Table S5. List of non-redundant protein groups detected by MudPIT analysis of Nuclear Envelopes (NEs) isolated from Human Peripheral Blood Mononuclear Cells (PBMCs) and compared to Microsomal Membranes (MMs) isolated from Rodent Liver

Human, mouse and rat proteins are compared based on their Ensembl orthologous group.
The number of times a protein is detected across replicates is listed in the "Detected # Out of" columns.
dNSAF are averaged across replicate runs ("dNSAF AVG" columns).
(Note that dNSAF values from 2 proteinase K digested samples with low spectral counts and protein identifications (HsSD-NE_NT_lymphocytes_PK_1 and HsNaOH-NE_PHA_lymphocytes_PK_1) were not included in the average and standard deviation calculations)
Ratios between dNSAF measured in NEs samples and dNSAF measured in MMs samples are reported in the "NEs:MMs" column.
Columns ending with PredHel and TMHMM_Topology list the number and position of transmembrane helices predicted for each protein by TMHMM.
The columns starting with "SIGNALP" are the output from SIGNALP HMM predictions on each protein for type of signal peptide sequences, their position (_POS) and probability (_SPROB).
Proteins that also appeared in separate mitochondrial datasets (Mootha et al, 2003) are listed in the "Detected in Mitochondria" column.

Nine protein classes are defined (within each class, proteins are ranked by decreasing dNSAF values and frequency of detection)

	Total	NT	unique NT	NT AND PHA	PHA	unique PHA	
rk 1-13	13	13	0	13	13	0	Proteins previously annotated as NETs
rk 14-52	39	33	5	28	34	4	Proteins previously annotated as liver NETs (Schirmer et al, 2003)
rk 53-139	87	75	12	63	75	12	Putative blood NETs (at least 1 predicted TM or membrane anchor, not detected in mitochondria and MMs, or with NEs:MMs ratio >5; plausible annotation)
rk 140-475	336	299	66	233	270	37	Membrane proteins enriched in NEs (at least 1 predicted TM or membrane anchor, not detected in mitochondria and MMs, or with NEs:MMs ratio >5; annotation not compatible with them being NETs)
rk 476-2593	2118	1808	322	1486	1796	310	Soluble proteins enriched in NEs (not detected in mitochondria and MMs, or with NEs:MMs ratio >5)
rk 2594-2885	292	265	41	224	251	27	Membrane proteins not enriched in NEs (at least 1 predicted TM or membrane anchor, not detected in mitochondria, and with NEs:MMs ratio <5)
rk 2886-3174	289	263	40	223	249	26	Soluble proteins not enriched in NEs (not detected in mitochondria, and with NEs:MMs ratio <5)
rk 3175-3214	40	37	6	31	34	3	Membrane proteins detected in previously published mitochondrial proteome dataset (Mootha et al, 2003) (at least 1 predicted TM or membrane anchor, detected in mitochondria)
rk 3215-3351	137	130	15	115	117	2	Soluble proteins detected in previously published mitochondrial proteome dataset (Mootha et al, 2003) (detected in mitochondria)

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB
1	9	0.007262	3	2.36E-05	307.2379		ENSG00000100242:E	UNC84B	SUN-2	Hodzic et al, 2	gi|31742498|ref|NP_	unc-84 homolog B [Homo sa	717	80311	6.7	1	i213-235o	Q	33	0
2	9	0.003763	3	2.21E-05	170.002		ENSG00000120802:E	TMPO	LAP2	Foisner and G	gi|73760405|ref|NP_	thymopoietin isoform beta [H	454	50670	9.4	1	o411-430i	Q	0	0
3	9	0.001601	1	4.6E-05	34.81905		ENSG00000143815:E	LBR	LBR	Worman et al,	gi|37595752|ref|NP_	lamin B receptor [Homo sapi	615	70703	9.4	8	i209-231o2	Q	35	0
4	9	0.001314	0	0	INF		ENSG00000132182:E	NUP210	gp210	Gerace et al,	gi|27477134|ref|NP_	nucleoporin 210 [Homo sapie	1887	205109	6.8	2	i7-26o1809	S	26	1
5	8	0.004068	3	0.000116	34.98206		ENSG00000170876:E	TMEM43	LUMA	Dreger et al, 2	gi|13236587|ref|NP_	transmembrane protein 43 [H	400	44876	8.1	4	o32-51i309	A	58	0.001
6	8	0.001596	1	3.36E-06	475.4389		ENSG00000143337:E	TOR1AIP1	LAP1	Senior and Ge	gi|39753957|ref|NP_	lamina-associated polypeptid	583	66248	8.2	0	o	Q	31	0
7	8	0.001407	1	2.22E-05	63.2545		ENSG00000102119:E	EMD	emerin	Manilal et al, 1	gi|4557553|ref|NP_0	emerin [Homo sapiens]	254	28994	5.5	1	i225-247o	Q	0	0
8	5	0.000168	0	0	INF		ENSG00000137404:E	NRM	Nurim	Rolls et al, 19	gi|25282391|ref|NP_	nurim [Homo sapiens]	262	29379	8.6	4	i5-27o59-8	S	21	0.999
9	5	2.84E-05	0	0	INF		ENSG00000054654:E	SYNE2	syne-2	Zhang et al, 2	gi|118918403|ref|NP	spectrin repeat containing, nu	6885	796457	5.4	0	o	Q	0	0
10	4	2.34E-05	0	0	INF		ENSG00000131018:E	SYNE1	syne-1	Apel et al, 200	gi|154277116|ref|NP	spectrin repeat containing, nu	8797	1011050	5.5	0	o	Q	0	0
11	3	7.19E-05	0	0	INF		ENSG00000174106:E	LEMD3	LEMD3;MAN1	Paulin-Levass	gi|7706607|ref|NP_0	LEM domain containing 3 [Ho	911	99997	7.5	2	o472-494i6	Q	20	0
12	2	5.69E-05	0	0	INF		ENSG00000164828:E	UNC84A	SUN-1	Dreger et al, 2	gi|110227866|ref|NP	unc-84 homolog A [Homo sa	702	77911	7.1	2	o177-199i2	S	21	0.933
13	2	2.87E-05	0	0	INF		ENSG00000196313:E	POM121C	POM121	Hallberg et al,	gi|150378545|ref|NP	POM121 membrane glycopro	987	99134	9.9	0	o	Q	39	0.002
14	8	0.00169	0	0	INF		ENSG00000184584:E	TMEM173	NET23	Malik et al, 20	gi|38093659|ref|NP_	transmembrane protein 173 [	379	42193	7.1	0	o	S	38	0.94
15	7	0.000217	0	0	INF		ENSG00000173821:E	RNF213	NET57		gi|66571327|ref|NP_	ring finger protein 213 [Homo	3280	373981	6.9	0	o	Q	35	0
16	6	0.001041	0	0	INF		ENSG00000100612:N	DHRS7	NET50	Malik et al, 20	gi|7706318|ref|NP_0	dehydrogenase/reductase (S	339	38299	8.3	1	i5-23o	S	29	0.986
17	6	0.000594	0	0	INF		ENSG00000161904:E	LEMD2	NET25	Brachner et al	gi|31044432|ref|NP_	LEM domain containing 2 [Ho	503	56975	9	2	o209-231i3	Q	27	0
18	6	0.000301	0	0	INF		ENSG00000176438:E	C14orf49	NET53; nesprin	Wilhelmsen et	gi|145580592|ref|NP	nesprin-3 [Homo sapiens]	975	112216	6.2	1	o927-946i	Q	0	0
19	6	0.000192	1	2.21E-06	86.92041		ENSG00000136699:E	SMPD4	NET13	Malik et al, 20	gi|102467484|ref|NP	neutral sphingomyelinase 3 i	837	94585	8.3	1	o799-821i	Q	58	0.05
20	6	0.000103	0	0	INF		ENSG00000135372:E	NAT10	NET43	no, Malik et al	gi|13399322|ref|NP_	N-acetyltransferase 10 [Hom	1025	115748	8.3	0	o	Q	25	0
21	5	0.000162	5	0.000463	0.349906		ENSG00000125912:E	NCLN	NET59	Malik et al, 20	gi|51873031|ref|NP_	nicalin [Homo sapiens]	563	62974	6.9	2	i12-34o521	A	43	0.293
22	5	0.000116	0	0	INF		ENSG00000158941:E	KIAA1967	NET35	no, Malik et al	gi|40548408|ref|NP_	p30 DBC protein [Homo sapi	923	102902	5.2	0	o	Q	35	0.062
23	5	0.000106	0	0	INF		ENSG00000184967:E	NOC4L	NET49	no, Malik et al	gi|13129068|ref|NP_	nucleolar complex associated	516	58468	7.5	0	o	Q	31	0.007
24	5	9.73E-05	0	0	INF		ENSG00000134186:E	PRPF38B	NET1		gi|8922358|ref|NP_0	PRP38 pre-mRNA processin	542	63753	10.5	0	o	Q	24	0.004
25	5	1.34E-05	1	2.01E-06	6.689513		ENSG00000164880:E	INTS1	NET28		gi|122937317|ref|NP	integrator complex subunit 1	2381	264069	6.6	0	o	Q	17	0.002
26	4	0.000342	2	6.61E-05	5.176487		ENSG00000113719:E	ERGIC1	NET24	Malik et al, 20	gi|72534712|ref|NP_	endoplasmic reticulum-golgi	290	32592	7.1	2	o20-42i248	A	47	0.002
27	4	0.000192	6	0.001935	0.099061		ENSG00000123684:E	LPGAT1	NET8	Schirmer et al	gi|7661996|ref|NP_0	lysophosphatidylglycerol acy	370	43089	8.9	4	o20-42i54-	Q	33	0.096
28	4	0.000133	0	0	INF		ENSG00000146842:E	TMEM209	NET31	Schirmer et al	gi|66348165|ref|NP_	transmembrane protein 209 [	561	62922	8.6	2	i28-45o58-	Q	41	0.104
29	4	7.71E-05	1	4.87E-06	15.83878		ENSG00000119707:E	RBM25	NET52		gi|55741709|ref|NP_	RNA binding motif protein 25	843	100186	6.3	0	o	Q	55	0.001
30	3	0.000212	0	0	INF		ENSG00000145569:E	FAM105A	NET20	Malik et al, 20	gi|9506641|ref|NP_0	hypothetical protein LOC544	356	42196	9.3	1	i40-62o	A	59	0.011
31	3	0.000163	6	0.002079	0.078174		ENSG00000143653:E	SCCPDH	NET11	Malik et al, 20	gi|55770836|ref|NP_	saccharopine dehydrogenase	429	47151	9.1	1	o277-299i	Q	21	0.175
32	3	6.62E-05	2	4.15E-05	1.597916		ENSG00000119523:E	ALG2	NET38	Malik et al, 20	gi|14861836|ref|NP_	asparagine-linked glycosylati	416	47092	7	0	o	Q	30	0
33	3	6.25E-05	0	0	INF		ENSG00000058804:E	TMEM48	NET3	Schirmer et al	gi|21359924|ref|NP_	transmembrane protein 48 [H	674	76363	9	5	i20-45o65-	A	42	0.061
34	3	3.11E-05	0	0	INF		ENSG00000116754:E	SFRS11	NET2		gi|4759100|ref|NP_0	splicing factor, arginine/serin	484	53542	10.5	0	o	Q	18	0.006
35	3	1.86E-05	1	8.1E-06	2.295792		ENSG00000162408:E	NOL9	NET6		gi|40217805|ref|NP_	nucleolar protein 9 [Homo sa	702	79277	9.2	0	o	Q	60	0.001
36	2	0.000473	1	8.22E-05	5.750196		ENSG00000133935:E	C14orf1	NET51	Schirmer et al	gi|6005719|ref|NP_0	hypothetical protein LOC111	140	15806	9.9	4	i5-27o47-6	S	27	0.923
37	2	8.87E-05	0	0	INF		ENSG00000188807:E	TMEM201	NET5	Malik et al, 20	gi|58197554|ref|NP_	transmembrane protein 201 [	392	43382	8.7	5	o13-35i214	S	28	0.722
38	2	7.93E-05	0	0	INF		ENSG00000147475:E	ERLIN2	NET32	Chen et al, 20	gi|6005721|ref|NP_0	ER lipid raft associated 2 iso	339	37840	5.6	0	o	S	22	0.977
39	2	5.68E-05	1	2.78E-05	2.047737		ENSG00000175826:E	DULLARD	NET56	Schirmer et al	gi|31542547|ref|NP_	dullard homolog [Homo sapie	244	28377	9.8	1	i7-29o	S	23	0.912
40	2	3.58E-05	0	0	INF		ENSG00000188976:N	NOC2L	NET7		gi|157694511|ref|NP	nucleolar complex associated	749	84905	5.6	0	o	Q	24	0.004
41	2	2.79E-05	5	0.000156	0.179127		ENSG00000149476:E	DAK	NET45	Malik et al, 20	gi|20149621|ref|NP_	dihydroxyacetone kinase 2 [H	575	58947	7.5	0	o	Q	20	0.213
42	2	2.55E-05	0	0	INF		ENSG00000101413:E	C20orf77	NET60		gi|11034845|ref|NP_	Regulation of nuclear pre-mR	326	36900	6	0	o	Q	38	0.004
43	2	2.02E-05	0	0	INF		ENSG00000163811:E	WDR43	NET12		gi|157743245|ref|NP	WD repeat domain 43 [Homo	677	74891	5.6	0	o	Q	28	0.09
44	2	1.18E-05	0	0	INF		ENSG00000163694:E	RBM47	NET18		gi|148833513|ref|NP	RNA binding motif protein 47	593	64099	7.7	0	o	Q	21	0.004
45	2	8.67E-06	0	0	INF		ENSG00000135763:E	KIAA0133	NET10		gi|7661932|ref|NP_0	hypothetical protein LOC981	1524	170569	7.3	0	o	Q	19	0.001
46	2	4.92E-06	0	0	INF		ENSG00000120733:E	JMJD1B	NET22		gi|38372909|ref|NP_	jumonji domain containing 1B	1761	191610	7.2	0	o	S	34	0.997
47	2	1.66E-06	0	0	INF		ENSG00000136709:E	WDR33	NET14	no, Malik et al	gi|56243590|ref|NP_	WD repeat domain 33 isofor	1331	145410	9.1	0	o	Q	21	0
48	1	7.81E-05	1	3.54E-05	2.205761	Y	ENSG00000111843:E	TMEM14C	NET26	Schirmer et al	gi|7705501|ref|NP_0	transmembrane protein 14C	112	11565	9.9	4	i7-29o33-5	Q	33	0.388
49	1	6.56E-05	6	0.002071	0.031667		ENSG00000149809:E	TM7SF2	NET47	Malik et al, 20	gi|117414150|ref|NP	transmembrane 7 superfamil	418	46406	8.9	7	i13-35o62-	S	37	0.997
50	1	2.31E-05	0	0	INF		ENSG00000115368:E	WDR75	NET16	no, Malik et al	gi|29789283|ref|NP_	WD repeat domain 75 [Homo	830	94499	6	0	o	Q	0	0
51	1	6.52E-06	0	0	INF		ENSG00000122515:E	ZMIZ2	NET27		gi|54607110|ref|NP_	zinc finger, MIZ-type containi	894	93981	7.2	0	o	Q	52	0.009
52	1	5.97E-06	4	0.000153	0.039004		ENSG00000169905:E	TOR1AIP2	NET9	Chen et al, 20	gi|21450775|ref|NP_	torsin A interacting protein 2	470	51263	5	1	i214-236o	Q	0	0
53	8	0.002867	8	0.004499	0.637299		ENSG00000101474:E	C20orf3	bNET	Fig. 4, 6	gi|24308201|ref|NP_	chromosome 20 open readin	416	46480	6.2	1	i38-60o	A	58	0
54	7	0.000971	4	0.000289	3.357254		ENSG00000144959:E	AADACL1	bNET	Fig. 4, 6	gi|68051721|ref|NP_	arylacetamide deacetylase-li	440	49063	7.9	1	i37-59o	A	48	0.037
55	7	0.000705	5	0.000109	6.479097		ENSG00000117868:E	FAM62B	bNET?		gi|45387945|ref|NP_	family with sequence similari	893	98902	8.7	1	i98-120o	Q	43	0.008
56	7	0.000217	5	0.000388	0.559766		ENSG00000134910:E	STT3A	bNET	Fig. 4, 6	gi|22749415|ref|NP_	integral membrane protein 1	705	80530	8.1	12	i20-39o83-	S	38	0.625
57	6	0.002261	0	0	INF		ENSG00000110108:E	TMEM109	bNET	Fig. 4, 6	gi|13129092|ref|NP_	transmembrane protein 109 [	243	26210	10.5	5	o10-32i84-	S	34	1
58	6	0.00068	4	7.91E-05	8.598374		ENSG00000166479:E	TXNDC10	bNET?		gi|38505222|ref|NP_	thioredoxin domain containin	454	51872	4.9	1	o374-396i	S	25	0.993
59	6	0.000282	6	0.000789	0.358009		ENSG00000185432:N	METTL7A	bNET	Fig. 4, 6	gi|89145417|ref|NP_	methyltransferase-like protei	244	28285	8.4	1	o10-32i	A	30	0.276
60	6	0.000238	0	0	INF		ENSG00000009790:E	TRAF3IP3	bNET?		gi|13435127|ref|NP_	TRAF3-interacting JNK-activ	531	61375	8.4	1	o507-524i	Q	22	0
61	5	0.000984	1	4.03E-06	244.0077		ENSG00000136026:E	CKAP4	bNET?		gi|19920317|ref|NP_	cytoskeleton-associated prot	602	66023	5.9	1	i109-131o	Q	24	0
62	5	0.000729	0	0	INF		ENSG00000166562:E	SEC11C	bNET	Fig. 4, 6	gi|15150809|ref|NP_	SEC11-like 3 [Homo sapiens	192	21542	9.2	1	i34-56o	Q	16	0.119
63	5	0.000452	0	0	INF		ENSG00000196329:E	GIMAP5	bNET?		gi|28416949|ref|NP_	GTPase, IMAP family membe	307	34846	7.7	1	o282-304i	Q	40	0
64	5	0.000443	0	0	INF		ENSG00000178927:E	C17orf62	bNET	Fig. 4, 5, 6	gi|154350204|ref|NP	hypothetical protein LOC794	173	19436	6.8	0	o	A	50	0.001
65	4	0.000862	2	5.21E-05	16.52813		ENSG00000125827:E	TXNDC13	bNET?		gi|40254947|ref|NP_	thioredoxin domain containin	349	38952	4.4	1	i188-210o	S	26	0.998
66	4	0.000513	0	0	INF		ENSG00000177917:E	ARL6IP6	bNET?		gi|22749091|ref|NP_	ADP-ribosylation-like factor 6	226	24676	6.3	3	i108-130o1	Q	30	0.004
67	4	0.000363	0	0	INF		ENSG00000106771:E	C9orf5	bNET?		gi|110681719|ref|NP	hypothetical protein LOC237	879	97357	8.9	14	i54-76o113	Q	44	0
68	4	0.000273	0	0	INF		ENSG00000156471:E	PTDSS1	bNET?		gi|7662647|ref|NP_0	phosphatidylserine synthase	473	55528	8.4	9	o37-59i72-	Q	0	0
69	4	0.000213	0	0	INF		ENSG00000122986:E	HVCN1	bNET?		gi|91992155|ref|NP_	hydrogen voltage-gated char	273	31683	6.8	3	i101-123o1	Q	38	0
70	4	0.000124	1	6.03E-06	20.5511		ENSG00000144320:E	KIAA1715	bNET?		gi|38176151|ref|NP_	Lunapark [Homo sapiens]	428	47740	5.1	2	i44-66o76-	A	0	0
71	4	8.57E-05	0	0	INF		ENSG00000107020:E	C9orf46	bNET?		gi|8923932|ref|NP_0	hypothetical protein LOC558	147	17229	9.7	1	i53-72o	Q	0	0
72	3	0.000894	1	4.25E-06	210.6973		ENSG00000153395:E	AYTL2	bNET?		gi|33946291|ref|NP_	acyltransferase like 2 [Homo	534	59151	6	1	i53-75o	S	62	0.688
73	3	0.000337	1	4.66E-06	72.29594		ENSG00000111684:E	MBOAT5	bNET?		gi|42542394|ref|NP_	O-acyltransferase (membran	487	56035	8.7	7	o40-62i69-	Q	25	0.041
74	3	0.000201	0	0	INF		ENSG00000144468:E	RHBDD1	bNET?		gi|33300639|ref|NP_	rhomboid domain containing	315	35823	8.2	2	i103-125o1	A	34	0.114
75	3	0.000182	1	1.76E-05	10.29334		ENSG00000155099:E	TMEM55A	bNET?		gi|24308165|ref|NP_	transmembrane protein 55A	257	28081	8.7	2	o193-212i2	Q	25	0
76	3	0.000126	3	0.00016	0.790371		ENSG00000196937:E	FAM3C	bNET?	Fig. 6	gi|91807125|ref|NP_	family with sequence similari	227	24680	8.3	1	i7-29o	S	25	0.906
77	3	9.07E-05	0	0	INF		ENSG00000171488:E	LRRC8C	bNET?		gi|19923729|ref|NP_	leucine rich repeat containing	803	92391	7.7	4	o26-48i126	A	46	0.004
78	3	7.91E-05	0	0	INF		ENSG00000160629:E	C17orf32	bNET	Fig. 4, 5	gi|22748979|ref|NP_	transmembrane protein 199 [	208	23130	9	2	o145-167i1	Q	15	0.013
79	3	6.58E-05	1	7.83E-06	8.409375		ENSG00000139192:E	TAPBPL	bNET	Fig. 4, 6	gi|31543801|ref|NP_	tapasin-related protein precu	468	50177	5.3	1	o407-426i	S	22	1
80	3	6.36E-05	0	0	INF		ENSG00000137500:E	CCDC90B	bNET?		gi|20149663|ref|NP_	coiled-coil domain containing	254	29506	7.5	1	o231-253i	Q	17	0.009
81	3	5.15E-05	1	8.43E-06	6.110866		ENSG00000169762:E	TAPT1	bNET?		gi|130977756|ref|NP	transmembrane anterior post	567	64260	8.3	5	o122-144i1	Q	17	0
82	3	4.91E-05	1	3.59E-05	1.368773		ENSG00000102158:E	IAG2	bNET	Fig. 4, 6	gi|40255229|ref|NP_	magnesium transporter 1 [Ho	335	38037	9.6	5	i7-29o186-	S	30	0.978
83	3	4.84E-05	0	0	INF		ENSG00000118308:E	LRMP	bNET?		gi|42789729|ref|NP_	lymphoid-restricted membrar	499	56213	5.6	1	i441-463o	Q	0	0
84	3	4.52E-05	0	0	INF		ENSG00000087253:E	AYTL1	bNET?		gi|47086907|ref|NP_	lysophosphatidylcholine acylt	544	60208	6.6	1	i58-80o	Q	17	0.091
85	3	3.2E-05	0	0	INF		ENSG00000133872:E	TMEM66	bNET?		gi|42476193|ref|NP_	transmembrane protein 66 [H	339	36975	7.6	3	o10-32i172	S	31	0.999
86	2	0.00021	0	0	INF		ENSG00000163479:E	SSR2	bNET?		gi|4507239|ref|NP_0	signal sequence receptor, be	183	20135	8.3	1	o147-169i	S	18	1
87	2	0.000199	0	0	INF		ENSG00000162976:E	PQLC3	bNET?		gi|22748837|ref|NP_	PQ loop repeat containing 3	202	22575	8.9	4	i34-56o66-	S	20	0.986
88	2	0.000193	0	0	INF		ENSG00000102007:E	PLP2	bNET?		gi|4505893|ref|NP_0	proteolipid protein 2 (colonic	152	16691	7.2	4	o25-42i49-	A	44	0.228
89	2	0.000149	0	0	INF		ENSG00000163867:E	LOC100130633	bNET?		gi|169161547|ref|XP	PREDICTED: similar to ZMY	154	16885	9.2	4	i5-22o60-7	S	23	0.968
90	2	0.000144	1	8.94E-06	16.14959		ENSG00000198060:E	MARCH5	bNET	Fig. 5	gi|8923415|ref|NP_0	membrane-associated ring fi	278	31232	8.7	4	i97-119o13	Q	20	0
91	2	0.000139	0	0	INF		ENSG00000166920:E	C15orf48	bNET?		gi|37694067|ref|NP_	hypothetical protein LOC844	83	9617	9.5	1	i13-35o	S	30	0.905
92	2	0.000133	0	0	INF		ENSG00000186501:E	TMEM222	bNET?		gi|14149779|ref|NP_	transmembrane protein 222 [	188	21179	6.8	3	o34-56i142	Q	0	0
93	2	0.000126	0	0	INF		ENSG00000164051:E	CCDC51	bNET?		gi|94536784|ref|NP_	coiled-coil domain containing	411	45811	8.2	1	o386-408i	Q	28	0.027
94	2	0.000123	1	7.02E-06	17.4602		ENSG00000134851:E	TMEM165	bNET?		gi|32189371|ref|NP_	transmembrane protein 165 [	324	34906	7	7	i12-34o91-	S	34	1
95	2	0.000117	0	0	INF		ENSG00000156738:E	MS4A1	bNET?		gi|23110989|ref|NP_	membrane-spanning 4-doma	297	33077	5	4	i55-77o82-	Q	54	0
96	2	0.000113	0	0	INF		ENSG00000188921:E	PTPLAD2	bNET?		gi|148226324|ref|NP	protein tyrosine phosphatase	232	27520	8.6	4	i20-42o126	A	33	0.048
97	2	8.07E-05	1	1.25E-05	6.484076		ENSG00000137522:E	RNF121	bNET?		gi|21361732|ref|NP_	ring finger protein 121 isofor	327	37882	7.1	6	o50-72i79-	Q	16	0.003
98	2	7.87E-05	0	0	INF		ENSG00000167904:E	TMEM68	bNET?		gi|22748883|ref|NP_	transmembrane protein 68 [H	257	29542	7.4	2	i43-74o124	A	34	0
99	2	6.55E-05	0	0	INF		ENSG00000197296:E	C20orf142	bNET?		gi|122937337|ref|NP_	fat-inducing transcript 2 [Hon	262	29855	8.6	5	i57-79o89-	A	39	0.151
100	2	6.36E-05	0	0	INF		ENSG00000177150:E	C18orf19	bNET?		gi|149408153|ref|NP	hypothetical protein LOC125	272	30777	9.8	1	i133-155o	Q	30	0

rk	RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs							
	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
1	0.008142	0.011739	0.004979	0.003474	0.001136	5	0.007083	0.003663	0.010524	0.015614	0	0.003141	0.000482	4	0.00744	0.006909
2	0.005001	0.005818	0.004138	0.000584	0	4	0.003885	0.002305	0.008799	0.004863	0.007701	0.000312	0.000592	5	0.003641	0.00402
3	0.003164	0.002579	0.000611	0.000345	0	4	0.001675	0.001407	0.001443	0.00332	0.002274	0.000451	0.000892	5	0.001526	0.001262
4	0.000859	0.001891	0.001792	0.0003	0	4	0.001211	0.000765	0.001176	0.002651	0.002223	0.000398	0.001444	5	0.001417	0.000935
5	0.00973	0.003207	0.004227	0.001544	0	4	0.004677	0.003545	0.006658	0.005945	0	0.000367	0.000864	4	0.003459	0.003302
6	0.00306	0.00208	0.000967	0.000545	0.002793	5	0.001663	0.001134	0.004568	0.001347	0	0	0.000198	3	0.001528	0.002112
7	0.002554	0.001286	0	0.000278	0	3	0.001029	0.001157	0.005243	0.001678	0.002753	6.43E-05	0.000151	5	0.001784	0.002422
8	0	8.9E-05	0	6.74E-05	0	2	3.91E-05	4.6E-05	0	0.000771	0	0.000125	0.000293	3	0.000297	0.000338
9	0	9.82E-05	0	2.05E-05	0	2	2.97E-05	4.67E-05	0	7.17E-05	0	1.42E-05	2.23E-05	3	2.71E-05	3.12E-05
10	0	6.89E-05	0	3.21E-05	0	2	2.53E-05	3.28E-05	0	7.91E-05	0	7.42E-06	0	2	2.16E-05	3.85E-05
11	0	0.000358	0	1.94E-05	0	2	9.45E-05	0.000176	0	0.000197	0	0	0	1	4.93E-05	9.85E-05
12	0	0.000199	0	0	0	1	4.98E-05	9.97E-05	0	0.000256	0	0	0	1	6.39E-05	0.000128
13	0	0.000118	0	0	0	1	2.95E-05	5.91E-05	0	0.000111	0	0	0	1	2.78E-05	5.56E-05
14	0.002995	0.000923	0.002974	0.000606	0	4	0.001875	0.001288	0.003514	0.002309	0.001845	0	0.000203	4	0.001506	0.001697
15	0	0.000505	0.000115	9.16E-05	0	3	0.000178	0.000224	0.000271	0.000499	0	5.47E-05	0.000199	4	0.000256	0.000185
16	0.00287	0.001445	0.001108	0.000208	0	4	0.001408	0.001106	0	0.002581	0	0	0.000113	2	0.000674	0.001273
17	0.000645	0.000371	0.001494	0	0	3	0.000627	0.000635	0.001765	0.000401	0	0	7.63E-05	3	0.000561	0.000821
18	0.000333	0.000359	0.000385	5.44E-05	0	4	0.000283	0.000154	0.000911	0.000368	0	0	0	2	0.00032	0.00043
19	0.000387	0.000334	0	0.000106	0	3	0.000207	0.000184	0	0.000214	0	3.9E-05	0.000459	3	0.000178	0.000209
20	0	6.83E-05	0	5.17E-05	0	2	3E-05	3.53E-05	0.000433	8.76E-05	0	0.000111	7.49E-05	4	0.000177	0.000172
21	0.000288	0.00029	0	0.000251	0	3	0.000207	0.000139	0	0.000438	0	2.9E-05	0	2	0.000117	0.000215
22	0	0.000227	0	0.000268	0	2	0.000124	0.000144	0	2.43E-05	0	3.54E-05	0.000374	3	0.000108	0.000178
23	0	0.000136	0	0.000205	0	2	8.53E-05	0.000102	0	0.000304	0	0.000127	7.44E-05	3	0.000126	0.00013
24	0	8.61E-05	0.000347	0.000163	0	3	0.000149	0.000148	0	4.14E-05	0	0	0.000142	2	4.58E-05	6.68E-05
25	0	3.92E-05	0	2.23E-05	0	2	1.54E-05	1.9E-05	0	9.42E-06	0	2.06E-05	1.61E-05	3	1.15E-05	8.95E-06
26	0	0.001367	0.000648	0.000183	0	3	0.000549	0.00061	0	0.000542	0	0	0	1	0.000135	0.000271
27	0	0.000693	0	0.000191	0	2	0.000221	0.000327	0	0.000546	0	0	0.000104	2	0.000162	0.00026
28	0	0.000499	0	0.000126	0.000726	3	0.000156	0.000236	0	0.00044	0	0	0	1	0.00011	0.00022
29	0	0	0	0.000356	0	1	8.91E-05	0.000178	0	7.98E-05	0	0.000136	4.55E-05	3	6.52E-05	5.71E-05
30	0	0.000655	0	0	0	1	0.000164	0.000328	0	0.000504	0	0	0.000539	2	0.000261	0.000302
31	0	0.000109	0	0	0	1	2.72E-05	5.44E-05	0.001035	0.000157	0	0	0	2	0.000298	0.000497
32	0	5.61E-05	0	4.25E-05	0	2	2.46E-05	2.9E-05	0	0.000431	0	0	0	1	0.000108	0.000216
33	0	0.000208	0	2.62E-05	0	2	5.85E-05	0.0001	0	0.000266	0	0	0	1	6.66E-05	0.000133
34	0	0.000145	0	3.65E-05	0	2	4.53E-05	6.84E-05	0	0	0	6.74E-05	0	1	1.69E-05	3.37E-05
35	0	6.65E-05	0	5.03E-05	0	2	2.92E-05	3.43E-05	0	3.2E-05	0	0	0	1	7.99E-06	1.6E-05
36	0	0.002499	0	0	0	1	0.000625	0.00125	0	0.001282	0	0	0	1	0.00032	0.000641
37	0	0.000595	0	0	0	1	0.000149	0.000298	0	0.000114	0	0	0	1	2.86E-05	5.72E-05
38	0.000478	0	0	0.000156	0	2	0.000159	0.000226	0	0	0	0	0	0	0	0
39	0	0.000382	0	7.24E-05	0	2	0.000114	0.000182	0	0	0	0	0	0	0	0
40	0	0	0	0	0	0	0	0	0	3E-05	0	0	0.000256	2	7.16E-05	0.000124
41	0	0	0	0.000184	0	1	4.61E-05	9.22E-05	0	3.9E-05	0	0	0	1	9.75E-06	1.95E-05
42	0	0	0	5.42E-05	0	1	1.35E-05	2.71E-05	0	0	0	0.00015	0	1	3.75E-05	7.51E-05
43	0	0	0	0	0	0	0	0	0	0	0	4.82E-05	0.000113	2	4.04E-05	5.37E-05
44	0	0	0	2.98E-05	0	1	7.45E-06	1.49E-05	0	0	0	0	6.47E-05	1	1.62E-05	3.24E-05
45	0	0	0	0	0	0	0	0	0	4.42E-05	0	0	2.52E-05	2	1.73E-05	2.15E-05
46	0	0	0	3.01E-05	0	1	7.52E-06	1.5E-05	0	0	0	9.27E-06	0	1	2.32E-06	4.63E-06
47	0	0	0	1.33E-05	0.000306	2	3.32E-06	6.64E-06	0	0	0	0	0	0	0	0
48	0	0.000625	0	0	0	1	0.000156	0.000312	0	0	0	0	0	0	0	0
49	0	0	0	0	0	0	0	0	0	0	0	0	0.000525	1	0.000131	0.000262
50	0	0	0	0	0	0	0	0	0	0	0	0	0.000185	1	4.63E-05	9.25E-05
51	0	5.22E-05	0	0	0	1	1.3E-05	2.61E-05	0	0	0	0	0	0	0	0
52	0	0	0	0	0	0	0	0	0	4.77E-05	0	0	0	1	1.19E-05	2.39E-05
53	0.002339	0.003588	0.003161	0.000552	0	4	0.00241	0.001343	0.007469	0.005065	0	0.000118	0.000646	4	0.003324	0.003543
54	0.001843	0.00053	0.000854	0.000161	0	4	0.000847	0.000722	0.004035	0.000255	0	0	8.72E-05	3	0.001094	0.001963
55	0.000545	0.001149	0.002525	7.91E-05	0	4	0.001074	0.001061	0	0.001105	0	1.83E-05	0.000215	3	0.000335	0.000523
56	0.00046	0.000298	0.000266	5.01E-05	0	4	0.000269	0.000169	0	0.000509	0	4.63E-05	0.000109	3	0.000166	0.000233
57	0.005339	0.00096	0	0	0.001676	3	0.001575	0.00255	0.01096	0.000831	0.01151	0	0	3	0.002948	0.005356
58	0.000357	0.001387	0.002069	3.89E-05	0	4	0.000963	0.000935	0	0.001334	0	0	0.000254	2	0.000397	0.000636
59	0.000665	0.000478	0	0.000145	0	3	0.000322	0.000304	0	0.000276	0	6.69E-05	0.000629	3	0.000243	0.000283
60	0.000611	0.000747	0	0.000166	0	3	0.000381	0.000355	0	0.000127	0	0.000184	7.23E-05	3	9.59E-05	7.86E-05
61	0.005657	0.000349	0	5.87E-05	0	3	0.001516	0.002765	0.001475	0.000335	0	0	0	2	0.000453	0.0007
62	0.001689	0.000243	0	0.000184	0	3	0.000529	0.00078	0.002312	0.001402	0	0	0	2	0.000929	0.001135
63	0	0.001216	0	0.000115	0	2	0.000333	0.000591	0.001446	0.000731	0	0.000106	0	3	0.000571	0.000667
64	0	0.000404	0	0.000306	0	2	0.000178	0.000209	0	0.002205	0	0.000189	0.000444	3	0.000709	0.001013
65	0.001859	0.002005	0.001615	0	0	3	0.00137	0.000927	0	0.001414	0	0	0	1	0.000354	0.000707
66	0	0.000206	0.003325	7.82E-05	0	3	0.000902	0.001617	0	0.000496	0	0	0	1	0.000124	0.000248
67	0.000369	7.96E-05	0.002351	0	0	3	0.0007	0.001112	0	0.000102	0	0	0	1	2.55E-05	5.1E-05
68	0.001029	0.00069	0	0	0	2	0.00043	0.000515	0	0.000427	0	3.45E-05	0	2	0.000115	0.000208
69	0.000594	0.000256	0.000688	0	0	3	0.000385	0.000316	0	0.000164	0	0	0	1	4.11E-05	8.22E-05
70	0	0.000545	0	4.13E-05	0	2	0.000147	0.000266	0	0.000367	0	3.81E-05	0	2	0.000101	0.000178
71	0	0.000159	0	0	0	1	3.97E-05	7.93E-05	0	0.000305	0.004757	0.000222	0	3	0.000132	0.000156
72	0	0.000786	0.005277	0	0	2	0.001516	0.002535	0	0.001092	0	0	0	1	0.000273	0.000546
73	0	0.000239	0.002315	0	0	2	0.000639	0.001123	0	0.000138	0	0	0	1	3.46E-05	6.91E-05
74	0.00103	0.000222	0	0	0	2	0.000313	0.000489	0	0.000356	0	0	0	1	8.9E-05	0.000178
75	0.000631	9.08E-05	0.000731	0	0	3	0.000363	0.000371	0	0	0	0	0	0	0	0
76	0	0.000205	0	0.000311	0	2	0.000129	0.000155	0	0.000494	0	0	0	1	0.000124	0.000247
77	0	0.000145	0	0	0	1	3.63E-05	7.26E-05	0.000553	2.79E-05	0	0	0	2	0.000145	0.000272
78	0	0.000224	0	8.49E-05	0	2	7.73E-05	0.000106	0	0.000324	0	0	0	1	8.09E-05	0.000162
79	0	0.000249	0	3.77E-05	0	2	7.17E-05	0.00012	0	0.00024	0	0	0	1	5.99E-05	0.00012
80	0	0	0	0.000139	0	1	3.48E-05	6.95E-05	0	0.000177	0	0.000193	0	2	9.24E-05	0.000107
81	0	4.11E-05	0.000331	0	0	2	9.31E-05	0.00016	0	3.96E-05	0	0	0	1	9.89E-06	1.98E-05
82	0	0.000278	0	0	0	1	6.96E-05	0.000139	0	0	0.002087	0	0.000115	2	2.86E-05	5.73E-05
83	0	0.000187	0	0	0	1	4.67E-05	9.35E-05	0	0.000135	0	6.54E-05	0	2	5.01E-05	6.44E-05
84	0	0.000214	0	6.49E-05	0	2	6.98E-05	0.000101	0	8.25E-05	0	0	0	1	2.06E-05	4.12E-05
85	0	0.000138	0	5.21E-05	0	2	4.74E-05	6.49E-05	0	6.62E-05	0	0	0	1	1.65E-05	3.31E-05
86	0	0	0	0	0	0	0	0	0	0	0.007642	0	0.001678	2	0.00042	0.000839
87	0	0.001039	0	0	0	1	0.00026	0.00052	0	0.000555	0	0	0	1	0.000139	0.000278
88	0	0.000307	0.001236	0	0	2	0.000386	0.000585	0	0	0	0	0	0	0	0
89	0	0.000606	0	0	0	1	0.000151	0.000303	0	0.000583	0	0	0	1	0.000146	0.000291
90	0	0.000671	0	0	0	1	0.000168	0.000336	0	0.000484	0	0	0	1	0.000121	0.000242
91	0	0.000843	0	0	0	1	0.000211	0.000422	0	0.00027	0	0	0	1	6.76E-05	0.000135
92	0	0.000248	0	0	0	1	6.2E-05	0.000124	0	0	0	0	0.000817	1	0.000204	0.000408
93	0	0.000567	0	0	0	1	0.000142	0.000284	0	0.000437	0	0	0	1	0.000109	0.000218
94	0	0.000288	0	0	0	1	7.2E-05	0.000144	0	0.000692	0	0	0	1	0.000173	0.000346
95	0	0.000707	0	0	0	1	0.000177	0.000353	0	0.000227	0	0	0	1	5.67E-05	0.000113
96	0.000699	0.000201	0	0	0	2	0.000225	0.00033	0	0	0	0	0	0	0	0
97	0	7.13E-05	0.000575	0	0	2	0.000161	0.000277	0	0	0	0	0	0	0	0
98	0	0.000182	0	0	0	1	4.54E-05	9.08E-05	0	0	0	0	0.000448	1	0.000112	0.000224
99	0	0.000267	0	0	0	1	6.68E-05	0.000134	0	0.000257	0	0	0	1	6.42E-05	0.000128
100	0	8.58E-05	0	0	0	1	2.14E-05	4.29E-05	0	0	0	0	0.000423	1	0.000106	0.000212

rk	MMs										
	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
1	0	0	5.73E-05	0.000112	0	1.94E-05	0	0	Sad1 / UNC-like C-terminal.	integral to membrane;	microtubule binding [pmid
2	0	0	0.000102	4.01E-05	0	3.46E-05	0	0	LEM domain. The LEM	chromosome; integral to	DNA binding; lamin binding
3	0	0	0	0	0	0	0.000368	0	Tudor domain; Domain of	integral to membrane [pmid	DNA binding [pmid 8157662];
4	0	0	0	0	0	0	0	0	Bacterial Ig-like domain	integral to membrane;	protein binding [pmid
5	0	0	0.000463	0.000272	0	0.000196	0	0	Protein of unknown function	Golgi apparatus [pmid	
6	0	0	0	0	0	2.68E-05	0	0	Lamina-associated	integral to membrane;	
7	0	0	0.000178	0	0	0	0	0	LEM domain. The LEM	integral to membrane;	protein binding [pmid
8	0	0	0	0	0	0	0	0			
9	0	0	0	0	0	0	0	0			
10	0	0	0	0	0	0	0	0			
11	0	0	0	0	0	0	0	0	LEM domain. The LEM	integral to membrane [pmid	nucleotide binding
12	0	0	0	0	0	0	0	0			
13	0	0	0	0	0	0	0	0			
14	0	0	0	0	0	0	0	0			
15	0	0	0	0	0	0	0	0	RING-finger (Really		metal ion binding; protein
16	0	0	0	0	0	0	0	0	Short-chain dehydrogenase		oxidoreductase activity
17	0	0	0	0	0	0	0	0	in nuclear membrane-	nuclear envelope	
18	0	0	0	0	0	0	0	0			
19	0	0	0	1.77E-05	0	0	0	0			
20	0	0	0	0	0	0	0	0	Putative ATPase	nucleus [pmid 11214970]	acyltransferase activity; ATP
21	0.000785	0	0.000986	0.000805	0.000684	0.000445	0	0	Predicted aminopeptidases	endoplasmic reticulum;	
22	0	0	0	0	0	0	0	0		cytoplasm [pmid 15824730];	calcium ion binding
23	0	0	0	0	0	0	0	0	CBF/Mak21 family;	integral to membrane;	protein binding [pmid
24	0	0	0	0	0	0	0	0	PRP38 family. Members of		
25	0	0	0	0	0	0	1.61E-05	0		integral to membrane;	actin binding; protein binding
26	0	0	0	0.00035	0	0	0.000179	0	Protein of unknown function	endoplasmic reticulum; ER-	protein binding [pmid
27	0	0	0.00325	0.002696	0.00598	0.003215	0.000176	0.000166	Phosphate	cytoplasm [pmid 10942595];	acyltransferase activity;
28	0	0	0	0	0	0	0	0	MLTD_N; pfam06474		
29	0	0	0	0	0	0	3.9E-05	0	RNA-binding proteins (RRM		mRNA binding; nucleic acid
30	0	0	0	0	0	0	0	0	RhoGAP_CdGAP: RhoGAP		
31	0	0	0.006254	0.003128	0.00213	0.00332	0.001443	0.000358	Saccharopine		oxidoreductase activity;
32	0	0	0	0.000219	0	0.000113	0	0	Glycosyl transferases	integral to membrane;	transferase activity,
33	0	0	0	0	0	0	0	0	Homeobox prospero-like	integral to membrane;	structural constituent of
34	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus [pmid 1896467]	nucleic acid binding;
35	0	0	6.48E-05	0	0	0	0	0	Predicted GTPase or GTP-	nucleus	
36	0	0	0	0	0	0	0	0.000658	Erg28 like protein. This is a	endoplasmic reticulum;	
37	0	0	0	0	0	0	0	0			
38	0	0	0	0	0	0	0	0	A subgroup of the band 7	endoplasmic reticulum [pmid	
39	0	0	0	0.000222	0	0	0	0	NLI interacting factor-like		phosphoric monoester
40	0	0	0	0	0	0	0	0			
41	0	0	0.00032	0.000377	8.32E-05	0.000298	0.000169	0	DAK2 domain. This domain		ATP binding; glycerone
42	0	0	0	0	0	0	0	0	CID (CTD-Interacting		
43	0	0	0	0	0	0	0	0			
44	0	0	0	0	0	0	0	0			
45	0	0	0	0	0	0	0	0		integral to membrane;	
46	0	0	0	0	0	0	0	0	JmjC domain. The JmjC	nucleus	iron ion binding; metal ion
47	0	0	0	0	0	0	0	0	WD40 domain, found in a	cytoplasm; nucleus [pmid	
48	0	0	0	0	0	0	0.000283	0	Transmembrane proteins	integral to membrane;	
49	0	0	0.000221	0.000434	0.00023	0.000599	0.003195	0.011892			
50	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus	
51	0	0	0	0	0	0	0	0	MIZ/SP-RING zinc finger.	nucleus	carbohydrate binding; metal
52	0	0	0.0004	0.000251	0.000166	0.000406	0	0	Lamina-associated	endoplasmic reticulum;	protein binding [pmid
53	0.002131	0.0018	0.00812	0.005065	0.003198	0.00562	0.004591	0.005468	Strictosidine synthase.	integral to membrane;	strictosidine synthase
54	0	0.001831	0	0.000178	0	0.000153	0	0.00015	alpha/beta hydrolase fold.		hydrolase activity
55	0	0	0	6.09E-05	0.000108	0.000175	0.000182	0.000344	Protein kinase C conserved		
56	0	0	0.000818	0.000898	0	0.000757	0.000307	0.000326	Oligosaccharyl transferase	endoplasmic reticulum;	dolichyl-
57	0	0	0	0	0	0	0	0		integral to membrane;	
58	0	0	0.000237	0.000124	0.000164	0.000107	0	0	PDIa family, TMX3	endoplasmic reticulum;	calcium ion binding; electron
59	0	0	0.001137	0.000892	0.001774	0.001604	0.0004	0.000503	Methyltransferase domain.	nucleus	S-adenosylmethionine-
60	0	0	0	0	0	0	0	0	Uncharacterized protein	integral to membrane;	kinase activity
61	0	0	0	3.23E-05	0	0	0	0	Chromosome segregation	integral to membrane [pmid	
62	0	0	0	0	0	0	0	0	Signal peptidase I	endoplasmic reticulum;	serine-type peptidase
63	0	0	0	0	0	0	0	0	AIG1 (avrRpt2-induced	integral to membrane;	GTP binding; nucleotide
64	0	0	0	0	0	0	0	0			
65	0	0	0	0.000324	0	9.32E-05	0	0	PDIa family, TMX	integral to membrane;	electron carrier activity;
66	0	0	0	0	0	0	0	0			
67	0	0	0	0	0	0	0	0			
68	0	0	0	0	0	0	0	0	Phosphatidyl serine	integral to membrane;	transferase activity
69	0	0	0	0	0	0	0	0		integral to membrane [pmid	ion channel activity; voltage-
70	0	0	0	4.82E-05	0	0	0	0	Predicted integral	integral to membrane;	
71	0	0	0	0	0	0	0	0		integral to membrane;	
72	0	0	0	3.4E-05	0	0	0	0	Acyltransferase. This family	endoplasmic reticulum;	1-acylglycerophosphocholine
73	0	0	0	3.72E-05	0	0	0	0	Predicted membrane	integral to membrane;	acyltransferase activity;
74	0	0	0	0	0	0	0	0	Rhomboid family. This		
75	0	0	0	0.000141	0	0	0	0		integral to membrane;	hydrolase activity
76	0	0	0	0.00024	0.000212	0.000827	0	0		extracellular region [pmid	cytokine activity [pmid
77	0	0	0	0	0	0	0	0	Leucine-rich repeats	integral to membrane;	transferase activity
78	0	0	0	0	0	0	0	0		integral to membrane;	
79	0	0	0	0	0	0	0	6.26E-05	Immunoglobulin domain	endoplasmic reticulum;	
80	0	0	0	0	0	0	0	0	Protein of unknown function	mitochondrion [pmid	
81	0	0	6.74E-05	0	0	0	0	0			
82	0	0	0	0	0.000287	0	0	0	OST3 / OST6 family. The	endoplasmic reticulum;	
83	0	0	0	0	0	0	0	0	MRVI1 protein. This family	endoplasmic reticulum;	
84	0	0	0	0	0	0	0	0	Eps15 homology domain;	integral to membrane;	acyltransferase activity;
85	0	0	0	0	0	0	0	0	Protein of unknown function	integral to membrane;	
86	0	0	0	0	0	0	0	0	Translocon-associated	endoplasmic reticulum [pmid	signal sequence binding
87	0	0	0	0	0	0	0	0		integral to membrane;	
88	0	0	0	0	0	0	0	0	Membrane-associating	endoplasmic reticulum [pmid	chemokine binding [pmid
89	0	0	0	0	0	0	0	0			
90	0	0	0	7.15E-05	0	0	0	0	The RING-variant domain is		protein binding; zinc ion
91	0	0	0	0	0	0	0	0		nucleus [pmid 12209954]	
92	0	0	0	0	0	0	0	0	Protein of unknown function	integral to membrane;	protein binding [pmid
93	0	0	0	0	0	0	0	0			
94	0	0	0	5.61E-05	0	0	0	0	Uncharacterized protein	integral to membrane;	
95	0	0	0	0	0	0	0	0	CD20/IgE Fc receptor beta	integral to plasma membrane	receptor activity; receptor
96	0	0	0	0	0	0	0	0			
97	0	0	0	0	0	0	9.96E-05	0	Ring finger; E3 ubiquitin-		metal ion binding; protein
98	0	0	0	0	0	0	0	0	Acyltransferase. This family		acyltransferase activity
99	0	0	0	0	0	0	0	0			
100	0	0	0	0	0	0	0	0			

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB
101	2	6.36E-05	0	0	INF		ENSG00000185905:E	C16orf54	bNET?		gi|148233642|ref|NP	hypothetical protein LOC283	224	24360	6.2	1	o31-53i	A	54	0.112
102	2	6.05E-05	0	0	INF		ENSG00000128973:E	CLN6	bNET?		gi|8923532|ref|NP_0	CLN6 protein [Homo sapiens	311	35919	8.9	7	i47-69o84-	Q	35	0.209
103	2	5.62E-05	0	0	INF		ENSG00000188167:E	TMPP	bNET?		gi|89886215|ref|NP_	hypothetical protein LOC643	453	49458	7	5	i13-32o42-	S	32	0.727
104	2	5.54E-05	0	0	INF		ENSG00000114023:E	C3orf28	bNET?		gi|49355721|ref|NP_	growth and transformation-de	154	17342	9.8	1	o103-120i	Q	15	0.105
105	2	5.32E-05	0	0	INF		ENSG00000124208:N	TMEM189	bNET?		gi|40806193|ref|NP_	transmembrane protein 189 [	270	31136	6.7	3	o46-68i75-	Q	65	0
106	2	4.95E-05	0	0	INF		ENSG00000172992:E	DCAKD	bNET?		gi|19923601|ref|NP_	dephospho-CoA kinase dom	231	26549	9.6	1	o207-229i	Q	16	0.213
107	2	3.98E-05	0	0	INF		ENSG00000104381:E	GDAP1	bNET?		gi|108773797|ref|NP	ganglioside-induced different	358	41346	8.4	2	i292-309o3	Q	35	0
108	2	3.88E-05	0	0	INF		ENSG00000136404:E	TM6SF1	bNET?		gi|13194199|ref|NP_	transmembrane 6 superfamil	370	41664	7.6	9	i5-27o32-5	S	17	0.742
109	2	3.59E-05	0	0	INF		ENSG00000196187:E	TMEM63A	bNET?		gi|7662308|ref|NP_0	transmembrane protein 63A	807	92160	7.3	11	o49-71i146	A	17	0
110	2	3.08E-05	0	0	INF		ENSG00000198513:E	SPG3A	bNET?		gi|19923445|ref|NP_	atlastin isoform a [Homo sap	558	63544	6.2	2	i449-468o4	Q	0	0
111	2	2.61E-05	0	0	INF		ENSG00000185475:E	TMEM179B	bNET?		gi|40786402|ref|NP_	transmembrane protein 179E	219	23550	7.9	3	i9-28o64-8	S	27	0.998
112	2	2.11E-05	0	0	INF		ENSG00000170088:E	TMEM192	bNET?		gi|154240704|ref|NP	transmembrane protein 192 [	271	30922	8	4	i48-70o92-	A	0	0
113	2	2.09E-05	0	0	INF		ENSG00000144567:E	FAM134A	bNET?		gi|31543176|ref|NP_	hypothetical protein LOC791	543	57789	4.5	1	o203-225i	S	36	0.93
114	2	2.08E-05	0	0	INF		ENSG00000166881:E	TMEM194A	bNET?		gi|58037093|ref|NP_	transmembrane protein 194 [	371	41999	6.2	4	i112-134o1	S	44	0.972
115	2	2.01E-05	0	0	INF		ENSG00000070269:E	C14orf101	bNET?		gi|93277080|ref|NP_	hypothetical protein LOC549	707	79536	8.4	8	i23-45o65-	A	51	0.208
116	2	1.85E-05	0	0	INF		ENSG00000090686:E	USP48	bNET?		gi|52630449|ref|NP_	ubiquitin specific protease 48	1035	119032	6.1	1	i87-109o	Q	18	0.001
117	2	1.84E-05	0	0	INF		ENSG00000177054:E	ZDHHC13	bNET?		gi|47933346|ref|NP_	zinc finger, DHHC domain co	622	70861	8.1	6	i290-312o3	Q	17	0
118	2	1.58E-05	0	0	INF		ENSG00000177119:E	TMEM16F	bNET?		gi|70778895|ref|NP_	transmembrane protein 16F [	910	106131	7.8	8	i295-317o3	Q	0	0
119	2	1.42E-05	0	0	INF		ENSG00000180776:E	ZDHHC20	bNET?		gi|49457851|ref|NP_	zinc finger, DHHC-type conta	354	41096	7.9	4	i13-32o52-	A	30	0.142
120	2	1.21E-05	0	0	INF		ENSG00000176915:E	ANKLE2	bNET?		gi|148664230|ref|NP	hypothetical protein LOC231	938	104114	7.1	1	i13-32o	S	38	0.994
121	2	9.13E-06	0	0	INF		ENSG00000182134:E	TDRKH	bNET?		gi|145312270|ref|NP	tudor and KH domain contain	561	62046	5	1	i17-34o	Q	31	0.22
122	2	4.75E-06	0	0	INF		ENSG00000075420:E	FNDC3B	bNET?		gi|27477059|ref|NP_	fibronectin type III domain co	1204	132900	5.9	1	o1179-120	Q	33	0.001
123	2	2.56E-06	0	0	INF		ENSG00000007202:E	KIAA0100	bNET?		gi|57242774|ref|NP_	hypothetical protein LOC970	2235	253698	7.1	1	i5-27o	S	19	0.995
124	1	0.001756	0	0	INF		ENSG00000183172:E	C22orf32	bNET?		gi|21314769|ref|NP_	hypothetical protein LOC916	107	11342	6.1	1	i65-84o	Q	17	0.793
125	1	0.000625	2	3.25E-05	19.24109		ENSG00000130748:E	TMEM160	bNET?		gi|8923477|ref|NP_0	transmembrane protein 160 [	188	19657	8	2	i99-121o13	S	48	0.759
126	1	0.000369	0	0	INF		ENSG00000173436:E	C1orf151	bNET?		gi|73912720|ref|NP_	chromosome 1 open reading	78	8808	8.5	1	i13-35o	A	59	0.002
127	1	0.000254	1	2.99E-05	8.487215		ENSG00000171202:E	TMEM126A	bNET	Fig. 4, 5, 6	gi|14150017|ref|NP_	transmembrane protein 126A	195	21527	9.3	2	i65-87o107	Q	0	0
128	1	0.000136	0	0	INF		ENSG00000183978:E	CCDC56	bNET?		gi|94536771|ref|NP_	coiled-coil domain containing	106	11731	9.6	1	i58-80o	Q	16	0
129	1	7.38E-05	0	0	INF		ENSG00000175606:E	TMEM70	bNET?		gi|34147498|ref|NP_	transmembrane protein 70 is	260	28969	8.9	2	i103-125o1	S	35	0.881
130	1	6.63E-05	0	0	INF		ENSG00000163900:E	TMEM41A	bNET	Fig. 4, 5	gi|18087813|ref|NP_	transmembrane protein 41A	264	29665	9	6	o4-21i68-8	S	18	0.981
131	1	5.3E-05	0	0	INF		ENSG00000127774:E	TMEM93	bNET?		gi|62339424|ref|NP_	transmembrane protein 93 [H	110	12017	10.1	2	o46-68i85-	A	52	0
132	1	3.06E-05	0	0	INF		ENSG00000112167:E	C6orf64	bNET?		gi|8922867|ref|NP_0	hypothetical protein LOC557	183	20163	8.8	1	i106-128o	Q	28	0.084
133	1	2.78E-05	0	0	INF		ENSG00000168569:E	MGC3196	bNET?		gi|122937442|ref|NP	hypothetical protein LOC790	202	22049	11	2	i44-66o96-	A	28	0.363
134	1	2.72E-05	0	0	INF		ENSG00000090971:E	NAT14	bNET?		gi|23943862|ref|NP_	N-acetyltransferase 14 [Hom	206	21650	10.7	1	o55-77i	A	61	0.005
135	1	1.91E-05	0	0	INF		ENSG00000152749:E	GPR180	bNET?		gi|30725877|ref|NP_	G protein-coupled receptor 1	440	49395	7.4	7	o173-192i2	S	23	1
136	1	1.91E-05	0	0	INF		ENSG00000175489:E	LRRC25	bNET?		gi|45593138|ref|NP_	leucine rich repeat containing	305	33179	5.1	1	o166-188i	S	21	0.998
137	1	1.51E-05	0	0	INF		ENSG00000162542:E	TMCO4	bNET?		gi|42476210|ref|NP_	transmembrane and coiled-c	634	67881	5.8	3	i190-212o2	Q	25	0.005
138	1	1.17E-05	0	0	INF		ENSG00000064545:E	TMEM161A	bNET?		gi|8923394|ref|NP_0	transmembrane protein 161A	479	53602	8.4	8	i105-127o1	S	29	0.994
139	1	1.08E-05	0	0	INF		ENSG00000163933:E	RFT1	bNET?		gi|16418361|ref|NP_	RFT1 homolog [Homo sapien	541	60335	8.9	12	i13-35o45-	S	34	0.602
140	10	0.002309	0	0	INF		ENSG00000204523:N	HLA-B			gi|17986001|ref|NP_	major histocompatibility comp	362	40460	5.9	1	o308-330i	S	25	1
141	10	0.001234	4	6.83E-05	18.06		ENSG00000081237:E	PTPRC			gi|18641347|ref|NP_	protein tyrosine phosphatase	1304	147254	6.2	2	o578-600i8	S	24	0.988
142	9	0.00153	4	9.72E-05	15.73675		ENSG00000168394:E	TAP1			gi|9665248|ref|NP_0	transporter 1, ATP-binding ca	808	87218	8	7	i74-96o116	Q	22	0.157
143	8	0.005807	0	0	INF		ENSG00000206503:N	HLA-A			gi|24797067|ref|NP_	major histocompatibility comp	365	40841	6	1	o308-330i	S	25	1
144	8	0.001967	0	0	INF		ENSG00000213203:E	GIMAP1			gi|18594498|ref|NP_	GTPase, IMAP family membe	306	34369	8.9	1	o273-292i	Q	0	0
145	8	0.001427	0	0	INF		ENSG00000112493:E	TAPBP			gi|27436893|ref|NP_	tapasin isoform 1 precursor [	448	47571	7	1	o414-436i	S	21	1
146	8	0.000541	0	0	INF		ENSG00000204525:N	1C07			gi|52630342|ref|NP_	major histocompatibility comp	366	40649	6	1	o306-328i	S	25	1
147	8	0.000535	1	4.49E-05	11.93138		ENSG00000005844:E	ITGAL			gi|4504757|ref|NP_0	integrin alpha L precursor [H	1170	128849	5.6	2	i5-27o1090	S	26	0.979
148	8	0.000515	3	4.49E-05	11.4917		ENSG00000167323:E	STIM1			gi|21070997|ref|NP_	stromal interaction molecule	685	77423	6.7	1	i214-232o	S	23	1
149	7	0.001226	2	1.18E-05	103.7688		ENSG00000074370:E	ATP2A3			gi|28373103|ref|NP_	sarco/endoplasmic reticulum	999	109256	5.5	8	i60-78o88-	Q	23	0.038
150	7	0.001218	0	0	INF		ENSG00000005022:E	SLC25A5			gi|156071459|ref|NP	solute carrier family 25, mem	298	32852	9.7	3	o109-131i1	Q	25	0.124
151	7	0.001153	0	0	INF		ENSG00000206306:N	HLA-DRB4			gi|169169220|ref|XP	PREDICTED: major histocon	279	31647	8.4	2	o6-28i241-	S	30	0.995
152	7	0.001003	2	2.37E-05	42.2588		ENSG00000160255:E	ITGB2			gi|89191865|ref|NP_	integrin, beta 2 precursor [Ho	769	84782	7	1	o701-723i	S	23	0.999
153	7	0.000837	4	8.55E-05	9.788422		ENSG00000165168:E	CYBB			gi|6996021|ref|NP_0	cytochrome b-245, beta poly	570	65336	8.6	4	o10-32i98-	A	26	0.171
154	7	0.000495	0	0	INF		ENSG00000163527:E	STT3B			gi|30578410|ref|NP_	source of immunodominant M	826	93674	8.9	10	o66-85i134	Q	33	0.012
155	7	0.00018	0	0	INF		ENSG00000204592:N	HLA-E			gi|62912479|ref|NP_	major histocompatibility comp	358	40058	5.8	1	o305-327i	S	22	0.999
156	6	0.003248	3	5.92E-05	54.86813		ENSG00000204287:E	HLA-DRA			gi|52426774|ref|NP_	major histocompatibility comp	254	28621	5	1	o217-239i	S	26	0.996
157	6	0.002483	0	0	INF		ENSG00000148175:E	STOM			gi|38016911|ref|NP_	stomatin isoform a [Homo sa	288	31731	7.9	1	o32-54i	A	46	0
158	6	0.001063	0	0	INF		ENSG00000056345:E	ITGB3			gi|47078292|ref|NP_	integrin beta chain, beta 3 pr	788	87058	5.2	1	o719-741i	S	27	0.971
159	6	0.000759	0	0	INF		ENSG00000086598:E	TMED2			gi|5803149|ref|NP_0	coated vesicle membrane pro	201	22761	5.2	2	o4-23i169-	S	21	0.998
160	6	0.000743	2	1.55E-05	47.84383		ENSG00000074582:E	BCS1L			gi|119964730|ref|NP	BCS1-like [Homo sapiens]	419	47534	8.5	0	o	A	33	0.097
161	6	0.00054	0	0	INF		ENSG00000196396:E	PTPN1			gi|4506289|ref|NP_0	protein tyrosine phosphatase	435	49967	6.3	1	o409-431i	Q	0	0
162	6	0.000477	0	0	INF		ENSG00000184270:E	HIST2H2AB			gi|28195394|ref|NP_	histone cluster 2, H2ab [Hom	130	13995	10.9	0	o	A	62	0.069
163	6	0.000424	0	0	INF		ENSG00000143554:E	SLC27A3			gi|13236579|ref|NP_	solute carrier family 27 meml	730	78644	7.5	1	i48-70o	A	65	0.01
164	6	0.000286	0	0	INF		ENSG00000026508:E	CD44			gi|48255935|ref|NP_	CD44 antigen isoform 1 prec	742	81538	5.3	1	o650-672i	S	21	0.997
165	6	0.000265	2	1.89E-05	13.96811		ENSG00000071537:E	SEL1L			gi|19923669|ref|NP_	sel-1 suppressor of lin-12-like	794	88755	5.4	1	o739-761i	S	22	1
166	5	0.003623	0	0	INF		ENSG00000169100:N	SLC25A6			gi|156071462|ref|NP	solute carrier family 25, mem	298	32866	9.7	2	i172-194o2	Q	25	0.049
167	5	0.001499	0	0	INF		ENSG00000065518:E	NDUFB4			gi|113414862|ref|XP	PREDICTED: similar to NAD	129	15209	9.8	1	o88-105i	Q	21	0
168	5	0.001229	0	0	INF		ENSG00000196126:E	HLA-DRB1			gi|4504411|ref|NP_0	major histocompatibility comp	266	29914	7.7	1	o228-250i	S	30	0.996
169	5	0.001185	0	0	INF		ENSG00000204642:N	HLA-F			gi|149158698|ref|NP	major histocompatibility comp	346	39062	5.6	1	o305-327i	S	22	1
170	5	0.000964	0	0	INF		ENSG00000204632:N	HLA-A29.1			gi|169168595|ref|XP	major histocompatibility comp	365	40789	6.7	1	o308-330i	S	25	1
171	5	0.000935	1	6.42E-06	145.7369		ENSG00000159348:E	CYB5R1			gi|49574502|ref|NP_	NAD(P)H:quinone oxidoredu	305	34095	9.4	1	i7-29o	S	27	0.809
172	5	0.000831	5	9.56E-05	8.693477		ENSG00000139921:E	TXNDC1			gi|151101292|ref|NP	thioredoxin domain containin	280	31791	5	3	o4-23i139-	S	27	1
173	5	0.000742	0	0	INF		ENSG00000197561:E	ELA2			gi|4503549|ref|NP_0	elastase 2, neutrophil prepro	267	28518	9.3	1	i7-26o	S	28	0.999
174	5	0.000718	0	0	INF		ENSG00000144867:E	SRPRB			gi|14917113|ref|NP_	signal recognition particle rec	271	29651	9	1	i37-54o	A	60	0
175	5	0.000691	0	0	INF		ENSG00000057252:E	SOAT1			gi|49533617|ref|NP_	sterol O-acyltransferase (acy	550	64735	8.9	8	i140-162o1	Q	0	0
176	5	0.000645	4	6.92E-05	9.321851		ENSG00000185896:E	LAMP1			gi|112380628|ref|NP	lysosomal-associated memb	417	44882	8.7	2	i11-33o384	S	29	1
177	5	0.000581	0	0	INF		ENSG00000198502:E	HLA-DRB5			gi|18641375|ref|NP_	major histocompatibility comp	266	30056	6.9	1	o228-250i	S	30	0.991
178	5	0.000432	1	1.97E-06	219.3482		ENSG00000169896:E	ITGAM			gi|88501734|ref|NP_	integrin alpha M precursor [H	1152	127178	7.2	1	o1109-113	S	17	0.999
179	5	0.000401	0	0	INF		ENSG00000101856:E	PGRMC1			gi|5729875|ref|NP_0	progesterone receptor memb	195	21671	4.7	1	o20-42i	Q	49	0.022
180	5	0.000333	0	0	INF		ENSG00000188486:E	H2AFX			gi|4504253|ref|NP_0	H2A histone family, member	143	15145	10.7	0	o	A	62	0.116
181	5	0.00032	0	0	INF		ENSG00000113441:E	LNPEP			gi|61742775|ref|NP_	leucyl/cystinyl aminopeptidas	1011	115636	5.7	1	i98-117o	Q	0	0
182	5	0.000314	0	0	INF		ENSG00000140678:E	ITGAX			gi|34452173|ref|NP_	integrin alpha X precursor [H	1163	127829	6.6	1	o1109-113	S	20	0.999
183	5	0.000278	3	3.32E-05	8.375647		ENSG00000101464:E	PIGU			gi|17998700|ref|NP_	phosphatidylinositol glycan a	435	50052	7.7	9	o77-99i165	S	18	1
184	5	0.000237	2	2.49E-05	9.520225		ENSG00000140983:E	RHOT2			gi|20270303|ref|NP_	ras homolog gene family, me	618	68118	5.9	1	o593-615i	Q	31	0.012
185	5	0.000236	4	3.37E-05	6.987656		ENSG00000141385:E	AFG3L2			gi|5802970|ref|NP_0	AFG3 ATPase family gene 3	797	88484	8.7	2	o146-163i2	Q	32	0.272
186	5	0.00023	1	3.21E-06	71.72433		ENSG00000132305:E	IMMT			gi|154354966|ref|NP	inner membrane protein, mito	747	82625	6.6	0	o	A	20	0.268
187	5	0.000201	1	2.11E-05	9.545084		ENSG00000124155:E	PIGT			gi|23397653|ref|NP_	phosphatidylinositol glycan a	578	65700	8.4	1	o522-544i	S	24	1
188	5	0.000196	0	0	INF		ENSG00000010278:E	CD9			gi|4502693|ref|NP_0	CD9 antigen [Homo sapiens]	228	25416	7.1	4	i13-35o60-	A	31	0.156
189	5	0.000174	0	0	INF		ENSG00000168383:N	HLA-DPB1			gi|24797076|ref|NP_	major histocompatibility comp	258	29159	8.6	1	o226-245i	S	30	0.999
190	5	0.000145	1	3.15E-06	46.05912		ENSG00000123983:E	ACSL3			gi|42794754|ref|NP_	acyl-CoA synthetase long-ch	720	80420	8.4	1	i21-43o	A	38	0.006
191	5	9.1E-05	1	1.76E-05	5.171329		ENSG00000032444:E	PNPLA6			gi|116256487|ref|NP	neuropathy target esterase [	1327	146215	7.8	1	i9-31o	A	26	0.002
192	5	6.95E-05	2	5.3E-06	13.09802		ENSG00000150995:E	ITPR1			gi|154354996|ref|NP	inositol 1,4,5-triphosphate re	2695	306840	6.4	6	o2220-224	Q	22	0.007
193	4	0.001192	0	0	INF		ENSG00000130288:E	NDUFA13			gi|156151369|ref|NP	NADH dehydrogenase (ubiqu	227	25821	9.8	1	i112-134o	Q	62	0
194	4	0.001058	4	2.4E-05	44.13573		ENSG00000133318:E	RTN3			gi|5174655|ref|NP_0	reticulon 3 isoform a [Homo s	236	25609	8.5	3	o69-91i149	Q	20	0.014
195	4	0.000983	0	0	INF		ENSG00000137078:E	SIT1			gi|7657577|ref|NP_0	SHP2-interacting transmemb	196	21126	6.3	1	o41-63i	A	25	0.078
196	4	0.000912	0	0	INF		ENSG00000134970:E	TMED7			gi|32996709|ref|NP_	transmembrane emp24 prote	224	25172	6.9	1	i186-208o	S	35	1
197	4	0.000904	0	0	INF		ENSG00000203618:E	GP1BB			gi|4504073|ref|NP_0	glycoprotein Ib, beta polypep	206	21718	9.3	1	o151-173i	S	26	1
198	4	0.000656	2	3.38E-05	19.40826		ENSG00000051523:E	CYBA			gi|68509914|ref|NP_	cytochrome b, alpha polypep	195	21013	9.5	3	i7-29o33-5	S	32	0.603
199	4	0.000619	0	0	INF		ENSG00000107819:E	SFXN3			gi|31621303|ref|NP_	sideroflexin 3 [Homo sapiens	325	35979	9.1	1	o268-290i	Q	0	0
200	4	0.000613	0	0	INF		ENSG00000185013:E	RDH14			gi|10190746|ref|NP_	retinol dehydrogenase 14 (al	336	36865	8.8	1	o4-26i	S	22	0.996
201	4	0.000548	0	0	INF		ENSG00000019582:E	CD74			gi|68448544|ref|NP_	CD74 antigen isoform a [Hon	296	33516	8.4	1	i49-71o	A	0	0
202	4	0.000547	0	0	INF		ENSG00000213402:E	PTPRCAP			gi|5032005|ref|NP_0	protein tyrosine phosphatase	206	21196	4.6	1	o32-54i	S	52	0.893
203	4	0.000513	0	0	INF		ENSG00000100300:E	TSPO			gi|74275350|ref|NP_	translocator protein isoform F	169	18828	9.4	5	o4-26i46-6	S	29	0.955
204	4	0.000449	0	0	INF		ENSG00000119537:E	FVT1			gi|4503817|ref|NP_0	3-ketodihydrosphingosine re	332	36187	7.1	1	i2-24o	S	22	0.991
205	4	0.000385	0	0	INF		ENSG00000110448:E	CD5			gi|7656965|ref|NP_0	CD5 molecule [Homo sapien	495	54625	8.3	1	o380-402i	S	25	0.982
206	4	0.000382	0	0	INF		ENSG00000184992:E	BRI3BP			gi|19923665|ref|NP_	BRI3-binding protein [Homo	251	27836	9.4	4	o10-32i125	S	35	1
207	4	0.000331	0	0	INF		ENSG00000115204:N	MPV17			gi|4505241|ref|NP_0	Mpv17 protein [Homo sapien	176	19733	9.5	2	i51-73o93-	S	35	0.761
208	4	0.000281	1	3.11E-05	9.036697		ENSG00000129255:E	MPDU1			gi|116517313|ref|NP	mannose-P-dolichol utilizatio	247	26638	8.9	6	o45-67i74-	Q	23	0
209	4	0.000265	0	0	INF		ENSG00000204257:E	HLA-DMA			gi|18765715|ref|NP_	major histocompatibility comp	261	29207	4.7	1	o232-254i	S	27	0.996
210	4	0.000264	0	0	INF		ENSG00000171791:E	BCL2			gi|72198189|ref|NP_	B-cell lymphoma protein 2 al	239	26266	7.3	1	o214-236i	Q	0	0
211	4	0.000243	1	6.89E-06	35.25623		ENSG00000140497:E	SCAMP2			gi|5730031|ref|NP_0	secretory carrier membrane	329	36649	6.1	4	i152-174o1	Q	0	0
212	4	0.000197	0	0	INF		ENSG00000135390:E	ATP5G2			gi|50593533|ref|NP_	ATP synthase, H+ transportin	157	16334	9	2	i96-118o13	Q	20	0.017
213	4	0.000171	0	0	INF		ENSG00000123146:E	CD97			gi|17978489|ref|NP_	CD97 antigen isoform 2 prec	742	81743	7.1	7	o460-482i4	S	21	1
214	4	0.000169	0	0	INF		ENSG00000067167:E	TRAM1			gi|7657655|ref|NP_0	translocation associated mer	374	43072	9.6	8	i30-52o80-	A	47	0.041
215	4	0.000149	0	0	INF		ENSG00000003056:E	M6PR			gi|4505061|ref|NP_0	cation-dependent mannose-6	277	30993	5.8	1	o188-210i	S	27	0.988
216	4	0.000112	0	0	INF		ENSG00000206305:N	HLA-DQA1			gi|169217612|ref|XP	HLA-DQA1 major histocompa	254	27937	5.4	1	o217-239i	S	24	0.997
217	4	8.75E-05	0	0	INF		ENSG00000088888:E	MAVS			gi|83776598|ref|NP_	virus-induced signaling adap	540	56528	5.5	1	o513-535i	Q	0	0
218	4	8.18E-05	0	0	INF		ENSG00000054219:E	LY75			gi|144446030|ref|NP	lymphocyte antigen 75 [Hom	1722	198310	6.7	1	o1669-169	S	32	1
219	4	6.19E-05	2	1.16E-05	5.361538		ENSG00000068366:E	ACSL4			gi|12669909|ref|NP_	acyl-CoA synthetase long-ch	711	79188	8.4	1	i12-34o	A	24	0.148
220	4	5.7E-05	0	0	INF		ENSG00000116824:E	CD2			gi|156071472|ref|NP	CD2 molecule [Homo sapien	351	39448	9.6	1	o212-234i	S	25	0.957
221	4	5.13E-05	0	0	INF		ENSG00000122224:E	LY9			gi|55925578|ref|NP_	lymphocyte antigen 9 isoforn	655	72139	5.5	1	o455-476i	A	48	0.294
222	4	4.61E-05	0	0	INF		ENSG00000128335:E	APOL2			gi|22035653|ref|NP_	apolipoprotein L2 [Homo sap	337	37092	6.7	3	i119-141o1	Q	0	0
223	4	4.2E-05	0	0	INF		ENSG00000111801:E	BTN3A3			gi|37574628|ref|NP_	butyrophilin, subfamily 3, me	542	60557	5.4	1	o206-228i	Q	19	0.001
224	4	3.63E-05	0	0	INF		ENSG00000096433:E	ITPR3			gi|153945846|ref|NP	inositol 1,4,5-triphosphate re	2671	304105	6.5	7	o2201-222	Q	21	0.011
225	4	3.25E-05	0	0	INF		ENSG00000077454:E	LRCH4			gi|30181233|ref|NP_	leucine-rich repeats and calp	683	73450	8.2	1	o653-675i	S	19	0.891
226	4	3.07E-05	0	0	INF		ENSG00000007541:E	PIGQ			gi|22538450|ref|NP_	phosphatidylinositol glycan a	581	65344	9	5	o276-298i3	Q	22	0.264
227	4	1.71E-05	0	0	INF		ENSG00000172046:E	USP19			gi|57529246|ref|NP_	ubiquitin specific peptidase 1	1318	145650	6.3	1	o1291-131	Q	16	0
228	3	0.00067	0	0	INF		ENSG00000151729:E	SLC25A4			gi|55749577|ref|NP_	solute carrier family 25 (mito	298	33064	9.8	3	o112-134i1	Q	25	0.255
229	3	0.000553	0	0	INF		ENSG00000141378:E	PTRH2			gi|7706351|ref|NP_0	Bcl-2 inhibitor of transcription	179	19194	8.7	1	o15-37i	S	31	0.804
230	3	0.000427	0	0	INF		ENSG00000198821:E	CD247			gi|37595565|ref|NP_	T-cell receptor zeta chain iso	164	18696	9.2	1	o31-53i	S	22	0.979
231	3	0.000344	0	0	INF		ENSG00000170310:E	STX8			gi|4759188|ref|NP_0	syntaxin 8 [Homo sapiens]	236	26907	5	1	i211-233o	Q	22	0
232	3	0.000335	0	0	INF		ENSG00000198851:E	CD3E			gi|4502671|ref|NP_0	CD3E antigen, epsilon polype	207	23147	6.8	1	o130-152i	S	22	0.997
233	3	0.000311	0	0	INF		ENSG00000173726:E	TOMM20			gi|7657257|ref|NP_0	translocase of outer mitochor	145	16298	8.6	1	o5-24i	A	22	0.212
234	3	0.000278	0	0	INF		ENSG00000169704:E	GP9			gi|4504077|ref|NP_0	glycoprotein IX (platelet) [Ho	177	19046	6.4	1	o147-169i	S	17	1
235	3	0.000274	0	0	INF		ENSG00000186529:N	CYP4F3			gi|119220562|ref|NP	cytochrome P450, family 4, s	520	59847	7.6	1	o15-37i	S	37	1
236	3	0.00027	0	0	INF		ENSG00000114544:E	SLC41A3			gi|56549671|ref|NP_	solute carrier family 41, mem	487	52449	6.9	10	i65-87o149	Q	36	0
237	3	0.000258	0	0	INF		ENSG00000069849:E	ATP1B3			gi|4502281|ref|NP_0	Na+/K+ -ATPase beta 3 subu	279	31513	8.3	1	i38-60o	A	56	0
238	3	0.000233	0	0	INF		ENSG00000076662:N	ICAM3			gi|4504559|ref|NP_0	intercellular adhesion molecu	547	59384	5.4	1	o487-509i	S	30	1
239	3	0.00022	2	2.94E-05	7.498593		ENSG00000108622:E	ICAM2			gi|153082722|ref|NP	intercellular adhesion molecu	275	30654	7.4	1	o225-247i	S	22	0.733
240	3	0.000207	2	2.65E-05	7.837453		ENSG00000103249:E	CLCN7			gi|14149607|ref|NP_	chloride channel 7 isoform a	805	88679	8.4	11	i126-148o1	Q	46	0
241	3	0.000194	0	0	INF		ENSG00000115652:E	UXS1			gi|42516563|ref|NP_	UDP-glucuronate decarboxyl	420	47577	8.9	1	i20-38o	S	36	0.99
242	3	0.000179	0	0	INF		ENSG00000030110:E	BCL2L7P1			gi|4502363|ref|NP_0	BCL2-antagonist/killer 1 [Hor	211	23409	6	1	o183-205i	Q	29	0
243	3	0.000164	1	1.53E-05	10.74749		ENSG00000165264:E	NDUFB6			gi|4505365|ref|NP_0	NADH dehydrogenase (ubiqu	128	15489	9.6	1	i68-86o	Q	0	0
244	3	0.000147	0	0	INF		ENSG00000206294:N	HLA-DMB			gi|4504399|ref|NP_0	major histocompatibility comp	263	28943	7.4	1	o219-238i	S	21	0.998
245	3	0.000146	1	2.07E-05	7.04479		ENSG00000090054:E	SPTLC1			gi|5454084|ref|NP_0	serine palmitoyltransferase s	473	52744	6	2	o20-40i161	Q	17	0.035
246	3	0.000142	0	0	INF		ENSG00000137409:E	MTCH1			gi|7657345|ref|NP_0	mitochondrial carrier homolo	372	39920	9.5	2	o255-277i2	Q	34	0.417

rk	RESTING LYMPHOCYTES NEs: HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	PHA-TREATED LYMPHOCYTES NEs: HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
101	0	0.000208	0	0	0	1	5.21E-05	0.000104	0	0.0003	0	0	0	1	7.51E-05	0.00015
102	0	0	0	0	0	0	0	0	0	0.000361	0	0	0.000123	2	0.000121	0.00017
103	0	0.000103	0	0	0	1	2.57E-05	5.15E-05	0	0.000347	0	0	0	1	8.67E-05	0.000173
104	0	0.000151	0	0	0	1	3.79E-05	7.57E-05	0	0.000291	0	0	0	1	7.28E-05	0.000146
105	0	0.000259	0	0	0	1	6.48E-05	0.00013	0	0.000166	0	0	0	1	4.15E-05	8.31E-05
106	0	0.000202	0	0	0	1	5.05E-05	0.000101	0	0.000194	0	0	0	1	4.86E-05	9.71E-05
107	0	0.00013	0	0	0	1	3.26E-05	6.52E-05	0	0.000188	0	0	0	1	4.7E-05	9.4E-05
108	0	0.000189	0	0	0	1	4.73E-05	9.46E-05	0	0.000121	0	0	0	1	3.03E-05	6.06E-05
109	0	0.000231	0	0	0	1	5.78E-05	0.000116	0	5.56E-05	0	0	0	1	1.39E-05	2.78E-05
110	0	0.000125	0	0	0	1	3.13E-05	6.27E-05	0	0.000121	0	0	0	1	3.02E-05	6.03E-05
111	0	0.000107	0	0	0	1	2.66E-05	5.33E-05	0	0.000102	0	0	0	1	2.56E-05	5.12E-05
112	0	8.61E-05	0	0	0	1	2.15E-05	4.3E-05	0	8.28E-05	0	0	0	1	2.07E-05	4.14E-05
113	0	4.3E-05	0	0	0	1	1.07E-05	2.15E-05	0	0.000124	0	0	0	1	3.1E-05	6.2E-05
114	0	6.29E-05	0	0	0	1	1.57E-05	3.14E-05	0	0	0	0	0.000103	1	2.59E-05	5.17E-05
115	0	6.6E-05	0	0	0	1	1.65E-05	3.3E-05	0	9.52E-05	0	0	0	1	2.38E-05	4.76E-05
116	0	0	0	0	0	0	0	0	0	0	0.000676	0	0.000148	2	3.71E-05	7.42E-05
117	0	7.5E-05	0	0	0	1	1.87E-05	3.75E-05	0	7.21E-05	0	0	0	1	1.8E-05	3.61E-05
118	0	7.69E-05	0	0	0	1	1.92E-05	3.84E-05	0	4.93E-05	0	0	0	1	1.23E-05	2.47E-05
119	0	0	0	4.99E-05	0	1	1.25E-05	2.49E-05	0	6.34E-05	0	0	0	1	1.58E-05	3.17E-05
120	0	2.49E-05	0	0	0	1	6.22E-06	1.24E-05	0	7.18E-05	0	0	0	1	1.79E-05	3.59E-05
121	0	4.16E-05	0	3.15E-05	0	2	1.83E-05	2.15E-05	0	0	0	0	0	0	0	0
122	0	1.94E-05	0	0	0	1	4.84E-06	9.69E-06	0	1.86E-05	0	0	0	1	4.66E-06	9.32E-06
123	0	1.04E-05	0	0	0	1	2.61E-06	5.22E-06	0	1E-05	0	0	0	1	2.51E-06	5.02E-06
124	0	0	0.014047	0	0	1	0.003512	0.007023	0	0	0	0	0	0	0	0
125	0	0	0.004997	0	0	1	0.001249	0.002498	0	0	0	0	0	0	0	0
126	0	0	0	0	0	0	0	0	0	0	0	0	0.002953	1	0.000738	0.001476
127	0	0.002033	0	0	0	1	0.000508	0.001017	0	0	0	0	0	0	0	0
128	0	0	0	0	0	0	0	0	0	0	0	0	0.001086	1	0.000272	0.000543
129	0	0	0	0	0	0	0	0	0	0	0	0	0.000591	1	0.000148	0.000295
130	0	0.00053	0	0	0	1	0.000133	0.000265	0	0	0	0	0	0	0	0
131	0	0.000424	0	0	0	1	0.000106	0.000212	0	0	0	0	0	0	0	0
132	0	0	0	0	0	0	0	0	0	0.000245	0	0	0	1	6.13E-05	0.000123
133	0	0	0	0	0	0	0	0	0	0.000222	0	0	0	1	5.55E-05	0.000111
134	0	0	0	0	0	0	0	0	0	0.000218	0	0	0	1	5.45E-05	0.000109
135	0	0	0	0	0	0	0	0	0	0.000153	0	0	0	1	3.82E-05	7.65E-05
136	0	0.000153	0	0	0	1	3.82E-05	7.65E-05	0	0	0	0	0	0	0	0
137	0	0	0	0	0	0	0	0	0	0	0	0	0.000121	1	3.03E-05	6.05E-05
138	0	0	0	0	0	0	0	0	0	9.37E-05	0	0	0	1	2.34E-05	4.68E-05
139	0	8.62E-05	0	0	0	1	2.16E-05	4.31E-05	0	0	0	0	0	0	0	0
140	0.000149	0.003452	0.008823	0.001026	0.001125	5	0.003363	0.003899	0.001226	0.003296	0.001932	0.000311	0.000186	5	0.001255	0.001438
141	0.001617	0.002629	0.002593	0.000433	0.001249	5	0.001818	0.001036	0.00034	0.001772	0.001072	0.00025	0.000236	5	0.00065	0.00075
142	0.001004	0.00153	0.003953	0.000175	0	4	0.001665	0.001624	0.002197	0.00236	0.001731	0.000121	0.000903	5	0.001395	0.001071
143	0.006664	0.005355	0.016986	0.001494	0	4	0.007625	0.006616	0.009729	0.004606	0	0.001436	0.000184	4	0.003989	0.004255
144	0.00371	0.003201	0.002456	0.001039	0	4	0.002602	0.001162	0.002901	0.002126	0	5.33E-05	0.000251	4	0.001333	0.001402
145	0	0.00026	0.003774	0.000828	0.000909	4	0.001216	0.00174	0	0.002153	0.006243	0.000546	0.003856	4	0.001639	0.001738
146	0.000148	0.001311	0	0.000899	0.001112	4	0.000589	0.000622	0.001213	0.000602	0.00191	0.000156	0	4	0.000493	0.000544
147	0.000832	0.000578	0.001606	6.04E-05	0	4	0.000769	0.000644	0.000759	0.000326	0	5.58E-05	6.56E-05	4	0.000302	0.000329
148	0.00142	0.000468	0.000274	0.000103	0	4	0.000567	0.000588	0.001296	0.000426	0	2.38E-05	0.000112	4	0.000464	0.000581
149	0.002381	0.001708	0.000272	0.000296	0	4	0.001164	0.001053	0.002666	0.0022	0	0.000287	0	3	0.001288	0.001341
150	0	0.001435	0	0.001656	0.004099	3	0.000773	0.000897	0	0.003808	0.009385	0.000698	0.002147	4	0.001663	0.001686
151	0.000387	0.002952	0	0.00038	0	3	0.00093	0.00136	0.003182	0.002021	0	0.000117	0.000183	4	0.001376	0.001493
152	0.002109	0.002335	0.000489	0.000436	0	4	0.001342	0.00102	0.001154	0.001459	0	4.24E-05	0	3	0.000664	0.000753
153	0.002561	0.000941	0.00033	0.000465	0	4	0.001074	0.001025	0.000779	0.000945	0	0	0.000673	3	0.000599	0.000415
154	0.000393	0.000452	0.000455	0.000214	0	4	0.000378	0.000113	0.001612	0.000462	0	0.000375	0	3	0.000612	0.000696
155	0.000151	0.000122	0	0.000161	0.001137	4	0.000109	7.43E-05	0	0.000855	0.001953	0.00015	0	3	0.000251	0.000409
156	0	0.001901	0.011835	0.001113	0	3	0.003712	0.005471	0	0.002616	0	6.43E-05	0.008458	3	0.002784	0.003974
157	0.009009	0.002511	0	0.000736	0	3	0.003064	0.004101	0.004624	0.002181	0	0	0.0008	3	0.001901	0.002026
158	0.003293	0.000296	0.003576	6.72E-05	0	4	0.001808	0.001884	0.000563	0.000712	0	0	0	2	0.000319	0.000373
159	0	0.001741	0.000935	8.79E-05	0	3	0.000691	0.000817	0	0.00279	0	0.000325	0.000191	3	0.000827	0.001316
160	0.001161	0.000946	0	8.43E-05	0	3	0.000548	0.000592	0.003178	0.000482	0	0	9.16E-05	3	0.000938	0.001508
161	0	0.000375	0.000432	0.000244	0	3	0.000263	0.000192	0	0.000877	0	0.00045	0.001941	3	0.000817	0.000831
162	0	0.000314	0	0.001223	0.039775	3	0.000384	0.000578	0	0.001079	0	0.000314	0.000886	3	0.00057	0.0005
163	0.000222	0.00016	0	7.26E-05	0	3	0.000114	9.75E-05	0.002432	0.0004	0	0	0.000105	3	0.000734	0.001145
164	0.000874	0.000314	0.00076	0.000167	0	4	0.000529	0.000341	0	0.000151	0	2.2E-05	0	2	4.33E-05	7.27E-05
165	0.000613	0.000118	0	2.22E-05	0	3	0.000188	0.000288	0.001118	0.000226	0	2.06E-05	0	3	0.000341	0.000528
166	0	0.005435	0	0.008658	0	2	0.003523	0.004276	0	0.012086	0.002346	0.002807	0	3	0.003723	0.00573
167	0.002514	0.000542	0.001456	0	0	3	0.001128	0.001102	0.006882	0	0	0	0.000595	2	0.001869	0.003353
168	0.000559	0	0.00565	0	0	2	0.001552	0.002745	0.003337	0	0	6.14E-05	0.000221	3	0.000905	0.001624
169	0	0.002059	0.002715	0.001032	0	3	0.001452	0.00119	0	0.00352	0	0.000151	0	2	0.000918	0.001736
170	0	0.004572	0.001029	0.000145	0	3	0.001437	0.002139	0	0.001778	0	0	0.000184	2	0.00049	0.000863
171	0	0.000918	0.004928	5.79E-05	0	3	0.001476	0.002339	0	0.001324	0	0	0.000252	2	0.000394	0.000631
172	0.001158	0.001083	0.003355	0.000252	0	4	0.001462	0.001327	0	0.000801	0	0	0	1	0.0002	0.000401
173	0	0.001485	0	0.001191	0	2	0.000669	0.000782	0.001662	0.000588	0	0	0.001006	3	0.000814	0.0007
174	0.001197	0.001377	0	0.000326	0	3	0.000725	0.000667	0	0.001573	0	0	0.001275	2	0.000712	0.000831
175	0.000885	0.000297	0	6.42E-05	0	3	0.000311	0.000403	0.004035	0.000245	0	0	0	2	0.00107	0.00198
176	0.001167	0.000559	0	0.000551	0	3	0.000569	0.000477	0.002129	0.000753	0	0	0	2	0.000721	0.001004
177	0.000559	0.000611	0	0	0	2	0.000292	0.000338	0.003337	0	0	6.14E-05	7.7E-05	3	0.000869	0.001646
178	0.002252	0.000587	0.000163	0.000123	0	4	0.000781	0.001003	0	0.000331	0	0	0	1	8.28E-05	0.000166
179	0	0.00012	0.001927	0.000272	0	3	0.00058	0.000905	0	0.00069	0	0	0.000197	2	0.000222	0.000326
180	0	0.000285	0	0.001112	0.036159	3	0.000349	0.000526	0	0.000981	0	0.000285	0	2	0.000316	0.000463
181	0	0.000461	0.001672	5.24E-05	0	3	0.000547	0.000778	0	0.000333	0	0	3.8E-05	2	9.27E-05	0.000161
182	0.000139	0.00016	0.001939	4.56E-05	0	4	0.000571	0.000913	0	0.000231	0	0	0	1	5.79E-05	0.000116
183	0.000746	0.000214	0	4.06E-05	0	3	0.00025	0.000343	0.00102	0.000206	0	0	0	2	0.000307	0.000486
184	0	0.000668	0	8.57E-05	0	2	0.000189	0.000322	0	0.000653	0	5.28E-05	0.000435	3	0.000285	0.000313
185	0	0.000585	0.000236	0.000199	0	3	0.000255	0.000243	0	0.000816	0	0	4.82E-05	2	0.000216	0.000401
186	0	0.000219	0	0.000591	0	2	0.000202	0.000279	0	0.00012	0	0.000502	0.000411	3	0.000258	0.000237
187	0.001122	0.000161	0	3.06E-05	0	3	0.000329	0.000534	0	0	0	2.82E-05	0.000266	2	7.35E-05	0.000129
188	0	0.000205	0.000824	7.75E-05	0	3	0.000277	0.000375	0	0.000295	0	0	0.000168	2	0.000116	0.000143
189	0	0.000271	0	6.85E-05	0	2	8.49E-05	0.000128	0	0.000435	0	6.33E-05	0.000558	3	0.000264	0.000274
190	0.000225	0.00051	0	2.45E-05	0	3	0.00019	0.000236	0	0.000187	0	0	0.000213	2	0.0001	0.000116
191	0.000244	0.000105	0	6.66E-05	0	3	0.000104	0.000103	0	0.000254	0	0	5.79E-05	2	7.79E-05	0.00012
192	0	0.000286	6.97E-05	6.55E-06	0	3	9.07E-05	0.000134	0	0.000136	0	0	5.7E-05	2	4.82E-05	6.43E-05
193	0.001429	0.000205	0	7.78E-05	0	3	0.000428	0.000673	0.007822	0	0	0	0	1	0.001955	0.003911
194	0.00481	0.000395	0.003184	7.48E-05	0	4	0.002116	0.002275	0	0	0	0	0	0	0	0
195	0	0.000833	0.00671	9.01E-05	0	3	0.001908	0.003223	0	0.000229	0	0	0	1	5.72E-05	0.000114
196	0	0.000625	0.005871	0	0	2	0.001624	0.002847	0	0.000801	0.003121	0	0	2	0.0002	0.000401
197	0.003936	0.000226	0.000912	0	0	3	0.001269	0.00182	0.002155	0	0	0	0	1	0.000539	0.001077
198	0	0.00012	0.004817	0	0	2	0.001234	0.002389	0	0.000115	0	0	0.000197	2	7.8E-05	9.6E-05
199	0.000499	0.000254	0	0	0	2	0.000188	0.000239	0.004097	0	0	0.0001	0	2	0.001049	0.002032
200	0	0.000347	0.003914	0.000105	0	3	0.001092	0.001887	0	0.000534	0	0	0	1	0.000134	0.000267
201	0	0.001812	0.001587	0	0	2	0.00085	0.000986	0	0.000819	0	0.000165	0	2	0.000246	0.00039
202	0	0.000793	0.002736	8.57E-05	0	3	0.000904	0.001272	0	0.000762	0	0	0	1	0.000191	0.000381
203	0	0.002622	0	0	0	1	0.000656	0.001311	0	0.000797	0.012412	0	0.000681	3	0.000369	0.000429
204	0.000977	0.000281	0.002264	0	0	3	0.00088	0.001009	0	6.76E-05	0	0	0	1	1.69E-05	3.38E-05
205	0	0.001319	0.000759	0.000143	0	3	0.000555	0.000607	0	0.000861	0	0	0	1	0.000215	0.000431
206	0.000646	0.000558	0.001497	0	0	3	0.000675	0.000618	0	0.000358	0	0	0	1	8.94E-05	0.000179
207	0	0.001193	0	0.000703	0	2	0.000474	0.000583	0	0.000382	0	0.000371	0	2	0.000188	0.000218
208	0	0.000189	0.000761	0	0	2	0.000237	0.00036	0	0.000363	0	0	0.000932	2	0.000324	0.00044
209	0	0.000715	0	0.000338	0	2	0.000263	0.000341	0	0.000774	0	0	0.000294	2	0.000267	0.000365
210	0	0	0	0.00037	0	1	9.24E-05	0.000185	0	0.001033	0	0.000546	0.000161	3	0.000435	0.00046
211	0.000986	0.000567	0	0	0	2	0.000388	0.00048	0	0.000341	0	4.96E-05	0	2	9.76E-05	0.000164
212	0.001033	0.000297	0	0	0	2	0.000333	0.000487	0	0	0.008907	0	0.000245	2	6.11E-05	0.000122
213	0	0.000314	0.000253	0.000167	0	3	0.000184	0.000137	0	0.000635	0	0	0	1	0.000159	0.000317
214	0	6.24E-05	0.001005	4.72E-05	0	3	0.000279	0.000485	0	0.00024	0	0	0	1	6E-05	0.00012
215	0	0.000505	0	6.38E-05	0	2	0.000142	0.000244	0	0.000486	0	0	0.000139	2	0.000156	0.000229
216	0	0.000211	0	0.000139	0	2	8.76E-05	0.000105	0	0.000387	0	0	0.000157	2	0.000136	0.000183
217	0	0.000259	0	0.000131	0	2	9.75E-05	0.000124	0	0.000249	0	6.04E-05	0	2	7.74E-05	0.000118
218	0	0.000257	0.000218	0	0	2	0.000119	0.000138	0	0.000156	0	0	2.23E-05	2	4.47E-05	7.52E-05
219	0.000228	7.38E-05	0	0	0	2	7.55E-05	0.000108	0	3.16E-05	0	0	0.000162	2	4.84E-05	7.72E-05
220	0	6.65E-05	0	0.000151	0	2	5.44E-05	7.16E-05	0	0.000192	0	4.65E-05	0	2	5.96E-05	9.08E-05
221	0	3.56E-05	0.000287	5.39E-05	0	3	9.41E-05	0.00013	0	3.43E-05	0	0	0	1	8.56E-06	1.71E-05
222	0	6.92E-05	0	5.24E-05	0	2	3.04E-05	3.58E-05	0	0.000133	0	0	0.000114	2	6.18E-05	7.17E-05
223	0	0.000172	0	3.26E-05	0	2	5.12E-05	8.21E-05	0	0	0	6.02E-05	7.08E-05	2	3.28E-05	3.81E-05
224	0	0.00011	0.000141	0	0	2	6.27E-05	7.35E-05	0	2.52E-05	0	0	1.44E-05	2	9.89E-06	1.22E-05
225	0	3.41E-05	0	0.000103	0	2	3.44E-05	4.88E-05	0	9.85E-05	0	2.39E-05	0	2	3.06E-05	4.67E-05
226	0	8.03E-05	0	6.08E-05	0	2	3.53E-05	4.15E-05	0	3.86E-05	0	0	6.61E-05	2	2.62E-05	3.22E-05
227	0	1.77E-05	0	2.68E-05	0	2	1.11E-05	1.34E-05	0	3.4E-05	0	0	5.83E-05	2	2.31E-05	2.84E-05
228	0	0.002679	0	0	0	1	0.00067	0.001339	0	0.00225	0	0	0.000429	2	0.00067	0.001073
229	0.001812	0.00013	0	0	0	2	0.000486	0.000886	0.00248	0	0	0	0	1	0.00062	0.00124
230	0	0.000711	0.002291	0	0	2	0.000751	0.00108	0	0.00041	0	0	0	1	0.000103	0.000205
231	0.002061	0.000593	0	0	0	2	0.000664	0.000973	0	9.51E-05	0	0	0	1	2.38E-05	4.75E-05
232	0	0.001127	0	0.000256	0	2	0.000346	0.000535	0	0.001301	0	0	0	1	0.000325	0.00065
233	0	0	0	0	0	0	0	0	0	0.000155	0	0.001013	0.001324	3	0.000623	0.000646
234	0.001832	0.000264	0	0	0	2	0.000524	0.000881	0	0.000127	0	0	0	1	3.17E-05	6.34E-05
235	0.000936	0.000404	0	0	0	2	0.000335	0.000443	0.000854	0	0	0	0	1	0.000213	0.000427
236	0	4.79E-05	0.001929	0	0	2	0.000494	0.000957	0	0.000184	0	0	0	1	4.61E-05	9.21E-05
237	0.000581	0.00092	0	0	0	2	0.000375	0.000455	0	0.000563	0	0	0	1	0.000141	0.000281
238	0.000889	0.000725	0	0	0	2	0.000404	0.000471	0	0.000246	0	0	0	1	6.15E-05	0.000123
239	0	0.000509	0	0.000193	0	2	0.000175	0.00024	0	0.001061	0	0	0	1	0.000265	0.00053
240	0	0.000232	0.0014	0	0	2	0.000408	0.00067	0	2.79E-05	0	0	0	1	6.97E-06	1.39E-05
241	0	0.000444	0	0	0	1	0.000111	0.000222	0.001057	5.34E-05	0	0	0	2	0.000278	0.00052
242	0	0.000221	0.00089	0	0	2	0.000278	0.000421	0	0.000319	0	0	0	1	7.97E-05	0.000159
243	0	0	0	0.000138	0	1	3.45E-05	6.9E-05	0	0.000876	0	0	0.0003	2	0.000294	0.000413
244	0	0.000532	0	0.000134	0	2	0.000167	0.000252	0	0.000512	0	0	0	1	0.000128	0.000256
245	0.000686	0.000148	0	0	0	2	0.000208	0.000326	0	0.000332	0	0	0	1	8.3E-05	0.000166
246	0	6.27E-05	0.00101	0	0	2	0.000268	0.000495	0	6.03E-05	0	0	0	1	1.51E-05	3.02E-05

rk	MMs: MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
101	0	0	0	0	0	0	0	0			
102	0	0	0	0	0	0	0	0		endoplasmic reticulum;	
103	0	0	0	0	0	0	0	0	Predicted		hydrolase activity
104	0	0	0	0	0	0	0	0	Protein of unknown function		
105	0	0	0	0	0	0	0	0			
106	0	0	0	0	0	0	0	0	Dephospho-coenzyme A		ATP binding; kinase activity
107	0	0	0	0	0	0	0	0			
108	0	0	0	0	0	0	0	0		integral to membrane;	
109	0	0	0	0	0	0	0	0	Domain of unknown	integral to membrane;	nucleotide binding
110	0	0	0	0	0	0	0	0	Guanylate-binding protein		GTP binding; GTPase
111	0	0	0	0	0	0	0	0			
112	0	0	0	0	0	0	0	0			
113	0	0	0	0	0	0	0	0		integral to membrane;	
114	0	0	0	0	0	0	0	0		integral to membrane;	
115	0	0	0	0	0	0	0	0		integral to membrane;	
116	0	0	0	0	0	0	0	0	A subfamily of Peptidase	nucleus	cysteine-type endopeptidase
117	0	0	0	0	0	0	0	0	ankyrin repeats; ankyrin	integral to membrane;	acyltransferase activity;
118	0	0	0	0	0	0	0	0	Frizzled/Smoothened family	integral to membrane;	
119	0	0	0	0	0	0	0	0	DHHC zinc finger domain.	integral to membrane;	acyltransferase activity;
120	0	0	0	0	0	0	0	0			
121	0	0	0	0	0	0	0	0			
122	0	0	0	0	0	0	0	0	Fibronectin type 3 domain;	integral to membrane;	receptor activity
123	0	0	0	0	0	0	0	0			malate dehydrogenase
124	0	0	0	0	0	0	0	0			
125	0	0	0	9.65E-05	0	0	0	0.000163		integral to membrane	
126	0	0	0	0	0	0	0	0	Domain of unknown		
127	0	0	0	0	0	0.00024	0	0	Protein of unknown function	integral to membrane;	
128	0	0	0	0	0	0	0	0		integral to membrane;	
129	0	0	0	0	0	0	0	0	Protein of unknown function	integral to membrane	
130	0	0	0	0	0	0	0	0	SNARE associated Golgi	integral to membrane	
131	0	0	0	0	0	0	0	0	Protein of unknown function		
132	0	0	0	0	0	0	0	0		integral to membrane;	
133	0	0	0	0	0	0	0	0			
134	0	0	0	0	0	0	0	0		nucleus [pmid 10873651]	N-acetyltransferase activity;
135	0	0	0	0	0	0	0	0		integral to membrane;	
136	0	0	0	0	0	0	0	0		integral to membrane;	transferase activity
137	0	0	0	0	0	0	0	0	Protein of unknown function	integral to membrane	
138	0	0	0	0	0	0	0	0			
139	0	0	0	0	0	0	0	0	Rft protein; pfam04506	integral to membrane	lipid transporter activity
140	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane; integral	MHC class I receptor activity
141	0	0	0.000338	0.000133	0	5.09E-05	0	2.49E-05	Fibronectin type 3 domain;	focal adhesion; integral to	hydrolase activity; protein
142	0	0	0	0.00025	0.000332	0.000151	4.49E-05	0	TAP, the Transporter	endoplasmic reticulum;	ATP binding; ATPase
143	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane; integral	MHC class I receptor activity
144	0	0	0	0	0	0	0	0	AIG1 (avrRpt2-induced	endoplasmic reticulum;	GTP binding
145	0	0	0	0	0	0	0	0	Immunoglobulin C1-set	endoplasmic reticulum [pmid	MHC class I protein binding
146	0	0	0	0	0	0	0	0	Immunoglobulin domain	axonemal dynein complex	MHC class I receptor activity
147	0	0	0.000359	0	0	0	0	0	Integrins are a class of	integral to membrane; integrin	calcium ion binding;
148	0	0	0.000135	0.000132	0	9.14E-05	0	0	Sterile alpha motif.	endoplasmic reticulum;	calcium ion binding [pmid
149	0	0	0	7.65E-05	0	1.8E-05	0	0	haloacid dehalogenase-like	integral to plasma membrane	ATP binding; ATPase
150	0	0	0	0	0	0	0	0			
151	0	0	0	0	0	0	0	0			
152	0	0	0	4.72E-05	0	0.000143	0	0	Integrin beta subunits (N-	integral to membrane; integrin	protein binding [pmid
153	0	0	0	0.00035	8.44E-05	0.000192	5.71E-05	0	Ferric reductase like	integral to plasma membrane	FAD binding; iron ion binding;
154	0	0	0	0	0	0	0	0	Oligosaccharyl transferase	membrane; oligosaccharyl	dolichyl-
155	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane;	MHC class I receptor activity
156	0	0	0	0.000284	0	6.14E-05	0.000128	0	Immunoglobulin domain	integral to plasma membrane	MHC class II receptor
157	0	0	0	0	0	0	0	0	Band_7_stomatin_like: A	cytoskeleton [pmid 7592848];	
158	0	0	0	0	0	0	0	0	Integrin beta subunits (N-	integrin complex [pmid	identical protein binding
159	0	0	0	0	0	0	0	0	emp24/gp25L/p24	ER-Golgi intermediate	
160	0	0	0	8.68E-05	0	3.74E-05	0	0			
161	0	0	0	0	0	0	0	0	Protein tyrosine	cytoplasm; endoplasmic	hydrolase activity; protein
162	0	0	0	0	0	0	0	0	Histone 2A; H2A is a	chromosome; nucleosome;	DNA binding
163	0	0	0	0	0	0	0	0	acyl-CoA synthase;	integral to membrane;	ligase activity; nucleotide
164	0	0	0	0	0	0	0	0	This domain is a	integral to plasma membrane	collagen binding [pmid
165	0	0	7.52E-05	0	0	7.64E-05	0	0	Fibronectin Type II domain:	integral to membrane;	binding
166	0	0	0	0	0	0	0	0			
167	0	0	0	0	0	0	0	0	NADH-ubiquinone		
168	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane;	MHC class II receptor
169	0	0	0	0	0	0	0	0			
170	0	0	0	0	0	0	0	0			
171	0	0	0	0	0	5.13E-05	0	0	Oxidoreductase NAD-		oxidoreductase activity
172	0	0	0.000166	0.000196	0.000173	0.000113	0.000117	0			
173	0	0	0	0	0	0	0	0	Trypsin-like serine	cell surface [pmid 12114510];	bacterial binding [pmid
174	0	0	0	0	0	0	0	0	Signal recognition particle	endoplasmic reticulum;	GTP binding; nucleotide
175	0	0	0	0	0	0	0	0	Acyl-CoA cholesterol	endoplasmic reticulum [pmid	acyltransferase activity
176	0	0	0.000227	8.91E-05	0	7.69E-05	0.00016	0			
177	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane; integral	MHC class II receptor
178	0	0	0	1.58E-05	0	0	0	0	Integrins are a class of	integral to membrane; integrin	calcium ion binding;
179	0	0	0	0	0	0	0	0	Cytochrome b5-like	cell surface [pmid 12493773];	lipid binding; receptor
180	0	0	0	0	0	0	0	0		chromosome; nucleosome;	DNA binding [pmid 2587254];
181	0	0	0	0	0	0	0	0	Peptidase family M1.	integral to plasma membrane	aminopeptidase activity
182	0	0	0	0	0	0	0	0	Integrins are a class of	integral to membrane; integrin	calcium ion binding;
183	0	0	0	8.34E-05	0.000111	7.2E-05	0	0	GPI transamidase subunit	endoplasmic reticulum;	GPI anchor binding [pmid
184	0	0	0.000149	0	0	5.03E-05	0	0	Miro1 subfamily. Miro	integral to membrane; integral	calcium ion binding; GTP
185	0	0	5.77E-05	0.000113	6E-05	3.9E-05	0	0	FtsH Extracellular. This	integral to membrane;	ATP binding; metal ion
186	0	0	0	0	0	2.57E-05	0	0			
187	0	0	0	0	0	0	0.000168	0	Gpi16 subunit, GPI	endoplasmic reticulum; GPI-	GPI-anchor transamidase
188	0	0	0	0	0	0	0	0	Tetraspanin, extracellular	integral to membrane; integral	protein binding [pmid
189	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane;	MHC class II receptor
190	0	0	0	2.52E-05	0	0	0	0	Long-chain acyl-CoA	integral to membrane;	fatty-acyl-CoA synthase
191	0	0.000141	0	0	0	0	0	0			
192	0	0	0	7.42E-06	3.5E-05	0	0	0			
193	0	0	0	0	0	0	0	0			
194	0	0	0	5.79E-05	0	6.66E-05	3.47E-05	3.26E-05	Reticulon. Reticulon, also	endoplasmic reticulum;	
195	0	0	0	0	0	0	0	0		integral to plasma membrane	kinase binding [pmid
196	0	0	0	0	0	0	0	0	emp24/gp25L/p24	endoplasmic reticulum;	
197	0	0	0	0	0	0	0	0	Leucine rich repeat C-	integral to plasma membrane	protein binding [pmid
198	0	0	0	0.000189	0	8.15E-05	0	0	Cytochrome Cytochrome	membrane; mitochondrion	electron carrier activity [pmid
199	0	0	0	0	0	0	0	0	Tricarboxylate carrier;		
200	0	0	0	0	0	0	0	0	Dehydrogenases with	endoplasmic reticulum [pmid	oxidoreductase activity
201	0	0	0	0	0	0	0	0	CLIP, MHC2 interacting.	integral to membrane [pmid	cytokine binding [pmid
202	0	0	0	0	0	0	0	0		integral to plasma membrane;	
203	0	0	0	0	0	0	0	0	TspO/MBR family.	integral to membrane;	benzodiazepine receptor
204	0	0	0	0	0	0	0	0	Dehydrogenases with	endoplasmic reticulum;	3-dehydrosphinganine
205	0	0	0	0	0	0	0	0	Scavenger receptor	integral to plasma membrane	protein binding [pmid
206	0	0	0	0	0	0	0	0		integral to membrane;	
207	0	0	0	0	0	0	0	0	Mpv17 / PMP22 family. The	integral to membrane; integral	
208	0	0	0	0	0	0	0	0.000248			
209	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane;	MHC class II receptor
210	0	0	0	0	0	0	0	0	Apoptosis regulator	endoplasmic reticulum;	identical protein binding
211	0	0	0	5.51E-05	0	0	0	0	SCAMP family; pfam04144	integral to membrane;	
212	0	0	0	0	0	0	0	0	ATP synthase subunit C;	membrane; membrane	hydrogen-transporting ATP
213	0	0	0	0	0	0	0	0	7 transmembrane receptor	integral to plasma membrane	calcium ion binding; G-
214	0	0	0	0	0	0	0	0	Longevity-assurance	endoplasmic reticulum [pmid	receptor activity [pmid
215	0	0	0	0	0	0	0	0	Cation-dependent mannose	cell surface [pmid 12493773];	mannose binding; mannose
216	0	0	0	0	0	0	0	0			
217	0	0	0	0	0	0	0	0		integral to membrane;	protein binding [pmid
218	0	0	0	0	0	0	0	0			
219	0	0	6.9E-05	0	0	2.34E-05	0	0	Long-chain acyl-CoA	integral to membrane;	ligase activity; long-chain-
220	0	0	0	0	0	0	0	0			
221	0	0	0	0	0	0	0	0	Immunoglobulin V-set	integral to membrane;	protein binding
222	0	0	0	0	0	0	0	0	Apolipoprotein L. Apo L	extracellular region;	high-density lipoprotein
223	0	0	0	0	0	0	0	0	Domain in SPla and the	integral to membrane;	
224	0	0	0	0	0	0	0	0			
225	0	0	0	0	0	0	0	0	Leucine-rich repeats	PML body [pmid 16449650]	transferase activity
226	0	0	0	0	0	0	0	0	N-acetylglucosaminyl	integral to membrane;	phosphatidylinositol N-
227	0	0	0	0	0	0	0	0	homolog to co-chaperone		cysteine-type endopeptidase
228	0	0	0	0	0	0	0	0	Mitochondrial carrier	integral to membrane; integral	adenine transporter activity
229	0	0	0	0	0	0	0	0	Peptidyl-tRNA hydrolase,	chromosome, pericentric	aminoacyl-tRNA hydrolase
230	0	0	0	0	0	0	0	0		cytoplasm [pmid 11390434];	protein binding [pmid
231	0	0	0	0	0	0	0	0	Soluble NSF (N-	endoplasmic reticulum [pmid	
232	0	0	0	0	0	0	0	0	Immunoglobulin C-2 Type;	external side of plasma	protein heterodimerization
233	0	0	0	0	0	0	0	0	MAS20 protein import	integral to membrane;	protein translocase activity
234	0	0	0	0	0	0	0	0	Leucine rich repeat C-	integral to plasma membrane	protein binding; transferase
235	0	0	0	0	0	0	0	0			
236	0	0	0	0	0	0	0	0	Divalent cation transporter.		cation transporter activity;
237	0	0	0	0	0	0	0	0	Sodium / potassium	integral to membrane;	potassium ion binding;
238	0	0	0	0	0	0	0	0	Immunoglobulin domain cell	integral to plasma membrane	integrin binding [pmid
239	0	0	0	6.55E-05	0	0.00017	0	0			
240	0	0	0.000173	0	0	3.9E-05	0	0	ClC-6-like chloride channel	integral to plasma membrane;	chloride ion binding; voltage-
241	0	0	0	0	0	0	0	0	Nucleoside-diphosphate-	integral to membrane;	coenzyme binding; lyase
242	0	0	0	0	0	0	0	0	Apoptosis regulator	integral to membrane;	identical protein binding
243	0	0	0	0	0	0.000122	0	0		mitochondrion	NADH dehydrogenase
244	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane;	MHC class II receptor
245	0	0	0	0	0	0.000165	0	0	7-keto-8-aminopelargonate	endoplasmic reticulum;	acyltransferase activity;
246	0	0	0	0	0	0	0	0	Mitochondrial carrier	integral to membrane;	binding; PDZ domain binding;

																					RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs										
rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
247	3	0.000135	0	0	INF		ENSG00000033011:E	ALG1			gi|41350216|ref|NP_	beta-1,4-mannosyltransferas	464	52518	7.2	1	i5-23o	S	22	0.998	0	0.000704	0	0	0	1	0.000176	0.000352	0	0.00029	0	0	8.27E-05	2	9.32E-05	0.000137	0	0	0	0	0	0	0	0	Glycosyl transferases	endoplasmic reticulum;	chitobiosyldiphosphodolichol
248	3	0.000122	1	4.96E-06	24.67023		ENSG00000010610:E	CD4			gi|10835167|ref|NP_	CD4 antigen precursor [Hom	458	51111	9.5	1	o398-420i	S	26	1	0	0.000611	0	0.00027	0	2	0.00022	0.00029	0	9.8E-05	0	0	0	1	2.45E-05	4.9E-05	0	0	0	3.97E-05	0	0	0	0	CD4, extracellular.	integral to membrane; plasma	coreceptor activity [pmid
249	3	0.000108	0	0	INF		ENSG00000155463:E	OXA1L			gi|4826880|ref|NP_0	oxidase (cytochrome c) asse	495	55298	9.7	4	o198-220i2	Q	55	0.066	0	0.000283	0	0	0	1	7.07E-05	0.000141	0	0.000272	0	0	0.00031	2	0.000146	0.000169	0	0	0	0	0	0	0	0	Preprotein translocase	integral to membrane;	
250	3	9.56E-05	1	1.78E-05	5.384833		ENSG00000011478:E	QPCTL			gi|92110027|ref|NP_	glutaminyl-peptide cyclotrans	382	42924	9.8	1	i33-55o	A	48	0.109	0	0.000366	0	4.62E-05	0	2	0.000103	0.000177	0	0.000352	0	0	0	1	8.81E-05	0.000176	0	0	0	0.000142	0	0	0	0	Peptidase family M28;		peptidase activity;
251	3	9.18E-05	0	0	INF		ENSG00000198053:S	SIRPA			gi|91105767|ref|NP_	signal-regulatory protein alph	504	54967	7	1	o372-394i	S	31	1	0.000644	4.63E-05	0	0	0	2	0.000172	0.000315	0	4.45E-05	0	0	0	1	1.11E-05	2.23E-05	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane; plasma	
252	3	8.8E-05	1	9.34E-06	9.425772		ENSG00000182220:E	ATP6AP2			gi|15011918|ref|NP_	ATPase, H+ transporting, lys	350	39008	6.1	1	o309-331i	S	17	1	0	0.000333	0	5.05E-05	0	2	9.59E-05	0.00016	0	0.00032	0	0	0	1	8.01E-05	0.00016	0	0	0	0	0	0	7.47E-05	0	Renin receptor-like protein.	integral to membrane;	receptor activity
253	3	8.51E-05	1	1.26E-05	6.755208		ENSG00000197858:E	GPAA1			gi|4504079|ref|NP_0	glycosylphosphatidylinositol	621	67623	8.1	7	o20-42i365	A	47	0.018	0	0.000263	0	5.69E-05	0	2	8E-05	0.000125	0	0.000361	0	0	0	1	9.03E-05	0.000181	0	0	0	0	0	0.000101	0	0	Gaa1-like, GPI	endoplasmic reticulum; GPI-	GPI anchor binding [pmid
254	3	8.29E-05	0	0	INF		ENSG00000139133:E	ALG10			gi|147904264|ref|NP	asparagine-linked glycosylati	473	55606	9.3	11	o5-27i61-8	S	31	0.936	0	0.000345	0	0	0	1	8.63E-05	0.000173	0	0.000237	0	0	8.12E-05	2	7.96E-05	0.000112	0	0	0	0	0	0	0	0			
255	3	8.26E-05	0	0	INF		ENSG00000062716:E	TMEM49			gi|20070349|ref|NP_	transmembrane protein 49 [H	406	46238	6.9	6	i44-63o78-	Q	0	0	0	0.000172	0	0	0	1	4.31E-05	8.62E-05	0	0.000111	0	0	0.000378	2	0.000122	0.000178	0	0	0	0	0	0	0	0	SNARE associated Golgi	endoplasmic reticulum [pmid	
256	3	8.25E-05	0	0	INF		ENSG00000182858:E	ALG12			gi|13129114|ref|NP_	asparagine-linked glycosylati	488	54655	9.6	11	i12-31o63-	S	26	0.969	0	0.000239	0	0.000145	0	2	9.59E-05	0.000117	0	0.000276	0	0	0	1	6.9E-05	0.000138	0	0	0	0	0	0	0	0	Alg9-like	endoplasmic reticulum;	transferase activity,
257	3	8.01E-05	1	6.87E-06	11.6479		ENSG00000204427:E	BAT5			gi|15100151|ref|NP_	HLA-B associated transcript	558	63243	8.1	2	o60-82i95-	Q	14	0	0	0.000376	0	6.33E-05	0	2	0.00011	0.00018	0	0.000201	0	0	0	1	5.03E-05	0.000101	0	0	0	0	0	0	0	5.50E-05	alpha/beta hydrolase fold.	integral to membrane;	protein binding [pmid
258	3	7.84E-05	0	0	INF		ENSG00000164171:E	ITGA2			gi|116295258|ref|NP	integrin alpha 2 precursor [H	1181	129296	5.3	1	o1132-115	S	30	0.999	0.000549	5.92E-05	0	0	0	2	0.000152	0.000266	0	1.9E-05	0	0	0	1	4.75E-06	9.5E-06	0	0	0	0	0	0	0	0			
259	3	7.66E-05	0	0	INF		ENSG00000135776:E	ABCB10			gi|9961244|ref|NP_0	ATP-binding cassette, sub-fa	738	79099	9.9	5	o171-193i2	S	39	0.767	0	0.00019	0	0	0	1	4.74E-05	9.48E-05	0	0.000319	0	0	0.000104	2	0.000106	0.00015	0	0	0	0	0	0	0	0	MTABC3 (also known as	ATP-binding cassette (ABC)	ATP binding [pmid
260	3	7.32E-05	0	0	INF		ENSG00000079385:N	CEACAM1			gi|19923195|ref|NP_	carcinoembryonic antigen-re	526	57560	6	1	o433-455i	S	35	0.999	0	0.000177	0	6.72E-05	0	2	6.11E-05	8.37E-05	0	0.000341	0	0	0	1	8.53E-05	0.000171	0	0	0	0	0	0	0	0		integral to membrane; integral	
261	3	7.28E-05	0	0	INF		ENSG00000187688:E	TRPV2			gi|20127551|ref|NP_	transient receptor potential c	764	85981	5.8	6	i391-413o4	Q	18	0	0	6.11E-05	0.000492	0	0	2	0.000138	0.000237	0	2.94E-05	0	0	0	1	7.34E-06	1.47E-05	0	0	0	0	0	0	0	0	ankyrin repeats; ankyrin	integral to plasma membrane	calcium channel activity;
262	3	6.66E-05	0	0	INF		ENSG00000138678:E	PLCH			gi|21362092|ref|NP_	lysophosphatidic acid acyltra	434	48705	8.9	2	o10-32i156	S	30	0.909	0.000374	0.000107	0	0	0	2	0.00012	0.000176	0	5.17E-05	0	0	0	1	1.29E-05	2.58E-05	0	0	0	0	0	0	0	0	Acyltransferase. This family		acyltransferase activity
263	3	6.45E-05	0	0	INF		ENSG00000059804:N	GTR3			gi|5902090|ref|NP_0	solute carrier family 2 (facilita	496	53924	7.2	10	i9-31o63-8	S	22	0.743	0	4.7E-05	0.000379	0	0	2	0.000106	0.000183	0	9.05E-05	0	0	0	1	2.26E-05	4.52E-05	0	0	0	0	0	0	0	0	Sugar (and other)	integral to membrane;	glucose transporter activity
264	3	6.37E-05	0	0	INF		ENSG00000112303:N	VNN2			gi|17865814|ref|NP_	vanin 2 isoform 1 precursor [	520	58521	6.5	1	o499-518i	S	23	0.942	0	0.000269	0	6.79E-05	0	2	8.43E-05	0.000127	0	0.000173	0	0	0	1	4.31E-05	8.63E-05	0	0	0	0	0	0	0	0	Predicted amidohydrolase	membrane	GPI anchor binding;
265	3	5.1E-05	0	0	INF		ENSG00000109736:E	TETRAN			gi|20127440|ref|NP_	tetracycline transporter-like p	455	48351	9.6	10	i24-46o86-	A	57	0.179	0	0.000359	0	0	0	1	8.97E-05	0.000179	0	4.93E-05	0.001537	0	0	2	1.23E-05	2.47E-05	0	0	0	0	0	0	0	0	Arabinose efflux permease	integral to membrane [pmid	tetracycline transporter
266	3	4.99E-05	2	7.19E-06	6.934904		ENSG00000152270:E	PDE3B			gi|40254434|ref|NP_	phosphodiesterase 3B, cGMI	1112	124333	5.9	5	i80-102o11	Q	0	0	0	0.000189	0	0	0	1	4.72E-05	9.44E-05	0	0.000141	0	0	6.9E-05	2	5.26E-05	6.75E-05	0	0	0	0	4.34E-05	1.41E-05	0	0	Metal dependent	membrane	3',5'-cyclic-nucleotide
267	3	4.94E-05	0	0	INF		ENSG00000149218:E	ENDOD1			gi|148225659|ref|NP	endonuclease domain contai	500	55017	5.7	3	o342-364i4	S	22	0.998	0	0.00028	0	7.07E-05	0	2	8.76E-05	0.000132	0	4.49E-05	0	0	0	1	1.12E-05	2.24E-05	0	0	0	0	0	0	0	0			
268	3	4.89E-05	0	0	INF		ENSG00000110057:E	UNC93B1			gi|45580709|ref|NP_	unc-93 homolog B1 [Homo s	597	66631	7	12	i60-82o111	Q	19	0	0	3.91E-05	0.000315	0	0	2	8.84E-05	0.000152	0	3.76E-05	0	0	0	1	9.39E-06	1.88E-05	0	0	0	0	0	0	0	0	Eukaryotic protein of	integral to membrane;	
269	3	4.55E-05	0	0	INF		ENSG00000176454:E	AGPAT7			gi|87116681|ref|NP_	PLSC domain containing pro	524	57219	9	1	i40-62o	A	55	0.001	0	0	0	3.37E-05	0	1	8.43E-06	1.69E-05	0	0.000257	0	0	7.33E-05	2	8.25E-05	0.000121	0	0	0	0	0	0	0	0	Phosphate	endoplasmic reticulum;	1-acylglycerol-3-phosphate
270	3	4.44E-05	1	1.64E-06	27.03432		ENSG00000197081:E	IGF2R			gi|119964726|ref|NP	insulin-like growth factor 2 re	2491	274274	5.9	1	o2305-232	S	41	1	0	7.49E-05	0.000226	0	0	2	7.53E-05	0.000107	0	5.4E-05	0	0	0	1	1.35E-05	2.7E-05	0	0	0	0	0	0	1.31E-05	0			
271	3	2.92E-05	0	0	INF		ENSG00000127526:S	SLC35E1			gi|19923607|ref|NP_	solute carrier family 35, mem	266	30218	9.6	6	i21-40o44-	A	53	0.36	0	8.77E-05	0	0	0	1	2.19E-05	4.38E-05	0	8.43E-05	0	6.14E-05	0	2	3.64E-05	4.31E-05	0	0	0	0	0	0	0	0	Triose-phosphate	integral to membrane;	
272	3	2.9E-05	0	0	INF		ENSG00000134061:E	CD180			gi|5031895|ref|NP_0	CD180 molecule [Homo sapi	661	74165	6.4	1	o627-649i	S	19	0.962	0	0.000106	0	0	0	1	2.65E-05	5.29E-05	0	6.79E-05	0	0	5.81E-05	2	3.15E-05	3.66E-05	0	0	0	0	0	0	0	0	Leucine-rich repeats	integral to membrane; plasma	protein binding [pmid
273	3	2.78E-05	0	0	INF		ENSG00000126353:E	CCR7			gi|4502641|ref|NP_0	chemokine (C-C motif) recep	378	42874	8.5	7	o63-85i97-	S	25	0.99	0	6.17E-05	0	0	0	1	1.54E-05	3.09E-05	0	5.94E-05	0	0	0.000102	2	4.02E-05	4.95E-05	0	0	0	0	0	0	0	0	7 transmembrane receptor	integral to plasma membrane	C-C chemokine receptor
274	3	2.7E-05	1	5.36E-06	5.03415		ENSG00000109572:E	CLCN3			gi|55770838|ref|NP_	chloride channel 3 isoform b	818	90966	6.3	11	i128-150o2	Q	0	0	0	5.7E-05	0	2.16E-05	0	2	1.97E-05	2.69E-05	0	0.000137	0	0	0	1	3.43E-05	6.86E-05	0	0	0	0	0	0	4.29E-05	0	ClC-3-like chloride channel	cell surface [pmid 12471024];	chloride ion binding; PDZ
275	3	2.57E-05	0	0	INF		ENSG00000161513:E	FDXR			gi|111118981|ref|NP	ferredoxin reductase isoform	491	53837	8.4	0	o	A	36	0.214	0	0	0	3.6E-05	0	1	8.99E-06	1.8E-05	0	9.14E-05	0	0	7.82E-05	2	4.24E-05	4.92E-05	0	0	0	0	0	0	0	0			
276	3	2.09E-05	0	0	INF		ENSG00000102401:E	ARMCX3			gi|29540566|ref|NP_	armadillo repeat containing,	379	42501	8.4	1	i7-29o	S	24	0.807	0	6.15E-05	0	4.66E-05	0	2	2.7E-05	3.18E-05	0	5.92E-05	0	0	0	1	1.48E-05	2.96E-05	0	0	0	0	0	0	0	0	Protein of unknown function	integral to membrane;	binding
277	3	1.91E-05	0	0	INF		ENSG00000136213:E	CHST12			gi|8922112|ref|NP_0	carbohydrate (chondroitin 4)	414	48414	9.3	1	i7-26o	S	32	0.575	0	5.63E-05	0	4.27E-05	0	2	2.48E-05	2.91E-05	0	5.42E-05	0	0	0	1	1.35E-05	2.71E-05	0	0	0	0	0	0	0	0	Sulfotransferase.	integral to Golgi membrane	3'-phosphoadenosine 5'-
278	3	1.77E-05	0	0	INF		ENSG00000101425:E	BPI			gi|157276599|ref|NP	bactericidal/permeability-incr	487	53900	9.4	1	i16-38o	S	31	0.919	0	9.58E-05	0	0	0.000836	2	2.39E-05	4.79E-05	0	4.61E-05	0	0	0	1	1.15E-05	2.3E-05	0	0	0	0	0	0	0	0			
279	3	1.52E-05	0	0	INF		ENSG00000125746:E	EML2			gi|6912356|ref|NP_0	echinoderm microtubule asso	649	70679	6.3	1	i71-93o	Q	0	0	0	0	0	2.72E-05	0	1	6.8E-06	1.36E-05	0	6.91E-05	0	2.51E-05	0	2	2.36E-05	3.26E-05	0	0	0	0	0	0	0	0	HELP motif. The HELP	microtubule; microtubule	
280	3	1.45E-05	0	0	INF		ENSG00000137642:S	SORL1			gi|4507157|ref|NP_0	sortilin-related receptor conta	2214	248440	5.5	1	o2136-215	S	29	1	0	2.11E-05	0	2.39E-05	0	2	1.13E-05	1.3E-05	0	7.09E-05	0	0	0	1	1.77E-05	3.55E-05	0	0	0	0	0	0	0	0	Low Density Lipoprotein	integral to plasma membrane	lipid transporter activity;
281	3	1.36E-05	0	0	INF		ENSG00000139626:E	ITGB7			gi|4504777|ref|NP_0	integrin, beta 7 [Homo sapier	798	86903	6	1	o724-746i	S	20	1	0	5.85E-05	0	2.21E-05	0	2	2.01E-05	2.76E-05	0	2.81E-05	0	0	0	1	7.03E-06	1.41E-05	0	0	0	0	0	0	0	0	Integrin beta subunits (N-	integral to membrane; integrin	identical protein binding
282	3	1.29E-05	0	0	INF		ENSG00000185803:E	GPR172A			gi|13375682|ref|NP_	G protein-coupled receptor 1	445	45777	7.2	11	i9-31o46-6	S	26	0.999	0	5.24E-05	0	0	0.000916	2	1.31E-05	2.62E-05	0	5.04E-05	0	0	0	1	1.26E-05	2.52E-05	0	0	0	0	0	0	0	0	Protein of unknown function	integral to membrane;	receptor activity
283	2	0.000883	1	7.21E-05	12.25209		ENSG00000129562:E	DAD1			gi|4503253|ref|NP_0	defender against cell death 1	113	12497	7.1	3	o29-51i56-	A	42	0.005	0	0.000413	0.006651	0	0	2	0.001766	0.003262	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000576	0	DAD family. Members of	integral to membrane;	dolichyl-
284	2	0.000487	2	6.77E-05	7.196949		ENSG00000166471:E	TMEM41B			gi|66392190|ref|NP_	transmembrane protein 41B	291	32513	9.6	6	i50-72o113	A	65	0.001	0	0	0	0	0	0	0	0	0.003051	0.000848	0	0	0	2	0.000975	0.001441	0	0	0	0.000436	0	0	0	0.000105	SNARE associated Golgi	integral to membrane	
285	2	0.000477	1	5.07E-05	9.414569		ENSG00000099203:E	TMED1			gi|5803040|ref|NP_0	interleukin 1 receptor-like 1 li	227	25206	4.5	1	o193-215i	S	24	1	0	0	0.003311	0	0	1	0.000828	0.001655	0	0	0	0	0.000507	1	0.000127	0.000254	0	0	0	0	0	0	0	0.000406	emp24/gp25L/p24	integral to membrane;	receptor binding [pmid
286	2	0.000361	0	0	INF		ENSG00000136732:N	GYPC			gi|4504229|ref|NP_0	glycophorin C isoform 1 [Hon	128	13811	4.8	1	o59-81i	Q	26	0.263	0.002534	0	0	0	0	1	0.000633	0.001267	0	0.000351	0	0	0	1	8.76E-05	0.000175	0	0	0	0	0	0	0	0	putative band 4.1	cortical cytoskeleton [pmid	protein binding [pmid
287	2	0.000297	0	0	INF		ENSG00000108958:E	LOC100132717			gi|169162550|ref|XP	PREDICTED: hypothetical pr	135	14770	9.7	3	o40-62i69-	A	56	0.019	0	0.001209	0	0	0	1	0.000302	0.000605	0	0.001163	0	0	0	1	0.000291	0.000582	0	0	0	0	0	0	0	0			
288	2	0.000283	0	0	INF		ENSG00000114902:E	SPCS1			gi|66472394|ref|NP_	signal peptidase complex sul	102	11805	9.3	2	o20-42i47-	A	40	0.002	0	0.001601	0	0	0	1	0.0004	0.0008	0	0.00066	0	0	0	1	0.000165	0.00033	0	0	0	0	0	0	0	0	Microsomal signal	endoplasmic reticulum;	signal peptidase activity
289	2	0.000271	0	0	INF		ENSG00000164919:E	COX6C			gi|4758040|ref|NP_0	cytochrome c oxidase subun	75	8781	10.4	1	o20-37i	A	36	0.286	0	0.001866	0	0	0	1	0.000466	0.000933	0	0.000299	0	0	0	1	7.48E-05	0.00015	0	0	0	0	0	0	0	0	Cytochrome c oxidase	integral to membrane;	cytochrome-c oxidase
290	2	0.000231	0	0	INF		ENSG00000179344:N	HLA-DQB1			gi|150418002|ref|NP	major histocompatibility comp	261	29791	7.9	1	o232-251i	S	31	0.975	0	0.001072	0	0	0	1	0.000268	0.000536	0	0	0	0	0.000772	1	0.000193	0.000386	0	0	0	0	0	0	0	0			
291	2	0.000219	0	0	INF		ENSG00000165233:E	C9orf89			gi|92087058|ref|NP_	bcl10-interacting CARD prote	183	20626	8.1	1	i126-143o	Q	0	0	0	0.00102	0	0	0	1	0.000255	0.00051	0	0.000736	0	0	0	1	0.000184	0.000368	0	0	0	0	0	0	0	0		cytosol [pmid 15637807];	CARD domain binding [pmid
292	2	0.000205	0	0	INF		ENSG00000170906:N	NDUFA3			gi|4758772|ref|NP_0	NADH dehydrogenase (ubiqu	84	9279	8.5	1	o20-39i	A	30	0.16	0	0	0	0	0	0	0	0	0	0.000267	0	0	0.001371	2	0.00041	0.000653	0	0	0	0	0	0	0	0		integral to membrane;	NADH dehydrogenase
293	2	0.000182	0	0	INF		ENSG00000204310:E	AGPAT1			gi|15100175|ref|NP_	1-acylglycerol-3-phosphate C	283	31717	9.4	3	i7-29o39-5	S	29	0.994	0	0.000824	0	0	0	1	0.000206	0.000412	0	0.000634	0	0	0	1	0.000159	0.000317	0	0	0	0	0	0	0	0	Acyltransferase. This family	endoplasmic reticulum [pmid	1-acylglycerol-3-phosphate
294	2	0.000175	0	0	INF		ENSG00000158714:S	SLAMF8			gi|9910342|ref|NP_0	SLAM family member 8 [Hon	285	31670	6.2	1	o234-256i	S	24	0.999	0	0	0.001318	0	0	1	0.00033	0.000659	0	7.87E-05	0	0	0	1	1.97E-05	3.94E-05	0	0	0	0	0	0	0	0		integral to membrane;	
295	2	0.000152	0	0	INF		ENSG00000177674:E	AGTRAP			gi|93588491|ref|NP_	angiotensin II receptor-assoc	152	16669	6.3	3	o24-46i53-	S	34	0.597	0.001067	0	0	0	0	1	0.000267	0.000533	0	0.000148	0	0	0	1	3.69E-05	7.38E-05	0	0	0	0	0	0	0	0	Angiotensin II, type I	endoplasmic reticulum;	
296	2	0.000138	0	0	INF		ENSG00000129450:S	SIGLEC9			gi|23943856|ref|NP_	sialic acid binding Ig-like lecti	463	50082	7.3	1	o348-370i	S	18	0.976	0.001051	5.04E-05	0	0	0	2	0.000275	0.000518	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Immunoglobulin V-set	integral to plasma membrane	protein binding; sugar binding
297	2	0.000123	0	0	INF		ENSG00000142892:E	PIGK			gi|23199983|ref|NP_	phosphatidylinositol glycan a	395	45252	6.2	2	i7-29o364-	S	28	0.999	0	0.000531	0	0	0	1	0.000133	0.000266	0	0.000454	0	0	0	1	0.000114	0.000227	0	0	0	0	0	0	0	0	Glycosylphosphatidylinosito	endoplasmic reticulum; GPI-	GPI anchor binding [pmid
298	2	0.000122	0	0	INF		ENSG00000173762:E	CD7			gi|5453613|ref|NP_0	CD7 antigen precursor [Hom	240	25409	7.2	1	o178-200i	S	26	1	0	0.000194	0.000783	0	0	2	0.000244	0.000371	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane [pmid	receptor activity [pmid
299	2	0.000121	0	0	INF		ENSG00000143119:E	CD53			gi|91106727|ref|NP_	CD53 antigen [Homo sapiens	219	24341	7.5	4	i13-35o50-	A	30	0.174	0	0.000107	0.000858	0	0	2	0.000241	0.000414	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Tetraspanin, extracellular	integral to plasma membrane;	
300	2	0.000118	0	0	INF		ENSG00000149564:E	ESAM			gi|148664205|ref|NP	endothelial cell adhesion mol	390	41176	9.3	1	o248-270i	S	30	0.997	0.000832	0	0	0	0	1	0.000208	0.000416	0	0.000115	0	0	0	1	2.88E-05	5.75E-05	0	0	0	0	0	0	0	0			
301	2	0.000116	0	0	INF		ENSG00000143753:E	DEGS1			gi|21614501|ref|NP_	degenerative spermatocyte h	323	37866	7.5	6	o43-61i68-	A	0	0	0	0.000578	0	0	0	1	0.000144	0.000289	0	0.000347	0	0	0	1	8.68E-05	0.000174	0	0	0	0	0	0	0	0	The Delta4-sphingolipid	endoplasmic reticulum [pmid	electron carrier activity [pmid
302	2	0.000115	0	0	INF		ENSG00000197471:E	SPN			gi|71979937|ref|NP_	sialophorin [Homo sapiens]	400	40322	5.1	1	o255-277i	S	20	1	0	0.000583	0	0	0	1	0.000146	0.000292	0	0.000337	0	0	0	1	8.41E-05	0.000168	0	0	0	0	0	0	0	0	Herpes virus major outer	extracellular space [pmid	bacterial binding [pmid
303	2	0.000115	0	0	INF		ENSG00000007312:E	CD79B			gi|11038674|ref|NP_	CD79B antigen isoform 1 pre	229	26048	5.9	1	o161-180i	S	29	1	0	0	0.00082	0	0	1	0.000205	0.00041	0	9.8E-05	0	0	0	1	2.45E-05	4.9E-05	0	0	0	0	0	0	0	0	Immunoglobulin V-set	integral to plasma membrane	transmembrane receptor
304	2	0.000108	0	0	INF		ENSG00000203896:N	LIME1			gi|157388906|ref|NP	Lck interacting transmembrai	295	31288	9.6	1	o5-27i	S	31	0.999	0	0.000633	0	0	0	1	0.000158	0.000316	0	0.000228	0	0	0	1	5.7E-05	0.000114	0	0	0	0	0	0	0	0			
305	2	0.0001	0	0	INF		ENSG00000168384:N	HLA-DPA1			gi|24797074|ref|NP_	major histocompatibility comp	260	29381	5.2	1	i223-245o	S	32	0.995	0	0.000718	0	0	0	1	0.000179	0.000359	0	8.63E-05	0	0	0	1	2.16E-05	4.31E-05	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to plasma membrane	MHC class II receptor
306	2	0.0001	0	0	INF		ENSG00000213689:E	TREX1			gi|18375535|ref|NP_	three prime repair exonuclea	314	33212	7.9	1	o287-309i	Q	24	0.021	0	0.000371	0	0	0	1	9.29E-05	0.000186	0	0.000429	0	0	0	1	0.000107	0.000214	0	0	0	0	0	0	0	0	exonuclease domain in	nuclear envelope [pmid	3'-5'-exodeoxyribonuclease
307	2	9.8E-05	0	0	INF		ENSG00000134049:N	IER3IP1			gi|7705819|ref|NP_0	immediate early response 3 i	82	8969	8.3	1	o62-81i	S	19	0.991	0	0.000569	0	0.000215	0	2	0.000196	0.000268	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Yos1-like. In yeast, Yos1 is	endoplasmic reticulum [pmid	
308	2	9.19E-05	0	0	INF		ENSG00000013725:E	CD6			gi|51036598|ref|NP_	CD6 molecule [Homo sapien	668	71889	4.9	1	o402-424i	S	17	0.998	0	0.000454	0.000281	0	0	2	0.000184	0.000224	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Scavenger receptor	cell surface [pmid 12493773];	protein binding; scavenger
309	2	9.14E-05	0	0	INF		ENSG00000104894:E	CD37			gi|4502663|ref|NP_0	CD37 antigen isoform A [Hor	281	31703	8	4	i13-38o58-	A	34	0.008	0	0.000332	0	0	0	1	8.3E-05	0.000166	0	0.000399	0	0	0	1	9.98E-05	0.0002	0	0	0	0	0	0	0	0	Tetraspanin, extracellular	integral to membrane; integral	
310	2	8.95E-05	0	0	INF		ENSG00000089012:S	SIRPG			gi|94538335|ref|NP_	signal-regulatory protein gam	387	42498	7.2	1	o361-383i	S	29	1	0	0.000542	0	0	0	1	0.000136	0.000271	0	0.000174	0	0	0	1	4.35E-05	8.7E-05	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane;	
311	2	8.59E-05	0	0	INF		ENSG00000134285:E	FKBP11			gi|7706131|ref|NP_0	FK506 binding protein precu	201	22180	9.4	1	o155-177i	S	26	1	0	0.000464	0	0	0	1	0.000116	0.000232	0	0.000223	0	0	0	1	5.58E-05	0.000112	0	0	0	0	0	0	0	0	FKBP-type peptidyl-prolyl		isomerase activity; peptidyl-
312	2	8.07E-05	0	0	INF		ENSG00000113845:E	C3orf1			gi|59710109|ref|NP_	hypothetical protein LOC513	285	32178	8.5	1	o187-209i	S	25	0.991	0	0.000409	0	0	0	1	0.000102	0.000205	0	0.000236	0	0	0	1	5.9E-05	0.000118	0	0	0	0	0	0	0	0	Tim17/Tim22/Tim23 family.	mitochondrial inner	protein transporter activity
313	2	7.7E-05	0	0	INF		ENSG00000111711:N	GOLT1B			gi|7705636|ref|NP_0	golgi transport 1 homolog B [	138	15426	10.3	3	i13-30o34-	A	36	0.036	0	0	0	0.000128	0	1	3.2E-05	6.4E-05	0	0.000488	0	0	0	1	0.000122	0.000244	0	0	0	0	0	0	0	0	Got1-like family. Traffic	endoplasmic reticulum [pmid	signal transducer activity
314	2	7.61E-05	0	0	INF		ENSG00000158769:E	F11R			gi|21464111|ref|NP_	F11 receptor precursor [Hom	299	32583	7.9	2	i12-31o239	S	28	0.993	0	0.000234	0	0	0	1	5.85E-05	0.000117	0	0.000375	0	0	0	1	9.38E-05	0.000188	0	0	0	0	0	0	0	0	Immunoglobulin domain cell	cytoplasm [pmid 12817473];	thiosulfate sulfurtransferase
315	2	7.41E-05	0	0	INF		ENSG00000165678:E	GHITM			gi|118200356|ref|NP	growth hormone inducible tra	345	37205	9.9	6	i81-103o12	Q	25	0.493	0	0.000203	0	0	0	1	5.07E-05	0.000101	0	0.00039	0	0	0	1	9.75E-05	0.000195	0	0	0	0	0	0	0	0			
316	2	7.23E-05	0	0	INF		ENSG00000204273:E	HLA-DOB			gi|4504403|ref|NP_0	major histocompatibility comp	273	30822	6.8	1	o225-247i	S	22	0.984	0	8.54E-05	0	0	0	1	2.14E-05	4.27E-05	0	0.000493	0	0	0	1	0.000123	0.000247	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane;	MHC class II receptor
317	2	6.78E-05	0	0	INF		ENSG00000196296:E	ATP2A1			gi|10835220|ref|NP_	ATPase, Ca++ transporting,	994	109283	5.2	7	i60-79o84-	Q	24	0.004	0	0.000164	0.000378	0	0	2	0.000136	0.000179	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	haloacid dehalogenase-like	integral to membrane;	ATP binding; calcium ion
318	2	6.22E-05	0	0	INF		ENSG00000157036:E	ENDOGL1			gi|4826714|ref|NP_0	endonuclease G-like 1 [Hom	368	41127	8.3	1	i16-38o	S	35	0.804	0	0.000254	0	0	0	1	6.34E-05	0.000127	0	0.000244	0	0	0	1	6.1E-05	0.000122	0	0	0	0	0	0	0	0	DNA/RNA non-specific		endonuclease activity [pmid
319	2	6.05E-05	0	0	INF		ENSG00000213496:E	NDUFA11			gi|28269681|ref|NP_	NADH dehydrogenase (ubiqu	141	14852	8.7	4	i21-43o58-	Q	39	0.005	0	0.000165	0	0	0	1	4.14E-05	8.27E-05	0	0.000318	0	0	0	1	7.96E-05	0.000159	0	0	0	0	0	0	0	0		integral to membrane;	NADH dehydrogenase
320	2	6E-05	0	0	INF		ENSG00000174165:E	ZDHHC24			gi|46409316|ref|NP_	zinc finger, DHHC-type conta	284	30176	8.6	5	i17-39o54-	S	31	0.983	0	0.000164	0	0	0	1	4.11E-05	8.21E-05	0	0.000316	0	0	0	1	7.9E-05	0.000158	0	0	0	0	0	0	0	0	DHHC zinc finger domain.	integral to membrane;	acyltransferase activity;
321	2	5.43E-05	0	0	INF		ENSG00000109743:E	BST1			gi|4757874|ref|NP_0	bone marrow stromal cell ant	318	35738	7.8	1	i7-29o	S	33	1	0	0.000293	0	0	0	1	7.33E-05	0.000147	0	0.000141	0	0	0	1	3.53E-05	7.06E-05	0	0	0	0	0	0	0	0	ADP-ribosyl cyclase. ADP-	extrinsic to membrane [pmid	GPI anchor binding;
322	2	5.12E-05	0	0	INF		ENSG00000133195:S	SLC39A11			gi|21040273|ref|NP_	solute carrier family 39 (meta	335	34711	5.4	7	o10-32i39-	S	27	0.751	0	0.000209	0	0	0	1	5.22E-05	0.000104	0	0.000201	0	0	0	1	5.02E-05	0.0001	0	0	0	0	0	0	0	0	ZIP Zinc transporter. The	membrane	metal ion transporter activity
323	2	4.94E-05	0	0	INF		ENSG00000115902:S	SLC1A4			gi|21314632|ref|NP_	solute carrier family 1, memb	532	55723	6.3	9	i43-65o85-	A	60	0.131	0	0	0.000353	0	0	1	8.83E-05	0.000177	0	4.22E-05	0	0	0	1	1.05E-05	2.11E-05	0	0	0	0	0	0	0	0	Sodium:dicarboxylate	integral to plasma membrane	neutral amino acid
324	2	4.84E-05	0	0	INF		ENSG00000121966:E	CXCR4			gi|4503175|ref|NP_0	chemokine (C-X-C motif) rec	352	39746	8.2	7	o43-65i78-	Q	0	0	0	0.000133	0	0	0	1	3.31E-05	6.63E-05	0	0.000255	0	0	0	1	6.37E-05	0.000127	0	0	0	0	0	0	0	0	7 transmembrane receptor	integral to membrane;	C-C chemokine receptor
325	2	4.78E-05	0	0	INF		ENSG00000155189:E	AGPAT5			gi|61743952|ref|NP_	1-acylglycerol-3-phosphate C	364	42072	9.1	3	i13-35o55-	S	32	0.965	0	0.00032	0	0	0	1	8.01E-05	0.00016	0	6.16E-05	0	0	0	1	1.54E-05	3.08E-05	0	0	0	0	0	0	0	0	Phosphate	integral to membrane;	1-acylglycerol-3-phosphate
326	2	4.69E-05	0	0	INF		ENSG00000128228:E	SDF2L1			gi|56243533|ref|NP_	stromal cell-derived factor 2-	221	23598	7	1	i7-29o	S	29	1	0	0	0	7.99E-05	0	1	2E-05	4E-05	0	0	0	0.000295	0	1	7.38E-05	0.000148	0	0	0	0	0	0	0	0	Domain in ryanodine and	membrane	hydrolase activity
327	2	4.52E-05	0	0	INF		ENSG00000089060:S	SLC24A6			gi|39995086|ref|NP_	solute carrier family 24 memb	584	64232	8	13	o96-118i13	S	30	1	0	3.99E-05	0.000322	0	0	2	9.04E-05	0.000155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Sodium/calcium exchanger	integral to membrane;	antiporter activity; calcium
328	2	4.46E-05	0	0	INF		ENSG00000131779:E	PEX11B			gi|4505719|ref|NP_0	peroxisomal biogenesis facto	259	28431	9.8	1	o233-255i	Q	37	0.155	0	0.00027	0	0	0	1	6.75E-05	0.000135	0	8.66E-05	0	0	0	1	2.17E-05	4.33E-05	0	0	0	0	0	0	0	0	Peroxisomal biogenesis	integral to membrane; integral	protein binding [pmid
329	2	4.46E-05	0	0	INF		ENSG00000001561:E	ENPP4			gi|7662358|ref|NP_0	ectonucleotide pyrophosphat	453	51641	6.1	1	o406-428i	S	16	0.998	0	0.000257	0	0	0	1	6.44E-05	0.000129	0	9.91E-05	0	0	0	1	2.48E-05	4.95E-05	0	0	0	0	0	0	0	0	Type I phosphodiesterase /		hydrolase activity
330	2	4.35E-05	0	0	INF		ENSG00000126858:E	RHOT1			gi|75750470|ref|NP_	ras homolog gene family, me	618	70784	6.3	1	o593-615i	Q	31	0.001	0	0.000275	0	0	0	1	6.88E-05	0.000138	0	7.26E-05	0	0	0	1	1.82E-05	3.63E-05	0	0	0	0	0	0	0	0	Miro1 subfamily. Miro	integral to membrane; integral	calcium ion binding; GTP
331	2	4.3E-05	1	1.94E-06	22.21941		ENSG00000124406:E	ATP8A1			gi|157649069|ref|NP	ATPase, aminophospholipid	1149	129723	7.3	8	i298-320o3	Q	0	0	0.000141	0.000203	0	0	0	2	8.6E-05	0.000103	0	0	0	0	0	0	0	0	0	0	0	1.55E-05	0	0	0	0			
332	2	4.22E-05	0	0	INF		ENSG00000115232:E	ITGA4			gi|67191027|ref|NP_	integrin alpha 4 precursor [H	1032	114899	6.5	1	o978-1000	S	34	0.922	0	0.000294	0	0	0	1	7.35E-05	0.000147	0	4.35E-05	0	0	0	1	1.09E-05	2.17E-05	0	0	0	0	0	0	0	0		integral to membrane; integrin	calcium ion binding; identical
333	2	4.19E-05	0	0	INF		ENSG00000183605:E	SFXN4			gi|47458811|ref|NP_	sideroflexin 4 [Homo sapiens	337	37998	9.2	4	o134-153i1	Q	0	0	0	6.92E-05	0	0	0	1	1.73E-05	3.46E-05	0	0.000266	0	0	0	1	6.66E-05	0.000133	0	0	0	0	0	0	0	0	Tricarboxylate carrier;	integral to membrane;	cation transporter activity;
334	2	4.17E-05	0	0	INF		ENSG00000158201:E	ABHD3			gi|23397663|ref|NP_	alpha/beta hydrolase domain	409	46009	7.2	1	i26-48o	A	46	0.009	0	0.000114	0	0	0	1	2.85E-05	5.7E-05	0	0.000219	0	0	0	1	5.49E-05	0.00011	0	0	0	0	0	0	0	0	Predicted hydrolase of the		hydrolase activity
335	2	4.01E-05	0	0	INF		ENSG00000204252:E	HLA-DOA			gi|4504401|ref|NP_0	major histocompatibility comp	250	27599	5.9	1	o226-248i	S	26	0.994	0	0	0	0.000141	0	1	3.53E-05	7.07E-05	0	0.000179	0	0	0	1	4.49E-05	8.97E-05	0	0	0	0	0	0	0	0	Immunoglobulin domain	integral to membrane; plasma	MHC class II receptor
336	2	3.94E-05	0	0	INF		ENSG00000001630:E	CYP51A1			gi|4503243|ref|NP_0	cytochrome P450, family 51	509	57278	8.5	2	o4-21i28-5	S	22	0.999	0	0.000183	0	0	0	1	4.58E-05	9.16E-05	0	0.000132	0	0	0	1	3.31E-05	6.61E-05	0	0	0	0	0	0	0	0	Cytochrome P450.	integral to membrane;	heme binding; iron ion
337	2	3.81E-05	0	0	INF		ENSG00000087502:E	ERGIC2			gi|50959176|ref|NP_	PTX1 protein [Homo sapiens	377	42549	6.8	0	o	A	48	0	0	0.000186	0	0	0	1	4.64E-05	9.28E-05	0	0.000119	0	0	0	1	2.98E-05	5.95E-05	0	0	0	0	0	0	0	0	Protein of unknown function	endoplasmic reticulum; ER-	protein binding [pmid
338	2	3.73E-05	0	0	INF		ENSG00000012124:E	CD22			gi|157168355|ref|NP	CD22 molecule [Homo sapie	847	95348	6.7	1	o684-706i	S	22	0.996	0	0.000193	0	0	0	1	4.82E-05	9.64E-05	0	0.000106	0	0	0	1	2.65E-05	5.3E-05	0	0	0	0	0	0	0	0			
339	2	3.68E-05	0	0	INF		ENSG00000158850:E	B4GALT3			gi|4502349|ref|NP_0	UDP-Gal:betaGlcNAc beta 1	393	43928	9.3	1	i12-31o	A	30	0.303	0	0.000237	0	0	0	1	5.93E-05	0.000119	0	5.71E-05	0	0	0	1	1.43E-05	2.85E-05	0	0	0	0	0	0	0	0	Galactosyltransferase. This	integral to membrane;	beta-N-
340	2	3.65E-05	0	0	INF		ENSG00000011260:E	UTP18			gi|118344456|ref|NP	UTP18, small subunit proces	556	62004	8.8	0	o	A	65	0.001	0	0.000252	0	0	0	1	6.29E-05	0.000126	0	4.04E-05	0	0	0	1	1.01E-05	2.02E-05	0	0	0	0	0	0	0	0			
341	2	3.6E-05	0	0	INF		ENSG00000198818:S	SFT2D1			gi|21553317|ref|NP_	SFT2 domain containing 1 [H	159	17804	8.6	4	i37-59o64-	A	56	0	0	0.000147	0	0	0	1	3.67E-05	7.33E-05	0	0.000141	0	0	0	1	3.53E-05	7.06E-05	0	0	0	0	0	0	0	0	SFT2-like protein. This is a	integral to membrane;	
342	2	3.5E-05	0	0	INF		ENSG00000104972:E	LILRB1			gi|116488411|ref|NP	leukocyte immunoglobulin-lik	650	70819	6	1	o461-483i	S	24	0.998	0	0.000108	0	0	0	1	2.69E-05	5.38E-05	0	0.000173	0	0	0	1	4.31E-05	8.63E-05	0	0	0	0	0	0	0	0			
343	2	3.36E-05	0	0	INF		ENSG00000145817:E	YIPF5			gi|68226422|ref|NP_	Yip1 domain family, member	257	27989	4.4	4	o147-169i1	Q	0	0	0	0.000182	0	0	0	1	4.54E-05	9.08E-05	0	8.73E-05	0	0	0	1	2.18E-05	4.36E-05	0	0	0	0	0	0	0	0	Rab GTPase interacting	endoplasmic reticulum;	
344	2	3.34E-05	0	0	INF		ENSG00000088035:E	ALG6			gi|38026892|ref|NP_	asparagine-linked glycosylati	507	58121	8.5	10	i5-22o110-	S	23	0.962	0	4.6E-05	0	0	0	1	1.15E-05	2.3E-05	0	0.000221	0	0	0	1	5.53E-05	0.000111	0	0	0	0	0	0	0	0	ALG6, ALG8	endoplasmic reticulum;	glucosyltransferase activity
345	2	3.32E-05	0	0	INF		ENSG00000138185:E	ENTPD1			gi|147905700|ref|NP	ectonucleoside triphosphate	517	58706	6.7	2	i24-46o484	A	46	0.002	0	0.000135	0	0	0	1	3.38E-05	6.77E-05	0	0.00013	0	0	0	1	3.25E-05	6.51E-05	0	0	0	0	0	0	0	0			
346	2	3.32E-05	0	0	INF		ENSG00000162600:E	OMA1			gi|21686999|ref|NP_	OMA1 homolog, zinc metallo	524	60120	9.2	1	i195-217o	Q	41	0.001	0	0.000223	0	0	0	1	5.56E-05	0.000111	0	4.28E-05	0	0	0	1	1.07E-05	2.14E-05	0	0	0	0	0	0	0	0	Peptidase family M48;	membrane	metalloendopeptidase
347	2	3.31E-05	0	0	INF		ENSG00000103064:S	SLC7A6			gi|115648063|ref|NP	solute carrier family 7 (cation	515	56828	5.9	12	i45-67o77-	Q	23	0	0	9.06E-05	0	0	0	1	2.26E-05	4.53E-05	0	0.000174	0	0	0	1	4.36E-05	8.71E-05	0	0	0	0	0	0	0	0			
348	2	3.31E-05	0	0	INF		ENSG00000198689:S	SLC9A6			gi|110227626|ref|NP	solute carrier family 9 (sodiur	701	77917	6.4	12	i28-42o74-	S	43	0.997	0.000231	3.33E-05	0	0	0	2	6.62E-05	0.000111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
349	2	2.82E-05	0	0	INF		ENSG00000197217:E	ENTPD4			gi|4758662|ref|NP_0	ectonucleoside triphosphate	616	70255	8.3	2	i35-54o561	A	24	0.003	0	0.000189	0	0	0	1	4.73E-05	9.47E-05	0	3.64E-05	0	0	0	1	9.11E-06	1.82E-05	0	0	0	0	0	0	0	0	Golgi nucleoside	integral to Golgi membrane	calcium ion binding;
350	2	2.75E-05	0	0	INF		ENSG00000162300:E	ZFPL1			gi|33300635|ref|NP_	zinc finger protein-like 1 [Hor	310	34114	8.1	1	i265-287o	Q	25	0	0	7.52E-05	0	0	0	1	1.88E-05	3.76E-05	0	0.000145	0	0	0	1	3.62E-05	7.24E-05	0	0	0	0	0	0	0	0		integral to membrane;	DNA binding [pmid 9653652];
351	2	2.68E-05	0	0	INF		ENSG00000137575:S	SDCBP			gi|55749504|ref|NP_	syntenin isoform 2 [Homo sa	292	31762	7.5	1	o251-273i	Q	24	0	0	0	0	6.05E-05	0	1	1.51E-05	3.02E-05	0	0.000154	0	0	0	1	3.84E-05	7.68E-05	0	0	0	0	0	0	0	0	PDZ domain found in a	adherens junction [pmid	cytoskeletal adaptor activity
352	2	2.62E-05	0	0	INF		ENSG00000166734:E	CASC4			gi|29826289|ref|NP_	cancer susceptibility candida	436	49498	5.3	1	i13-35o	S	30	0.663	0	0.000107	0	0	0	1	2.67E-05	5.35E-05	0	0.000103	0	0	0	1	2.57E-05	5.15E-05	0	0	0	0	0	0	0	0	Chromosome segregation		
353	2	2.58E-05	0	0	INF		ENSG00000149541:E	B3GAT3			gi|12408654|ref|NP_	beta-1,3-glucuronyltransferas	335	37122	8.3	1	i7-29o	S	29	0.694	0	0.000139	0	0	0	1	3.48E-05	6.96E-05	0	6.7E-05	0	0	0	1	1.67E-05	3.35E-05	0	0	0	0	0	0	0	0	Beta1,3-	Golgi membrane; integral to	galactosylgalactosylxylosylpr
354	2	2.55E-05	0	0	INF		ENSG00000185862:E	EVI2B			gi|148227044|ref|NP	ecotropic viral integration site	448	48666	4.8	1	i203-225o	Q	19	0.175	0	0.000104	0	0	0	1	2.6E-05	5.21E-05	0	0.0001	0	0	0	1	2.5E-05	5.01E-05	0	0	0	0	0	0	0	0			
355	2	2.41E-05	2	4.7E-06	5.116448		ENSG00000102531:E	FNDC3A			gi|118918395|ref|NP	fibronectin type III domain co	1198	131852	6.7	1	o1175-119	Q	29	0.091	0	0.000136	0	0	0	1	3.41E-05	6.81E-05	0	5.62E-05	0	0	0	1	1.4E-05	2.81E-05	0	0	0	0	0	1.22E-05	2.54E-05	0			
356	2	2.38E-05	0	0	INF		ENSG00000125257:E	ABCC4			gi|157502201|ref|NP	ATP-binding cassette, sub-fa	1325	149526	8.2	11	i91-113o13	Q	35	0	0.000122	0	0	0	0	1	3.06E-05	6.12E-05	0	6.77E-05	0	0	0	1	1.69E-05	3.39E-05	0	0	0	0	0	0	0	0			
357	2	2.08E-05	0	0	INF		ENSG00000160013:E	PTGIR			gi|4506263|ref|NP_0	prostaglandin I2 (prostacyclir	386	40956	8.5	7	o15-37i49-	Q	35	0.251	0	0.000121	0	4.58E-05	0	2	4.17E-05	5.7E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7 transmembrane receptor	integral to plasma membrane	receptor activity; rhodopsin-
358	2	2.06E-05	0	0	INF		ENSG00000204420:E	C6orf25			gi|19913375|ref|NP_	G6B protein isoform G6b-B p	241	26163	9.6	1	o143-165i	S	18	0.999	0	9.68E-05	0	0	0	1	2.42E-05	4.84E-05	0	0	0	6.77E-05	0	1	1.69E-05	3.39E-05	0	0	0	0	0	0	0	0		endoplasmic reticulum;	receptor activity
359	2	2.02E-05	0	0	INF		ENSG00000163513:E	TGFBR2			gi|67782324|ref|NP_	transforming growth factor, b	567	64568	5.9	1	o167-189i	S	24	0.96	0	8.23E-05	0	0	0	1	2.06E-05	4.11E-05	0	7.91E-05	0	0	0	1	1.98E-05	3.96E-05	0	0	0	0	0	0	0	0	Transforming growth factor	integral to membrane;	ATP binding; magnesium ion
360	2	2E-05	0	0	INF		ENSG00000151651:E	ADAM8			gi|69354859|ref|NP_	ADAM metallopeptidase dom	856	92205	7.6	1	o656-678i	S	21	0.999	0	8.17E-05	0	0	0	1	2.04E-05	4.09E-05	0	7.86E-05	0	0	0	1	1.97E-05	3.93E-05	0	0	0	0	0	0	0	0	Zinc-dependent	integral to plasma membrane	metal ion binding;
361	2	1.98E-05	0	0	INF		ENSG00000178660:E	LOC389137			gi|169165133|ref|XP	similar to SVH protein isoforr	253	27688	7.2	1	o5-27i	S	24	0.984	0	0	0	6.98E-05	0	1	1.75E-05	3.49E-05	0	8.87E-05	0	0	0	1	2.22E-05	4.43E-05	0	0	0	0	0	0	0	0			
362	2	1.95E-05	0	0	INF		ENSG00000197540:E	GZMM			gi|4885369|ref|NP_0	granzyme M precursor [Hom	257	27446	10	1	i7-29o	S	24	0.998	0	0	0	6.87E-05	0	1	1.72E-05	3.44E-05	0	8.73E-05	0	0	0	1	2.18E-05	4.36E-05	0	0	0	0	0	0	0	0	Trypsin-like serine		serine-type endopeptidase
363	2	1.95E-05	0	0	INF		ENSG00000124532:E	MRS2L			gi|10190702|ref|NP_	MRS2-like, magnesium home	443	50318	6.9	2	o338-360i3	S	39	0.744	0	0.000105	0	0	0	1	2.63E-05	5.27E-05	0	5.06E-05	0	0	0	1	1.27E-05	2.53E-05	0	0	0	0	0	0	0	0	CorA-like Mg2+ transporter	integral to membrane;	DNA binding; magnesium ion
364	2	1.8E-05	0	0	INF		ENSG00000090520:E	DNAJB11			gi|7706495|ref|NP_0	DnaJ (Hsp40) homolog, subf	358	40514	6.2	1	i5-27o	S	23	0.982	0	0	0	9.87E-05	0	1	2.47E-05	4.93E-05	0	0	0	4.56E-05	0	1	1.14E-05	2.28E-05	0	0	0	0	0	0	0	0	DnaJ domain. DnaJ	endoplasmic reticulum [pmid	heat shock protein binding;
365	2	1.74E-05	0	0	INF		ENSG00000132965:E	ALOX5AP			gi|15718675|ref|NP_	arachidonate 5-lipoxygenase	161	18157	8.4	3	i7-26o71-9	A	28	0.094	0	0	0	0	0.002529	1	0	0	0	0.000139	0	0	0	1	3.48E-05	6.97E-05	0	0	0	0	0	0	0	0		integral to membrane;	binding [pmid 2300173];
366	2	1.73E-05	0	0	INF		ENSG00000162739:S	SLAMF6			gi|16418407|ref|NP_	activating NK receptor precu	331	37274	6.8	1	o226-248i	S	22	0.997	0	7.05E-05	0	0	0	1	1.76E-05	3.52E-05	0	6.78E-05	0	0	0	1	1.69E-05	3.39E-05	0	0	0	0	0	0	0	0	Immunoglobulin V-set	integral to membrane;	receptor activity
367	2	1.68E-05	1	2.69E-06	6.227928		ENSG00000185344:E	ATP6V0A2			gi|42741679|ref|NP_	ATPase, H+ transporting, lys	856	98082	6.6	6	o408-430i4	S	23	0.945	0	8.17E-05	0	0	0	1	2.04E-05	4.09E-05	0	5.24E-05	0	0	0	1	1.31E-05	2.62E-05	0	0	0	0	2.15E-05	0	0	0	V-type ATPase 116kDa	integral to membrane;	hydrogen ion transporter
368	2	1.67E-05	0	0	INF		ENSG00000128203:E	ASPHD2			gi|10092629|ref|NP_	aspartate beta-hydroxylase c	343	38855	7.3	0	o	A	22	0.007	0	6.8E-05	0	0	0	1	1.7E-05	3.4E-05	0	6.54E-05	0	0	0	1	1.64E-05	3.27E-05	0	0	0	0	0	0	0	0	Aspartyl/Asparaginyl beta-	integral to endoplasmic	peptide-aspartate beta-
369	2	1.59E-05	0	0	INF		ENSG00000182162:N	P2RY8			gi|30023826|ref|NP_	G-protein coupled purinergic	359	40635	9.5	6	o23-45i58-	Q	36	0.183	0	6.5E-05	0	0	0	1	1.62E-05	3.25E-05	0	6.25E-05	0	0	0	1	1.56E-05	3.12E-05	0	0	0	0	0	0	0	0	7 transmembrane receptor	integral to membrane;	purinergic nucleotide
370	2	1.54E-05	0	0	INF		ENSG00000136770:E	DNAJC1			gi|21361912|ref|NP_	DnaJ (Hsp40) homolog, subf	554	63883	8.6	1	i153-175o	S	48	0.997	0	4.21E-05	0	0	0	1	1.05E-05	2.11E-05	0	8.1E-05	0	0	0	1	2.02E-05	4.05E-05	0	0	0	0	0	0	0	0	'SWI3, ADA2, N-CoR and	endoplasmic reticulum;	ATPase stimulator activity
371	2	1.49E-05	0	0	INF		ENSG00000177239:N	MAN1B1			gi|7706437|ref|NP_0	alpha 1,2-mannosidase [Hon	699	79553	7.7	1	i86-105o	Q	27	0.035	0	0	0	0	0	0	0	0	0	6.42E-05	0	0	5.49E-05	2	2.98E-05	3.46E-05	0	0	0	0	0	0	0	0	Glycosyl hydrolase family	endoplasmic reticulum [pmid	calcium ion binding [pmid
372	2	1.45E-05	0	0	INF		ENSG00000065665:S	SEC61A2			gi|14589847|ref|NP_	Sec61 alpha form 2 [Homo s	476	52248	8.1	8	i33-55o75-	A	47	0.001	0	6.26E-05	0	0	0	1	1.57E-05	3.13E-05	0	5.33E-05	0	0	0	1	1.33E-05	2.67E-05	0	0	0	0	0	0	0	0	Preprotein translocase	endoplasmic reticulum;	protein translocase activity
373	2	1.44E-05	0	0	INF		ENSG00000006756:N	ARSD			gi|71852584|ref|NP_	arylsulfatase D isoform a pre	593	64860	7.2	3	i206-225o2	S	34	0.998	0	3.93E-05	0	0	0	1	9.83E-06	1.97E-05	0	7.57E-05	0	0	0	1	1.89E-05	3.78E-05	0	0	0	0	0	0	0	0	Arylsulfatase A and related	lysosome	arylsulfatase activity [pmid
374	2	1.24E-05	0	0	INF		ENSG00000213186:E	TRIM59			gi|27436877|ref|NP_	tripartite motif-containing 59	403	47114	6.8	1	o329-348i	Q	25	0	0	0	0	4.38E-05	0	1	1.1E-05	2.19E-05	0	5.57E-05	0	0	0	1	1.39E-05	2.78E-05	0	0	0	0	0	0	0	0	RING-finger (Really	integral to membrane;	metal ion binding; protein
375	2	1.24E-05	0	0	INF		ENSG00000081307:E	UBE1DC1			gi|13376212|ref|NP_	ubiquitin-activating enzyme 5	404	44863	4.8	1	i71-93o	Q	0	0	0	0	0	4.37E-05	0	1	1.09E-05	2.19E-05	0	5.55E-05	0	0	0	1	1.39E-05	2.78E-05	0	0	0	0	0	0	0	0	Dinucleotide-utilizing	cytoplasm [pmid 11256614]	catalytic activity;
376	2	1.17E-05	0	0	INF		ENSG00000023171:E	GRAMD1B			gi|144227752|ref|NP	GRAM domain containing 1B	738	85400	6.2	1	o624-646i	Q	19	0.007	0	6.32E-05	0	0	0	1	1.58E-05	3.16E-05	0	3.04E-05	0	0	0	1	7.6E-06	1.52E-05	0	0	0	0	0	0	0	0			
377	2	1.16E-05	0	0	INF		ENSG00000146828:S	SLC12A9			gi|31881740|ref|NP_	solute carrier family 12 (pota	914	96110	8.1	10	o41-63i76-	A	21	0.01	0	5.1E-05	0	0	0	1	1.28E-05	2.55E-05	0	0	0	0	4.2E-05	1	1.05E-05	2.1E-05	0	0	0	0	0	0	0	0	Gamma-aminobutyrate	integral to membrane [pmid	cation:chloride symporter
378	2	1.15E-05	0	0	INF		ENSG00000146555:S	SDK1			gi|119220552|ref|NP	sidekick 1 isoform 1 [Homo s	2213	242109	6.4	1	o2008-203	Q	18	0.018	0	0	8.49E-05	0	0	1	2.12E-05	4.24E-05	0	0	0	7.37E-06	0	1	1.84E-06	3.69E-06	0	0	0	0	0	0	0	0			
379	2	1.14E-05	0	0	INF		ENSG00000105963:E	CENTA1			gi|6806913|ref|NP_0	centaurin, alpha 1 [Homo sap	374	43425	9	0	o	A	22	0.01	0	0	0	4.72E-05	0	1	1.18E-05	2.36E-05	0	0	0	4.36E-05	0	1	1.09E-05	2.18E-05	0	0	0	0	0	0	0	0	Pleckstrin homology (PH)	cytoplasm [pmid 10333475]	ARF GTPase activator
380	2	1.11E-05	0	0	INF		ENSG00000085563:E	ABCB1			gi|42741659|ref|NP_	ATP-binding cassette sub-fan	1280	141478	9	10	i49-71o114	Q	0	0	0	3.64E-05	0	0	0	1	9.11E-06	1.82E-05	0	5.26E-05	0	0	0	1	1.31E-05	2.63E-05	0	0	0	0	0	0	0	0	MTABC3 (also known as	cell surface [pmid 12493773];	ATP binding [pmid 3768958];
381	2	9.68E-06	0	0	INF		ENSG00000105609:E	LILRB5			gi|125987591|ref|NP	leukocyte immunoglobulin-lik	591	64197	7.3	1	o458-480i	S	24	0.998	0	3.95E-05	0	0	0	1	9.87E-06	1.97E-05	0	3.8E-05	0	0	0	1	9.49E-06	1.9E-05	0	0	0	0	0	0	0	0			
382	2	9.58E-06	0	0	INF		ENSG00000071073:E	MGAT4A			gi|6912502|ref|NP_0	mannosyl (alpha-1,3-)-glycop	535	61544	7.4	1	i5-27o	S	23	0.656	0	4.36E-05	0	3.3E-05	0	2	1.92E-05	2.25E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	N-	membrane	alpha-1,3-
383	2	9.14E-06	0	0	INF		ENSG00000154118:E	JPH3			gi|21704283|ref|NP_	junctophilin 3 [Homo sapiens	748	81469	9.4	1	o725-747i	Q	27	0	0	0	0	0	0	0	0	0	0	0	0	2.18E-05	5.13E-05	2	1.83E-05	2.43E-05	0	0	0	0	0	0	0	0	Uncharacterized protein	endoplasmic reticulum;	
384	2	8.78E-06	0	0	INF		ENSG00000185245:E	GP1BA			gi|150417978|ref|NP	platelet glycoprotein Ib alpha	639	70248	6.5	1	o520-542i	S	17	1	0	0	0	0	0.000637	1	0	0	0	7.02E-05	0	0	0	1	1.76E-05	3.51E-05	0	0	0	0	0	0	0	0			
385	2	8.67E-06	0	0	INF		ENSG00000159640:E	ACE			gi|4503273|ref|NP_0	angiotensin I converting enzy	1306	149714	6.4	1	o1257-127	S	30	1	0	1.79E-05	0	0	0	1	4.46E-06	8.93E-06	0	5.15E-05	0	0	0	1	1.29E-05	2.58E-05	0	0	0	0	0	0	0	0	Angiotensin-converting	integral to membrane [pmid	carboxypeptidase activity;
386	2	7.69E-06	0	0	INF		ENSG00000040933:E	INPP4A			gi|4504705|ref|NP_0	inositol polyphosphate-4-pho	954	107297	6.9	1	o926-948i	Q	36	0.048	0	2.44E-05	0	3.7E-05	0	2	1.54E-05	1.85E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			hydrolase activity;
387	2	7.05E-06	0	0	INF		ENSG00000174123:N	TLR10			gi|62865621|ref|NP_	toll-like receptor 10 precurso	811	94564	6.8	1	o577-599i	S	20	0.638	0	2.88E-05	0	0	0	1	7.19E-06	1.44E-05	0	2.77E-05	0	0	0	1	6.92E-06	1.38E-05	0	0	0	0	0	0	0	0	Leucine-rich repeats	integral to membrane;	transferase activity;
388	2	7.04E-06	0	0	INF		ENSG00000133657:E	ATP13A3			gi|148839292|ref|NP	ATPase type 13A3 [Homo sa	1226	138043	6.6	10	i29-51o231	A	0	0	0	3.8E-05	0	0	0	1	9.51E-06	1.9E-05	0	1.83E-05	0	0	0	1	4.57E-06	9.15E-06	0	0	0	0	0	0	0	0			
389	2	5.76E-06	0	0	INF		ENSG00000165240:E	ATP7A			gi|115529486|ref|NP	ATPase, Cu++ transporting,	1500	163373	6.2	7	o654-673i7	Q	20	0.005	0	3.11E-05	0	0	0	1	7.77E-06	1.55E-05	0	1.5E-05	0	0	0	1	3.74E-06	7.48E-06	0	0	0	0	0	0	0	0			
390	2	4.79E-06	0	0	INF		ENSG00000169851:N	PCDH7			gi|14589931|ref|NP_	protocadherin 7 isoform a pre	1069	116071	5.2	2	i7-29o878-	S	31	1	0	2.18E-05	0	1.65E-05	0	2	9.59E-06	1.13E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Cadherin repeat domain;	integral to plasma membrane	calcium ion binding; protein
391	2	3.79E-06	0	0	INF		ENSG00000136531:E	SCN2A			gi|93141212|ref|NP_	sodium channel, voltage-gate	2005	227973	5.7	17	i126-148o2	Q	24	0	0	0	0	0	0	0	0	0	0	1.12E-05	0	0	1.91E-05	2	7.58E-06	9.34E-06	0	0	0	0	0	0	0	0	Ion transport protein. This	membrane; voltage-gated	calcium ion binding; sodium
392	2	2.98E-06	0	0	INF		ENSG00000177103:E	DSCAML1			gi|21359935|ref|NP_	Down syndrome cell adhesio	2113	230632	8.3	1	o1652-167	A	0	0	0	0	0	8.36E-06	0	1	2.09E-06	4.18E-06	0	0	0	1.54E-05	0	1	3.86E-06	7.72E-06	0	0	0	0	0	0	0	0	Paramyxovirus P	cell surface [pmid 11453658];	protein binding; protein
393	2	1.26E-06	0	0	INF		ENSG00000165323:N	FAT3			gi|148886692|ref|NP	protocadherin Fat 3; FAT tun	4557	501983	4.9	1	o4156-417	S	33	0.992	0	5.12E-06	0	0	0	1	1.28E-06	2.56E-06	0	4.92E-06	0	0	0	1	1.23E-06	2.46E-06	0	0	0	0	0	0	0	0			

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB
394	1	0.000746	0	0	INF		ENSG00000184076:N	UCRC			gi|41281885|ref|NP_	ubiquinol-cytochrome c reduc	63	7308	9.5	1	i13-32o	A	43	0.121
395	1	0.000569	0	0	INF		ENSG00000105374:E	NKG7			gi|5031949|ref|NP_0	natural killer cell group 7 seq	165	17665	6.4	4	i7-29o63-8	S	38	0.755
396	1	0.000561	0	0	INF		ENSG00000167754:E	KLK5			gi|117306176|ref|NP	kallikrein-related peptidase 5	293	32020	8.3	1	i7-29o	S	30	0.986
397	1	0.000439	0	0	INF		ENSG00000149516:E	MS4A3			gi|73486649|ref|NP_	membrane-spanning 4-doma	214	22933	5.3	4	i50-72o87-	Q	25	0.001
398	1	0.000414	0	0	INF		gi|169163403|ref|XP_	LOC100132060			gi|169163403|ref|XP	PREDICTED: hypothetical pr	170	17494	4.1	1	o5-27i	S	33	0.997
399	1	7.54E-05	0	0	INF		ENSG00000163519:E	TRAT1			gi|54607137|ref|NP_	T-cell receptor interacting mo	186	21211	5.4	1	o10-32i	S	26	0.612
400	1	7.52E-05	0	0	INF		ENSG00000206302:N	LOC100133583			gi|169168591|ref|XP	PREDICTED: similar to majo	261	29673	8.5	1	i231-253o	S	33	0.996
401	1	7.44E-05	0	0	INF		ENSG00000153563:E	CD8A			gi|22902134|ref|NP_	CD8 antigen alpha polypepti	235	25729	9.5	1	o184-206i	S	22	1
402	1	6.86E-05	0	0	INF		ENSG00000164047:E	CAMP			gi|39753970|ref|NP_	cathelicidin antimicrobial pep	170	19301	9.4	1	i13-35o	S	31	0.904
403	1	5.83E-05	0	0	INF		ENSG00000141524:E	TMC6			gi|23943902|ref|NP_	EVIN1 [Homo sapiens]	805	90079	8.7	10	o212-234i2	Q	17	0.013
404	1	5.83E-05	0	0	INF		ENSG00000117013:E	KCNQ4			gi|26638653|ref|NP_	potassium voltage-gated cha	695	77101	9.5	5	i99-121o13	Q	37	0.056
405	1	5.61E-05	0	0	INF		ENSG00000166091:E	CMTM5			gi|19923993|ref|NP_	chemokine-like factor superfa	156	17444	5.5	4	i35-56o60-	A	59	0
406	1	5.5E-05	0	0	INF		ENSG00000146066:E	HIGD2A			gi|20270389|ref|NP_	HIG1 domain family, membe	106	11529	10.2	2	o48-70i83-	Q	24	0
407	1	4.49E-05	0	0	INF		ENSG00000185885:N	IFITM1			gi|150010589|ref|NP	interferon induced transmem	125	13938	7.9	2	o37-59i85-	Q	21	0.001
408	1	4.37E-05	0	0	INF		ENSG00000116337:E	AMPD2			gi|21264318|ref|NP_	adenosine monophosphate d	879	100688	6.9	0	o	A	27	0.015
409	1	4E-05	0	0	INF		ENSG00000164054:E	SCOTIN			gi|21703710|ref|NP_	scotin [Homo sapiens]	240	25582	6.7	1	o106-128i	S	29	1
410	1	3.56E-05	0	0	INF		ENSG00000090661:E	LASS4			gi|13375717|ref|NP_	LAG1 homolog, ceramide sy	394	46399	9	5	o39-56i140	A	56	0.005
411	1	3.45E-05	1	6.71E-06	5.144154		ENSG00000120942:E	UBIAD1			gi|7019551|ref|NP_0	UbiA prenyltransferase doma	338	36831	8.2	7	i83-105o13	Q	22	0
412	1	3.4E-05	0	0	INF		ENSG00000204152:E	LOC653252			gi|113421523|ref|XP	PREDICTED: similar to MGC	257	28048	9.4	2	i74-96o123	Q	30	0.195
413	1	3.4E-05	0	0	INF		ENSG00000196785:E	APOL6			gi|13449281|ref|NP_	apolipoprotein L6 [Homo sap	343	38128	8.4	3	i79-101o11	Q	0	0
414	1	3.24E-05	0	0	INF		ENSG00000050426:E	LETMD1			gi|67089165|ref|NP_	LETM1 domain containing 1	360	41790	10.3	1	i139-161o	S	22	0.547
415	1	3.19E-05	0	0	INF		ENSG00000171135:E	JAGN1			gi|31982911|ref|NP_	jagunal homolog 1 [Homo sa	183	21155	9.7	3	i40-62o97-	A	59	0
416	1	3.09E-05	0	0	INF		ENSG00000153933:E	DGKE			gi|4503313|ref|NP_0	diacylglycerol kinase epsilon	567	63927	7.7	1	o20-42i	A	38	0.005
417	1	2.98E-05	0	0	INF		ENSG00000105369:E	CD79A			gi|11038672|ref|NP_	CD79A antigen isoform 2 pre	188	20786	4.6	2	i13-35o105	S	33	0.997
418	1	2.98E-05	0	0	INF		ENSG00000157916:E	RER1			gi|116812591|ref|NP	RER1 retention in endoplasm	196	22958	9.5	3	o39-61i63-	Q	0	0
419	1	2.95E-05	0	0	INF		ENSG00000198246:E	SLC29A3			gi|148596922|ref|NP	solute carrier family 29 (nucle	475	51815	7.8	11	i50-72o107	Q	0	0
420	1	2.93E-05	0	0	INF		ENSG00000033170:E	FUT8			gi|30410728|ref|NP_	fucosyltransferase 8 isoform	575	66516	7.7	1	i7-29o	S	28	0.533
421	1	2.6E-05	0	0	INF		ENSG00000106560:N	GIMAP2			gi|28416431|ref|NP_	GTPase, IMAP family membe	337	38017	8.2	2	i271-290o2	Q	35	0
422	1	2.51E-05	0	0	INF		ENSG00000100568:E	VTI1B			gi|5454166|ref|NP_0	vesicle transport through inte	232	26688	9	1	i207-229o	Q	0	0
423	1	2.34E-05	0	0	INF		ENSG00000163590:E	PPM1L			gi|63003905|ref|NP_	protein phosphatase 1 (forme	360	41053	5.9	0	o	A	38	0.009
424	1	2.25E-05	0	0	INF		ENSG00000173535:E	TNFRSF10C			gi|22547121|ref|NP_	tumor necrosis factor recepto	259	27395	4.8	2	i7-29o236-	S	24	0.981
425	1	2.22E-05	0	0	INF		ENSG00000100100:E	PIK3IP1			gi|51317358|ref|NP_	HGFL protein [Homo sapiens	263	28248	5	1	o169-191i	S	22	0.988
426	1	2.18E-05	0	0	INF		ENSG00000078124:E	PHCA			gi|19923527|ref|NP_	phytoceramidase, alkaline [H	267	31566	8.6	7	o29-51i63-	Q	22	0
427	1	2.15E-05	0	0	INF		ENSG00000122557:E	HERPUD2			gi|19923834|ref|NP_	HERPUD family member 2 [H	406	45177	5.1	1	o292-314i	Q	23	0
428	1	2.02E-05	0	0	INF		ENSG00000139370:E	SLC15A4			gi|21717816|ref|NP_	solute carrier family 15, mem	577	62034	9	13	o15-32i45-	S	36	0.899
429	1	1.82E-05	0	0	INF		ENSG00000160404:E	TOR2A			gi|145386578|ref|NP	torsin family 2, member A isc	321	35715	7.6	1	i12-31o	S	27	0.999
430	1	1.81E-05	0	0	INF		ENSG00000184292:E	TACSTD2			gi|4505057|ref|NP_0	tumor-associated calcium sig	323	35723	8.9	1	o275-297i	S	31	1
431	1	1.76E-05	0	0	INF		ENSG00000205060:E	SLC35B4			gi|14249528|ref|NP_	solute carrier family 35, mem	331	37424	9.1	9	o5-24i31-5	S	17	0.993
432	1	1.74E-05	0	0	INF		ENSG00000136816:E	TOR1B			gi|14149653|ref|NP_	torsin family 1, member B (to	336	37979	8.6	1	i21-43o	S	25	1
433	1	1.73E-05	0	0	INF		ENSG00000139826:E	ABHD13			gi|49355781|ref|NP_	abhydrolase domain containi	337	38548	8.6	2	o15-37i39-	A	55	0
434	1	1.66E-05	0	0	INF		ENSG00000103257:E	SLC7A5			gi|71979932|ref|NP_	solute carrier family 7 (cation	507	55010	7.7	11	i53-75o85-	Q	23	0
435	1	1.66E-05	0	0	INF		ENSG00000090432:E	C1orf166			gi|13375705|ref|NP_	mitochondrial ubiquitin ligase	352	39717	8.1	2	o10-29i242	S	24	0.713
436	1	1.62E-05	0	0	INF		ENSG00000105281:E	SLC1A5			gi|5032093|ref|NP_0	solute carrier family 1 (neutra	541	56598	5.5	9	i53-75o95-	A	36	0.001
437	1	1.57E-05	0	0	INF		ENSG00000174600:E	CMKLR1			gi|4758014|ref|NP_0	chemokine-like receptor 1 [H	371	42035	8.3	7	o39-61i74-	A	0	0
438	1	1.57E-05	0	0	INF		ENSG00000188404:E	SELL			gi|4506875|ref|NP_0	selectin L precursor [Homo s	372	42187	6.6	1	o333-355i	Q	39	0.133
439	1	1.55E-05	0	0	INF		ENSG00000119714:E	GPR68			gi|40217829|ref|NP_	G protein-coupled receptor 6	375	42088	8	7	o34-56i68-	Q	53	0.002
440	1	1.5E-05	0	0	INF		ENSG00000171044:E	XKR6			gi|89886484|ref|NP_	XK, Kell blood group comple:	641	71638	7.9	6	i130-149o1	Q	26	0.01
441	1	1.46E-05	0	0	INF		ENSG00000108405:E	P2RX1			gi|4505545|ref|NP_0	purinergic receptor P2X1 [Ho	399	44980	8.5	2	i29-51o335	A	51	0
442	1	1.44E-05	0	0	INF		ENSG00000178607:E	ERN1			gi|153946421|ref|NP	endoplasmic reticulum to nuc	977	109735	6.4	1	i7-29o	S	19	0.998
443	1	1.39E-05	0	0	INF		ENSG00000125875:E	TBC1D20			gi|21389447|ref|NP_	TBC1 domain family, membe	403	45855	6.9	2	o238-260i3	Q	0	0
444	1	1.38E-05	0	0	INF		ENSG00000204977:E	TRIM13			gi|47132524|ref|NP_	ret finger protein 2 isoform 1	407	46988	6	1	o319-341i	Q	25	0.001
445	1	1.36E-05	0	0	INF		ENSG00000181804:E	SLC9A9			gi|27734935|ref|NP_	solute carrier family 9 (sodiu	645	72565	6.2	10	o20-41i48-	A	41	0
446	1	1.28E-05	0	0	INF		ENSG00000157181:E	C1orf27			gi|57527756|ref|NP_	hypothetical protein LOC549	454	51103	5.9	1	o431-453i	Q	37	0.002
447	1	1.28E-05	0	0	INF		ENSG00000152291:N	TGOLN2			gi|42518068|ref|NP_	trans-golgi network protein 2	437	45880	5.6	1	o385-402i	S	16	1
448	1	1.22E-05	0	0	INF		ENSG00000198855:E	FICD			gi|42794620|ref|NP_	Huntingtin interacting protein	458	51778	7.7	1	i20-42o	S	40	0.914
449	1	1.21E-05	0	0	INF		ENSG00000134249:E	ADAM30			gi|31881770|ref|NP_	ADAM metallopeptidase dom	790	88940	7.6	1	o686-708i	S	28	0.994
450	1	1.19E-05	0	0	INF		ENSG00000163297:E	ANTXR2			gi|50513243|ref|NP_	anthrax toxin receptor 2 [Hon	488	53493	8.3	1	o319-341i	S	34	0.994
451	1	1.16E-05	0	0	INF		ENSG00000089351:E	GRAMD1A			gi|92110010|ref|NP_	GRAM domain containing 1A	724	80680	6.7	1	o608-630i	Q	36	0
452	1	1.13E-05	0	0	INF		ENSG00000120451:E	SNX19			gi|157502171|ref|NP	sorting nexin 19 [Homo sapie	992	108632	5	2	o29-51i53-	A	63	0.002
453	1	1.12E-05	0	0	INF		ENSG00000137462:E	TLR2			gi|19718734|ref|NP_	toll-like receptor 2 [Homo sap	784	89838	6.6	1	o588-610i	S	19	0.936
454	1	1.1E-05	0	0	INF		ENSG00000028116:E	VRK2			gi|71164884|ref|NP_	vaccinia related kinase 2 [Ho	508	58141	8.8	1	o487-506i	Q	0	0
455	1	1.02E-05	0	0	INF		ENSG00000100385:E	IL2RB			gi|4504665|ref|NP_0	interleukin 2 receptor beta pr	551	61117	5.1	2	o10-32i243	S	27	1
456	1	9.62E-06	0	0	INF		ENSG00000168685:E	IL7R			gi|28610151|ref|NP_	interleukin 7 receptor precurs	459	51579	5.4	1	o241-263i	S	21	0.979
457	1	9.59E-06	0	0	INF		ENSG00000153283:E	CD96			gi|38683840|ref|NP_	CD96 antigen isoform 1 prec	585	65634	7.1	1	o518-540i	Q	22	0.009
458	1	9.12E-06	0	0	INF		ENSG00000125999:E	C20orf114			gi|40807482|ref|NP_	LPLUNC1 protein precursor	484	52442	7.2	1	i7-29o	S	22	0.997
459	1	8.31E-06	0	0	INF		ENSG00000135392:E	DNAJC14			gi|119943096|ref|NP	dopamine receptor interactin	702	78569	8.1	2	o298-320i3	Q	32	0.001
460	1	8.02E-06	0	0	INF		ENSG00000091409:E	ITGA6			gi|119395740|ref|NP	integrin alpha chain, alpha 6	1091	122053	6.8	1	o1015-103	S	24	0.999
461	1	7.64E-06	0	0	INF		ENSG00000084234:E	APLP2			gi|4502147|ref|NP_0	amyloid beta (A4) precursor-	763	86956	4.8	2	i13-35o694	S	32	1
462	1	7.17E-06	0	0	INF		ENSG00000021574:E	SPAST			gi|11875211|ref|NP_	spastin isoform 1 [Homo sap	616	67197	9.6	1	i57-79o	Q	39	0.002
463	1	5.72E-06	0	0	INF		ENSG00000203710:N	CR1			gi|86793036|ref|NP_	complement receptor 1 isofo	2039	223675	6.9	1	o1974-199	S	42	0.979
464	1	5.6E-06	0	0	INF		ENSG00000136141:E	LRCH1			gi|33859670|ref|NP_	leucine-rich repeats and calp	728	80885	5.9	1	o704-726i	Q	41	0.345
465	1	4.88E-06	0	0	INF		ENSG00000196547:E	MAN2A2			gi|51477716|ref|NP_	mannosidase, alpha, class 2	1150	130538	6.8	1	i7-26o	A	22	0.148
466	1	4.75E-06	0	0	INF		ENSG00000159363:E	ATP13A2			gi|13435129|ref|NP_	ATPase type 13A2 [Homo sa	1180	128793	8.1	11	o45-67i236	Q	18	0.008
467	1	4.59E-06	0	0	INF		ENSG00000143515:E	ATP8B2			gi|40316837|ref|NP_	ATPase, class I, type 8B, me	1223	138719	6.9	9	o102-124i3	Q	26	0.389
468	1	4.47E-06	0	0	INF		ENSG00000111670:E	GNPTAB			gi|38202211|ref|NP_	N-acetylglucosamine-1-phos	1256	143621	7.2	2	i20-42o121	A	35	0.088
469	1	4.06E-06	0	0	INF		ENSG00000108582:E	CPD			gi|22202611|ref|NP_	carboxypeptidase D precurso	1380	152931	6	1	o1300-132	S	32	1
470	1	3.98E-06	0	0	INF		ENSG00000187790:E	FANCM			gi|74959747|ref|NP_	Fanconi anemia, complemen	2048	232190	6.1	1	i102-124o	Q	22	0.411
471	1	2.95E-06	0	0	INF		ENSG00000065618:E	COL17A1			gi|119829187|ref|NP	alpha 1 type XVII collagen [H	1497	150419	8.8	1	i467-489o	Q	0	0
472	1	2.28E-06	0	0	INF		ENSG00000103335:E	FAM38A			gi|169210119|ref|XP	PREDICTED: family with seq	2561	290660	7.5	30	i119-141o1	Q	28	0.022
473	1	0	0	0	INF		ENSG00000213918:E	DNASE1			gi|21361254|ref|NP_	deoxyribonuclease I precurso	282	31434	4.9	1	i7-29o	S	23	1
474	1	0	0	0	INF		ENSG00000076351:E	SLC46A1			gi|31543204|ref|NP_	proton-coupled folate transpo	459	49771	8.8	11	o85-107i11	S	45	0.456
475	1	0	0	0	INF		ENSG00000196950:E	SLC39A10			gi|55741750|ref|NP_	solute carrier family 39 (zinc	831	94132	6.8	7	o404-426i4	S	26	0.977
476	10	0.033733	2	0.001683	20.03996		ENSG00000075624:E	ACTB			gi|4501885|ref|NP_0	beta actin [Homo sapiens]	375	41737	5.5	0	o	Q	20	0
477	10	0.028573	3	0.000356	80.3237		ENSG00000198327:E	HIST2H4B			gi|77539758|ref|NP_	histone cluster 2, H4b [Homo	103	11367	11.4	0	o	Q	0	0
478	10	0.019888	0	0	INF		ENSG00000223609:N	HBB			gi|4504349|ref|NP_0	beta globin [Homo sapiens]	147	15998	7.3	0	o	Q	27	0
479	10	0.009913	6	0.000357	27.73958		ENSG00000196230:E	TUBB			gi|29788785|ref|NP_	tubulin, beta [Homo sapiens]	444	49671	4.9	0	o	Q	19	0
480	10	0.00462	0	0	INF		ENSG00000121053:E	EPX			gi|4503595|ref|NP_0	eosinophil peroxidase [Homo	715	81040	10.3	0	o	S	18	1
481	10	0.003378	0	0	INF		ENSG00000167552:E	TUBA1A			gi|17986283|ref|NP_	tubulin, alpha 1a [Homo sapi	451	50136	5.1	0	o	Q	20	0.005
482	10	0.003003	0	0	INF		ENSG00000102879:E	CORO1A			gi|5902134|ref|NP_0	coronin, actin binding protein	461	51026	6.7	0	o	Q	17	0
483	10	0.00216	0	0	INF		ENSG00000153187:E	HNRNPU			gi|74136883|ref|NP_	heterogeneous nuclear ribon	825	90585	6	0	o	Q	0	0
484	9	0.010618	0	0	INF		ENSG00000111640:N	GAPDH			gi|7669492|ref|NP_0	glyceraldehyde-3-phosphate	335	36053	8.5	0	o	Q	22	0
485	9	0.009152	1	3.19E-05	286.6359		ENSG00000206172:E	HBA2			gi|4504347|ref|NP_0	alpha 1 globin [Homo sapien	142	15258	8.7	0	o	Q	23	0
486	9	0.009139	0	0	INF		ENSG00000186652:E	PRG2			gi|46276889|ref|NP_	proteoglycan 2 preproprotein	222	25206	6.8	0	o	S	17	1
487	9	0.008271	5	0.000279	29.64165		ENSG00000127824:E	TUBA4A			gi|17921989|ref|NP_	tubulin, alpha 4a [Homo sapi	448	49924	5.1	0	o	Q	20	0.006
488	9	0.005931	0	0	INF		ENSG00000122566:E	HNRNPA2B1			gi|14043072|ref|NP_	heterogeneous nuclear ribon	353	37430	8.9	0	o	Q	0	0
489	9	0.004731	0	0	INF		ENSG00000026025:E	VIM			gi|62414289|ref|NP_	vimentin [Homo sapiens]	466	53652	5.1	0	o	Q	30	0.015
490	9	0.002312	1	1.18E-05	195.7657		ENSG00000128340:E	RAC2			gi|4506381|ref|NP_0	ras-related C3 botulinum toxi	192	21429	7.6	0	o	Q	16	0.02
491	9	0.001771	0	0	INF		ENSG00000044574:E	HSPA5			gi|16507237|ref|NP_	heat shock 70kDa protein 5 [	654	72333	5.2	0	o	S	19	1
492	9	0.00161	0	0	INF		ENSG00000149781:E	URP2			gi|28626504|ref|NP_	fermitin family homolog 3 sho	663	75430	6.8	0	o	Q	0	0
493	9	0.001281	0	0	INF		ENSG00000166598:N	HSP90B1			gi|4507677|ref|NP_0	tumor rejection antigen (gp96	803	92469	4.8	0	o	S	22	1
494	9	0.001016	1	1.48E-06	687.2353		ENSG00000196924:E	FLNA			gi|116063573|ref|NP	filamin A, alpha isoform 1 [Ho	2639	280016	6	0	o	Q	24	0.061
495	9	0.0008	0	0	INF		ENSG00000116560:E	SFPQ			gi|4826998|ref|NP_0	splicing factor proline/glutam	707	76150	9.4	0	o	Q	23	0
496	8	0.015025	2	0.000287	52.39936		NA:ENSMUSG00000	H3F3B; HIST2H3D			gi|4885385|ref|NP_0	H3 histone, family 3B [Homo	136	15328	11.3	0	i	Q	36	0
497	8	0.00655	0	0	INF		ENSG00000203812:E	HIST2H2AA4			gi|106775678|ref|NP	histone cluster 2, H2aa4 [Ho	130	14095	10.9	0	o	Q	62	0.022
498	8	0.006529	0	0	INF		ENSG00000185918:N	DEFA3			gi|4885179|ref|NP_0	defensin, alpha 3 preproprote	94	10245	6	0	o	S	20	1
499	8	0.004299	0	0	INF		ENSG00000156508:E	EEF1A1			gi|4503471|ref|NP_0	eukaryotic translation elonga	462	50141	9	0	o	Q	19	0.003
500	8	0.003588	4	0.000214	16.7421		ENSG00000114353:E	GNAI2			gi|4504041|ref|NP_0	guanine nucleotide binding p	355	40451	5.5	0	o	Q	0	0
501	8	0.003334	4	4.92E-05	67.74661		ENSG00000115091:E	ACTR3			gi|5031573|ref|NP_0	ARP3 actin-related protein 3	418	47371	5.9	0	o	Q	23	0.013
502	8	0.003223	1	7.2E-05	44.78652		NA:ENSMUSG00000	HIST1H2BD			gi|20336752|ref|NP_	histone cluster 1, H2bd [Hom	126	13936	10.3	0	o	Q	52	0
503	8	0.003005	0	0	INF		ENSG00000156575:E	PRG3			gi|5174531|ref|NP_0	proteoglycan 3 [Homo sapier	225	25447	4.9	0	o	S	18	1
504	8	0.002788	1	7.2E-05	38.73907		NA:ENSMUSG00000	HIST1H2BL			gi|4504259|ref|NP_0	histone cluster 1, H2bl [Homo	126	13952	10.3	0	o	Q	52	0
505	8	0.00271	1	1.26E-05	215.5495		ENSG00000169813:E	HNRNPF			gi|148470406|ref|NP	heterogeneous nuclear ribon	415	45672	5.6	0	o	Q	24	0
506	8	0.002373	4	0.000171	13.87461		ENSG00000167658:E	EEF2			gi|4503483|ref|NP_0	eukaryotic translation elonga	858	95338	6.8	0	o	Q	0	0
507	8	0.002235	1	3.78E-05	59.16064		ENSG00000198931:E	APRT			gi|4502171|ref|NP_0	adenine phosphoribosyltrans	180	19608	6	0	o	Q	16	0
508	8	0.002172	0	0	INF		ENSG00000135486:E	HNRNPA1			gi|14043070|ref|NP_	heterogeneous nuclear ribon	372	38747	9.1	0	o	Q	33	0
509	8	0.002051	0	0	INF		ENSG00000115415:E	STAT1			gi|21536301|ref|NP_	signal transducer and activat	712	83043	6.4	0	o	Q	0	0
510	8	0.001908	3	3.54E-05	53.87472		ENSG00000137076:E	TLN1			gi|16753233|ref|NP_	talin 1 [Homo sapiens]	2541	269665	6	0	o	Q	17	0.003
511	8	0.001816	0	0	INF		ENSG00000169045:E	HNRNPH1			gi|5031753|ref|NP_0	heterogeneous nuclear ribon	449	49229	6.3	0	o	Q	25	0.003
512	8	0.001708	6	0.000317	5.391573		ENSG00000096384:E	HSP90AB1			gi|20149594|ref|NP_	heat shock 90kDa protein 1,	724	83264	5	0	o	Q	0	0
513	8	0.001581	0	0	INF		ENSG00000147604:N	RPL7			gi|15431301|ref|NP_	ribosomal protein L7 [Homo s	248	29226	10.7	0	o	Q	0	0
514	8	0.001571	0	0	INF		ENSG00000102144:E	PGK1			gi|4505763|ref|NP_0	phosphoglycerate kinase 1 [H	417	44615	8.1	0	o	Q	0	0
515	8	0.001559	1	2.5E-05	62.43656		ENSG00000165119:E	HNRNPK			gi|14165435|ref|NP_	heterogeneous nuclear ribon	463	50976	5.5	0	o	Q	0	0
516	8	0.00144	1	1.62E-05	88.83591		ENSG00000113648:E	H2AFY			gi|93141018|ref|NP_	H2A histone family, member	372	39617	9.8	0	o	Q	59	0.01
517	8	0.00141	0	0	INF		ENSG00000011304:E	PTBP1			gi|14165464|ref|NP_	polypyrimidine tract-binding p	550	59037	9.2	0	o	Q	39	0
518	8	0.000801	0	0	INF		ENSG00000160789:E	LMNA			gi|27436946|ref|NP_	lamin A/C isoform 1 precurso	664	74140	7	0	o	Q	30	0.001
519	8	0.000795	0	0	INF		ENSG00000198563:E	BAT1			gi|18375623|ref|NP_	HLA-B associated transcript	428	48991	5.7	0	o	Q	0	0
520	8	0.000673	0	0	INF		ENSG00000148841:E	KIAA1754			gi|29789287|ref|NP_	KIAA1754 [Homo sapiens]	547	62060	5.9	0	o	S	16	0.815
521	8	0.000626	0	0	INF		ENSG00000168028:N	RPSA			gi|59859885|ref|NP_	ribosomal protein SA [Homo	295	32854	4.9	0	o	Q	31	0
522	8	0.000567	0	0	INF		ENSG00000156515:E	HK1			gi|15991827|ref|NP_	hexokinase 1 isoform HKI-R	916	102201	6.6	0	o	Q	17	0.004
523	8	0.000565	0	0	INF		ENSG00000176619:E	LMNB2			gi|27436951|ref|NP_	lamin B2 [Homo sapiens]	600	67689	5.3	0	o	Q	22	0.008
524	8	0.000544	0	0	INF		ENSG00000135829:E	DHX9			gi|100913206|ref|NP	DEAH (Asp-Glu-Ala-His) box	1270	140958	6.8	0	o	Q	19	0
525	8	0.000472	0	0	INF		ENSG00000121031:E	PRKDC			gi|13654237|ref|NP_	protein kinase, DNA-activate	4128	469093	7.1	0	o	Q	23	0.34
526	8	0.000465	1	5.48E-06	84.86589		ENSG00000142347:E	MYO1F			gi|27544941|ref|NP_	myosin IF [Homo sapiens]	1098	124844	9.1	0	o	Q	35	0
527	8	0.000304	0	0	INF		ENSG00000214052:E	FLJ21438			gi|130502162|ref|NP	hypothetical protein LOC649	1011	111898	8.8	0	o	Q	60	0
528	7	0.004943	0	0	INF		ENSG00000127314:E	RAP1B			gi|58219792|ref|NP_	RAP1B, member of RAS onc	184	20825	5.8	0	o	Q	19	0.196
529	7	0.004915	3	0.000275	17.85609		ENSG00000108518:E	PFN1			gi|4826898|ref|NP_0	profilin 1 [Homo sapiens]	140	15054	8.3	0	o	Q	19	0
530	7	0.004597	1	9.72E-05	47.301		ENSG00000167088:E	SNRPD1			gi|5902102|ref|NP_0	small nuclear ribonucleoprote	119	13282	11.6	0	o	Q	17	0.002
531	7	0.004224	0	0	INF		ENSG00000206047:N	LOC728358			gi|124248516|ref|NP	alpha-defensin 1 [Homo sapi	94	10201	7	0	o	S	20	1
532	7	0.002992	0	0	INF		ENSG00000147140:E	NONO			gi|34932414|ref|NP_	non-POU domain containing,	471	54232	8.9	0	o	Q	0	0
533	7	0.002813	0	0	INF		ENSG00000196866:N	HIST1H2AH			gi|10800132|ref|NP_	histone cluster 1, H2ag [Hom	130	14091	10.9	0	o	Q	62	0.06
534	7	0.002781	0	0	INF		ENSG00000111348:E	ARHGDIB			gi|56676393|ref|NP_	Rho GDP dissociation inhibit	201	22988	5.2	0	o	Q	0	0
535	7	0.002702	1	3.01E-05	89.76859		ENSG00000183558:E	HIST2H2AA4			gi|10800130|ref|NP_	histone cluster 1, H2ad [Hom	130	14107	10.9	0	o	Q	62	0.046
536	7	0.002135	0	0	INF		ENSG00000108561:E	C1QBP			gi|4502491|ref|NP_0	complement component 1, q	282	31362	4.8	0	o	S	25	0.849
537	7	0.001976	0	0	INF		ENSG00000113368:E	LMNB1			gi|5031877|ref|NP_0	lamin B1 [Homo sapiens]	586	66408	5.2	0	o	Q	28	0.003
538	7	0.001895	0	0	INF		ENSG00000100911:E	PSME2			gi|30410792|ref|NP_	proteasome activator subunit	239	27402	5.7	0	o	Q	17	0
539	7	0.001855	0	0	INF		ENSG00000069974:E	RAB27A			gi|34485711|ref|NP_	Ras-related protein Rab-27A	221	24868	5.2	0	o	Q	22	0

rk	RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs							
	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
394	0	0	0.005964	0	0	1	0.001491	0.002982	0	0	0	0	0	0	0	0
395	0	0	0.004555	0	0	1	0.001139	0.002277	0	0	0	0	0	0	0	0
396	0	0	0.004489	0	0	1	0.001122	0.002244	0	0	0	0	0	0	0	0
397	0	0	0.003512	0	0	1	0.000878	0.001756	0	0	0	0	0	0	0	0
398	0	0	0.003315	0	0	1	0.000829	0.001658	0	0	0	0	0	0	0	0
399	0	0	0	0	0	0	0	0	0	0.000603	0	0	0	1	0.000151	0.000302
400	0	0	0	0	0	0	0	0	0	0.000602	0	0	0	1	0.00015	0.000301
401	0	0.000596	0	0	0	1	0.000149	0.000298	0	0	0	0	0	0	0	0
402	0	0.000549	0	0	0	1	0.000137	0.000274	0	0	0	0	0	0	0	0
403	0	0	0.000467	0	0	1	0.000117	0.000233	0	0	0	0	0	0	0	0
404	0.000467	0	0	0	0	1	0.000117	0.000233	0	0	0	0	0	0	0	0
405	0	0.000449	0	0	0	1	0.000112	0.000224	0	0	0	0	0	0	0	0
406	0	0.00044	0	0	0	1	0.00011	0.00022	0	0	0	0	0	0	0	0
407	0	0	0	0	0	0	0	0	0	0.000359	0	0	0	1	8.97E-05	0.000179
408	0	0	0	0	0	0	0	0	0	0	0	0	0.000349	1	8.73E-05	0.000175
409	0	0	0	0	0	0	0	0	0	0	0	0	0.00032	1	8E-05	0.00016
410	0	0	0	0	0	0	0	0	0	0.000285	0	0	0	1	7.12E-05	0.000142
411	0	0.000276	0	0	0	1	6.9E-05	0.000138	0	0	0	0	0	0	0	0
412	0	0.000272	0	0	0	1	6.81E-05	0.000136	0	0	0	0	0	0	0	0
413	0	0.000272	0	0	0	1	6.8E-05	0.000136	0	0	0	0	0	0	0	0
414	0	0.000259	0	0	0	1	6.48E-05	0.00013	0	0	0	0	0	0	0	0
415	0	0.000255	0	0	0	1	6.37E-05	0.000127	0	0	0	0	0	0	0	0
416	0	0.000247	0	0	0	1	6.17E-05	0.000123	0	0	0	0	0	0	0	0
417	0	0	0	0	0	0	0	0	0	0.000239	0	0	0	1	5.97E-05	0.000119
418	0	0.000238	0	0	0	1	5.95E-05	0.000119	0	0	0	0	0	0	0	0
419	0	0	0	0	0	0	0	0	0	0.000236	0	0	0	1	5.9E-05	0.000118
420	0	0	0	0	0	0	0	0	0	0.000234	0	0	0	1	5.85E-05	0.000117
421	0	0.000208	0	0	0	1	5.19E-05	0.000104	0	0	0	0	0	0	0	0
422	0	0.000201	0	0	0	1	5.03E-05	0.000101	0	0	0	0	0	0	0	0
423	0	0	0	0	0	0	0	0	0	0.000187	0	0	0	1	4.67E-05	9.35E-05
424	0	0.00018	0	0	0	1	4.5E-05	9.01E-05	0	0	0	0	0	0	0	0
425	0	0.000177	0	0	0	1	4.43E-05	8.87E-05	0	0	0	0	0	0	0	0
426	0	0.000175	0	0	0	1	4.37E-05	8.74E-05	0	0	0	0	0	0	0	0
427	0	0.000172	0	0	0	1	4.31E-05	8.62E-05	0	0	0	0	0	0	0	0
428	0	0.000162	0	0	0	1	4.04E-05	8.08E-05	0	0	0	0	0	0	0	0
429	0	0.000145	0	0	0	1	3.63E-05	7.27E-05	0	0	0	0	0	0	0	0
430	0	0.000144	0	0	0	1	3.61E-05	7.22E-05	0	0	0	0	0	0	0	0
431	0	0.000141	0	0	0	1	3.52E-05	7.05E-05	0	0	0	0	0	0	0	0
432	0	0.000139	0	0	0	1	3.47E-05	6.94E-05	0	0	0	0	0	0	0	0
433	0	0.000138	0	0	0	1	3.46E-05	6.92E-05	0	0	0	0	0	0	0	0
434	0	0	0	0	0	0	0	0	0	0.000133	0	0	0	1	3.32E-05	6.64E-05
435	0	0.000133	0	0	0	1	3.31E-05	6.63E-05	0	0	0	0	0	0	0	0
436	0	0.000129	0	0	0	1	3.23E-05	6.47E-05	0	0	0	0	0	0	0	0
437	0	0.000126	0	0	0	1	3.14E-05	6.29E-05	0	0	0	0	0	0	0	0
438	0	0.000125	0	0	0	1	3.13E-05	6.27E-05	0	0	0	0	0	0	0	0
439	0	0.000124	0	0	0	1	3.11E-05	6.22E-05	0	0	0	0	0	0	0	0
440	0	0	0	0	0	0	0	0	0	0	0	0	0.00012	1	2.99E-05	5.99E-05
441	0	0.000117	0	0	0	1	2.92E-05	5.85E-05	0	0	0	0	0	0	0	0
442	0	0	0	0	0	0	0	0	0	0.000115	0	0	0	1	2.87E-05	5.74E-05
443	0	0	0	0	0	0	0	0	0	0.000111	0	0	0	1	2.78E-05	5.57E-05
444	0	0	0	0	0	0	0	0	0	0.00011	0	0	0	1	2.76E-05	5.51E-05
445	0	0.000108	0	0	0	1	2.71E-05	5.42E-05	0	0	0	0	0	0	0	0
446	0	0.000103	0	0	0	1	2.57E-05	5.14E-05	0	0	0	0	0	0	0	0
447	0	0	0	0	0	0	0	0	0	0.000103	0	0	0	1	2.57E-05	5.13E-05
448	0	0	0	0	0	0	0	0	0	9.8E-05	0	0	0	1	2.45E-05	4.9E-05
449	0	0	0	0	0	0	0	0	0	0	0	0	9.72E-05	1	2.43E-05	4.86E-05
450	0	9.56E-05	0	0	0	1	2.39E-05	4.78E-05	0	0	0	0	0	0	0	0
451	0	0	0	0	0	0	0	0	0	9.3E-05	0	0	0	1	2.32E-05	4.65E-05
452	0	0	0	0	0	0	0	0	0	9.05E-05	0	0	0	1	2.26E-05	4.52E-05
453	0	8.93E-05	0	0	0	1	2.23E-05	4.46E-05	0	0	0	0	0	0	0	0
454	0	0	0	0	0	0	0	0	0	8.83E-05	0	0	0	1	2.21E-05	4.42E-05
455	0	0	0	0	0	0	0	0	0	8.14E-05	0	0	0	1	2.04E-05	4.07E-05
456	0	0	0	7.7E-05	0	1	1.92E-05	3.85E-05	0	0	0	0	0	0	0	0
457	0	0	0	0	0	0	0	0	0	7.67E-05	0	0	0	1	1.92E-05	3.84E-05
458	0	0	0	7.3E-05	0	1	1.82E-05	3.65E-05	0	0	0	0	0	0	0	0
459	0	6.65E-05	0	0	0	1	1.66E-05	3.32E-05	0	0	0	0	0	0	0	0
460	0	6.41E-05	0	0	0	1	1.6E-05	3.21E-05	0	0	0	0	0	0	0	0
461	0	6.11E-05	0	0	0	1	1.53E-05	3.06E-05	0	0	0	0	0	0	0	0
462	0	0	0	5.74E-05	0	1	1.43E-05	2.87E-05	0	0	0	0	0	0	0	0
463	0	4.58E-05	0	0	0	1	1.14E-05	2.29E-05	0	0	0	0	0	0	0	0
464	0	0	0	0	0	0	0	0	0	0	0	4.48E-05	0	1	1.12E-05	2.24E-05
465	0	0	0	0	0	0	0	0	0	3.9E-05	0	0	0	1	9.75E-06	1.95E-05
466	0	0	0	0	0	0	0	0	0	3.8E-05	0	0	0	1	9.51E-06	1.9E-05
467	0	0	0	0	0	0	0	0	0	3.67E-05	0	0	0	1	9.17E-06	1.83E-05
468	0	0	0	0	0	0	0	0	0	3.57E-05	0	0	0	1	8.93E-06	1.79E-05
469	0	0	0	0	0	0	0	0	0	3.25E-05	0	0	0	1	8.13E-06	1.63E-05
470	0	0	0	0	0	0	0	0	0	0	0	3.19E-05	0	1	7.97E-06	1.59E-05
471	0	0	0	2.36E-05	0	1	5.9E-06	1.18E-05	0	0	0	0	0	0	0	0
472	0	1.82E-05	0	0	0	1	4.55E-06	9.11E-06	0	0	0	0	0	0	0	0
473	0	0	0	0	0	0	0	0	0	0	0.004959	0	0	1	0	0
474	0	0	0	0	0.001774	1	0	0	0	0	0	0	0	0	0	0
475	0	0	0	0	0.00098	1	0	0	0	0	0	0	0	0	0	0
476	0.015568	0.030066	0.019539	0.048634	0.312493	5	0.028452	0.01478	0.023081	0.028791	0.182461	0.061122	0.043059	5	0.039013	0.016966
477	0.045659	0.020154	0.038305	0.015606	0.039529	5	0.029931	0.014356	0.056023	0.021999	0.08825	0.018538	0.012299	5	0.027215	0.01962
478	0.061778	0.008208	0.011503	0.011907	0.011079	5	0.023349	0.025673	0.015098	0.013609	0.01427	0.010627	0.026375	5	0.016427	0.006887
479	0.00672	0.00554	0.000282	0.012945	0.007336	5	0.006372	0.0052	0.014996	0.006659	0.003675	0.014703	0.017457	5	0.013454	0.004695
480	0.006866	0.006421	0.003679	0.004141	0.009111	5	0.005277	0.0016	0.011101	0.002851	0.001956	0.001575	0.000322	5	0.003962	0.00487
481	0.002133	0.002405	0.004305	0.000418	0.004454	5	0.002315	0.001592	0.003281	0.002016	0.006977	0.00739	0.005079	5	0.004442	0.002333
482	0.001759	0.002682	0.001223	0.002491	0.000883	5	0.002038	0.000674	0.001926	0.003017	0.001517	0.006266	0.004663	5	0.003968	0.001901
483	0.000786	0.001385	0.00296	0.00227	0.001481	5	0.00185	0.000959	0.000538	0.000789	0.000848	0.004827	0.003722	5	0.002469	0.002136
484	0.00242	0.00369	0.008973	0.021619	0.002431	5	0.009176	0.008767	0.001325	0.003148	0	0.03873	0.005042	4	0.012061	0.017844
485	0.012562	0.002628	0	0.004105	0.037274	4	0.004824	0.005431	0.018755	0.010427	0.044316	0.01609	0.008651	5	0.013481	0.004736
486	0.004383	0.03257	0.007617	0.011378	0.06419	5	0.013987	0.012714	0	0.012531	0.009449	0.001176	0.003458	4	0.004291	0.005678
487	0.002299	0.003566	0	0.013761	0.004862	4	0.004906	0.006085	0.026751	0.003245	0.007023	0.009407	0.007141	5	0.011636	0.010393
488	0.000919	0.000859	0.006919	0.008957	0.00346	5	0.004413	0.004154	0.002515	0.001716	0	0.023717	0.001842	4	0.007448	0.010852
489	0.005568	0.001251	0.002016	0.01539	0.006116	5	0.006056	0.0065	0.00381	0.001252	0	0.007985	0.000577	4	0.003406	0.003355
490	0.003378	0.001458	0.000734	0.001705	0.004241	5	0.001819	0.001118	0	0.001655	0.003642	0.000765	0.008797	4	0.002804	0.004052
491	0.000868	0.000999	0.004596	0.001783	0.00083	5	0.002061	0.001738	0.000679	0.000617	0	0.004154	0.00047	4	0.00148	0.001785
492	0.006115	0.001583	0.001984	0.000693	0	4	0.002594	0.002409	0.000669	0.001354	0.001055	0.000197	0.000289	5	0.000627	0.000526
493	0.000606	0.000639	0.001638	0.000726	0.002535	5	0.000902	0.000493	0.002211	0.000754	0	0.00128	0.00239	4	0.001659	0.000775
494	0.00381	0.000492	0.000641	0.000848	0.000463	5	0.001448	0.001582	0.001346	0.000502	0	0.000315	0.000175	4	0.000584	0.000525
495	0.001147	0.000594	0.000266	0.000325	0.001152	5	0.000583	0.000402	0.001883	0.000952	0	0.000416	0.000814	4	0.001016	0.000621
496	0.017886	0.014015	0.005526	0.019223	0	4	0.014162	0.006167	0.022846	0.018946	0	0.01908	0.002681	4	0.015888	0.008988
497	0.007485	0.003947	0	0.012005	0.048858	4	0.005859	0.005112	0.013658	0.011037	0.096504	0.004268	0	4	0.007241	0.006241
498	0.013801	0.000248	0.01599	0.002819	0	4	0.008214	0.007837	0.014166	0.002148	0.007438	0	0.003063	4	0.004844	0.006346
499	0.000351	0.004342	0.000407	0.007876	0.007931	5	0.003244	0.003609	0	0.003836	0	0.014342	0.003241	3	0.005355	0.006224
500	0.004111	0.002428	0.007613	0.002418	0	4	0.004142	0.002447	0.005001	0.00205	0	0.00346	0.001622	4	0.003033	0.001529
501	0.000388	0.000725	0.000899	0.002409	0	4	0.001105	0.000895	0.005309	0.001234	0	0.001327	0.014376	4	0.005562	0.006175
502	0.006435	0.000555	0.001491	0.010374	0.006463	5	0.004714	0.004571	0	0.001068	0	0.001684	0.004178	3	0.001733	0.001773
503	0.002162	0.002592	0.01336	0.003533	0.003619	5	0.005412	0.00533	0	0.001296	0	7.25E-05	0.001024	3	0.000598	0.000659
504	0.006435	0.000555	0.001491	0.010374	0.006463	5	0.004714	0.004571	0	0.001068	0	0.001684	0.000696	3	0.000862	0.000704
505	0	0.001455	0.002113	0.003505	0.003924	4	0.001768	0.001456	0.002139	0.001591	0	0.00981	0.001068	4	0.003652	0.004128
506	0.001323	0.000625	0	0.005023	0.000475	4	0.001743	0.002253	0.001035	0.001778	0	0.007989	0.001208	4	0.003002	0.003339
507	0.001802	0.001037	0	0.004416	0.004524	4	0.001814	0.001886	0.004932	0.001371	0	0.003899	0.000427	4	0.002657	0.002109
508	0.000872	0.00094	0	0.003134	0.003283	4	0.001237	0.001335	0.002386	0.000543	0	0.009388	0.000109	4	0.003107	0.004303
509	0.000683	0.001671	0.001319	0.000744	0	4	0.001104	0.000474	0.006234	0.00063	0	0.001352	0.003774	4	0.002998	0.002542
510	0.009059	0.000679	0.000222	0.000834	0	4	0.002699	0.004248	0.003668	0.000406	0	0.000321	7.55E-05	4	0.001118	0.001706
511	0	0.000839	0.000976	0.002777	0.003627	4	0.001148	0.001169	0.001977	0.000668	0	0.00686	0.000432	4	0.002484	0.002996
512	0.000672	0.000984	0.002595	0.001785	0	4	0.001509	0.000862	0.001226	0.000995	0	0.002251	0.003156	4	0.001907	0.000996
513	0.002616	0.000658	0.00303	0.000712	0	4	0.001754	0.001246	0.00179	0.002895	0	0.000329	0.000619	4	0.001408	0.001175
514	0.000778	0.000727	0	0.001652	0.001953	4	0.000789	0.000676	0.002129	0.001775	0	0.005323	0.000184	4	0.002353	0.002153
515	0.001051	0.001209	0.001217	0.002785	0.001759	5	0.001566	0.000817	0	0.000775	0	0.004195	0.001244	3	0.001553	0.001834
516	0.001744	0.000752	0	0.003229	0.019701	4	0.001431	0.001395	0	0.000965	0.006696	0.004519	0.00031	4	0.001448	0.002086
517	0.001179	0.001866	0.000342	0.000931	0.00074	5	0.00108	0.000631	0	0.002774	0	0.003353	0.000838	3	0.001741	0.001582
518	0.000977	0.000211	0	0.000479	0.001226	4	0.000417	0.000422	0.004011	0.000169	0	0.00027	0.000289	4	0.001185	0.001885
519	0.001137	0.000736	0	0.00066	0.002854	4	0.000633	0.000471	0.001037	0.000786	0	0.001787	0.000215	4	0.000956	0.000652
520	0	0.000512	0.002061	0.000161	0	3	0.000683	0.000943	0.001623	0.000615	0.001278	0.000269	0.00014	5	0.000662	0.000671
521	0.00055	0.000474	0	0.000539	0	3	0.000391	0.000263	0.001505	0.000304	0.00237	0.000332	0.001301	5	0.000861	0.000632
522	0.001416	0.000637	0.000205	0.000771	0	4	0.000757	0.000501	0.000969	0.000367	0	8.91E-05	8.38E-05	4	0.000377	0.000416
523	0.000297	0.000272	0.001566	0.00092	0.000679	5	0.000764	0.000613	0	0.000449	0	0.000571	0.000448	3	0.000367	0.000251
524	0.000255	0.000588	0.000296	0.000348	0	4	0.000372	0.000149	0.00035	0.000406	0	0.000565	0.001542	4	0.000716	0.000558
525	3.93E-05	0.000593	0.000728	0.000329	0	4	0.000423	0.000304	0.000108	0.000446	0	0.000352	0.001181	4	0.000522	0.000462
526	0.000148	0.000191	0.000342	0.000273	0	4	0.000239	8.65E-05	0.002021	0.000266	0	0.000372	0.000105	4	0.000691	0.000894
527	0.00016	0.000369	0.000929	6.99E-05	0	4	0.000382	0.000386	0.000439	0.000244	0	3.23E-05	0.00019	4	0.000226	0.000168
528	0.007051	0.002789	0	0.007008	0	3	0.004212	0.003447	0.009649	0.002682	0	0.008692	0.001669	4	0.005673	0.004078
529	0.003475	0.001666	0	0.011986	0.008725	4	0.004282	0.005329	0	0.003365	0	0.011424	0.007403	3	0.005548	0.00495
530	0.008176	0.001568	0	0.001781	0	3	0.002881	0.003618	0.01865	0.004525	0	0.000137	0.001936	4	0.006312	0.00842
531	0.013801	0.000248	0	0.002819	0	3	0.004217	0.006515	0.014166	0.002148	0.007438	0	0.000613	4	0.004232	0.006684
532	0.003443	0.001188	0	0.001388	0.001729	4	0.001505	0.00143	0.013194	0.001572	0	0.003153	0	3	0.00448	0.00595
533	0.007485	4.49E-05	0	0.000136	0	3	0.001916	0.003713	0.013658	4.31E-05	0	0.000251	0.000886	4	0.003709	0.006642
534	0.000807	0.000696	0.001246	0.004746	0	4	0.001874	0.001929	0	0.001228	0	0.004547	0.008976	3	0.003688	0.004015
535	0.007485	4.49E-05	0	0.000136	0	3	0.001916	0.003713	0.013658	4.31E-05	0.223184	0.000251	0	4	0.003488	0.006781
536	0	0.001323	0.003997	0.003633	0.001444	4	0.002238	0.001905	0	0.001671	0	0.000463	0.00599	3	0.002031	0.002732
537	0.00274	0.000995	0.001924	0.002584	0	4	0.002061	0.000794	0	0.000957	0	0.001699	0.004913	3	0.001892	0.002131
538	0.00475	0.00039	0	0.000222	0	3	0.00134	0.002278	0.009286	0.000282	0	6.83E-05	0.000161	4	0.002449	0.004559
539	0.004403	0.001126	0	0.00032	0	3	0.001462	0.002017	0.008034	0.000711	0	7.38E-05	0.000174	4	0.002248	0.003867

rk	MMs										
	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
394	0	0	0	0	0	0	0	0	Ubiquinol-cytochrome C	membrane; mitochondrial	oxidoreductase activity;
395	0	0	0	0	0	0	0	0		integral to plasma membrane	
396	0	0	0	0	0	0	0	0			
397	0	0	0	0	0	0	0	0	CD20/IgE Fc receptor beta	integral to membrane;	receptor activity
398	0	0	0	0	0	0	0	0			
399	0	0	0	0	0	0	0	0		integral to membrane; plasma	
400	0	0	0	0	0	0	0	0			
401	0	0	0	0	0	0	0	0	Immunoglobulin V-set	integral to plasma membrane	coreceptor activity [pmid
402	0	0	0	0	0	0	0	0	Cathelicidin. A novel protein	extracellular region	
403	0	0	0	0	0	0	0	0	TMC domain. These	endoplasmic reticulum;	
404	0	0	0	0	0	0	0	0	Ion transport protein. This	membrane; membrane	potassium ion binding;
405	0	0	0	0	0	0	0	0	Membrane-associating	extracellular space; integral to	cytokine activity
406	0	0	0	0	0	0	0	0	Hypoxia induced protein	integral to membrane;	
407	0	0	0	0	0	0	0	0			
408	0	0	0	0	0	0	0	0	AMP deaminase (AMPD)		AMP deaminase activity
409	0	0	0	0	0	0	0	0		nucleus	signal transducer activity
410	0	0	0	0	0	0	0	0	Longevity-assurance	endoplasmic reticulum;	sequence-specific DNA
411	0	0	0	5.37E-05	0	0	0	0	1,4-dihydroxy-2-naphthoate	cytoplasm [pmid 11314041];	prenyltransferase activity
412	0	0	0	0	0	0	0	0	Tim17/Tim22/Tim23 family.		
413	0	0	0	0	0	0	0	0	Apolipoprotein L. Apo L	cytoplasm; extracellular region	lipid binding; lipid transporter
414	0	0	0	0	0	0	0	0	LETM1-like protein.		
415	0	0	0	0	0	0	0	0	Protein of unknown function		
416	0	0	0	0	0	0	0	0	Protein kinase C conserved	integral to membrane;	ATP binding [pmid 8626589];
417	0	0	0	0	0	0	0	0		integral to membrane;	transmembrane receptor
418	0	0	0	0	0	0	0	0			
419	0	0	0	0	0	0	0	0			
420	0	0	0	0	0	0	0	0	Src homology 3 domains;	Golgi apparatus [pmid	glycoprotein 6-alpha-L-
421	0	0	0	0	0	0	0	0	AIG1 (avrRpt2-induced	integral to membrane;	GTP binding; nucleotide
422	0	0	0	0	0	0	0	0	Helical region found in	integral to membrane;	
423	0	0	0	0	0	0	0	0	Serine/threonine	integral to membrane;	hydrolase activity;
424	0	0	0	0	0	0	0	0	Tumor necrosis factor	integral to plasma membrane	GPI anchor binding;
425	0	0	0	0	0	0	0	0	Kringle domain; Kringle		
426	0	0	0	0	0	0	0	0	Alkaline phytoceramidase	endoplasmic reticulum;	hydrolase activity; hydrolase
427	0	0	0	0	0	0	0	0	Herp (Homocysteine-		
428	0	0	0	0	0	0	0	0	POT family. The POT	integral to membrane;	transporter activity
429	0	0	0	0	0	0	0	0			
430	0	0	0	0	0	0	0	0	Thyroglobulin type I	cytosol [pmid 10192395];	receptor activity [pmid
431	0	0	0	0	0	0	0	0	Triose-phosphate	Golgi apparatus [pmid	nucleotide-sugar transporter
432	0	0	0	0	0	0	0	0	Torsin. This family consists	endoplasmic reticulum	ATP binding; nucleoside-
433	0	0	0	0	0	0	0	0	Hydrolases of the		hydrolase activity
434	0	0	0	0	0	0	0	0	Amino acid transporters	integral to membrane;	amino acid permease
435	0	0	0	0	0	0	0	0	RING-finger (Really	mitochondrion [pmid	metal ion binding; protein
436	0	0	0	0	0	0	0	0	Sodium:dicarboxylate	integral to plasma membrane	neutral amino acid
437	0	0	0	0	0	0	0	0	7 transmembrane receptor	integral to membrane; integral	C5a anaphylatoxin receptor
438	0	0	0	0	0	0	0	0	Domain abundant in	integral to plasma membrane	protein binding; sugar binding
439	0	0	0	0	0	0	0	0	7 transmembrane receptor	integral to plasma membrane	receptor activity; rhodopsin-
440	0	0	0	0	0	0	0	0		integral to membrane;	
441	0	0	0	0	0	0	0	0	ATP P2X receptor;	integral to plasma membrane	ATP binding; ATP-gated
442	0	0	0	0	0	0	0	0			
443	0	0	0	0	0	0	0	0	Domain in Tre-2, BUB2p,	integral to membrane;	GTPase activator activity
444	0	0	0	0	0	0	0	0	RING-finger (Really	intracellular	metal ion binding; protein
445	0	0	0	0	0	0	0	0	NhaP-type Na+/H+ and	integral to membrane;	antiporter activity; sodium
446	0	0	0	0	0	0	0	0			oxidoreductase activity; zinc
447	0	0	0	0	0	0	0	0	DNA polymerase III	Golgi trans face [pmid	
448	0	0	0	0	0	0	0	0	Tetratricopeptide repeat		protein binding [pmid
449	0	0	0	0	0	0	0	0	Zinc-dependent	integral to membrane [pmid	metal ion binding;
450	0	0	0	0	0	0	0	0	Anthrax receptor	endoplasmic reticulum;	metal ion binding; protein
451	0	0	0	0	0	0	0	0	domain in		
452	0	0	0	0	0	0	0	0			
453	0	0	0	0	0	0	0	0	TIR domain. The	cell surface [pmid 12443841];	Gram-positive bacterial
454	0	0	0	0	0	0	0	0	Serine/threonine protein	integral to membrane;	ATP binding; nucleotide
455	0	0	0	0	0	0	0	0	Fibronectin type 3 domain;	external side of plasma	hematopoietin/interferon-
456	0	0	0	0	0	0	0	0	Fibronectin type III domain;	integral to membrane;	antigen binding [pmid
457	0	0	0	0	0	0	0	0	Immunoglobulin V-set	integral to plasma membrane	
458	0	0	0	0	0	0	0	0	BPI/LBP/CETP N-terminal		lipid binding
459	0	0	0	0	0	0	0	0			
460	0	0	0	0	0	0	0	0			
461	0	0	0	0	0	0	0	0	BPTI/Kunitz family of serine	integral to membrane [pmid	binding; DNA binding [pmid
462	0	0	0	0	0	0	0	0	Magnesium chelatase,	nucleus [pmid 10610178]	ATP binding; nucleoside-
463	0	0	0	0	0	0	0	0	Domain abundant in	integral to plasma membrane	complement component C3b
464	0	0	0	0	0	0	0	0	Leucine-rich repeats		sugar porter activity;
465	0	0	0	0	0	0	0	0	Alpha mannosidase, middle	Golgi membrane; integral to	alpha-mannosidase activity;
466	0	0	0	0	0	0	0	0	haloacid dehalogenase-like	endoplasmic reticulum;	ATP binding; ATPase
467	0	0	0	0	0	0	0	0	Cation transport ATPase	integral to membrane;	ATP binding; ATPase
468	0	0	0	0	0	0	0	0	Domain found in Notch and	integral to membrane;	calcium ion binding;
469	0	0	0	0	0	0	0	0	Prophage tail fibre N-	integral to membrane;	carboxypeptidase A activity;
470	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; ATP-dependent
471	0	0	0	0	0	0	0	0			
472	0	0	0	0	0	0	0	0			
473	0	0	0	0	0	0	0	0	deoxyribonuclease I;	extracellular region [pmid	actin binding; calcium ion
474	0	0	0	0	0	0	0	0	NAD(P) transhydrogenase	integral to membrane;	transporter activity
475	0	0	0	0	0	0	0	0	ZIP Zinc transporter. The	membrane	metal ion transporter activity
476	0.012968	0.000498	0	0	0	0	0	0	Actin; An ubiquitous protein	actin filament; cytoskeleton;	ATP binding; nucleotide
477	0	0.001813	0	0.00088	0	0.000152	0	0	Histone H4, one of the four		
478	0	0	0	0	0	0	0	0	Globins are heme proteins,	hemoglobin complex [pmid	heme binding; hemoglobin
479	0	0	0.000231	0.000353	0.00065	0.001075	0.000367	0.000183	The tubulin superfamily	cytoplasm; microtubule;	GTP binding; GTPase
480	0	0	0	0	0	0	0	0	Animal haem peroxidase;		calcium ion binding; iron ion
481	0	0	0	0	0	0	0	0	The tubulin superfamily	microtubule; protein complex	GTP binding; GTPase
482	0	0	0	0	0	0	0	0	WD40 domain, found in a	actin cytoskeleton [pmid	actin binding; structural
483	0	0	0	0	0	0	0	0	SPRY domain. SPRY	heterogeneous nuclear	ATP binding; DNA binding
484	0	0	0	0	0	0	0	0	Glyceraldehyde 3-	cytoplasm	glyceraldehyde-3-phosphate
485	0	0	0	0.000255	0	0	0	0	Globins are heme proteins,	hemoglobin complex	heme binding; iron ion
486	0	0	0	0	0	0	0	0	CLECT_EMBP_like: C-type	cytoplasm; extracellular region	heparin binding; sugar
487	0	0	0.000774	0.000294	0.000832	0.000264	0	6.85E-05	The tubulin superfamily	microtubule; protein complex	GTP binding; GTPase
488	0	0	0	0	0	0	0	0	RNA recognition motif.	heterogeneous nuclear	nucleotide binding; protein
489	0	0	0	0	0	0	0	0	Intermediate filament head	cytoplasm [pmid 9150946];	protein binding [pmid
490	0	0	0	9.45E-05	0	0	0	0	Rac1-like subfamily. The	intracellular	GTP binding; GTPase
491	0	0	0	0	0	0	0	0	Hydantoinase/oxoprolinase.	caspase complex [pmid	ATP binding [pmid
492	0	0	0	0	0	0	0	0	Band 4.1 homologues; Also	cytoskeleton; membrane	protein binding [pmid
493	0	0	0	0	0	0	0	0	Histidine kinase-, DNA	cytosol [pmid 9596688];	ATP binding; calcium ion
494	0	0	0	0	0	1.18E-05	0	0			
495	0	0	0	0	0	0	0	0	NOPS (NUC059) domain.	nucleus	DNA binding; nucleotide
496	0	0	0.001361	0.000933	0	0	0	0	Histone H3; smart00428		
497	0	0	0	0	0	0	0	0	Histone 2A; H2A is a		
498	0	0	0	0	0	0	0	0	Defensin propeptide;	extracellular region	
499	0	0	0	0	0	0	0	0	EF1_alpha_II: this family	cytoplasm	GTP binding; GTPase
500	0	0	0.000521	0.000582	0	0.000427	0.000184	0	G-protein alpha subunit. G		GTP binding; GTPase
501	0	0	0.000111	0.00013	0	7.49E-05	7.79E-05	0	Actin; An ubiquitous protein	Arp2/3 protein complex [pmid	ATP binding; nucleotide
502	0	0	0	0.000576	0	0	0	0	Histone H2B; smart00427	chromosome; nucleosome;	DNA binding
503	0	0	0	0	0	0	0	0	CLECT_EMBP_like: C-type		sugar binding
504	0	0	0	0.000576	0	0	0	0	Histone H2B; smart00427	chromosome; nucleosome	DNA binding [pmid 9439656]
505	0	0	0	0	0	0.000101	0	0			
506	0	0	0.000162	0.000338	0.000449	0.00042	0	0	EF2_snRNP_like_II: this		GTP binding; nucleotide
507	0	0	0	0.000302	0	0	0	0	adenine	cytoplasm [pmid 16130169]	adenine
508	0	0	0	0	0	0	0	0	RNA recognition motif.	cytoplasm [pmid 8521471];	nucleotide binding; protein
509	0	0	0	0	0	0	0	0	STAT protein, DNA binding	cytoplasm [pmid 10820245];	calcium ion binding;
510	0	0	9.1E-05	9.99E-05	0	9.24E-05	0	0	Vinculin Binding Site.	cytoskeleton; cytosol; focal	actin binding; binding; LIM
511	0	0	0	0	0	0	0	0	RNPHF zinc finger. This	heterogeneous nuclear	nucleotide binding; poly(U)
512	0	0	0.000575	0.000358	0.000532	0.00054	0.00036	0.00017	Histidine kinase-, DNA	cytoplasm	ATP binding; nitric-oxide
513	0	0	0	0	0	0	0	0	The archeal/eukaryotic	cytosolic large ribosomal	RNA binding [pmid 8441630];
514	0	0	0	0	0	0	0	0	Phosphoglycerate kinase		ATP binding; nucleotide
515	0	0	0.0002	0	0	0	0	0	ROKNT (NUC014) domain.	nucleus; ribonucleoprotein	DNA binding; nucleic acid
516	0	0	0	0	0.00013	0	0	0	Histone 2A; H2A is a	Barr body [pmid 11331621];	DNA binding [pmid 9714746]
517	0	0	0	0	0	0	0	0	RNA recognition motif.	heterogeneous nuclear	nucleic acid binding;
518	0	0	0	0	0	0	0	0	Intermediate filament tail	intermediate filament; nucleus	protein binding [pmid
519	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus [pmid 7601445];	ATP binding; ATP-dependent
520	0	0	0	0	0	0	0	0			
521	0	0	0	0	0	0	0	0	Ribosomal protein S2;	cytoplasm [pmid 16130169];	laminin receptor activity
522	0	0	0	0	0	0	0	0	Hexokinase. Hexokinase	membrane	ATP binding; hexokinase
523	0	0	0	0	0	0	0	0	Intermediate filament tail	intermediate filament; nuclear	structural molecule activity
524	0	0	0	0	0	0	0	0			
525	0	0	0	0	0	0	0	0	Phosphatidylinositol kinase	nucleus	ATP binding; DNA binding;
526	0	0	0	0	4.38E-05	0	0	0	Src homology 3 domains;	myosin; unconventional	actin binding [pmid
527	0	0	0	0	0	0	0	0			
528	0	0	0	0	0	0	0	0	Rap1 subgroup. The Rap1	intracellular; membrane [pmid	GTP binding; nucleotide
529	0	0	0	0.000389	0.001031	0.000783	0	0	Profilin binds actin	actin cytoskeleton	actin monomer binding
530	0	0	0.000777	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus; ribonucleoprotein	protein binding [pmid
531	0	0	0	0	0	0	0	0			
532	0	0	0	0	0	0	0	0	NOPS (NUC059) domain.	nucleus [pmid 9360842]	DNA binding; nucleotide
533	0	0	0	0	0	0	0	0	Histone 2A; H2A is a		
534	0	0	0	0	0	0	0	0	RHO protein GDP	cytoplasm [pmid 16130169];	GTPase activator activity;
535	0	0	0	0	0	0.000241	0	0	Histone 2A; H2A is a		
536	0	0	0	0	0	0	0	0	Mitochondrial glycoprotein.	mitochondrial matrix;	protein binding [pmid
537	0	0	0	0	0	0	0	0	Intermediate filament tail	lamin filament [pmid 7557986];	structural molecule activity
538	0	0	0	0	0	0	0	0	Proteasome activator pa28	cytosol; proteasome activator	proteasome activator activity
539	0	0	0	0	0	0	0	0	Rab27a subfamily. The		GTP binding; GTPase

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description
540	7	0.001762	0	0	INF		ENSG00000198618:N	PPIA			gi|10863927|ref|NP_	peptidylprolyl isomerase A [H
541	7	0.00171	3	8.69E-05	19.68235		ENSG00000161960:E	EIF4A1			gi|4503529|ref|NP_0	eukaryotic translation initiatio
542	7	0.001412	2	2.59E-05	54.54841		ENSG00000080824:E	HSP90AA1			gi|153792590|ref|NP	heat shock protein 90kDa alp
543	7	0.001345	0	0	INF		ENSG00000105202:E	FBL			gi|12056465|ref|NP_	fibrillarin [Homo sapiens]
544	7	0.001343	0	0	INF		ENSG00000172232:N	AZU1			gi|11342670|ref|NP_	azurocidin 1 preproprotein [H
545	7	0.001334	2	7.23E-05	18.44439		ENSG00000135046:E	ANXA1			gi|4502101|ref|NP_0	annexin I [Homo sapiens]
546	7	0.001325	0	0	INF		ENSG00000136167:E	LCP1			gi|4504965|ref|NP_0	L-plastin [Homo sapiens]
547	7	0.001252	0	0	INF		ENSG00000197785:E	ATAD3A			gi|42476028|ref|NP_	ATPase family, AAA domain
548	7	0.00113	0	0	INF		ENSG00000145779:E	TNFAIP8			gi|117676365|ref|NP	tumor necrosis factor, alpha-
549	7	0.00107	4	0.000147	7.296393		ENSG00000117592:E	PRDX6			gi|4758638|ref|NP_0	peroxiredoxin 6 [Homo sapie
550	7	0.000978	0	0	INF		ENSG00000171863:N	RPS7			gi|4506741|ref|NP_0	ribosomal protein S7 [Homo
551	7	0.000941	0	0	INF		ENSG00000115053:E	NCL			gi|55956788|ref|NP_	nucleolin [Homo sapiens]
552	7	0.000935	0	0	INF		ENSG00000214078:E	CPNE1			gi|23397708|ref|NP_	copine I [Homo sapiens]
553	7	0.000925	2	6.92E-05	13.35397		ENSG00000166128:E	RAB8B			gi|7706563|ref|NP_0	RAB8B, member RAS oncog
554	7	0.000903	0	0	INF		ENSG00000130985:E	UBE1			gi|23510340|ref|NP_	ubiquitin-activating enzyme E
555	7	0.000833	0	0	INF		ENSG00000072110:E	ACTN1			gi|4501891|ref|NP_0	actinin, alpha 1 [Homo sapie
556	7	0.000809	0	0	INF		ENSG00000071127:E	WDR1			gi|9257257|ref|NP_0	WD repeat-containing protei
557	7	0.000732	0	0	INF		ENSG00000212860:N	HSPA1A			gi|4885431|ref|NP_0	heat shock 70kDa protein 1B
558	7	0.000705	0	0	INF		ENSG00000110047:E	EHD1			gi|30240932|ref|NP_	EH-domain containing 1 [Hor
559	7	0.000629	0	0	INF		ENSG00000136286:E	MYO1G			gi|54873627|ref|NP_	myosin IG [Homo sapiens]
560	7	0.000619	0	0	INF		ENSG00000197111:E	PCBP2			gi|14141166|ref|NP_	poly(rC)-binding protein 2 iso
561	7	0.000563	0	0	INF		ENSG00000140105:E	WARS			gi|47419916|ref|NP_	tryptophanyl-tRNA synthetas
562	7	0.000542	0	0	INF		ENSG00000123136:E	DDX39			gi|21040371|ref|NP_	DEAD (Asp-Glu-Ala-Asp) bo
563	7	0.000533	0	0	INF		ENSG00000099783:E	HNRPM			gi|14141152|ref|NP_	heterogeneous nuclear ribon
564	7	0.000533	0	0	INF		ENSG00000108424:E	KPNB1			gi|19923142|ref|NP_	karyopherin beta 1 [Homo sa
565	7	0.000477	0	0	INF		ENSG00000182718:E	ANXA2P3			gi|50845386|ref|NP_	annexin A2 isoform 2 [Homo
566	7	0.00046	2	5.41E-06	84.9245		ENSG00000148180:E	GSN			gi|38044288|ref|NP_	gelsolin isoform b [Homo sap
567	7	0.000449	0	0	INF		ENSG00000115085:E	ZAP70			gi|31455611|ref|NP_	zeta-chain associated protei
568	7	0.000448	0	0	INF		ENSG00000094914:E	AAAS			gi|12962937|ref|NP_	achalasia, adrenocortical ins
569	7	0.000427	0	0	INF		ENSG00000092929:E	UNC13D			gi|46195765|ref|NP_	unc-13 homolog D [Homo sa
570	7	0.000404	0	0	INF		ENSG00000140575:E	IQGAP1			gi|4506787|ref|NP_0	IQ motif containing GTPase a
571	7	0.000377	0	0	INF		ENSG00000030066:E	NUP160			gi|54859722|ref|NP_	nucleoporin 160kDa [Homo s
572	7	0.000345	1	3.18E-06	108.457		ENSG00000014216:E	CAPN1			gi|12408656|ref|NP_	calpain 1, large subunit [Hom
573	7	0.000337	0	0	INF		ENSG00000076928:E	ARHGEF1			gi|15011972|ref|NP_	Rho guanine nucleotide exch
574	7	0.000329	0	0	INF		ENSG00000184922:E	FMNL1			gi|33356148|ref|NP_	formin-like 1 [Homo sapiens]
575	7	0.000304	0	0	INF		ENSG00000113013:E	HSPA9			gi|24234688|ref|NP_	heat shock 70kDa protein 9 p
576	7	0.000301	0	0	INF		ENSG00000155561:E	NUP205			gi|57634534|ref|NP_	nucleoporin 205kDa [Homo s
577	7	0.00025	0	0	INF		ENSG00000111335:E	OAS2			gi|74229017|ref|NP_	2'-5'-oligoadenylate syntheta
578	7	0.000247	2	1.43E-05	17.26184		ENSG00000168610:E	STAT3			gi|21618340|ref|NP_	signal transducer and activat
579	7	0.000208	0	0	INF		ENSG00000180448:E	HMHA1			gi|47834348|ref|NP_	minor histocompatibility antig
580	7	0.00019	0	0	INF		ENSG00000137801:E	THBS1			gi|40317626|ref|NP_	thrombospondin 1 precursor
581	7	0.000188	0	0	INF		ENSG00000077150:E	NFKB2			gi|117320531|ref|NP	nuclear factor of kappa light p
582	7	0.000166	0	0	INF		ENSG00000178209:E	PLEC1			gi|41322908|ref|NP_	plectin 1 isoform 3 [Homo sa
583	7	0.000147	2	1.38E-05	10.61619		ENSG00000170248:E	PDCD6IP			gi|22027538|ref|NP_	programmed cell death 6 inte
584	7	0.000131	0	0	INF		ENSG00000160883:E	HK3			gi|4504395|ref|NP_0	hexokinase 3 [Homo sapiens
585	6	0.009426	0	0	INF		ENSG00000172757:N	CFL1			gi|5031635|ref|NP_0	cofilin 1 (non-muscle) [Homo
586	6	0.004728	0	0	INF		ENSG00000118680:E	MRLC2			gi|15809016|ref|NP_	myosin regulatory light chain
587	6	0.00329	0	0	INF		ENSG00000074800:N	ENO1			gi|4503571|ref|NP_0	enolase 1 [Homo sapiens]
588	6	0.002952	4	0.000165	17.91427		ENSG00000143761:E	ARF1			gi|66879664|ref|NP_	ADP-ribosylation factor 1 [Ho
589	6	0.001955	0	0	INF		ENSG00000108774:E	RAB5C			gi|41393614|ref|NP_	RAB5C, member RAS oncog
590	6	0.00183	0	0	INF		ENSG00000166913:E	YWHAB			gi|21328448|ref|NP_	tyrosine 3-monooxygenase/tr
591	6	0.001722	3	6.68E-05	25.77178		NA:ENSMUSG00000	ARPC4			gi|5031595|ref|NP_0	actin related protein 2/3 com
592	6	0.001714	0	0	INF		ENSG00000067560:N	RHOA			gi|10835049|ref|NP_	ras homolog gene family, me
593	6	0.001695	0	0	INF		ENSG00000104824:E	HNRNPL			gi|52632383|ref|NP_	heterogeneous nuclear ribon
594	6	0.001658	0	0	INF		ENSG00000092199:N	HNRNPC			gi|117190254|ref|NP	heterogeneous nuclear ribon
595	6	0.001452	0	0	INF		ENSG00000213719:E	CLIC1			gi|14251209|ref|NP_	chloride intracellular channel
596	6	0.001358	1	4.07E-05	33.3419		ENSG00000163466:E	ARPC2			gi|23238211|ref|NP_	actin related protein 2/3 com
597	6	0.001192	0	0	INF		ENSG00000170144:E	HNRPA3			gi|34740329|ref|NP_	heterogeneous nuclear ribon
598	6	0.001185	0	0	INF		ENSG00000079246:E	XRCC5			gi|10863945|ref|NP_	ATP-dependent DNA helicas
599	6	0.001159	0	0	INF		ENSG00000115875:E	SFRS7			gi|72534660|ref|NP_	splicing factor, arginine/serin
600	6	0.001078	3	0.000156	6.895708		ENSG00000080371:E	RAB21			gi|7661922|ref|NP_0	RAB21, member RAS oncog
601	6	0.001061	0	0	INF		ENSG00000141522:N	ARHGDIA			gi|4757768|ref|NP_0	Rho GDP dissociation inhibit
602	6	0.000929	3	5.13E-05	18.09723		ENSG00000131236:E	CAP1			gi|157649073|ref|NP	adenylyl cyclase-associated
603	6	0.000878	0	0	INF		ENSG00000101347:E	SAMHD1			gi|38016914|ref|NP_	SAM domain- and HD domai
604	6	0.000852	0	0	INF		ENSG00000198034:E	RPS4X			gi|4506725|ref|NP_0	ribosomal protein S4, X-linke
605	6	0.000851	2	8.21E-05	10.36689		ENSG00000143878:E	RHOB			gi|4757764|ref|NP_0	ras homolog gene family, me
606	6	0.00085	0	0	INF		ENSG00000189403:N	HMGB1			gi|4504425|ref|NP_0	high-mobility group box 1 [Ho
607	6	0.000827	0	0	INF		ENSG00000164587:E	RPS14			gi|68160922|ref|NP_	ribosomal protein S14 [Homo
608	6	0.000794	0	0	INF		ENSG00000181163:N	NPM1			gi|10835063|ref|NP_	nucleophosmin 1 isoform 1 [
609	6	0.000791	0	0	INF		ENSG00000110958:E	PTGES3			gi|23308579|ref|NP_	unactive progesterone recep
610	6	0.000785	0	0	INF		ENSG00000133574:E	GIMAP4			gi|8922873|ref|NP_0	GTPase, IMAP family memb
611	6	0.00078	0	0	INF		ENSG00000130429:E	ARPC1B			gi|5031601|ref|NP_0	actin related protein 2/3 com
612	6	0.000686	0	0	INF		ENSG00000188846:N	RPL14			gi|78000183|ref|NP_	ribosomal protein L14 [Homo
613	6	0.000673	0	0	INF		ENSG00000166441:N	RPL27A			gi|4506625|ref|NP_0	ribosomal protein L27a [Hom
614	6	0.000629	0	0	INF		ENSG00000148834:E	GSTO1			gi|4758484|ref|NP_0	glutathione-S-transferase om
615	6	0.000609	0	0	INF		ENSG00000115956:E	PLEK			gi|156616273|ref|NP	pleckstrin [Homo sapiens]
616	6	0.000575	0	0	INF		ENSG00000170027:E	YWHAG			gi|21464101|ref|NP_	tyrosine 3-monooxygenase/tr
617	6	0.000549	0	0	INF		ENSG00000141543:E	EIF4A3			gi|7661920|ref|NP_0	eukaryotic translation initiatio
618	6	0.000536	0	0	INF		ENSG00000160211:E	G6PD			gi|108773793|ref|NP	glucose-6-phosphate dehydr
619	6	0.000532	1	9.49E-06	56.01025		ENSG00000196419:E	XRCC6			gi|4503841|ref|NP_0	ATP-dependent DNA helicas
620	6	0.000499	2	2.12E-05	23.53648		ENSG00000100347:E	SAMM50			gi|31542301|ref|NP_	sorting and assembly machir
621	6	0.000489	0	0	INF		ENSG00000132383:E	RPA1			gi|4506583|ref|NP_0	replication protein A1, 70kDa
622	6	0.000477	0	0	INF		ENSG00000134308:E	YWHAQ			gi|5803227|ref|NP_0	tyrosine 3/tryptophan 5 -mon
623	6	0.000466	0	0	INF		ENSG00000089157:N	RPLP0			gi|16933546|ref|NP_	ribosomal protein P0 [Homo
624	6	0.000451	0	0	INF		ENSG00000082898:E	XPO1			gi|4507943|ref|NP_0	exportin 1 [Homo sapiens]
625	6	0.000441	0	0	INF		ENSG00000142657:E	PGD			gi|40068518|ref|NP_	phosphogluconate dehydrog
626	6	0.000438	2	1.41E-05	31.00001		ENSG00000141959:E	PFKL			gi|48762920|ref|NP_	liver phosphofructokinase is
627	6	0.000429	0	0	INF		ENSG00000111679:E	PTPN6			gi|18104989|ref|NP_	protein tyrosine phosphatase
628	6	0.00042	0	0	INF		ENSG00000085491:E	SLC25A24			gi|148491091|ref|NP	solute carrier family 25 memb
629	6	0.000388	0	0	INF		ENSG00000196101:N	LOC100133811			gi|169217452|ref|XP	PREDICTED: similar to hCG
630	6	0.000384	0	0	INF		ENSG00000120948:E	TARDBP			gi|6678271|ref|NP_0	TAR DNA binding protein [Ho
631	6	0.000358	0	0	INF		ENSG00000169564:E	PCBP1			gi|5453854|ref|NP_0	poly(rC) binding protein 1 [Ho
632	6	0.000339	2	1.66E-05	20.46989		ENSG00000124207:E	CSE1L			gi|29029559|ref|NP_	CSE1 chromosome segregat
633	6	0.000334	0	0	INF		ENSG00000015479:E	MATR3			gi|62750354|ref|NP_	matrin 3 [Homo sapiens]
634	6	0.00032	0	0	INF		ENSG00000127483:E	HP1BP3			gi|56676330|ref|NP_	HP1-BP74 [Homo sapiens]
635	6	0.000315	2	5.05E-05	6.243112		ENSG00000130204:E	TOMM40			gi|5174723|ref|NP_0	mitochondrial outer membran
636	6	0.000312	0	0	INF		ENSG00000125944:E	HNRNPR			gi|5031755|ref|NP_0	heterogeneous nuclear ribon
637	6	0.000301	0	0	INF		ENSG00000144028:E	ASCC3L1			gi|40217847|ref|NP_	activating signal cointegrator
638	6	0.000276	0	0	INF		ENSG00000054118:E	THRAP3			gi|4827040|ref|NP_0	thyroid hormone receptor ass
639	6	0.000271	0	0	INF		ENSG00000170542:E	SERPINB9			gi|4758906|ref|NP_0	serine (or cysteine) proteinas
640	6	0.000247	0	0	INF		ENSG00000065135:E	GNAI3			gi|5729850|ref|NP_0	guanine nucleotide binding p
641	6	0.000242	2	8.8E-06	27.50945		ENSG00000010256:E	UQCRC1			gi|46593007|ref|NP_	ubiquinol-cytochrome c redu
642	6	0.00024	0	0	INF		ENSG00000174231:E	PRPF8			gi|91208426|ref|NP_	U5 snRNP-specific protein [H
643	6	0.000239	0	0	INF		ENSG00000163565:E	IFI16			gi|112789562|ref|NP	interferon, gamma-inducible
644	6	0.000229	0	0	INF		ENSG00000125450:E	NUP85			gi|13376259|ref|NP_	nucleoporin 85 [Homo sapien
645	6	0.00022	0	0	INF		ENSG00000155849:E	ELMO1			gi|18765700|ref|NP_	engulfment and cell motility 1
646	6	0.000203	0	0	INF		ENSG00000126261:E	SAE2			gi|4885649|ref|NP_0	SUMO-1 activating enzyme s
647	6	0.000198	0	0	INF		ENSG00000079785:E	DDX1			gi|4826686|ref|NP_0	DEAD (Asp-Glu-Ala-Asp) bo
648	6	0.000184	0	0	INF		ENSG00000100092:E	PDXP			gi|85815829|ref|NP_	SH3-domain binding protein
649	6	0.00018	0	0	INF		ENSG00000092820:E	VIL2			gi|21614499|ref|NP_	ezrin [Homo sapiens]
650	6	0.000177	0	0	INF		ENSG00000113569:E	NUP155			gi|24430149|ref|NP_	nucleoporin 155kDa isoform
651	6	0.000175	0	0	INF		ENSG00000069248:E	NUP133			gi|26051235|ref|NP_	nucleoporin 133kDa [Homo s
652	6	0.000173	0	0	INF		ENSG00000100201:E	DDX17			gi|148613856|ref|NP	DEAD box polypeptide 17 is
653	6	0.000166	0	0	INF		ENSG00000137752:E	CASP1			gi|15431328|ref|NP_	caspase 1 isoform alpha pre
654	6	0.000155	2	1.14E-05	13.67593		ENSG00000087470:E	DNM1L			gi|5031677|ref|NP_0	dynamin 1-like protein isofor
655	6	0.00015	0	0	INF		ENSG00000165271:E	NOL6			gi|18644728|ref|NP_	nucleolar protein family 6 alp
656	6	0.000145	0	0	INF		ENSG00000177189:E	RPS6KA3			gi|4759050|ref|NP_0	ribosomal protein S6 kinase,
657	6	0.00014	0	0	INF		ENSG00000166501:E	PRKCB1			gi|20127450|ref|NP_	protein kinase C, beta isofor
658	6	0.000137	0	0	INF		ENSG00000108592:E	FTSJ3			gi|17017991|ref|NP_	FtsJ homolog 3 [Homo sapie
659	6	0.000134	1	2.38E-06	56.47165		ENSG00000173692:E	PSMD1			gi|25777600|ref|NP_	proteasome 26S non-ATPas
660	6	0.000125	0	0	INF		ENSG00000112062:E	MAPK14			gi|20986512|ref|NP_	mitogen-activated protein kin
661	6	0.000124	0	0	INF		ENSG00000106105:E	GARS			gi|116805340|ref|NP	glycyl-tRNA synthetase [Hom
662	6	0.000122	0	0	INF		ENSG00000131504:E	DIAPH1			gi|119395758|ref|NP	diaphanous 1 isoform 1 [Hom
663	6	0.000115	0	0	INF		ENSG00000095319:E	NUP188			gi|62955803|ref|NP_	nucleoporin 188kDa [Homo s
664	6	0.000107	0	0	INF		ENSG00000075856:E	SART3			gi|7661952|ref|NP_0	squamous cell carcinoma an
665	6	9.12E-05	0	0	INF		ENSG00000038358:E	EDC4			gi|45827771|ref|NP_	autoantigen RCD8 [Homo sa
666	6	8.55E-05	0	0	INF		ENSG00000145703:E	IQGAP2			gi|116089337|ref|NP	IQ motif containing GTPase a
667	6	8.02E-05	0	0	INF		ENSG00000055163:E	CYFIP2			gi|116805788|ref|NP	cytoplasmic FMR1 interacting
668	6	6.17E-05	1	8.88E-07	69.53903		ENSG00000124486:E	USP9X			gi|145309309|ref|NP	ubiquitin specific protease 9,
669	6	4.86E-05	0	0	INF		ENSG00000153827:E	TRIP12			gi|10863903|ref|NP_	thyroid hormone receptor inte
670	6	4.47E-05	0	0	INF		ENSG00000086758:E	HUWE1			gi|61676188|ref|NP_	HECT, UBA and WWE doma
671	6	4.47E-05	0	0	INF		ENSG00000153201:E	RANBP2			gi|150418007|ref|NP	RAN binding protein 2 [Homo
672	6	1.42E-05	0	0	INF		ENSG00000129003:E	VPS13C			gi|42544121|ref|NP_	vacuolar protein sorting 13C
673	5	0.011547	0	0	INF		ENSG00000163221:N	S100A12			gi|5032059|ref|NP_0	S100 calcium-binding protein
674	5	0.003312	0	0	INF		ENSG00000143546:E	S100A8			gi|21614544|ref|NP_	S100 calcium-binding protein
675	5	0.00269	0	0	INF		ENSG00000164032:E	H2AFZ			gi|4504255|ref|NP_0	H2A histone family, member
676	5	0.002443	0	0	INF		ENSG00000163220:E	S100A9			gi|4506773|ref|NP_0	S100 calcium-binding protein
677	5	0.001926	0	0	INF		ENSG00000169397:E	RNASE3			gi|45243507|ref|NP_	ribonuclease, RNase A family
678	5	0.001765	3	8.53E-05	20.69303		ENSG00000138071:E	ACTR2			gi|5031571|ref|NP_0	actin-related protein 2 isofor
679	5	0.00172	0	0	INF		ENSG00000158710:E	TAGLN2			gi|4507357|ref|NP_0	transgelin 2 [Homo sapiens]
680	5	0.001685	0	0	INF		ENSG00000198191:N	PGAM1			gi|4505753|ref|NP_0	phosphoglycerate mutase 1 (
681	5	0.001613	0	0	INF		ENSG00000177105:E	RHOG			gi|46249393|ref|NP_	ras homolog gene family, me
682	5	0.001597	0	0	INF		ENSG00000132507:E	EIF5A			gi|169211223|ref|XP	PREDICTED: similar to euka
683	5	0.00159	0	0	INF		ENSG00000140988:N	RPS2			gi|15055539|ref|NP_	ribosomal protein S2 [Homo
684	5	0.001528	0	0	INF		ENSG00000084207:E	GSTP1			gi|4504183|ref|NP_0	glutathione transferase [Hom
685	5	0.00128	0	0	INF		NA:ENSMUSG00000	LOC100130553			gi|169168597|ref|XP	PREDICTED: hypothetical pr
686	5	0.001199	0	0	INF		ENSG00000134419:E	RPS15A			gi|71772415|ref|NP_	ribosomal protein S15a [Hom

									RESTING LYMPHOCYTES NEs							
rk	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S=signal; A=Anchor; Q=none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV
540	165	18012	7.8	0	o	Q	15	0.001	0.002948	0.001555	0	0.003426	0.004936	4	0.001982	0.001542
541	406	46154	5.5	0	o	Q	0	0	0.001598	0.002052	0	0.000557	0	3	0.001052	0.00094
542	854	98161	5.2	0	o	Q	17	0	0.00057	0.000668	0	0.002293	0	3	0.000882	0.000985
543	321	33784	10.2	0	o	Q	20	0	0.00101	0.002035	0.002341	0.001156	0	4	0.001635	0.000653
544	251	26886	9.5	0	o	S	20	1	0.001938	0.001301	0.002246	0.000141	0	4	0.001406	0.000931
545	346	38714	7	0	o	Q	20	0	0.00375	0.002427	0.001086	0.000562	0	4	0.001956	0.001431
546	627	70289	5.3	0	o	Q	0	0	0.002328	0.000893	0	0.00231	0	3	0.001383	0.001141
547	634	71357	9	0	o	Q	16	0	0.002302	0.001246	0.000889	5.57E-05	0	4	0.001123	0.000931
548	198	23003	7.9	0	o	Q	0	0	0.001638	0.000118	0.004744	0.000892	0	4	0.001848	0.002028
549	224	25035	6.4	0	o	Q	17	0.007	0.000724	0.001145	0.000839	0.000631	0	4	0.000835	0.000224
550	194	22127	10.1	0	o	Q	0	0	0.000836	0.001496	0	0.001184	0.002099	4	0.000879	0.000645
551	710	76615	4.7	0	o	Q	0	0	0	0.000361	0.000265	0.000697	0	3	0.000331	0.000288
552	537	59059	5.8	0	o	Q	15	0.081	0.000906	0.00013	0	0.000395	0	3	0.000358	0.000401
553	207	23584	9.1	0	o	Q	21	0.022	0.001567	0.000225	0	0.000171	0	3	0.000491	0.000724
554	1058	117849	5.8	0	o	Q	36	0.001	0.002146	0.000551	0	0.001102	0	3	0.00095	0.000916
555	892	103058	5.4	0	o	Q	0	0	0.003384	0.000311	0	0.000208	0	3	0.000976	0.001611
556	606	66194	6.7	0	o	Q	21	0.001	0.000268	0.000462	0.00093	0.001661	0	4	0.00083	0.00062
557	641	70025	5.6	0	o	Q	17	0.049	0.000253	3.64E-05	0.001465	0.001399	0	4	0.000789	0.000749
558	534	60627	6.8	0	o	Q	31	0.001	0.001215	0.00052	0.001407	0.000681	0	4	0.000956	0.000423
559	1018	116440	8.8	0	o	Q	0	0	0.000637	0.001511	0.000185	0.000729	0	4	0.000765	0.000551
560	362	38222	6.8	0	o	Q	23	0.001	0.001792	0.000193	0.000519	0.000683	0.002249	5	0.000797	0.000694
561	471	53165	6.2	0	o	Q	21	0.026	0.000689	4.95E-05	0	0.000638	0	3	0.000344	0.00037
562	427	49130	5.7	0	o	Q	0	0	0.001139	0.000901	0	8.27E-05	0	3	0.000531	0.000574
563	730	77516	8.7	0	o	Q	14	0	0.000222	0.000863	0.000257	0.000823	0	4	0.000541	0.000349
564	876	97170	4.8	0	o	Q	46	0	0.00037	0.000346	0	0.000807	0	3	0.000381	0.00033
565	339	38604	7.8	0	o	Q	19	0.001	0.000478	0.000826	0.001108	0.000469	0	4	0.00072	0.000307
566	731	80641	5.8	0	o	Q	0	0	0.000666	0.000128	0.001799	0.000314	0	4	0.000727	0.000749
567	619	69872	7.7	0	o	Q	21	0.211	0	0.000829	0.000304	0.000457	0	3	0.000397	0.000345
568	546	59574	7.5	0	o	Q	15	0	0.000594	0.000555	0	9.71E-05	0	3	0.000312	0.000307
569	1090	123282	6.7	0	o	Q	19	0	0.001637	0.000257	0.000345	0.000146	0	4	0.000596	0.000698
570	1657	189251	6.5	0	o	Q	19	0	0.000196	0.00038	0.000227	0.000885	0	4	0.000422	0.000319
571	1436	162121	5.5	0	o	Q	18	0.029	0	0.000471	0.000916	0.000148	0	3	0.000384	0.000406
572	714	81890	5.7	0	o	Q	17	0.012	0.000454	0.000359	0.000789	0.000396	0	4	0.0005	0.000197
573	912	102435	5.7	0	o	Q	27	0.001	0.000356	0.000435	0.000206	0.000291	0	4	0.000322	9.71E-05
574	1100	121827	5.7	0	o	Q	16	0	0.000295	0.000276	0.000342	0.000337	0	4	0.000312	3.23E-05
575	679	73681	6.2	0	o	S	25	0.825	0.000239	0.000275	0	0.00065	0.0006	4	0.000291	0.000269
576	2012	227918	6.2	0	o	Q	16	0.005	0.000242	0.000371	0	0.000114	0	3	0.000182	0.00016
577	687	78787	8	0	o	Q	18	0	0	0.000373	0	7.71E-05	0.001185	3	0.000113	0.000178
578	770	88068	6.3	0	o	Q	0	0	0.000211	0.000394	0.000244	0.00039	0	4	0.00031	9.6E-05
579	1136	124614	6.1	0	o	Q	22	0	0.000428	8.21E-05	0.000165	0.000109	0	4	0.000196	0.000159
580	1170	129383	4.9	0	o	S	19	0.994	0.000277	0.000319	0.000161	0.000196	0	4	0.000238	7.26E-05
581	900	96749	6.2	0	o	Q	0	0	0.00036	0.000104	0	0.000157	0	3	0.000155	0.000151
582	4525	513712	5.8	0	o	Q	0	0	0.000251	0.000182	0	0.00041	0	3	0.000211	0.00017
583	868	96023	6.5	0	o	Q	19	0	0.000187	2.69E-05	0.000433	0.000285	0	4	0.000233	0.000171
584	923	98919	5.4	0	o	Q	18	0	0.000176	0.000152	0	9.57E-05	0	3	0.000106	7.81E-05
585	166	18502	8.1	0	o	Q	0	0	0	0.003934	0	0.016803	0.009811	3	0.005184	0.007965
586	172	19779	4.8	0	i	Q	30	0	0	0.00122	0.002185	0.015302	0	3	0.004677	0.00714
587	434	47169	7.4	0	o	Q	42	0	0	0.000645	0	0.005519	0	2	0.001541	0.00267
588	181	20697	6.8	0	o	Q	30	0	0.001792	0.002593	0	0.00527	0	3	0.002414	0.002191
589	216	23483	8.4	0	o	Q	34	0.021	0.002252	0.001836	0	8.18E-05	0	3	0.001042	0.001169
590	246	28082	4.8	0	o	Q	0	0	0	0.001016	0	0.003508	0.001655	3	0.001131	0.001655
591	168	19667	8.4	0	o	S	22	0.568	0	0.000139	0.001118	0.002313	0	3	0.000893	0.00107
592	193	21768	6.1	0	o	Q	23	0.009	0	0.001473	0.005273	0.001239	0	3	0.001996	0.002278
593	589	64133	8.2	0	o	Q	46	0.001	0	0.000713	0.000319	0.00147	0	3	0.000625	0.000634
594	293	32338	5.1	0	o	Q	36	0	0	0.000876	0.002565	0.002945	0.004169	4	0.001596	0.001394
595	241	26923	5.2	0	o	Q	19	0	0	0.000484	0.006237	0.001759	0	3	0.00212	0.002843
596	300	34333	7.3	0	o	Q	17	0	0	0.000622	0.000626	0.002826	0	3	0.001019	0.00124
597	378	39595	9	0	o	Q	0	0	0	0.000864	0.000994	0.001542	0	3	0.00085	0.000638
598	732	82705	5.8	0	o	Q	22	0.279	0	0.00102	0.000513	0.002244	0	3	0.000944	0.000961
599	238	27367	11.8	0	o	Q	26	0	0	0.000343	0	0.000148	0.001711	3	0.000123	0.000163
600	225	24348	7.9	0	o	Q	20	0.354	0.001441	0.002073	0.002505	0.000393	0	4	0.001603	0.000918
601	204	23207	5.1	0	o	Q	0	0	0	0.000229	0.002456	0.000779	0	3	0.000866	0.001109
602	475	51673	8	0	o	Q	33	0	0.00239	0.000196	0	0.000893	0	3	0.00087	0.001083
603	626	72201	7.1	0	o	Q	0	0	0.000518	0.00149	0	0.001383	0	3	0.000848	0.000713
604	263	29598	10.2	0	o	Q	58	0.011	0	0.000355	0.001429	0.000977	0	3	0.00069	0.000637
605	196	22123	5.2	0	o	Q	23	0.011	0	0.000323	0.004234	0.000867	0	3	0.001356	0.001952
606	215	24894	5.7	0	o	Q	24	0	0	0.000325	0.000874	0.000164	0	3	0.000341	0.000379
607	151	16273	10.1	0	i	Q	25	0.001	0	0.000309	0.002488	0	0	2	0.000699	0.001202
608	294	32575	4.8	0	o	Q	0	0	0	7.93E-05	0	0.001202	0.00277	3	0.00032	0.000589
609	160	18697	4.5	0	o	Q	0	0	0	0.000437	0.002348	0.000773	0	3	0.00089	0.001023
610	329	37534	7.8	0	o	Q	19	0.001	0.000986	0.001418	0	0.00043	0	3	0.000708	0.000622
611	372	40950	8.4	0	o	Q	16	0.003	0	0.000376	0.001515	0.000617	0	3	0.000627	0.000644
612	215	23432	10.9	0	o	Q	27	0.006	0	0.000976	0	0.000246	0.003787	3	0.000306	0.000462
613	148	16561	11	0	i	Q	24	0	0	0.000315	0.002539	0.000477	0	3	0.000833	0.001154
614	241	27566	6.6	0	o	Q	0	0	0.001346	0.000387	0	0.000147	0	3	0.00047	0.000605
615	350	40125	8.3	0	o	Q	0	0	0	0.001066	0.001074	0.00106	0	3	0.0008	0.000533
616	247	28303	4.9	0	o	Q	0	0	0	0.000202	0	0.000801	0.001648	3	0.000251	0.000379
617	411	46871	6.7	0	o	Q	14	0.002	0	0.00042	0	0.000559	0	2	0.000245	0.000288
618	515	59257	6.8	0	o	Q	26	0	0.000315	0.000951	0	0.000549	0	3	0.000454	0.000401
619	609	69843	6.6	0	o	Q	0	0	0.000266	0.000881	0	0.00116	0	3	0.000577	0.000536
620	469	51962	6.9	0	o	Q	24	0	0	0.000995	0.000801	0.000226	0	3	0.000505	0.000469
621	616	68138	7.2	0	o	Q	20	0.001	0	0.000151	0.002135	0.000459	0	3	0.000686	0.000984
622	245	27764	4.8	0	o	Q	0	0	0	0.000612	0	0.001394	0.001662	3	0.000502	0.000661
623	317	34274	6	0	o	Q	0	0	0	0.000294	0.000593	0.00078	0	3	0.000417	0.000342
624	1071	123386	6.1	0	o	Q	16	0.006	0	0.000174	0.001228	0.000214	0	3	0.000404	0.000557
625	483	53140	7.2	0	o	Q	16	0.119	0	0.000241	0.001556	0.000439	0	3	0.000559	0.000688
626	780	85018	7.5	0	o	Q	30	0.035	0.000208	0.000329	0	0.000584	0	3	0.00028	0.000244
627	595	67561	7.8	0	o	Q	26	0	0.000545	0.000392	0	0.000742	0	3	0.00042	0.000314
628	477	53354	6.3	0	o	Q	19	0.046	0	0.001027	0	0.000444	0.000854	3	0.000368	0.000487
629	223	25700	6.9	0	o	Q	28	0.005	0.000182	0.001121	0	0.000158	0	3	0.000365	0.00051
630	414	44740	6.2	0	o	Q	0	0	0	0.000282	0	0.00064	0	2	0.00023	0.000304
631	356	37526	7.1	0	o	Q	23	0.002	0.001367	0.000131	0	0.000248	0	3	0.000436	0.000628
632	971	110417	5.8	0	o	Q	0	0	0	0.000504	0.000774	0.000528	0	3	0.000451	0.000325
633	847	94623	6.3	0	o	S	38	0.611	0.000383	0.000606	0	0.000626	0	3	0.000404	0.000291
634	553	61207	9.7	0	o	Q	28	0.141	0.000293	0.000169	0	0.000799	0	3	0.000315	0.000344
635	361	37893	7.3	0	o	Q	46	0.085	0	0.001034	0	0.000147	0	2	0.000295	0.000497
636	633	70943	8.1	0	o	Q	0	0	0.000769	0.000147	0	0.000865	0	3	0.000445	0.000435
637	2136	244505	6.1	0	o	Q	0	0	0	0.000273	0	0.000686	0.000572	3	0.00024	0.000324
638	955	108694	10.2	0	o	Q	58	0	0	7.33E-05	0.001377	0.000185	0	3	0.000409	0.00065
639	376	42404	5.9	0	o	Q	21	0.016	0.000863	0.000186	0	0.000329	0.001083	4	0.000344	0.000371
640	354	40532	5.7	0	o	Q	0	0	0	0.000189	0.000694	0.00017	0	3	0.000263	0.0003
641	480	52646	6.4	0	o	S	42	0.68	0.000338	9.72E-05	0	0.00092	0	3	0.000339	0.000413
642	2335	273599	8.8	0	o	Q	27	0	0	0.00022	0.000241	0.000409	0	3	0.000217	0.000168
643	729	82096	9.3	0	o	Q	0	0	0	0.000196	0.000258	0.000412	0	3	0.000216	0.00017
644	656	75019	5.6	0	o	Q	19	0	0	0.000107	0.001146	5.39E-05	0	3	0.000327	0.000548
645	727	83829	6.3	0	o	Q	20	0	0	0.000192	0	9.72E-05	0	2	7.24E-05	9.22E-05
646	640	71224	5.3	0	o	Q	28	0.204	0	0.000182	0.000294	0.000414	0	3	0.000222	0.000176
647	740	82432	7.2	0	o	Q	17	0.01	0.000219	0.000221	0	0.000358	0	3	0.000199	0.000148
648	701	75713	6.8	0	o	Q	26	0.003	0.000231	0.0002	0	0.000176	0	3	0.000152	0.000104
649	586	69413	6.3	0	o	Q	17	0	0.000277	0.000119	0	0.000332	0	3	0.000182	0.000151
650	1391	155199	6.2	0	o	S	17	0.976	0.000233	0.000285	0	0.000216	0	3	0.000184	0.000126
651	1156	128979	5.1	0	o	Q	57	0.129	0.00014	0.000262	0	0.000153	0	3	0.000139	0.000108
652	731	80458	8.4	0	o	S	22	0.985	0	9.57E-05	0	0.000252	0	2	8.7E-05	0.000119
653	404	45159	5.9	0	o	Q	25	0	0.000401	0.000115	0	0.000219	0	3	0.000184	0.00017
654	699	78061	6.7	0	o	Q	21	0	0.000464	6.67E-05	0	0.000202	0	3	0.000183	0.000205
655	1146	127593	7.6	0	o	Q	16	0	0	0.000122	0	0.000123	0	2	6.14E-05	7.09E-05
656	740	83736	6.9	0	o	Q	15	0	0	6.3E-05	0.000508	7.16E-05	0	3	0.000161	0.000234
657	673	77012	7	0	o	Q	0	0	0.000241	0.000243	0	5.25E-05	0	3	0.000134	0.000126
658	847	96576	8.2	0	o	Q	64	0.005	0	0.00011	0.000665	2.09E-05	0	3	0.000199	0.000315
659	953	105836	5.4	0	o	Q	18	0.004	0	2.45E-05	0.000591	5.56E-05	0	3	0.000168	0.000283
660	360	41293	5.8	0	o	Q	41	0	0.00045	0.00013	0	9.81E-05	0	3	0.00017	0.000195
661	739	83166	7	0	o	S	27	0.999	0.000219	0.000126	0	0.000287	0	3	0.000158	0.000124
662	1272	141347	5.4	0	o	Q	0	0	0.000255	9.17E-05	0	0.000236	0	3	0.000146	0.000121
663	1749	196041	6.7	0	o	Q	35	0.104	9.27E-05	0.00012	0	2.02E-05	0	3	5.82E-05	5.73E-05
664	963	109935	5.6	0	o	Q	17	0	0	0.000121	0.000195	5.5E-05	0	3	9.28E-05	8.43E-05
665	1401	151661	5.9	0	o	Q	0	0	0	0.000166	0	3.78E-05	0	2	5.11E-05	7.9E-05
666	1575	180578	5.6	0	o	Q	0	0	0	4.44E-05	0.000239	0.000101	0	3	9.6E-05	0.000104
667	1253	145673	7.1	0	o	Q	18	0	0.000129	3.1E-05	0	5.64E-05	0	3	5.42E-05	5.52E-05
668	2570	292278	5.8	0	o	Q	18	0	6.31E-05	2.72E-05	0	4.81E-05	0	3	3.46E-05	2.74E-05
669	1992	220432	8.5	0	o	Q	0	0	0	1.17E-05	0	6.21E-05	0	2	1.84E-05	2.96E-05
670	4374	481896	5.2	0	o	Q	0	0	7.42E-05	4.27E-05	0	2.83E-05	0	3	3.63E-05	3.09E-05
671	3224	358201	6.2	0	o	Q	21	0	0	1.93E-05	5.83E-05	2.74E-05	0	3	2.62E-05	2.43E-05
672	3710	417279	6.6	0	o	Q	17	0.001	0	3.77E-05	0	1.43E-05	0.00011	3	1.3E-05	1.78E-05
673	92	10575	6.2	0	o	Q	0	0	0	0.001521	0	0.020736	0	2	0.005564	0.01014
674	93	10834	7	0	o	Q	0	0	0.003487	0	0	0.00019	0.004378	3	0.000919	0.001714
675	128	13553	10.6	0	o	Q	65	0.029	0	0.001822	0.004403	0.004781	0	3	0.002752	0.002257
676	114	13242	6.1	0	o	Q	28	0	0.007113	0.002046	0	0.00124	0	3	0.0026	0.003124
677	160	18385	10	0	o	S	28	0.998	0.002027	0.001895	0	0	0	2	0.000981	0.001134
678	394	44761	6.7	0	o	Q	24	0	0	0.000178	0	0.002062	0	2	0.00056	0.001005
679	199	22391	8.2	0	o	Q	17	0	0	0.000586	0.004721	0.003639	0	3	0.002236	0.0023
680	254	28804	7.2	0	o	Q	16	0	0	0.001928	0	0.001252	0	2	0.000795	0.000959
681	191	21308	8.1	0	o	Q	28	0.015	0	0.000977	0.008853	0.000555	0	3	0.002596	0.00419
682	184	20170	7	0	o	Q	0	0	0	0.00038	0	0.005472	0	2	0.001463	0.002679
683	293	31324	10.2	0	o	Q	21	0	0	0.000955	0	0.000784	0	2	0.000435	0.000507
684	210	23356	5.6	0	o	Q	29	0.084	0	0.000222	0	0.001598	0.021327	3	0.000455	0.000769
685	152	17719	11	0	o	Q	42	0	0.002134	0.000921	0.00618	0.000116	0	4	0.002338	0.002693
686	130	14839	10.1	0	o	Q	18	0	0	0.001076	0	0.000408	0	2	0.000371	0.000508

	PHA-TREATED LYMPHOCYTES NEs							
rk	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
540	0	0.000952	0	0.004748	0.000465	3	0.001541	0.002173
541	0.002187	0.000737	0	0.000965	0.005586	4	0.002368	0.002237
542	0.00052	0.000786	0	0.004952	0.001505	4	0.001941	0.00205
543	0	0.002376	0	0.000763	0.001076	3	0.001054	0.000991
544	0.003537	0.000358	0	0	0.001224	3	0.001279	0.00159
545	0.001283	0.000908	0	0.00066	0	3	0.000713	0.00054
546	0.00354	0.000501	0	0.000234	0.000796	4	0.001268	0.001532
547	0.003501	0.001762	0	0.000257	0	3	0.00138	0.001613
548	0	0.00068	0	0.000577	0.000388	3	0.000411	0.0003
549	0	0.001302	0	0.00306	0.000857	3	0.001305	0.001289
550	0	0.00081	0	0.000336	0.003166	3	0.001078	0.001431
551	0.000625	0.000822	0	0.004436	0.000324	4	0.001552	0.001934
552	0.003306	0.000209	0	3.04E-05	0.002502	4	0.001512	0.001642
553	0.004289	0.000325	0	7.88E-05	0.000742	4	0.001359	0.001972
554	0.001259	0.000191	0	0.000524	0.001451	4	0.000856	0.000597
555	0.002488	5.03E-05	0	0.000181	4.3E-05	4	0.000691	0.0012
556	0	0.000481	0	0.002478	0.00019	3	0.000787	0.001144
557	0	0.00049	0	0.001553	0.000659	3	0.000675	0.000648
558	0	0.000403	0	0.000764	0.000647	3	0.000453	0.000338
559	0	0.000793	0	0.000497	0.000679	3	0.000492	0.00035
560	0	0.000599	0	0	0.001166	2	0.000441	0.00056
561	0.001885	0.000476	0	3.46E-05	0.000734	4	0.000782	0.00079
562	0.00104	0.000263	0	4.37E-05	0.000863	4	0.000552	0.000475
563	0	0.000645	0	0.00114	0.000316	3	0.000525	0.000487
564	0.001013	0.000333	0	0.000428	0.000964	4	0.000685	0.000354
565	0	0.000662	0	4.81E-05	0.000226	3	0.000234	0.000301
566	0	3.07E-05	0	0.000112	0.00063	3	0.000193	0.000295
567	0.000717	0.000616	0	0.000422	0.000248	4	0.000501	0.000208
568	0.000813	0.000904	0	0.000269	0.000352	4	0.000584	0.00032
569	0.000814	0.000144	0	0	7.04E-05	3	0.000257	0.000376
570	0	0.000284	0	0.001054	0.000209	3	0.000387	0.000461
571	0.000309	0.000406	0	0.000205	0.000561	4	0.00037	0.000152
572	0	3.14E-05	0	0.000137	0.000591	3	0.00019	0.000274
573	0	0.000221	0	0.000179	0.00101	3	0.000353	0.000449
574	0	0.000388	0	0.000371	0.000628	3	0.000347	0.000259
575	0	9.91E-05	0	0.001058	0.000113	3	0.000317	0.000496
576	0.000441	0.000357	0	4.06E-05	0.000839	4	0.00042	0.000329
577	0	0.000588	0.001018	7.13E-05	0.000894	4	0.000388	0.000427
578	0	0.000291	0	0.000148	0.000299	3	0.000185	0.000141
579	0.000781	0	0	2.87E-05	6.76E-05	3	0.000219	0.000376
580	0.000379	0.000173	0	1.39E-05	0	3	0.000141	0.000177
581	0.000493	0.000199	0	1.81E-05	0.000171	4	0.00022	0.000199
582	0.000196	0.000178	0	7.57E-05	3.39E-05	4	0.000121	7.87E-05
583	0	5.17E-05	0	5.64E-05	0.000133	3	6.02E-05	5.47E-05
584	0.000481	8.1E-05	0	1.77E-05	4.16E-05	4	0.000155	0.000219
585	0	0.003919	0	0.040112	0.010638	3	0.013667	0.018169
586	0	0.00261	0	0.018407	0.000446	3	0.004779	0.009088
587	0.001023	0.001034	0	0.016771	0.001327	4	0.005039	0.007823
588	0	0.003426	0	0.008797	0.001739	3	0.003491	0.003804
589	0.010275	0.000742	0	0.000453	0	3	0.002868	0.004948
590	0	0.001733	0	0.004047	0.004336	3	0.002529	0.002049
591	0	0.001469	0	0.005537	0.003199	3	0.002551	0.002382
592	0	0.001893	0	0.003237	0.000597	3	0.001432	0.00144
593	0	0.00099	0	0.006872	0.003194	3	0.002764	0.003046
594	0	0.000919	0	0.005957	0	2	0.001719	0.002858
595	0	0.000559	0	0.001219	0.001363	3	0.000785	0.00063
596	0	0.000823	0	0.003917	0.002047	3	0.001697	0.001702
597	0	0.00089	0	0.004231	0.001016	3	0.001534	0.001854
598	0	0.001134	0	0.002051	0.002517	3	0.001426	0.001111
599	0.00746	0.001255	0	6.86E-05	0	3	0.002196	0.003556
600	0	0.001994	0	0.000218	0	2	0.000553	0.000966
601	0	0.00022	0	0.00104	0.003763	3	0.001256	0.001731
602	0	0.000331	0	0.003058	0.000566	3	0.000989	0.001399
603	0	0.001039	0	0.001486	0.001104	3	0.000907	0.000636
604	0	0.001549	0	0.002358	0.000146	3	0.001013	0.001136
605	0	0.000687	0	0.000309	0.000392	3	0.000347	0.000282
606	0	0.00167	0	0.003409	0.000357	3	0.001359	0.001544
607	0.00294	0.000297	0	0.000324	0.000254	4	0.000954	0.001324
608	0	0.000382	0	0.001554	0.003134	3	0.001267	0.001409
609	0	0.000421	0	0.001632	0.00072	3	0.000693	0.000692
610	0	0.002114	0	0.000397	0.000933	3	0.000861	0.000919
611	0	0.000844	0	0.000614	0.00227	3	0.000932	0.000961
612	0	0.000522	0	0.003568	0.000179	3	0.001067	0.001681
613	0	0.00091	0	0.000882	0.000259	3	0.000513	0.000455
614	0	0.000559	0	0.000203	0.002389	3	0.000788	0.001092
615	0	0.001282	0	0.00028	0.00011	3	0.000418	0.000587
616	0	0.000636	0	0.00218	0.000777	3	0.000898	0.000919
617	0.00216	0.000509	0	0.000278	0.000467	4	0.000854	0.000877
618	0	0.000523	0	0.000158	0.001789	3	0.000618	0.000811
619	0	0.00081	0	0.000884	0.000252	3	0.000487	0.00043
620	0	0.000813	0	0.000174	0.000982	3	0.000492	0.000478
621	0	0.000182	0	0.000238	0.000748	3	0.000292	0.00032
622	0	0.000183	0	0.001266	0.000363	3	0.000453	0.000562
623	0	0.000212	0	0.000154	0.001695	3	0.000516	0.000792
624	0	0.000168	0	0.000107	0.00172	3	0.000499	0.000817
625	0	0.000604	0	0.000372	0.000318	3	0.000323	0.000249
626	0	0.000374	0	0.000879	0.001132	3	0.000596	0.000507
627	0	0.000377	0	0.000603	0.000774	3	0.000439	0.000335
628	0	0.000658	0	0.000103	0.001127	3	0.000472	0.000524
629	0	0.001537	0	7.32E-05	3.44E-05	3	0.000411	0.000751
630	0.001072	0.000271	0	0.000434	0.000371	4	0.000537	0.000363
631	0	0.000273	0	0.000525	0.000323	3	0.00028	0.000216
632	0	0.000347	0	0.000286	0.000277	3	0.000227	0.000155
633	0	0.000583	0	0.000154	0.000317	3	0.000264	0.000249
634	0	0.000406	0	5.9E-05	0.000833	3	0.000324	0.000383
635	0	0.000932	0.001937	9.04E-05	0.000319	4	0.000335	0.00042
636	0	0.000142	0	0.000516	6.06E-05	3	0.00018	0.000231
637	0	0.000252	0	0.000229	0.00097	3	0.000363	0.000421
638	0	0.000164	0	0.000325	8.04E-05	3	0.000142	0.000139
639	0	0.000179	0	0	0.000613	2	0.000198	0.000289
640	0	0.000162	0	0.000541	0.000217	3	0.00023	0.000227
641	0	9.35E-05	0	0.000408	8E-05	3	0.000145	0.00018
642	0	0.000231	0	6.29E-05	0.000756	3	0.000262	0.000343
643	0	0.000277	0	0.000403	0.000369	3	0.000262	0.000183
644	0	0.000308	0	9.95E-05	0.000117	3	0.000131	0.000129
645	0.001221	3.09E-05	0	0.000112	0.000106	4	0.000367	0.00057
646	0	0.000175	0	0.000383	0.00018	3	0.000184	0.000156
647	0	0.000455	0	0.000176	0.000156	3	0.000197	0.000189
648	0.000633	0.00016	0	6.98E-05	0	3	0.000216	0.000286
649	0	0.000191	0	0.000195	0.000328	3	0.000178	0.000135
650	0	0.000339	0	1.17E-05	0.000331	3	0.00017	0.00019
651	0	0.000737	0	7.06E-05	3.32E-05	3	0.00021	0.000353
652	0.000607	0.000173	0	4.47E-05	0.00021	4	0.000259	0.000243
653	0	0.000278	0	0.000121	0.00019	3	0.000147	0.000117
654	0	6.42E-05	0	0.000117	0.00033	3	0.000128	0.000143
655	0.000775	0.000117	0	2.85E-05	3.35E-05	4	0.000239	0.00036
656	0	0.000121	0	0.000154	0.000242	3	0.000129	0.0001
657	0	0.00019	0	4.85E-05	0.000342	3	0.000145	0.000154
658	0	0.000212	0	3.85E-05	4.53E-05	3	7.39E-05	9.41E-05
659	0	2.35E-05	0	1.71E-05	0.000363	3	0.000101	0.000175
660	0	6.23E-05	0	4.53E-05	0.000213	3	8.02E-05	9.25E-05
661	0	0.000152	0	0.000155	5.19E-05	3	8.96E-05	7.65E-05
662	0	8.82E-05	0	0.000244	6.04E-05	3	9.81E-05	0.000104
663	0.000508	0.000167	0	9.33E-06	0	3	0.000171	0.000237
664	0	2.33E-05	0	0.00022	0.000239	3	0.000121	0.000127
665	0.000317	3.2E-05	0	1.16E-05	0.000164	4	0.000131	0.000141
666	0	7.12E-05	0	8.29E-05	0.000146	3	7.51E-05	5.99E-05
667	0	0.000179	0	3.91E-05	0.000207	3	0.000106	0.000102
668	0	6.11E-05	0	2.54E-05	0.000269	3	8.88E-05	0.000123
669	0.000223	5.63E-05	0	1.64E-05	1.93E-05	4	7.87E-05	9.78E-05
670	0.000101	4.1E-05	0	0	7.02E-05	3	5.32E-05	4.32E-05
671	0	0.000125	0	5.57E-05	7.14E-05	3	6.31E-05	5.15E-05
672	0	1.81E-05	0	4.4E-06	3.88E-05	3	1.53E-05	1.74E-05
673	0	0.001951	0	0.002661	0.065509	3	0.01753	0.032006
674	0	0	0	0.000526	0.02229	2	0.005704	0.01106
675	0	0.004389	0	0.00612	0	2	0.002627	0.003115
676	0	0.000394	0	0	0.008755	2	0.002287	0.004316
677	0.008323	0.001963	0	0	0.0012	3	0.002871	0.003723
678	0	0.000911	0	0.005302	0.00567	3	0.002971	0.002932
679	0	0.001127	0	0.00369	0	2	0.001204	0.00174
680	0	0.00212	0	0.005911	0.002267	3	0.002574	0.002454
681	0	0.001665	0	0.000854	0	2	0.00063	0.000799
682	0	0.000975	0	0.005322	0.000626	3	0.001731	0.002428
683	0	0.000153	0	0.007687	0.003144	3	0.002746	0.003598
684	0	0	0	0.002176	0.008226	2	0.0026	0.003888
685	0	0.000886	0	0	0	1	0.000221	0.000443
686	0	0.002071	0	0.004268	0.001772	3	0.002028	0.001751

	MMs										
rk	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
540	0	0	0	0	0	0	0	0	cyclophilin_ABH_like:		isomerase activity; peptide
541	0	0	0.000114	0.000107	0.000474	0	0	0	Helicase superfamily c-		ATP binding; ATP-dependent
542	0	0	0	0.000141	6.56E-05	0	0	0			
543	0	0	0	0	0	0	0	0	Fibrillarin; pfam01269	nucleus; ribonucleoprotein	methyltransferase activity;
544	0	0	0	0	0	0	0	0	Trypsin-like serine	azurophil granule [pmid	heparin binding [pmid
545	0	0	0	0.000262	0	0.000317	0	0	Annexin. This family of	cornified envelope [pmid	calcium ion binding [pmid
546	0	0	0	0	0	0	0	0	EF-hand, calcium binding	cytoplasm [pmid 2378651];	actin binding [pmid
547	0	0	0	0	0	0	0	0	ATPase family associated		ATP binding; nucleoside-
548	0	0	0	0	0	0	0	0			
549	0	0	0.000413	0.000405	0	0.00021	0.000145	0	Peroxiredoxin (PRX) family,	cytosol [pmid 9497358];	hydrolase activity;
550	0	0	0	0	0	0	0	0	Ribosomal protein S7e;	cytosolic small ribosomal	protein binding [pmid
551	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleolus [pmid 2394707];	DNA binding; nucleotide
552	0	0	0	0	0	0	0	0	VWA Copine: Copines are		calcium-dependent
553	0	0	0.000439	0.000115	0	0	0	0	Rab8/Sec4/Ypt2.	intracellular; membrane	ATP binding; GTP binding;
554	0	0	0	0	0	0	0	0	Ubiquitin activating enzyme		ATP binding; catalytic
555	0	0	0	0	0	0	0	0	Spectrin repeats, found in	cytoskeleton; focal adhesion	actin binding; calcium ion
556	0	0	0	0	0	0	0	0	WD40 domain, found in a	cytoskeleton	actin binding; protein binding
557	0	0	0	0	0	0	0	0	Hsp70 protein. Hsp70	cytoplasm [pmid 16130169];	ATP binding; nucleotide
558	0	0	0	0	0	0	0	0	Eps15 homology domain;		ATP binding; calcium ion
559	0	0	0	0	0	0	0	0	Myosin motor domain, type	myosin	ATP binding; motor activity
560	0	0	0	0	0	0	0	0	K homology RNA-binding	cytoplasm; nucleus;	DNA binding; nucleic acid
561	0	0	0	0	0	0	0	0	Tryptophanyl-tRNA	cytoplasm [pmid 16130169];	ATP binding; ligase activity;
562	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus [pmid 15047853]	ATP binding; ATP-dependent
563	0	0	0	0	0	0	0	0	N-acetylglucosamine-	integral to plasma membrane	nucleotide binding; RNA
564	0	0	0	0	0	0	0	0	Karyopherin (importin) beta	cytoplasm [pmid 7615630];	nuclear localization
565	0	0	0	0	0	0	0	0	Annexin. This family of	plasma membrane [pmid	calcium ion binding; calcium-
566	0	0	0	2.33E-05	0	2.01E-05	0	0	Gelsolin homology domain;	actin cytoskeleton [pmid	actin binding; calcium ion
567	0	0	0	0	0	0	0	0	Serine/Threonine protein	cytoplasm [pmid 12359715];	ATP binding [pmid 1423621];
568	0	0	0	0	0	0	0	0	WD40 domain, found in a	nuclear pore [pmid 12730363]	
569	0	0	0	0	0	0	0	0	Domain of Unknown		
570	0	0	0	0	0	0	0	0		actin filament [pmid 8670801];	calmodulin binding [pmid
571	0	0	0	0	0	0	0	0	Polyphosphate kinase	nuclear pore [pmid 11564755]	nucleocytoplasmic
572	0	0	0	2.54E-05	0	0	0	0	Calpains, domains IIa, IIb;	intracellular	calcium ion binding; calpain
573	0	0	0	0	0	0	0	0	Guanine nucleotide	cytoplasm [pmid 10747909];	GTPase activator activity;
574	0	0	0	0	0	0	0	0	Diaphanous GTPase-		actin binding; Rho GTPase
575	0	0	0	0	0	0	0	0	molecular chaperone DnaK;	cell surface [pmid 12493773];	ATP binding; nucleotide
576	0	0	0	0	0	0	0	0		nuclear pore [pmid 9348540];	protein binding [pmid
577	0	0	0	0	0	0	0	0		membrane [pmid 2440675];	ATP binding;
578	0	0	0	9.42E-05	0	2.03E-05	0	0	STAT protein, DNA binding	cytoplasm [pmid 7512451];	calcium ion binding;
579	0	0	0	0	0	0	0	0	RhoGAP_PARG1: RhoGAP	intracellular	
580	0	0	0	0	0	0	0	0	Thrombospondin C-terminal	extracellular region [pmid	calcium ion binding;
581	0	0	0	0	0	0	0	0			
582	0	0	0	0	0	0	0	0	Spectrin repeats, found in	cytoskeleton; intermediate	actin binding; structural
583	0	0	0	2.08E-05	0	8.96E-05	0	0	Ly49-like protein, N-	cytosol [pmid 9880530]	signal transducer activity
584	0	0	0	0	0	0	0	0	Hexokinase. Hexokinase	membrane	ATP binding; hexokinase
585	0	0	0	0	0	0	0	0	Actin depolymerisation	cytoplasm [pmid 16130169];	actin binding; protein binding
586	0	0	0	0	0	0	0	0	EF-hand, calcium binding		calcium ion binding
587	0	0	0	0	0	0	0	0	Enolase: Enolases are	cytoplasm [pmid 11256614];	DNA binding; lyase activity;
588	0	0	0.000558	0.000301	0	0.00028	0.00018	0	Arf1-Arf5-like subfamily.	intracellular; plasma	GTP binding; GTPase
589	0	0	0	0	0	0	0	0	Rab5-related subfamily.		GTP binding; GTPase
590	0	0	0	0	0	0	0	0	14-3-3 protein; pfam00244	cytoplasm [pmid 12963375];	monooxygenase activity;
591	0	0	0	0.000284	0.000189	6.14E-05	0	0	ARP2/3 complex 20 kDa	Arp2/3 protein complex [pmid	actin filament binding [pmid
592	0	0	0	0	0	0	0	0		cytoskeleton; intracellular;	GTP binding; GTPase
593	0	0	0	0	0	0	0	0	RNA recognition motif;	heterogeneous nuclear	nucleic acid binding;
594	0	0	0	0	0	0	0	0			
595	0	0	0	0	0	0	0	0	GST_C family, Chloride	brush border [pmid	chloride ion binding; protein
596	0	0	0.000326	0	0	0	0	0	Arp2/3 complex, 34 kD	Arp2/3 protein complex [pmid	structural constituent of
597	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus; ribonucleoprotein	nucleotide binding; RNA
598	0	0	0	0	0	0	0	0	Ku C terminal domain like.	DNA-dependent protein kinase	ATP binding; ATP-dependent
599	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus [pmid 8013463]	metal ion binding; nucleotide
600	0	0	0.000622	0.000488	0	0.00014	0	0	Rab21 subfamily. The	endosome [pmid 11256614]	GTP binding; nucleotide
601	0	0	0	0	0	0	0	0	RHO protein GDP	cytoplasm; cytoskeleton [pmid	GTPase activator activity;
602	0	0	9.76E-05	3.83E-05	0	0	0.000275	0			
603	0	0	0	0	0	0	0	0	Sterile alpha motif.;	intracellular [pmid 11064105];	3',5'-cyclic-nucleotide
604	0	0	0	0	0	0	0	0	RS4NT (NUC023) domain.	intracellular; ribosome [pmid	rRNA binding; structural
605	0	0	0.000472	0.000185	0	0	0	0	RhoA-like subfamily. The	endosome membrane [pmid	GTP binding [pmid 1400319];
606	0	0	0	0	0	0	0	0	HMGB-UBF_HMG-box,	chromatin; condensed	DNA bending activity [pmid
607	0	0	0	0	0	0	0	0	30S ribosomal protein	cytosolic small ribosomal	RNA binding [pmid 3785212];
608	0	0	0	0	0	0	0	0	Nucleoplasmin.	centrosome [pmid 11051553];	NF-kappaB binding [pmid
609	0	0	0	0	0	0	0	0	homolog to co-chaperone	chromosome, telomeric region	isomerase activity;
610	0	0	0	0	0	0	0	0	AIG1 (avrRpt2-induced		GTP binding; nucleotide
611	0	0	0	0	0	0	0	0	WD40 domain, found in a	Arp2/3 protein complex [pmid	structural constituent of
612	0	0	0	0	0	0	0	0	Ribosomal protein L14.	cytosolic large ribosomal	protein binding [pmid
613	0	0	0	0	0	0	0	0	50S ribosomal protein	cytosolic large ribosomal	RNA binding [pmid 7772601];
614	0	0	0	0	0	0	0	0	GST_N family, Class	cytoplasm	glutathione transferase
615	0	0	0	0	0	0	0	0			
616	0	0	0	0	0	0	0	0	14-3-3 protein; pfam00244	cytoplasm	actin binding; insulin-like
617	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; ATP-dependent
618	0	0	0	0	0	0	0	0			
619	0	0	7.6E-05	0	0	0	0	0	Ku-core domain, Ku70	DNA-dependent protein kinase	ATP binding; ATP-dependent
620	0	0	0	0	0	0.0001	6.95E-05	0	Surface antigen. This entry	integral to membrane;	
621	0	0	0	0	0	0	0	0	RPA1_DBD_C: A subfamily	DNA replication factor A	DNA binding; metal ion
622	0	0	0	0	0	0	0	0	14-3-3 protein; pfam00244		protein domain specific
623	0	0	0	0	0	0	0	0	acidic ribosomal protein P0;	cytosolic large ribosomal	protein binding [pmid
624	0	0	0	0	0	0	0	0	CRM1 C terminal. CRM1	cytoplasm [pmid 9368044];	protein binding [pmid
625	0	0	0	0	0	0	0	0	6-phosphogluconate		NADP binding;
626	0	0	0	9.3E-05	0	2.01E-05	0	0	Phosphofructokinase, a key	6-phosphofructokinase	6-phosphofructokinase
627	0	0	0	0	0	0	0	0	Protein tyrosine	cytoskeleton; membrane [pmid	hydrolase activity; protein
628	0	0	0	0	0	0	0	0			
629	0	0	0	0	0	0	0	0			
630	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus [pmid 7745706]	microtubule binding [pmid
631	0	0	0	0	0	0	0	0	K homology RNA-binding	cytoplasm; nucleus;	DNA binding; protein binding
632	0	0	9.53E-05	3.74E-05	0	0	0	0	CAS/CSE protein, C-	cytoplasm [pmid 9323134];	binding; importin-alpha export
633	0	0	0	0	0	0	0	0	U1-like zinc finger; Family	intracellular; nuclear inner	metal ion binding; nucleic
634	0	0	0	0	0	0	0	0	linker histone 1 and histone	nucleosome; nucleus	DNA binding
635	0	0	0	0.0001	0	0.000304	0	0	Eukaryotic porin;	integral to membrane;	voltage-gated ion-selective
636	0	0	0	0	0	0	0	0		heterogeneous nuclear	nucleotide binding; RNA
637	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus; snRNP U5 [pmid	ATP binding [pmid 9539711];
638	0	0	0	0	0	0	0	0		mediator complex [pmid	ATP binding; ligand-
639	0	0	0	0	0	0	0	0	Plasminogen Activator	cytoplasm [pmid 16130169];	protein binding [pmid
640	0	0	0	0	0	0	0	0	G-protein alpha subunit. G		GTP binding; GTPase
641	0	0	0	3.78E-05	0	3.26E-05	0	0	Peptidase M16 inactive	membrane; mitochondrial	oxidoreductase activity;
642	0	0	0	0	0	0	0	0	JAB/MPN domain; Domain	nucleus; spliceosome complex	protein binding [pmid
643	0	0	0	0	0	0	0	0			
644	0	0	0	0	0	0	0	0	Nup85 Nucleoporin. A	plasma membrane [pmid	protein binding [pmid
645	0	0	0	0	0	0	0	0	Phospholipase C (PLC)	cytoplasm [pmid 11595183];	protein binding [pmid
646	0	0	0	0	0	0	0	0	Ubiquitin activating enzyme		ATP binding; enzyme
647	0	0	0	0	0	0	0	0	Helicase superfamily c-		ATP binding; ATP-dependent
648	0	0	0	0	0	0	0	0	BAR domain. The BAR	cytoplasm; intracellular	GTPase activator activity;
649	0	0	0	0	0	0	0	0	The FERM_C domain is the	actin filament [pmid	actin filament binding [pmid
650	0	0	0	0	0	0	0	0	Non-repetitive/WGA-	nuclear pore; nucleus	nucleocytoplasmic
651	0	0	0	0	0	0	0	0	Nup133 N terminal like.	integral to membrane; nuclear	nucleocytoplasmic
652	0	0	0	0	0	0	0	0			
653	0	0	0	0	0	0	0	0	Caspase, interleukin-1 beta	intracellular	caspase activator activity
654	0	0	0	2.53E-05	0	6.56E-05	0	0	Dynamin, GTPase; Large	endoplasmic reticulum [pmid	GTP binding; GTPase
655	0	0	0	0	0	0	0	0	Nrap protein. Members of	condensed nuclear	protein binding; snoRNA
656	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; magnesium ion
657	0	0	0	0	0	0	0	0	Protein kinase C conserved	cytoplasm [pmid 10828076];	ATP binding; calcium ion
658	0	0	0	0	0	0	0	0	Spb1 C-terminal domain.	integral to membrane; nucleus	copper ion binding;
659	0	0	0	1.9E-05	0	0	0	0	26S proteasome regulatory	cytosol; proteasome	binding
660	0	0	0	0	0	0	0	0	Serine/Threonine protein	cytoplasm; nucleus	ATP binding; MAP kinase
661	0	0	0	0	0	0	0	0			
662	0	0	0	0	0	0	0	0			
663	0	0	0	0	0	0	0	0		integral to membrane; outer	porin activity
664	0	0	0	0	0	0	0	0	HAT (Half-A-TPR) repeats;	intracellular; nucleus	nucleotide binding; RNA
665	0	0	0	0	0	0	0	0	WD40 domain, found in a	cytoplasm [pmid 9067524];	protein binding [pmid
666	0	0	0	0	0	0	0	0			
667	0	0	0	0	0	0	0	0			
668	0	0	0	7.1E-06	0	0	0	0			
669	0	0	0	0	0	0	0	0	WWE domain. The WWE	cytosol; intracellular; protein	binding; ligase activity;
670	0	0	0	0	0	0	0	0	WWE domain. The WWE	cytoplasm; intracellular;	binding; DNA binding; ligase
671	0	0	0	0	0	0	0	0			
672	0	0	0	0	0	0	0	0	Protein of unknown function		
673	0	0	0	0	0	0	0	0	S-100/ICaBP-like domain;	cytosol [pmid 7626002];	calcium ion binding [pmid
674	0	0	0	0	0	0	0	0	S-100/ICaBP-like domain;	extracellular space	calcium ion binding [pmid
675	0	0	0	0	0	0	0	0	Histone 2A; H2A is a	chromosome; nucleosome;	DNA binding
676	0	0	0	0	0	0	0	0	S-100/ICaBP-like domain;	extracellular space	calcium ion binding [pmid
677	0	0	0	0	0	0	0	0	Pancreatic ribonucleases	extracellular region [pmid	endonuclease activity;
678	0	0	0.000235	0.000368	0	7.95E-05	0	0	Actin; An ubiquitous protein	cytoskeleton	protein binding; structural
679	0	0	0	0	0	0	0	0	Calponin homology domain;	nuclear membrane [pmid	
680	0	0	0	0	0	0	0	0	Phosphoglycerate mutase	cytosol	bisphosphoglycerate mutase
681	0	0	0	0	0	0	0	0	RhoG subfamily. RhoG is a	intracellular; membrane	GTP binding; GTPase
682	0	0	0	0	0	0	0	0			
683	0	0	0	0	0	0	0	0	Ribosomal protein S5, N-	cytosolic small ribosomal	RNA binding [pmid 2308862];
684	0	0	0	0	0	0	0	0	GST_N family, Class Pi	cytoplasm [pmid 16130169]	glutathione transferase
685	0	0	0	0	0	0	0	0			
686	0	0	0	0	0	0	0	0	30S ribosomal protein S8P;	cytosolic small ribosomal	protein binding [pmid

																					RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs										
rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
687	5	0.001172	0	0	INF		ENSG00000103187:E	COTL1			gi|21624607|ref|NP_	coactosin-like 1 [Homo sapie	142	15945	5.7	0	o	Q	24	0	0	0.00115	0	0.000622	0	2	0.000443	0.000555	0	0.00158	0	0.004942	0.001081	3	0.001901	0.002132	0	0	0	0	0	0	0	0	Actin depolymerisation	cytoskeleton; intracellular	actin binding [pmid
688	5	0.001159	1	1.05E-05	110.444		ENSG00000132341:E	RAN			gi|5453555|ref|NP_0	ras-related nuclear protein [H	216	24423	7.5	0	o	Q	23	0.004	0	0.000324	0	0.001636	0	2	0.00049	0.000779	0	0.00135	0	0.003476	0.002488	3	0.001828	0.001497	0	0	0	8.4E-05	0	0	0	0	Ran (Ras-related nuclear	chromatin [pmid 1961752];	androgen receptor binding
689	5	0.001055	0	0	INF		ENSG00000124614:N	RPS10			gi|4506679|ref|NP_0	ribosomal protein S10 [Homo	165	18898	10.2	0	o	Q	24	0.001	0	0.001272	0	0.001392	0	2	0.000666	0.000771	0	0.000816	0	0.003561	0.001396	3	0.001443	0.001523	0	0	0	0	0	0	0	0	Plectin/S10 domain. This	cytosolic small ribosomal	RNA binding [pmid 7772601];
690	5	0.001048	6	0.00012	8.761176		ENSG00000035403:E	VCL			gi|4507877|ref|NP_0	vinculin isoform VCL [Homo	1066	116722	6.1	0	o	Q	19	0	0.006237	0.000175	0	9.94E-05	0	3	0.001628	0.003074	0.001666	0.00021	0	0	0	2	0.000469	0.000804	0.000415	0.000175	0.000122	8E-05	0	0.000138	0	2.71E-05	Vinculin family; pfam01044	actin cytoskeleton; adherens	actin binding [pmid
691	5	0.001008	0	0	INF		ENSG00000143401:E	ANP32E			gi|13569879|ref|NP_	acidic (leucine-rich) nuclear p	268	30692	3.8	0	o	Q	0	0	0	0.000609	0	0.00145	0	2	0.000515	0.000686	0	0.000251	0	0.001888	0.003867	3	0.001502	0.001786	0	0	0	0	0	0	0	0		cytoplasmic membrane-bound	phosphatase inhibitor
692	5	0.000885	0	0	INF		ENSG00000100448:E	CTSG			gi|4503149|ref|NP_0	cathepsin G preproprotein [H	255	28837	11.2	0	o	S	19	1	0.003816	0.001281	0	6.93E-05	0	3	0.001291	0.001783	0.001741	0.000176	0	0	0	2	0.000479	0.000845	0	0	0	0	0	0	0	0	Trypsin-like serine	insoluble fraction	cathepsin G activity [pmid
693	5	0.000869	0	0	INF		ENSG00000111229:E	ARPC3			gi|5031597|ref|NP_0	actin related protein 2/3 com	178	20547	8.6	0	o	Q	27	0.001	0	0.000262	0	0.002282	0	2	0.000636	0.001104	0	0.000126	0	0.000183	0.004098	3	0.001102	0.001999	0	0	0	0	0	0	0	0	P21-ARC (ARP2/3 complex	Arp2/3 protein complex [pmid	structural constituent of
694	5	0.000841	0	0	INF		ENSG00000214754:E	SFRS2			gi|47271443|ref|NP_	splicing factor, arginine/serin	221	25476	11.9	0	o	Q	0	0	0	0.00095	0	7.99E-05	0	2	0.000257	0.000463	0.004017	0.001015	0	0.000665	0	3	0.001424	0.001779	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus [pmid 15652350];	nucleotide binding; protein
695	5	0.000808	4	0.000121	6.680291		ENSG00000114779:E	ABHD14B			gi|14249382|ref|NP_	abhydrolase domain containi	210	22346	6.4	0	o	Q	27	0.002	0	0.000777	0	0.000336	0	2	0.000278	0.000369	0	0.000107	0	0.000311	0.004936	3	0.001338	0.002402	0	0	0.00022	0.000518	0	7.45E-05	0.000155	0	Predicted hydrolases or	nucleus	
696	5	0.000804	0	0	INF		ENSG00000100028:E	SNRPD3			gi|4759160|ref|NP_0	small nuclear ribonucleoprote	126	13916	10.3	0	o	Q	16	0.015	0	0.000555	0	0.00028	0	2	0.000209	0.000266	0.003523	0.001424	0	0.000648	0	3	0.001399	0.001531	0	0	0	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus; ribonucleoprotein	protein binding [pmid
697	5	0.000766	0	0	INF		ENSG00000138385:E	SSB			gi|10835067|ref|NP_	autoantigen La [Homo sapier	408	46837	7.1	0	o	Q	0	0	0	0.0004	0	0.000476	0	2	0.000219	0.000255	0	0.00066	0	0.00196	0.002634	3	0.001314	0.001199	0	0	0	0	0	0	0	0	RNA binding motif. This	cytoplasm; nucleus;	mRNA binding [pmid
698	5	0.000765	2	3.52E-05	21.71852		ENSG00000004059:E	ARF5			gi|4502209|ref|NP_0	ADP-ribosylation factor 5 [Ho	180	20530	6.8	0	o	Q	15	0.054	0.001802	0.000249	0	0	0	2	0.000513	0.000867	0	0.000627	0	0.000113	0.003327	3	0.001017	0.001564	0	0	0	0.000101	0	0	0.000181	0	Arf1-Arf5-like subfamily.	intracellular	GTP binding; GTPase
699	5	0.000762	0	0	INF		ENSG00000182754:N	RPL9P7			gi|67944630|ref|NP_	ribosomal protein L9 [Homo	192	21863	10	0	o	Q	0	0	0	0.00085	0	0.00092	0	2	0.000443	0.000512	0	0.001402	0	0.002125	0.0008	3	0.001082	0.000902	0	0	0	0	0	0	0	0	50S ribosomal protein L6P;	intracellular; ribosome [pmid	RNA binding [pmid 8597601];
700	5	0.000675	3	0.000107	6.308424		ENSG00000150753:E	CCT5			gi|24307939|ref|NP_	chaperonin containing TCP1	541	59671	5.6	0	o	Q	16	0	0	0.000517	0	0.000849	0	2	0.000342	0.000417	0	0.000373	0	0.002805	0.000851	3	0.001008	0.001248	0	0	0.000342	0.000369	0	0.000145	0	0	TCP-1 (CTT or eukaryotic		ATP binding; nucleotide
701	5	0.000624	0	0	INF		ENSG00000155366:N	RHOC			gi|111494251|ref|NP	ras homolog gene family, me	193	22006	6.6	0	o	Q	23	0.009	0	0.000737	0.002353	0.000992	0	3	0.00102	0.000983	0	0.000316	0	0	0.000597	2	0.000228	0.000287	0	0	0	0	0	0	0	0			
702	5	0.000521	0	0	INF		ENSG00000186468:E	RPS23			gi|4506701|ref|NP_0	ribosomal protein S23 [Homo	143	15808	10.5	0	o	Q	48	0	0	0.000326	0	0.000247	0	2	0.000143	0.000169	0	0.000471	0	0.002853	0.000268	3	0.000898	0.001318	0	0	0	0	0	0	0	0	S12-like family, 40S	cytosolic small ribosomal	structural constituent of
703	5	0.000494	0	0	INF		ENSG00000100823:E	APEX1			gi|18375505|ref|NP_	APEX nuclease [Homo sapie	318	35554	8.1	0	o	Q	0	0	0	0	0.001182	0.000611	0	2	0.000448	0.000568	0	0.000282	0	0.000308	0.001569	3	0.00054	0.0007	0	0	0	0	0	0	0	0	Exonuclease III [DNA	endoplasmic reticulum [pmid	3'-5' exonuclease activity
704	5	0.000489	0	0	INF		ENSG00000101361:E	NOL5A			gi|32483374|ref|NP_	nucleolar protein 5A [Homo s	594	66050	9.2	0	o	Q	19	0.067	0	0.00051	0	0.000624	0	2	0.000284	0.000331	0	0.000604	0	0.000687	0.001486	3	0.000694	0.00061	0	0	0	0	0	0	0	0	Putative snoRNA binding	nucleolus [pmid 9372940];	RNA binding [pmid 9372940]
705	5	0.000482	2	4.5E-05	10.69798		ENSG00000170458:E	CD14			gi|91105159|ref|NP_	CD14 antigen precursor [Hor	375	40076	6.2	0	o	S	20	1	0.002162	0.000187	0	0.000141	0	3	0.000623	0.00103	0.001184	0.000179	0	0	0	2	0.000341	0.000568	0	0	0	9.75E-05	0	0	0.000263	0		extrinsic to membrane; plasma	GPI anchor binding;
706	5	0.000479	1	1.55E-05	30.82888		ENSG00000169567:E	HINT1			gi|4885413|ref|NP_0	histidine triad nucleotide binc	126	13802	7	0	o	Q	0	0	0	0	0.001491	0.000561	0	2	0.000513	0.000704	0	0.000178	0	0.001295	0.000305	3	0.000444	0.000581	0	0	0	0	0	0.000124	0	0	Protein Kinase C	cytoskeleton [pmid 8812426];	hydrolase activity; protein
707	5	0.000466	0	0	INF		ENSG00000166197:E	NOLC1			gi|148596949|ref|NP	nucleolar and coiled-body ph	699	73603	9.5	0	o	Q	28	0.001	0.000928	0.000601	0	0.000126	0	3	0.000414	0.000429	0.00127	0.000802	0	0	0	2	0.000518	0.000628	0	0	0	0	0	0	0	0			
708	5	0.000462	1	1E-05	46.01303		ENSG00000178952:E	TUFM			gi|34147630|ref|NP_	Tu translation elongation fact	455	49875	7.6	0	o	S	39	0.913	0.001069	0.000666	0	0.000971	0	3	0.000677	0.000483	0	0.000197	0	0.000789	0	2	0.000247	0.000373	0	0	0	8.02E-05	0	0	0	0	EF-Tu subfamily. This	intracellular; mitochondrion	GTP binding; nucleotide
709	5	0.000443	2	8.17E-05	5.425807		ENSG00000125741:E	OPA3			gi|13376717|ref|NP_	OPA3 protein isoform b [Hom	179	19996	8.9	0	o	Q	19	0.004	0	0.000912	0	0.000197	0	2	0.000277	0.000433	0	0.000877	0	0.000274	0.001287	3	0.000609	0.000582	0	0	0	0.000304	0	0.00035	0	0	Optic atrophy 3 protein	mitochondrion	
710	5	0.000442	2	1.64E-05	26.98778		ENSG00000166226:E	CCT2			gi|5453603|ref|NP_0	chaperonin containing TCP1	535	57488	6.4	0	o	Q	17	0.092	0	0.000523	0	0.000594	0	2	0.000279	0.000324	0	0.00021	0	0.002135	7.18E-05	3	0.000604	0.001024	0	0	0	0.000102	0	2.93E-05	0	0	TCP-1 (CTT or eukaryotic	cytosol [pmid 11532003]	ATP binding; nucleotide
711	5	0.000424	0	0	INF		ENSG00000063177:E	RPL18			gi|4506607|ref|NP_0	ribosomal protein L18 [Homo	188	21634	11.7	0	o	Q	0	0	0	0.001117	0	0.000564	0	2	0.00042	0.000535	0	0.001193	0.003719	0.000521	0	3	0.000429	0.000566	0	0	0	0	0	0	0	0	Ribosomal protein L18E	cytosolic large ribosomal	RNA binding [pmid 8218404];
712	5	0.000407	3	5.84E-05	6.956397		ENSG00000122545:E	SEPT7			gi|148352329|ref|NP	cell division cycle 10 isoform	436	50581	8.6	0	o	Q	18	0	0	0.000428	0	0.000365	0	2	0.000198	0.00023	0	0.00036	0	7.49E-05	0.002025	3	0.000615	0.000953	0	0	0.000318	4.16E-05	0	0.000108	0	0			
713	5	0.000398	0	0	INF		ENSG00000063244:E	U2AF2			gi|6005926|ref|NP_0	U2 (RNU2) small nuclear RN	475	53501	9.1	0	o	Q	0	0	0	0.000344	0	0.000595	0	2	0.000235	0.00029	0	0.000331	0	0.001752	0.000162	3	0.000561	0.000805	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus; spliceosome complex	nucleotide binding; protein
714	5	0.000388	0	0	INF		ENSG00000138069:E	RAB1A			gi|4758988|ref|NP_0	RAB1A, member RAS oncog	205	22678	6.2	0	o	Q	24	0.002	0	0.00041	0.000916	0.000414	0	3	0.000435	0.000375	0	0	0	0.000239	0.001124	2	0.000341	0.000534	0	0	0	0	0	0	0	0	Rab1/Ypt1 subfamily. Rab1	cytoplasm [pmid 11256614];	ATP binding; GTP binding;
715	5	0.000384	1	2.01E-05	19.17398		ENSG00000156976:E	EIF4A2			gi|83700235|ref|NP_	eukaryotic translation initiatio	407	46402	5.5	0	o	Q	0	0	0	0.000108	0	0.000139	0	2	6.17E-05	7.23E-05	0.002181	0.000184	0	0	0.000464	3	0.000707	0.001001	0	0	0	0.00016	0	0	0	0	Helicase superfamily c-	eukaryotic translation	ATP binding; ATP-dependent
716	5	0.000378	0	0	INF		ENSG00000105568:E	PPP2R1A			gi|21361399|ref|NP_	alpha isoform of regulatory s	589	65309	5.1	0	o	Q	21	0	0	0.000346	0	0.000821	0	2	0.000292	0.000389	0	0.000419	0	0.000332	0.001108	3	0.000465	0.000465	0	0	0	0	0	0	0	0		cytosol [pmid 11007961];	antigen binding [pmid
717	5	0.000373	0	0	INF		ENSG00000188170:N	HBD			gi|4504351|ref|NP_0	delta globin [Homo sapiens]	147	16055	8	0	o	Q	24	0	0	0.001216	0	0.00107	0	2	0.000572	0.000663	0	0.000555	0.01427	0.000142	0	3	0.000174	0.000263	0	0	0	0	0	0	0	0	Globins are heme proteins,	hemoglobin complex [pmid	heme binding; iron ion
718	5	0.00037	0	0	INF		ENSG00000073578:N	SDHA			gi|156416003|ref|NP	succinate dehydrogenase co	664	72692	7.4	0	o	S	33	0.743	0	0.000246	0	0.00125	0	2	0.000374	0.000596	0	0.000372	0	0.00086	0.000231	3	0.000366	0.000364	0	0	0	0	0	0	0	0			
719	5	0.000369	0	0	INF		ENSG00000055044:E	NOL5			gi|7706254|ref|NP_0	nucleolar protein NOP5/NOP	529	59578	8.9	0	o	Q	23	0	0	0.000485	0	0.000467	0	2	0.000238	0.000275	0	0.000212	0	0.000555	0.001234	3	0.0005	0.00054	0	0	0	0	0	0	0	0	Putative snoRNA binding	nucleolus [pmid 10925205];	snoRNP binding [pmid
720	5	0.000354	0	0	INF		ENSG00000179335:E	CLK3			gi|153791372|ref|NP	CDC-like kinase 3 [Homo sa	490	58588	9.5	0	o	Q	0	0	0.000662	0.00019	0	0	0	2	0.000213	0.000312	0.001812	9.16E-05	0	0	7.83E-05	3	0.000495	0.000878	0	0	0	0	0	0	0	0			
721	5	0.000346	0	0	INF		ENSG00000099624:E	ATP5D			gi|50345991|ref|NP_	ATP synthase, H+ transporti	168	17490	5.5	0	o	S	34	0.564	0	0.000278	0	0.00021	0	2	0.000122	0.000144	0	0.000267	0	0.001554	0.000457	3	0.00057	0.000683	0	0	0	0	0	0	0	0	ATP synthase,	membrane fraction;	hydrogen-transporting ATP
722	5	0.000345	0	0	INF		ENSG00000197958:N	RPL12			gi|4506597|ref|NP_0	ribosomal protein L12 [Homo	165	17819	9.4	0	o	Q	28	0	0	0.000283	0	0.000642	0	2	0.000231	0.000305	0	0.00068	0	0.000692	0.000465	3	0.000459	0.000323	0	0	0	0	0	0	0	0	Ribosomal protein L11.	cytosolic large ribosomal	RNA binding; structural
723	5	0.000345	0	0	INF		ENSG00000146963:E	LUC7L2			gi|116812577|ref|NP	LUC7-like 2 [Homo sapiens]	392	46514	10	0	o	Q	22	0.001	0	0.000272	0	0.000766	0	2	0.00026	0.000361	0	0.001537	0	8.33E-05	9.79E-05	3	0.000429	0.000739	0	0	0	0	0	0	0	0			
724	5	0.000338	0	0	INF		ENSG00000182866:E	LCK			gi|112789548|ref|NP	lymphocyte-specific protein t	509	58001	5.4	0	o	Q	0	0	0	0.000958	0	0.000416	0	2	0.000344	0.000454	0	0.000793	0	0.00016	0.000377	3	0.000333	0.000344	0	0	0	0	0	0	0	0			
725	5	0.000332	0	0	INF		ENSG00000013016:E	EHD3			gi|7657056|ref|NP_0	EH-domain containing 3 [Hor	535	60887	6.6	0	o	Q	0	0	0	0.000222	0.001405	7.99E-05	0	3	0.000427	0.000658	0	0.000302	0	0	0.000646	2	0.000237	0.000307	0	0	0	0	0	0	0	0	Eps15 homology domain;	nucleus [pmid 10673336]	ATP binding; calcium ion
726	5	0.000324	0	0	INF		ENSG00000113460:E	BXDC2			gi|55770900|ref|NP_	BRIX [Homo sapiens]	353	41401	9.9	0	o	Q	0	0	0	6.61E-05	0	0.0003	0	2	9.16E-05	0.000143	0	6.36E-05	0	9.25E-05	0.002066	3	0.000556	0.001008	0	0	0	0	0	0	0	0	RNA-binding protein	nucleus	
727	5	0.000318	0	0	INF		ENSG00000156261:E	CCT8			gi|48762932|ref|NP_	chaperonin containing TCP1	548	59621	5.6	0	o	Q	19	0	0	0.000298	0	0.000677	0	2	0.000244	0.000321	0	0.000287	0	0.000864	0.00042	3	0.000393	0.00036	0	0	0	0	0	0	0	0	TCP-1 (CTT or eukaryotic	cytosol	ATP binding; ATPase
728	5	0.000317	0	0	INF		ENSG00000078369:E	GNB1			gi|11321585|ref|NP_	guanine nucleotide-binding p	340	37377	6	0	o	Q	0	0	0	0.000172	0	0.001889	0	2	0.000515	0.000919	0	0.000264	0	0.000096	0.000113	3	0.000118	0.000109	0	0	0	0	0	0	0	0	WD40 domain, found in a		signal transducer activity
729	5	0.000306	2	1.95E-05	15.66243		ENSG00000059377:E	TBXAS1			gi|13699840|ref|NP_	thromboxane A synthase 1 (	460	52444	6.5	0	o	S	37	0.707	0.001058	0.000558	0	0	0	2	0.000404	0.000509	0	0.00039	0	0.000106	0.000334	3	0.000208	0.000185	0	0	0	6.81E-05	0	8.81E-05	0	0	Cytochrome P450.	integral to membrane;	heme binding; iron ion
730	5	0.000302	0	0	INF		ENSG00000143621:E	ILF2			gi|24234747|ref|NP_	interleukin enhancer binding	390	43062	5.3	0	o	Q	47	0.001	0	0.00012	0.000482	0.000453	0	3	0.000264	0.000241	0	0	0	8.37E-05	0.00128	2	0.000341	0.000627	0	0	0	0	0	0	0	0	domain in DSRM or	nucleolus [pmid 11790298];	DNA binding [pmid 7519613]
731	5	0.00029	0	0	INF		ENSG00000138668:E	HNRPD			gi|14110414|ref|NP_	heterogeneous nuclear ribon	306	32835	8.2	0	o	Q	25	0.201	0	0.00061	0	0.000346	0	2	0.000239	0.000296	0	0.000147	0	0.000587	0.000627	3	0.00034	0.000314	0	0	0	0	0	0	0	0	RNA recognition motif.	chromosome; chromosome,	DNA binding; mRNA binding
732	5	0.000286	0	0	INF		ENSG00000105401:E	CDC37			gi|5901922|ref|NP_0	cell division cycle 37 protein	378	44468	5.2	0	o	Q	0	0	0.000858	6.17E-05	0	9.35E-05	0	3	0.000253	0.000405	0.001174	0	0	0	0.000102	2	0.000319	0.000572	0	0	0	0	0	0	0	0	Cdc37 Hsp90 binding	cytoplasm [pmid 11256614]	unfolded protein binding
733	5	0.000285	0	0	INF		ENSG00000096746:E	HNRPH3			gi|14141157|ref|NP_	heterogeneous nuclear ribon	346	36926	6.9	0	o	Q	0	0	0	0.00027	0.001086	5.11E-05	0	3	0.000352	0.000503	0	0	0	0.000472	0.000399	2	0.000218	0.000253	0	0	0	0	0	0	0	0	RNA recognition motif.	heterogeneous nuclear	nucleotide binding; RNA
734	5	0.000284	3	5.67E-05	5.009123		ENSG00000163931:E	TKT			gi|4507521|ref|NP_0	transketolase [Homo sapiens	623	67878	7.7	0	o	Q	37	0	0.00026	0	0	0.000312	0	2	0.000143	0.000167	0	0.000288	0	0.000733	0.000678	3	0.000425	0.000346	0	0	0.000212	0.000194	0	4.78E-05	0	0	Thiamine pyrophosphate		calcium ion binding;
735	5	0.000283	2	2.58E-05	10.95478		ENSG00000137106:E	GRHPR			gi|6912396|ref|NP_0	glyoxylate reductase/hydroxy	328	35668	7.4	0	o	Q	27	0.019	0	0.000427	0	0.000108	0	2	0.000134	0.000202	0	0.001163	0	9.95E-05	0.000468	3	0.000433	0.000527	0	0	0	0.000109	0	0	9.78E-05	0	D-isomer specific 2-	cytoplasm [pmid 11256614]	glycerate dehydrogenase
736	5	0.000282	0	0	INF		ENSG00000168000:E	HNRNPUL2			gi|118601081|ref|NP	heterogeneous nuclear ribon	747	85105	4.9	0	o	Q	0	0	0	0.000375	0	0.000497	0	2	0.000218	0.000256	0	0.00021	0	0.000459	0.000719	3	0.000347	0.000311	0	0	0	0	0	0	0	0			
737	5	0.00028	0	0	INF		ENSG00000175220:E	ARHGAP1			gi|4757766|ref|NP_0	Rho GTPase activating prote	439	50436	6.3	0	o	Q	0	0	0	0.000213	0	0.000282	0	2	0.000124	0.000145	0	0.000307	0	3.72E-05	0.001399	3	0.000436	0.000657	0	0	0	0	0	0	0	0	RhoGAP-p50rhoGAP:	intracellular	GTP binding [pmid 8253717];
738	5	0.000275	0	0	INF		ENSG00000023892:E	DEF6			gi|145312241|ref|NP	differentially expressed in FD	631	73910	6	0	o	Q	24	0.007	0	0.000111	0	0.000168	0	2	6.97E-05	8.38E-05	0	7.11E-05	0	0.000388	0.00146	3	0.00048	0.000675	0	0	0	0	0	0	0	0			
739	5	0.000274	0	0	INF		ENSG00000143799:E	PARP1			gi|156523968|ref|NP	poly (ADP-ribose) polymeras	1014	113084	8.9	0	o	Q	0	0	0	0.000414	0	0.000401	0	2	0.000204	0.000235	0	0.000332	0	0.000708	0.000341	3	0.000345	0.000289	0	0	0	0	0	0	0	0			
740	5	0.000272	0	0	INF		ENSG00000101162:E	TUBB1			gi|13562114|ref|NP_	beta tubulin 1, class VI [Hom	451	50327	5.2	0	o	Q	19	0	0.00036	0.000765	0	0.000454	0	3	0.000395	0.000315	0	0.000509	0	0	8.51E-05	2	0.000148	0.000243	0	0	0	0	0	0	0	0	The tubulin superfamily	microtubule; protein complex	GTP binding; GTPase
741	5	0.000269	0	0	INF		ENSG00000004700:E	RECQL			gi|14591904|ref|NP_	RecQ protein-like isoform 1 [	649	73457	7.9	0	o	Q	21	0.001	0	0.000252	0	0.000299	0	2	0.000138	0.00016	0	0.000449	0	0.000151	0.001002	3	0.000401	0.000442	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus [pmid 7961977]	ATP binding; ATP-dependent
742	5	0.000269	0	0	INF		ENSG00000109606:E	DHX15			gi|68509926|ref|NP_	DEAH (Asp-Glu-Ala-His) box	795	90933	7.5	0	o	Q	0	0	0	0.000235	0	0.000356	0	2	0.000148	0.000177	0	0.000113	0	0.000287	0.001159	3	0.00039	0.000526	0	0	0	0	0	0	0	0	Helicase superfamily c-	minor (U12-dependent)	ATP binding; ATP-dependent
743	5	0.000264	0	0	INF		ENSG00000154451:E	GBP5			gi|16418425|ref|NP_	guanylate-binding protein 5 [	586	66617	5.6	0	o	Q	0	0	0	0.000398	0	0.000151	0	2	0.000137	0.000188	0	0.000383	0	0.000195	0.000983	3	0.00039	0.000425	0	0	0	0	0	0	0	0	Guanylate-binding protein,	membrane	GTP binding; GTPase
744	5	0.000262	0	0	INF		ENSG00000175333:N	LOC645296			gi|148228985|ref|NP	hypothetical protein LOC645	184	21313	10.1	0	o	Q	0	0	0	0.000254	0	0.000192	0	2	0.000111	0.000131	0	0.00061	0	0.000621	0.000417	3	0.000412	0.00029	0	0	0	0	0	0	0	0			
745	5	0.000262	0	0	INF		ENSG00000125753:E	VASP			gi|4507869|ref|NP_0	vasodilator-stimulated phosp	380	39830	8.9	0	o	Q	16	0	0.000427	6.14E-05	0	9.3E-05	0	3	0.000145	0.000192	0.001168	0	0	0.000344	0	2	0.000378	0.000551	0	0	0	0	0	0	0	0	Enabled-VASP-type	actin cytoskeleton [pmid	actin binding
746	5	0.000261	0	0	INF		ENSG00000130726:E	TRIM28			gi|5032179|ref|NP_0	tripartite motif-containing 28	835	88550	5.8	0	o	S	19	0.998	0	0.00014	0	0.000338	0	2	0.00012	0.00016	0	0.000403	0	0.000704	0.000506	3	0.000403	0.000296	0	0	0	0	0	0	0	0	B-Box-type zinc finger; zinc	intracellular; nucleus	metal ion binding; protein
747	5	0.000258	0	0	INF		ENSG00000163154:E	TNFAIP8L2			gi|157389001|ref|NP	tumor necrosis factor, alpha-	184	20556	8.4	0	o	Q	37	0.002	0	0.000127	0	0.000672	0	2	0.0002	0.00032	0	0.00061	0	0.000443	0.000209	3	0.000315	0.000267	0	0	0	0	0	0	0	0			
748	5	0.000255	0	0	INF		ENSG00000178950:E	GAK			gi|157384971|ref|NP	cyclin G associated kinase [H	1311	143190	5.7	0	o	S	23	0.655	0.000247	3.56E-05	0	1.35E-05	0	3	7.41E-05	0.000116	0.001693	0	0	4.98E-05	0	2	0.000436	0.000838	0	0	0	0	0	0	0	0			
749	5	0.000254	3	4.44E-05	5.728217		ENSG00000069329:E	VPS35			gi|17999541|ref|NP_	vacuolar protein sorting 35 [H	796	91707	5.5	0	o	Q	0	0	0	0.000264	0	0.000222	0	2	0.000121	0.000141	0	0.000169	0	0.000513	0.000868	3	0.000387	0.000385	0	0	0.000173	4.53E-05	0	0.000137	0	0	Vacuolar protein sorting-	cytosol [pmid 11102511];	protein binding [pmid
750	5	0.000253	0	0	INF		ENSG00000197214:N	TCEA1			gi|45439355|ref|NP_	transcription elongation facto	280	31664	8.5	0	o	Q	0	0	0	8.33E-05	0	0.000189	0	2	6.81E-05	8.98E-05	0	0.00016	0	0.001457	0.000137	3	0.000439	0.000683	0	0	0	0	0	0	0	0	N-terminal domain (domain	nucleus	DNA binding; general RNA
751	5	0.000251	0	0	INF		ENSG00000136450:E	SFRS1			gi|5902076|ref|NP_0	splicing factor, arginine/serin	248	27745	10.4	0	o	Q	17	0	0	0.000188	0	0.000285	0.001642	3	0.000118	0.000142	0	0.000452	0	0	0.001084	2	0.000384	0.000513	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus	nucleotide binding; protein
752	5	0.00025	0	0	INF		ENSG00000070756:N	PABPC1			gi|46367787|ref|NP_	poly(A) binding protein, cytop	636	70671	9.5	0	o	Q	26	0.012	0.000255	0.000183	0	0	0	2	0.00011	0.00013	0.001396	0.000106	0	0	6.04E-05	3	0.000391	0.000672	0	0	0	0	0	0	0	0	Poly-adenylate binding	cytoplasm [pmid 9582337]	nucleotide binding; poly(A)
753	5	0.000249	0	0	INF		ENSG00000104518:E	GSDMDC1			gi|83320070|ref|NP_	gasdermin domain containing	484	52801	5.1	0	o	Q	34	0	0	4.82E-05	0	0.000219	0	2	6.68E-05	0.000104	0	0.000185	0	0.00027	0.001269	3	0.000431	0.00057	0	0	0	0	0	0	0	0	Gasdermin family. The		
754	5	0.000249	0	0	INF		ENSG00000108883:E	EFTUD2			gi|41152056|ref|NP_	elongation factor Tu GTP bin	972	109478	5	0	o	Q	0	0	0	9.6E-05	0	0.000781	0	2	0.000219	0.000377	0	0.000115	0	0.000285	0.000711	3	0.000278	0.000312	0	0	0	0	0	0	0	0	EF-2_domain IV_snRNP	nucleus; spliceosome complex	GTP binding; GTPase
755	5	0.000247	0	0	INF		ENSG00000120438:E	TCP1			gi|57863257|ref|NP_	T-complex protein 1 isoform	556	60344	6.1	0	o	Q	35	0	0	0.000126	0	0.000635	0	2	0.00019	0.000303	0	4.04E-05	0	0.000763	0.000414	3	0.000304	0.000358	0	0	0	0	0	0	0	0	TCP-1 (CTT or eukaryotic	cytosol [pmid 1630491]	ATP binding; nucleotide
756	5	0.000244	0	0	INF		ENSG00000188529:N	LOC642558			gi|169161109|ref|XP	PREDICTED: hypothetical pr	183	22222	10.3	0	o	Q	24	0.001	0	0	0	0.000386	0.00445	2	9.65E-05	0.000193	0	0.00049	0	0.000446	0.000629	3	0.000391	0.000272	0	0	0	0	0	0	0	0			
757	5	0.000239	2	1.14E-05	20.84934		ENSG00000141127:E	PRPSAP2			gi|4506133|ref|NP_0	phosphoribosyl pyrophospha	369	40926	7.4	0	o	Q	32	0.001	0	6.32E-05	0	9.57E-05	0	2	3.97E-05	4.78E-05	0.001203	6.08E-05	0	0.000487	0	3	0.000438	0.000554	0	0	0	4.92E-05	0	4.24E-05	0	0	Phosphoribosylpyrophosph		enzyme inhibitor activity
758	5	0.000232	0	0	INF		ENSG00000180096:E	SEPT1			gi|16604248|ref|NP_	septin 1 [Homo sapiens]	367	41971	5.8	0	o	Q	38	0	0	0.000318	0	0.000578	0	2	0.000224	0.000279	0	0.000428	0	0.000222	0.000314	3	0.000241	0.000181	0	0	0	0	0	0	0	0	CDC/Septin. Septins are a		GTP binding; nucleotide
759	5	0.000231	0	0	INF		ENSG00000031698:E	SARS			gi|16306548|ref|NP_	seryl-tRNA synthetase [Hom	514	58777	6.4	0	o	Q	0	0	0	0.000272	0	0.000687	0	2	0.00024	0.000325	0	0.000131	0	0.000159	0.000597	3	0.000222	0.00026	0	0	0	0	0	0	0	0	Seryl-tRNA synthetase N-	cytoplasm; soluble fraction	ATP binding; ligase activity;
760	5	0.00023	1	1.53E-05	15.08024		ENSG00000057608:E	GDI2			gi|6598323|ref|NP_0	GDP dissociation inhibitor 2 [	445	50663	6.5	0	o	Q	21	0.004	0.000729	0.00021	0	0.000232	0	3	0.000293	0.000309	0	0.000454	0	0.00022	0	2	0.000168	0.000217	0	0	0	0.000122	0	0	0	0	GDP dissociation inhibitor;	cell surface [pmid 12493773];	GTPase activator activity;
761	5	0.000228	0	0	INF		ENSG00000176390:E	CRLF3			gi|156142186|ref|NP	cytokine receptor-like factor	442	49766	5.1	0	o	Q	23	0	0	0.000106	0	0.00056	0	2	0.000166	0.000267	0	0.000406	0	0.000406	0.000347	3	0.00029	0.000195	0	0	0	0	0	0	0	0			
762	5	0.000226	0	0	INF		ENSG00000103653:E	CSK			gi|4758078|ref|NP_0	c-src tyrosine kinase [Homo	450	50704	7.1	0	o	Q	17	0.012	0.000721	0.000415	0	0.000118	0	3	0.000313	0.000323	0	0.000299	0	0.000254	0	2	0.000138	0.000161	0	0	0	0	0	0	0	0	Src homology 3 domains;	cytoplasm [pmid 8890164];	ATP binding; nucleotide
763	5	0.000223	0	0	INF		ENSG00000092841:E	MYL6			gi|17986258|ref|NP_	myosin, light chain 6, alkali,	151	16930	4.7	0	o	Q	0	0	0	0.000309	0	0.000819	0	2	0.000282	0.000386	0	0.000297	0	0.000108	0.000254	3	0.000165	0.000136	0	0	0	0	0	0	0	0	EF-hand, calcium binding	unconventional myosin [pmid	calcium ion binding; motor
764	5	0.000222	2	2.59E-05	8.584209		ENSG00000109072:E	VTN			gi|88853069|ref|NP_	vitronectin precursor [Homo	478	54306	5.8	0	o	S	20	0.999	0.000679	9.76E-05	0	3.7E-05	0	3	0.000203	0.000319	0.000929	0	0	3.41E-05	0	2	0.000241	0.000459	0	0	0	7.59E-05	0	0.000131	0	0	Hemopexin-like repeats.	extracellular region [pmid	heparin binding; protein
765	5	0.000221	0	0	INF		ENSG00000011009:E	LYPLA2			gi|9966764|ref|NP_0	lysophospholipase II [Homo	231	24737	7.2	0	o	Q	20	0.249	0	0.000404	0	0.000765	0	2	0.000292	0.000368	0	0.000291	0	0.000141	0.000166	3	0.00015	0.000119	0	0	0	0	0	0	0	0	Phospholipase/Carboxylest		hydrolase activity
766	5	0.000218	0	0	INF		ENSG00000162909:E	CAPN2			gi|157389005|ref|NP	calpain 2, large subunit [Hon	700	80009	5	0	o	Q	15	0	0	0.000333	0	0.000227	0	2	0.00014	0.000167	0	6.41E-05	0	0.000513	0.000603	3	0.000295	0.000307	0	0	0	0	0	0	0	0			
767	5	0.000216	0	0	INF		ENSG00000023191:E	RNH1			gi|42822874|ref|NP_	ribonuclease/angiogenin inhi	461	49974	4.8	0	o	Q	36	0	0	0.000253	0	0.00069	0	2	0.000236	0.000325	0	0.000146	0	0.000389	0.00025	3	0.000196	0.000165	0	0	0	0	0	0	0	0	Leucine-rich repeats		protein binding [pmid
768	5	0.000215	0	0	INF		ENSG00000105953:E	OGDH			gi|51873036|ref|NP_	oxoglutarate (alpha-ketogluta	1023	115935	6.9	0	o	Q	17	0.015	0	0.000342	0	0.000311	0	2	0.000163	0.000189	0	0.000154	0	0.000128	0.000788	3	0.000267	0.000354	0	0	0	0	0	0	0	0	Thiamine pyrophosphate	mitochondrion; oxoglutarate	oxidoreductase activity;
769	5	0.000214	0	0	INF		ENSG00000168291:E	PDHB			gi|156564403|ref|NP	pyruvate dehydrogenase (lip	359	39233	6.6	0	o	Q	39	0.066	0	0	0	0.000443	0.001134	2	0.000111	0.000221	0	0.000125	0	0.0005	0.000642	3	0.000317	0.000303	0	0	0	0	0	0	0	0			
770	5	0.000214	0	0	INF		ENSG00000085662:E	AKR1B1			gi|4502049|ref|NP_0	aldo-keto reductase family 1,	316	35853	7	0	o	Q	32	0.007	0	0.000295	0	0.000112	0	2	0.000102	0.000139	0	0.000284	0	0.000775	0.000243	3	0.000325	0.000325	0	0	0	0	0	0	0	0	Aldo/keto reductase family.	extracellular space [pmid	aldehyde reductase activity
771	5	0.00021	0	0	INF		ENSG00000092010:E	PSME1			gi|5453990|ref|NP_0	proteasome activator subunit	249	28723	6	0	o	Q	0	0	0	0.000281	0	0.000213	0	2	0.000123	0.000145	0	9.01E-05	0	0.000328	0.000771	3	0.000297	0.000345	0	0	0	0	0	0	0	0	Proteasome activator pa28	cytoplasm [pmid 16130169];	proteasome activator activity
772	5	0.000209	0	0	INF		ENSG00000108953:E	YWHAE			gi|5803225|ref|NP_0	tyrosine 3/tryptophan 5 -mon	255	29174	4.7	0	o	Q	0	0	0	0	0	0.000282	0.001597	2	7.05E-05	0.000141	0	8.8E-05	0	0.001152	0.000151	3	0.000348	0.00054	0	0	0	0	0	0	0	0	14-3-3 protein; pfam00244		enzyme binding [pmid
773	5	0.000205	1	1.06E-05	19.37686		ENSG00000132589:E	FLOT2			gi|94538362|ref|NP_	flotillin 2 [Homo sapiens]	428	47064	5.3	0	o	Q	22	0.003	0.000379	0.000599	0	0.000206	0	3	0.000296	0.000255	0	0.000419	0	3.81E-05	0	2	0.000114	0.000204	0	0	0	8.47E-05	0	0	0	0	Band_7_flotillin: a subgroup	cell surface [pmid 12493773];	protein binding [pmid
774	5	0.000205	0	0	INF		ENSG00000099901:E	RANBP1			gi|4506407|ref|NP_0	RAN binding protein 1 [Homo	201	23310	5.3	0	o	Q	0	0	0	0.000464	0	0.000439	0	2	0.000226	0.000261	0	0.000112	0	0.000244	0.000382	3	0.000184	0.000165	0	0	0	0	0	0	0	0	Ran-binding domain; This	cytoplasm [pmid 16130169];	GDP-dissociation inhibitor
775	5	0.000203	0	0	INF		ENSG00000131051:E	RBM39			gi|35493811|ref|NP_	RNA binding motif protein 39	530	59380	10.1	0	o	Q	0	0	0.000612	0.000528	0	0.000133	0	3	0.000318	0.000298	0	0.000169	0	0.000185	0	2	8.85E-05	0.000102	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleoplasm [pmid 8227358];	nucleic acid binding;
776	5	0.0002	0	0	INF		ENSG00000105323:E	HNRPUL1			gi|21536320|ref|NP_	E1B-55kDa-associated prote	756	84794	8.8	0	o	Q	0	0	0	0.000216	0	0.000234	0	2	0.000112	0.00013	0	0.000297	0	0.000497	0.000355	3	0.000287	0.000209	0	0	0	0	0	0	0	0	SPRY domain. SPRY	nucleus; ribonucleoprotein	DNA binding; RNA binding
777	5	0.000199	0	0	INF		ENSG00000117593:E	DARS2			gi|40789249|ref|NP_	aspartyl-tRNA synthetase 2,	645	73563	8	0	o	Q	16	0.015	0	7.23E-05	0	5.48E-05	0	2	3.18E-05	3.74E-05	0	0.000139	0	0.000253	0.001071	3	0.000366	0.000482	0	0	0	0	0	0	0	0	EcAspRS_like_N: N-	cytoplasm	aspartate-tRNA ligase
778	5	0.000195	0	0	INF		ENSG00000111642:E	CHD4			gi|51599156|ref|NP_	chromodomain helicase DNA	1912	218003	5.9	0	o	Q	16	0.003	0	0.000122	0	0.000139	0	2	6.51E-05	7.55E-05	0	0.000153	0	8.54E-05	0.001064	3	0.000325	0.000496	0	0	0	0	0	0	0	0	Helicase superfamily c-	chromatin; nucleus	ATP binding; ATP-dependent
779	5	0.000193	0	0	INF		ENSG00000139684:E	ESD			gi|33413400|ref|NP_	esterase D/formylglutathione	282	31463	7	0	o	Q	27	0	0	0.000165	0	0.000564	0	2	0.000182	0.000266	0	7.96E-05	0	5.79E-05	0.000681	3	0.000205	0.000319	0	0	0	0	0	0	0	0	Putative esterase. This	cytoplasmic membrane-bound	hydrolase activity; S-
780	5	0.00019	0	0	INF		ENSG00000187109:E	NAP1L1			gi|21327708|ref|NP_	nucleosome assembly protei	391	45374	4.5	0	o	Q	0	0	0	5.97E-05	0	0.000335	0	2	9.86E-05	0.00016	0	0.000344	0	0.000584	0.000196	3	0.000281	0.000246	0	0	0	0	0	0	0	0	Nucleosome assembly	chromatin assembly complex	protein binding [pmid
781	5	0.000189	2	2.02E-05	9.382236		ENSG00000014123:E	KIAA0776			gi|24308039|ref|NP_	hypothetical protein LOC233	794	89595	6.8	0	o	Q	24	0	0	0.00047	0	0.000156	0	2	0.000156	0.000222	0	0.000509	0	0.000185	0.000193	3	0.000222	0.000211	0	0	0	0.000141	0	2.03E-05	0	0			
782	5	0.000188	4	1.42E-05	13.21525		ENSG00000171490:E	RSL1D1			gi|118498359|ref|NP	ribosomal L1 domain contain	490	54973	10.1	0	o	S	24	0.558	0	0.000238	0	0.000216	0	2	0.000114	0.000131	0	0.000412	0	0.000167	0.00047	3	0.000262	0.000219	0	0	1.43E-05	2.24E-05	7.13E-05	5.8E-06	0	0			
783	5	0.000185	0	0	INF		ENSG00000065357:E	DGKA			gi|41872500|ref|NP_	diacylglycerol kinase, alpha 8	735	82630	6.7	0	o	Q	17	0	0	0.000381	0	0.000312	0	2	0.000173	0.000202	0	0.000366	0	0.000111	0.000313	3	0.000198	0.000172	0	0	0	0	0	0	0	0	Protein kinase C conserved		calcium ion binding;
784	5	0.000185	0	0	INF		ENSG00000110031:E	LPXN			gi|4758670|ref|NP_0	leupaxin [Homo sapiens]	386	43332	6	0	o	Q	17	0	0	0.000363	0	0.000137	0	2	0.000125	0.000171	0	0.000232	0	0.00055	0.000199	3	0.000245	0.000227	0	0	0	0	0	0	0	0	LIM domain. This family	cytoplasm	metal ion binding; zinc ion
785	5	0.000183	0	0	INF		ENSG00000205531:E	NAP1L4			gi|5174613|ref|NP_0	nucleosome assembly protei	375	42823	4.7	0	o	Q	18	0	0	0.000249	0	0.000499	0	2	0.000187	0.000239	0	0.000179	0	0.000131	0.000409	3	0.00018	0.000171	0	0	0	0	0	0	0	0	Nucleosome assembly	chromatin assembly complex	unfolded protein binding
786	5	0.00018	0	0	INF		ENSG00000103426:E	CORO7			gi|88702975|ref|NP_	coronin 7 [Homo sapiens]	925	100635	5.8	0	o	Q	57	0.001	0	0.000403	0	0.000535	0	2	0.000235	0.000276	0	0.00017	0	0.000247	8.3E-05	3	0.000125	0.000107	0	0	0	0	0	0	0	0	WD40 domain, found in a	Golgi apparatus; integral to	
787	5	0.000179	3	1.48E-05	12.10385		ENSG00000135624:E	CCT7			gi|5453607|ref|NP_0	chaperonin containing TCP1	543	59367	7.6	0	o	Q	19	0.002	0	0.000215	0	0.000586	0	2	0.0002	0.000276	0	8.26E-05	0	0.000481	7.07E-05	3	0.000159	0.000218	0	0	0	3.33E-05	0	2.88E-05	0	5.64E-05	TCP-1 (CTT or eukaryotic	cytoplasm [pmid 9819444]	ATP binding; nucleotide
788	5	0.000176	2	2.76E-05	6.38986		ENSG00000115866:E	DARS			gi|45439306|ref|NP_	aspartyl-tRNA synthetase [H	501	57136	6.5	0	o	Q	0	0	0	0.000559	0	0.000212	0	2	0.000193	0.000264	0	0.000313	0	9.77E-05	0.00023	3	0.00016	0.000139	0	0	0.000185	3.62E-05	0	0	0	0	AspRS_cyto_N: N-terminal,	cytoplasm [pmid 8449960];	aminoacylase activity [pmid
789	5	0.00017	0	0	INF		ENSG00000122406:E	RPL5			gi|14591909|ref|NP_	ribosomal protein L5 [Homo	297	34363	9.7	0	o	Q	0	0	0	0.000314	0	0.000178	0	2	0.000123	0.000153	0	7.55E-05	0	0.000659	0.000129	3	0.000216	0.0003	0	0	0	0	0	0	0	0	50S ribosomal protein	cytosolic large ribosomal	5S rRNA binding; protein
790	5	0.000169	0	0	INF		ENSG00000111530:E	CAND1			gi|21361794|ref|NP_	TIP120 protein [Homo sapier	1230	136375	5.8	0	o	Q	19	0	0	0.000152	0	0.000302	0	2	0.000113	0.000144	0	0.000201	0	0.000106	0.000593	3	0.000225	0.000259	0	0	0	0	0	0	0	0	TATA-binding protein	nucleus; ubiquitin ligase	protein binding [pmid
791	5	0.000165	1	5.81E-06	28.4116		ENSG00000126945:E	HNRPH2			gi|74099697|ref|NP_	heterogeneous nuclear ribon	449	49264	6.3	0	o	Q	25	0.003	0	0.000258	0	0.000357	0	2	0.000154	0.000182	0	6.07E-05	0	0.00032	0.000325	3	0.000176	0.000171	0	0	0	0	0	4.65E-05	0	0	RNPHF zinc finger. This	heterogeneous nuclear	nucleotide binding; RNA
792	5	0.000165	0	0	INF		ENSG00000167770:E	OTUB1			gi|109148508|ref|NP	otubain 1 [Homo sapiens]	271	31284	4.9	0	o	Q	0	0	0	0.000172	0	0.000456	0	2	0.000157	0.000215	0	0.000248	0	0.000301	0.000142	3	0.000173	0.000133	0	0	0	0	0	0	0	0			
793	5	0.000165	3	2.86E-05	5.752139		ENSG00000181789:E	COPG			gi|11559929|ref|NP_	coatomer protein complex, s	874	97718	5.5	0	o	Q	0	0	0	0.00032	0	0.000382	0	2	0.000176	0.000204	0	0.00022	0	0.000131	0.000264	3	0.000154	0.000116	0	0	0.000106	8.75E-05	0	0	0	3.52E-05	Coatomer gamma subunit	COPI vesicle coat; membrane	binding
794	5	0.000164	0	0	INF		ENSG00000102054:E	RBBP7			gi|4506439|ref|NP_0	retinoblastoma binding prote	425	47820	5	0	o	Q	0	0	0	5.49E-05	0	0.000125	0	2	4.49E-05	5.92E-05	0	0.000264	0	0.000691	0.000181	3	0.000284	0.000293	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus	protein binding [pmid
795	5	0.000164	0	0	INF		ENSG00000119314:E	ROD1			gi|38569466|ref|NP_	ROD1 regulator of differentia	552	59690	9	0	o	Q	17	0.001	0	0.000338	0	0.00032	0	2	0.000165	0.00019	0	0.000488	0	2.96E-05	0.000139	3	0.000164	0.000224	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus	nucleic acid binding;
796	5	0.000162	0	0	INF		ENSG00000122692:E	SMU1			gi|109948304|ref|NP	smu-1 suppressor of mec-8 a	513	57544	7.2	0	o	Q	0	0	0	0.000136	0	0.000172	0	2	7.71E-05	9.03E-05	0	0.000262	0	0.000127	0.000599	3	0.000247	0.000258	0	0	0	0	0	0	0	0			
797	5	0.00016	2	2.96E-05	5.396352		ENSG00000117448:E	AKR1A1			gi|24497577|ref|NP_	aldo-keto reductase family 1,	325	36573	6.8	0	o	Q	21	0.038	0	0.000359	0	0.000326	0	2	0.000171	0.000198	0	0.000207	0	0.000151	0.000236	3	0.000148	0.000105	0	0	0	0	0	4.82E-05	0	0.000189	Aldo/keto reductase family.		alcohol dehydrogenase
798	5	0.000155	0	0	INF		ENSG00000092201:E	SUPT16H			gi|6005757|ref|NP_0	chromatin-specific transcripti	1047	119914	5.7	0	o	Q	0	0	0	0.000111	0	0.000388	0	2	0.000125	0.000183	0	2.14E-05	0	0.000281	0.00044	3	0.000185	0.000212	0	0	0	0	0	0	0	0	FACT complex subunit	chromosome; nucleus	metalloexopeptidase activity;
799	5	0.000153	0	0	INF		ENSG00000100994:E	PYGB			gi|21361370|ref|NP_	brain glycogen phosphorylas	843	96696	6.9	0	o	Q	27	0	0	0.000111	0	0.000147	0	2	6.43E-05	7.57E-05	0.000527	0	0	7.74E-05	0.000364	3	0.000242	0.000246	0	0	0	0	0	0	0	0	Carbohydrate		phosphorylase activity;
800	5	0.000151	0	0	INF		ENSG00000150867:E	PIP5K2A			gi|6857820|ref|NP_0	phosphatidylinositol-5-phosp	406	46225	7	0	o	Q	49	0.009	0.000399	5.74E-05	0	0.000174	0	3	0.000158	0.000177	0	0	0	0.000201	0.000378	2	0.000145	0.000182	0	0	0	0	0	0	0	0	Phosphatidylinositol		1-phosphatidylinositol-4-
801	5	0.000151	0	0	INF		ENSG00000111667:E	USP5			gi|148727247|ref|NP	ubiquitin specific peptidase 5	835	93308	5.1	0	o	Q	22	0.006	0	0.000168	0	0.000233	0	2	0.0001	0.000119	0	0.000457	0	0.000215	0.000138	3	0.000202	0.000191	0	0	0	0	0	0	0	0			
802	5	0.00015	0	0	INF		ENSG00000066044:E	ELAVL1			gi|38201714|ref|NP_	ELAV-like 1 [Homo sapiens]	326	36092	9.2	0	o	Q	0	0	0	0.000143	0	0.000163	0	2	7.64E-05	8.86E-05	0	0.000275	0	0.000501	0.000118	3	0.000223	0.000216	0	0	0	0	0	0	0	0	RNA recognition motif.		identical protein binding
803	5	0.000148	0	0	INF		ENSG00000183431:E	SF3A3			gi|5803167|ref|NP_0	splicing factor 3a, subunit 3 [	501	58849	5.4	0	o	Q	0	0	0	0.00014	0	0.000106	0	2	6.14E-05	7.22E-05	0	4.48E-05	0	0.000358	0.000536	3	0.000235	0.000257	0	0	0	0	0	0	0	0	Splicing factor 3a, subunit 3	intracellular; nucleus;	metal ion binding; nucleic
804	5	0.000148	0	0	INF		ENSG00000182944:E	EWSR1			gi|4885225|ref|NP_0	Ewing sarcoma breakpoint re	656	68478	9.3	0	o	Q	20	0.001	0	0.000213	0.000573	0	0	2	0.000197	0.00027	0	0.000137	0	2.49E-05	0.000234	3	9.89E-05	0.000108	0	0	0	0	0	0	0	0	Zn-finger in Ran binding	intracellular; nucleus	calmodulin binding; metal ion
805	5	0.000147	0	0	INF		ENSG00000179051:E	RCC2			gi|29789090|ref|NP_	regulator of chromosome co	522	56085	8.8	0	o	Q	24	0.005	0	0.000313	0	3.38E-05	0	2	8.67E-05	0.000152	0	0.000129	0	0.000625	7.35E-05	3	0.000207	0.000284	0	0	0	0	0	0	0	0	Alpha-tubulin suppressor	chromosome, pericentric	
806	5	0.000146	0	0	INF		ENSG00000099942:E	CRKL			gi|4885153|ref|NP_0	v-crk sarcoma virus CT10 on	303	33777	6.7	0	o	Q	25	0	0	7.7E-05	0	0.000117	0	2	4.84E-05	5.82E-05	0	7.4E-05	0	0.000269	0.000633	3	0.000244	0.000283	0	0	0	0	0	0	0	0	Variant SH3 domain. SH3		protein binding [pmid
807	5	0.000146	0	0	INF		ENSG00000138363:E	ATIC			gi|20127454|ref|NP_	5-aminoimidazole-4-carboxa	592	64616	6.7	0	o	Q	39	0.156	0.000274	0.000236	0	0.000388	0	3	0.000225	0.000163	0	7.58E-05	0	0.000193	0	2	6.72E-05	9.11E-05	0	0	0	0	0	0	0	0	Inosine monophosphate		hydrolase activity; IMP
808	5	0.000143	0	0	INF		ENSG00000172340:E	SUCLG2			gi|157779135|ref|NP	succinate-CoA ligase, GDP-f	432	46511	6.4	0	o	S	30	0.654	0	0.00027	0	0.000245	0	2	0.000129	0.000149	0	0.000208	0	0.000151	0.000267	3	0.000156	0.000114	0	0	0	0	0	0	0	0			
809	5	0.000141	0	0	INF		ENSG00000166508:E	MCM7			gi|33469968|ref|NP_	minichromosome maintenanc	719	81308	6.5	0	o	Q	0	0	0	0.000422	0	0.000147	0	2	0.000142	0.000199	0	0.000437	0	6.81E-05	5.34E-05	3	0.00014	0.0002	0	0	0	0	0	0	0	0	ATPase family associated	chromatin [pmid 8798650];	ATP binding; DNA binding;
810	5	0.000141	1	3.82E-06	36.89277		ENSG00000076944:E	STXBP2			gi|5902128|ref|NP_0	syntaxin binding protein 2 [H	593	66439	6.5	0	o	Q	17	0.001	0.000547	0.000197	0	0.000149	0	3	0.000223	0.000232	0	0.000151	0	8.26E-05	0	2	5.85E-05	7.31E-05	0	0	0	3.05E-05	0	0	0	0	Proteins involved in		syntaxin-2 binding; syntaxin-
811	5	0.000135	3	1.35E-05	9.982807		ENSG00000204463:E	BAT3			gi|149158692|ref|NP	HLA-B associated transcript-	1132	119409	5.6	0	o	Q	0	0	0	0.000124	0.000664	6.24E-05	0	3	0.000212	0.000305	0	0.000159	0	0	6.78E-05	2	5.66E-05	7.51E-05	0	0	0	4.96E-05	4.39E-05	1.43E-05	0	0			
812	5	0.000134	0	0	INF		ENSG00000088930:E	XRN2			gi|18860916|ref|NP_	5'-3' exoribonuclease 2 [Hom	950	108583	7.5	0	o	Q	16	0.001	0	4.91E-05	0	0.000112	0	2	4.02E-05	5.29E-05	0	4.72E-05	0	0.000137	0.000727	3	0.000228	0.000338	0	0	0	0	0	0	0	0	XRN 5'-3' exonuclease N-	nucleus	5'-3' exoribonuclease activity
813	5	0.000134	0	0	INF		ENSG00000115524:E	SF3B1			gi|54112117|ref|NP_	splicing factor 3b, subunit 1 i	1304	145830	7.1	0	o	Q	0	0	0	5.37E-05	0	0.000244	0	2	7.44E-05	0.000116	0	3.44E-05	0	6.26E-05	0.000677	3	0.000194	0.000323	0	0	0	0	0	0	0	0	U2 snRNP spliceosome	nucleus; spliceosome complex	binding; RNA splicing factor
814	5	0.000133	0	0	INF		ENSG00000083312:E	TNPO1			gi|133925811|ref|NP	transportin 1 isoform 1 [Hom	898	102355	5	0	o	Q	33	0	0	2.6E-05	0	0.000212	0	2	5.95E-05	0.000102	0	0.000125	0	6.36E-05	0.000639	3	0.000207	0.000293	0	0	0	0	0	0	0	0			
815	5	0.000133	0	0	INF		ENSG00000102900:E	NUP93			gi|41281437|ref|NP_	nucleoporin 93kDa [Homo sa	819	93557	5.8	0	o	Q	19	0	0	2.85E-05	0	0.000173	0	2	5.03E-05	8.26E-05	0	0.000137	0	1.99E-05	0.000703	3	0.000215	0.000331	0	0	0	0	0	0	0	0	Nucleoporin interacting	nuclear pore; nucleus	
816	5	0.000132	0	0	INF		ENSG00000115419:E	GLS			gi|156104878|ref|NP	glutaminase [Homo sapiens]	669	73461	7.8	0	o	Q	29	0.487	0	0.000174	0	0.000396	0	2	0.000143	0.000188	0	0.000402	0	2.44E-05	5.74E-05	3	0.000121	0.000189	0	0	0	0	0	0	0	0			
817	5	0.000131	1	1.93E-06	67.68439		ENSG00000047315:E	POLR2B			gi|4505941|ref|NP_0	DNA directed RNA polymera	1174	133896	6.9	0	o	Q	0	0	0	0	0	3.01E-05	0	1	7.52E-06	1.5E-05	0.000756	0.000115	0	1.39E-05	0.000131	4	0.000254	0.000339	0	0	0	1.54E-05	0	0	0	0	RNA polymerase Rpb2,	DNA-directed RNA	DNA binding [pmid 1518060];
818	5	0.000131	0	0	INF		ENSG00000100304:E	TTLL12			gi|11056036|ref|NP_	tubulin tyrosine ligase-like fa	644	74404	5.5	0	o	Q	42	0.001	0.000252	0.00029	0	0.000165	0	3	0.000177	0.000129	0	0.000314	0	2.53E-05	0	2	8.47E-05	0.000153	0	0	0	0	0	0	0	0	Tubulin-tyrosine ligase		ligase activity; tubulin-
819	5	0.000129	0	0	INF		ENSG00000100297:E	MCM5			gi|23510448|ref|NP_	minichromosome maintenanc	734	82286	8.4	0	o	Q	22	0	0	0.000254	0	9.63E-05	0	2	8.76E-05	0.00012	0	9.17E-05	0	6.67E-05	0.000523	3	0.00017	0.000238	0	0	0	0	0	0	0	0	Magnesium chelatase,	nucleus [pmid 8751386]	ATP binding; DNA binding;
820	5	0.000126	0	0	INF		ENSG00000168918:E	Q6P5A4			gi|40254823|ref|NP_	SH2 containing inositol phos	1188	133193	7.6	0	o	Q	42	0	0	0.000216	0	0.000104	0	2	8E-05	0.000103	0	0.000275	0	0.000124	0.000291	3	0.000172	0.000137	0	0	0	0	0	0	0	0	Inositol polyphosphate		inositol or
821	5	0.000125	0	0	INF		ENSG00000124357:E	NAGK			gi|49574508|ref|NP_	N-Acetylglucosamine kinase	344	37376	6.2	0	o	Q	16	0.001	0.000471	6.78E-05	0	0.000154	0	3	0.000173	0.000208	0	0.000261	0	4.74E-05	0	2	7.71E-05	0.000125	0	0	0	0	0	0	0	0	BadF/BadG/BcrA/BcrD		ATP binding; kinase activity;
822	5	0.000124	1	2.5E-06	49.61837		ENSG00000175166:E	PSMD2			gi|25777602|ref|NP_	proteasome 26S non-ATPas	908	100200	5.2	0	o	Q	0	0	0.000179	2.57E-05	0	0.000331	0	3	0.000134	0.000153	0	2.47E-05	0	0.000431	0	2	0.000114	0.000212	0	0	0	2E-05	0	0	0	0	26S proteasome regulatory	cytosol; proteasome	binding; protein binding [pmid
823	5	0.000123	0	0	INF		ENSG00000166750:E	SLFN5			gi|145580600|ref|NP	schlafen family member 5 [H	891	101055	8.2	0	o	Q	0	0	0	0.000256	0	0.000159	0	2	0.000104	0.000126	0	0.000126	0	0.000275	0.000172	3	0.000143	0.000114	0	0	0	0	0	0	0	0			
824	5	0.000122	0	0	INF		ENSG00000004478:E	FKBP4			gi|4503729|ref|NP_0	FK506-binding protein 4 [Hor	459	51805	5.4	0	o	Q	23	0	0	5.08E-05	0	0.000346	0	2	9.93E-05	0.000166	0	0.000244	0	0.000249	8.36E-05	3	0.000144	0.000123	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	cytoplasm [pmid 2378870];	FK506 binding [pmid
825	5	0.000121	0	0	INF		ENSG00000126561:E	STAT5A			gi|21618342|ref|NP_	signal transducer and activat	794	90647	6.4	0	o	Q	15	0	0	0.000101	0	0.000289	0	2	9.75E-05	0.000136	0	0.00017	0	2.06E-05	0.000387	3	0.000144	0.000178	0	0	0	0	0	0	0	0	STAT protein, DNA binding	nucleus	calcium ion binding; signal
826	5	0.000119	0	0	INF		NA:ENSMUSG00000	C14orf169			gi|106879206|ref|NP	chromosome 14 open readin	641	71086	6.5	0	o	Q	58	0.017	0	0.000218	0	0.00011	0	2	8.21E-05	0.000105	0	0.000245	0	7.64E-05	0.000299	3	0.000155	0.00014	0	0	0	0	0	0	0	0			
827	5	0.000118	0	0	INF		ENSG00000102871:E	TRADD			gi|13378137|ref|NP_	TNFRSF1A-associated via d	312	34247	6.3	0	o	Q	24	0.002	0.00052	0	0	5.66E-05	0	2	0.000144	0.000252	0	7.19E-05	0	5.23E-05	0.000246	3	9.26E-05	0.000107	0	0	0	0	0	0	0	0	DEATH domain, found in		identical protein binding
828	5	0.000116	0	0	INF		ENSG00000105063:E	SAPS1			gi|151101459|ref|NP	SAPS domain family, membe	881	96724	4.6	0	o	Q	26	0	0	0.000265	0	0.000261	0	2	0.000131	0.000152	0	7.64E-05	0	0.000111	0.000218	3	0.000101	9.05E-05	0	0	0	0	0	0	0	0			
829	5	0.000116	1	1.23E-06	94.04644		ENSG00000134516:E	DOCK2			gi|31377468|ref|NP_	dedicator of cytokinesis 2 [H	1830	211947	6.9	0	o	Q	25	0.001	0	0.000319	0	0.000145	0	2	0.000116	0.000151	0	0.000319	0	6.24E-05	8.39E-05	3	0.000116	0.00014	0	0	0	9.87E-06	0	0	0	0	Src homology 3 domains;	cytoskeleton; membrane	protein binding [pmid
830	5	0.000114	0	0	INF		ENSG00000161847:E	RAVER1			gi|123173757|ref|NP	RAVER1 [Homo sapiens]	756	79579	8.9	0	o	Q	21	0.007	0	0.000247	0	0.00028	0	2	0.000132	0.000153	0	0.000178	0	0.000108	0.000102	3	9.69E-05	7.33E-05	0	0	0	0	0	0	0	0			
831	5	0.000113	0	0	INF		ENSG00000149136:E	SSRP1			gi|4507241|ref|NP_0	structure specific recognition	709	81075	6.9	0	o	Q	0	0	0	6.58E-05	0	0.000324	0	2	9.74E-05	0.000154	0	0.000127	0	0.000276	0.000108	3	0.000128	0.000114	0	0	0	0	0	0	0	0	HMGB-UBF_HMG-box,	chromatin; chromosome;	DNA binding [pmid 1372440];
832	5	0.00011	1	2.22E-06	49.5966		ENSG00000189091:E	SF3B3			gi|54112121|ref|NP_	splicing factor 3b, subunit 3 [	1217	135577	5.3	0	o	Q	24	0.014	0	0	0	0.000305	0.000336	2	7.62E-05	0.000152	0	3.69E-05	0	6.71E-05	0.000473	3	0.000144	0.000221	0	0	0	1.78E-05	0	0	0	0	CPSF A subunit region.	nucleus; small nuclear	nucleic acid binding; protein
833	5	0.00011	0	0	INF		ENSG00000112118:E	MCM3			gi|6631095|ref|NP_0	minichromosome maintenanc	808	90981	5.8	0	o	Q	16	0	0	0.000115	0.000233	0.000306	0	3	0.000164	0.000134	0	0.000167	0	6.06E-05	0	2	5.68E-05	7.86E-05	0	0	0	0	0	0	0	0	Magnesium chelatase,	alpha DNA	ATP binding; DNA binding

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB
834	5	0.000109	2	8.48E-06	12.85653		ENSG00000138768:E	USO1			gi|4505541|ref|NP_0	USO1 homolog, vesicle dock	962	107907	4.9	0	o	Q	21	0.019
835	5	0.000109	0	0	INF		ENSG00000104365:E	IKBKB			gi|41352712|ref|NP_	inhibitor of kappa light polype	756	86564	5.8	0	o	Q	15	0.004
836	5	0.000109	0	0	INF		ENSG00000104852:E	SNRP70			gi|29568103|ref|NP_	U1 small nuclear ribonucleop	437	51557	9.9	0	o	Q	19	0.031
837	5	0.000108	0	0	INF		ENSG00000123338:E	NCKAP1L			gi|34485727|ref|NP_	NCK-associated protein 1-lik	1127	128153	6.9	0	o	Q	25	0
838	5	0.000103	1	1.63E-06	63.17037		ENSG00000138095:E	LRPPRC			gi|31621305|ref|NP_	leucine-rich PPR motif-conta	1394	157904	6.1	0	o	S	37	0.99
839	5	1E-04	0	0	INF		ENSG00000067057:E	PFKP			gi|11321601|ref|NP_	phosphofructokinase, platele	784	85596	7.6	0	o	Q	39	0.001
840	5	9.93E-05	0	0	INF		ENSG00000072786:E	STK10			gi|126362971|ref|NP	serine/threonine kinase 10 [H	968	112135	6.9	0	o	Q	21	0
841	5	9.85E-05	0	0	INF		ENSG00000117228:N	GBP1			gi|4503939|ref|NP_0	guanylate binding protein 1, i	592	67903	6.3	0	o	Q	20	0.002
842	5	9.82E-05	0	0	INF		ENSG00000134333:E	LDHA			gi|5031857|ref|NP_0	lactate dehydrogenase A [Ho	332	36689	8.3	0	o	Q	37	0
843	5	9.57E-05	0	0	INF		ENSG00000173366:E	TLR9			gi|6005846|ref|NP_0	twinfilin-like protein [Homo sa	349	39548	6.9	0	o	Q	23	0
844	5	9.49E-05	0	0	INF		ENSG00000105939:E	ZC3HAV1			gi|27477136|ref|NP_	zinc finger antiviral protein is	902	101431	8.4	0	o	Q	19	0.036
845	5	9.32E-05	0	0	INF		ENSG00000183808:E	RBM12B			gi|118722349|ref|NP	RNA binding motif protein 12	1001	118103	6.8	0	o	Q	17	0.162
846	5	9.26E-05	0	0	INF		ENSG00000184432:E	COPB2			gi|4758032|ref|NP_0	coatomer protein complex, su	906	102487	5.3	0	o	Q	41	0
847	5	9.21E-05	0	0	INF		ENSG00000126934:E	MAP2K2			gi|13489054|ref|NP_	mitogen-activated protein kin	400	44424	6.5	0	o	S	20	0.816
848	5	9.19E-05	0	0	INF		ENSG00000104738:E	MCM4			gi|33469919|ref|NP_	minichromosome maintenanc	863	96558	6.7	0	o	Q	32	0
849	5	9.19E-05	0	0	INF		ENSG00000205609:E	EIF3CL			gi|153791492|ref|NP	eukaryotic translation initiatio	914	105473	5.6	0	o	Q	20	0
850	5	8.91E-05	0	0	INF		ENSG00000155229:E	MMS19			gi|157738692|ref|NP	MMS19 nucleotide excision r	1051	115705	6.5	0	o	S	31	0.747
851	5	8.89E-05	0	0	INF		ENSG00000180644:E	PRF1			gi|133908621|ref|NP	perforin 1 precursor [Homo s	555	61377	7.8	0	o	S	26	1
852	5	8.89E-05	0	0	INF		ENSG00000133706:E	LARS			gi|108773810|ref|NP	leucyl-tRNA synthetase [Hom	1176	134466	7.3	0	o	Q	0	0
853	5	8.85E-05	0	0	INF		ENSG00000113407:E	TARS			gi|38202255|ref|NP_	threonyl-tRNA synthetase [H	723	83435	6.7	0	o	Q	0	0
854	5	8.76E-05	0	0	INF		ENSG00000213965:E	NUDT19			gi|157739940|ref|NP	nudix (nucleoside diphospha	375	42233	7.6	0	o	S	28	0.977
855	5	8.52E-05	0	0	INF		ENSG00000145833:E	DDX46			gi|41327773|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	1031	117362	9.3	0	o	Q	25	0
856	5	8.38E-05	0	0	INF		ENSG00000065427:E	KARS			gi|5031815|ref|NP_0	lysyl-tRNA synthetase [Homo	597	68048	6.4	0	o	Q	14	0
857	5	8.14E-05	0	0	INF		ENSG00000124491:E	F13A1			gi|119395709|ref|NP	coagulation factor XIII A1 sub	732	83268	6	0	o	Q	23	0
858	5	8.14E-05	0	0	INF		ENSG00000136937:E	NCBP1			gi|4505343|ref|NP_0	nuclear cap binding protein s	790	91839	6.4	0	o	Q	0	0
859	5	8E-05	1	2.64E-06	30.27558		ENSG00000072818:E	CENTB1			gi|7661880|ref|NP_0	centaurin beta1 [Homo sapie	740	81536	7.7	0	o	Q	0	0
860	5	7.88E-05	0	0	INF		ENSG00000047410:E	TPR			gi|114155142|ref|NP	nuclear pore complex-associ	2363	267290	5	0	o	Q	15	0
861	5	7.85E-05	0	0	INF		ENSG00000116584:E	ARHGEF2			gi|15011974|ref|NP_	rho/rac guanine nucleotide e	958	108242	6.9	0	o	Q	29	0.029
862	5	7.66E-05	1	2.2E-06	34.75541		ENSG00000163714:E	SR140			gi|122937227|ref|NP	U2-associated SR140 protein	1029	118292	8.5	0	o	Q	0	0
863	5	7.36E-05	1	4.5E-06	16.35258		ENSG00000073111:E	MCM2			gi|33356547|ref|NP_	minichromosome maintenanc	904	101896	5.5	0	o	Q	21	0
864	5	7.31E-05	0	0	INF		ENSG00000121892:E	PDS5A			gi|155030216|ref|NP	PDS5, regulator of cohesion	1337	150830	7.9	0	o	Q	25	0.21
865	5	7.21E-05	0	0	INF		ENSG00000140632:E	N-PAC			gi|40556376|ref|NP_	cytokine-like nuclear factor n	553	60547	9.2	0	o	Q	18	0.007
866	5	7.14E-05	0	0	INF		ENSG00000088205:E	DDX18			gi|38327634|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	670	75407	9.5	0	o	Q	39	0
867	5	7.14E-05	0	0	INF		ENSG00000111581:E	NUP107			gi|9966881|ref|NP_0	nucleoporin 107kDa [Homo s	925	106374	5.4	0	o	Q	18	0
868	5	7.08E-05	0	0	INF		ENSG00000128245:E	YWHAH			gi|4507951|ref|NP_0	tyrosine 3/tryptophan 5 -mon	246	28219	4.8	0	o	Q	0	0
869	5	6.97E-05	0	0	INF		ENSG00000187555:E	USP7			gi|150378533|ref|NP	ubiquitin specific protease 7	1102	128302	5.6	0	o	Q	0	0
870	5	6.93E-05	0	0	INF		ENSG00000177963:E	RIC8A			gi|27883866|ref|NP_	resistance to inhibitors of cho	537	60372	5.3	0	o	Q	0	0
871	5	6.86E-05	0	0	INF		ENSG00000159131:E	GART			gi|4503915|ref|NP_0	phosphoribosylglycinamide fo	1010	107767	6.7	0	o	Q	19	0.047
872	5	6.83E-05	0	0	INF		ENSG00000110367:E	DDX6			gi|4758140|ref|NP_0	DEAD (Asp-Glu-Ala-Asp) box	472	53216	8.7	0	o	Q	30	0
873	5	6.77E-05	0	0	INF		ENSG00000100220:E	C22orf28			gi|7657015|ref|NP_0	hypothetical protein LOC514	505	55210	7.2	0	o	Q	0	0
874	5	6.71E-05	0	0	INF		ENSG00000089737:E	DDX24			gi|9966805|ref|NP_0	DEAD (Asp-Glu-Ala-Asp) box	859	96332	9.1	0	o	Q	0	0
875	5	6.63E-05	0	0	INF		ENSG00000010810:E	FYN			gi|23510362|ref|NP_	protein-tyrosine kinase fyn is	534	60141	6.2	0	o	Q	0	0
876	5	6.6E-05	1	1.79E-06	36.86244		ENSG00000119285:E	HEATR1			gi|73695475|ref|NP_	protein BAP28 [Homo sapien	2144	242368	6.5	0	o	Q	19	0.028
877	5	6.59E-05	2	3.49E-06	18.85091		ENSG00000107099:E	DOCK8			gi|44889960|ref|NP_	dedicator of cytokinesis 8 [Ho	2031	230818	6.8	0	o	Q	17	0
878	5	6.45E-05	0	0	INF		ENSG00000196305:E	IARS			gi|94721241|ref|NP_	isoleucyl-tRNA synthetase [H	1262	144498	6.1	0	o	Q	0	0
879	5	6.39E-05	0	0	INF		ENSG00000177731:E	FLII			gi|4503743|ref|NP_0	flightless I homolog [Homo sa	1269	144751	6.1	0	o	Q	16	0.014
880	5	6.36E-05	0	0	INF		ENSG00000076003:E	MCM6			gi|7427519|ref|NP_0	minichromosome maintenanc	821	92889	5.4	0	o	Q	14	0
881	5	6.15E-05	0	0	INF		ENSG00000110713:E	NUP98			gi|21264365|ref|NP_	nucleoporin 98kD isoform 1 [	1800	195816	6.4	0	o	Q	25	0.034
882	5	5.99E-05	1	3.89E-06	15.39086		ENSG00000136628:E	EPRS			gi|62241042|ref|NP_	glutamyl-prolyl tRNA synthet	1512	170590	7.3	0	o	Q	20	0.024
883	5	5.98E-05	0	0	INF		ENSG00000107937:E	GTPBP4			gi|55953087|ref|NP_	G protein-binding protein CR	634	73965	9.5	0	o	Q	25	0
884	5	5.83E-05	0	0	INF		ENSG00000158417:N	EIF5B			gi|84043963|ref|NP_	eukaryotic translation initiatio	1220	138827	5.5	0	o	Q	0	0
885	5	5.75E-05	0	0	INF		ENSG00000183486:N	MX2			gi|11342664|ref|NP_	myxovirus resistance protein	715	82089	8.8	0	o	Q	52	0
886	5	5.71E-05	0	0	INF		ENSG00000149480:E	MTA2			gi|14141170|ref|NP_	metastasis-associated protei	668	75023	9.7	0	o	Q	0	0
887	5	5.53E-05	0	0	INF		ENSG00000163932:E	PRKCD			gi|47157325|ref|NP_	protein kinase C, delta [Hom	676	77505	7.8	0	o	Q	20	0.018
888	5	5.31E-05	0	0	INF		ENSG00000137265:E	IRF4			gi|4505287|ref|NP_0	interferon regulatory factor 4	451	51712	6.7	0	o	Q	23	0
889	5	5.14E-05	0	0	INF		ENSG00000111144:E	LTA4H			gi|4505029|ref|NP_0	leukotriene A4 hydrolase [Ho	611	69285	6.2	0	o	Q	20	0.022
890	5	5.03E-05	0	0	INF		ENSG00000143924:E	EML4			gi|19923497|ref|NP_	echinoderm microtubule asso	981	108903	6.3	0	o	Q	18	0
891	5	5.01E-05	0	0	INF		ENSG00000160710:E	ADAR			gi|70166852|ref|NP_	adenosine deaminase, RNA-	1226	135967	8.6	0	o	Q	20	0
892	5	5E-05	0	0	INF		ENSG00000077097:E	TOP2B			gi|19913408|ref|NP_	DNA topoisomerase II, beta i	1621	182661	8.1	0	o	Q	19	0.229
893	5	4.92E-05	0	0	INF		ENSG00000125755:E	SYMPK			gi|124028529|ref|NP	symplekin [Homo sapiens]	1274	141148	6.1	0	o	Q	30	0
894	5	4.83E-05	0	0	INF		ENSG00000123130:E	ACOT9			gi|81295407|ref|NP_	acyl-Coenzyme A thioesteras	448	50851	8.5	0	o	S	17	0.594
895	5	4.59E-05	0	0	INF		ENSG00000138698:E	RAP1GDS1			gi|155030192|ref|NP	RAP1, GTP-GDP dissociatio	608	66388	5.3	0	o	Q	37	0
896	5	4.58E-05	0	0	INF		ENSG00000101596:E	SMCHD1			gi|148839305|ref|NP	structural maintenance of chr	2005	226372	7.3	0	o	Q	25	0
897	5	4.4E-05	1	2.04E-06	21.53212		ENSG00000148843:E	PDCD11			gi|70980549|ref|NP_	programmed cell death 11 [H	1871	208699	8.9	0	o	Q	0	0
898	5	4.35E-05	0	0	INF		ENSG00000144895:E	EIF2A			gi|54873624|ref|NP_	eukaryotic translation initiatio	585	64990	8.9	0	o	Q	16	0.049
899	5	4.26E-05	0	0	INF		ENSG00000060339:E	CCAR1			gi|46852388|ref|NP_	cell-cycle and apoptosis regu	1150	132821	5.8	0	o	Q	29	0.259
900	5	4.25E-05	0	0	INF		ENSG00000213445:E	SIPA1			gi|24497629|ref|NP_	signal-induced proliferation-a	1042	112116	6.6	0	o	Q	21	0.004
901	5	4.21E-05	0	0	INF		ENSG00000108055:E	SMC3			gi|4885399|ref|NP_0	structural maintenance of chr	1217	141541	7.2	0	o	Q	0	0
902	5	4.11E-05	0	0	INF		ENSG00000197943:E	PLCG2			gi|117320537|ref|NP	phospholipase C, gamma 2 [	1265	147870	6.6	0	o	Q	37	0
903	5	4.09E-05	0	0	INF		ENSG00000137497:E	NUMA1			gi|71361682|ref|NP_	nuclear mitotic apparatus pro	2115	238257	5.8	0	o	S	24	0.897
904	5	4.02E-05	0	0	INF		ENSG00000134905:E	CARS2			gi|13375695|ref|NP_	cysteinyl-tRNA synthetase 2	564	62224	8.3	0	o	S	34	0.92
905	5	4E-05	0	0	INF		ENSG00000133511:E	PI4KA			gi|155030226|ref|NP	phosphatidylinositol 4-kinase	2044	231317	6.9	0	o	Q	33	0.001
906	5	3.98E-05	0	0	INF		ENSG00000162775:E	RBM15			gi|47933339|ref|NP_	RNA binding motif protein 15	977	107188	10.1	0	o	Q	37	0.011
907	5	3.81E-05	0	0	INF		ENSG00000171793:E	CTPS			gi|148491070|ref|NP	CTP synthase [Homo sapien	591	66690	6.5	0	o	Q	21	0.166
908	5	3.64E-05	0	0	INF		ENSG00000153147:E	SMARCA5			gi|21071058|ref|NP_	SWI/SNF-related matrix-asso	1052	121933	8.1	0	o	Q	57	0.017
909	5	3.62E-05	0	0	INF		ENSG00000111331:N	OAS3			gi|45007007|ref|NP_	2'-5'oligoadenylate synthetas	1087	121170	8.4	0	o	Q	49	0.019
910	5	3.52E-05	1	2.43E-06	14.47864		ENSG00000197694:E	SPTAN1			gi|154759259|ref|NP	spectrin, alpha, non-erythroc	2472	284538	5.3	0	o	Q	0	0
911	5	3.47E-05	0	0	INF		ENSG00000149311:E	LOC651610			gi|169218268|ref|XP	PREDICTED: similar to muta	2934	336125	6.5	0	o	Q	0	0
912	5	3.21E-05	0	0	INF		ENSG00000119638:E	NEK9			gi|31543286|ref|NP_	NIMA related kinase 9 [Homo	979	107034	5.7	0	o	Q	0	0
913	5	2.88E-05	0	0	INF		ENSG00000084774:E	CAD			gi|18105007|ref|NP_	carbamoylphosphate synthet	2225	242981	6.5	0	o	Q	25	0.007
914	5	2.86E-05	0	0	INF		ENSG00000009335:E	UBE3C			gi|7661856|ref|NP_0	ubiquitin protein ligase E3C [	1083	123937	6.7	0	o	Q	0	0
915	5	2.74E-05	0	0	INF		ENSG00000181222:E	POLR2A			gi|4505939|ref|NP_0	DNA directed RNA polymera	1970	217204	7.4	0	o	Q	0	0
916	5	1.9E-05	0	0	INF		ENSG00000160796:E	NBEAL2			gi|149944548|ref|NP	neurobeachin-like 2 [Homo s	2754	302515	6.4	0	o	Q	22	0.003
917	5	1.75E-05	0	0	INF		ENSG00000159140:E	SON			gi|21040326|ref|NP_	SON DNA-binding protein iso	2426	263827	5.6	0	o	Q	0	0
918	5	1.32E-05	1	1.75E-06	7.556342		ENSG00000048828:E	FAM120A			gi|39652628|ref|NP_	hypothetical protein LOC231	1118	121888	8.9	0	o	Q	30	0
919	5	1.24E-05	1	1.48E-06	8.420621		ENSG00000127481:E	UBR4			gi|82659109|ref|NP_	retinoblastoma-associated fa	5183	573849	6	0	o	Q	23	0.109
920	5	1.19E-05	0	0	INF		ENSG00000153922:E	CHD1			gi|68299795|ref|NP_	chromodomain helicase DNA	1710	196687	7.1	0	o	Q	0	0
921	5	1.19E-05	0	0	INF		ENSG00000172534:E	HCFC1			gi|98986457|ref|NP_	host cell factor 1 [Homo sapi	2035	208730	7.5	0	o	Q	25	0.105
922	5	1.09E-05	0	0	INF		ENSG00000136813:E	KIAA0368			gi|122937211|ref|NP	KIAA0368 protein [Homo sap	2017	223692	8.7	0	o	Q	0	0
923	5	6.69E-06	0	0	INF		ENSG00000112159:E	MDN1			gi|24415404|ref|NP_	MDN1, midasin homolog [Ho	5596	632827	5.7	0	o	Q	19	0.216
924	4	0.001769	2	0.00012	14.68075		ENSG00000142676:E	RPL11			gi|15431290|ref|NP_	ribosomal protein L11 [Homo	178	20252	9.6	0	o	Q	37	0
925	4	0.001211	0	0	INF		ENSG00000087086:N	FTL			gi|20149498|ref|NP_	ferritin, light polypeptide [Hor	175	20020	5.8	0	o	Q	28	0
926	4	0.001038	0	0	INF		ENSG00000136527:E	SFRS10			gi|4759098|ref|NP_0	splicing factor, arginine/serin	288	33666	11.2	0	o	Q	0	0
927	4	0.000831	0	0	INF		ENSG00000100138:E	NHP2L1			gi|51317376|ref|NP_	NHP2 non-histone chromoso	128	14174	8.5	0	o	Q	0	0
928	4	0.000821	0	0	INF		ENSG00000136942:E	RPL35			gi|6005860|ref|NP_0	ribosomal protein L35 [Homo	123	14551	11	0	i	Q	0	0
929	4	0.000817	0	0	INF		ENSG00000092531:E	SNAP23			gi|18765729|ref|NP_	synaptosomal-associated pro	211	23354	5	0	o	Q	0	0
930	4	0.000809	0	0	INF		ENSG00000182774:E	LOC402057			gi|122937438|ref|NP	similar to 40S ribosomal prot	135	15602	9.6	0	i	Q	0	0
931	4	0.000808	0	0	INF		ENSG00000140350:E	ANP32A			gi|5453880|ref|NP_0	acidic (leucine-rich) nuclear p	249	28585	4.1	0	o	Q	0	0
932	4	0.000755	0	0	INF		ENSG00000100632:E	ERH			gi|4758302|ref|NP_0	enhancer of rudimentary hom	104	12259	5.9	0	o	Q	17	0.001
933	4	0.000733	0	0	INF		ENSG00000162385:E	MAGOH			gi|4505087|ref|NP_0	mago-nashi homolog [Homo	146	17164	6.1	0	o	Q	0	0
934	4	0.000718	0	0	INF		ENSG00000109332:E	UBE2D3			gi|33149320|ref|NP_	ubiquitin-conjugating enzyme	147	16687	7.8	0	o	Q	24	0
935	4	0.000709	0	0	INF		ENSG00000172809:E	RPL38			gi|78214522|ref|NP_	ribosomal protein L38 [Homo	70	8218	10.1	0	i	Q	0	0
936	4	0.000658	0	0	INF		ENSG00000124469:N	CEACAM8			gi|21314600|ref|NP_	carcinoembryonic antigen-rel	349	38154	7.4	0	o	S	35	0.994
937	4	0.000629	2	8.25E-05	7.621154		ENSG00000111737:E	RAB35			gi|5803135|ref|NP_0	RAB35, member RAS oncog	201	23025	8.3	0	o	Q	21	0.001
938	4	0.00058	1	2.37E-05	24.46436		ENSG00000008988:E	RPS20			gi|4506697|ref|NP_0	ribosomal protein S20 [Homo	119	13373	9.9	0	o	Q	0	0
939	4	0.000553	0	0	INF		ENSG00000163191:E	S100A11			gi|5032057|ref|NP_0	S100 calcium binding protein	105	11740	7.2	0	o	Q	26	0
940	4	0.000547	0	0	INF		ENSG00000144566:E	RAB5A			gi|19923262|ref|NP_	RAB5A, member RAS oncog	215	23659	8.1	0	o	Q	33	0.004
941	4	0.000539	0	0	INF		ENSG00000134287:E	ARF3			gi|4502203|ref|NP_0	ADP-ribosylation factor 3 [Ho	181	20601	7.4	0	o	Q	30	0
942	4	0.000532	0	0	INF		ENSG00000167283:E	ATP5L			gi|51479156|ref|NP_	ATP synthase, H+ transporti	103	11428	9.6	0	o	Q	29	0.003
943	4	0.000528	0	0	INF		ENSG00000143862:E	ARL8A			gi|20270343|ref|NP_	ADP-ribosylation factor-like 8	186	21416	7.8	0	o	Q	36	0
944	4	0.000493	3	7.94E-05	6.207288		ENSG00000072506:E	HSD17B10			gi|4758504|ref|NP_0	hydroxysteroid (17-beta) deh	261	26923	7.8	0	o	S	28	0.976
945	4	0.000484	0	0	INF		ENSG00000105640:E	RPL18A			gi|11415026|ref|NP_	ribosomal protein L18a [Hom	176	20762	10.7	0	o	Q	25	0
946	4	0.000464	0	0	INF		ENSG00000100445:E	C14orf124			gi|116812630|ref|NP	hypothetical protein LOC569	293	31077	9	0	o	S	18	0.778
947	4	0.000446	2	3.31E-05	13.44848		ENSG00000138796:E	HADH			gi|94557308|ref|NP_	L-3-hydroxyacyl-Coenzyme A	314	34294	8.9	0	o	S	48	0.513
948	4	0.000444	0	0	INF		ENSG00000213639:E	PPP1CB			gi|46249376|ref|NP_	protein phosphatase 1, catal	327	37187	6.2	0	o	Q	21	0
949	4	0.000429	0	0	INF		ENSG00000205937:E	RNPS1			gi|18379334|ref|NP_	RNA-binding protein S1, seri	305	34208	11.8	0	o	Q	0	0
950	4	0.000427	1	7.89E-06	54.14494		ENSG00000143549:E	TPM3			gi|114155144|ref|NP	tropomyosin 3 isoform 4 [Hor	248	28870	4.8	0	o	Q	0	0
951	4	0.000425	0	0	INF		ENSG00000115268:E	RPS15			gi|4506687|ref|NP_0	ribosomal protein S15 [Homo	145	17040	10.4	0	i	Q	0	0
952	4	0.000403	0	0	INF		ENSG00000169067:E	ACTBL2			gi|63055057|ref|NP_	hypothetical protein LOC345	376	42003	5.6	0	o	Q	21	0
953	4	0.000398	0	0	INF		ENSG00000197894:E	ADH5			gi|71565154|ref|NP_	class III alcohol dehydrogena	374	39724	7.5	0	o	Q	18	0
954	4	0.000389	0	0	INF		ENSG00000100365:E	NCF4			gi|47519798|ref|NP_	neutrophil cytosolic factor 4 i	339	39032	6.8	0	o	Q	0	0
955	4	0.000362	0	0	INF		ENSG00000177733:E	HNRNPA0			gi|5803036|ref|NP_0	heterogeneous nuclear ribon	305	30841	9.3	0	o	Q	22	0.01
956	4	0.000353	2	6.75E-05	5.229378		ENSG00000077549:E	CAPZB			gi|4826659|ref|NP_0	F-actin capping protein beta	272	30629	6	0	o	Q	19	0
957	4	0.000349	1	1.54E-05	22.66855		ENSG00000113387:E	SUB1			gi|19923784|ref|NP_	activated RNA polymerase II	127	14365	9.6	0	o	Q	20	0.003
958	4	0.000339	0	0	INF		ENSG00000198113:E	C9orf167			gi|116063568|ref|NP	hypothetical protein LOC548	423	46914	9.9	0	o	Q	20	0.015
959	4	0.000322	0	0	INF		ENSG00000063438:E	PDCD6			gi|7019485|ref|NP_0	programmed cell death 6 [Ho	191	21868	5.4	0	o	Q	29	0.009
960	4	0.000319	1	9.41E-06	33.891		ENSG00000142937:E	RPS8			gi|4506743|ref|NP_0	ribosomal protein S8 [Homo	208	24205	10.3	0	o	Q	0	0
961	4	0.000319	0	0	INF		ENSG00000167461:E	RAB8A			gi|16933567|ref|NP_	mel transforming oncogene [	207	23668	9.1	0	o	Q	21	0.034
962	4	0.000312	0	0	INF		ENSG00000146731:E	CCT6A			gi|4502643|ref|NP_0	chaperonin containing TCP1	531	58024	6.7	0	o	Q	30	0.212
963	4	0.000279	0	0	INF		ENSG00000086548:N	CEACAM6			gi|40255013|ref|NP_	carcinoembryonic antigen-rel	344	37195	5.8	0	o	S	35	0.978
964	4	0.000276	0	0	INF		ENSG00000115271:E	GCA			gi|6912388|ref|NP_0	grancalcin, EF-hand calcium	217	24010	5.2	0	o	Q	24	0.001
965	4	0.000276	0	0	INF		ENSG00000126247:E	CAPNS1			gi|51599151|ref|NP_	calpain, small subunit 1 [Hon	268	28316	5.2	0	o	Q	39	0.036
966	4	0.000274	0	0	INF		ENSG00000137312:E	FLOT1			gi|5031699|ref|NP_0	flotillin 1 [Homo sapiens]	427	47355	7.5	0	o	Q	27	0.015
967	4	0.000272	0	0	INF		ENSG00000106399:E	RPA3			gi|4506587|ref|NP_0	replication protein A3, 14kDa	121	13569	5.1	0	o	Q	27	0
968	4	0.000268	0	0	INF		ENSG00000167005:E	NUDT21			gi|5901926|ref|NP_0	cleavage and polyadenylatio	227	26227	8.8	0	o	Q	0	0
969	4	0.000266	0	0	INF		ENSG00000164069:N	LOC100131205			gi|169162497|ref|XP	PREDICTED: similar to hCG	160	18535	10.5	0	i	Q	38	0
970	4	0.000262	0	0	INF		ENSG00000168461:E	RAB31			gi|33589861|ref|NP_	RAB31, member RAS oncog	195	21700	7.1	0	o	Q	19	0.003
971	4	0.000262	0	0	INF		ENSG00000090013:E	BLVRB			gi|4502419|ref|NP_0	biliverdin reductase B (flavin	206	22119	7.6	0	o	S	22	0.853
972	4	0.000259	1	5.38E-06	48.04152		ENSG00000006530:E	AGK			gi|8922701|ref|NP_0	acylglycerol kinase [Homo sa	422	47137	8.1	0	o	S	32	0.935
973	4	0.00025	0	0	INF		ENSG00000104408:E	EIF3E			gi|4503521|ref|NP_0	eukaryotic translation initiatio	445	52221	6	0	o	Q	22	0
974	4	0.000248	0	0	INF		ENSG00000137818:N	RPLP1			gi|4506669|ref|NP_0	ribosomal protein P1 isoform	114	11514	4.3	0	o	Q	25	0.042
975	4	0.000239	0	0	INF		ENSG00000179144:E	GIMAP7			gi|23397516|ref|NP_	GTPase, IMAP family membe	300	34509	6.4	0	o	Q	21	0.002
976	4	0.000234	0	0	INF		ENSG00000170515:E	PA2G4			gi|124494254|ref|NP	ErbB3-binding protein 1 [Hon	394	43787	6.6	0	o	Q	0	0
977	4	0.000232	0	0	INF		ENSG00000160201:E	U2AF1			gi|5803207|ref|NP_0	U2 small nuclear RNA auxilla	240	27872	8.8	0	o	Q	19	0
978	4	0.000232	0	0	INF		ENSG00000187608:E	ISG15			gi|4826774|ref|NP_0	ISG15 ubiquitin-like modifier	165	17887	7.5	0	o	Q	31	0.011
979	4	0.000231	0	0	INF		ENSG00000101911:E	PRPS2			gi|4506129|ref|NP_0	phosphoribosyl pyrophospha	318	34769	6.6	0	o	Q	17	0.03
980	4	0.000224	0	0	INF		ENSG00000113575:E	PPP2CA			gi|4506017|ref|NP_0	protein phosphatase 2, cataly	309	35594	5.5	0	o	Q	0	0

rk	RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs										
	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
834	0	7.27E-05	0.000391	3.67E-05	0	3	0.000125	0.00018	0	9.33E-05	0	0	0.000279	2	9.32E-05	0.000132	0	0	0	1.89E-05	0	4.9E-05	0	0	Chromosome segregation	cytoplasm; Golgi membrane	binding; protein transporter
835	0	0.000216	0.000249	0.000187	0	3	0.000163	0.000111	0	0.000178	0	4.32E-05	0	2	5.53E-05	8.43E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	cytoplasm	ATP binding; nucleotide
836	0.000371	0.000107	0	0.000202	0	3	0.00017	0.000157	0	0.000154	0	3.73E-05	0	2	4.78E-05	7.29E-05	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus; spliceosome complex	nucleotide binding; protein
837	0	0.000103	0	9.4E-05	0	2	4.94E-05	5.71E-05	0	0.000338	0	8.69E-05	0.000238	3	0.000166	0.000151	0	0	0	0	0	0	0	0		integral to plasma membrane	
838	0	0.000268	0	0.000228	0	2	0.000124	0.000144	0	9.66E-05	0	0.000176	5.51E-05	3	8.18E-05	7.4E-05	0	0	0	1.3E-05	0	0	0	0		cytoplasm; mitochondrion	binding; RNA binding [pmid
839	0	8.93E-05	0	0.000163	0	2	6.3E-05	7.86E-05	0	0.000114	0	4.16E-05	0.000392	3	0.000137	0.000176	0	0	0	0	0	0	0	0	Phosphofructokinase, a key	6-phosphofructokinase	6-phosphofructokinase
840	0	0.000261	0	0.000219	0	2	0.00012	0.00014	0	0.000139	0	1.69E-05	0.000159	3	7.86E-05	8.18E-05	0	0	0	0	0	0	0	0			
841	0	0.000315	0	0.000179	0	2	0.000124	0.000153	0	0.000136	0	2.76E-05	0.00013	3	7.34E-05	6.98E-05	0	0	0	0	0	0	0	0	Guanylate-binding protein,	membrane	GTP binding [pmid 1715024];
842	0	7.03E-05	0	0.000213	0	2	7.08E-05	0.0001	0	0.000338	0	4.92E-05	0.000116	3	0.000126	0.000149	0	0	0	0	0	0	0	0	L-lactate dehydrogenases	cytoplasm; cytosol [pmid	L-lactate dehydrogenase
843	0	0.000134	0	0.000253	0	2	9.67E-05	0.000122	0	0.000129	0	0.00014	0.00011	3	9.47E-05	6.44E-05	0	0	0	0	0	0	0	0	Actin depolymerisation	cytoskeleton; intracellular	actin binding
844	0.00036	0.000129	0	0.000137	0	3	0.000156	0.000149	0	0	0	9.05E-05	4.26E-05	2	3.33E-05	4.31E-05	0	0	0	0	0	0	0	0	Poly(ADP-ribose)	nucleus	metal ion binding; NAD+ ADP
845	0	6.99E-05	0	0.000229	0	2	7.48E-05	0.000108	0	0.000179	0	0.000228	3.83E-05	3	0.000111	0.00011	0	0	0	0	0	0	0	0			
846	0	7.72E-05	0	9.75E-05	0	2	4.37E-05	5.11E-05	0	0.000149	0	3.6E-05	0.000381	3	0.000141	0.000172	0	0	0	0	0	0	0	0	WD40 domain, found in a	COPI vesicle coat [pmid	protein transporter activity
847	0	0.000175	0	0.000194	0	2	9.23E-05	0.000107	0	0.00015	0	0.000122	9.6E-05	3	9.2E-05	6.51E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	extracellular region [pmid	ATP binding; nucleotide
848	0	0.000108	0	8.19E-05	0	2	4.75E-05	5.59E-05	0	0.000286	0	0.00017	8.9E-05	3	0.000136	0.000122	0	0	0	0	0	0	0	0	ATPase family associated	nucleus [pmid 8265339]	ATP binding; DNA binding;
849	0	2.55E-05	0	9.66E-05	0	2	3.05E-05	4.57E-05	0	4.91E-05	0	1.79E-05	0.000546	3	0.000153	0.000263	0	0	0	0	0	0	0	0			
850	0	0.000155	0	3.36E-05	0	2	4.72E-05	7.38E-05	0	0.000107	0	1.55E-05	0.000402	3	0.000131	0.000187	0	0	0	0	0	0	0	0			
851	0	0.00042	0	6.37E-05	0	2	0.000121	0.000202	0	4.04E-05	0	0.000118	6.92E-05	3	5.68E-05	4.95E-05	0	0	0	0	0	0	0	0			
852	0	7.93E-05	0	9.01E-05	0	2	4.24E-05	4.91E-05	0	7.63E-05	0	0.000139	0.000326	3	0.000135	0.000139	0	0	0	0	0	0	0	0			
853	0	0.000129	0	0.000147	0	2	6.89E-05	7.99E-05	0	6.21E-05	0	0.000158	0.000212	3	0.000108	9.52E-05	0	0	0	0	0	0	0	0	Threonyl-tRNA synthetase	cytoplasm [pmid 2033077];	ATP binding; electron carrier
854	0	0.000124	0	9.42E-05	0	2	5.47E-05	6.43E-05	0	5.98E-05	0	0.000218	0.000205	3	0.000121	0.000108	0	0	0	0	0	0	0	0			
855	0	0.000181	0	8.57E-05	0	2	6.67E-05	8.63E-05	0	0.000283	0	9.5E-05	3.72E-05	3	0.000104	0.000126	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; ATP-dependent
856	0	7.81E-05	0	8.88E-05	0	2	4.17E-05	4.84E-05	0	3.76E-05	0	0.000273	0.000193	3	0.000126	0.000129	0	0	0	0	0	0	0	0	LysRS_N: N-terminal,	cytoplasm [pmid 9278442];	ATP binding; ligase activity;
857	0	0.000127	0	0.000169	0	2	7.41E-05	8.72E-05	0	0.000153	0	4.46E-05	0.000157	3	8.88E-05	7.89E-05	0	0	0	0	0	0	0	0	activation peptide		
858	0	8.86E-05	0	8.94E-05	0	2	4.45E-05	5.14E-05	0	0.000114	0	0.000165	0.000194	3	0.000118	8.57E-05	0	0	0	0	0	0	0	0	Middle domain of	nucleoplasm [pmid 7937105];	protein binding [pmid
859	0.000219	0.000315	0	2.39E-05	0	3	0.00014	0.000153	0	3.03E-05	0	0	5.19E-05	2	2.05E-05	2.53E-05	0	0	0	0	0	2.12E-05	0	0	Putative GTPase activating		GTPase activator activity;
860	0.000137	1.97E-05	0	0	0	2	3.92E-05	6.6E-05	0.000376	2.85E-05	0	6.91E-05	0	3	0.000118	0.000174	0	0	0	0	0	0	0	0			
861	0	0.00017	0	9.22E-05	0	2	6.57E-05	8.23E-05	0	0.000234	0	5.11E-05	8.01E-05	3	9.14E-05	0.000101	0	0	0	0	0	0	0	0	Protein kinase C conserved	intracellular; microtubule [pmid	diacylglycerol binding; metal
862	0	2.27E-05	0	5.15E-05	0	2	1.85E-05	2.44E-05	0.000431	4.36E-05	0	6.34E-05	0	3	0.000135	0.0002	0	0	0	1.76E-05	0	0	0	0			
863	0	2.58E-05	0.000208	9.77E-05	0	3	8.28E-05	9.3E-05	0	0.000149	0	0.000108	0	2	6.43E-05	7.61E-05	0	0	0	0	0	0	3.6E-05	0	Magnesium chelatase,	chromatin [pmid 8798650];	ATP binding; DNA binding
864	0	0.000105	0	0.000167	0	2	6.8E-05	8.26E-05	0	0.000161	0	3.66E-05	0.000115	3	7.81E-05	7.32E-05	0	0	0	0	0	0	0	0			
865	0	8.44E-05	0	0.000224	0	2	7.7E-05	0.000106	0	8.11E-05	0	0.000118	6.94E-05	3	6.72E-05	4.93E-05	0	0	0	0	0	0	0	0	NAD binding domain of 6-		phosphogluconate
866	0	6.96E-05	0	0.000237	0	2	7.67E-05	0.000112	0	0.000134	0	7.31E-05	5.73E-05	3	6.61E-05	5.51E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-		ATP binding; ATP-dependent
867	0	0.000126	0	0.000115	0	2	6.02E-05	6.96E-05	0	0.000218	0	7.06E-05	4.15E-05	3	8.26E-05	9.5E-05	0	0	0	0	0	0	0	0	Nuclear pore protein 84 /	nuclear pore [pmid 11564755]	nucleocytoplasmic
868	0	0.000203	0	7.31E-05	0.001655	3	6.91E-05	9.58E-05	0	9.12E-05	0	0.000199	0	2	7.26E-05	9.46E-05	0	0	0	0	0	0	0	0		cytoplasm	actin binding; glucocorticoid
869	0	0.000127	0	0.00016	0	2	7.18E-05	8.4E-05	0	8.14E-05	0	1.48E-05	0.000174	3	6.76E-05	7.94E-05	0	0	0	0	0	0	0	0			
870	0.000302	4.34E-05	0	6.58E-05	0.000758	4	0.000103	0.000136	0	0	0	0	0.000143	1	3.57E-05	7.15E-05	0	0	0	0	0	0	0	0	PUL domain. The PUL		guanyl-nucleotide exchange
871	0	0.000185	0	0.00014	0	2	8.12E-05	9.55E-05	0	8.89E-05	0	9.7E-05	3.8E-05	3	5.6E-05	4.55E-05	0	0	0	0	0	0	0	0	PurM (Aminoimidazole	cytoplasm	ATP binding; catalytic
872	0	9.88E-05	0	3.74E-05	0	2	3.41E-05	4.66E-05	0	0.00019	0	0.000138	8.13E-05	3	0.000102	8.15E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; ATP-dependent
873	0	9.24E-05	0	7E-05	0	2	4.06E-05	4.77E-05	0	4.44E-05	0	0.000259	7.6E-05	3	9.47E-05	0.000114	0	0	0	0	0	0	0	0	Uncharacterized conserved		
874	0	5.43E-05	0	0.000165	0	2	5.47E-05	7.76E-05	0	0.000235	0	3.8E-05	4.47E-05	3	7.94E-05	0.000106	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleolus [pmid 11256614]	ATP binding; ATP-dependent
875	0	4.8E-05	0	0.000132	0	2	4.51E-05	6.24E-05	0	8.4E-05	0	0.000122	0.000144	3	8.75E-05	6.34E-05	0	0	0	0	0	0	0	0	Src homology 3 domains;		ATP binding; identical protein
876	0	0.000109	0	9.06E-05	0	2	4.99E-05	5.8E-05	0	7.32E-05	0	7.61E-05	0.000179	3	8.21E-05	7.36E-05	0	0	0	0	0	0	0	1.43E-05	BP28CT (NUC211) domain.	nucleus	binding; protein binding [pmid
877	0	0.000115	0	0.000165	0	2	7E-05	8.34E-05	0	6.63E-05	0	4.82E-05	0.000132	3	6.17E-05	5.48E-05	0	0	2.09E-05	0	0	7.07E-06	0	0	Dedicator of cytokinesis.		binding; GTP binding;
878	0	0.000129	0	7E-05	0	2	4.98E-05	6.24E-05	0	1.78E-05	0	0.000116	0.000183	3	7.92E-05	8.58E-05	0	0	0	0	0	0	0	0	This is the catalytic core	cytoplasm [pmid 7721108];	aminoacyl-tRNA ligase
879	0	0.00011	0	0.000111	0	2	5.54E-05	6.4E-05	0	1.77E-05	0	9E-05	0.000182	3	7.23E-05	8.26E-05	0	0	0	0	0	0	0	0	Leucine-rich repeats	cytoskeleton; nucleus	actin binding [pmid
880	0	8.52E-05	0	6.45E-05	0	2	3.74E-05	4.41E-05	0	2.73E-05	0	0.000239	9.35E-05	3	8.98E-05	0.000107	0	0	0	0	0	0	0	0	Magnesium chelatase,	nucleus [pmid 9286856]	ATP binding [pmid 9286856];
881	0	0.000155	0	5.89E-05	0	2	5.36E-05	7.34E-05	0	2.49E-05	0	1.81E-05	0.000235	3	6.94E-05	0.000111	0	0	0	0	0	0	0	0	Nucleoporin autopeptidase;	nuclear pore [pmid 9348540]	protein binding [pmid
882	0	0.000108	0	8.18E-05	0	2	4.74E-05	5.58E-05	0	2.97E-05	0	0.000183	7.62E-05	3	7.23E-05	8.05E-05	0	0	3.11E-05	0	0	0	0	0	GST_C family, Gamma	cytoplasm [pmid 8188258];	ATP binding; glutamate-tRNA
883	0	7.36E-05	0	0.000223	0	2	7.41E-05	0.000105	0	3.54E-05	0	2.57E-05	0.000121	3	4.56E-05	5.25E-05	0	0	0	0	0	0	0	0	NOG1 is a nucleolar GTP-	nucleus	GTP binding; nucleotide
884	0	7.65E-05	0	4.34E-05	0	2	3E-05	3.71E-05	0	5.52E-05	0	0.000134	0.000157	3	8.66E-05	7.24E-05	0	0	0	0	0	0	0	0	IF2/eIF5B (initiation factors	intracellular	GTP binding; nucleotide
885	0	0.000163	0	4.94E-05	0	2	5.31E-05	7.69E-05	0	0.000126	0	6.85E-05	5.37E-05	3	6.19E-05	5.16E-05	0	0	0	0	0	0	0	0	Dynamin, GTPase; Large	cytoplasm [pmid 8798556];	GTP binding; GTPase
886	0	6.98E-05	0	0.000132	0	2	5.05E-05	6.36E-05	0	3.36E-05	0	4.89E-05	0.000172	3	6.37E-05	7.53E-05	0	0	0	0	0	0	0	0	ELM2 domain. The ELM2	histone deacetylase complex	metal ion binding; sequence-
887	0.00024	3.45E-05	0	7.84E-05	0	3	8.82E-05	0.000106	0	3.32E-05	0	0	5.68E-05	2	2.25E-05	2.77E-05	0	0	0	0	0	0	0	0	Protein kinase C conserved	cytoplasm [pmid 16611985];	ATP binding; diacylglycerol
888	0	0.000103	0	7.83E-05	0	2	4.54E-05	5.35E-05	0	4.97E-05	0	0.000109	8.51E-05	3	6.09E-05	4.72E-05	0	0	0	0	0	0	0	0	Interferon Regulatory	nucleus [pmid 8657101] [pmid	RNA polymerase II
889	0	3.82E-05	0	8.67E-05	0	2	3.12E-05	4.11E-05	0	3.67E-05	0	0.000187	6.28E-05	3	7.16E-05	8.11E-05	0	0	0	0	0	0	0	0	Peptidase family M1.		epoxide hydrolase activity
890	0	4.76E-05	0	9E-05	0	2	3.44E-05	4.33E-05	0	0.000114	0	3.33E-05	0.000117	3	6.63E-05	5.89E-05	0	0	0	0	0	0	0	0	HELP motif. The HELP	cytoplasm [pmid 10995578];	
891	0	0.000152	0	8.64E-05	0	2	5.97E-05	7.39E-05	0	7.32E-05	0	2.66E-05	6.26E-05	3	4.06E-05	3.36E-05	0	0	0	0	0	0	0	0	Double-stranded RNA	cytoplasm [pmid 7565688];	DNA binding; double-
892	0	7.19E-05	0	0.000128	0	2	5E-05	6.2E-05	0	2.77E-05	0	3.02E-05	0.000142	3	5E-05	6.29E-05	0	0	0	0	0	0	0	0	TOPRIM_TopoIIA:	chromosome; cytosol [pmid	ATP binding; chromatin
893	0	7.32E-05	0	0.000139	0	2	5.3E-05	6.67E-05	0	3.52E-05	0	2.56E-05	0.000121	3	4.53E-05	5.23E-05	0	0	0	0	0	0	0	0			
894	0	5.21E-05	0	3.94E-05	0	2	2.29E-05	2.69E-05	0	0.0001	0	0.000109	8.57E-05	3	7.38E-05	5.01E-05	0	0	0	0	0	0	0	0	Brown fat-inducible	mitochondrion	acetyl-CoA hydrolase
895	0	0.000153	0	8.72E-05	0	2	6.02E-05	7.45E-05	0	3.69E-05	0	2.68E-05	6.31E-05	3	3.17E-05	2.61E-05	0	0	0	0	0	0	0	0			
896	0	9.31E-05	0	7.93E-05	0	2	4.31E-05	5.01E-05	0	4.48E-05	0	0.00013	1.91E-05	3	4.85E-05	5.75E-05	0	0	0	0	0	0	0	0			
897	0	2.49E-05	0	3.78E-05	0	2	1.57E-05	1.88E-05	0	0.000108	0	1.74E-05	0.000164	3	7.24E-05	7.73E-05	0	0	0	0	0	0	0	1.64E-05	Tetratricopeptide repeat	intracellular; nucleus [pmid	RNA binding; transcription
898	0	0.00012	0	3.02E-05	0	2	3.75E-05	5.66E-05	0	7.67E-05	0	5.58E-05	6.56E-05	3	4.95E-05	3.41E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a	cytoplasm; eukaryotic	ribosome binding; translation
899	0	4.06E-05	0	4.61E-05	0	2	2.17E-05	2.51E-05	0	5.85E-05	0	2.84E-05	0.000167	3	6.35E-05	7.3E-05	0	0	0	0	0	0	0	0			calcium ion binding; DNA
900	0	8.95E-05	0	0.000102	0	2	4.78E-05	5.54E-05	0	6.46E-05	0	4.7E-05	3.68E-05	3	3.71E-05	2.73E-05	0	0	0	0	0	0	0	0	Nnf1. NNF1 is an essential	membrane; nucleus [pmid	protein binding; Rap GTPase
901	0	3.83E-05	0	1.45E-05	0	2	1.32E-05	1.81E-05	0	1.84E-05	0	1.34E-05	0.000252	3	7.1E-05	0.000121	0	0	0	0	0	0	0	0	SMC proteins Flexible	basement membrane [pmid	ATP binding; ATPase
902	0	7.38E-05	0	9.77E-05	0	2	4.29E-05	5.05E-05	0	5.32E-05	0	1.29E-05	9.1E-05	3	3.93E-05	4.13E-05	0	0	0	0	0	0	0	0			
903	7.67E-05	4.41E-05	0	0.000167	0	3	7.2E-05	7.07E-05	0	2.12E-05	0	0	1.82E-05	2	9.84E-06	1.14E-05	0	0	0	0	0	0	0	0	Chromosome segregation	nucleus [pmid 1541636];	protein binding [pmid
904	0	8.27E-05	0	6.26E-05	0	2	3.63E-05	4.28E-05	0	7.96E-05	0	2.89E-05	6.81E-05	3	4.41E-05	3.65E-05	0	0	0	0	0	0	0	0	This is the catalytic core		ATP binding; cysteine-tRNA
905	0	2.28E-05	0	1.73E-05	0	2	1E-05	1.18E-05	0.000217	4.39E-05	0	0	1.88E-05	3	7E-05	9.98E-05	0	0	0	0	0	0	0	0			
906	0.000166	2.39E-05	0	7.23E-05	0	3	6.55E-05	7.34E-05	0	2.3E-05	0	3.34E-05	0	2	1.41E-05	1.68E-05	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus	nucleotide binding; RNA
907	0	7.89E-05	0	2.99E-05	0	2	2.72E-05	3.73E-05	0	7.59E-05	0	5.52E-05	6.5E-05	3	4.9E-05	3.38E-05	0	0	0	0	0	0	0	0			
908	0	2.22E-05	0	1.68E-05	0	2	9.74E-06	1.15E-05	0	2.13E-05	0	0.00014	9.12E-05	3	6.3E-05	6.42E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	condensed chromosome [pmid	ATP binding [pmid
909	0	4.29E-05	0	4.88E-05	0	2	2.29E-05	2.66E-05	0	6.19E-05	0	3E-05	0.000106	3	4.95E-05	4.53E-05	0	0	0	0	0	0	0	0	Nucleotidyltransferase	microsome [pmid 2440675]	ATP binding;
910	6.56E-05	3.77E-05	0	0.000114	0	3	5.44E-05	4.81E-05	0	0	0	3.3E-05	3.11E-05	2	1.6E-05	1.85E-05	0	0	0	0	0	0	0	0			
911	0	4.77E-05	0	5.42E-05	0	2	2.55E-05	2.95E-05	0	2.29E-05	0	2.22E-05	0.000131	3	4.4E-05	5.89E-05	0	0	0	0	1.95E-05	0	0	0			
912	0	2.38E-05	0	3.61E-05	0	2	1.5E-05	1.8E-05	0	4.58E-05	0	3.33E-05	0.000118	3	4.92E-05	4.96E-05	0	0	0	0	0	0	0	0	Alpha-tubulin suppressor	nucleus	ATP binding; magnesium ion
913	0	2.1E-05	0	5.56E-05	0	2	1.91E-05	2.62E-05	0	6.05E-05	0	7.33E-06	8.63E-05	3	3.85E-05	4.17E-05	0	0	0	0	0	0	0	0	Methylglyoxal synthase-like	cytoplasm	amino acid binding;
914	0	2.15E-05	0	6.52E-05	0	2	2.17E-05	3.08E-05	0	2.07E-05	0	1.51E-05	0.000106	3	3.55E-05	4.8E-05	0	0	0	0	0	0	0	0	Domain Homologous to E6-	intracellular [pmid 11278995];	ligase activity; protein
915	0	7.1E-05	0	3.59E-05	0	2	2.67E-05	3.4E-05	0	5.69E-05	0	1.66E-05	3.9E-05	3	2.81E-05	2.5E-05	0	0	0	0	0	0	0	0	RNA polymerase Rpb1,	DNA-directed RNA	DNA binding [pmid 7622068];
916	0	4.23E-05	0	1.92E-05	0.000148	3	1.54E-05	2.01E-05	0	4.89E-05	0	0	4.18E-05	2	2.27E-05	2.63E-05	0	0	0	0	0	0	0	0			
917	0	9.61E-06	0	5.1E-05	0	2	1.51E-05	2.43E-05	0	3.7E-05	0	2.69E-05	1.58E-05	3	1.99E-05	1.59E-05	0	0	0	0	0	0	0	0	Double-stranded RNA	intracellular; nucleus	DNA binding [pmid 8031013];
918	0	2.09E-05	0	1.58E-05	0	2	9.17E-06	1.08E-05	0	2.01E-05	0	1.46E-05	3.43E-05	3	1.73E-05	1.42E-05	0	0	0	1.4E-05	0	0	0	0	Xeroderma pigmentosum G		
919	0	4.5E-06	0	2.73E-05	0	2	7.94E-06	1.31E-05	0	8.66E-06	0	2.2E-05	3.7E-05	3	1.69E-05	1.62E-05	0	0	0	0	0	0	0	1.18E-05	Putative zinc finger in N-		binding; ubiquitin-protein
920	0	1.64E-05	0	2.07E-05	0	2	9.26E-06	1.08E-05	0	2.62E-05	0	9.54E-06	2.24E-05	3	1.46E-05	1.21E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	chromatin; nucleus	ATP binding; ATP-dependent
921	0	2.29E-05	0	2.6E-05	0	2	1.22E-05	1.42E-05	0	1.1E-05	0	1.6E-05	1.89E-05	3	1.15E-05	8.31E-06	0	0	0	0	0	0	0	0			
922	0	2.31E-05	0	1.75E-05	0	2	1.02E-05	1.2E-05	0	1.11E-05	0	1.62E-05	1.9E-05	3	1.16E-05	8.39E-06	0	0	0	0	0	0	0	0			
923	0	1.25E-05	0	9.47E-06	0	2	5.49E-06	6.46E-06	0	1.2E-05	0	5.83E-06	1.37E-05	3	7.89E-06	6.26E-06	0	0	0	0	0	0	0	0	VWA_Midasin: Midasin is a	nucleus [pmid 12102729]	ATP binding; ATPase activity
924	0	0	0	0.001092	0	1	0.000273	0.000546	0	0.000378	0	0.001467	0.011214	3	0.003265	0.005336	0	0	0	0	0	0	0.00078	0.000184	ribosomal L5P family C-	intracellular; ribosome	rRNA binding; structural
925	0.001853	0.000133	0	0	0	2	0.000497	0.000907	0.005073	0	0	0	0.002632	2	0.001926	0.002437	0	0	0	0	0	0	0	0	Eukaryotic Ferritin	ferritin complex [pmid	binding; ferric iron binding;
926	0	0.001296	0	0.002883	0	2	0.001045	0.001369	0	0.002259	0	0.00187	0	2	0.001032	0.001202	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus [pmid 9546399]	nucleic acid binding;
927	0	0.000182	0	0.00069	0	2	0.000218	0.000326	0	0	0	0.001275	0.004499	2	0.001443	0.002124	0	0	0	0	0	0	0	0	Ribosomal protein HS6-	nucleolus [pmid 10593953];	RNA binding [pmid
928	0.002637	0.00019	0	0	0	2	0.000707	0.00129	0.003609	0	0	0.000133	0	2	0.000935	0.001783	0	0	0	0	0	0	0	0		cytosolic large ribosomal	mRNA binding [pmid
929	0.001537	0.000442	0.004452	0	0	3	0.001608	0.002003	0	0.000106	0	0	0	1	2.66E-05	5.32E-05	0	0	0	0	0	0	0	0	Soluble NSF (N-	plasma membrane [pmid	protein binding [pmid
930	0	0	0.002783	0.00157	0	2	0.001088	0.001351	0	0.001994	0	0.000121	0	2	0.000529	0.000979	0	0	0	0	0	0	0	0			
931	0	0	0	0.000607	0	1	0.000152	0.000303	0	0.00036	0	0.000721	0.004779	3	0.001465	0.002229	0	0	0	0	0	0	0	0		cytoplasm [pmid 11729309];	protein binding [pmid
932	0	0	0	0.001359	0	1	0.00034	0.000679	0	0.000216	0	0.001883	0.002584	3	0.001171	0.001263	0	0	0	0	0	0	0	0	Enhancer of rudimentary.		
933	0	0	0	0.002541	0	1	0.000635	0.00127	0	0.000154	0	0.002906	0.000263	3	0.000831	0.001388	0	0	0	0	0	0	0	0	Mago nashi protein. This	nucleus	protein binding [pmid
934	0	0	0.002556	0.00024	0	2	0.000699	0.001243	0	0	0	0.000333	0.002611	2	0.000736	0.00126	0	0	0	0	0	0	0	0	Ubiquitin-conjugating		ligase activity; protein
935	0	0.000333	0	0.000505	0	2	0.000209	0.000252	0	0.003205	0	0.001632	0	2	0.001209	0.001537	0	0	0	0	0	0	0	0	Ribosomal L38e protein	intracellular; ribosome	structural constituent of
936	0.003253	0.000267	0.001615	0	0	3	0.001284	0.001491	0	0.000129	0	0	0	1	3.21E-05	6.43E-05	0	0	0	0	0	0	0	0	Immunoglobulin domain cell	extracellular space [pmid	GPI anchor binding
937	0	0.001625	0	0.000352	0	2	0.000494	0.000772	0	0.002567	0	0.000487	0	2	0.000764	0.001224	0	0	0	0.000271	0	0.000389	0	0	Rab35 subfamily. Rab35 is	membrane	GTP binding; GTPase
938	0	0.001372	0	0.000148	0	2	0.00038	0.000665	0	0.001508	0	0	0.001613	2	0.00078	0.000902	0	0	0	0	0	0.00019	0	0	Ribosomal protein	cytosolic small ribosomal	protein binding [pmid
939	0	0.000666	0	0.001178	0	2	0.000461	0.000572	0	0.001496	0	0.001088	0	2	0.000646	0.000764	0	0	0	0	0	0	0	0	S-100/ICaBP-like domain;	cytoplasm [pmid 10913138]	calcium ion binding; calcium-
940	0	0.000651	0.003495	8.22E-05	0	3	0.001057	0.001651	0	0.000149	0	0	0	1	3.73E-05	7.45E-05	0	0	0	0	0	0	0	0	Rab5-related subfamily.	early endosome [pmid	GTP binding; GTPase
941	0.001792	0.000432	0	0	0	2	0.000556	0.000849	0	0.000685	0	0.001402	0	2	0.000522	0.00067	0	0	0	0	0	0	0	0	Arf1-Arf5-like subfamily.	intracellular	GTP binding; nucleotide
942	0	0.001132	0	0.000171	0	2	0.000326	0.000544	0	0.001089	0	0	0.001863	2	0.000738	0.000909	0	0	0	0	0	0	0	0	Mitochondrial ATP	mitochondrion; proton-	hydrogen-transporting ATP
943	0	0.001317	0	0.00095	0	2	0.000567	0.000671	0	0.001608	0	0.000351	0	2	0.00049	0.000764	0	0	0	0	0	0	0	0	Arl10-like subfamily.	cytoplasm [pmid 15331635];	alpha-tubulin binding [pmid
944	0	0.000804	0	0.001489	0	2	0.000573	0.000719	0	0.000774	0	0.000875	0	2	0.000412	0.000478	0	0	0.000177	0.000278	0	0.00018	0	0	3-ketoacyl-(acyl-carrier-	cytoplasm [pmid 9338779];	3-hydroxy-2-methylbutyryl-
945	0	0.001325	0	0.000703	0	2	0.000507	0.000638	0	0.001657	0	0.000185	0	2	0.000461	0.000802	0	0	0	0	0	0	0	0	Ribosomal L18ae protein	cytosolic large ribosomal	RNA binding [pmid 9582194];
946	0	0.000239	0	6.03E-05	0	2	7.48E-05	0.000113	0.00303	0.000383	0	0	0	2	0.000853	0.001462	0	0	0	0	0	0	0	0			
947	0	0.000669	0	0.00135	0	2	0.000505	0.000646	0	0.000714	0	0.000832	0	2	0.000387	0.000449	0	0	0	0.000116	0	0.00015	0	0	3-hydroxyacyl-CoA	cytoplasm [pmid 11256614];	3-hydroxyacyl-CoA
948	0	0	0	0.000556	0	1	0.000139	0.000278	0	0.000137	0	0.000216	0.002641	3	0.000749	0.001265	0	0	0	0	0	0	0	0	Protein phosphatase 2A		hydrolase activity; iron ion
949	0	0.001147	0.001232	0.000174	0	3	0.000638	0.000641	0	0.000883	0	0	0	1	0.000221	0.000441	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus [pmid 9580558]	nucleotide binding; RNA
950	0.002943	9.4E-05	0	7.12E-05	0	3	0.000777	0.001444	0	0	0	0	0.00031	1	7.74E-05	0.000155	0	0	0	0	0	6.31E-05	0	0			
951	0	0	0	0.001096	0	1	0.000274	0.000548	0	0.001702	0	0.000338	0.000265	3	0.000576	0.000764	0	0	0	0	0	0	0	0	30S ribosomal protein	cytosolic small ribosomal	protein binding [pmid
952	0	0	0	0.000143	0.003982	2	3.56E-05	7.13E-05	0.002951	0	0	0.00013	0	2	0.00077	0.001455	0	0	0	0	0	0	0	0	Actin; An ubiquitous protein		protein binding
953	0	0.000187	0	0.000425	0	2	0.000153	0.000202	0	0	0	0.00144	0.001129	2	0.000642	0.000752	0	0	0	0	0	0	0	0	Alcohol dehydrogenase		alcohol dehydrogenase
954	0	0	0	0.000313	0	1	7.82E-05	0.000156	0.002619	6.62E-05	0	0	0.000113	3	0.0007	0.00128	0	0	0	0	0	0	0	0	Src homology 3 domains;	cytosol [pmid 8280052];	phosphoinositide binding;
955	0	0.000535	0	0.000579	0	2	0.000279	0.000322	0	0	0	0.001659	0.000126	2	0.000446	0.000811	0	0	0	0	0	0	0	0		heterogeneous nuclear	nucleotide binding; RNA
956	0	8.58E-05	0	0.000844	0	2	0.000232	0.00041	0	0	0	0.00006	0.001835	2	0.000474	0.000908	0	0	0.00034	0.0002	0	0	0	0	F-actin capping protein,	F-actin capping protein	actin binding [pmid 7665558]
957	0	0.000367	0.001479	0.000417	0	3	0.000566	0.000637	0	0.00053	0	0	0	1	0.000132	0.000265	0	0	0	0	0	0.000123	0	0	Transcriptional Coactivator	nucleus; transcription factor	DNA binding; single-stranded
958	0.001533	0.000551	0	4.18E-05	0	3	0.000532	0.000713	0	0.000583	0	0	0	1	0.000146	0.000292	0	0	0	0	0	0	0	0			
959	0	0.000122	0.001967	0.00037	0	3	0.000615	0.000915	0	0.000117	0	0	0	1	2.94E-05	5.87E-05	0	0	0	0	0	0	0	0	EF-hand, calcium binding		calcium ion binding
960	0	0.000897	0	0.000849	0	2	0.000437	0.000504	0	0.000647	0	0.000157	0	2	0.000201	0.000306	0	0	0	0	0	7.53E-05	0	0	Ribosomal protein S8e;	cytosolic small ribosomal	structural constituent of
961	0.001567	0.000563	0	0.000341	0	3	0.000618	0.000674	0	0	0	7.88E-05	0	1	1.97E-05	3.94E-05	0	0	0	0	0	0	0	0		membrane	GTP binding; nucleotide
962	0	0.000132	0	0.000699	0	2	0.000208	0.000333	0	0.000127	0	0.001537	0	2	0.000416	0.00075	0	0	0	0	0	0	0	0	TCP-1 (CTT or eukaryotic	cytoplasm [pmid 8034610]	ATP binding; nucleotide
963	0	0.000203	0.000546	0	0	2	0.000187	0.000258	0.00129	0.000196	0	0	0	2	0.000371	0.000619	0	0	0	0	0	0	0	0	Immunoglobulin domain cell	integral to plasma membrane	GPI anchor binding
964	0	0.000107	0.001732	0.000163	0	3	0.0005	0.000824	0	0.000207	0	0	0	1	5.17E-05	0.000103	0	0	0	0	0	0	0	0	EF-hand, calcium binding	cytoplasm [pmid 1530588];	calcium ion binding [pmid
965	0.000605	0	0	0.000725	0	2	0.000333	0.000387	0	0	0	0.000304	0.000573	2	0.000219	0.000276	0	0	0	0	0	0	0	0	EF-hand, calcium binding		calcium ion binding; calpain
966	0.00076	0.000819	0	0.000248	0	3	0.000457	0.000398	0	0.000368	0	0	0	1	9.19E-05	0.000184	0	0	0	0	0	0	0	0	Band_7_flotillin: a subgroup	caveola [pmid 9153235];	protein binding [pmid
967	0	0	0	0.000584	0	1	0.000146	0.000292	0	0.000371	0	0.00027	0.000952	3	0.000398	0.000401	0	0	0	0	0	0	0	0	RPA3: A subfamily of OB	DNA replication factor A	nucleic acid binding; single-
968	0	0	0	0.000623	0	1	0.000156	0.000311	0	0.000198	0	0.000647	0.000676	3	0.00038	0.000335	0	0	0	0	0	0	0	0	Members of the Nudix	centrosome [pmid 11256614];	protein binding [pmid
969	0	0.001458	0	0.000221	0	2	0.00042	0.0007	0	0.00014	0	0.000306	0	2	0.000112	0.000146	0	0	0	0	0	0	0	0			
970	0.000832	0.000598	0	9.06E-05	0	3	0.00038	0.0004	0	0.000575	0	0	0	1	0.000144	0.000288	0	0	0	0	0	0	0	0	Rab5-related subfamily.	membrane	GTP binding; GTPase
971	0	0.000113	0	0.001286	0	2	0.00035	0.000627	0	0.000218	0	0.000475	0	2	0.000173	0.000226	0	0	0	0	0	0	0	0	NmrA-like family. NmrA is a		biliverdin reductase activity
972	0	0.000276	0	0.00067	0	2	0.000237	0.000317	0	0.000851	0	0	0.000273	2	0.000281	0.000401	0	0	0	4.31E-05	0	0	0	0	Diacylglycerol kinase		diacylglycerol kinase activity
973	0	0.000314	0	0.000556	0	2	0.000218	0.00027	0	0.000353	0	0	0.000776	2	0.000282	0.000369	0	0	0	0	0	0	0	0	PCI domain. This domain		protein binding [pmid
974	0	0.000409	0	0.000174	0	2	0.000146	0.000194	0	0.000394	0	0	0.00101	2	0.000351	0.000477	0	0	0	0	0	0	0	0	60s Acidic ribosomal	cytosolic large ribosomal	protein binding [pmid
975	0	0.0007	0	0.000412	0	2	0.000278	0.000342	0	0.000673	0	0	0.000128	2	0.0002	0.000321	0	0	0	0	0	0	0	0	AIG1 (avrRpt2-induced		GTP binding; nucleotide
976	0	0.000296	0	0.000403	0	2	0.000175	0.000207	0	0	0	0.001077	9.74E-05	2	0.000294	0.000524	0	0	0	0	0	0	0	0			
977	0	0.000292	0	0.000736	0	2	0.000257	0.000348	0	0.000187	0	0	0.00064	2	0.000207	0.000302	0	0	0	0	0	0	0	0	RNA recognition motif;	Cajal body [pmid 1388271];	metal ion binding; nucleotide
978	0	0.000707	0	0.000321	0	2	0.000257	0.000336	0	0	0	0.000593	0.000233	2	0.000207	0.00028	0	0	0	0	0	0	0	0	ISG15 is a ubiquitin-like	cytoplasm; extracellular space	protein binding
979	0.00102	0.00022	0	0.000555	0	3	0.000449	0.000444	0	0	0	5.13E-05	0	1	1.28E-05	2.57E-05	0	0	0	0	0	0	0	0	Phosphoribosylpyrophosph		kinase activity; lipoate-
980	0	0.000151	0	0	0	1	3.77E-05	7.55E-05	0	0.000218	0	5.28E-05	0.001367	3	0.000409	0.000645	0	0	0	0	0	0	0	0	Protein phosphatase 2A	cytosol [pmid 11007961];	hydrolase activity; iron ion

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_S PROB
981	4	0.000222	0	0	INF		ENSG00000116489:E	CAPZA1			gi|5453597|ref|NP_0	F-actin capping protein alpha	286	32923	5.7	0	o	Q	0	0
982	4	0.00022	0	0	INF		ENSG00000197756:N	RPL37A			gi|4506643|ref|NP_0	ribosomal protein L37a [Hom	92	10275	10.4	0	i	Q	20	0
983	4	0.000219	0	0	INF		ENSG00000111669:E	TPI1			gi|4507645|ref|NP_0	triosephosphate isomerase 1	249	26669	6.9	0	o	Q	37	0.013
984	4	0.000217	0	0	INF		ENSG00000110107:E	PRPF19			gi|7657381|ref|NP_0	PRP19/PSO4 pre-mRNA pro	504	55181	6.6	0	o	Q	20	0
985	4	0.000213	0	0	INF		ENSG00000117450:E	PRDX1			gi|32455266|ref|NP_	peroxiredoxin 1 [Homo sapie	199	22110	8.1	0	o	Q	20	0
986	4	0.000213	0	0	INF		ENSG00000145425:N	RPS3A			gi|4506723|ref|NP_0	ribosomal protein S3a [Homo	264	29945	9.7	0	o	Q	0	0
987	4	0.000201	0	0	INF		ENSG00000101367:E	MAPRE1			gi|6912494|ref|NP_0	microtubule-associated prote	268	29999	5.1	0	o	Q	17	0
988	4	0.000197	0	0	INF		ENSG00000117748:E	RPA2			gi|4506585|ref|NP_0	replication protein A2, 32kDa	270	29247	6.1	0	o	Q	22	0.001
989	4	0.000192	0	0	INF		ENSG00000140395:E	WDR61			gi|13376840|ref|NP_	WD repeat domain 61 [Homo	305	33581	5.5	0	o	Q	0	0
990	4	0.000191	0	0	INF		ENSG00000069345:E	DNAJA2			gi|5031741|ref|NP_0	DnaJ subfamily A member 2	412	45746	6.5	0	o	Q	21	0
991	4	0.000191	0	0	INF		ENSG00000167460:E	TPM4			gi|4507651|ref|NP_0	tropomyosin 4 [Homo sapien	248	28522	4.7	0	o	Q	17	0
992	4	0.00019	0	0	INF		ENSG00000103342:E	GSPT1			gi|4504167|ref|NP_0	G1 to S phase transition 1 [H	499	55756	5.6	0	o	Q	0	0
993	4	0.000183	0	0	INF		ENSG00000100519:E	PSMC6			gi|24430160|ref|NP_	proteasome 26S ATPase sub	389	44173	7.5	0	o	Q	0	0
994	4	0.000183	0	0	INF		ENSG00000108312:E	UBTF			gi|115529451|ref|NP	upstream binding transcriptio	727	84937	5.6	0	o	Q	0	0
995	4	0.00018	0	0	INF		ENSG00000124795:E	DEK			gi|4503249|ref|NP_0	DEK oncogene [Homo sapie	375	42674	8.6	0	o	Q	16	0
996	4	0.000179	0	0	INF		ENSG00000157020:E	SEC13			gi|34335134|ref|NP_	SEC13 protein [Homo sapien	322	35541	5.5	0	o	Q	0	0
997	4	0.000177	0	0	INF		ENSG00000106605:E	BLVRA			gi|33589854|ref|NP_	biliverdin reductase A [Homo	296	33428	6.4	0	o	Q	22	0.067
998	4	0.000177	0	0	INF		ENSG00000149925:E	ALDOA			gi|34577112|ref|NP_	aldolase A [Homo sapiens]	364	39420	8.1	0	o	Q	33	0
999	4	0.000176	0	0	INF		ENSG00000111605:E	CPSF6			gi|5901928|ref|NP_0	cleavage and polyadenylatio	551	59209	7.4	0	o	Q	0	0
1000	4	0.000175	0	0	INF		ENSG00000068831:E	RASGRP2			gi|149158729|ref|NP	RAS guanyl releasing protein	609	69249	7.8	0	o	Q	24	0
1001	4	0.000174	0	0	INF		ENSG00000166986:E	MARS			gi|14043022|ref|NP_	methionyl-tRNA synthetase [	900	101116	6.2	0	o	S	25	0.821
1002	4	0.000174	0	0	INF		ENSG00000125354:E	SEPT6			gi|21361478|ref|NP_	septin 6 isoform B [Homo sap	434	49717	6.7	0	o	Q	17	0
1003	4	0.000167	0	0	INF		ENSG00000125414:E	MYH2			gi|153792663|ref|NP	myosin, heavy chain 2, skele	1941	223042	5.8	0	o	Q	14	0
1004	4	0.000166	0	0	INF		ENSG00000146729:E	GBAS			gi|4503937|ref|NP_0	nipsnap homolog 2 [Homo sa	286	33743	9.4	0	o	S	24	0.96
1005	4	0.000166	0	0	INF		ENSG00000184730:N	APOB48R			gi|119220598|ref|NP	apolipoprotein B48 receptor [	1088	114874	4.4	0	o	Q	34	0.07
1006	4	0.000163	0	0	INF		ENSG00000100811:E	YY1			gi|4507955|ref|NP_0	YY1 transcription factor [Hom	414	44713	6.3	0	o	Q	14	0
1007	4	0.00016	0	0	INF		ENSG00000168496:E	FEN1			gi|4758356|ref|NP_0	flap structure-specific endonu	380	42593	8.6	0	o	Q	17	0.003
1008	4	0.000156	0	0	INF		ENSG00000214014:E	OVCA2			gi|18201880|ref|NP_	candidate tumor suppressor	227	24418	6.9	0	o	Q	19	0.134
1009	4	0.000156	0	0	INF		ENSG00000105419:E	MEIS3			gi|57863281|ref|NP_	Meis1, myeloid ecotropic vira	421	46175	5.3	0	o	Q	31	0.002
1010	4	0.000152	0	0	INF		ENSG00000156110:E	ADK			gi|32484973|ref|NP_	adenosine kinase isoform a [	345	38703	6.7	0	o	Q	22	0.001
1011	4	0.00015	0	0	INF		ENSG00000162645:E	GBP2			gi|38327558|ref|NP_	guanylate binding protein 2, i	591	67209	5.7	0	o	Q	20	0.001
1012	4	0.00015	1	2.63E-05	5.708902		ENSG00000203879:E	GDI1			gi|4503971|ref|NP_0	GDP dissociation inhibitor 1 [	447	50583	5.1	0	o	Q	21	0.002
1013	4	0.000147	0	0	INF		ENSG00000072062:E	PRKACA			gi|4506055|ref|NP_0	cAMP-dependent protein kina	351	40590	8.8	0	o	Q	0	0
1014	4	0.000144	0	0	INF		ENSG00000175463:E	TBC1D10C			gi|38348348|ref|NP_	TBC1 domain family, membe	446	49712	8.8	0	o	Q	0	0
1015	4	0.000144	0	0	INF		ENSG00000064666:E	CNN2			gi|4758018|ref|NP_0	calponin 2 isoform a [Homo s	309	33697	7.3	0	o	Q	25	0
1016	4	0.000139	0	0	INF		ENSG00000125691:E	RPL23			gi|4506605|ref|NP_0	ribosomal protein L23 [Homo	140	14865	10.5	0	o	S	29	0.645
1017	4	0.000139	0	0	INF		ENSG00000117118:E	SDHB			gi|115387094|ref|NP	succinate dehydrogenase co	280	31630	8.8	0	o	S	29	0.987
1018	4	0.000139	1	2.52E-06	55.1025		ENSG00000135316:E	SYNCRIP			gi|23397427|ref|NP_	synaptotagmin binding, cytop	623	69633	8.6	0	o	Q	0	0
1019	4	0.000135	0	0	INF		ENSG00000100941:E	PNN			gi|33356174|ref|NP_	pinin, desmosome associated	717	81614	7.2	0	o	Q	0	0
1020	4	0.000134	2	8.57E-06	15.66123		ENSG00000138107:E	ACTR1A			gi|5031569|ref|NP_0	ARP1 actin-related protein 1	376	42614	6.6	0	o	Q	20	0
1021	4	0.000134	0	0	INF		ENSG00000130810:N	PPAN-P2RY11			gi|47174861|ref|NP_	peter pan homolog [Homo sa	473	53194	10.1	0	o	Q	41	0.001
1022	4	0.000132	0	0	INF		ENSG00000163468:E	CCT3			gi|58761486|ref|NP_	chaperonin containing TCP1	544	60463	6.5	0	o	Q	20	0.001
1023	4	0.000131	0	0	INF		ENSG00000034152:E	MAP2K3			gi|21618349|ref|NP_	mitogen-activated protein kin	347	39318	7.4	0	o	Q	18	0
1024	4	0.00013	0	0	INF		ENSG00000165025:E	SYK			gi|21361553|ref|NP_	spleen tyrosine kinase [Homo	635	72066	8.2	0	o	Q	26	0
1025	4	0.000127	3	1.39E-05	9.145446		ENSG00000163346:E	PBXIP1			gi|19923830|ref|NP_	pre-B-cell leukemia homeobo	731	80643	5.3	0	o	Q	24	0.001
1026	4	0.000125	0	0	INF		ENSG00000071626:E	DAZAP1			gi|25470886|ref|NP_	DAZ associated protein 1 iso	407	43383	8.6	0	o	Q	23	0
1027	4	0.000125	0	0	INF		ENSG00000134001:E	EIF2S1			gi|4758256|ref|NP_0	eukaryotic translation initiatio	315	36112	5.1	0	o	Q	0	0
1028	4	0.000124	0	0	INF		ENSG00000101444:E	AHCY			gi|9951915|ref|NP_0	S-adenosylhomocysteine hyd	432	47716	6.3	0	o	Q	22	0.001
1029	4	0.000124	0	0	INF		ENSG00000148908:E	RGS10			gi|52694755|ref|NP_	regulator of G-protein signali	181	21210	7.5	0	o	Q	0	0
1030	4	0.000122	0	0	INF		ENSG00000079332:E	SAR1A			gi|9910542|ref|NP_0	SAR1a gene homolog 1 [Hom	198	22367	6.7	0	o	Q	27	0.002
1031	4	0.000121	0	0	INF		ENSG00000146223:E	RPL7L1			gi|50053872|ref|NP_	ribosomal protein L7-like 1 [H	246	28661	10.5	0	o	Q	0	0
1032	4	0.00012	2	9.24E-06	12.9689		ENSG00000173959:E	RBM14			gi|5454064|ref|NP_0	RNA binding motif protein 14	669	69492	9.7	0	o	Q	31	0.001
1033	4	0.000118	0	0	INF		ENSG00000100596:E	SPTLC2			gi|4758668|ref|NP_0	serine palmitoyltransferase, l	562	62924	7.8	0	o	Q	44	0.002
1034	4	0.000116	0	0	INF		ENSG00000145907:E	G3BP1			gi|38327552|ref|NP_	Ras-GTPase-activating prote	466	52164	5.5	0	o	Q	19	0
1035	4	0.000116	0	0	INF		ENSG00000196415:E	PRTN3			gi|71361688|ref|NP_	proteinase 3 (serine proteina	256	27807	8.3	0	o	S	26	1
1036	4	0.000115	0	0	INF		NA:ENSMUSG00000	RPL26			gi|4506621|ref|NP_0	ribosomal protein L26 [Homo	145	17258	10.6	0	o	Q	0	0
1037	4	0.000115	0	0	INF		ENSG00000162704:E	ARPC5			gi|5031593|ref|NP_0	actin related protein 2/3 com	151	16320	5.7	0	o	Q	0	0
1038	4	0.000114	0	0	INF		ENSG00000180817:E	PPA1			gi|11056044|ref|NP_	pyrophosphatase 1 [Homo sa	289	32660	5.9	0	o	Q	0	0
1039	4	0.000114	0	0	INF		ENSG00000185627:E	PSMD13			gi|157502193|ref|NP	proteasome 26S non-ATPase	376	42946	5.8	0	o	Q	20	0
1040	4	0.000111	0	0	INF		ENSG00000159339:E	PADI4			gi|6912576|ref|NP_0	peptidyl arginine deiminase,	663	74095	6.6	0	o	Q	33	0.483
1041	4	0.00011	0	0	INF		ENSG00000166974:E	MAPRE2			gi|10346135|ref|NP_	microtubule-associated prote	327	37031	5.6	0	o	Q	0	0
1042	4	0.00011	1	1.21E-05	9.090467		ENSG00000068120:E	COASY			gi|110227611|ref|NP	coenzyme A synthase isoforn	564	62329	7	0	o	S	24	0.997
1043	4	0.000108	0	0	INF		ENSG00000108559:E	NUP88			gi|24497453|ref|NP_	nucleoporin 88kDa [Homo sa	741	83542	5.7	0	o	Q	31	0
1044	4	0.000108	0	0	INF		ENSG00000110063:E	DCPS			gi|7661734|ref|NP_0	mRNA decapping enzyme [H	337	38609	6.4	0	o	Q	0	0
1045	4	0.000105	1	1.27E-05	8.277605		ENSG00000185129:E	PURA			gi|5032007|ref|NP_0	purine-rich element binding p	322	34911	6.4	0	o	Q	23	0.009
1046	4	0.000105	1	4.5E-06	23.23836		ENSG00000095261:E	PSMD5			gi|4826952|ref|NP_0	proteasome 26S non-ATPase	504	56196	5.5	0	o	Q	16	0.053
1047	4	0.000104	0	0	INF		ENSG00000132382:E	MYBBP1A			gi|157694492|ref|NP	MYB binding protein 1a isofo	1328	148854	9.3	0	o	Q	21	0
1048	4	0.000101	1	2.18E-06	46.29048		ENSG00000205339:E	IPO7			gi|5453998|ref|NP_0	importin 7 [Homo sapiens]	1038	119516	4.8	0	o	Q	22	0
1049	4	0.000101	0	0	INF		ENSG00000125970:E	RALY			gi|21396480|ref|NP_	RNA binding protein (autoan	290	30364	9.6	0	o	Q	0	0
1050	4	0.0001	0	0	INF		ENSG00000159692:E	CTBP1			gi|4557497|ref|NP_0	C-terminal binding protein 1 i	440	47535	6.8	0	o	Q	27	0
1051	4	9.92E-05	0	0	INF		ENSG00000079462:E	PAFAH1B3			gi|4505587|ref|NP_0	platelet-activating factor acet	231	25734	6.8	0	o	Q	0	0
1052	4	9.86E-05	0	0	INF		ENSG00000197915:N	HRNR			gi|57864582|ref|NP_	hornerin [Homo sapiens]	2850	282389	10	0	o	Q	20	0.019
1053	4	9.77E-05	0	0	INF		ENSG00000134602:E	MST4			gi|15011880|ref|NP_	serine/threonine protein kina	416	46529	5.3	0	o	Q	19	0.004
1054	4	9.77E-05	0	0	INF		ENSG00000171763:E	SPATA5L1			gi|13129040|ref|NP_	spermatogenesis associated	753	80682	8	0	o	Q	47	0.001
1055	4	9.62E-05	1	3.47E-06	27.73937		ENSG00000168883:E	USP39			gi|56550051|ref|NP_	ubiquitin specific protease 39	565	65381	8.9	0	o	Q	0	0
1056	4	9.33E-05	1	5.19E-06	17.978		ENSG00000132612:E	VPS4A			gi|7019569|ref|NP_0	vacuolar protein sorting facto	437	48898	7.8	0	o	Q	17	0
1057	4	9.31E-05	0	0	INF		ENSG00000170379:E	FAM139A			gi|27734979|ref|NP_	hypothetical protein LOC285	845	91978	7.3	0	o	S	19	0.853
1058	4	9.24E-05	0	0	INF		ENSG00000160194:E	NDUFV3			gi|48255924|ref|NP_	NADH-ubiquinone oxidoredu	473	50984	9.2	0	o	Q	39	0.071
1059	4	9.15E-05	1	1.02E-05	8.935403		ENSG00000100129:E	EIF3EIP			gi|7705433|ref|NP_0	eukaryotic translation initiatio	564	66727	6.3	0	o	Q	0	0
1060	4	9.14E-05	0	0	INF		ENSG00000096060:E	FKBP5			gi|4758384|ref|NP_0	FK506 binding protein 5 [Hor	457	51212	5.9	0	o	Q	0	0
1061	4	8.85E-05	0	0	INF		ENSG00000159753:E	RLTPR			gi|66392157|ref|NP_	RGD motif, leucine rich repea	1435	154688	6.8	0	o	Q	38	0
1062	4	8.73E-05	0	0	INF		ENSG00000130592:E	LSP1			gi|10880979|ref|NP_	lymphocyte-specific protein 1	339	37192	4.7	0	o	Q	0	0
1063	4	8.59E-05	0	0	INF		ENSG00000116791:E	CRYZ			gi|13236495|ref|NP_	crystallin, zeta [Homo sapien	329	35207	8.4	0	o	Q	20	0
1064	4	8.46E-05	0	0	INF		ENSG00000119414:E	PPP6C			gi|4506029|ref|NP_0	protein phosphatase 6, cataly	305	35144	5.7	0	o	Q	0	0
1065	4	8.35E-05	0	0	INF		ENSG00000135842:E	FAM129A			gi|16757970|ref|NP_	niban protein isoform 2 [Hom	928	103135	4.8	0	o	Q	15	0
1066	4	8.33E-05	0	0	INF		ENSG00000176393:E	RNPEP			gi|40316915|ref|NP_	arginyl aminopeptidase (amin	650	72596	5.8	0	o	Q	29	0.013
1067	4	8.32E-05	0	0	INF		ENSG00000085415:E	SEH1L			gi|61743969|ref|NP_	sec13-like protein isoform 2 [	360	39649	8.1	0	o	Q	0	0
1068	4	8.17E-05	1	4.52E-06	18.0756		ENSG00000161057:E	PSMC2			gi|4506209|ref|NP_0	proteasome 26S ATPase sub	433	48634	5.9	0	o	Q	0	0
1069	4	8.06E-05	0	0	INF		ENSG00000166888:E	STAT6			gi|23397678|ref|NP_	signal transducer and activat	847	94135	6.2	0	o	Q	56	0
1070	4	7.83E-05	0	0	INF		ENSG00000130775:E	C1orf38			gi|157738677|ref|NP	basement membrane-induce	643	72049	6.1	0	o	Q	28	0
1071	4	7.77E-05	0	0	INF		ENSG00000108270:E	AATF			gi|7657013|ref|NP_0	apoptosis antagonizing trans	560	63133	4.9	0	o	Q	23	0.205
1072	4	7.62E-05	0	0	INF		ENSG00000116478:N	HDAC1			gi|13128860|ref|NP_	histone deacetylase 1 [Homo	482	55103	5.5	0	o	Q	0	0
1073	4	7.5E-05	0	0	INF		ENSG00000146476:E	C6orf211			gi|13375746|ref|NP_	hypothetical protein LOC796	441	51172	5.8	0	o	Q	18	0.021
1074	4	7.37E-05	1	9.05E-06	8.149434		ENSG00000143368:E	SF3B4			gi|5032069|ref|NP_0	splicing factor 3b, subunit 4 [	424	44386	8.6	0	o	Q	26	0
1075	4	7.35E-05	0	0	INF		ENSG00000108946:E	PRKAR1A			gi|47132583|ref|NP_	cAMP-dependent protein kina	381	42982	5.3	0	o	Q	15	0
1076	4	7.16E-05	0	0	INF		ENSG00000089280:E	FUS			gi|4826734|ref|NP_0	fusion (involved in t(12;16) in	526	53426	9.4	0	o	Q	25	0
1077	4	7.13E-05	0	0	INF		ENSG00000105364:E	MRPL4			gi|22547138|ref|NP_	mitochondrial ribosomal prote	311	34919	9.7	0	o	Q	32	0.215
1078	4	7.07E-05	1	1.12E-05	6.332259		ENSG00000087191:E	PSMC5			gi|24497435|ref|NP_	proteasome 26S ATPase sub	406	45626	7.5	0	o	Q	0	0
1079	4	7.06E-05	1	2.86E-06	24.64327		ENSG00000100813:E	ACIN1			gi|7662238|ref|NP_0	apoptotic chromatin condens	1341	151887	6.4	0	o	Q	23	0.005
1080	4	7.03E-05	0	0	INF		ENSG00000010671:E	BTK			gi|4557377|ref|NP_0	Bruton agammaglobulinemia	659	76281	7.8	0	o	Q	17	0.022
1081	4	6.98E-05	0	0	INF		ENSG00000077809:E	GTF2I			gi|14670350|ref|NP_	general transcription factor II	998	112416	6.4	0	o	Q	20	0.002
1082	4	6.93E-05	0	0	INF		ENSG00000129351:E	ILF3			gi|24234750|ref|NP_	interleukin enhancer binding	894	95339	8.8	0	o	Q	0	0
1083	4	6.93E-05	0	0	INF		ENSG00000064419:E	TNPO3			gi|6912734|ref|NP_0	transportin 3 [Homo sapiens]	923	104203	5.6	0	o	Q	18	0.012
1084	4	6.81E-05	0	0	INF		ENSG00000100353:E	EIF3D			gi|4503523|ref|NP_0	eukaryotic translation initiatio	548	63973	6	0	o	Q	20	0
1085	4	6.8E-05	0	0	INF		ENSG00000185811:E	IKZF1			gi|5174501|ref|NP_0	zinc finger protein, subfamily	519	57528	6.6	0	o	Q	0	0
1086	4	6.74E-05	0	0	INF		ENSG00000048740:E	CUGBP2			gi|134152680|ref|NP	CUG triplet repeat, RNA bind	521	55732	8.6	0	o	Q	18	0
1087	4	6.74E-05	0	0	INF		ENSG00000104812:E	GYS1			gi|31542868|ref|NP_	glycogen synthase 1 (muscle	737	83786	6.2	0	o	Q	16	0
1088	4	6.72E-05	0	0	INF		ENSG00000134996:E	OSTF1			gi|38257157|ref|NP_	osteoclast stimulating factor	214	23799	5.4	0	o	Q	29	0
1089	4	6.65E-05	0	0	INF		ENSG00000033178:E	UBA6			gi|150417996|ref|NP	ubiquitin-activating enzyme E	1052	117970	6.1	0	o	Q	18	0
1090	4	6.64E-05	0	0	INF		ENSG00000182446:E	NPLOC4			gi|157426879|ref|NP	nuclear protein localization 4	608	68120	6.4	0	o	Q	21	0
1091	4	6.63E-05	0	0	INF		ENSG00000100401:E	RANGAP1			gi|4506411|ref|NP_0	Ran GTPase activating prote	587	63542	4.7	0	o	Q	22	0
1092	4	6.58E-05	0	0	INF		ENSG00000153310:E	FAM49B			gi|42734438|ref|NP_	hypothetical protein LOC515	324	36748	6.1	0	o	Q	16	0.001
1093	4	6.57E-05	0	0	INF		ENSG00000143624:E	INTS3			gi|39995084|ref|NP_	integrator complex subunit 3	1042	118013	5.8	0	o	S	21	0.858
1094	4	6.55E-05	0	0	INF		ENSG00000012779:E	ALOX5			gi|4502057|ref|NP_0	arachidonate 5-lipoxygenase	674	77983	5.8	0	o	Q	17	0.031
1095	4	6.45E-05	0	0	INF		ENSG00000180843:N	KIAA1618			gi|66529203|ref|NP_	hypothetical protein LOC577	1063	118436	5.7	0	o	Q	0	0
1096	4	6.45E-05	0	0	INF		ENSG00000108604:E	SMARCD2			gi|148536862|ref|NP	SWI/SNF-related matrix-asso	510	57173	9.6	0	o	S	27	0.87
1097	4	6.44E-05	0	0	INF		ENSG00000104814:E	MAP4K1			gi|110611908|ref|NP	mitogen-activated protein kin	821	90425	8.2	0	o	Q	0	0
1098	4	6.42E-05	0	0	INF		ENSG00000087087:E	ARS2			gi|33383233|ref|NP_	arsenate resistance protein 2	796	90251	5.7	0	o	Q	0	0
1099	4	6.4E-05	0	0	INF		ENSG00000108654:E	DDX5			gi|4758138|ref|NP_0	DEAD (Asp-Glu-Ala-Asp) box	614	69148	8.9	0	o	Q	27	0
1100	4	6.35E-05	0	0	INF		ENSG00000111445:E	RFC5			gi|6677723|ref|NP_0	replication factor C 5 isoform	340	38497	7.2	0	o	Q	0	0
1101	4	6.29E-05	0	0	INF		ENSG00000176715:E	LOC197322			gi|28372537|ref|NP_	acyl-CoA synthetase family n	576	64131	8.1	0	o	S	25	0.873
1102	4	6.08E-05	0	0	INF		ENSG00000117676:E	RPS6KA1			gi|20149547|ref|NP_	ribosomal protein S6 kinase,	735	82723	7.8	0	o	Q	24	0.001
1103	4	6.04E-05	0	0	INF		ENSG00000138772:E	ANXA3			gi|4826643|ref|NP_0	annexin A3 [Homo sapiens]	323	36375	5.9	0	o	Q	17	0
1104	4	6.01E-05	0	0	INF		ENSG00000101557:E	USP14			gi|4827050|ref|NP_0	ubiquitin specific protease 14	494	56069	5.3	0	o	Q	45	0
1105	4	6.01E-05	0	0	INF		ENSG00000197872:E	FAM49A			gi|13540580|ref|NP_	family with sequence similari	323	37313	6	0	o	Q	0	0
1106	4	5.98E-05	0	0	INF		ENSG00000134371:E	CDC73			gi|40018640|ref|NP_	parafibromin [Homo sapiens]	531	60577	9.6	0	o	Q	0	0
1107	4	5.97E-05	0	0	INF		ENSG00000125458:E	NT5C			gi|7657033|ref|NP_0	5',3'-nucleotidase, cytosolic [	201	23383	6.6	0	o	Q	17	0.012
1108	4	5.77E-05	0	0	INF		ENSG00000136518:E	ACTL6A			gi|4757718|ref|NP_0	actin-like 6A isoform 1 [Homo	429	47461	5.6	0	o	Q	29	0.001
1109	4	5.75E-05	0	0	INF		ENSG00000164163:E	ABCE1			gi|108773784|ref|NP	ATP-binding cassette, sub-fa	599	67314	8.3	0	o	Q	0	0
1110	4	5.71E-05	0	0	INF		ENSG00000090861:E	AARS			gi|109148542|ref|NP	alanyl-tRNA synthetase [Hon	968	106810	5.5	0	o	Q	0	0
1111	4	5.65E-05	0	0	INF		ENSG00000123064:E	DDX54			gi|51094101|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	881	98595	10	0	o	Q	19	0
1112	4	5.54E-05	0	0	INF		ENSG00000102882:E	MAPK3			gi|158138507|ref|NP	mitogen-activated protein kin	335	38275	6.2	0	o	Q	20	0.002
1113	4	5.39E-05	0	0	INF		ENSG00000125817:E	CENPB			gi|21735415|ref|NP_	centromere protein B [Homo	599	65171	4.6	0	o	Q	0	0
1114	4	5.39E-05	0	0	INF		ENSG00000136270:E	TBRG4			gi|40217812|ref|NP_	cell cycle progression 2 prote	631	70738	7.4	0	o	Q	45	0.088
1115	4	5.37E-05	0	0	INF		ENSG00000037474:E	NSUN2			gi|39995082|ref|NP_	NOL1/NOP2/Sun domain fan	767	86471	6.8	0	o	Q	0	0
1116	4	5.35E-05	0	0	INF		ENSG00000163655:E	GMPS			gi|4504035|ref|NP_0	guanine monophosphate syn	693	76715	6.9	0	o	Q	0	0
1117	4	5.34E-05	0	0	INF		ENSG00000214133:E	COPG2			gi|109134349|ref|NP	coatomer protein complex, su	871	97622	5.8	0	o	Q	0	0
1118	4	5.31E-05	0	0	INF		ENSG00000117226:N	GBP3			gi|112382372|ref|NP	guanylate binding protein 3 [	595	68114	6.5	0	o	Q	20	0.003
1119	4	5.26E-05	0	0	INF		ENSG00000065613:E	SLK			gi|41281453|ref|NP_	serine/threonine kinase 2 [Ho	1235	142695	5.1	0	o	Q	0	0
1120	4	5.19E-05	0	0	INF		ENSG00000108848:E	CROP			gi|52426743|ref|NP_	cisplatin resistance-associate	432	51466	9.8	0	o	Q	19	0
1121	4	5.19E-05	0	0	INF		ENSG00000149016:E	TUT1			gi|12383074|ref|NP_	terminal uridylyl transferase 1	874	93789	6.2	0	o	Q	27	0.003
1122	4	5.12E-05	0	0	INF		ENSG00000049541:E	RFC2			gi|28882049|ref|NP_	replication factor C 2 isoform	320	35244	5.5	0	o	Q	16	0.022
1123	4	5.1E-05	0	0	INF		ENSG00000135596:E	MICAL1			gi|20127616|ref|NP_	microtubule associated mono	1067	117932	6.5	0	o	Q	29	0.011
1124	4	5.09E-05	0	0	INF		ENSG00000130227:E	XPO7			gi|154448892|ref|NP	exportin 7 isoform b [Homo s	1087	123907	6.3	0	o	Q	18	0
1125	4	5.07E-05	0	0	INF		ENSG00000083642:E	PDS5B			gi|7657269|ref|NP_0	PDS5, regulator of cohesion	1447	164666	8.5	0	o	Q	0	0
1126	4	4.94E-05	0	0	INF		ENSG00000133316:E	WDR74			gi|8922422|ref|NP_0	WD repeat domain 74 [Homo	385	42286	8.2	0	o	Q	26	0.017
1127	4	4.93E-05	0	0	INF		ENSG00000085872:E	CHERP			gi|119226260|ref|NP	calcium homeostasis endopla	916	103702	9	0	o	Q	0	0

	RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs							
rk	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
981	0.000567	0.000326	0	0.000618	0	3	0.000378	0.000282	0	0	0	0	0.000268	1	6.71E-05	0.000134
982	0	0.000761	0	0.000576	0	2	0.000334	0.000393	0	0.000244	0	0.000177	0	2	0.000105	0.000125
983	0	0.000281	0	0.000284	0	2	0.000141	0.000163	0	0.00027	0	0.000918	0	2	0.000297	0.000433
984	0	0.000231	0	0.000631	0	2	0.000216	0.000298	0	0	0	0.000648	0.000228	2	0.000219	0.000305
985	0	0.000117	0	0.000533	0	2	0.000162	0.000253	0	0.000564	0	0.000492	0	2	0.000264	0.000306
986	0	0	0	0.000268	0	1	6.69E-05	0.000134	0	0.00102	0	0.000124	0.000291	3	0.000359	0.000457
987	0	0.000435	0	0.000461	0	2	0.000224	0.000259	0	0.000586	0	0.000122	0	2	0.000177	0.000279
988	0	0	0	0.000262	0	1	6.54E-05	0.000131	0	0.000166	0	0.000725	0.000427	3	0.00033	0.000317
989	0	0.000153	0	0.000463	0	2	0.000154	0.000218	0	0.000221	0	0.000696	0	2	0.000229	0.000328
990	0	5.66E-05	0	0.000686	0	2	0.000186	0.000335	0	0.000272	0	0.000515	0	2	0.000197	0.000248
991	0.000981	9.4E-05	0	0.000142	0	3	0.000304	0.000455	0	0	0	0	0.00031	1	7.74E-05	0.000155
992	0	0	0	0.000159	0	1	3.98E-05	7.96E-05	0	8.99E-05	0	0.000196	0.001077	3	0.000341	0.000497
993	0	6E-05	0	0.000136	0	2	4.9E-05	6.46E-05	0.001141	0	0	0.000126	0	2	0.000317	0.000553
994	0	0.000738	0	9.72E-05	0	2	0.000209	0.000356	0	0.000401	0	0.000224	0	2	0.000156	0.000194
995	0	0.000311	0	0.000236	0	2	0.000137	0.000161	0	0.000239	0	0.000653	0	2	0.000223	0.000308
996	0	0.000145	0	0.000823	0	2	0.000242	0.000393	0	0.000209	0	0.000253	0	2	0.000116	0.000135
997	0	0.000473	0	0	0	1	0.000118	0.000236	0	7.58E-05	0	0.000221	0.000648	3	0.000236	0.00029
998	0.000446	0	0	0.000437	0	2	0.000221	0.000255	0	0.000308	0	0.000224	0	2	0.000133	0.000157
999	0	4.23E-05	0	0.000609	0	2	0.000163	0.000298	0	0.000407	0	0	0.000348	2	0.000189	0.000219
1000	0	0	0.000617	0.000377	0	2	0.000249	0.000303	0	0	0	2.68E-05	0.000378	2	0.000101	0.000185
1001	0	0.000259	0	0	0	1	6.48E-05	0.00013	0	0.000125	0	7.25E-05	0.000938	3	0.000284	0.000439
1002	0	0	0	0.000366	0	1	9.16E-05	0.000183	0	5.17E-05	0	0.00018	0.000796	3	0.000257	0.000367
1003	0	9.07E-05	0.001162	7.63E-05	0	3	0.000332	0.000554	0	5.78E-06	0	0	0	1	1.44E-06	2.89E-06
1004	0	0.000163	0	0	0	1	4.08E-05	8.16E-05	0	7.84E-05	0	0.000685	0.000403	3	0.000291	0.000315
1005	0	6.43E-05	0	1.62E-05	0	2	2.01E-05	3.04E-05	0.001224	2.06E-05	0	0	0	2	0.000311	0.000609
1006	0	5.63E-05	0	0.000341	0	2	9.94E-05	0.000163	0	0	0	0.000631	0.000278	2	0.000227	0.000299
1007	0	0.00043	0	0.000139	0	2	0.000142	0.000203	0	0.000236	0	0.000472	0	2	0.000177	0.000226
1008	0	0.000103	0	0.000311	0	2	0.000104	0.000147	0	0.000692	0	0.000144	0	2	0.000209	0.000329
1009	0	5.54E-05	0	8.39E-05	0	2	3.48E-05	4.19E-05	0.001054	5.33E-05	0	0	0	2	0.000277	0.000519
1010	0	0.000135	0	0.000461	0	2	0.000149	0.000217	0	0.000195	0	0.000426	0	2	0.000155	0.000202
1011	0	0	0	0.000239	0	1	5.98E-05	0.00012	0	0.00038	0	0.000387	0.000195	3	0.00024	0.000183
1012	0.000726	0.000209	0	4.61E-05	0	3	0.000245	0.000333	0	0	0	0.000219	0	1	5.48E-05	0.00011
1013	0.000462	0	0	0.000403	0	2	0.000216	0.000251	0	0	0	9.3E-05	0.000219	2	7.79E-05	0.000104
1014	0.000364	0.000209	0	0	0	2	0.000143	0.000177	0	0.000151	0	0	0.00043	2	0.000145	0.000203
1015	0.000525	0.000151	0	0.0004	0	3	0.000269	0.000237	0	7.26E-05	0	0	0	1	1.82E-05	3.63E-05
1016	0	0.0005	0	0.000379	0	2	0.00022	0.000258	0	0	0.004994	0.000233	0	2	5.83E-05	0.000117
1017	0	8.33E-05	0	0.000442	0	2	0.000131	0.000211	0	0	0	0.000175	0.000411	2	0.000147	0.000195
1018	0	0.000112	0	0.00068	0	2	0.000198	0.000326	0	0.000108	0	0.00021	0	2	7.94E-05	0.000101
1019	0	0.00039	0.000262	4.93E-05	0	3	0.000175	0.000183	0	0.000375	0	0	0	1	9.39E-05	0.000188
1020	0	0.000186	0	0.000141	0	2	8.18E-05	9.62E-05	0	0.000269	0	0	0.000478	2	0.000187	0.000232
1021	0	4.93E-05	0	3.73E-05	0	2	2.17E-05	2.55E-05	0.000938	4.74E-05	0	0	0	2	0.000246	0.000462
1022	0	8.58E-05	0	0.000487	0.000748	3	0.000143	0.000233	0	0	0	0.00048	0	1	0.00012	0.00024
1023	0.000467	0.000202	0	5.09E-05	0	3	0.00018	0.00021	0	0	0	0	0.000332	1	8.3E-05	0.000166
1024	0	0	0	0.000306	0	1	7.65E-05	0.000153	0	0.000177	0	7.71E-05	0.000484	3	0.000184	0.000212
1025	0	0.000319	0.000257	0	0	2	0.000144	0.000168	0	0.000123	0	0	0.000315	2	0.000109	0.000149
1026	0	0.000172	0	0.000174	0	2	8.64E-05	9.97E-05	0	0	0	0.000281	0.000377	2	0.000164	0.000194
1027	0	0.000148	0	0.000224	0	2	9.31E-05	0.000112	0	0.000214	0	0.000414	0	2	0.000157	0.000199
1028	0	0.000162	0	8.18E-05	0	2	6.09E-05	7.76E-05	0	0	0	3.78E-05	0.000711	2	0.000187	0.00035
1029	0	0.000129	0	0.000195	0	2	8.1E-05	9.74E-05	0	0.000124	0	0.000541	0	2	0.000166	0.000257
1030	0	0.000236	0	0.000428	0	2	0.000166	0.000207	0	0.000227	0	8.24E-05	0	2	7.73E-05	0.000107
1031	0	0.000284	0	7.18E-05	0	2	8.91E-05	0.000135	0	0.000456	0	0	0.000156	2	0.000153	0.000215
1032	0	0.000244	0	0.000132	0	2	9.4E-05	0.000118	0	0.000168	0	0.000415	0	2	0.000146	0.000196
1033	0.000577	8.3E-05	0	0.000126	0	3	0.000196	0.000259	0	0.00016	0	0	0	1	3.99E-05	7.98E-05
1034	0	5.01E-05	0.000806	3.79E-05	0	3	0.000224	0.000389	0	0	0	3.5E-05	0	1	8.76E-06	1.75E-05
1035	0.000633	9.11E-05	0	0.000138	0	3	0.000216	0.000284	0	0	0	6.38E-05	0	1	1.59E-05	3.19E-05
1036	0	0	0	0.000122	0	1	3.05E-05	6.09E-05	0	0.000309	0	0.000225	0.000265	3	0.0002	0.000138
1037	0	0.000154	0	0.000468	0.002696	3	0.000156	0.000221	0	0.000297	0	0	0	1	7.43E-05	0.000149
1038	0	0	0	6.11E-05	0	1	1.53E-05	3.06E-05	0	7.76E-05	0	0.000508	0.000266	3	0.000213	0.000226
1039	0	0.000124	0	4.7E-05	0	2	4.28E-05	5.86E-05	0	0	0	0.000434	0.000306	2	0.000185	0.00022
1040	0.000489	3.52E-05	0	0.000293	0	3	0.000204	0.00023	0	6.77E-05	0	0	0	1	1.69E-05	3.38E-05
1041	0	0.000285	0	5.4E-05	0	2	8.48E-05	0.000136	0	0.000343	0	0.0002	0	2	0.000136	0.000167
1042	0	0.000207	0	0	0	1	5.17E-05	0.000103	0	7.96E-05	0	0.000116	0.000476	3	0.000168	0.000211
1043	0	0	0.000254	0.000238	0	2	0.000123	0.000142	0	6.06E-05	0	0	0.000311	2	9.28E-05	0.000148
1044	0	0	0	0.000419	0	1	0.000105	0.00021	0	0.000133	0	0.000194	0.000114	3	0.00011	8.09E-05
1045	0.000504	7.24E-05	0	5.49E-05	0	3	0.000158	0.000233	0	0.000209	0	0	0	1	5.23E-05	0.000105
1046	0	0.000324	0	0.000175	0	2	0.000125	0.000156	0	0	0	3.24E-05	0.000305	2	8.43E-05	0.000148
1047	0	0.000299	0	0.0002	0	2	0.000125	0.000149	0	0.000237	0	9.83E-05	0	2	8.37E-05	0.000112
1048	0	6.74E-05	0	0.000119	0	2	4.66E-05	5.78E-05	0	0	0	0.000142	0.000481	2	0.000156	0.000227
1049	0	0.000402	0	6.09E-05	0	2	0.000116	0.000193	0	0.000232	0	0.000113	0	2	8.62E-05	0.000111
1050	0	0.000159	0	0.000281	0	2	0.00011	0.000136	0	0.000102	0	0.00026	0	2	9.04E-05	0.000123
1051	0	0.000202	0	0.000229	0	2	0.000108	0.000125	0	0.000291	0	7.06E-05	0	2	9.05E-05	0.000138
1052	0	0.000275	0	4.96E-05	0	2	8.11E-05	0.000131	0	0.000464	0.000491	0	0	2	0.000116	0.000232
1053	0	7.48E-05	0	0.000364	0	2	0.00011	0.000173	0	0.000108	0	0.000235	0	2	8.58E-05	0.000112
1054	0	6.19E-05	0	7.04E-05	0	2	3.31E-05	3.84E-05	0.000589	5.96E-05	0	0	0	2	0.000162	0.000286
1055	0	0	0	0.000188	0	1	4.69E-05	9.38E-05	0	7.94E-05	0	0.000231	0.000272	3	0.000146	0.000128
1056	0	0.000107	0	0.000121	0	2	5.7E-05	6.61E-05	0	0.000257	0	0.000261	0	2	0.00013	0.00015
1057	0	5.52E-05	0	0	0	1	1.38E-05	2.76E-05	0	0.000106	0	3.86E-05	0.000545	3	0.000172	0.000252
1058	0	0.000197	0	7.47E-05	0	2	6.8E-05	9.31E-05	0	0.000142	0	0	0.000325	2	0.000117	0.000154
1059	0	4.14E-05	0	0.000157	0	2	4.95E-05	7.4E-05	0	0	0	5.79E-05	0.000476	2	0.000134	0.00023
1060	0	0.000102	0	0.000425	0	2	0.000132	0.000201	0	0	0	3.57E-05	0.000168	2	5.09E-05	7.98E-05
1061	0	4.88E-05	0	2.46E-05	0	2	1.83E-05	2.34E-05	0.000619	1.56E-05	0	0	0	2	0.000159	0.000307
1062	0	0.000275	0	0.000261	0	2	0.000134	0.000155	0	6.62E-05	0	9.63E-05	0	2	4.06E-05	4.85E-05
1063	0	0.000354	0	0.000215	0	2	0.000142	0.000174	0	6.82E-05	0	4.96E-05	0	2	2.94E-05	3.48E-05
1064	0	7.65E-05	0	0.000116	0	2	4.81E-05	5.78E-05	0	0	0	0.000107	0.000378	2	0.000121	0.000178
1065	0	0	0	0.000171	0	1	4.28E-05	8.57E-05	0	2.42E-05	0	1.76E-05	0.000455	3	0.000124	0.000221
1066	0	0.000108	0	0.000245	0	2	8.81E-05	0.000116	0	0.000138	0	0.000176	0	2	7.85E-05	9.19E-05
1067	0	0	0	0.000147	0	1	3.68E-05	7.36E-05	0	6.23E-05	0	0.000136	0.00032	3	0.00013	0.000139
1068	0	5.39E-05	0	0.000163	0	2	5.43E-05	7.69E-05	0	0.000259	0	0	0.000177	2	0.000109	0.00013
1069	0	0.00011	0	2.09E-05	0	2	3.28E-05	5.25E-05	0	0.000106	0	0	0.000408	2	0.000128	0.000193
1070	0	3.63E-05	0	0.000137	0	2	4.34E-05	6.49E-05	0	3.49E-05	0	0	0.000418	2	0.000113	0.000204
1071	0	8.33E-05	0	0.000189	0	2	6.81E-05	8.98E-05	0	0.00028	0	0	6.85E-05	2	8.72E-05	0.000133
1072	0	9.68E-05	0	0	0	1	2.42E-05	4.84E-05	0	4.65E-05	0	6.77E-05	0.000398	3	0.000128	0.000182
1073	0	0	0	0.0002	0	1	5.01E-05	0.0001	0	0.000102	0	3.7E-05	0.000261	3	1E-04	0.000115
1074	0	0	0	8.33E-05	0	1	2.08E-05	4.17E-05	0	0.000106	0	3.85E-05	0.000362	3	0.000127	0.000163
1075	0	0.000122	0	0.000278	0	2	0.0001	0.000132	0	5.89E-05	0	0.000129	0	2	4.68E-05	6.11E-05
1076	0	8.87E-05	0.000357	3.36E-05	0	3	0.00012	0.000162	0	0	0	9.31E-05	0	1	2.33E-05	4.65E-05
1077	0	7.5E-05	0	5.68E-05	0	2	3.29E-05	3.88E-05	0	0	0	0.000315	0.000123	2	0.00011	0.000149
1078	0	0.000172	0	0.000218	0	2	9.75E-05	0.000114	0	5.53E-05	0	0.000121	0	2	4.4E-05	5.73E-05
1079	0	0.000174	0	0.000158	0	2	0.000083	9.61E-05	0	5.02E-05	0	0.000183	0	2	5.82E-05	8.62E-05
1080	0	0.000177	0	0.000107	0	2	7.1E-05	8.68E-05	0	0.000204	0	7.43E-05	0	2	6.96E-05	9.63E-05
1081	0	4.67E-05	0	0.000124	0	2	4.27E-05	5.85E-05	0	0.000157	0	0	0.000231	2	9.7E-05	0.000116
1082	0.000181	0.00013	0	0.000217	0	3	0.000132	9.51E-05	0	2.51E-05	0	0	0	1	6.27E-06	1.25E-05
1083	0	0.000101	0	0.000172	0	2	6.83E-05	8.41E-05	0	7.29E-05	0	0	0.000208	2	7.02E-05	9.8E-05
1084	0	4.26E-05	0	0.00029	0	2	8.32E-05	0.000139	0	0.000123	0	8.93E-05	0	2	5.3E-05	6.28E-05
1085	0	0.000404	0	3.4E-05	0	2	0.00011	0.000197	0	0	0	3.14E-05	7.4E-05	2	2.64E-05	3.5E-05
1086	0	0.000224	0	0.000136	0	2	8.99E-05	0.00011	0	8.61E-05	0	9.4E-05	0	2	4.5E-05	5.21E-05
1087	0	0.000285	0	0.00012	0	2	0.000101	0.000135	0	3.04E-05	0	0	0.000104	2	3.37E-05	4.92E-05
1088	0	0.000109	0	0.000248	0	2	8.92E-05	0.000117	0	0.000105	0	7.63E-05	0	2	4.53E-05	5.36E-05
1089	0	0.000111	0	0.000134	0	2	6.13E-05	7.14E-05	0	8.53E-05	0	0.000202	0	2	7.17E-05	9.55E-05
1090	0	3.84E-05	0	8.72E-05	0	2	3.14E-05	4.13E-05	0	0	0	2.68E-05	0.000379	2	0.000101	0.000185
1091	0	3.97E-05	0	0.000331	0	2	9.27E-05	0.00016	0	7.64E-05	0	8.34E-05	0	2	4E-05	4.62E-05
1092	0	0.000288	0	0	0	1	7.2E-05	0.000144	0	6.92E-05	0	5.04E-05	0.000118	3	5.95E-05	4.9E-05
1093	0	0.000179	0	0.000186	0	2	9.14E-05	0.000106	0	8.61E-05	0	0	7.37E-05	2	4E-05	4.64E-05
1094	0	0.000208	0	2.62E-05	0	2	5.85E-05	0.0001	0	0.000266	0	2.42E-05	0	2	7.26E-05	0.00013
1095	0	0.000176	0	3.32E-05	0	2	5.22E-05	8.37E-05	0	0.000127	0	0	0.000181	2	7.68E-05	9.14E-05
1096	0	0.000137	0	0.000139	0	2	6.89E-05	7.96E-05	0	0.000176	0	0.000064	0	2	6E-05	8.3E-05
1097	0	0.000114	0	0	0	1	2.84E-05	5.68E-05	0	5.47E-05	0	1.99E-05	0.000327	3	0.0001	0.000153
1098	0	8.79E-05	0	0.000111	0	2	4.97E-05	5.82E-05	0	0	0	0.000267	4.82E-05	2	7.87E-05	0.000127
1099	0	7.6E-05	0	0.00018	0	2	6.4E-05	8.53E-05	0	0.000123	0	0.000133	0	2	6.41E-05	7.41E-05
1100	0	6.86E-05	0	0.00026	0	2	8.21E-05	0.000123	0	0.000132	0	0.000048	0	2	4.5E-05	6.22E-05
1101	0	0.000121	0	0.000276	0	2	9.94E-05	0.000131	0	3.89E-05	0	0	6.66E-05	2	2.64E-05	3.25E-05
1102	0	0.000127	0	2.4E-05	0	2	3.77E-05	6.05E-05	0	0.000214	0	0	0.000122	2	8.39E-05	0.000104
1103	0	0.000144	0	0.000219	0	2	9.08E-05	0.000109	0	6.95E-05	0	5.05E-05	0	2	3E-05	3.55E-05
1104	0	4.72E-05	0	0.000179	0	2	5.65E-05	8.45E-05	0	0	0	9.91E-05	0.000155	2	6.36E-05	7.7E-05
1105	0	7.22E-05	0	0.000219	0	2	7.27E-05	0.000103	0	0.000139	0	5.05E-05	0	2	4.74E-05	6.55E-05
1106	0	4.39E-05	0	0.000133	0	2	4.42E-05	6.27E-05	0	8.45E-05	0	0	0.000217	2	7.53E-05	0.000102
1107	0	0.000116	0	8.79E-05	0	2	5.1E-05	6E-05	0	0.000112	0	0.000162	0	2	6.85E-05	8.18E-05
1108	0	5.44E-05	0	0.000165	0	2	5.48E-05	7.76E-05	0	5.23E-05	0	0.00019	0	2	6.06E-05	8.98E-05
1109	0	0.000156	0	0.000147	0	2	7.58E-05	8.76E-05	0	7.49E-05	0	8.17E-05	0	2	3.92E-05	4.53E-05
1110	0	9.64E-05	0	0.000274	0	2	9.25E-05	0.000129	0	6.95E-05	0	1.69E-05	0	2	2.16E-05	3.29E-05
1111	0	0.000159	0	2.01E-05	0	2	4.47E-05	7.67E-05	0	0.000229	0	0	4.36E-05	2	6.82E-05	0.000109
1112	0	0.000209	0	7.03E-05	0	2	6.98E-05	9.85E-05	0	6.7E-05	0	9.74E-05	0	2	4.11E-05	4.91E-05
1113	0	3.89E-05	0	0.000236	0	2	6.87E-05	0.000113	0	7.49E-05	0	8.17E-05	0	2	3.92E-05	4.53E-05
1114	0	0.000185	0	2.8E-05	0	2	5.32E-05	8.87E-05	0	3.56E-05	0	0	0.000183	2	5.45E-05	8.7E-05
1115	0	0.000182	0	6.91E-05	0	2	6.29E-05	8.61E-05	0	0	0	0.000128	5E-05	2	4.44E-05	6.03E-05
1116	0	6.73E-05	0	0.000178	0	2	6.14E-05	8.42E-05	0	6.47E-05	0	0.000118	0	2	4.56E-05	5.7E-05
1117	0	0.000107	0	0.000144	0	2	6.27E-05	7.4E-05	0	8.83E-05	0	0	8.81E-05	2	4.41E-05	5.09E-05
1118	0	0	0	0.000178	0	1	4.45E-05	8.91E-05	0	9.05E-05	0	2.74E-05	0.000129	3	6.17E-05	5.87E-05
1119	0	4.09E-05	0	1.43E-05	0	2	1.38E-05	1.93E-05	0	5.45E-05	0	0	0.000311	2	9.13E-05	0.000149
1120	0	0.000162	0	0.000164	0	2	8.14E-05	9.4E-05	0	5.19E-05	0	3.78E-05	0	2	2.24E-05	2.65E-05
1121	0	8.01E-05	0	2.02E-05	0	2	2.51E-05	3.79E-05	0	5.13E-05	0	0	0.000264	2	7.87E-05	0.000126
1122	0	7.29E-05	0	0.000166	0	2	5.96E-05	7.86E-05	0	0	0	0.000051	0.00012	2	4.27E-05	5.68E-05
1123	0.000152	0.000131	0	8.28E-05	0	3	9.15E-05	6.75E-05	0	4.21E-05	0	0	0	1	1.05E-05	2.1E-05
1124	0	0.00015	0	9.75E-05	0	2	6.19E-05	7.47E-05	0	0.000124	0	0	3.53E-05	2	3.98E-05	5.85E-05
1125	0	9.67E-05	0	7.73E-05	0	2	4.35E-05	5.09E-05	0	9.92E-05	0	0	0.000133	2	5.8E-05	6.83E-05
1126	0	0.000121	0	4.59E-05	0	2	4.18E-05	5.72E-05	0	5.83E-05	0	0.00017	0	2	5.7E-05	7.99E-05
1127	0	2.55E-05	0	0.000135	0	2	4.01E-05	6.44E-05	0	7.35E-05	0	0.00016	0	2	5.85E-05	7.62E-05

	MMs										
rk	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
981	0	0	0	0	0	0	0	0	F-actin capping protein	F-actin capping protein	actin binding [pmid 7665558]
982	0	0	0	0	0	0	0	0	Ribosomal L37ae protein	intracellular; ribosome	metal ion binding; structural
983	0	0	0	0	0	0	0	0	Triosephosphate		isomerase activity; triose-
984	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus; ubiquitin ligase	DNA binding; ubiquitin-protein
985	0	0	0	0	0	0	0	0	Peroxiredoxin (PRX) family,		oxidoreductase activity;
986	0	0	0	0	0	0	0	0	Ribosomal S3Ae family;	cytosol; cytosolic small	protein binding; structural
987	0	0	0	0	0	0	0	0	Calponin homology (CH)	cortical microtubule	microtubule plus-end binding
988	0	0	0	0	0	0	0	0	RPA2_DBD_D: A subfamily	DNA replication factor A	DNA-directed DNA
989	0	0	0	0	0	0	0	0	WD40 domain, found in a		
990	0	0	0	0	0	0	0	0	DnaJ central domain (4	membrane	heat shock protein binding;
991	0	0	0	0	0	0	0	0	Tropomyosin; pfam00261	cytoskeleton	actin binding
992	0	0	0	0	0	0	0	0	This family represents	intracellular [pmid 15326224]	GTP binding; GTPase
993	0	0	0	0	0	0	0	0	AAA-superfamily of	cytoplasm; cytosol; nucleus	ATP binding; ATPase activity
994	0	0	0	0	0	0	0	0			
995	0	0	0	0	0	0	0	0	DEK C terminal domain.	nucleus [pmid 9050861];	DNA binding; GTP binding;
996	0	0	0	0	0	0	0	0	WD40 domain, found in a		
997	0	0	0	0	0	0	0	0	Biliverdin reductase,		biliverdin reductase activity
998	0	0	0	0	0	0	0	0	Fructose-1,6-bisphosphate		fructose-bisphosphate
999	0	0	0	0	0	0	0	0	RNA recognition motif;	mRNA cleavage factor	nucleotide binding; protein
1000	0	0	0	0	0	0	0	0			
1001	0	0	0	0	0	0	0	0	Glutathione S-transferase	cytoplasm; soluble fraction	ATP binding; ligase activity;
1002	0	0	0	0	0	0	0	0	CDC/Septin. Septins are a		GTP binding [pmid
1003	0	0	0	0	0	0	0	0			
1004	0	0	0	0	0	0	0	0	NIPSNAP. Members of this	integral to plasma membrane	
1005	0	0	0	0	0	0	0	0			
1006	0	0	0	0	0	0	0	0	FOG: Zn-finger [General	intracellular; nucleus	metal ion binding; protein
1007	0	0	0	0	0	0	0	0	Xeroderma pigmentosum G	nucleus [pmid 7961795]	5'-3' exonuclease activity
1008	0	0	0	0	0	0	0	0	Serine hydrolase (FSH1).		
1009	0	0	0	0	0	0	0	0	Homeodomain; DNA binding	nucleus	sequence-specific DNA
1010	0	0	0	0	0	0	0	0	Adenosine kinase (AK)		adenosine kinase activity
1011	0	0	0	0	0	0	0	0	Guanylate-binding protein,	membrane	GTP binding [pmid 1715024];
1012	0	0	0	0	0	0.00021	0	0	GDP dissociation inhibitor;	cytoplasm [pmid 11256614]	GTPase activator activity;
1013	0	0	0	0	0	0	0	0	Serine/Threonine protein	cAMP-dependent protein	ATP binding; cAMP-
1014	0	0	0	0	0	0	0	0	TBC domain. Identification		
1015	0	0	0	0	0	0	0	0	Calponin homology domain;	cytoskeleton [pmid 8889829];	actin binding [pmid
1016	0	0	0	0	0	0	0	0	50S ribosomal protein	intracellular; ribosome [pmid	structural constituent of
1017	0	0	0	0	0	0	0	0			
1018	0	0	0	2.02E-05	0	0	0	0	RNA recognition motif;	endoplasmic reticulum;	nucleotide binding; RNA
1019	0	0	0	0	0	0	0	0	pinin/SDK/memA/ protein	nucleus	DNA binding
1020	0	0	0	3.68E-05	0	3.17E-05	0	0	Actin; An ubiquitous protein	actin filament; cytoplasm	ATP binding; nucleotide
1021	0	0	0	0	0	0	0	0	Brix domain; pfam04427	nucleus [pmid 15302935]	
1022	0	0	0	0	0	0	0	0	TCP-1 (CTT or eukaryotic	cytoskeleton [pmid 8001976]	ATP binding; nucleotide
1023	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; MAP kinase
1024	0	0	0	0	0	0	0	0	Serine/Threonine protein	cytoplasm; T cell receptor	ATP binding; integrin binding
1025	0	0	6.41E-05	2.51E-05	0	2.17E-05	0	0		cytosol [pmid 10825160];	transcription corepressor
1026	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus	nucleotide binding; RNA
1027	0	0	0	0	0	0	0	0		eukaryotic translation	RNA binding; translation
1028	0	0	0	0	0	0	0	0	S-adenosyl-L-	cytoplasm	adenosylhomocysteinase
1029	0	0	0	0	0	0	0	0	Regulator of G protein		signal transducer activity
1030	0	0	0	0	0	0	0	0	Sar1 subfamily. Sar1 is an	cytoplasm; endoplasmic	GTP binding; GTPase
1031	0	0	0	0	0	0	0	0	The archeal/eukaryotic	intracellular; large ribosomal	structural constituent of
1032	0	0	0	2.71E-05	0	4.68E-05	0	0	RNA recognition motif;	mediator complex [pmid	ligand-dependent nuclear
1033	0	0	0	0	0	0	0	0	7-keto-8-aminopelargonate	endoplasmic reticulum;	acyltransferase activity;
1034	0	0	0	0	0	0	0	0	Nuclear transport factor 2	cytoplasm; intracellular;	ATP binding; ATP-dependent
1035	0	0	0	0	0	0	0	0	Trypsin-like serine		protein binding [pmid
1036	0	0	0	0	0	0	0	0	50S ribosomal protein	intracellular; large ribosomal	structural constituent of
1037	0	0	0	0	0	0	0	0	ARP2/3 complex 16 kDa	Arp2/3 protein complex [pmid	structural constituent of
1038	0	0	0	0	0	0	0	0	Inorganic pyrophosphatase.	cytoplasm [pmid 16130169]	hydrolase activity; inorganic
1039	0	0	0	0	0	0	0	0			
1040	0	0	0	0	0	0	0	0	Protein-arginine deiminase	nucleus	calcium ion binding;
1041	0	0	0	0	0	0	0	0	Calponin homology (CH)	microtubule	microtubule binding
1042	0	0	0	9.66E-05	0	0	0	0			
1043	0	0	0	0	0	0	0	0	RecF/RecN/SMC N	nuclear pore [pmid 9049309];	transporter activity [pmid
1044	0	0	0	0	0	0	0	0	Scavenger mRNA	nucleus	hydrolase activity
1045	0	0	0	0	0	0	0.000101	0	DNA/RNA-binding repeats	DNA replication factor A	DNA binding; double-
1046	0	0	0	3.6E-05	0	0	0	0		cytosol; proteasome complex	binding
1047	0	0	0	0	0	0	0	0			
1048	0	0	0	1.75E-05	0	0	0	0	Importin, protein involved in	cytoplasm; nuclear pore [pmid	protein binding [pmid
1049	0	0	0	0	0	0	0	0	RNA recognition motif;	heterogeneous nuclear	nucleic acid binding;
1050	0	0	0	0	0	0	0	0	D-isomer specific 2-	nucleus	NAD binding; oxidoreductase
1051	0	0	0	0	0	0	0	0	PAF_acetylhydrolase (PAF-	cytoplasm; soluble fraction	1-alkyl-2-
1052	0	0	0	0	0	0	0	0	S-100/ICaBP-like domain;		calcium ion binding;
1053	0	0	0	0	0	0	0	0	Serine/Threonine protein	Golgi apparatus	ATP binding [pmid
1054	0	0	0	0	0	0	0	0	AAA-superfamily of		ATP binding; nucleoside-
1055	0	0	0	0	0	2.78E-05	0	0	A subfamily of Peptidase	intracellular; nucleus	cysteine-type endopeptidase
1056	0	0	0	4.15E-05	0	0	0	0	MIT: domain contained	cytoplasm [pmid 11563910];	ATP binding; nucleoside-
1057	0	0	0	0	0	0	0	0			
1058	0	0	0	0	0	0	0	0		mitochondrion	NADH dehydrogenase
1059	0	0	0	0	0	8.2E-05	0	0			binding; protein binding [pmid
1060	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	nucleus	FK506 binding [pmid
1061	0	0	0	0	0	0	0	0	Leucine-rich repeats		transferase activity
1062	0	0	0	0	0	0	0	0	Caldesmon; pfam02029	actin cytoskeleton [pmid	actin binding [pmid
1063	0	0	0	0	0	0	0	0	Alcohol dehydrogenase		NADPH:quinone reductase
1064	0	0	0	0	0	0	0	0	Protein phosphatase 2A		hydrolase activity; iron ion
1065	0	0	0	0	0	0	0	0			
1066	0	0	0	0	0	0	0	0	Peptidase family M1.	extracellular region [pmid	aminopeptidase B activity
1067	0	0	0	0	0	0	0	0	WD40 domain, found in a		
1068	0	0	0	0	0	3.61E-05	0	0	AAA-superfamily of	cytoplasm [pmid 16130169];	ATP binding; hydrolase
1069	0	0	0	0	0	0	0	0	STAT protein, DNA binding	nucleus	calcium ion binding; signal
1070	0	0	0	0	0	0	0	0			
1071	0	0	0	0	0	0	0	0	TRAUB (NUC102) domain.	nucleus [pmid 12429849]	protein binding [pmid
1072	0	0	0	0	0	0	0	0	Histone deacetylase	cytoplasm [pmid 12711221];	enzyme binding [pmid
1073	0	0	0	0	0	0	0	0	Protein of unknown function		
1074	0	0	0	0	0	0	0	7.24E-05	RNA recognition motif;	nucleus; spliceosome complex	nucleic acid binding;
1075	0	0	0	0	0	0	0	0	effector domain of the CAP	cAMP-dependent protein	cAMP binding; cAMP-
1076	0	0	0	0	0	0	0	0	RNA recognition motif.	intracellular; nucleus [pmid	DNA binding; metal ion
1077	0	0	0	0	0	0	0	0	50S ribosomal protein L4;	intracellular; mitochondrion;	structural constituent of
1078	0	0	0	8.93E-05	0	0	0	0	AAA-superfamily of	cytoplasm [pmid 9927201];	ATP binding; ATPase activity
1079	0	0	0	0	0	0	0	2.29E-05	SAP domain. The SAP	nucleus [pmid 10490026]	ATPase activity [pmid
1080	0	0	0	0	0	0	0	0	BTK motif. Zinc-binding	cytoplasm [pmid 15046600];	ATP binding [pmid
1081	0	0	0	0	0	0	0	0	GTF2I-like repeat. This	nucleus	general RNA polymerase II
1082	0	0	0	0	0	0	0	0	Double-stranded RNA	intracellular; nucleus [pmid	DNA binding [pmid 7519613]
1083	0	0	0	0	0	0	0	0	Exportin 1-like protein. The	nucleus	binding; receptor activity
1084	0	0	0	0	0	0	0	0	Eukaryotic translation	eukaryotic translation	protein binding [pmid
1085	0	0	0	0	0	0	0	0	Zinc finger, C2H2 type. The	intracellular; nucleus	DNA binding [pmid 8543809];
1086	0	0	0	0	0	0	0	0			
1087	0	0	0	0	0	0	0	0	Glycogen synthase. This		glycogen (starch) synthase
1088	0	0	0	0	0	0	0	0	Src homology 3 domains;	intracellular [pmid 10092216]	protein binding [pmid
1089	0	0	0	0	0	0	0	0			
1090	0	0	0	0	0	0	0	0			
1091	0	0	0	0	0	0	0	0	Leucine-rich repeats	cytoplasm [pmid 8978815];	Ran GTPase activator
1092	0	0	0	0	0	0	0	0	Protein of unknown function		
1093	0	0	0	0	0	0	0	0		integrator complex [pmid	protein binding [pmid
1094	0	0	0	0	0	0	0	0	PLAT domain of 12/15-		arachidonate 5-lipoxygenase
1095	0	0	0	0	0	0	0	0	Ryanodine Receptor TM 4-		
1096	0	0	0	0	0	0	0	0			
1097	0	0	0	0	0	0	0	0			
1098	0	0	0	0	0	0	0	0	Arsenite-resistance protein		nucleotide binding
1099	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus [pmid 2451786]	ATP binding; ATP-dependent
1100	0	0	0	0	0	0	0	0	AAA-superfamily of	DNA replication factor C	ATP binding; enzyme binding
1101	0	0	0	0	0	0	0	0	Acyl-CoA synthetases		catalytic activity
1102	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; magnesium ion
1103	0	0	0	0	0	0	0	0	Annexin. This family of	cytoplasm [pmid 16130169]	calcium ion binding; calcium-
1104	0	0	0	0	0	0	0	0	A subfamily of Peptidase		cysteine-type endopeptidase
1105	0	0	0	0	0	0	0	0	Protein of unknown function	intracellular [pmid 11256614]	
1106	0	0	0	0	0	0	0	0	RNA pol II accessory	nucleus	protein binding [pmid
1107	0	0	0	0	0	0	0	0	5' nucleotidase, deoxy	cytoplasm [pmid 10681516];	hydrolase activity;
1108	0	0	0	0	0	0	0	0	Actin; An ubiquitous protein	actin filament; nucleus;	ATP binding; chromatin
1109	0	0	0	0	0	0	0	0			
1110	0	0	0	0	0	0	0	0			
1111	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleolus [pmid 12466272];	ATP binding; ATP-dependent
1112	0	0	0	0	0	0	0	0			
1113	0	0	0	0	0	0	0	0	CENP-B N-terminal DNA-	chromosome; chromosome,	chromatin binding [pmid
1114	0	0	0	0	0	0	0	0	RAP domain. This domain	mitochondrion [pmid	ATP binding; protein kinase
1115	0	0	0	0	0	0	0	0	tRNA and rRNA cytosine-		
1116	0	0	0	0	0	0	0	0	The C-terminal domain of		ATP binding; GMP synthase
1117	0	0	0	0	0	0	0	0			
1118	0	0	0	0	0	0	0	0			
1119	0	0	0	0	0	0	0	0	Ezrin/radixin/moesin family.		ATP binding; DNA binding;
1120	0	0	0	0	0	0	0	0	U1 snRNP component,	nucleus	DNA binding
1121	0	0	0	0	0	0	0	0	Poly(A) polymerase. This	intracellular	nucleic acid binding;
1122	0	0	0	0	0	0	0	0	AAA-superfamily of	DNA replication factor C	ATP binding [pmid 1313560];
1123	0	0	0	0	0	0	0	0	Calponin homology domain;	cytoplasm [pmid 11827972];	metal ion binding;
1124	0	0	0	0	0	0	0	0			
1125	0	0	0	0	0	0	0	0		membrane; nucleus [pmid	ATP binding [pmid
1126	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus	
1127	0	0	0	0	0	0	0	0			

																					RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs										
rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
1128	4	4.93E-05	0	0	INF		ENSG00000076924:E	XAB2			gi|55770906|ref|NP_	XPA binding protein 2 [Homo	855	100010	6.2	0	o	Q	0	0	0	0	0	4.13E-05	0	1	1.03E-05	2.07E-05	0	2.62E-05	0	5.73E-05	0.000269	3	8.82E-05	0.000123	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	intracellular; nucleus [pmid	protein binding [pmid
1129	4	4.84E-05	0	0	INF		ENSG00000100029:E	PES1			gi|7657455|ref|NP_0	pescadillo homolog 1, contai	588	68003	7.3	0	o	Q	0	0	0	0.000119	0	6.01E-05	0	2	4.48E-05	5.7E-05	0	0.000153	0	5.55E-05	0	2	5.2E-05	7.2E-05	0	0	0	0	0	0	0	0	Pescadillo N-terminus. This	intracellular; nucleolus;	
1130	4	4.79E-05	0	0	INF		ENSG00000171608:E	PIK3CD			gi|156564405|ref|NP	phosphoinositide-3-kinase, c	1044	119479	7.2	0	o	Q	33	0	0	0.000156	0	0	0	1	3.91E-05	7.82E-05	0	6.45E-05	0	1.56E-05	0.000147	3	5.68E-05	6.62E-05	0	0	0	0	0	0	0	0			
1131	4	4.74E-05	0	0	INF		ENSG00000027869:E	SH2D2A			gi|4503633|ref|NP_0	SH2 domain protein 2A [Hom	389	42907	7.4	0	o	Q	17	0	0	0.00012	0	4.54E-05	0	2	4.13E-05	5.66E-05	0	0.000115	0	0	9.87E-05	2	5.35E-05	6.22E-05	0	0	0	0	0	0	0	0	Src homology 2 domains;	cytoplasm [pmid 9468509];	protein binding [pmid
1132	4	4.73E-05	0	0	INF		ENSG00000157881:E	PANK4			gi|8922665|ref|NP_0	pantothenate kinase 4 [Homo	773	85991	6.3	0	o	Q	16	0	0	9.05E-05	0	2.29E-05	0	2	2.83E-05	4.28E-05	0	0.000116	0	0	0.000149	2	6.63E-05	7.77E-05	0	0	0	0	0	0	0	0	Fumble. Fumble is required		ATP binding; nucleotide
1133	4	4.72E-05	0	0	INF		ENSG00000052749:E	RRP12			gi|15987121|ref|NP_	ribosomal RNA processing 1	1297	143732	8.8	0	o	Q	24	0	0	1.8E-05	0	9.53E-05	0	2	2.83E-05	4.55E-05	0	8.65E-05	0	0	0.000178	2	6.6E-05	8.48E-05	0	0	0	0	0	0	0	0	NUC173 domain. This is	integral to membrane;	binding
1134	4	4.68E-05	0	0	INF		ENSG00000123143:E	PKN1			gi|47132589|ref|NP_	protein kinase N1 isoform 2 [	942	103932	6.4	0	o	Q	28	0.108	0	0	0	7.5E-05	0	1	1.88E-05	3.75E-05	0	0.000119	0	1.73E-05	0.000163	3	7.49E-05	7.88E-05	0	0	0	0	0	0	0	0	Protein kinase C-related	intracellular	ATP binding; nucleotide
1135	4	4.61E-05	0	0	INF		ENSG00000198055:E	GRK6			gi|51896035|ref|NP_	G protein-coupled receptor k	589	67258	8.5	0	o	Q	19	0.001	0	7.92E-05	0	0.00012	0	2	4.98E-05	5.99E-05	0	0.000114	0	5.54E-05	0	2	4.24E-05	5.46E-05	0	0	0	0	0	0	0	0	Regulator of G protein	membrane	ATP binding; G-protein
1136	4	4.47E-05	0	0	INF		ENSG00000184575:E	XPOT			gi|8051636|ref|NP_0	tRNA exportin [Homo sapien	962	109964	5.4	0	o	Q	16	0	0	2.42E-05	0.000195	1.84E-05	0	3	5.95E-05	9.11E-05	0	0	0	0	0.00012	1	2.99E-05	5.99E-05	0	0	0	0	0	0	0	0	Exportin 1-like protein. The	nucleus	binding; tRNA binding [pmid
1137	4	4.38E-05	0	0	INF		ENSG00000087365:E	SF3B2			gi|55749531|ref|NP_	splicing factor 3B subunit 2 [	895	100228	5.7	0	o	Q	35	0	0	0	0	9.87E-05	0	1	2.47E-05	4.93E-05	0	5.01E-05	0	7.29E-05	0.000129	3	6.29E-05	5.34E-05	0	0	0	0	0	0	0	0	Domain of unknown	nucleus; spliceosome complex	DNA binding
1138	4	4.32E-05	0	0	INF		ENSG00000088247:E	KHSRP			gi|154355000|ref|NP	KH-type splicing regulatory p	711	73115	7.3	0	o	Q	29	0.001	0	0	0	0.000174	0	1	4.35E-05	8.7E-05	0	9.47E-05	0	2.3E-05	5.4E-05	3	4.29E-05	4.1E-05	0	0	0	0	0	0	0	0			
1139	4	4.19E-05	1	3.43E-06	12.22772		ENSG00000113643:E	RARS			gi|15149476|ref|NP_	arginyl-tRNA synthetase [Ho	660	75379	6.7	0	o	Q	16	0.001	0	3.53E-05	0	2.68E-05	0	2	1.55E-05	1.83E-05	0	0	0	9.89E-05	0.000174	2	6.83E-05	8.47E-05	0	0	0	2.74E-05	0	0	0	0	DALR anticodon binding	cytoplasm [pmid 7590355];	arginine-tRNA ligase activity;
1140	4	4.1E-05	0	0	INF		ENSG00000058272:E	PPP1R12A			gi|4505317|ref|NP_0	protein phosphatase 1, regul	1030	115281	5.4	0	o	Q	54	0	0	2.26E-05	0	0.000171	0	2	4.85E-05	8.27E-05	0	2.18E-05	0	0	0.000112	2	3.34E-05	5.33E-05	0	0	0	0	0	0	0	0	ankyrin repeats; ankyrin	actin cytoskeleton	signal transducer activity
1141	4	4.07E-05	1	4.05E-06	10.04783		ENSG00000021776:E	AQR			gi|38788372|ref|NP_	aquarius [Homo sapiens]	1485	171294	6.4	0	o	Q	21	0.006	0	1.57E-05	0	0.000107	0	2	3.07E-05	5.14E-05	0	0	0	2.2E-05	0.000181	2	5.07E-05	8.74E-05	0	0	0	0	3.24E-05	0	0	0	Superfamily I DNA and RNA		
1142	4	3.99E-05	0	0	INF		ENSG00000179950:E	PUF60			gi|17298690|ref|NP_	poly-U binding splicing factor	542	58172	5.3	0	o	Q	19	0.061	0	4.3E-05	0	0.000163	0	2	5.15E-05	7.7E-05	0	8.28E-05	0	3.01E-05	0	2	2.82E-05	3.9E-05	0	0	0	0	0	0	0	0	RNA recognition motif;	ribonucleoprotein complex	nucleic acid binding;
1143	4	3.96E-05	0	0	INF		ENSG00000140750:E	ARHGAP17			gi|54860079|ref|NP_	nadrin isoform 1 [Homo sapie	881	95437	7.6	0	o	Q	27	0	0	0.000132	0	0.00014	0	2	6.82E-05	7.88E-05	0	2.55E-05	0	1.85E-05	0	2	1.1E-05	1.3E-05	0	0	0	0	0	0	0	0	BAR domain. The BAR	cytoplasm; intracellular	aminoacyl-tRNA ligase
1144	4	3.85E-05	0	0	INF		ENSG00000132323:E	ILKAP			gi|13540531|ref|NP_	integrin-linked kinase-associ	392	42907	7.1	0	o	Q	0	0	0	0.000119	0	9.01E-05	0	2	5.23E-05	6.15E-05	0	5.72E-05	0	4.16E-05	0	2	2.47E-05	2.92E-05	0	0	0	0	0	0	0	0	Serine/threonine	protein serine/threonine	hydrolase activity; kinase
1145	4	3.77E-05	0	0	INF		ENSG00000113163:E	COL4A3BP			gi|14165452|ref|NP_	alpha 3 type IV collagen bind	598	68007	5.5	0	o	Q	0	0	0	3.9E-05	0	5.91E-05	0	2	2.45E-05	2.95E-05	0	7.5E-05	0	0	0.000128	2	5.09E-05	6.26E-05	0	0	0	0	0	0	0	0	Goodpasture antigen		protein serine/threonine
1146	4	3.74E-05	0	0	INF		ENSG00000008869:E	HEATR5B			gi|55749742|ref|NP_	HEAT repeat containing 5B [	2071	224300	7.2	0	o	Q	16	0.389	0	4.5E-05	0.000181	0	0	2	5.66E-05	8.59E-05	0	5.42E-05	0	0	1.85E-05	2	1.82E-05	2.55E-05	0	0	0	0	0	0	0	0			binding
1147	4	3.68E-05	0	0	INF		ENSG00000144591:E	GMPPA			gi|45447090|ref|NP_	GDP-mannose pyrophospho	420	46291	7.2	0	o	Q	46	0.006	0	0.000111	0	0	0	1	2.78E-05	5.55E-05	0	5.34E-05	0	3.89E-05	9.14E-05	3	4.59E-05	3.78E-05	0	0	0	0	0	0	0	0	Nucleoside-diphosphate-		acyltransferase activity;
1148	4	3.67E-05	0	0	INF		ENSG00000123329:E	ARHGAP9			gi|122939147|ref|NP	Rho GTPase activating prote	731	81150	8.2	0	o	S	41	0.964	0	6.38E-05	0	2.42E-05	0	2	2.2E-05	3.01E-05	0	0.000153	0	0	5.25E-05	2	5.15E-05	7.23E-05	0	0	0	0	0	0	0	0			
1149	4	3.63E-05	0	0	INF		ENSG00000100284:E	TOM1			gi|4885637|ref|NP_0	target of myb1 [Homo sapien	492	53818	4.7	0	o	Q	16	0.001	0	9.48E-05	0	7.18E-05	0	2	4.17E-05	4.9E-05	0	4.56E-05	0	0	7.8E-05	2	3.09E-05	3.81E-05	0	0	0	0	0	0	0	0	GAT domain. The GAT	cytosol [pmid 14613930];	protein binding [pmid
1150	4	3.58E-05	0	0	INF		ENSG00000174243:E	DDX23			gi|41327771|ref|NP_	DEAD (Asp-Glu-Ala-Asp) bo	820	95583	9.6	0	o	Q	0	0	0	0	0	8.62E-05	0	1	2.15E-05	4.31E-05	0	2.74E-05	0	7.96E-05	9.36E-05	3	5.01E-05	4.39E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus; snRNP U5 [pmid	ATP binding; ATP-dependent
1151	4	3.58E-05	0	0	INF		ENSG00000113522:E	RAD50			gi|19924129|ref|NP_	RAD50 homolog isoform 1 [H	1312	153892	6.9	0	o	Q	41	0.001	0	1.78E-05	0	0.000121	0	2	3.47E-05	5.82E-05	0	8.55E-05	0	6.22E-05	0	2	3.69E-05	4.37E-05	0	0	0	0	0	0	0	0	The catalytic domains of	chromosome; chromosome,	3'-5' exonuclease activity
1152	4	3.57E-05	0	0	INF		ENSG00000005007:E	UPF1			gi|18375673|ref|NP_	regulator of nonsense transc	1118	123036	6.7	0	o	Q	26	0.001	0	0.000146	0	3.16E-05	0	2	4.44E-05	6.94E-05	0	2.01E-05	0	8.76E-05	0	2	2.69E-05	4.15E-05	0	0	0	0	0	0	0	0	DEXH-box helicases. A	chromatin [pmid 16488880];	ATP binding; ATP-dependent
1153	4	3.55E-05	0	0	INF		ENSG00000120694:E	HSPH1			gi|42544159|ref|NP_	heat shock 105kD [Homo sa	858	96865	5.4	0	o	Q	21	0.028	0	8.16E-05	0	4.12E-05	0	2	3.07E-05	3.91E-05	0	0.000105	0	5.71E-05	0	2	4.04E-05	5.05E-05	0	0	0	0	0	0	0	0	Hsp70 protein. Hsp70	cytoplasm [pmid 9931472]	ATP binding; nucleotide
1154	4	3.54E-05	0	0	INF		ENSG00000163219:E	ARHGAP25			gi|55770898|ref|NP_	Rho GTPase activating prote	645	73435	6.4	0	o	Q	42	0	0	7.23E-05	0	8.22E-05	0	2	3.86E-05	4.48E-05	0	6.96E-05	0	0	5.95E-05	2	3.23E-05	3.75E-05	0	0	0	0	0	0	0	0	RhoGAP_ARHGAP22_24_	intracellular	GTPase activator activity
1155	4	3.53E-05	0	0	INF		ENSG00000055332:E	EIF2AK2			gi|4506103|ref|NP_0	eukaryotic translation initiatio	551	62094	8.4	0	o	Q	17	0	0	0	0	3.21E-05	0	1	8.01E-06	1.6E-05	0	8.14E-05	0	2.96E-05	0.000139	3	6.26E-05	6.12E-05	0	0	0	0	0	0	0	0	Double-stranded RNA	intracellular	ATP binding; double-stranded
1156	4	3.51E-05	0	0	INF		ENSG00000135899:E	SP110			gi|17986252|ref|NP_	SP110 nuclear body protein	549	61941	9.6	0	o	Q	27	0.001	0	8.5E-05	0	9.65E-05	0	2	4.54E-05	5.26E-05	0	0	0	2.97E-05	6.99E-05	2	2.49E-05	3.31E-05	0	0	0	0	0	0	0	0	Sp100 domain. The	nucleus [pmid 7693701]	DNA binding [pmid 7693701];
1157	4	3.51E-05	0	0	INF		ENSG00000109320:E	NFKB1			gi|34577122|ref|NP_	nuclear factor kappa-B, subu	969	105427	5.4	0	o	Q	0	0	0	0	0	0.000128	0	1	3.19E-05	6.38E-05	0	4.63E-05	0	6.74E-05	3.96E-05	3	3.83E-05	2.82E-05	0	0	0	0	0	0	0	0	Rel homology domain	cytoplasm [pmid 11819787];	protein binding [pmid
1158	4	3.5E-05	0	0	INF		ENSG00000141569:E	TRIM65			gi|38679905|ref|NP_	tripartite motif-containing 65	517	57353	6.7	0	o	Q	27	0.103	0	4.51E-05	0	3.42E-05	0	2	1.98E-05	2.33E-05	0	0	0	0.000126	7.43E-05	2	5.01E-05	6.17E-05	0	0	0	0	0	0	0	0	RING-finger (Really	intracellular	metal ion binding; protein
1159	4	3.5E-05	0	0	INF		ENSG00000169375:E	SIN3A			gi|23397666|ref|NP_	transcriptional co-repressor S	1273	145175	7.3	0	o	Q	27	0	0	0	0	5.55E-05	0	1	1.39E-05	2.78E-05	0	1.76E-05	0	2.56E-05	0.000181	3	5.6E-05	8.39E-05	0	0	0	0	0	0	0	0	Paired amphipathic helix	nucleus	protein binding [pmid
1160	4	3.48E-05	0	0	INF		ENSG00000188986:E	NELFB			gi|20070260|ref|NP_	cofactor of BRCA1 [Homo sa	580	65697	6.1	0	o	Q	14	0	0	0	0	6.09E-05	0	1	1.52E-05	3.05E-05	0	3.87E-05	0	0.000113	6.62E-05	3	5.44E-05	4.74E-05	0	0	0	0	0	0	0	0	Cofactor of BRCA1	cytoplasm [pmid 11256614];	protein binding [pmid
1161	4	3.47E-05	0	0	INF		ENSG00000039123:E	SKIV2L2			gi|39930353|ref|NP_	superkiller viralicidic activity 2	1042	117761	6.7	0	o	Q	21	0	0	2.24E-05	0	5.09E-05	0	2	1.83E-05	2.41E-05	0	0	0	9.4E-05	0.000111	2	5.11E-05	5.94E-05	0	0	0	0	0	0	0	0	DEAD-like helicases	nucleus	ATP binding; ATP-dependent
1162	4	3.45E-05	0	0	INF		ENSG00000062650:E	WAPAL			gi|42734325|ref|NP_	wings apart-like homolog [Ho	1190	132945	5.4	0	o	Q	0	0	0	9.8E-05	0	4.45E-05	0	2	3.56E-05	4.66E-05	0	3.77E-05	0	0.000096	0	2	3.34E-05	4.53E-05	0	0	0	0	0	0	0	0	Wings apart-like protein.	nucleus	
1163	4	3.42E-05	0	0	INF		ENSG00000121060:E	TRIM25			gi|68160937|ref|NP_	tripartite motif-containing 25	630	70974	8.1	0	o	Q	17	0.002	0	7.4E-05	0	0.000112	0	2	4.65E-05	5.6E-05	0	3.56E-05	0	5.18E-05	0	2	2.19E-05	2.61E-05	0	0	0	0	0	0	0	0	RING-finger (Really		metal ion binding; protein
1164	4	3.33E-05	0	0	INF		ENSG00000105618:E	PRPF31			gi|40254869|ref|NP_	pre-mRNA processing factor	499	55442	5.8	0	o	Q	15	0	0	4.67E-05	0	0.000142	0	2	4.71E-05	6.67E-05	0	4.5E-05	0	3.27E-05	0	2	1.94E-05	2.3E-05	0	0	0	0	0	0	0	0	Putative snoRNA binding	Cajal body [pmid 11867543];	protein binding [pmid
1165	4	3.31E-05	0	0	INF		ENSG00000116350:E	SFRS4			gi|21361282|ref|NP_	splicing factor, arginine/serin	494	56678	11.5	0	o	Q	0	0	0	4.72E-05	0	3.58E-05	0.000824	3	2.07E-05	2.44E-05	0	0.000182	0	0	0	1	4.54E-05	9.08E-05	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus [pmid 8321209]	nucleotide binding; RNA
1166	4	3.29E-05	0	0	INF		ENSG00000198721:E	PECI			gi|45643119|ref|NP_	peroxisomal D3,D2-enoyl-Co	364	40183	8.8	0	o	Q	0	0	0	6.41E-05	0	4.85E-05	0	2	2.82E-05	3.31E-05	0	0	0	4.48E-05	0.000105	2	3.76E-05	4.99E-05	0	0	0	0	0	0	0	0	Acyl CoA binding protein	mitochondrion [pmid	acyl-CoA binding;
1167	4	3.25E-05	0	0	INF		ENSG00000095002:E	MSH2			gi|4557761|ref|NP_0	mutS homolog 2 [Homo sapi	934	104743	5.8	0	o	Q	26	0	0	4.99E-05	0	0.000151	0	2	5.03E-05	7.13E-05	0	0	0	1.75E-05	4.11E-05	2	1.46E-05	1.95E-05	0	0	0	0	0	0	0	0	MutS2 homolog in	nucleus [pmid 7923193]	ATP binding; damaged DNA
1168	4	3.19E-05	0	0	INF		ENSG00000009954:E	BAZ1B			gi|14670392|ref|NP_	bromodomain adjacent to zin	1483	170902	8.5	0	o	Q	25	0	0	7.86E-05	0	9.53E-05	0	2	4.35E-05	5.07E-05	0	1.51E-05	0	6.6E-05	0	2	2.03E-05	3.13E-05	0	0	0	0	0	0	0	0	PHD-finger. PHD folds into	nucleus [pmid 11124022]	metal ion binding; protein
1169	4	3.16E-05	2	5.21E-06	6.064498		ENSG00000099331:E	MYO9B			gi|33356170|ref|NP_	myosin IXB [Homo sapiens]	2157	243398	8.8	0	o	Q	31	0.001	0	9.73E-05	0	0.000106	0	2	5.09E-05	5.89E-05	0	3.12E-05	0	0	1.78E-05	2	1.22E-05	1.52E-05	0	0	2.34E-05	1.83E-05	0	0	0	0	Myosin motor domain, type	intracellular; myosin	actin binding; ATP binding;
1170	4	3.16E-05	0	0	INF		ENSG00000164754:E	RAD21			gi|5453994|ref|NP_0	RAD21 homolog [Homo sapi	631	71690	4.7	0	o	Q	31	0.004	0	7.39E-05	0	5.6E-05	0	2	3.25E-05	3.82E-05	0	7.11E-05	0	5.17E-05	0	2	3.07E-05	3.63E-05	0	0	0	0	0	0	0	0	N terminus of Rad21 / Rec8	nuclear chromosome; nucleus	protein binding [pmid
1171	4	3.13E-05	0	0	INF		ENSG00000106263:E	EIF3B			gi|83367072|ref|NP_	eukaryotic translation initiatio	814	92482	5	0	o	Q	0	0	0	0	0	0.000109	0	1	2.71E-05	5.43E-05	0	2.76E-05	0	2E-05	9.43E-05	3	3.55E-05	4.09E-05	0	0	0	0	0	0	0	0	Uncharacterized protein,	eukaryotic translation	nucleotide binding; RNA
1172	4	3.08E-05	0	0	INF		ENSG00000186517:E	ARHGAP30			gi|71040096|ref|NP_	Rho GTPase activating prote	890	95528	5.1	0	o	Q	31	0	0	7.86E-05	0	1.98E-05	0	2	2.46E-05	3.72E-05	0	0	0	1.83E-05	0.000129	2	3.69E-05	6.22E-05	0	0	0	0	0	0	0	0	RhoGAP_CdGAP: RhoGAP	intracellular	
1173	4	3.06E-05	0	0	INF		ENSG00000101343:E	CRNKL1			gi|124256489|ref|NP	crooked neck-like 1 protein [H	848	100452	8	0	o	Q	17	0	0	2.75E-05	0	6.25E-05	0	2	2.25E-05	2.96E-05	0	0	0	1.92E-05	0.000136	2	3.88E-05	6.53E-05	0	0	0	0	0	0	0	0			
1174	4	3.05E-05	0	0	INF		ENSG00000215305:E	VPS16			gi|17978479|ref|NP_	vacuolar protein sorting 16 is	839	94694	6.8	0	o	Q	0	0	0	8.34E-05	0	4.21E-05	0	2	3.14E-05	4E-05	0	2.67E-05	0	0	9.15E-05	2	2.96E-05	4.32E-05	0	0	0	0	0	0	0	0	Vps16, N-terminal region.	cytoplasm; membrane	
1175	4	3.04E-05	0	0	INF		ENSG00000124571:E	XPO5			gi|22748937|ref|NP_	exportin 5 [Homo sapiens]	1204	136311	5.8	0	o	Q	17	0	0	1.94E-05	0	0	0	1	4.84E-06	9.69E-06	0	1.86E-05	0	1.36E-05	0.000191	3	5.59E-05	9.06E-05	0	0	0	0	0	0	0	0	Exportin 1-like protein. The	nucleus	binding; protein binding [pmid
1176	4	2.98E-05	0	0	INF		ENSG00000119397:E	CEP110			gi|87298937|ref|NP_	centrosomal protein 110kDa	2325	268883	5.6	0	o	Q	51	0.001	0.000139	3.01E-05	0	3.04E-05	0	3	5E-05	6.13E-05	0	3.86E-05	0	0	0	1	9.65E-06	1.93E-05	0	0	0	0	0	0	0	0	Chromosome segregation	centrosome [pmid 15337773];	RNA polymerase II
1177	4	2.97E-05	0	0	INF		ENSG00000163660:E	CCNL1			gi|9945320|ref|NP_0	cyclin L1 [Homo sapiens]	526	59634	10.7	0	o	S	25	0.977	0	8.87E-05	0	3.36E-05	0	2	3.06E-05	4.19E-05	0	4.27E-05	0	0	7.3E-05	2	2.89E-05	3.56E-05	0	0	0	0	0	0	0	0	Cyclin box fold. Protein	nucleus	
1178	4	2.97E-05	0	0	INF		ENSG00000151779:E	NAG			gi|41393547|ref|NP_	neuroblastoma-amplified pro	2371	268569	6	0	o	Q	18	0.006	0	9.84E-06	0	7.45E-06	0	2	4.32E-06	5.08E-06	0	9.46E-06	0	0	0.00021	2	5.5E-05	0.000104	0	0	0	0	0	0	0	0	Secretory pathway protein		
1179	4	2.96E-05	0	0	INF		ENSG00000172349:E	IL16			gi|148833504|ref|NP	interleukin 16 isoform 2 [Hom	1332	141752	8.1	0	o	Q	29	0.012	0	5.25E-05	0	2.65E-05	0	2	1.98E-05	2.52E-05	0	8.42E-05	0	7.35E-05	0	2	3.94E-05	4.57E-05	0	0	0	0	0	0	0	0			
1180	4	2.86E-05	0	0	INF		ENSG00000129515:E	SNX6			gi|88703041|ref|NP_	sorting nexin 6 isoform b [Ho	418	47804	6.4	0	o	Q	17	0.007	0	5.58E-05	0	4.23E-05	0	2	2.45E-05	2.88E-05	0	0	0	3.9E-05	9.18E-05	2	3.27E-05	4.35E-05	0	0	0	0	0	0	0	0	Vps5 C terminal like. Vps5	intracellular [pmid 11279102]	intracellular transporter
1181	4	2.83E-05	0	0	INF		ENSG00000072501:E	SMC1A			gi|30581135|ref|NP_	structural maintenance of chr	1233	143233	7.6	0	o	Q	0	0	0	9.46E-05	0	4.3E-05	0	2	3.44E-05	4.5E-05	0	0	0	2.65E-05	6.23E-05	2	2.22E-05	2.95E-05	0	0	0	0	0	0	0	0	SMC proteins Flexible	chromosome; cohesin core	ATP binding; chromatin
1182	4	2.83E-05	0	0	INF		ENSG00000125484:E	GTF3C4			gi|156119605|ref|NP	general transcription factor II	822	91982	6.7	0	o	Q	0	0	0	5.67E-05	0	2.15E-05	0	2	1.96E-05	2.68E-05	0	5.46E-05	0	0	9.34E-05	2	3.7E-05	4.56E-05	0	0	0	0	0	0	0	0			
1183	4	2.82E-05	0	0	INF		ENSG00000065150:E	RANBP5			gi|24797086|ref|NP_	RAN binding protein 5 [Homo	1115	125545	4.9	0	o	Q	27	0	0	0.000105	0	3.17E-05	0	2	3.41E-05	4.93E-05	0	2.01E-05	0	0	6.89E-05	2	2.22E-05	3.25E-05	0	0	0	0	0	0	0	0	HEAT repeat. The HEAT	cytoplasm [pmid 9114010];	binding; GTPase inhibitor
1184	4	2.77E-05	0	0	INF		ENSG00000196235:E	SUPT5H			gi|20149524|ref|NP_	suppressor of Ty 5 homolog	1087	121000	5.1	0	o	Q	0	0	0	6.44E-05	0	6.5E-05	0	2	3.23E-05	3.73E-05	0	6.19E-05	0	3E-05	0	2	2.3E-05	2.96E-05	0	0	0	0	0	0	0	0	Aflatoxin regulatory protein.	nucleus	negative transcription
1185	4	2.75E-05	0	0	INF		ENSG00000164815:E	ORC5L			gi|4505525|ref|NP_0	origin recognition complex su	435	50283	7.7	0	o	Q	24	0.001	0	5.36E-05	0	4.06E-05	0	2	2.36E-05	2.77E-05	0	0	0	3.75E-05	8.82E-05	2	3.14E-05	4.18E-05	0	0	0	0	0	0	0	0	Archaeal ATPase. This	nuclear origin of replication	ATP binding; DNA replication
1186	4	2.74E-05	0	0	INF		ENSG00000205744:E	DENND1C			gi|113205087|ref|NP	DENN/MADD domain contai	801	87065	5.7	0	o	Q	26	0.016	0	2.91E-05	0	6.62E-05	0	2	2.38E-05	3.14E-05	0	2.8E-05	0	0	9.58E-05	2	3.1E-05	4.52E-05	0	0	0	0	0	0	0	0			
1187	4	2.68E-05	0	0	INF		ENSG00000120690:E	ELF1			gi|27363484|ref|NP_	E74-like factor 1 (ets domain	619	67498	5.2	0	o	Q	16	0	0	3.77E-05	0	0.000114	0	2	3.8E-05	5.38E-05	0	3.62E-05	0	2.64E-05	0	2	1.57E-05	1.85E-05	0	0	0	0	0	0	0	0	Ets-domain; pfam00178	nucleus [pmid 14970218]	protein binding [pmid
1188	4	2.64E-05	0	0	INF		ENSG00000140464:E	PML			gi|67089149|ref|NP_	promyelocytic leukemia prote	882	97551	6.2	0	o	Q	0	0	0	5.29E-05	0	2E-05	0	2	1.82E-05	2.5E-05	0	5.09E-05	0	0	8.7E-05	2	3.45E-05	4.25E-05	0	0	0	0	0	0	0	0	RING-finger (Really	insoluble fraction [pmid	metal ion binding; nucleic
1189	4	2.64E-05	0	0	INF		ENSG00000101161:E	PRPF6			gi|40807485|ref|NP_	PRP6 pre-mRNA processing	941	106925	8.3	0	o	Q	25	0.211	0	7.44E-05	0	3.75E-05	0	2	2.8E-05	3.56E-05	0	0	0	1.73E-05	8.16E-05	2	2.47E-05	3.88E-05	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	intracellular; nucleus [pmid	androgen receptor binding
1190	4	2.61E-05	0	0	INF		ENSG00000006744:E	ELAC2			gi|145553959|ref|NP	elaC homolog 2 [Homo sapie	826	92219	7.9	0	o	S	18	0.822	0	0.000113	0	2.14E-05	0	2	3.36E-05	5.39E-05	0	5.43E-05	0	1.98E-05	0	2	1.85E-05	2.56E-05	0	0	0	0	0	0	0	0			
1191	4	2.56E-05	0	0	INF		ENSG00000102241:E	HTATSF1			gi|21361437|ref|NP_	HIV-1 Tat specific factor 1 [H	755	85853	4.4	0	o	Q	0	0	0	6.18E-05	0	7.02E-05	0	2	3.3E-05	3.83E-05	0	2.97E-05	0	4.32E-05	0	2	1.82E-05	2.18E-05	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus [pmid 10454543]	nucleic acid binding;
1192	4	2.49E-05	0	0	INF		ENSG00000107201:E	DDX58			gi|27881482|ref|NP_	DEAD/H (Asp-Glu-Ala-Asp/H	925	106600	6.4	0	o	Q	0	0	0	5.04E-05	0	1.91E-05	0	2	1.74E-05	2.38E-05	0	0	0	8.82E-05	4.15E-05	2	3.24E-05	4.2E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-		ATP binding; ATP-dependent
1193	4	2.46E-05	0	0	INF		ENSG00000157601:E	MX1			gi|4505291|ref|NP_0	myxovirus resistance protein	662	75534	5.8	0	o	Q	30	0.002	0	3.52E-05	0	5.34E-05	0	2	2.21E-05	2.66E-05	0	3.39E-05	0	7.4E-05	0	2	2.7E-05	3.52E-05	0	0	0	0	0	0	0	0	Dynamin, GTPase; Large	cytoplasm	GTP binding [pmid 2154602];
1194	4	2.37E-05	0	0	INF		ENSG00000173193:E	PARP14			gi|154813199|ref|NP	poly (ADP-ribose) polymeras	1801	202799	7.2	0	o	Q	17	0.226	0	5.18E-05	0	2.94E-05	0	2	2.03E-05	2.52E-05	0	8.72E-05	0	0	2.13E-05	2	2.71E-05	4.13E-05	0	0	0	0	0	0	0	0			
1195	4	2.37E-05	0	0	INF		ENSG00000131747:E	TOP2A			gi|19913406|ref|NP_	DNA topoisomerase II, alpha	1531	174384	8.7	0	o	Q	0	0	0	0	0	4.92E-05	0	1	1.23E-05	2.46E-05	0	2.93E-05	0	1.07E-05	0.0001	3	3.51E-05	4.51E-05	0	0	0	0	0	0	0	0	TOPRIM_TopoIIA:	centriole [pmid 9049244];	ATP binding; chromatin
1196	4	2.36E-05	0	0	INF		ENSG00000160208:E	RRP1B			gi|57863269|ref|NP_	ribosomal RNA processing 1	758	84428	9.8	0	o	Q	20	0.001	0	6.15E-05	0	4.66E-05	0	2	2.7E-05	3.18E-05	0	5.92E-05	0	2.15E-05	0	2	2.02E-05	2.79E-05	0	0	0	0	0	0	0	0	Nucleolar protein,Nop52.	nucleolar preribosome, small	metal ion binding; protein
1197	4	2.36E-05	0	0	INF		ENSG00000168067:E	MAP4K2			gi|22035600|ref|NP_	mitogen-activated protein kin	820	91556	6.3	0	o	Q	29	0	0	5.69E-05	0	6.46E-05	0	2	3.04E-05	3.52E-05	0	2.74E-05	0	3.98E-05	0	2	1.68E-05	2E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	Golgi membrane [pmid	ATP binding [pmid
1198	4	2.34E-05	0	0	INF		ENSG00000120899:E	PTK2B			gi|27886588|ref|NP_	PTK2B protein tyrosine kinas	967	111183	5.9	0	o	Q	24	0	0	4.82E-05	0	3.65E-05	0	2	2.12E-05	2.49E-05	0	2.32E-05	0	0	7.94E-05	2	2.56E-05	3.75E-05	0	0	0	0	0	0	0	0	Focal adhesion targeting	cytoplasm [pmid 7499242];	ATP binding; non-membrane
1199	4	2.33E-05	0	0	INF		ENSG00000133104:E	SPG20			gi|21703346|ref|NP_	spastic paraplegia 20 [Homo	666	72833	5.9	0	o	Q	0	0	0	3.5E-05	0	2.65E-05	0	2	1.54E-05	1.81E-05	0	6.74E-05	0	0	5.76E-05	2	3.13E-05	3.63E-05	0	0	0	0	0	0	0	0	Senescence-associated		
1200	4	2.27E-05	1	3.7E-06	6.136922		ENSG00000147162:E	OGT			gi|32307148|ref|NP_	O-linked GlcNAc transferase	1046	116924	6.7	0	o	Q	35	0	0	2.23E-05	0	0.000101	0	2	3.09E-05	4.81E-05	0	2.14E-05	0	0	3.67E-05	2	1.45E-05	1.79E-05	0	0	0	0	0	0	0	2.96E-05	Tetratricopeptide repeat	cytosol [pmid 9083067];	acetylglucosaminyltransferas
1201	4	2.26E-05	0	0	INF		ENSG00000136068:E	FLNB			gi|105990514|ref|NP	filamin B, beta (actin binding	2602	278162	5.7	0	o	Q	0	0	0.000125	2.13E-05	0	2.88E-05	0	3	4.37E-05	5.53E-05	0	0	0	6.4E-06	0	1	1.6E-06	3.2E-06	0	0	0	0	0	0	0	0			
1202	4	2.21E-05	0	0	INF		ENSG00000130479:E	MAP1S			gi|50428935|ref|NP_	BPY2 interacting protein 1 [H	1059	112211	7.3	0	o	S	22	0.957	0	4.4E-05	0	5E-05	0	2	2.35E-05	2.73E-05	0	2.12E-05	0	6.16E-05	0	2	2.07E-05	2.91E-05	0	0	0	0	0	0	0	0		cell soma [pmid 15528209];	actin filament binding [pmid
1203	4	2.18E-05	0	0	INF		ENSG00000189369:E	GSPT2			gi|46094014|ref|NP_	peptide chain release factor 3	628	68883	5.4	0	o	Q	0	0	0	0	0	4.22E-05	0.000648	2	1.05E-05	2.11E-05	0	7.14E-05	0	0	6.11E-05	2	3.31E-05	3.85E-05	0	0	0	0	0	0	0	0	This family represents	intracellular	GTP binding; GTPase
1204	4	2.16E-05	0	0	INF		ENSG00000152556:E	PFKM			gi|4505749|ref|NP_0	phosphofructokinase, muscle	780	85182	8	0	o	Q	28	0.033	0	0	0	4.53E-05	0	1	1.13E-05	2.26E-05	0	5.75E-05	0	2.09E-05	4.92E-05	3	3.19E-05	2.64E-05	0	0	0	0	0	0	0	0	Phosphofructokinase, a key	6-phosphofructokinase	6-phosphofructokinase
1205	4	2.15E-05	0	0	INF		ENSG00000112739:E	PRPF4B			gi|89276756|ref|NP_	serine/threonine-protein kina	1007	116987	10.3	0	o	Q	0	0	0	0.000116	0	1.75E-05	0	2	3.33E-05	5.56E-05	0	2.23E-05	0	1.62E-05	0	2	9.62E-06	1.14E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	nucleus	ATP binding; nucleotide
1206	4	2.08E-05	0	0	INF		ENSG00000144711:E	IQSEC1			gi|50582989|ref|NP_	IQ motif and Sec7 domain 1	963	108314	6.9	0	o	Q	26	0	0	4.84E-05	0	5.5E-05	0	2	2.59E-05	3E-05	0	2.33E-05	0	0	3.99E-05	2	1.58E-05	1.94E-05	0	0	0	0	0	0	0	0	Pleckstrin homology (PH)	intracellular; nucleus	ARF guanyl-nucleotide
1207	4	1.98E-05	0	0	INF		ENSG00000125637:E	PSD4			gi|56788370|ref|NP_	pleckstrin and Sec7 domain c	1056	116249	5.5	0	o	Q	28	0	0	0	0	3.35E-05	0	1	8.36E-06	1.67E-05	0	2.12E-05	0	3.09E-05	7.27E-05	3	3.12E-05	3.05E-05	0	0	0	0	0	0	0	0	Sec7 domain; Domain	intracellular	ARF guanyl-nucleotide
1208	4	1.96E-05	0	0	INF		ENSG00000162654:E	GBP4			gi|31377634|ref|NP_	guanylate binding protein 4 [	640	73165	6	0	o	Q	17	0.001	0	3.64E-05	0	0	0	1	9.11E-06	1.82E-05	0	3.51E-05	0	2.55E-05	6E-05	3	3.01E-05	2.48E-05	0	0	0	0	0	0	0	0	Guanylate-binding protein,		
1209	4	1.92E-05	0	0	INF		ENSG00000110048:E	OSBP			gi|4505531|ref|NP_0	oxysterol binding protein [Ho	807	89421	7.3	0	o	S	26	0.731	0	2.89E-05	0	2.19E-05	0	2	1.27E-05	1.49E-05	0	5.56E-05	0	0	4.76E-05	2	2.58E-05	3E-05	0	0	0	0	0	0	0	0	Oxysterol binding protein	cytoplasm	oxysterol binding [pmid
1210	4	1.88E-05	0	0	INF		ENSG00000080503:E	SMARCA2			gi|48255898|ref|NP_	SWI/SNF-related matrix-asso	1572	179280	7.3	0	o	Q	43	0	0	4.45E-05	0	2.25E-05	0	2	1.67E-05	2.13E-05	0	0	0	1.04E-05	7.33E-05	2	2.09E-05	3.52E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleoplasm [pmid 8670841];	ATP binding; DNA binding;
1211	4	1.79E-05	1	1.8E-06	9.965131		ENSG00000160218:E	TMEM1			gi|48928029|ref|NP_	transmembrane protein 1 iso	1259	142189	6	0	o	Q	24	0	0	5.56E-05	0	1.4E-05	0	2	1.74E-05	2.63E-05	0	0	0	1.3E-05	6.1E-05	2	1.85E-05	2.9E-05	0	0	0	1.44E-05	0	0	0	0		integral to membrane [pmid	binding; sodium ion
1212	4	1.74E-05	0	0	INF		ENSG00000163939:E	PBRM1			gi|30794372|ref|NP_	polybromo 1 isoform 1 [Hom	1602	183689	6.7	0	o	Q	23	0	0	1.46E-05	0	2.21E-05	0	2	9.15E-06	1.1E-05	0	0	0	3.06E-05	7.19E-05	2	2.56E-05	3.4E-05	0	0	0	0	0	0	0	0	High Mobility Group (HMG)-	nucleus	DNA binding; protein binding
1213	4	1.65E-05	0	0	INF		ENSG00000175073:E	VCPIP1			gi|36029914|ref|NP_	valosin containing protein (p9	1222	134320	7.2	0	o	Q	38	0.012	0	1.91E-05	0	1.45E-05	0	2	8.39E-06	9.87E-06	0	1.84E-05	0	8.01E-05	0	2	2.46E-05	3.8E-05	0	0	0	0	0	0	0	0	OTU-like cysteine	cytoplasm [pmid 11256614];	cysteine-type peptidase
1214	4	1.61E-05	1	2.45E-06	6.559977		ENSG00000204256:E	BRD2			gi|4826806|ref|NP_0	bromodomain containing 2 [H	801	88061	9.1	0	o	Q	28	0.001	0	5.82E-05	0	2.21E-05	0	2	2.01E-05	2.75E-05	0	2.8E-05	0	2.04E-05	0	2	1.21E-05	1.43E-05	0	0	0	0	0	1.96E-05	0	0	bromo domain; smart00297	nucleus	protein serine/threonine
1215	4	1.6E-05	0	0	INF		ENSG00000147251:E	DOCK11			gi|145699123|ref|NP	dedicator of cytokinesis 11 [H	2073	237669	7.7	0	o	Q	31	0	0	5.63E-05	0	4.26E-05	0	2	2.47E-05	2.91E-05	0	2.16E-05	0	7.87E-06	0	2	7.38E-06	1.02E-05	0	0	0	0	0	0	0	0			
1216	4	1.59E-05	0	0	INF		ENSG00000066777:E	ARFGEF1			gi|51479145|ref|NP_	brefeldin A-inhibited guanine	1849	208766	5.9	0	o	Q	22	0	0	3.15E-05	0	3.82E-05	0	2	1.74E-05	2.03E-05	0	4.85E-05	0	8.83E-06	0	2	1.43E-05	2.32E-05	0	0	0	0	0	0	0	0	Sec7 domain; Domain	intracellular	ARF guanyl-nucleotide
1217	4	1.54E-05	0	0	INF		ENSG00000175115:E	PACS1			gi|30089916|ref|NP_	phosphofurin acidic cluster s	963	104898	7.7	0	o	Q	20	0.005	0	4.84E-05	0	1.83E-05	0	2	1.67E-05	2.29E-05	0	0	0	1.69E-05	3.99E-05	2	1.42E-05	1.89E-05	0	0	0	0	0	0	0	0			protein binding [pmid
1218	4	1.52E-05	0	0	INF		ENSG00000125676:E	THOC2			gi|125656165|ref|NP	THO complex 2 isoform 1 [H	1593	182774	8.4	0	o	Q	23	0.001	0	1.46E-05	0	4.44E-05	0	2	1.47E-05	2.09E-05	0	1.41E-05	0	0	4.82E-05	2	1.56E-05	2.27E-05	0	0	0	0	0	0	0	0			
1219	4	1.5E-05	0	0	INF		ENSG00000126883:E	NUP214			gi|33946327|ref|NP_	nucleoporin 214kDa [Homo s	2090	213618	7.5	0	o	Q	0	0	0	2.23E-05	0	4.23E-05	0.000196	3	1.61E-05	2.03E-05	0	0	0	0	5.51E-05	1	1.38E-05	2.76E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a	integral to membrane; nuclear	porin activity; protein binding
1220	4	1.47E-05	0	0	INF		ENSG00000073910:E	FRYL			gi|119874201|ref|NP	furry-like [Homo sapiens]	3013	339598	5.6	0	o	Q	0	0	0	2.32E-05	0	4.1E-05	0	2	1.61E-05	1.99E-05	0	1.49E-05	0	0	3.82E-05	2	1.33E-05	1.81E-05	0	0	0	0	0	0	0	0			
1221	4	1.4E-05	3	1.53E-06	9.191027		ENSG00000127603:E	MACF1			gi|33188445|ref|NP_	microfilament and actin filam	5430	620426	5.4	0	o	Q	0	0	0	4.3E-06	0	9.76E-06	0	2	3.51E-06	4.63E-06	8.17E-05	1.65E-05	0	0	0	2	2.46E-05	3.89E-05	0	0	0	3.34E-06	0	2.88E-06	6E-06	0	Spectrin repeats, found in	cytoplasm [pmid 10559237];	actin binding; actin filament
1222	4	1.33E-05	0	0	INF		ENSG00000164190:E	NIPBL			gi|47578105|ref|NP_	delangin isoform A [Homo sa	2804	316051	7.9	0	o	Q	26	0.047	0	5.82E-05	0	1.26E-05	0	2	1.77E-05	2.77E-05	0	2.4E-05	0	1.16E-05	0	2	8.91E-06	1.15E-05	0	0	0	0	0	0	0	0	GRASP55/65 family.	nucleus	binding
1223	4	8.83E-06	1	1.08E-06	8.173105		ENSG00000162402:E	USP24			gi|149192845|ref|NP	ubiquitin specific protease 24	2460	277414	6.3	0	o	Q	19	0.008	0	1.9E-05	0	3.59E-05	0	2	1.37E-05	1.73E-05	0	9.12E-06	0	6.63E-06	0	2	3.94E-06	4.66E-06	0	0	0	8.64E-06	0	0	0	0			
1224	4	8.15E-06	0	0	INF		ENSG00000197386:E	HD			gi|90903231|ref|NP_	huntingtin [Homo sapiens]	3144	347859	6.2	0	o	Q	19	0	0	1.48E-05	0	2.25E-05	0	2	9.33E-06	1.12E-05	0	7.14E-06	0	2.08E-05	0	2	6.97E-06	9.79E-06	0	0	0	0	0	0	0	0	23Q repeat	cytoplasm [pmid 7568002];	microtubule binding [pmid
1225	4	7.77E-06	0	0	INF		ENSG00000205413:N	SAMD9			gi|38201706|ref|NP_	sterile alpha motif domain co	1589	184280	7.8	0	o	Q	0	0	0	1.47E-05	0	3.33E-05	0	2	1.2E-05	1.58E-05	0	1.41E-05	0.00044	0	0	2	3.53E-06	7.06E-06	0	0	0	0	0	0	0	0	AAA-superfamily of		binding
1226	3	0.000914	0	0	INF		ENSG00000145349:E	CAMK2D			gi|26667180|ref|NP_	calcium/calmodulin-depende	499	56369	7.2	0	o	Q	0	0	0	0	0	0.000142	0	1	3.54E-05	7.08E-05	0	8.99E-05	0	0	0.007077	2	0.001792	0.003524	0	0	0	0	0	0	0	0	Calcium/calmodulin	calcium- and calmodulin-	ATP binding; calcium- and
1227	3	0.000754	0	0	INF		ENSG00000099246:N	RAB18			gi|10880989|ref|NP_	RAB18, member RAS oncog	206	22977	5.2	0	o	Q	21	0.001	0	0.001585	0	0.001286	0	2	0.000718	0.000838	0	0.003158	0	0	0	1	0.00079	0.001579	0	0	0	0	0	0	0	0	Rab18 subfamily.	intracellular [pmid 11256614];	ATP binding; GTP binding;
1228	3	0.000451	0	0	INF		ENSG00000169020:E	ATP5I			gi|6005717|ref|NP_0	ATP synthase, H+ transportin	69	7933	9.4	0	o	Q	27	0.136	0	0	0	0.000768	0.005901	2	0.000192	0.000384	0	0	0	0.002838	0	1	0.00071	0.001419	0	0	0	0	0	0	0	0	ATP synthase E chain. This	mitochondrion; proton-	hydrogen-transporting ATP
1229	3	0.000427	0	0	INF		ENSG00000186298:E	PPP1CC			gi|4506007|ref|NP_0	protein phosphatase 1, catal	323	36984	6.5	0	o	Q	22	0	0	0	0	0.000402	0	1	0.000101	0.000201	0	0	0	0.000219	0.002793	2	0.000753	0.001364	0	0	0	0	0	0	0	0	Protein phosphatase 2A		hydrolase activity; iron ion
1230	3	0.000412	0	0	INF		ENSG00000116251:E	RPL22			gi|4506613|ref|NP_0	ribosomal protein L22 propro	128	14787	9.2	0	o	Q	29	0	0	0.000729	0	0.001518	0	2	0.000562	0.000724	0	0.001052	0	0	0	1	0.000263	0.000526	0	0	0	0	0	0	0	0	Ribosomal L22e protein	cytosolic large ribosomal	heparin binding; RNA binding
1231	3	0.000391	0	0	INF		ENSG00000041353:E	RAB27B			gi|5729997|ref|NP_0	RAB27B, member RAS onco	218	24608	5.5	0	o	Q	22	0	0.002232	0.000571	0	0.000324	0	3	0.000782	0.000995	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Rab27a subfamily. The		GTP binding; GTPase
1232	3	0.000379	0	0	INF		ENSG00000105993:E	DNAJB6			gi|17388799|ref|NP_	DnaJ (Hsp40) homolog, subf	326	36087	9.1	0	o	Q	17	0	0	0.000358	0	0.000433	0	2	0.000198	0.00023	0	0	0	0	0.002237	1	0.000559	0.001119	0	0	0	0	0	0	0	0	DnaJ domain. DnaJ		heat shock protein binding
1233	3	0.000353	0	0	INF		ENSG00000131795:E	RBM8A			gi|4826972|ref|NP_0	RNA binding motif protein 8A	174	19889	5.7	0	o	Q	0	0	0	0	0.00108	0.000203	0	2	0.000321	0.000515	0	0	0	0	0.001544	1	0.000386	0.000772	0	0	0	0	0	0	0	0	RNA recognition motif;	cytoplasm [pmid 11030346];	mRNA binding [pmid
1234	3	0.00032	0	0	INF		ENSG00000135604:E	STX11			gi|33667038|ref|NP_	syntaxin 11 [Homo sapiens]	287	33196	6.5	0	o	Q	18	0	0.001695	0.000163	0	0	0	2	0.000464	0.000824	0	0.000704	0	0	0	1	0.000176	0.000352	0	0	0	0	0	0	0	0	Syntaxin N-terminus	membrane	protein binding [pmid
1235	3	0.000312	0	0	INF		ENSG00000142444:E	C19orf52			gi|24308410|ref|NP_	hypothetical protein LOC905	260	29233	8.1	0	o	Q	46	0.354	0	0.000269	0	0	0	1	6.73E-05	0.000135	0.001707	0.000518	0	0	0	2	0.000556	0.000805	0	0	0	0	0	0	0	0	RNA polymerase sigma		
1236	3	0.000296	0	0	INF		ENSG00000173221:N	GLRX			gi|4504025|ref|NP_0	glutaredoxin (thioltransferase	106	11776	8.1	0	o	Q	30	0	0	0	0	0.000667	0	1	0.000167	0.000333	0	0	0	0.000616	0.001086	2	0.000426	0.000528	0	0	0	0	0	0	0	0	Glutaredoxin (GRX) family,		electron carrier activity;
1237	3	0.000279	0	0	INF		ENSG00000182004:N	SNRPE			gi|4507129|ref|NP_0	small nuclear ribonucleoprote	92	10804	9.4	0	i	Q	26	0	0	0	0	0.000384	0	1	9.6E-05	0.000192	0	0	0	0.000177	0.001669	2	0.000462	0.000809	0	0	0	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus; small nuclear	protein binding [pmid
1238	3	0.000242	0	0	INF		ENSG00000136279:E	DBNL			gi|21361670|ref|NP_	drebrin-like isoform a [Homo	431	48294	5	0	o	Q	22	0	0	0	0	4.1E-05	0	1	1.02E-05	2.05E-05	0	0	0	0.000114	0.001781	2	0.000474	0.000873	0	0	0	0	0	0	0	0	Src homology 3 domains;	cell cortex; cytoplasm;	actin binding; enzyme
1239	3	0.000237	0	0	INF		NA:NA:ENSRNOG00	HMGB2			gi|11321591|ref|NP_	high-mobility group box 2 [Ho	209	24034	7.8	0	o	Q	24	0	0	0	0	8.45E-05	0	1	2.11E-05	4.23E-05	0	0.000322	0	0.00149	0	2	0.000453	0.000708	0	0	0	0	0	0	0	0	HMGB-UBF_HMG-box,	chromatin; condensed	DNA bending activity [pmid
1240	3	0.000235	0	0	INF		ENSG00000177600:E	RPLP2			gi|4506671|ref|NP_0	ribosomal protein P2 [Homo	115	11665	4.5	0	o	S	17	0.835	0	0	0	0.00121	0	1	0.000302	0.000605	0	0.00039	0	0.000284	0	2	0.000168	0.000199	0	0	0	0	0	0	0	0	Ribosomal protein	cytosolic large ribosomal	RNA binding [pmid 3323886];
1241	3	0.000231	0	0	INF		ENSG00000172780:E	ISY1			gi|50234889|ref|NP_	RAB43 protein [Homo sapien	212	23339	5.7	0	o	Q	31	0	0.000765	0.00055	0	0	0	2	0.000329	0.00039	0	0.000529	0	0	0	1	0.000132	0.000265	0	0	0	0	0	0	0	0	Rab19 subfamily. Rab19	exosome (RNase complex);	GTP binding; nucleotide
1242	3	0.000218	0	0	INF		ENSG00000156136:E	DCK			gi|4503269|ref|NP_0	deoxycytidine kinase [Homo	260	30519	5.2	0	o	Q	19	0.001	0	0	0	6.79E-05	0	1	1.7E-05	3.4E-05	0	0.000345	0	0	0.001329	2	0.000418	0.000628	0	0	0	0	0	0	0	0	Deoxyribonucleoside	nucleus	ATP binding; deoxycytidine
1243	3	0.000217	0	0	INF		ENSG00000105887:E	MTPN			gi|21956645|ref|NP_	myotrophin [Homo sapiens]	118	12895	5.5	0	o	Q	0	0	0	0	0	0.000299	0	1	7.48E-05	0.00015	0	0.00019	0	0.001245	0	2	0.000359	0.000597	0	0	0	0	0	0	0	0	ankyrin repeats; ankyrin	intracellular [pmid 11256614]	protein binding [pmid
1244	3	0.000206	0	0	INF		ENSG00000143727:E	ACP1			gi|4757714|ref|NP_0	acid phosphatase 1 isoform c	158	18042	6.8	0	o	Q	26	0.413	0	0.000148	0	0.000671	0	2	0.000205	0.000318	0	0	0	0.000826	0	1	0.000207	0.000413	0	0	0	0	0	0	0	0	Low molecular weight	cytoplasm; soluble fraction	acid phosphatase activity
1245	3	0.000202	0	0	INF		ENSG00000160014:N	CALM3			gi|58218968|ref|NP_	calmodulin 3 [Homo sapiens]	149	16838	4.2	0	o	Q	0	0	0	0.00047	0	0.000119	0	2	0.000147	0.000222	0	0	0	0	0.001031	1	0.000258	0.000515	0	0	0	0	0	0	0	0	EF-hand, calcium binding		calcium ion binding
1246	3	0.000201	0	0	INF		ENSG00000143222:E	UFC1			gi|156416000|ref|NP	ubiquitin-fold modifier conjug	167	19458	7.4	0	o	Q	21	0.001	0	0	0	0.000529	0	1	0.000132	0.000264	0	0	0	0.000391	0.00069	2	0.00027	0.000335	0	0	0	0	0	0	0	0			
1247	3	0.000197	0	0	INF		ENSG00000134748:E	PRPF38A			gi|24762236|ref|NP_	PRP38 pre-mRNA processin	312	37477	10	0	o	Q	0	0	0	0.000374	0	0.00034	0	2	0.000178	0.000206	0	0	0	0	0.000861	1	0.000215	0.000431	0	0	0	0	0	0	0	0	PRP38 family. Members of		
1248	3	0.000194	0	0	INF		ENSG00000142875:E	PRKACB			gi|33636738|ref|NP_	cAMP-dependent protein kin	398	46236	8.7	0	o	Q	25	0	0	0	0	0.000355	0	1	8.88E-05	0.000178	0.001115	0	0	8.2E-05	0	2	0.000299	0.000545	0	0	0	0	0	0	0	0	Serine/Threonine protein	cAMP-dependent protein	ATP binding [pmid
1249	3	0.000193	0	0	INF		ENSG00000142669:E	SH3BGRL3			gi|13775198|ref|NP_	SH3 domain binding glutamic	93	10438	4.9	0	o	Q	20	0.001	0	0	0	0.00019	0	1	4.75E-05	9.5E-05	0	0	0	0.000526	0.000826	2	0.000338	0.000409	0	0	0	0	0	0	0	0	Glutaredoxin (GRX) family,	nucleus	
1250	3	0.000188	0	0	INF		ENSG00000204390:E	HSPA1L			gi|124256496|ref|NP	heat shock 70kDa protein 1-l	641	70375	6	0	o	Q	19	0.024	0	3.64E-05	0.001465	0	0.000847	3	0.000375	0.000727	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1251	3	0.000183	1	1.12E-05	16.365		ENSG00000165527:E	ARF6			gi|4502211|ref|NP_0	ADP-ribosylation factor 6 [Ho	175	20082	9	0	o	Q	26	0.001	0	0.0004	0	0.000808	0	2	0.000302	0.000386	0	0.000256	0	0	0	1	6.41E-05	0.000128	0	0	0	0	0	8.94E-05	0	0	Arf6 subfamily. Arf6 (ADP	cell cortex [pmid 10913182];	GTP binding [pmid
1252	3	0.000172	0	0	INF		ENSG00000106733:E	C9orf95			gi|8923530|ref|NP_0	nicotinamide riboside kinase	199	23193	4.9	0	o	Q	21	0.151	0	0.000352	0	0.000444	0	2	0.000199	0.000233	0	0	0	0	0.000579	1	0.000145	0.000289	0	0	0	0	0	0	0	0	Nicotinamide riboside		ATP binding; kinase activity;
1253	3	0.000171	3	2.14E-05	7.992915		ENSG00000159023:E	EPB41			gi|42716291|ref|NP_	erythrocyte membrane protei	641	71956	6.6	0	o	Q	22	0	0	3.64E-05	0	0	0	1	9.1E-06	1.82E-05	0	0	0	7.64E-05	0.001258	2	0.000334	0.000617	0	0	0	0	0	9.15E-05	5.44E-05	2.56E-05	SAB domain. This	cortical cytoskeleton [pmid	actin binding; binding;
1254	3	0.000169	0	0	INF		ENSG00000103275:E	UBE2I			gi|35494003|ref|NP_	ubiquitin-conjugating enzyme	158	18007	8.7	0	o	Q	16	0.001	0	0	0	0	0	0	0	0	0	0.000284	0	0.000826	0.000243	3	0.000338	0.000349	0	0	0	0	0	0	0	0	Ubiquitin-conjugating		ligase activity; protein
1255	3	0.000168	0	0	INF		ENSG00000188313:N	PLSCR1			gi|10863877|ref|NP_	phospholipid scramblase 1 [H	318	35049	4.9	0	o	Q	0	0	0.00102	0	0	0.000111	0	2	0.000283	0.000494	0	0.000212	0	0	0	1	5.29E-05	0.000106	0	0	0	0	0	0	0	0	Scramblase. Scramblase is	integral to membrane; plasma	calcium ion binding [pmid
1256	3	0.000163	0	0	INF		ENSG00000149100:E	EIF3M			gi|23397429|ref|NP_	eukaryotic translation initiatio	374	42503	5.6	0	o	Q	16	0	0	0	0	0	0	0	0	0	0	0.00018	0	0.000611	0.000513	3	0.000326	0.000285	0	0	0	0	0	0	0	0	motif in proteasome		
1257	3	0.000158	0	0	INF		ENSG00000131876:E	SNRPA1			gi|50593002|ref|NP_	small nuclear ribonucleoprote	255	28416	8.6	0	o	Q	19	0.001	0	0	0	0.000554	0	1	0.000139	0.000277	0	0	0	0.000256	0.000452	2	0.000177	0.000219	0	0	0	0	0	0	0	0		nucleus; ribonucleoprotein	protein binding [pmid
1258	3	0.000156	0	0	INF		ENSG00000172531:E	PPP1CA			gi|4506003|ref|NP_0	protein phosphatase 1, catal	330	37512	6.3	0	o	Q	22	0	0	0.000636	0	0.000394	0	2	0.000257	0.000313	0	0	0	0.000214	0	1	5.36E-05	0.000107	0	0	0	0	0	0	0	0	Protein phosphatase 2A		hydrolase activity; iron ion
1259	3	0.000153	0	0	INF		ENSG00000117751:E	PPP1R8			gi|13699256|ref|NP_	protein phosphatase 1 regula	351	38479	7.4	0	o	Q	21	0.281	0.000924	0	0	0	0	1	0.000231	0.000462	0	0.000256	0	4.65E-05	0	2	7.55E-05	0.000122	0	0	0	0	0	0	0	0	Forkhead associated	nucleus [pmid 7499293];	DNA binding; endonuclease
1260	3	0.000151	0	0	INF		ENSG00000042493:E	CAPG			gi|63252913|ref|NP_	gelsolin-like capping protein	348	38499	6.2	0	o	Q	18	0	0	0	0	0.000406	0	1	0.000102	0.000203	0	0	0	0.000469	0.000331	2	0.0002	0.000238	0	0	0	0	0	0	0	0	Gelsolin homology domain;	F-actin capping protein	actin binding
1261	3	0.00015	0	0	INF		ENSG00000126457:E	PRMT1			gi|150456457|ref|NP	HMT1 hnRNP methyltransfer	347	39929	5.6	0	o	Q	15	0	0	0	0	0.000204	0	1	5.09E-05	0.000102	0	0	0	0.000329	0.000664	2	0.000248	0.000318	0	0	0	0	0	0	0	0			
1262	3	0.000149	0	0	INF		ENSG00000213931:N	HBE1			gi|4885393|ref|NP_0	epsilon globin [Homo sapiens	147	16203	8.6	0	o	Q	27	0.001	0	0.000413	0	0	0	1	0.000103	0.000207	0	0.000334	0	0.000444	0	2	0.000195	0.000229	0	0	0	0	0	0	0	0	Globins are heme proteins,	hemoglobin complex [pmid	heme binding; iron ion
1263	3	0.000146	0	0	INF		ENSG00000141456:E	PELP1			gi|155030232|ref|NP	proline, glutamic acid and leu	1130	119700	4.3	0	o	S	17	0.904	0	2.06E-05	0	6.25E-05	0	2	2.08E-05	2.95E-05	0	0	0	0	0.001087	1	0.000272	0.000544	0	0	0	0	0	0	0	0			
1264	3	0.000145	0	0	INF		ENSG00000132792:E	CTNNBL1			gi|18644734|ref|NP_	beta catenin-like 1 [Homo sa	563	65173	5	0	o	Q	0	0	0	0	0	9.41E-05	0	1	2.35E-05	4.71E-05	0	3.98E-05	0	0	0.001023	2	0.000266	0.000505	0	0	0	0	0	0	0	0	Eukaryotic domain of	nucleus	binding
1265	3	0.000143	0	0	INF		ENSG00000167578:E	RAB4B			gi|82659107|ref|NP_	ras-related GTP-binding prot	213	23587	6	0	o	Q	21	0.066	0	0.000438	0	0	0	1	0.00011	0.000219	0	0.000632	0	7.66E-05	0	2	0.000177	0.000305	0	0	0	0	0	0	0	0	Rab4 subfamily. Rab4 has	intracellular; membrane	GTP binding; GTPase
1266	3	0.000141	0	0	INF		ENSG00000134440:E	NARS			gi|4758762|ref|NP_0	asparaginyl-tRNA synthetase	548	62943	6.3	0	o	Q	17	0	0	0.000128	0	0.000161	0	2	7.22E-05	8.45E-05	0	0	0	0	0.000841	1	0.00021	0.00042	0	0	0	0	0	0	0	0	AsnRS_cyto_like_N: N-	cytoplasm [pmid 9421509];	asparagine-tRNA ligase
1267	3	0.000138	0	0	INF		ENSG00000149357:E	C11orf59			gi|8923579|ref|NP_0	hypothetical protein LOC550	161	17745	5.1	0	o	Q	0	0	0	0.000724	0	0	0	1	0.000181	0.000362	0	0.000279	0	0.000101	0	2	9.5E-05	0.000131	0	0	0	0	0	0	0	0			
1268	3	0.000136	0	0	INF		ENSG00000108468:E	CBX1			gi|5803076|ref|NP_0	chromobox homolog 1 (HP1	185	21418	4.9	0	i	Q	0	0	0	0.000126	0	0.000255	0	2	9.52E-05	0.000122	0	0	0	0.000706	0	1	0.000176	0.000353	0	0	0	0	0	0	0	0	Chromo Shadow Domain,	chromatin; chromosome,	chromatin binding [pmid
1269	3	0.000135	0	0	INF		ENSG00000213654:E	GPSM3			gi|11545817|ref|NP_	G-protein signaling modulato	160	17866	5	0	o	Q	0	0	0	0.000292	0	0.000552	0	2	0.000211	0.000266	0	0	0	0	0.00024	1	6E-05	0.00012	0	0	0	0	0	0	0	0			GTPase activator activity;
1270	3	0.000133	0	0	INF		ENSG00000158882:E	TOMM40L			gi|21362030|ref|NP_	translocase of outer mitocho	308	33917	7.2	0	o	Q	19	0.005	0	0.000454	0	0	0	1	0.000114	0.000227	0	0.000364	0	0	0.000249	2	0.000153	0.000183	0	0	0	0	0	0	0	0	Eukaryotic porin;	integral to membrane;	voltage-gated ion-selective
1271	3	0.000133	0	0	INF		ENSG00000104529:E	EEF1D			gi|25453472|ref|NP_	eukaryotic translation elonga	281	31122	5	0	o	Q	0	0	0.000577	0	0	0.000251	0	2	0.000207	0.000274	0	0	0	0.000232	0	1	5.81E-05	0.000116	0	0	0	0	0	0	0	0	Elongation factor 1 beta	eukaryotic translation	guanyl-nucleotide exchange
1272	3	0.000129	0	0	INF		ENSG00000074071:E	MRPS34			gi|13027604|ref|NP_	mitochondrial ribosomal prot	218	25650	10	0	o	Q	21	0.015	0	0.000749	0	8.1E-05	0	2	0.000207	0.000363	0	0.000206	0	0	0	1	5.15E-05	0.000103	0	0	0	0	0	0	0	0		mitochondrion;	
1273	3	0.000129	0	0	INF		ENSG00000110172:E	CHORDC1			gi|6912304|ref|NP_0	cysteine and histidine-rich do	332	37437	7.7	0	o	Q	21	0	0	0	0	0.000372	0	1	9.31E-05	0.000186	0	6.76E-05	0	0.00059	0	2	0.000164	0.000285	0	0	0	0	0	0	0	0	CHORD. CHORD		
1274	3	0.000125	1	1.2E-05	10.38056		ENSG00000116288:E	PARK7			gi|31543380|ref|NP_	DJ-1 protein [Homo sapiens]	189	19891	6.8	0	o	Q	20	0.02	0	0	0	0.000467	0	1	0.000117	0.000234	0	0.000356	0	0.000173	0	2	0.000132	0.00017	0	0	0	9.6E-05	0	0	0	0	Type 1 glutamine	cytoplasm [pmid 12446870];	

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB
1275	3	0.000124	0	0	INF		ENSG00000089220:	PEBP1			gi|4505621|ref|NP_0	prostatic binding protein [Hor	187	21057	7.5	0	o	Q	16	0
1276	3	0.000124	0	0	INF		ENSG00000142634:	EFHD2			gi|20149675|ref|NP_	EF-hand domain family, mem	240	26697	5.2	0	o	Q	45	0
1277	3	0.000122	0	0	INF		ENSG00000104522:	TSTA3			gi|4507709|ref|NP_0	tissue specific transplantation	321	35893	6.6	0	o	Q	29	0.034
1278	3	0.000116	0	0	INF		ENSG00000152795:	HNRPDL			gi|14110407|ref|NP_	heterogeneous nuclear ribon	420	46437	9.6	0	o	S	51	0.814
1279	3	0.000114	0	0	INF		ENSG00000021355:	SERPINB1			gi|13489087|ref|NP_	serine (or cysteine) proteinas	379	42742	6.3	0	o	Q	25	0.015
1280	3	0.000112	0	0	INF		ENSG00000099817:	POLR2E			gi|14589951|ref|NP_	DNA directed RNA polymera	210	24611	6	0	o	Q	0	0
1281	3	0.000112	0	0	INF		ENSG00000178307:	TMEM11			gi|4505901|ref|NP_0	transmembrane protein 11 [H	192	21541	7.3	0	o	Q	26	0.013
1282	3	0.000109	0	0	INF		ENSG00000101109:	STK4			gi|5454096|ref|NP_0	serine/threonine kinase 4 [Ho	487	55630	5.1	0	o	Q	0	0
1283	3	0.000106	0	0	INF		ENSG00000162521:	RBBP4			gi|5032027|ref|NP_0	retinoblastoma binding protei	425	47656	4.9	0	o	Q	0	0
1284	3	0.000105	0	0	INF		ENSG00000029363:	BCLAF1			gi|117938251|ref|NP	BCL2-associated transcriptio	869	100232	10	0	o	Q	0	0
1285	3	0.000103	0	0	INF		ENSG00000105669:	COPE			gi|31542319|ref|NP_	epsilon subunit of coatomer p	308	34482	5.1	0	o	Q	15	0
1286	3	0.000103	0	0	INF		ENSG00000161217:	PCYT1A			gi|31543385|ref|NP_	phosphate cytidylyltransferas	367	41731	7.3	0	o	Q	0	0
1287	3	0.000103	0	0	INF		ENSG00000060688:	WDR57			gi|115298668|ref|NP	WD repeat domain 57 (U5 sr	357	39311	8.1	0	o	Q	37	0.005
1288	3	0.000102	1	1.39E-05	7.355007		ENSG00000111726:	CMAS			gi|8923900|ref|NP_0	cytidine 5'-monophosphate N	434	48379	7.9	0	o	Q	58	0.002
1289	3	0.0001	0	0	INF		ENSG00000183207:	RUVBL2			gi|5730023|ref|NP_0	RuvB-like 2 [Homo sapiens]	463	51157	5.6	0	o	Q	0	0
1290	3	9.97E-05	0	0	INF		ENSG00000154473:	BUB3			gi|4757880|ref|NP_0	BUB3 budding uninhibited by	328	37155	6.8	0	o	Q	42	0
1291	3	9.68E-05	1	1.37E-05	7.080232		ENSG00000100764:	PSMC1			gi|24430151|ref|NP_	proteasome 26S ATPase sub	440	49185	6.2	0	o	Q	0	0
1292	3	9.64E-05	0	0	INF		ENSG00000087302:	C14orf166			gi|7706322|ref|NP_0	homeobox prox 1 [Homo sap	244	28068	6.7	0	o	Q	20	0
1293	3	9.42E-05	0	0	INF		ENSG00000163563:	MNDA			gi|4505227|ref|NP_0	myeloid cell nuclear different	407	45836	9.8	0	o	Q	31	0
1294	3	9.11E-05	0	0	INF		ENSG00000130826:	DKC1			gi|4503337|ref|NP_0	dyskerin [Homo sapiens]	514	57674	9.4	0	o	Q	0	0
1295	3	9.02E-05	0	0	INF		ENSG00000126005:	EIF6			gi|31563378|ref|NP_	eukaryotic translation initiatio	245	26599	4.7	0	o	Q	32	0
1296	3	8.94E-05	0	0	INF		ENSG00000136938:	ANP32B			gi|5454088|ref|NP_0	acidic (leucine-rich) nuclear p	251	28788	4.1	0	o	Q	30	0
1297	3	8.94E-05	0	0	INF		ENSG00000086189:	DIMT1L			gi|7657198|ref|NP_0	dimethyladenosine transferas	313	35236	10	0	o	Q	36	0.001
1298	3	8.91E-05	0	0	INF		ENSG00000132002:	DNAJB1			gi|5453690|ref|NP_0	DnaJ (Hsp40) homolog, subf	340	38044	8.6	0	o	Q	17	0
1299	3	8.87E-05	0	0	INF		ENSG00000169627:	BOLA2B			gi|85797673|ref|NP_	bolA-like protein 2B [Homo s	152	16932	8.2	0	o	S	30	0.571
1300	3	8.67E-05	0	0	INF		ENSG00000100030:	MAPK1			gi|66932916|ref|NP_	mitogen-activated protein kin	360	41390	7	0	o	Q	17	0.383
1301	3	8.64E-05	0	0	INF		ENSG00000186940:	CHCHD9			gi|58219034|ref|NP_	coiled-coil-helix-coiled-coil-he	151	15490	9.9	0	o	S	49	0.839
1302	3	8.64E-05	0	0	INF		ENSG00000138430:	OLA1			gi|58761500|ref|NP_	GTP-binding protein PTD004	396	44744	7.8	0	o	Q	50	0
1303	3	8.64E-05	0	0	INF		NA:ENSMUSG00000	SET			gi|4506891|ref|NP_0	SET translocation (myeloid le	277	32134	4.2	0	o	Q	0	0
1304	3	8.63E-05	0	0	INF		ENSG00000168564:	CDKN2AIP			gi|8923040|ref|NP_0	CDKN2A interacting protein [	580	61125	9	0	o	Q	27	0
1305	3	8.58E-05	0	0	INF		ENSG00000043093:	DCUN1D1			gi|36030883|ref|NP_	RP42 homolog [Homo sapier	259	30124	5.3	0	o	Q	30	0
1306	3	8.55E-05	0	0	INF		ENSG00000161542:	PRPSAP1			gi|4506131|ref|NP_0	phosphoribosyl pyrophospha	356	39480	7.2	0	o	Q	23	0.082
1307	3	8.44E-05	0	0	INF		ENSG00000078304:	PPP2R5C			gi|31083236|ref|NP_	gamma isoform of regulatory	485	56661	7.2	0	o	Q	36	0
1308	3	8.36E-05	1	7.73E-06	10.81372		ENSG00000169504:	CLIC4			gi|7330335|ref|NP_0	chloride intracellular channel	253	28772	5.6	0	o	Q	30	0
1309	3	8.21E-05	0	0	INF		ENSG00000129824:	LOC100133662			gi|169216331|ref|XP	PREDICTED: hypothetical pr	263	29456	10.2	0	o	Q	58	0.014
1310	3	8.05E-05	0	0	INF		ENSG00000130764:	LRRC47			gi|24308207|ref|NP_	leucine rich repeat containing	583	63473	8.3	0	o	Q	38	0.005
1311	3	7.97E-05	0	0	INF		ENSG00000139725:	RHOF			gi|38016957|ref|NP_	ras homolog gene family, me	211	23625	8.6	0	o	Q	17	0.001
1312	3	7.94E-05	0	0	INF		ENSG00000147274:	RBMX			gi|56699409|ref|NP_	RNA binding motif protein, X-	391	42332	10.1	0	o	Q	27	0
1313	3	7.93E-05	0	0	INF		ENSG00000105835:	PBEF1			gi|5031977|ref|NP_0	visfatin precursor [Homo sap	491	55521	7.2	0	o	Q	18	0
1314	3	7.91E-05	0	0	INF		ENSG00000204574:	ABCF1			gi|10947135|ref|NP_	ATP-binding cassette, sub-fa	807	91680	7.7	0	o	Q	0	0
1315	3	7.91E-05	0	0	INF		ENSG00000146677:	LOC644907			gi|147900596|ref|NP	hypothetical protein LOC644	135	15751	10.9	0	o	Q	0	0
1316	3	7.91E-05	0	0	INF		ENSG00000178035:	IMPDH2			gi|66933016|ref|NP_	inosine monophosphate dehy	514	55805	6.9	0	o	Q	21	0.001
1317	3	7.91E-05	0	0	INF		ENSG00000070761:	C16orf80			gi|8392875|ref|NP_0	transcription factor IIB [Homo	193	22774	9.8	0	o	Q	20	0.089
1318	3	7.88E-05	0	0	INF		ENSG00000128739:	SNRPN			gi|13027650|ref|NP_	small nuclear ribonucleoprote	240	24614	11.2	0	o	Q	0	0
1319	3	7.85E-05	0	0	INF		ENSG00000104889:	RNASEH2A			gi|38455391|ref|NP_	ribonuclease H2, large subur	299	33395	5.3	0	o	Q	33	0
1320	3	7.77E-05	0	0	INF		ENSG00000160691:	SHC1			gi|32261324|ref|NP_	SHC (Src homology 2 domai	474	51682	7.2	0	o	Q	17	0
1321	3	7.72E-05	0	0	INF		ENSG00000043462:	LCP2			gi|5031855|ref|NP_0	lymphocyte cytosolic protein	533	60188	6.3	0	o	Q	22	0
1322	3	7.65E-05	0	0	INF		ENSG00000120265:	PCMT1			gi|4885539|ref|NP_0	protein-L-isoaspartate (D-asp	227	24636	7.2	0	o	Q	44	0
1323	3	7.45E-05	1	7.26E-06	10.26057		ENSG00000115484:	CCT4			gi|38455427|ref|NP_	chaperonin containing TCP1,	539	57924	7.8	0	o	Q	23	0.005
1324	3	7.37E-05	0	0	INF		ENSG00000121774:	KHDRBS1			gi|5730027|ref|NP_0	KH domain containing, RNA	443	48227	8.7	0	o	Q	27	0
1325	3	7.29E-05	0	0	INF		ENSG00000100591:	AHSA1			gi|6912280|ref|NP_0	AHA1, activator of heat shoc	338	38274	5.5	0	o	Q	0	0
1326	3	7.29E-05	0	0	INF		ENSG00000108591:	DRG2			gi|4557537|ref|NP_0	developmentally regulated G	364	40746	8.9	0	o	Q	0	0
1327	3	7.23E-05	0	0	INF		ENSG00000143851:	PTPN7			gi|18375658|ref|NP_	protein tyrosine phosphatase	360	40529	6.8	0	o	S	24	0.814
1328	3	7.18E-05	0	0	INF		ENSG00000133226:	SRRM1			gi|42542379|ref|NP_	serine/arginine repetitive mat	904	102335	11.8	0	o	Q	14	0
1329	3	7.16E-05	0	0	INF		ENSG00000128394:	APOBEC3G			gi|13399304|ref|NP_	apolipoprotein B mRNA editi	384	46408	8	0	o	Q	0	0
1330	3	7.1E-05	0	0	INF		ENSG00000143353:	LYPLAL1			gi|20270341|ref|NP_	lysophospholipase-like 1 [Ho	237	26334	7.8	0	o	Q	37	0.202
1331	3	6.94E-05	0	0	INF		ENSG00000101336:	HCK			gi|30795229|ref|NP_	hemopoietic cell kinase isofo	526	59600	6.7	0	o	Q	0	0
1332	3	6.94E-05	0	0	INF		ENSG00000163344:	PMVK			gi|5729980|ref|NP_0	phosphomevalonate kinase [	192	21995	5.7	0	o	Q	22	0.036
1333	3	6.92E-05	0	0	INF		ENSG00000196531:	NACA			gi|5031931|ref|NP_0	nascent polypeptide-associat	215	23384	4.6	0	o	Q	0	0
1334	3	6.8E-05	0	0	INF		ENSG00000137513:	NARS2			gi|39725683|ref|NP_	asparaginyl-tRNA synthetase	477	54077	7.2	0	o	Q	17	0.114
1335	3	6.7E-05	0	0	INF		ENSG00000188677:	PARVB			gi|20127528|ref|NP_	parvin, beta isoform b [Homo	364	41714	6.7	0	o	Q	36	0.001
1336	3	6.69E-05	0	0	INF		ENSG00000132646:	PCNA			gi|33239451|ref|NP_	proliferating cell nuclear antig	261	28769	4.7	0	o	Q	19	0.001
1337	3	6.68E-05	0	0	INF		ENSG00000023318:	TXNDC4			gi|52487191|ref|NP_	thioredoxin domain containin	406	46971	5.3	0	o	S	30	0.984
1338	3	6.66E-05	0	0	INF		ENSG00000138757:	G3BP2			gi|45359846|ref|NP_	Ras-GTPase activating prote	449	50817	5.4	0	o	Q	19	0
1339	3	6.6E-05	0	0	INF		ENSG00000186432:	KPNA4			gi|4504901|ref|NP_0	karyopherin alpha 4 [Homo s	521	57887	5	0	o	Q	0	0
1340	3	6.55E-05	0	0	INF		ENSG00000106211:	HSPB1			gi|4504517|ref|NP_0	heat shock 27kDa protein 1 [	205	22783	6.4	0	o	Q	19	0
1341	3	6.52E-05	0	0	INF		ENSG00000147471:	PROSC			gi|6005842|ref|NP_0	proline synthetase co-transcr	275	30344	7.5	0	o	Q	20	0.211
1342	3	6.49E-05	0	0	INF		ENSG00000147443:	DOK2			gi|41406050|ref|NP_	docking protein 2 [Homo sap	412	45379	6	0	o	Q	40	0.001
1343	3	6.42E-05	0	0	INF		ENSG00000084623:	EIF3I			gi|4503513|ref|NP_0	eukaryotic translation initiatio	325	36502	5.6	0	o	Q	15	0
1344	3	6.36E-05	1	3.93E-06	16.15627		ENSG00000134760:	DSG1			gi|119703744|ref|NP	desmoglein 1 preproprotein [	1049	113748	5	0	o	S	24	0.672
1345	3	6.26E-05	0	0	INF		ENSG00000023734:	STRAP			gi|148727341|ref|NP	serine/threonine kinase recep	350	38438	5.1	0	o	Q	24	0.005
1346	3	6.26E-05	0	0	INF		ENSG00000141048:	MYH4			gi|110611903|ref|NP	myosin, heavy polypeptide 4,	1939	223069	5.8	0	o	Q	14	0
1347	3	6.23E-05	0	0	INF		ENSG00000213782:	DDX47			gi|20149629|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	455	50647	9.1	0	o	Q	0	0
1348	3	6.17E-05	0	0	INF		ENSG00000132780:	NASP			gi|27262628|ref|NP_	nuclear autoantigenic sperm	788	85238	4.3	0	o	S	19	0.881
1349	3	6.13E-05	0	0	INF		ENSG00000129103:	SUMF2			gi|110227848|ref|NP	sulfatase modifying factor 2 i	304	34290	8.4	0	o	S	26	0.999
1350	3	6.13E-05	0	0	INF		ENSG00000108669:	CYTH1			gi|110349763|ref|NP	pleckstrin homology, Sec7 ar	397	46356	5.5	0	o	Q	0	0
1351	3	6.12E-05	0	0	INF		ENSG00000113384:	GOLPH3			gi|11545859|ref|NP_	golgi phosphoprotein 3 [Hom	298	33811	6.4	0	o	Q	19	0
1352	3	6.07E-05	0	0	INF		ENSG00000157191:	NECAP2			gi|8922416|ref|NP_0	NECAP endocytosis associat	263	28339	8.4	0	o	Q	0	0
1353	3	6.05E-05	0	0	INF		ENSG00000180370:	PAK2			gi|32483399|ref|NP_	p21-activated kinase 2 [Hom	524	58043	6	0	o	Q	0	0
1354	3	6.03E-05	0	0	INF		ENSG00000134954:	ETS1			gi|4885219|ref|NP_0	v-ets erythroblastosis virus E	441	50408	5.2	0	o	Q	17	0
1355	3	6.03E-05	0	0	INF		ENSG00000147457:	CHMP7			gi|22748641|ref|NP_	CHMP family, member 7 [Ho	453	50911	5.3	0	o	Q	20	0
1356	3	6.01E-05	0	0	INF		ENSG00000150593:	PDCD4			gi|21735596|ref|NP_	programmed cell death 4 isof	469	51735	5.2	0	o	Q	0	0
1357	3	5.96E-05	0	0	INF		ENSG00000105576:	TNPO2			gi|48675813|ref|NP_	transportin 2 (importin 3, kary	887	100408	5	0	o	Q	23	0
1358	3	5.95E-05	0	0	INF		ENSG00000105607:	GCDH			gi|4503943|ref|NP_0	glutaryl-Coenzyme A dehydro	438	48127	8.1	0	o	Q	28	0.39
1359	3	5.91E-05	0	0	INF		ENSG00000168497:	SDPR			gi|4759082|ref|NP_0	serum deprivation response	425	47173	5.2	0	o	Q	0	0
1360	3	5.88E-05	0	0	INF		ENSG00000169032:	MAP2K1			gi|5579478|ref|NP_0	mitogen-activated protein kin	393	43439	6.6	0	o	Q	20	0.001
1361	3	5.87E-05	0	0	INF		ENSG00000151553:	KIAA1600			gi|61098052|ref|NP_	hypothetical protein LOC577	765	86415	5.3	0	o	Q	22	0.088
1362	3	5.78E-05	0	0	INF		ENSG00000100749:	VRK1			gi|4507903|ref|NP_0	vaccinia related kinase 1 [Ho	396	45476	8.9	0	o	Q	31	0
1363	3	5.72E-05	0	0	INF		ENSG00000132604:	TERF2			gi|5032169|ref|NP_0	telomeric repeat binding facto	500	55551	9.2	0	o	Q	17	0
1364	3	5.63E-05	0	0	INF		ENSG00000185049:	WHSC2			gi|19913363|ref|NP_	Wolf-Hirschhorn syndrome c	528	57277	9	0	o	Q	36	0.005
1365	3	5.61E-05	0	0	INF		ENSG00000177830:	CHID1			gi|24431994|ref|NP_	chitinase domain containing	393	44883	8.8	0	o	S	20	1
1366	3	5.53E-05	1	5.8E-06	9.537754		ENSG00000101266:	CSNK2A1			gi|29570791|ref|NP_	casein kinase II alpha 1 subu	391	45144	7.7	0	o	Q	18	0
1367	3	5.49E-05	0	0	INF		ENSG00000186283:	TOR3A			gi|115647957|ref|NP	torsin family 3, member A [H	397	46199	6	0	o	S	22	0.999
1368	3	5.49E-05	0	0	INF		ENSG00000131378:	RFTN1			gi|41872577|ref|NP_	raft-linking protein [Homo sap	578	63146	5.7	0	o	Q	0	0
1369	3	5.42E-05	0	0	INF		ENSG00000163564:	PYHIN1			gi|39540514|ref|NP_	pyrin and HIN domain family,	492	55065	9.8	0	o	Q	0	0
1370	3	5.42E-05	0	0	INF		ENSG00000158793:	NIT1			gi|5031947|ref|NP_0	nitrilase 1 [Homo sapiens]	327	35896	7.7	0	o	S	31	0.799
1371	3	5.4E-05	0	0	INF		ENSG00000129968:	FAM108A1			gi|21361949|ref|NP_	hypothetical protein LOC819	361	39136	7	0	o	S	21	0.837
1372	3	5.37E-05	0	0	INF		ENSG00000147010:	SH3KBP1			gi|13994242|ref|NP_	SH3-domain kinase binding p	665	73126	6.6	0	o	Q	0	0
1373	3	5.32E-05	0	0	INF		ENSG00000173110:	HSPA6			gi|34419635|ref|NP_	heat shock 70kDa protein 6 (	643	71028	6.1	0	o	Q	19	0.009
1374	3	5.24E-05	0	0	INF		ENSG00000101972:	STAG2			gi|112789528|ref|NP	stromal antigen 2 isoform a [	1268	145751	5.5	0	o	Q	20	0
1375	3	5.18E-05	0	0	INF		ENSG00000117899:	MESDC2			gi|74136552|ref|NP_	mesoderm development cand	234	26077	7.8	0	o	S	34	1
1376	3	5.17E-05	0	0	INF		ENSG00000025800:	KPNA6			gi|6912478|ref|NP_0	karyopherin alpha 6 [Homo s	536	60030	5	0	o	Q	0	0
1377	3	5.14E-05	0	0	INF		ENSG00000136891:	TEX10			gi|8923269|ref|NP_0	testis expressed 10 [Homo sa	929	105693	9.4	0	o	Q	0	0
1378	3	5.1E-05	0	0	INF		ENSG00000089820:	ARHGAP4			gi|156071465|ref|NP	Rho GTPase activating prote	946	105026	6.3	0	o	Q	0	0
1379	3	5.09E-05	0	0	INF		ENSG00000169756:	LIMS1			gi|13518026|ref|NP_	LIM and senescent cell antig	325	37251	8	0	o	Q	16	0.014
1380	3	5.07E-05	0	0	INF		ENSG00000126456:	IRF3			gi|4504725|ref|NP_0	interferon regulatory factor 3	427	47219	5.3	0	o	Q	24	0.261
1381	3	4.98E-05	0	0	INF		ENSG00000213551:	DNAJC9			gi|27597059|ref|NP_	DnaJ homolog, subfamily C,	260	29910	5.7	0	o	Q	17	0
1382	3	4.92E-05	0	0	INF		ENSG00000067048:	LOC100130220			gi|169216131|ref|XP	PREDICTED: hypothetical pr	660	73154	7.6	0	o	Q	0	0
1383	3	4.91E-05	1	7.19E-06	6.830332		ENSG00000007392:	LUC7L			gi|41393554|ref|NP_	LUC7-like isoform b [Homo s	371	43728	9.9	0	o	Q	22	0.006
1384	3	4.9E-05	0	0	INF		ENSG00000170606:	HSPA4			gi|38327039|ref|NP_	heat shock 70kDa protein 4 [	840	94331	5.2	0	o	Q	21	0.111
1385	3	4.89E-05	0	0	INF		ENSG00000142230:	SAE1			gi|4885585|ref|NP_0	SUMO1 activating enzyme su	346	38450	5.3	0	o	Q	0	0
1386	3	4.84E-05	0	0	INF		ENSG00000119541:	VPS4B			gi|17865802|ref|NP_	vacuolar protein sorting facto	444	49302	7.2	0	o	Q	19	0
1387	3	4.73E-05	0	0	INF		ENSG00000108039:	XPNPEP1			gi|21359929|ref|NP_	X-prolyl aminopeptidase (am	623	69918	5.7	0	o	Q	17	0
1388	3	4.69E-05	0	0	INF		ENSG00000119383:	PPP2R4			gi|30065643|ref|NP_	protein phosphatase 2A, regu	323	36775	6.3	0	o	Q	0	0
1389	3	4.68E-05	0	0	INF		ENSG00000141968:	VAV1			gi|7108367|ref|NP_0	vav 1 guanine nucleotide exc	845	98314	6.6	0	o	Q	19	0.004
1390	3	4.68E-05	0	0	INF		ENSG00000165934:	CPSF2			gi|34101288|ref|NP_	cleavage and polyadenylation	782	88487	5.1	0	o	Q	21	0.01
1391	3	4.67E-05	0	0	INF		ENSG00000077420:	APBB1IP			gi|56118221|ref|NP_	amyloid beta (A4) precursor p	666	73183	5.6	0	o	Q	28	0
1392	3	4.64E-05	0	0	INF		ENSG00000159593:	APPBP1			gi|4502169|ref|NP_0	NEDD8 activating enzyme E	534	60246	5.4	0	o	Q	43	0
1393	3	4.63E-05	0	0	INF		ENSG00000132274:	TRIM22			gi|117938316|ref|NP	tripartite motif-containing 22	498	56947	7.7	0	o	Q	28	0
1394	3	4.59E-05	0	0	INF		ENSG00000130254:	SAFB2			gi|7661936|ref|NP_0	scaffold attachment factor B2	953	107474	6.2	0	o	Q	24	0.001
1395	3	4.55E-05	0	0	INF		ENSG00000165732:	DDX21			gi|50659095|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	783	87344	9.3	0	o	Q	0	0
1396	3	4.54E-05	0	0	INF		ENSG00000155438:	MKI67IP			gi|21314753|ref|NP_	MKI67 (FHA domain) interac	293	34253	9.9	0	o	Q	17	0.002
1397	3	4.51E-05	0	0	INF		ENSG00000147677:	EIF3H			gi|4503515|ref|NP_0	eukaryotic translation initiatio	352	39930	6.5	0	o	Q	22	0.087
1398	3	4.51E-05	0	0	INF		ENSG00000102575:	ACP5			gi|4501873|ref|NP_0	tartrate resistant acid phosph	325	36599	8.7	0	o	S	22	1
1399	3	4.47E-05	0	0	INF		ENSG00000105972:	C7orf20			gi|38570062|ref|NP_	hypothetical protein LOC516	327	36504	5.4	0	o	Q	17	0
1400	3	4.45E-05	3	7.62E-06	5.839374		ENSG00000118873:	RAB3GAP2			gi|19923790|ref|NP_	rab3 GTPase-activating prote	1393	155984	5.6	0	o	Q	17	0.125
1401	3	4.42E-05	0	0	INF		ENSG00000086589:	RBM22			gi|8922328|ref|NP_0	RNA binding motif protein 22	420	46896	8.5	0	o	Q	30	0
1402	3	4.42E-05	0	0	INF		ENSG00000060491:	OGFR			gi|33286446|ref|NP_	opioid growth factor receptor	677	73325	4.8	0	o	Q	0	0
1403	3	4.35E-05	0	0	INF		ENSG00000148660:	CAMK2G			gi|26667191|ref|NP_	calcium/calmodulin-depende	495	55961	7.2	0	o	Q	16	0
1404	3	4.33E-05	0	0	INF		ENSG00000104835:	SARS2			gi|8923421|ref|NP_0	seryl-tRNA synthetase 2 [Ho	518	58283	8.1	0	o	Q	25	0.005
1405	3	4.3E-05	0	0	INF		ENSG00000154727:	GABPA			gi|34452721|ref|NP_	GA binding protein transcript	454	51295	5	0	o	Q	0	0
1406	3	4.27E-05	0	0	INF		ENSG00000095380:	NANS			gi|12056473|ref|NP_	N-acetylneuraminic acid pho	359	40308	6.7	0	o	Q	16	0.004
1407	3	4.26E-05	0	0	INF		ENSG00000162231:	NXF1			gi|125625324|ref|NP	nuclear RNA export factor 1	356	40476	9	0	o	Q	0	0
1408	3	4.17E-05	0	0	INF		ENSG00000139436:	GIT2			gi|17149830|ref|NP_	G protein-coupled receptor k	759	84543	7.2	0	o	Q	23	0.004
1409	3	4.15E-05	0	0	INF		ENSG00000013275:	PSMC4			gi|24430155|ref|NP_	proteasome 26S ATPase sub	387	43508	5.3	0	o	Q	0	0
1410	3	4.14E-05	0	0	INF		ENSG00000183751:	TBL3			gi|19913369|ref|NP_	transducin beta-like 3 [Homo	808	89035	6.9	0	o	Q	17	0
1411	3	4.14E-05	0	0	INF		ENSG00000020922:	MRE11A			gi|24234690|ref|NP_	meiotic recombination 11 hor	680	77642	5.8	0	o	Q	0	0
1412	3	4.12E-05	0	0	INF		ENSG00000174780:	SRP72			gi|109638749|ref|NP	signal recognition particle 72	671	74606	9.3	0	o	Q	17	0.028
1413	3	4.06E-05	0	0	INF		ENSG00000133313:	CNDP2			gi|8922699|ref|NP_0	CNDP dipeptidase 2 [Homo s	475	52779	5.9	0	o	Q	34	0
1414	3	4.06E-05	0	0	INF		ENSG00000090857:	PDPR			gi|32261326|ref|NP_	pyruvate dehydrogenase pho	878	99233	6.4	0	o	Q	58	0.027
1415	3	4.06E-05	0	0	INF		ENSG00000135269:	TES			gi|7661666|ref|NP_0	testin isoform 1 [Homo sapie	421	47996	7.7	0	o	Q	0	0
1416	3	4.04E-05	0	0	INF		ENSG00000107625:	DDX50			gi|13129006|ref|NP_	nucleolar protein GU2 [Homo	737	82565	9.2	0	o	Q	23	0
1417	3	4.04E-05	0	0	INF		ENSG00000105254:	TBCB			gi|50428925|ref|NP_	cytoskeleton associated prote	244	27326	5.1	0	o	Q	19	0.051
1418	3	4.03E-05	0	0	INF		ENSG00000141030:	COPS3			gi|23238222|ref|NP_	COP9 constitutive photomorp	423	47873	6.7	0	o	Q	18	0.004
1419	3	4.02E-05	0	0	INF		ENSG00000139083:	ETV6			gi|4503611|ref|NP_0	ets variant gene 6 [Homo sap	452	53000	7.4	0	o	Q	0	0
1420	3	3.94E-05	2	7.55E-06	5.21877		ENSG00000138496:	PARP9			gi|13899297|ref|NP_	poly (ADP-ribose) polymeras	854	96283	7.9	0	o	S	32	0.528
1421	3	3.92E-05	0	0	INF		ENSG00000000938:	FGR			gi|112382244|ref|NP	proto-oncogene tyrosine-prot	529	59479	5.6	0	o	Q	16	0

rk	RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs							
	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
1275	0	0.000125	0	0.000661	0	2	0.000196	0.000315	0	0	0	0	0.000205	1	5.13E-05	0.000103
1276	0.000676	0	0	0.000221	0	2	0.000224	0.000319	0	9.35E-05	0	0	0	1	2.34E-05	4.67E-05
1277	0	0	0	0	0	0	0	0	0	0.00028	0	0.000102	0.000598	3	0.000245	0.000262
1278	0	0	0	0	0	0	0	0	0	5.34E-05	0	0.000505	0.000366	3	0.000231	0.000244
1279	0	0	0	0	0	0	0	0	0	5.92E-05	0	0.000344	0.000506	3	0.000228	0.000239
1280	0	0.000222	0	0	0	1	5.55E-05	0.000111	0	0	0	0.000311	0.000366	2	0.000169	0.000197
1281	0	0.000243	0	0.000184	0	2	0.000107	0.000126	0	0.000467	0	0	0	1	0.000117	0.000234
1282	0	0.000192	0	0.000363	0	2	0.000139	0.000175	0	0	0	0	0.000315	1	7.88E-05	0.000158
1283	0	0	0	0.000166	0	1	4.16E-05	8.31E-05	0	0.000106	0	0.000576	0	2	0.00017	0.000275
1284	0	0.000376	0	0.000183	0	2	0.00014	0.000179	0	0.000284	0	0	0	1	7.1E-05	0.000142
1285	0	0	0	0.000574	0	1	0.000143	0.000287	0	0.000146	0	0.000106	0	2	6.29E-05	7.44E-05
1286	0	0.000445	0	0.000193	0	2	0.000159	0.000211	0	0.000183	0	0	0	1	4.58E-05	9.17E-05
1287	0	0	0	0.000495	0	1	0.000124	0.000247	0	0.000189	0	0.000137	0	2	8.14E-05	9.63E-05
1288	0	0.000161	0	0.000244	0	2	0.000101	0.000122	0	0.000414	0	0	0	1	0.000103	0.000207
1289	0	0.000151	0	0.000153	0	2	7.59E-05	8.77E-05	0	0	0	0	0.000497	1	0.000124	0.000249
1290	0	0	0	0.000431	0	1	0.000108	0.000215	0	6.84E-05	0	0.000299	0	2	9.17E-05	0.000142
1291	0	0	0	0.000241	0	1	6.02E-05	0.00012	0	5.1E-05	0	0.000482	0	2	0.000133	0.000234
1292	0	0.000287	0	0.000217	0	2	0.000126	0.000148	0	0	0	0.000268	0	1	6.69E-05	0.000134
1293	0	0.000229	0	0.000304	0	2	0.000133	0.000157	0	0.00022	0	0	0	1	5.51E-05	0.00011
1294	0	0	0	0.000137	0	1	3.44E-05	6.87E-05	0	0.000218	0	0	0.000373	2	0.000148	0.000182
1295	0	0	0	0.000288	0	1	7.21E-05	0.000144	0	0.000366	0	6.66E-05	0	2	0.000108	0.000175
1296	0	0.000186	0	0.000172	0	2	8.95E-05	0.000103	0	0.000358	0	0	0	1	8.94E-05	0.000179
1297	0	7.45E-05	0	0.000282	0	2	8.92E-05	0.000133	0	0.000358	0	0	0	1	8.96E-05	0.000179
1298	0	0	0	5.2E-05	0	1	1.3E-05	2.6E-05	0	0	0	0.000096	0.000565	2	0.000165	0.00027
1299	0	0.000307	0	0	0	1	7.67E-05	0.000153	0	0.000295	0	0.000107	0	2	0.000101	0.000139
1300	0	0	0	0.000131	0	1	3.27E-05	6.54E-05	0	0	0	0.000136	0.000427	2	0.000141	0.000201
1301	0	0.000309	0	0.000234	0	2	0.000136	0.00016	0	0.000149	0	0	0	1	3.71E-05	7.43E-05
1302	0	0.000177	0	0.000401	0	2	0.000145	0.00019	0	0.000113	0	0	0	1	2.83E-05	5.67E-05
1303	0	8.42E-05	0	0.000191	0	2	6.89E-05	9.08E-05	0	0	0	0	0.000416	1	0.000104	0.000208
1304	0.000559	4.02E-05	0	9.14E-05	0	3	0.000173	0.00026	0	0	0	0	0	0	0	0
1305	0	0	0	6.82E-05	0	1	1.71E-05	3.41E-05	0	0.000173	0	0	0.000445	2	0.000154	0.00021
1306	0	0	0	9.92E-05	0	1	2.48E-05	4.96E-05	0	0	0	4.58E-05	0.000539	2	0.000146	0.000263
1307	0	4.81E-05	0	0	0	1	1.2E-05	2.4E-05	0	0.000231	0	0	0.000396	2	0.000157	0.000193
1308	0	0	0	0.000209	0	1	5.24E-05	0.000105	0	8.87E-05	0	0	0.000371	2	0.000115	0.000176
1309	0	0	0	9.77E-05	0	1	2.44E-05	4.88E-05	0	0.000413	0	0	0.000146	2	0.00014	0.000195
1310	0.000278	0	0	0.000212	0	2	0.000123	0.000144	0	0.000154	0	0	0	1	3.85E-05	7.7E-05
1311	0	0.000332	0.000223	8.37E-05	0	3	0.000159	0.000147	0	0	0	0	0	0	0	0
1312	0	0.000418	0	4.52E-05	0	2	0.000116	0.000202	0	0.000172	0	0	0	1	4.3E-05	8.61E-05
1313	0	0	0	0.000144	0	1	3.6E-05	7.2E-05	0	0	0	9.97E-05	0.000391	2	0.000123	0.000185
1314	0	2.89E-05	0	0	0	1	7.23E-06	1.45E-05	0	0	0	8.09E-05	0.000523	2	0.000151	0.000251
1315	0	0.000346	0	0	0	1	8.64E-05	0.000173	0	0.000166	0	0.000121	0	2	7.18E-05	8.49E-05
1316	0	4.54E-05	0	0.000206	0	2	6.29E-05	9.79E-05	0	0	0	0.000381	0	1	9.53E-05	0.000191
1317	0	0.000242	0	0.000275	0	2	0.000129	0.00015	0	0.000116	0	0	0	1	2.91E-05	5.81E-05
1318	0	0.000194	0	0.000368	0	2	0.000141	0.000177	0	0	0	0.000068	0	1	0.000017	0.000034
1319	0	7.8E-05	0	5.91E-05	0	2	3.43E-05	4.03E-05	0	0	0	0.000491	0	1	0.000123	0.000246
1320	0	0.000246	0	0.000186	0	2	0.000108	0.000127	0	0.000189	0	0	0	1	4.73E-05	9.47E-05
1321	0	0	0	0.000265	0	1	6.63E-05	0.000133	0	0.000168	0	0.000184	0	2	8.8E-05	0.000102
1322	0	0.000103	0	0.000311	0	2	0.000104	0.000147	0	0.000198	0	0	0	1	4.94E-05	9.88E-05
1323	0	8.65E-05	0	0.000328	0	2	0.000104	0.000155	0	0	0	0.000182	0	1	4.54E-05	9.08E-05
1324	0	0.000105	0	0	0	1	2.63E-05	5.27E-05	0	5.06E-05	0	0	0.000433	2	0.000121	0.00021
1325	0	0.000138	0	0.000105	0	2	6.06E-05	7.13E-05	0	0	0	0	0.000341	1	8.52E-05	0.00017
1326	0	6.41E-05	0	9.71E-05	0	2	4.03E-05	4.84E-05	0	0	0	0	0.000422	1	0.000105	0.000211
1327	0	0	0	9.81E-05	0	1	2.45E-05	4.91E-05	0	0.000374	0	0	0.000107	2	0.00012	0.000176
1328	0	0.000129	0	9.77E-05	0	2	5.67E-05	6.67E-05	0	0.000347	0	0	0	1	8.69E-05	0.000174
1329	0	0	0	0	0	0	0	0	0	0.000175	0	0.000298	1E-04	3	0.000143	0.000125
1330	0	0	0	0.000149	0	1	3.73E-05	7.45E-05	0	9.47E-05	0	0	0.000324	2	0.000105	0.000153
1331	0.000308	0	0	3.36E-05	0	2	8.55E-05	0.000149	0	0.000213	0	0	0	1	5.33E-05	0.000107
1332	0	0.000121	0	0	0	1	3.04E-05	6.07E-05	0	0.000234	0	0	0.0002	2	0.000108	0.000126
1333	0	0	0	0.000164	0	1	4.11E-05	8.22E-05	0	0.000313	0	7.59E-05	0	2	9.72E-05	0.000148
1334	0	0	0	0.000222	0.000854	2	5.55E-05	0.000111	0	0	0	0	0.000322	1	8.05E-05	0.000161
1335	0	0	0	4.85E-05	0	1	1.21E-05	2.43E-05	0	0.000308	0	0.000179	0	2	0.000122	0.00015
1336	0	0.000179	0	0.000271	0	2	0.000112	0.000135	0	8.6E-05	0	0	0	1	2.15E-05	4.3E-05
1337	0.000399	0	0	0	0	1	9.99E-05	0.0002	0	0	0	4.02E-05	9.46E-05	2	3.37E-05	4.48E-05
1338	0	0.000312	0	3.93E-05	0	2	8.78E-05	0.00015	0	0	0	0.000182	0	1	4.54E-05	9.09E-05
1339	0	0	0	0.000305	0	1	7.63E-05	0.000153	0	0.000129	0	9.4E-05	0	2	5.58E-05	6.6E-05
1340	0	0.000228	0	0	0	1	5.69E-05	0.000114	0	0.000109	0	0	0.000187	2	7.42E-05	9.14E-05
1341	0	0	0	6.42E-05	0	1	1.61E-05	3.21E-05	0	0	0	0.000178	0.000279	2	0.000114	0.000138
1342	0.000394	0	0	8.57E-05	0	2	0.00012	0.000187	0	0	0	3.96E-05	0	1	9.9E-06	1.98E-05
1343	0	0.000287	0	0.000109	0	2	9.89E-05	0.000135	0	0	0	0	0.000118	1	2.95E-05	5.91E-05
1344	0	0.000133	0.000358	1.68E-05	0	3	0.000127	0.000165	0	0	0	0	0	0	0	0
1345	0	0	0	0.000151	0	1	3.79E-05	7.57E-05	0	0.000256	0	9.33E-05	0	2	8.74E-05	0.000121
1346	0	0.000257	0	0.000151	0	2	0.000102	0.000126	0	9.26E-05	0	0	0	1	2.31E-05	4.63E-05
1347	0	0.00041	0	3.88E-05	0	2	0.000112	0.000199	0	4.93E-05	0	0	0	1	1.23E-05	2.47E-05
1348	0	0	0	0.000112	0	1	2.8E-05	5.6E-05	0	0	0	0.000186	0.000195	2	9.53E-05	0.00011
1349	0	0	0	5.81E-05	0	1	1.45E-05	2.91E-05	0	0	0	5.37E-05	0.000379	2	0.000108	0.000182
1350	0	5.88E-05	0	4.45E-05	0	2	2.58E-05	3.04E-05	0	0	0	0	0.000387	1	9.67E-05	0.000193
1351	0	0	0	5.93E-05	0	1	1.48E-05	2.96E-05	0	0.000301	0	0	0.000129	2	0.000107	0.000143
1352	0	0.000266	0	0.000134	0	2	0.0001	0.000127	0	8.53E-05	0	0	0	1	2.13E-05	4.27E-05
1353	0	0	0	6.74E-05	0	1	1.69E-05	3.37E-05	0	4.28E-05	0	0.000374	0	2	0.000104	0.000181
1354	0	0	0	0.00016	0	1	4.01E-05	8.01E-05	0	0	0	0.000148	0.000174	2	8.05E-05	9.36E-05
1355	0	0.000206	0	7.8E-05	0	2	7.1E-05	9.72E-05	0	0.000198	0	0	0	1	4.95E-05	9.91E-05
1356	0	0	0	0	0	0	0	0	0	0.000144	0	0.000174	0.000164	3	0.00012	8.12E-05
1357	0	0	0	6.43E-05	0	1	1.61E-05	3.22E-05	0	0	0	6.44E-05	0.000348	2	0.000103	0.000166
1358	0	5.33E-05	0	0	0	1	1.33E-05	2.66E-05	0	0	0	0.000335	8.76E-05	2	0.000106	0.000159
1359	0.000382	0	0	0	0	1	9.54E-05	0.000191	0	5.28E-05	0	3.84E-05	0	2	2.28E-05	2.7E-05
1360	0	0	0	0.000297	0	1	7.42E-05	0.000148	0	7.61E-05	0	0	9.77E-05	2	4.34E-05	5.09E-05
1361	0	0	0	6.93E-05	0	1	1.73E-05	3.46E-05	0	0	0	0.000149	0.000251	2	0.0001	0.000123
1362	0	0	0	8.92E-05	0	1	2.23E-05	4.46E-05	0	0	0	8.24E-05	0.000291	2	9.33E-05	0.000137
1363	0	9.33E-05	0	7.07E-05	0	2	4.1E-05	4.82E-05	0	0	0	0.000294	0	1	7.34E-05	0.000147
1364	0	8.83E-05	0	0.000234	0	2	8.06E-05	0.000111	0	0.000127	0	0	0	1	3.19E-05	6.37E-05
1365	0	0.000119	0	4.49E-05	0	2	4.09E-05	5.6E-05	0	0.000285	0	0	0	1	7.14E-05	0.000143
1366	0	0	0	0.000136	0	1	3.39E-05	6.78E-05	0	0	0	0.000209	9.82E-05	2	7.67E-05	9.94E-05
1367	0	5.88E-05	0	0	0	1	1.47E-05	2.94E-05	0	0.000339	0	4.11E-05	0	2	9.5E-05	0.000164
1368	0	0.000161	0	0.000122	0	2	7.09E-05	8.34E-05	0	0.000155	0	0	0	1	3.88E-05	7.76E-05
1369	0	0.000232	0	0	0	1	5.79E-05	0.000116	0	4.56E-05	0	0	0.000156	2	5.04E-05	7.36E-05
1370	0	0	0	0.000216	0	1	5.4E-05	0.000108	0	0	0	9.98E-05	0.000117	2	5.43E-05	6.31E-05
1371	0	0.000258	0	4.89E-05	0	2	7.68E-05	0.000123	0	0.000124	0	0	0	1	3.11E-05	6.21E-05
1372	0	0	0	7.97E-05	0	1	1.99E-05	3.98E-05	0	0.000202	0	0.000147	0	2	8.74E-05	0.000103
1373	0.000252	0.000145	0	2.8E-05	0	3	0.000106	0.000116	0	0	0	0	0	0	0	0
1374	0	0	0.000296	6.97E-05	0	2	9.15E-05	0.00014	0	5.31E-05	0	0	0	1	1.33E-05	2.65E-05
1375	0	0.000199	0	7.55E-05	0	2	6.87E-05	9.41E-05	0	0	0	0.000139	0	1	3.49E-05	6.97E-05
1376	0	0.000131	0	0.000253	0	2	9.58E-05	0.000121	0	0	0	3.04E-05	0	1	7.61E-06	1.52E-05
1377	0	2.51E-05	0	0	0	1	6.28E-06	1.26E-05	0	9.66E-05	0	0	0.000289	2	9.65E-05	0.000136
1378	0	7.4E-05	0	0.000168	0	2	6.05E-05	7.97E-05	0	0.000166	0	0	0	1	4.15E-05	8.3E-05
1379	0	0.000144	0	0.000163	0	2	7.66E-05	8.89E-05	0	0	0	0.0001	0	1	2.51E-05	5.02E-05
1380	0	0.000164	0	0.000165	0	2	8.23E-05	9.51E-05	0	0	0	7.64E-05	0	1	1.91E-05	3.82E-05
1381	0	8.97E-05	0	0.000136	0	2	5.64E-05	6.78E-05	0	0.000173	0	0	0	1	4.31E-05	8.63E-05
1382	0	0	0	0.000187	0	1	4.68E-05	9.35E-05	0	0	0	0.000148	5.82E-05	2	5.16E-05	7.01E-05
1383	0	0.000216	0	4.76E-05	0	2	6.58E-05	0.000102	0	0.00013	0	0	0	1	3.25E-05	6.5E-05
1384	0	0	0	0.00021	0	1	5.26E-05	0.000105	0	0	0	0.000136	4.57E-05	2	4.54E-05	6.41E-05
1385	0	6.74E-05	0	0.000102	0	2	4.24E-05	5.09E-05	0	0	0	0	0.000222	1	5.55E-05	0.000111
1386	0	0.000158	0	0.000119	0	2	6.92E-05	8.15E-05	0	0	0	0.00011	0	1	2.76E-05	5.51E-05
1387	0	7.49E-05	0	0.000198	0	2	6.83E-05	9.37E-05	0	0	0	0.000105	0	1	2.62E-05	5.24E-05
1388	0	7.22E-05	0	0.000164	0	2	5.91E-05	7.78E-05	0	0.000139	0	0	0	1	3.47E-05	6.95E-05
1389	0	0.000221	0	2.09E-05	0	2	6.04E-05	0.000107	0	0.000133	0	0	0	1	3.32E-05	6.64E-05
1390	0	2.98E-05	0	0.000136	0	2	4.13E-05	6.43E-05	0	0	0	0.000209	0	1	5.22E-05	0.000104
1391	0	0	0	0.000292	0	1	7.29E-05	0.000146	0	0	0	2.45E-05	5.76E-05	2	2.05E-05	2.73E-05
1392	0	0	0	3.31E-05	0	1	8.27E-06	1.65E-05	0	0	0	0.000122	0.000216	2	8.45E-05	0.000105
1393	0	0	0	0.000106	0	1	2.66E-05	5.32E-05	0	0	0	3.28E-05	0.000231	2	6.6E-05	0.000111
1394	0	0.000147	0.000197	0	0	2	8.6E-05	0.000101	0	2.35E-05	0	0	0	1	5.89E-06	1.18E-05
1395	0	0.000119	0	0.000203	0	2	8.05E-05	9.91E-05	0	0	0	4.17E-05	0	1	1.04E-05	2.08E-05
1396	0	0	0	0.000121	0	1	3.01E-05	6.03E-05	0	0	0	0.000111	0.000131	2	6.06E-05	7.04E-05
1397	0	0	0	5.02E-05	0	1	1.25E-05	2.51E-05	0	0	0	9.27E-05	0.000218	2	7.77E-05	0.000103
1398	0	7.18E-05	0	0	0	1	1.79E-05	3.59E-05	0	0.000138	0	0.000151	0	2	7.22E-05	8.35E-05
1399	0	0	0	5.4E-05	0	1	1.35E-05	2.7E-05	0	6.86E-05	0	0	0.000235	2	7.58E-05	0.000111
1400	0.000233	0	0	1.27E-05	0	2	6.14E-05	0.000114	0	0	0	0	0.00011	1	2.76E-05	5.51E-05
1401	0	0	0	0	0	0	0	0	0	0.000107	0	0.000155	9.14E-05	3	8.84E-05	6.5E-05
1402	0	0.000207	0	0	0	1	5.17E-05	0.000103	0	3.31E-05	0	0	0.000113	2	3.66E-05	5.35E-05
1403	0	0.000141	0	0	0	1	3.53E-05	7.07E-05	0	9.06E-05	0	0	0.000116	2	5.17E-05	6.07E-05
1404	0	9.01E-05	0	3.41E-05	0	2	3.1E-05	4.25E-05	0	0	0	0	0.000222	1	5.56E-05	0.000111
1405	0	5.14E-05	0	3.89E-05	0	2	2.26E-05	2.66E-05	0	0	0	0	0.000254	1	6.34E-05	0.000127
1406	0	0	0	9.84E-05	0	1	2.46E-05	4.92E-05	0	0	0	0.000136	0.000107	2	6.08E-05	7.13E-05
1407	0	6.55E-05	0	0.000149	0	2	5.36E-05	7.06E-05	0	0.000126	0	0	0	1	3.15E-05	6.3E-05
1408	0	0	0	0.000155	0	1	3.88E-05	7.76E-05	0	5.91E-05	0	0.000119	0	2	4.46E-05	5.71E-05
1409	0	0	0	9.13E-05	0	1	2.28E-05	4.56E-05	0	0	0	4.22E-05	0.000198	2	6.01E-05	9.43E-05
1410	0	0.000144	0	0.000131	0	2	6.89E-05	7.97E-05	0	5.55E-05	0	0	0	1	1.39E-05	2.78E-05
1411	0	0	0	0	0	0	0	0	0	3.3E-05	0	0.000072	0.000226	3	8.27E-05	9.98E-05
1412	0	0.000174	0	0.000132	0	2	7.64E-05	8.98E-05	0	0	0	2.43E-05	0	1	6.08E-06	1.22E-05
1413	0	0.000147	0	7.44E-05	0	2	5.54E-05	7.06E-05	0	0	0	0.000103	0	1	2.58E-05	5.15E-05
1414	0	0	0	8.05E-05	0	1	2.01E-05	4.02E-05	0	2.56E-05	0	0	0.000219	2	6.1E-05	0.000106
1415	0	0.000166	0	4.2E-05	0	2	5.2E-05	7.86E-05	0	0	0	0.000116	0	1	2.91E-05	5.81E-05
1416	0.00022	3.16E-05	0	7.19E-05	0	3	8.09E-05	9.73E-05	0	0	0	0	0	0	0	0
1417	0	0	0	7.24E-05	0	1	1.81E-05	3.62E-05	0	0.000184	0	6.69E-05	0	2	6.27E-05	8.67E-05
1418	0	0	0	0.000125	0	1	3.13E-05	6.26E-05	0	0.000106	0	0	9.08E-05	2	4.92E-05	5.72E-05
1419	0	0	0	7.82E-05	0	1	1.95E-05	3.91E-05	0	9.93E-05	0	0.000144	0	2	6.09E-05	7.27E-05
1420	0	2.73E-05	0	0	0	1	6.83E-06	1.37E-05	0	0	0	0.000153	0.000135	2	7.19E-05	8.34E-05
1421	0	4.41E-05	0	0.0001	0	2	3.61E-05	4.75E-05	0	0.00017	0	0	0	1	4.24E-05	8.48E-05

rk	MMs										
	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
1275	0	0	0	0	0	0	0	0	eukaryotic Raf Kinase		ATP binding; lipid binding;
1276	0	0	0	0	0	0	0	0	EF-hand, calcium binding		calcium ion binding
1277	0	0	0	0	0	0	0	0	NAD dependent	cytoplasm [pmid 11698403]	coenzyme binding; electron
1278	0	0	0	0	0	0	0	0	RNA recognition motif.	heterogeneous nuclear	double-stranded DNA binding
1279	0	0	0	0	0	0	0	0	Plasminogen Activator	cytoplasm	serine-type endopeptidase
1280	0	0	0	0	0	0	0	0	RNA polymerase Rpb5, N-	DNA-directed RNA	DNA binding; DNA-directed
1281	0	0	0	0	0	0	0	0		integral to plasma membrane	G-protein coupled receptor
1282	0	0	0	0	0	0	0	0	Serine/Threonine protein	integral to membrane; nucleus	ATP binding [pmid 8566796];
1283	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus [pmid 14609955]	DNA-dependent ATPase
1284	0	0	0	0	0	0	0	0			
1285	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	COPI vesicle coat; cytoplasm;	binding; protein transporter
1286	0	0	0	0	0	0	0	0	CTP:phosphocholine	membrane; soluble fraction	choline-phosphate
1287	0	0	0	0	0	0	0	0			
1288	0	0	0	0	0.000111	0	0	0	Cytidylyltransferase. This	nucleus	N-acylneuraminate
1289	0	0	0	0	0	0	0	0	DnaB-like helicase C	cytosol [pmid 10524211];	ATP binding; ATP-dependent
1290	0	0	0	0	0	0	0	0	WD40 domain, found in a	kinetochore [pmid 9660858];	protein binding [pmid
1291	0	0	0	0	0.000109	0	0	0	AAA-superfamily of	cytoplasm; cytosol; nucleus;	ATP binding; hydrolase
1292	0	0	0	0	0	0	0	0		nucleus	
1293	0	0	0	0	0	0	0	0	PAAD/DAPIN/Pyrin domain.	nucleus	DNA binding
1294	0	0	0	0	0	0	0	0	PseudoU_synth_hDyskerin	nucleolus [pmid 10556300];	isomerase activity;
1295	0	0	0	0	0	0	0	0	Ribosome anti-association	nucleus [pmid 9374518]	protein binding [pmid
1296	0	0	0	0	0	0	0	0		nucleus	transferase activity
1297	0	0	0	0	0	0	0	0	Dimethyladenosine	nucleus	methyltransferase activity;
1298	0	0	0	0	0	0	0	0	DnaJ domain. DnaJ	nucleus	heat shock protein binding;
1299	0	0	0	0	0	0	0	0	Stress-induced morphogen		
1300	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; MAP kinase
1301	0	0	0	0	0	0	0	0			
1302	0	0	0	0	0	0	0	0	YchF subfamily. YchF is a	cytoplasm [pmid 11256614];	GTP binding; nucleotide
1303	0	0	0	0	0	0	0	0	Nucleosome assembly	endoplasmic reticulum [pmid	histone binding [pmid
1304	0	0	0	0	0	0	0	0		intracellular	double-stranded RNA binding
1305	0	0	0	0	0	0	0	0	Domain of unknown		
1306	0	0	0	0	0	0	0	0	Phosphoribosylpyrophosph		enzyme inhibitor activity
1307	0	0	0	0	0	0	0	0	Protein phosphatase 2A	integral to membrane [pmid	peptidase activity [pmid
1308	0	0	0	0	0	6.19E-05	0	0	GST_C family, Chloride	actin cytoskeleton [pmid	chloride ion binding; protein
1309	0	0	0	0	0	0	0	0			
1310	0	0	0	0	0	0	0	0	Leucine-rich repeats		transferase activity
1311	0	0	0	0	0	0	0	0	Rho4-like subfamily. Rho4	cytoskeleton [pmid	GTP binding; GTPase
1312	0	0	0	0	0	0	0	0	RBM1CTR (NUC064)	heterogeneous nuclear	nucleotide binding; protein
1313	0	0	0	0	0	0	0	0	pre-B-cell colony-enhancing		cytokine activity [pmid
1314	0	0	0	0	0	0	0	0	Domain I of the ABC		ATP binding [pmid 9790762];
1315	0	0	0	0	0	0	0	0			
1316	0	0	0	0	0	0	0	0	The CBS domain, named		IMP dehydrogenase activity
1317	0	0	0	0	0	0	0	0	Protein of unknown function		
1318	0	0	0	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus; ribonucleoprotein	RNA binding
1319	0	0	0	0	0	0	0	0	Ribonuclease HII [DNA	nucleus	endonuclease activity;
1320	0	0	0	0	0	0	0	0	SHC phosphotyrosine-	plasma membrane [pmid	insulin receptor binding [pmid
1321	0	0	0	0	0	0	0	0	Src homology 2 domains;		protein binding [pmid
1322	0	0	0	0	0	0	0	0	Protein-L-isoaspartate(D-	endoplasmic reticulum [pmid	methyltransferase activity;
1323	0	0	0	0	0	5.81E-05	0	0	TCP-1 (CTT or eukaryotic	cytoplasm	ATP binding; nucleotide
1324	0	0	0	0	0	0	0	0	Splicing factor 1 (SF1) K	membrane [pmid 1374686];	DNA binding [pmid 1374686];
1325	0	0	0	0	0	0	0	0	Activator of Hsp90 ATPase	cytoplasm; endoplasmic	ATPase stimulator activity;
1326	0	0	0	0	0	0	0	0	The developmentally	intracellular	GTP binding [pmid 7929244];
1327	0	0	0	0	0	0	0	0	Protein tyrosine	cytoplasm [pmid 7545170]	hydrolase activity; protein
1328	0	0	0	0	0	0	0	0	PWI domain; pfam01480	nucleus	DNA binding; RNA binding
1329	0	0	0	0	0	0	0	0	APOBEC-like N-terminal	nucleus	cytidine deaminase activity
1330	0	0	0	0	0	0	0	0	Phospholipase/Carboxylest		hydrolase activity
1331	0	0	0	0	0	0	0	0	Src homology 3 domains;	membrane	ATP binding; nucleotide
1332	0	0	0	0	0	0	0	0	Phosphomevalonate	cytoplasm; peroxisome [pmid	phosphomevalonate kinase
1333	0	0	0	0	0	0	0	0	Transcription factor	cytoplasm [pmid 8047162];	DNA binding
1334	0	0	0	0	0	0	0	0	EcAsnRS_like_N: N-	cytoplasm	asparagine-tRNA ligase
1335	0	0	0	0	0	0	0	0	Calponin homology (CH)	cytoskeleton	actin binding; protein binding
1336	0	0	0	0	0	0	0	0	Proliferating Cell Nuclear	DNA replication factor C	DNA binding; DNA
1337	0	0	0	0	0	0	0	0	PDIb' family, ERp44	endoplasmic reticulum;	electron carrier activity;
1338	0	0	0	0	0	0	0	0	Nuclear transport factor 2	cytoplasm [pmid 10969074];	nucleotide binding; receptor
1339	0	0	0	0	0	0	0	0	Importin beta binding	nucleus	binding; protein transporter
1340	0	0	0	0	0	0	0	0	alpha-crystallin-type heat	cell surface [pmid 12493773];	protein binding [pmid
1341	0	0	0	0	0	0	0	0	PLP dependent enzymes	cytoplasm [pmid 10496079];	
1342	0	0	0	0	0	0	0	0	Pleckstrin homology		insulin receptor binding;
1343	0	0	0	0	0	0	0	0	WD40 domain, found in a	eukaryotic translation	protein binding [pmid
1344	0	0	0	0	0	0	3.15E-05	0			
1345	0	0	0	0	0	0	0	0			
1346	0	0	0	0	0	0	0	0			
1347	0	0	0	0	0	0	0	0	Helicase superfamily c-	cytoplasm [pmid 11024137];	ATP binding; ATP-dependent
1348	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	nucleus [pmid 1426632]	binding
1349	0	0	0	0	0	0	0	0			
1350	0	0	0	0	0	0	0	0			
1351	0	0	0	0	0	0	0	0	Golgi phosphoprotein 3	membrane	
1352	0	0	0	0	0	0	0	0	Protein of unknown function	clathrin vesicle coat; coated	protein binding
1353	0	0	0	0	0	0	0	0	PAK (p21 activated kinase)		ATP binding; nucleotide
1354	0	0	0	0	0	0	0	0	SAM / Pointed domain; A	nucleus	sequence-specific DNA
1355	0	0	0	0	0	0	0	0	Snf7. This family of proteins		
1356	0	0	0	0	0	0	0	0	MA3 domain. Domain in	cytoplasm [pmid 16357133];	protein binding [pmid
1357	0	0	0	0	0	0	0	0	HEAT repeat. The HEAT	cytoplasm [pmid 9298975];	binding; nuclear localization
1358	0	0	0	0	0	0	0	0	Glutaryl-CoA	mitochondrion [pmid 8541831]	FAD binding; glutaryl-CoA
1359	0	0	0	0	0	0	0	0	RecF/RecN/SMC N	caveola; cytosol [pmid	phosphatidylserine binding
1360	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; MAP kinase
1361	0	0	0	0	0	0	0	0			
1362	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
1363	0	0	0	0	0	0	0	0	'SWI3, ADA2, N-CoR and	chromosome; chromosome,	DNA binding; protein binding
1364	0	0	0	0	0	0	0	0		nucleus	
1365	0	0	0	0	0	0	0	0	Glyco_18 domain;		catalytic activity; cation
1366	0	0	0	4.64E-05	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
1367	0	0	0	0	0	0	0	0			
1368	0	0	0	0	0	0	0	0			
1369	0	0	0	0	0	0	0	0	PAAD/DAPIN/Pyrin domain.		
1370	0	0	0	0	0	0	0	0	Predicted amidohydrolase		hydrolase activity, acting on
1371	0	0	0	0	0	0	0	0	Hydrolases of the		hydrolase activity
1372	0	0	0	0	0	0	0	0	Src homology 3 domains;	membrane; nucleus	kinase activity; protein
1373	0	0	0	0	0	0	0	0	Hsp70 protein. Hsp70		ATP binding; nucleotide
1374	0	0	0	0	0	0	0	0			
1375	0	0	0	0	0	0	0	0			
1376	0	0	0	0	0	0	0	0	Importin beta binding		binding; protein transporter
1377	0	0	0	0	0	0	0	0		extracellular space; integral to	binding; carrier activity
1378	0	0	0	0	0	0	0	0			
1379	0	0	0	0	0	0	0	0	Zinc-binding domain		metal ion binding; zinc ion
1380	0	0	0	0	0	0	0	0	Interferon Regulatory	nucleus	RNA polymerase II
1381	0	0	0	0	0	0	0	0	DnaJ domain. DnaJ		heat shock protein binding
1382	0	0	0	0	0	0	0	0			
1383	0	0	0	0	0	5.75E-05	0	0	LUC7 N_terminus. This		metal ion binding; zinc ion
1384	0	0	0	0	0	0	0	0	Hsp70 protein. Hsp70	cytoplasm	ATP binding [pmid 8335910];
1385	0	0	0	0	0	0	0	0	Ubiquitin activating enzyme	nucleus [pmid 10187858]	ATP-dependent protein
1386	0	0	0	0	0	0	0	0	MIT: domain contained	endosome [pmid 11563910];	ATP binding; ATPase
1387	0	0	0	0	0	0	0	0	Creatinase/Prolidase N-	cytoplasm	aminopeptidase activity;
1388	0	0	0	0	0	0	0	0	Phosphotyrosyl	protein phosphatase type 2A	phosphatase activator
1389	0	0	0	0	0	0	0	0	Src homology 3 domains;	intracellular; nucleus	diacylglycerol binding; metal
1390	0	0	0	0	0	0	0	0	RNA-metabolising metallo-	nucleus	RNA binding
1391	0	0	0	0	0	0	0	0	Grb7_RA The RA (RAS-	cytoskeleton	
1392	0	0	0	0	0	0	0	0	Ubiquitin activating enzyme	cytoplasm [pmid 8626687];	catalytic activity; ligase
1393	0	0	0	0	0	0	0	0			
1394	0	0	0	0	0	0	0	0	SAP domain. The SAP	nucleus	DNA binding; nucleotide
1395	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleolus [pmid 8614622];	ATP binding; ATP-dependent
1396	0	0	0	0	0	0	0	0	RNA recognition motif;	condensed nuclear	nucleotide binding; protein
1397	0	0	0	0	0	0	0	0	JAB/MPN domain; Domain	eukaryotic translation	protein binding [pmid
1398	0	0	0	0	0	0	0	0	Calcineurin-like	integral to membrane [pmid	acid phosphatase activity
1399	0	0	0	0	0	0	0	0	Protein of unknown function		
1400	0	0	0	2.62E-05	0	1.13E-05	2.35E-05	0		soluble fraction	enzyme regulator activity;
1401	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus [pmid 11256614];	nucleic acid binding;
1402	0	0	0	0	0	0	0	0	Opioid growth factor	membrane	opioid receptor activity [pmid
1403	0	0	0	0	0	0	0	0	Calcium/calmodulin	calcium- and calmodulin-	ATP binding; calcium- and
1404	0	0	0	0	0	0	0	0	Seryl-tRNA synthetase	mitochondrion [pmid	ATP binding [pmid
1405	0	0	0	0	0	0	0	0	SAM / Pointed domain; A	nucleus [pmid 9016666]	protein binding [pmid
1406	0	0	0	0	0	0	0	0	NeuB family. NeuB is the	cytoplasm [pmid 10749855]	N-acetylneuraminate
1407	0	0	0	0	0	0	0	0			
1408	0	0	0	0	0	0	0	0	Putative GTP-ase	nucleoplasm [pmid 10942595]	GTPase activator activity;
1409	0	0	0	0	0	0	0	0	AAA-superfamily of	cytoplasm; cytosol; nucleus;	ATP binding; ATPase activity
1410	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus	receptor signaling protein
1411	0	0	0	0	0	0	0	0	Mre11 DNA-binding	nucleoplasm [pmid 9651580];	3'-5' exonuclease activity
1412	0	0	0	0	0	0	0	0			
1413	0	0	0	0	0	0	0	0	hypothetical protein;		carboxypeptidase activity;
1414	0	0	0	0	0	0	0	0	Glycine cleavage T-protein	cytoplasm	aminomethyltransferase
1415	0	0	0	0	0	0	0	0	Zinc-binding domain		metal ion binding; zinc ion
1416	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; ATP-dependent
1417	0	0	0	0	0	0	0	0	CAP-Gly domain.	microtubule	protein binding [pmid
1418	0	0	0	0	0	0	0	0	PCI domain. This domain	nucleus; signalosome complex	protein binding [pmid
1419	0	0	0	0	0	0	0	0	SAM / Pointed domain; A	nucleus	sequence-specific DNA
1420	0	0	0	2.16E-05	0	0	3.88E-05	0	Macro domain, BAL_like	nucleus [pmid 11110709]	NAD+ ADP-
1421	0	0	0	0	0	0	0	0			

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW
1422	3	3.92E-05	0	0	INF		ENSG00000100982:E	C20orf67			gi|18034767|ref|NP_	phosphorylated CTD interact	704	80670
1423	3	3.9E-05	0	0	INF		ENSG00000115216:E	NRBP1			gi|7019333|ref|NP_0	nuclear receptor binding prot	535	59845
1424	3	3.89E-05	0	0	INF		ENSG00000132356:E	PRKAA1			gi|94557299|ref|NP_	protein kinase, AMP-activate	574	65523
1425	3	3.88E-05	0	0	INF		ENSG00000133789:E	SWP70			gi|93102364|ref|NP_	SWAP-70 protein [Homo sap	585	68998
1426	3	3.86E-05	0	0	INF		ENSG00000083896:E	YTHDC1			gi|72534750|ref|NP_	splicing factor YT521-B isofo	727	84700
1427	3	3.84E-05	0	0	INF		ENSG00000129675:E	ARHGEF6			gi|22027525|ref|NP_	Rac/Cdc42 guanine nucleotic	776	87499
1428	3	3.84E-05	1	3.85E-06	9.964984		ENSG00000116120:E	FARSB			gi|124028525|ref|NP	phenylalanyl-tRNA synthetas	589	66116
1429	3	3.78E-05	0	0	INF		ENSG00000108010:E	GLRX3			gi|95113651|ref|NP_	glutaredoxin 3 [Homo sapien	335	37432
1430	3	3.74E-05	0	0	INF		ENSG00000028528:E	SNX1			gi|23111032|ref|NP_	sorting nexin 1 isoform b [Ho	457	51813
1431	3	3.72E-05	0	0	INF		ENSG00000155961:E	RAB39B			gi|25188193|ref|NP_	RAB39B, member RAS onco	213	24622
1432	3	3.71E-05	0	0	INF		ENSG00000143889:E	HNRPLL			gi|20149709|ref|NP_	heterogeneous nuclear ribon	542	60083
1433	3	3.71E-05	0	0	INF		ENSG00000119471:E	HSDL2			gi|40254986|ref|NP_	hydroxysteroid dehydrogena	418	45395
1434	3	3.67E-05	0	0	INF		ENSG00000068079:E	IFI35			gi|24307901|ref|NP_	interferon-induced protein 35	288	31745
1435	3	3.59E-05	0	0	INF		ENSG00000196139:E	AKR1C3			gi|24497583|ref|NP_	aldo-keto reductase family 1,	323	36853
1436	3	3.57E-05	0	0	INF		ENSG00000168066:E	SF1			gi|42544123|ref|NP_	splicing factor 1 isoform 3 [H	548	59712
1437	3	3.56E-05	0	0	INF		ENSG00000115808:E	STRN			gi|51242945|ref|NP_	striatin, calmodulin binding p	780	86132
1438	3	3.54E-05	0	0	INF		ENSG00000104897:E	SF3A2			gi|21361376|ref|NP_	splicing factor 3a, subunit 2 [	464	49256
1439	3	3.52E-05	0	0	INF		ENSG00000185875:E	THNSL1			gi|153792148|ref|NP	threonine synthase-like 1 [Ho	743	83070
1440	3	3.48E-05	0	0	INF		ENSG00000198218:E	QRICH1			gi|38570099|ref|NP_	glutamine-rich 1 [Homo sapie	776	86436
1441	3	3.48E-05	0	0	INF		ENSG00000143409:E	FAM63A			gi|31377841|ref|NP_	hypothetical protein LOC557	469	51805
1442	3	3.47E-05	0	0	INF		ENSG00000104419:E	NDRG1			gi|37655183|ref|NP_	N-myc downstream regulated	394	42835
1443	3	3.47E-05	0	0	INF		ENSG00000164916:E	FOXK1			gi|82546824|ref|NP_	forkhead box K1 [Homo sapi	733	75457
1444	3	3.46E-05	0	0	INF		ENSG00000147416:E	ATP6V1B2			gi|19913428|ref|NP_	vacuolar H+ATPase B2 [Hon	511	56501
1445	3	3.43E-05	0	0	INF		ENSG00000138594:E	TMOD3			gi|7657649|ref|NP_0	tropomodulin 3 (ubiquitous) [	352	39595
1446	3	3.43E-05	0	0	INF		ENSG00000178685:E	PARP10			gi|157738665|ref|NP	poly (ADP-ribose) polymeras	1025	109998
1447	3	3.41E-05	0	0	INF		ENSG00000027075:E	PRKCH			gi|28557781|ref|NP_	protein kinase C, eta [Homo	683	77829
1448	3	3.36E-05	0	0	INF		ENSG00000137996:E	RTCD1			gi|4506589|ref|NP_0	RNA terminal phosphate cyc	366	39337
1449	3	3.3E-05	0	0	INF		ENSG00000120868:E	APAF1			gi|32483359|ref|NP_	apoptotic peptidase activating	1248	141840
1450	3	3.29E-05	1	5.78E-06	5.693317		ENSG00000142864:E	SERBP1			gi|66346679|ref|NP_	SERPINE1 mRNA binding pr	408	44965
1451	3	3.27E-05	0	0	INF		ENSG00000012223:E	LTF			gi|54607120|ref|NP_	lactotransferrin [Homo sapien	710	78182
1452	3	3.27E-05	0	0	INF		ENSG00000134684:E	YARS			gi|4507947|ref|NP_0	tyrosyl-tRNA synthetase [Hon	528	59144
1453	3	3.26E-05	0	0	INF		ENSG00000163510:E	KIAA1604			gi|55749769|ref|NP_	hypothetical protein LOC577	908	105466
1454	3	3.24E-05	0	0	INF		ENSG00000121390:E	PSPC1			gi|109240550|ref|NP	paraspeckle protein 1 [Homo	523	58744
1455	3	3.21E-05	0	0	INF		ENSG00000214122:E	PPP2R2A			gi|4506019|ref|NP_0	alpha isoform of regulatory s	447	51692
1456	3	3.21E-05	0	0	INF		ENSG00000100034:E	PPM1F			gi|7661862|ref|NP_0	protein phosphatase 1F [Hon	454	49831
1457	3	3.2E-05	0	0	INF		ENSG00000196943:E	C14orf21			gi|28212272|ref|NP_	hypothetical protein LOC161	636	69438
1458	3	3.18E-05	1	4.39E-06	7.238315		ENSG00000070814:E	TCOF1			gi|57164975|ref|NP_	Treacher Collins-Francesche	1411	144314
1459	3	3.16E-05	0	0	INF		ENSG00000168397:E	LOC727737			gi|113413583|ref|XP	PREDICTED: similar to APG	380	42622
1460	3	3.16E-05	0	0	INF		ENSG00000182196:E	ARL6IP4			gi|50409691|ref|NP_	SRp25 nuclear protein isofor	338	36211
1461	3	3.13E-05	0	0	INF		ENSG00000083750:E	RRAGB			gi|46249395|ref|NP_	Ras-related GTP binding B s	346	40172
1462	3	3.12E-05	0	0	INF		ENSG00000047249:E	ATP6V1H			gi|47717100|ref|NP_	ATPase, H+ transporting, lys	465	54151
1463	3	3.11E-05	0	0	INF		ENSG00000160633:E	SAFB			gi|21264343|ref|NP_	scaffold attachment factor B	915	102642
1464	3	3.08E-05	0	0	INF		ENSG00000196591:E	HDAC2			gi|116284376|ref|NP	histone deacetylase 2 [Homo	582	65538
1465	3	3.07E-05	0	0	INF		ENSG00000173757:E	STAT5B			gi|21618344|ref|NP_	signal transducer and activat	787	89866
1466	3	3.07E-05	0	0	INF		ENSG00000096063:N	SRPK1			gi|47419936|ref|NP_	SFRS protein kinase 1 [Hom	655	74325
1467	3	3.07E-05	0	0	INF		ENSG00000149499:E	EML3			gi|110227615|ref|NP	echinoderm microtubule ass	896	95197
1468	3	3.06E-05	0	0	INF		ENSG00000145220:E	LYAR			gi|8923398|ref|NP_0	Ly1 antibody reactive homol	379	43634
1469	3	3.03E-05	0	0	INF		ENSG00000137776:E	SLTM			gi|62244004|ref|NP_	modulator of estrogen induce	1016	115409
1470	3	3.03E-05	0	0	INF		ENSG00000139613:E	SMARCC2			gi|21237805|ref|NP_	SWI/SNF-related matrix-ass	1214	132879
1471	3	3.01E-05	0	0	INF		ENSG00000102572:E	STK24			gi|110349738|ref|NP	serine/threonine kinase 24 is	431	47913
1472	3	2.99E-05	0	0	INF		ENSG00000114861:E	FOXP1			gi|18644886|ref|NP_	forkhead box P1 isoform 1 [H	677	75317
1473	3	2.98E-05	0	0	INF		ENSG00000180198:E	RCC1			gi|114796644|ref|NP	regulator of chromosome co	452	48146
1474	3	2.9E-05	0	0	INF		ENSG00000101096:E	NFATC2			gi|27886539|ref|NP_	nuclear factor of activated T-	921	99784
1475	3	2.89E-05	1	1.82E-06	15.92233		ENSG00000153207:E	AHCTF1P			gi|67551265|ref|NP_	transcription factor ELYS [Ho	2266	252496
1476	3	2.87E-05	0	0	INF		ENSG00000158290:E	CUL4B			gi|121114298|ref|NP	cullin 4B isoform 1 [Homo sa	913	103982
1477	3	2.84E-05	0	0	INF		ENSG00000118007:E	STAG1			gi|62243696|ref|NP_	stromal antigen 1 [Homo sap	1258	144427
1478	3	2.8E-05	0	0	INF		ENSG00000144589:E	STK11IP			gi|116235474|ref|NP	LKB1 interacting protein [Hor	1099	121401
1479	3	2.8E-05	0	0	INF		ENSG00000172939:E	OXSR1			gi|4826878|ref|NP_0	oxidative-stress responsive 1	527	58022
1480	3	2.78E-05	0	0	INF		ENSG00000160752:E	FDPS			gi|4503685|ref|NP_0	farnesyl diphosphate synthas	419	48276
1481	3	2.77E-05	0	0	INF		ENSG00000089639:E	GMIP			gi|91208437|ref|NP_	GEM interacting protein [Hor	970	106683
1482	3	2.69E-05	0	0	INF		ENSG00000166189:E	HPS6			gi|31881785|ref|NP_	Hermansky-Pudlak syndrome	775	82975
1483	3	2.63E-05	0	0	INF		ENSG00000090989:E	EXOC1			gi|30410716|ref|NP_	Sec3 isoform 2 [Homo sapier	879	100283
1484	3	2.58E-05	0	0	INF		ENSG00000162777:E	DENND2D			gi|21361991|ref|NP_	DENN/MADD domain contai	471	53672
1485	3	2.56E-05	0	0	INF		ENSG00000169220:E	RGS14			gi|21361304|ref|NP_	regulator of G-protein signalli	566	61447
1486	3	2.56E-05	0	0	INF		ENSG00000109111:E	SUPT6H			gi|27597090|ref|NP_	suppressor of Ty 6 homolog	1726	199071
1487	3	2.53E-05	0	0	INF		ENSG00000154305:E	MIA3			gi|122891870|ref|NP	melanoma inhibitory activity f	1907	213700
1488	3	2.53E-05	0	0	INF		ENSG00000178127:E	NDUFV2			gi|10835025|ref|NP_	NADH dehydrogenase (ubiqu	249	27364
1489	3	2.47E-05	0	0	INF		ENSG00000092621:E	PHGDH			gi|23308577|ref|NP_	phosphoglycerate dehydroge	533	56651
1490	3	2.46E-05	0	0	INF		ENSG00000197122:E	SRC			gi|38202217|ref|NP_	proto-oncogene tyrosine-prot	536	59835
1491	3	2.45E-05	0	0	INF		ENSG00000152256:E	PDK1			gi|4505689|ref|NP_0	pyruvate dehydrogenase kina	436	49244
1492	3	2.43E-05	0	0	INF		ENSG00000110321:E	EIF4G2			gi|110630018|ref|NP	eukaryotic translation initiatio	869	98150
1493	3	2.39E-05	0	0	INF		ENSG00000166477:E	LEO1			gi|20270337|ref|NP_	Leo1, Paf1/RNA polymerase	666	75404
1494	3	2.38E-05	0	0	INF		ENSG00000042088:E	TDP1			gi|57242805|ref|NP_	tyrosyl-DNA phosphodiestera	608	68420
1495	3	2.38E-05	0	0	INF		ENSG00000138442:E	WDR12			gi|16445424|ref|NP_	WD repeat domain 12 protei	423	47544
1496	3	2.34E-05	0	0	INF		ENSG00000067900:E	ROCK1			gi|4885583|ref|NP_0	Rho-associated, coiled-coil c	1354	158174
1497	3	2.33E-05	0	0	INF		ENSG00000140829:E	DHX38			gi|17999539|ref|NP_	DEAH (Asp-Glu-Ala-His) box	1227	140502
1498	3	2.31E-05	0	0	INF		ENSG00000170759:E	KIF5B			gi|4758648|ref|NP_0	kinesin family member 5B [H	963	109685
1499	3	2.29E-05	0	0	INF		ENSG00000105639:E	JAK3			gi|47157315|ref|NP_	Janus kinase 3 [Homo sapier	1124	125099
1500	3	2.29E-05	0	0	INF		ENSG00000180228:E	PRKRAP1			gi|4505581|ref|NP_0	protein kinase, interferon-ind	313	34404
1501	3	2.27E-05	0	0	INF		ENSG00000134987:E	WDR36			gi|21281677|ref|NP_	WD repeat domain 36 [Homo	951	105322
1502	3	2.21E-05	0	0	INF		ENSG00000196497:E	IPO4			gi|62460637|ref|NP_	importin 4 [Homo sapiens]	1081	118715
1503	3	2.16E-05	0	0	INF		ENSG00000096696:N	DSP			gi|58530840|ref|NP_	desmoplakin isoform I [Homo	2871	331774
1504	3	2.14E-05	0	0	INF		ENSG00000145715:E	RASA1			gi|12545406|ref|NP_	RAS p21 protein activator 1 i	870	100398
1505	3	2.14E-05	0	0	INF		ENSG00000105287:E	PRKD2			gi|120659785|ref|NP	protein kinase D2 isoform A [	878	96722
1506	3	2.13E-05	0	0	INF		ENSG00000124789:E	NUP153			gi|24430146|ref|NP_	nucleoporin 153kDa [Homo s	1475	153938
1507	3	2.06E-05	0	0	INF		ENSG00000196504:E	PRPF40A			gi|151301228|ref|NP	formin binding protein 3 [Hon	930	105927
1508	3	2.05E-05	0	0	INF		ENSG00000109805:E	NCAPG			gi|21359945|ref|NP_	chromosome condensation p	1015	114334
1509	3	2.04E-05	0	0	INF		ENSG00000114098:E	ARMC8			gi|32526896|ref|NP_	armadillo repeat containing 8	659	73994
1510	3	2.03E-05	0	0	INF		ENSG00000127084:E	FGD3			gi|134133265|ref|NP	FYVE, RhoGEF and PH dom	725	79401
1511	3	2E-05	0	0	INF		ENSG00000120437:E	ACAT2			gi|148539872|ref|NP	acetyl-Coenzyme A acetyltra	397	41351
1512	3	2E-05	0	0	INF		ENSG00000140598:N	EFTUD1			gi|94966752|ref|NP_	elongation factor Tu GTP bin	1069	119887
1513	3	1.96E-05	0	0	INF		ENSG00000170727:E	LOC727967			gi|169172744|ref|XP	PREDICTED: hypothetical pr	771	86489
1514	3	1.9E-05	0	0	INF		ENSG00000108839:E	ALOX12			gi|154426292|ref|NP	arachidonate 12-lipoxygenas	663	75694
1515	3	1.9E-05	0	0	INF		ENSG00000185085:E	INTS5			gi|44771201|ref|NP_	integrator complex subunit 5	1019	107995
1516	3	1.88E-05	0	0	INF		ENSG00000113593:E	PPWD1			gi|24308049|ref|NP_	peptidylprolyl isomerase dom	646	73575
1517	3	1.86E-05	0	0	INF		ENSG00000065413:E	ANKRD44			gi|24233530|ref|NP_	ankyrin repeat domain 44 [H	919	99819
1518	3	1.83E-05	0	0	INF		ENSG00000120254:E	MTHFD1L			gi|36796743|ref|NP_	methylenetetrahydrofolate de	978	105790
1519	3	1.82E-05	0	0	INF		ENSG00000111596:E	CNOT2			gi|7657385|ref|NP_0	CCR4-NOT transcription con	540	59738
1520	3	1.77E-05	0	0	INF		ENSG00000086827:E	ZW10			gi|4759344|ref|NP_0	centromere/kinetochore prote	779	88830
1521	3	1.75E-05	0	0	INF		ENSG00000141279:E	NPEPPS			gi|15451907|ref|NP_	aminopeptidase puromycin s	875	98503
1522	3	1.75E-05	0	0	INF		ENSG00000138035:E	PNPT1			gi|24308348|ref|NP_	polyribonucleotide nucleotidy	783	85937
1523	3	1.72E-05	0	0	INF		ENSG00000172053:E	QARS			gi|4826960|ref|NP_0	glutaminyl-tRNA synthetase [	775	87799
1524	3	1.68E-05	0	0	INF		ENSG00000102038:E	SMARCA1			gi|21071044|ref|NP_	SWI/SNF-related matrix-ass	1054	122605
1525	3	1.68E-05	0	0	INF		ENSG00000198700:E	IPO9			gi|21361659|ref|NP_	importin 9 [Homo sapiens]	1041	115963
1526	3	1.66E-05	0	0	INF		ENSG00000135597:E	REPS1			gi|39812394|ref|NP_	RALBP1 associated Eps don	743	80698
1527	3	1.66E-05	0	0	INF		ENSG00000076513:E	ANKRD13A			gi|38683799|ref|NP_	ankyrin repeat domain 13 [H	590	67619
1528	3	1.64E-05	0	0	INF		ENSG00000167632:E	TRAPPC9			gi|40255276|ref|NP_	NIK and IKK(beta) binding pr	1246	139423
1529	3	1.56E-05	0	0	INF		ENSG00000128815:E	C10orf64			gi|169194808|ref|XP	PREDICTED: similar to hCG	3184	353625
1530	3	1.52E-05	0	0	INF		ENSG00000121749:E	TBC1D15			gi|21362084|ref|NP_	TBC1 domain family, membe	691	79461
1531	3	1.5E-05	0	0	INF		ENSG00000177613:E	CSTF2T			gi|14149675|ref|NP_	cleavage stimulation factor, 3	616	64436
1532	3	1.49E-05	0	0	INF		ENSG00000143374:E	TARS2			gi|20070344|ref|NP_	threonyl-tRNA synthetase 2,	718	81036
1533	3	1.49E-05	0	0	INF		ENSG00000062822:E	POLD1			gi|156616275|ref|NP	polymerase (DNA directed),	1107	123631
1534	3	1.48E-05	1	2.08E-06	7.152784		ENSG00000112249:E	ASCC3			gi|76880486|ref|NP_	activating signal cointegrator	2202	251458
1535	3	1.48E-05	0	0	INF		ENSG00000182872:E	RBM10			gi|20127479|ref|NP_	RNA binding motif protein 10	930	103533
1536	3	1.45E-05	0	0	INF		ENSG00000103549:E	RNF40			gi|7662230|ref|NP_0	ring finger protein 40 [Homo	1001	113678
1537	3	1.45E-05	0	0	INF		ENSG00000164944:E	KIAA1429			gi|33946282|ref|NP_	hypothetical protein LOC259	1812	202023
1538	3	1.44E-05	0	0	INF		ENSG00000121486:E	C1orf25			gi|30181238|ref|NP_	N2,N2-dimethylguanosine tR	733	81790
1539	3	1.43E-05	0	0	INF		ENSG00000068796:E	KIF2A			gi|148612849|ref|NP	kinesin heavy chain member	744	84089
1540	3	1.43E-05	0	0	INF		ENSG00000197548:E	ATG7			gi|5453668|ref|NP_0	APG7 autophagy 7-like [Hom	703	77960
1541	3	1.43E-05	0	0	INF		ENSG00000096401:E	CDC5L			gi|11067747|ref|NP_	CDC5-like [Homo sapiens]	802	92251
1542	3	1.43E-05	0	0	INF		ENSG00000204209:E	DAXX			gi|4503257|ref|NP_0	death-associated protein 6 [H	740	81373
1543	3	1.42E-05	0	0	INF		ENSG00000130475:E	FCHO1			gi|29789054|ref|NP_	FCH domain only 1 [Homo s	889	96861
1544	3	1.42E-05	0	0	INF		ENSG00000079263:E	SP140			gi|52487219|ref|NP_	SP140 nuclear body protein	867	98286
1545	3	1.37E-05	0	0	INF		ENSG00000085224:E	LOC728849			gi|169216549|ref|XP	PREDICTED: similar to putat	2494	282912
1546	3	1.36E-05	0	0	INF		ENSG00000167615:E	LENG8			gi|24308382|ref|NP_	leukocyte receptor cluster (L	800	88157
1547	3	1.31E-05	0	0	INF		ENSG00000065183:E	WDR3			gi|5803221|ref|NP_0	WD repeat-containing protein	943	106099
1548	3	1.3E-05	0	0	INF		ENSG00000135905:E	DOCK10			gi|154146189|ref|NP	dedicator of cytokinesis 10 [H	2186	249529
1549	3	1.27E-05	0	0	INF		ENSG00000120915:E	EPHX2			gi|27597073|ref|NP_	epoxide hydrolase 2, cytopla	555	62616
1550	3	1.27E-05	0	0	INF		ENSG00000124228:E	DDX27			gi|19743937|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	796	89865
1551	3	1.24E-05	0	0	INF		ENSG00000114867:E	EIF4G1			gi|38201619|ref|NP_	eukaryotic translation initiatio	1403	154804
1552	3	1.2E-05	0	0	INF		ENSG00000166887:E	VPS39			gi|54234024|ref|NP_	vacuolar protein sorting 39 [H	875	100769
1553	3	1.19E-05	0	0	INF		ENSG00000176783:E	RUFY1			gi|94721332|ref|NP_	RUN and FYVE domain-cont	600	69078
1554	3	1.18E-05	0	0	INF		ENSG00000180900:E	SCRIB			gi|45827729|ref|NP_	scribble isoform b [Homo sap	1630	174930
1555	3	1.18E-05	0	0	INF		ENSG00000180917:E	FTSJD1			gi|153792086|ref|NP	hypothetical protein LOC557	770	88120
1556	3	1.15E-05	0	0	INF		ENSG00000170471:E	KIAA1219			gi|34787409|ref|NP_	hypothetical protein LOC571	1494	166798
1557	3	1.15E-05	0	0	INF		ENSG00000145041:E	VPRBP			gi|7662316|ref|NP_0	VprBP protein [Homo sapien	1507	169007
1558	3	1.13E-05	0	0	INF		ENSG00000130816:E	DNMT1			gi|4503351|ref|NP_0	DNA (cytosine-5-)-methyltrar	1616	183164
1559	3	1.11E-05	0	0	INF		ENSG00000114374:E	LOC100130216			gi|169216129|ref|XP	PREDICTED: hypothetical pr	2555	291075
1560	3	1.11E-05	0	0	INF		ENSG00000174485:E	DENND4A			gi|125628677|ref|NP	DENN/MADD domain contai	1863	209227
1561	3	1.1E-05	0	0	INF		ENSG00000176986:E	SEC24C			gi|38373671|ref|NP_	SEC24-related protein C [Ho	1094	118325
1562	3	1.07E-05	0	0	INF		ENSG00000137145:E	DENND4C			gi|94818781|ref|NP_	DENN/MADD domain contai	1673	186856
1563	3	1.01E-05	0	0	INF		ENSG00000137628:E	DDX60			gi|29725619|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	1712	197824
1564	3	9.98E-06	0	0	INF		ENSG00000196367:E	TRRAP			gi|4507691|ref|NP_0	transformation/transcription c	3830	434416
1565	3	9.85E-06	0	0	INF		ENSG00000164941:E	INTS8			gi|70608109|ref|NP_	integrator complex subunit 8	995	113088
1566	3	9.75E-06	0	0	INF		ENSG00000131375:E	CAPN7			gi|7656959|ref|NP_0	calpain 7 [Homo sapiens]	813	92652
1567	3	9.66E-06	0	0	INF		ENSG00000156802:E	ATAD2			gi|24497618|ref|NP_	ATPase family, AAA domain	1390	158554
1568	3	9.49E-06	0	0	INF		ENSG00000153064:E	BANK1			gi|144953889|ref|NP	B-cell scaffold protein with ar	755	86460

rk	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S=signal; A=Anchor; Q=none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	RESTING LYMPHOCYTES NEs: HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	PHA-TREATED LYMPHOCYTES NEs: HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
1422	7.4	0	o	Q	27	0	0	0	0	5.02E-05	0	1	1.25E-05	2.51E-05	0	0	0	0.000209	5.45E-05	2	6.58E-05	9.86E-05
1423	5.1	0	o	Q	41	0	0	0	0	6.6E-05	0	1	1.65E-05	3.3E-05	0	0	0	3.05E-05	0.000215	2	6.14E-05	0.000104
1424	8.2	0	o	Q	40	0	0	0	0	9.23E-05	0	1	2.31E-05	4.62E-05	0	0	0	8.53E-05	0.000134	2	5.48E-05	6.63E-05
1425	5.9	0	o	Q	25	0.005	0	0	0	3.02E-05	0	1	7.55E-06	1.51E-05	0	0	0	8.37E-05	0.000197	2	7.01E-05	9.32E-05
1426	6.2	0	o	Q	0	0	0	0	0	7.29E-05	0	1	1.82E-05	3.64E-05	0	0.000123	0	0.000112	0	2	5.89E-05	6.82E-05
1427	6	0	o	Q	26	0.136	0	0	0	0.000137	0	1	3.41E-05	6.83E-05	0	8.67E-05	0	8.41E-05	0	2	4.27E-05	4.93E-05
1428	6.8	0	o	Q	21	0.002	0	0.000119	0	0.00015	0	2	6.72E-05	7.86E-05	0	3.81E-05	0	0	0	1	9.52E-06	1.9E-05
1429	5.4	0	o	Q	19	0.182	0	0.000139	0	0	0	1	3.48E-05	6.96E-05	0	0	0	4.87E-05	0.000115	2	4.08E-05	5.43E-05
1430	5.6	0	o	Q	16	0	0	0	0	0.000116	0	1	2.9E-05	5.8E-05	0	0.000147	0	3.57E-05	0	2	4.57E-05	6.97E-05
1431	7.8	0	o	Q	21	0.033	0	0.00011	0	8.29E-05	0	2	4.81E-05	5.66E-05	0	0.000105	0	0	0	1	2.63E-05	5.27E-05
1432	7.7	0	o	Q	0	0	0	0	0	0.000196	0	1	4.89E-05	9.78E-05	0	4.14E-05	0	6.02E-05	0	2	2.54E-05	3.03E-05
1433	8	0	o	S	22	0.544	0	0	0	0.000127	0	1	3.17E-05	6.34E-05	0	0	0	7.81E-05	9.18E-05	2	4.25E-05	4.94E-05
1434	6.1	0	o	Q	18	0.001	0	8.1E-05	0	0	0	1	2.02E-05	4.05E-05	0	0.000156	0	5.67E-05	0	2	5.31E-05	7.35E-05
1435	7.9	0	o	Q	26	0	0	7.22E-05	0	0.000164	0	2	5.91E-05	7.78E-05	0	0	0	5.05E-05	0	1	1.26E-05	2.53E-05
1436	9.5	0	o	Q	46	0	0	0	0	3.22E-05	0	1	8.06E-06	1.61E-05	0	0.000164	0	8.93E-05	0	2	6.33E-05	7.91E-05
1437	5.3	0	o	Q	40	0.002	0	2.99E-05	0	0.000226	0	2	6.41E-05	0.000109	0	2.88E-05	0	0	0	1	7.19E-06	1.44E-05
1438	9.6	0	o	Q	23	0	0	0	0	0.000152	0	1	3.81E-05	7.61E-05	0	4.84E-05	0	0	8.27E-05	2	3.28E-05	4.04E-05
1439	7.1	0	o	Q	30	0	0	3.14E-05	0	0	0	1	7.85E-06	1.57E-05	0	0	0	4.39E-05	0.000207	2	6.26E-05	9.82E-05
1440	5.9	0	o	Q	20	0	0	0	0	2.28E-05	0	1	5.69E-06	1.14E-05	0	5.78E-05	0	0	0.000198	2	6.39E-05	9.34E-05
1441	4.9	0	o	Q	30	0	0	0	0	0.000113	0	1	2.82E-05	5.65E-05	0	9.57E-05	0	6.96E-05	0	2	4.13E-05	4.89E-05
1442	5.8	0	o	Q	0	0	0	0	0	0.000179	0	1	4.48E-05	8.97E-05	0	5.69E-05	0	4.14E-05	0	2	2.46E-05	2.91E-05
1443	9.3	0	o	S	45	0.984	0	9.55E-05	0	4.82E-05	0	2	3.59E-05	4.57E-05	0	0	0	0.000134	0	1	3.34E-05	6.68E-05
1444	5.8	0	o	Q	28	0.01	0	4.56E-05	0	0.000104	0	2	3.73E-05	4.92E-05	0	0	0	0.000128	0	1	3.19E-05	6.39E-05
1445	5.2	0	o	Q	0	0	0	0	0	0.0001	0	1	2.51E-05	5.02E-05	0	0.000127	0	4.64E-05	0	2	4.35E-05	6.01E-05
1446	5	0	o	Q	18	0.004	0	9.1E-05	0	0.000103	0	2	4.86E-05	5.64E-05	0	0	0	7.96E-05	0	1	1.99E-05	3.98E-05
1447	7.8	0	o	Q	29	0	0	0.000137	0	0	0	1	3.41E-05	6.83E-05	0	0	0	2.39E-05	0.000112	2	3.41E-05	5.34E-05
1448	7.9	0	o	Q	42	0.011	0	0.000127	0	9.65E-05	0	2	5.6E-05	6.59E-05	0	0	0	4.46E-05	0	1	1.11E-05	2.23E-05
1449	6.4	0	o	Q	16	0	0	0	0	5.66E-05	0	1	1.42E-05	2.83E-05	0	5.39E-05	0	0	0.000154	2	5.19E-05	7.25E-05
1450	8.6	0	o	Q	21	0	0	0.000114	0	0	0	1	2.86E-05	5.72E-05	0	5.5E-05	0	0	9.41E-05	2	3.73E-05	4.59E-05
1451	8.1	0	o	S	20	1	0	9.86E-05	0	9.95E-05	0	2	4.95E-05	5.72E-05	0	6.32E-05	0	0	0	1	1.58E-05	3.16E-05
1452	7	0	o	Q	24	0	0	0.000133	0	6.69E-05	0	2	4.99E-05	6.35E-05	0	0	0	6.18E-05	0	1	1.55E-05	3.09E-05
1453	7	0	o	Q	14	0	0	0.000205	0	1.95E-05	0	2	5.62E-05	9.99E-05	0	0	0	3.59E-05	0	1	8.99E-06	1.8E-05
1454	6.7	0	o	Q	49	0.107	0	4.46E-05	0	6.75E-05	0	2	2.8E-05	3.37E-05	0	0	0	0	0.000147	1	3.67E-05	7.34E-05
1455	6.2	0	o	Q	20	0	0	5.22E-05	0	0.000119	0	2	4.27E-05	5.62E-05	0	0	0	0	8.59E-05	1	2.15E-05	4.29E-05
1456	5.1	0	o	Q	22	0	0	5.14E-05	0	0.000156	0	2	5.18E-05	7.34E-05	0	4.94E-05	0	0	0	1	1.24E-05	2.47E-05
1457	7.3	0	o	Q	0	0	0	0.000147	0	8.33E-05	0	2	5.75E-05	7.13E-05	0	0	0	2.57E-05	0	1	6.42E-06	1.28E-05
1458	9	0	o	Q	27	0.385	0	0.000116	0	7.51E-05	0	2	4.77E-05	5.75E-05	0	6.36E-05	0	0	0	1	1.59E-05	3.18E-05
1459	5.5	0	o	Q	15	0	0	0	0	9.3E-05	0	1	2.32E-05	4.65E-05	0	5.9E-05	0	0	0.000101	2	4E-05	4.93E-05
1460	11.2	0	o	Q	45	0.012	0	0.000138	0	0	0	1	3.45E-05	6.9E-05	0	6.64E-05	0	4.83E-05	0	2	2.87E-05	3.39E-05
1461	6.1	0	o	Q	0	0	0	0.000135	0	5.11E-05	0	2	4.65E-05	6.36E-05	0	6.48E-05	0	0	0	1	1.62E-05	3.24E-05
1462	6.5	0	o	Q	24	0.002	0	0.0001	0	0.000114	0	2	5.36E-05	6.21E-05	0	0	0	3.51E-05	0	1	8.77E-06	1.75E-05
1463	5.5	0	o	Q	25	0.337	0	0	0.000205	1.93E-05	0	2	5.62E-05	9.99E-05	0	2.45E-05	0	0	0	1	6.13E-06	1.23E-05
1464	7	0	o	S	24	0.922	0	0	0	0.000152	0	1	3.79E-05	7.59E-05	0	3.85E-05	0	5.61E-05	0	2	2.37E-05	2.82E-05
1465	6.1	0	o	Q	15	0.003	0	0.000135	0	8.98E-05	0	2	5.63E-05	6.77E-05	0	0	0	2.07E-05	0	1	5.18E-06	1.04E-05
1466	6.2	0	o	Q	18	0	0	0	0	5.39E-05	0	1	1.35E-05	2.7E-05	0	0	0	7.47E-05	0.000117	2	4.8E-05	5.81E-05
1467	7.1	0	o	Q	0	0	0	5.21E-05	0	0.000118	0	2	4.26E-05	5.61E-05	0	7.51E-05	0	0	0	1	1.88E-05	3.76E-05
1468	9.6	0	o	Q	13	0	0	6.15E-05	0	0.00014	0	2	5.03E-05	6.63E-05	0	0	0	4.31E-05	0	1	1.08E-05	2.15E-05
1469	8.1	0	o	S	20	0.971	0	2.3E-05	0.000185	3.48E-05	0	3	6.07E-05	8.41E-05	0	0	0	0	0	0	0	0
1470	5.7	0	o	Q	0	0	0	0	0	0.000125	0	1	3.12E-05	6.24E-05	0	3.7E-05	0	8.07E-05	0	2	2.94E-05	3.84E-05
1471	5.4	0	o	Q	19	0.002	0	0.000144	0	5.85E-05	0	2	5.07E-05	6.82E-05	0	0	0	3.79E-05	0	1	9.47E-06	1.89E-05
1472	6.7	0	o	Q	0	0	0	0	0	5.22E-05	0	1	1.3E-05	2.61E-05	0	6.63E-05	0	0.000121	0	2	4.67E-05	5.83E-05
1473	8.2	0	o	Q	43	0	0	5.16E-05	0	7.82E-05	0	2	3.24E-05	3.9E-05	0	0	0	0.000108	0	1	2.71E-05	5.42E-05
1474	7.1	0	o	Q	0	0	0	0.000177	0	1.92E-05	0	2	4.91E-05	8.59E-05	0	0	0	3.54E-05	0	1	8.86E-06	1.77E-05
1475	6.6	0	o	Q	21	0.181	0	3.09E-05	0	0	0	1	7.72E-06	1.54E-05	0	9.9E-05	0	0	0.000102	2	5.02E-05	5.79E-05
1476	7.4	0	o	Q	41	0	0	0	0	6.77E-05	0	1	1.69E-05	3.39E-05	0	0	0	3.58E-05	0.000126	2	4.05E-05	5.95E-05
1477	5.6	0	o	Q	19	0	0	0	0	0	0	0	0	0	0	1.78E-05	0	2.59E-05	0.000183	3	5.67E-05	8.49E-05
1478	5.4	0	o	Q	51	0.2	0	2.12E-05	0	8.04E-05	0	2	2.54E-05	3.8E-05	0	0.000122	0	0	0	1	3.06E-05	6.12E-05
1479	6.4	0	o	Q	37	0	0	8.85E-05	0	0	0	1	2.21E-05	4.43E-05	0	4.26E-05	0	9.29E-05	0	2	3.39E-05	4.42E-05
1480	6.2	0	o	S	52	0.939	0	0	0	0	0.000972	1	0	0	0	0	0	3.89E-05	0.000183	2	5.55E-05	8.71E-05
1481	5.7	0	o	Q	0	0	0	4.81E-05	0	0.000127	0	2	4.39E-05	6.02E-05	0	4.63E-05	0	0	0	1	1.16E-05	2.31E-05
1482	6.3	0	o	Q	23	0.384	0	0	0	2.28E-05	0	1	5.7E-06	1.14E-05	0	8.68E-05	0	0.000105	0	2	4.8E-05	5.6E-05
1483	6.6	0	o	Q	0	0	0	0	0	0.000141	0	1	3.52E-05	7.03E-05	0	5.1E-05	0	1.86E-05	0	2	1.74E-05	2.41E-05
1484	7.6	0	o	Q	23	0.001	0	4.95E-05	0	7.5E-05	0	2	3.11E-05	3.74E-05	0	0	0	0	8.15E-05	1	2.04E-05	4.08E-05
1485	8.2	0	o	Q	23	0.003	0	8.24E-05	0	9.36E-05	0	2	4.4E-05	5.1E-05	0	0	0	2.88E-05	0	1	7.21E-06	1.44E-05
1486	4.9	0	o	Q	0	0	0	0	0	3.07E-05	0	1	7.68E-06	1.54E-05	0	1.3E-05	0	0.000161	0	2	4.34E-05	7.84E-05
1487	4.8	0	o	S	23	1	0	0.000122	0	9.26E-06	0	2	3.29E-05	5.98E-05	0	7.06E-05	0	0	0	1	1.76E-05	3.53E-05
1488	8.1	0	o	Q	20	0.072	0	0	0	7.09E-05	0.00327	2	1.77E-05	3.55E-05	0	0	0	0.000131	0	1	3.28E-05	6.55E-05
1489	6.7	0	o	Q	15	0	0	0.000131	0	6.63E-05	0.000764	3	4.94E-05	6.29E-05	0	0	0	0	0	0	0	0
1490	7.4	0	o	Q	45	0	0	0	0	3.3E-05	0	1	8.24E-06	1.65E-05	0	4.19E-05	0	0.000122	0	2	4.09E-05	5.74E-05
1491	8.8	0	o	S	22	0.885	0	0.000107	0	0	0	1	2.67E-05	5.35E-05	0	5.15E-05	0	3.74E-05	0	2	2.22E-05	2.63E-05
1492	7	0	o	Q	25	0.005	0	8.05E-05	0	0	0	1	2.01E-05	4.03E-05	0	2.58E-05	0	0	8.83E-05	2	2.85E-05	4.17E-05
1493	4.5	0	o	Q	0	0	0	0.00014	0	2.65E-05	0	2	4.17E-05	6.68E-05	0	0	0	2.45E-05	0	1	6.13E-06	1.23E-05
1494	7.6	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	7.38E-05	0	5.37E-05	6.31E-05	3	4.77E-05	3.28E-05
1495	6	0	o	Q	0	0	0	0.00011	0	4.18E-05	0	2	3.8E-05	5.2E-05	0	0	0	3.86E-05	0	1	9.65E-06	1.93E-05
1496	5.9	0	o	Q	0	0	0	0	0	6.52E-05	0	1	1.63E-05	3.26E-05	0	4.97E-05	0	7.23E-05	0	2	3.05E-05	3.64E-05
1497	6.5	0	o	Q	0	0	0	0	0	4.32E-05	0	1	1.08E-05	2.16E-05	0	1.83E-05	0	0	0.000125	2	3.59E-05	6.01E-05
1498	6.5	0	o	Q	0	0	0	9.69E-05	0	3.67E-05	0	2	3.34E-05	4.57E-05	0	0	0	5.08E-05	0	1	1.27E-05	2.54E-05
1499	7.2	0	o	Q	32	0.018	0	2.08E-05	0	6.29E-05	0	2	2.09E-05	2.96E-05	0	9.98E-05	0	0	0	1	2.49E-05	4.99E-05
1500	8.4	0	o	Q	30	0	0	7.45E-05	0	5.64E-05	0	2	3.27E-05	3.85E-05	0	0	0	5.21E-05	0	1	1.3E-05	2.61E-05
1501	7.5	0	o	Q	32	0.021	0	0	0	3.71E-05	0	1	9.29E-06	1.86E-05	0	2.36E-05	0	0	0.000121	2	3.62E-05	5.77E-05
1502	5	0	o	Q	49	0.003	0	6.47E-05	0	8.17E-05	0	2	3.66E-05	4.28E-05	0	0	0	3.02E-05	0	1	7.55E-06	1.51E-05
1503	6.8	0	o	Q	23	0	0	0.000122	0	4.31E-05	0	2	4.12E-05	5.75E-05	0	7.81E-06	0	0	0	1	1.95E-06	3.91E-06
1504	7.6	0	o	Q	60	0	0	0	0	0.000102	0	1	2.54E-05	5.08E-05	0	2.58E-05	0	0	4.41E-05	2	1.75E-05	2.15E-05
1505	6.8	0	o	Q	19	0.007	0	7.97E-05	0	4.02E-05	0	2	3E-05	3.82E-05	0	5.11E-05	0	0	0	1	1.28E-05	2.56E-05
1506	8.7	0	o	Q	19	0.001	0	3.16E-05	0.000127	0	0	2	3.97E-05	6.03E-05	0	0	0	1.11E-05	0	1	2.77E-06	5.53E-06
1507	8	0	o	Q	23	0.005	0	7.52E-05	0	1.9E-05	0	2	2.36E-05	3.56E-05	0	0	0	7.02E-05	0	1	1.75E-05	3.51E-05
1508	5.6	0	o	Q	26	0.001	0	0	0	3.48E-05	0	1	8.7E-06	1.74E-05	0	0	0	1.61E-05	0.000113	2	3.24E-05	5.46E-05
1509	6.7	0	o	Q	0	0	0	0	0	8.04E-05	0	1	2.01E-05	4.02E-05	0	0	0	2.48E-05	5.83E-05	2	2.08E-05	2.76E-05
1510	6.2	0	o	Q	26	0.005	0	0	0	2.44E-05	0	1	6.09E-06	1.22E-05	0	9.28E-05	0	4.5E-05	0	2	3.45E-05	4.43E-05
1511	6.9	0	o	Q	27	0.429	0	5.88E-05	0	4.45E-05	0	2	2.58E-05	3.04E-05	0	5.65E-05	0	0	0	1	1.41E-05	2.83E-05
1512	5.8	0	o	Q	32	0	0	2.18E-05	0	6.61E-05	0	2	2.2E-05	3.12E-05	0	0	0	0	7.18E-05	1	1.8E-05	3.59E-05
1513	9.6	0	o	S	48	0.9	0	3.03E-05	0	6.87E-05	0	2	2.47E-05	3.26E-05	0	5.82E-05	0	0	0	1	1.45E-05	2.91E-05
1514	6.2	0	o	Q	25	0.211	0	0	0	2.66E-05	0	1	6.66E-06	1.33E-05	0	6.77E-05	0	0	5.79E-05	2	3.14E-05	3.65E-05
1515	7	0	o	Q	29	0.001	0	2.29E-05	0	0	0	1	5.72E-06	1.14E-05	0	0	0	1.6E-05	0.000113	2	3.23E-05	5.44E-05
1516	7.1	0	o	Q	0	0	0	3.61E-05	0	5.47E-05	0	2	2.27E-05	2.73E-05	0	0	0	0	5.94E-05	1	1.49E-05	2.97E-05
1517	6.4	0	o	Q	30	0	0	7.61E-05	0	1.92E-05	0	2	2.38E-05	3.6E-05	0	0	0	5.33E-05	0	1	1.33E-05	2.66E-05
1518	8.1	0	o	Q	42	0.002	0	0	0	1.81E-05	0	1	4.52E-06	9.03E-06	0	0	0	5.01E-05	7.85E-05	2	3.21E-05	3.89E-05
1519	7.7	0	o	Q	0	0	0	0	0	3.27E-05	0	1	8.18E-06	1.64E-05	0	4.15E-05	0	0	7.11E-05	2	2.82E-05	3.47E-05
1520	6.3	0	o	Q	16	0.013	0	8.98E-05	0	2.27E-05	0	2	2.81E-05	4.25E-05	0	2.88E-05	0	0	0	1	7.2E-06	1.44E-05
1521	5.4	0	o	Q	23	0	0	2.67E-05	0	0	0	1	6.66E-06	1.33E-05	0	2.56E-05	0	0	8.77E-05	2	2.83E-05	4.14E-05
1522	7.8	0	o	Q	47	0.052	0	0	0	0	0.00052	1	0	0	0	0	0	4.17E-05	9.81E-05	2	3.49E-05	4.64E-05
1523	7.2	0	o	Q	19	0.459	0	0	0	4.56E-05	0	1	1.14E-05	2.28E-05	0	0	0	4.21E-05	4.95E-05	2	2.29E-05	2.66E-05
1524	8.1	0	o	S	20	0.708	0	2.21E-05	0	0	0	1	5.53E-06	1.11E-05	0	2.13E-05	0	0	9.11E-05	2	2.81E-05	4.32E-05
1525	4.8	0	o	S	21	0.884	0	4.48E-05	0	0	0	1	1.12E-05	2.24E-05	0	0	0	1.57E-05	7.38E-05	2	2.24E-05	3.51E-05
1526	5.9	0	o	Q	30	0.06	0	3.14E-05	0	7.13E-05	0	2	2.57E-05	3.38E-05	0	3.02E-05	0	0	0	1	7.55E-06	1.51E-05
1527	5	0	o	Q	0	0	0	3.95E-05	0	0	0	1	9.88E-06	1.98E-05	0	3.8E-05	0	5.53E-05	0	2	2.33E-05	2.79E-05
1528	7.2	0	o	Q	50	0	0	0	0	5.67E-05	0	1	1.42E-05	2.84E-05	0	0	0	1.31E-05	6.16E-05	2	1.87E-05	2.93E-05
1529	6.3	0	o	Q	0	0	0	7.33E-06	0	0	0	1	1.83E-06	3.66E-06	0	2.11E-05	0	0	9.65E-05	2	2.94E-05	4.58E-05
1530	5.7	0	o	Q	18	0	0	3.38E-05	0	0	0	1	8.44E-06	1.69E-05	0	3.25E-05	0	0	5.56E-05	2	2.2E-05	2.71E-05
1531	7.3	0	o	Q	28	0	0	0	0	5.74E-05	0	1	1.43E-05	2.87E-05	0	3.64E-05	0	2.65E-05	0	2	1.57E-05	1.86E-05
1532	7.3	0	o	Q	34	0.208	0	3.25E-05	0	2.46E-05	0	2	1.43E-05	1.68E-05	0	6.25E-05	0	0	0	1	1.56E-05	3.12E-05
1533	7	0	o	Q	21	0	0	2.11E-05	0	6.38E-05	0	2	2.12E-05	3.01E-05	0	0	0	0	3.47E-05	1	8.67E-06	1.73E-05
1534	7.1	0	o	Q	20	0.007	0	6.36E-05	0	0	0	1	1.59E-05	3.18E-05	0	2.04E-05	0	0	3.49E-05	2	1.38E-05	1.7E-05
1535	6	0	o	Q	0	0	0	2.51E-05	0	7.6E-05	0	2	2.53E-05	3.58E-05	0	0	0	1.75E-05	0	1	4.39E-06	8.77E-06
1536	6.3	0	o	Q	0	0	0	2.33E-05	0	7.06E-05	0	2	2.35E-05	3.33E-05	0	2.24E-05	0	0	0	1	5.6E-06	1.12E-05
1537	5	0	o	Q	21	0.001	0	6.44E-05	0	3.9E-05	0	2	2.58E-05	3.16E-05	0	1.24E-05	0	0	0	1	3.1E-06	6.19E-06
1538	8	0	o	Q	0	0	0	3.18E-05	0	0	0	1	7.96E-06	1.59E-05	0	6.12E-05	0	2.23E-05	0	2	2.09E-05	2.89E-05
1539	6.4	0	o	Q	23	0	0	6.27E-05	0	0	0	1	1.57E-05	3.13E-05	0	3.02E-05	0	2.19E-05	0	2	1.3E-05	1.54E-05
1540	6.2	0	o	Q	22	0.018	0	6.64E-05	0	2.51E-05	0	2	2.29E-05	3.13E-05	0	0	0	2.32E-05	0	1	5.8E-06	1.16E-05
1541	8.2	0	o	Q	44	0	0	0	0	6.61E-05	0	1	1.65E-05	3.3E-05	0	2.8E-05	0	2.03E-05	0	2	1.21E-05	1.43E-05
1542	4.9	0	o	Q	21	0	0	3.15E-05	0	0	0	1	7.88E-06	1.58E-05	0	6.06E-05	0	2.21E-05	0	2	2.07E-05	2.86E-05
1543	7	0	o	Q	0	0	0	0	0	1.99E-05	0	1	4.97E-06	9.93E-06	0	5.05E-05	0	0	4.32E-05	2	2.34E-05	2.72E-05
1544	5.3	0	o	Q	31	0	0	5.38E-05	0	4.07E-05	0	2	2.36E-05	2.78E-05	0	0	0	1.88E-05	0	1	4.71E-06	9.41E-06
1545	6.6	0	o	Q	0	0	0	1.87E-05	7.53E-05	0	0	2	2.35E-05	3.57E-05	0	0	0	0	1.54E-05	1	3.85E-06	7.7E-06
1546	9.1	0	o	Q	25	0	0	5.83E-05	0	2.21E-05	0	2	2.01E-05	2.75E-05	0	2.8E-05	0	0	0	1	7.01E-06	1.4E-05
1547	6.6	0	o	Q	22	0.036	0	2.47E-05	0	5.62E-05	0	2	2.02E-05	2.67E-05	0	2.38E-05	0	0	0	1	5.95E-06	1.19E-05
1548	7.1	0	o	Q	39	0.351	0	0	0	4.04E-05	0	1	1.01E-05	2.02E-05	0	4.11E-05	0	2.24E-05	0	2	1.59E-05	1.98E-05
1549	6.3	0	o	S	32	0.753	0	0	0	3.18E-05	0	1	7.96E-06	1.59E-05	0	4.04E-05	0	2.94E-05	0	2	1.75E-05	2.07E-05
1550	9.3	0	o	Q	30	0.057	0	5.86E-05	0	2.22E-05	0	2	2.02E-05	2.77E-05	0	0	0	2.05E-05	0	1	5.13E-06	1.03E-05
1551	5.2	0	o	Q	19	0.002	0	0	0	1.26E-05	0	1	3.15E-06	6.3E-06	0	3.2E-05	0	0	5.47E-05	2	2.17E-05	2.67E-05
1552	7.1	0	o	Q	23	0	0	2.67E-05	0	0	0	1	6.66E-06	1.33E-05	0	2.56E-05	0	0	4.39E-05	2	1.74E-05	2.14E-05
1553	5.9	0	o	Q	33	0.273	0	3.89E-05	0	2.94E-05	0	2	1.71E-05	2.01E-05	0	0	0	2.72E-05	0	1	6.8E-06	1.36E-05
1554	5.1	0	o	Q	17	0.001	0	2.86E-05	0	1.08E-05	0	2	9.86E-06	1.35E-05	0	5.51E-05	0	0	0	1	1.38E-05	2.75E-05
1555	7	0	o	Q	25	0.064	0	0	0	2.29E-05	0	1	5.74E-06	1.15E-05	0	2.91E-05	0	4.24E-05	0	2	1.79E-05	2.13E-05
1556	6.8	0	o	Q	20	0.001	0	3.12E-05	0	3.55E-05	0	2	1.67E-05	1.93E-05	0	0	0	0	2.57E-05	1	6.42E-06	1.28E-05
1557	5.1	0	o	Q	19	0	0	0	0	2.34E-05	0	1	5.86E-06	1.17E-05	0	0	0	4.33E-05	2.55E-05	2	1.72E-05	2.12E-05
1558	7.8	0	o	Q	22	0.207	0	0	0	1.09E-05	0	1	2.73E-06	5.47E-06	0	5.55E-05	0	0	2.38E-05	2	1.98E-05	2.63E-05
1559	5.9	0	o	Q	18	0.001	6.35E-05	0	0	0	0.000159	2	1.59E-05	3.17E-05	0	0	0	2.55E-05	0	1	6.39E-06	1.28E-05
1560	7.3	0	o	Q	25	0	0	0	0	4.74E-05	0	1	1.19E-05	2.37E-05	0	0	0.000375	0	4.12E-05	2	1.03E-05	2.06E-05
1561	7.1	0	o	Q	17	0	0	0	0	3.23E-05	0	1	8.07E-06	1.61E-05	0	2.05E-05	0	0	3.51E-05	2	1.39E-05	1.71E-05
1562	6.9	0	o	Q	30	0.103	0	4.18E-05	0	2.11E-05	0	2	1.57E-05	2E-05	0	0	0	0	2.29E-05	1	5.74E-06	1.15E-05
1563	7.7	0	o	Q	17	0	0	0	0	1.03E-05	0	1	2.58E-06	5.16E-06	0	1.31E-05	0	5.72E-05	0	2	1.76E-05	2.71E-05
1564	8.2	0	o	Q	18	0.006	0	0	0	1.38E-05	0	1	3.46E-06	6.92E-06	0	5.86E-06	0	0	6.01E-05	2	1.65E-05	2.92E-05
1565	7.1	0	o	Q	35	0	0	2.34E-05	0	0	0	1	5.86E-06	1.17E-05	0	2.25E-05	0	3.28E-05	0	2	1.38E-05	1.65E-05
1566	7.7	0	o	Q	20	0	0	2.87E-05	0	2.17E-05	0	2	1.26E-05	1.48E-05	0	2.76E-05	0	0	0	1	6.9E-06	1.38E-05
1567	6.3	0	o	Q	19	0.008	0	3.36E-05	0	0	0	1	8.39E-06	1.68E-05	0	1.61E-05	0	0	2.76E-05	2	1.09E-05	1.35E-05
1568	5.4	0	o	Q	27	0	0	3.09E-05	0	2.34E-05	0	2	1.36E-05	1.6E-05	0	0	0	2.16E-05	0	1	5.4E-06	1.08E-05

rk	MMs: MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
1422	0	0	0	0	0	0	0	0	Two conserved tryptophans	nucleus	
1423	0	0	0	0	0	0	0	0	Serine/Threonine protein	endomembrane system [pmid	ATP binding; protein binding
1424	0	0	0	0	0	0	0	0	Serine/Threonine protein	intracellular [pmid 8557660]	ATP binding; cAMP-
1425	0	0	0	0	0	0	0	0	Pleckstrin homology (PH)	membrane; nucleus	calcium ion binding; DNA
1426	0	0	0	0	0	0	0	0	YT521-B-like family. This	nucleus	
1427	0	0	0	0	0	0	0	0	Src homology 3 domains;	intracellular [pmid 11017088]	GTPase activator activity
1428	0	0	0	3.08E-05	0	0	0	0			
1429	0	0	0	0	0	0	0	0			
1430	0	0	0	0	0	0	0	0	Sorting nexin, N-terminal		phosphoinositide binding;
1431	0	0	0	0	0	0	0	0	Rab39 subfamily. Found in	intracellular [pmid 11256614];	GTP binding; nucleotide
1432	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus; ribonucleoprotein	nucleotide binding; RNA
1433	0	0	0	0	0	0	0	0	SCP-2 sterol transfer		oxidoreductase activity;
1434	0	0	0	0	0	0	0	0	Interferon-induced 35 kDa	nucleus [pmid 8288566]	protein binding [pmid
1435	0	0	0	0	0	0	0	0	Aldo/keto reductase family.	intracellular [pmid 11256614]	3-alpha-hydroxysteroid
1436	0	0	0	0	0	0	0	0	Splicing factor 1 (SF1) K	nucleus [pmid 7912130];	metal ion binding [pmid
1437	0	0	0	0	0	0	0	0	WD40 domain, found in a		calmodulin binding [pmid
1438	0	0	0	0	0	0	0	0	U1-like zinc finger; Family	intracellular; nucleus; small	metal ion binding; nucleic
1439	0	0	0	0	0	0	0	0			
1440	0	0	0	0	0	0	0	0	Caspase recruitment		
1441	0	0	0	0	0	0	0	0	Protein of unknown function		protein binding [pmid
1442	0	0	0	0	0	0	0	0	Ndr family. This family	nucleus	
1443	0	0	0	0	0	0	0	0	Forkhead associated	nucleus	sequence-specific DNA
1444	0	0	0	0	0	0	0	0	V/A-type ATP synthase	cytoplasm; proton-transporting	ATP binding; hydrogen-
1445	0	0	0	0	0	0	0	0	Leucine-rich repeats	cytoskeleton; F-actin capping	actin binding; tropomyosin
1446	0	0	0	0	0	0	0	0			
1447	0	0	0	0	0	0	0	0	Protein kinase C conserved		ATP binding; diacylglycerol
1448	0	0	0	0	0	0	0	0	RNA 3' phosphate cyclase	nucleoplasm [pmid 9184239];	RNA binding [pmid 9184239];
1449	0	0	0	0	0	0	0	0	WD40 domain, found in a	cytosol [pmid 9267021];	ATP binding; caspase
1450	0	0	0	4.63E-05	0	0	0	0	Hyaluronan / mRNA binding	nucleus	mRNA 3'-UTR binding [pmid
1451	0	0	0	0	0	0	0	0	Transferrin; smart00094	extracellular region;	ferric iron binding; metal ion
1452	0	0	0	0	0	0	0	0	Tyrosinyl-tRNA synthetase	cytoplasm [pmid 9162081];	ATP binding; interleukin-8
1453	0	0	0	0	0	0	0	0	MIF4G domain. MIF4G is		protein binding [pmid
1454	0	0	0	0	0	0	0	0			
1455	0	0	0	0	0	0	0	0	WD40 domain, found in a	protein phosphatase type 2A	protein binding [pmid
1456	0	0	0	0	0	0	0	0	Serine/threonine	protein serine/threonine	hydrolase activity;
1457	0	0	0	0	0	0	0	0			binding; RNA binding
1458	0	0	3.51E-05	0	0	0	0	0	Treacher Collins syndrome	nucleolus [pmid 15249688];	transporter activity [pmid
1459	0	0	0	0	0	0	0	0	Peptidase family C54;		
1460	0	0	0	0	0	0	0	0		nucleus [pmid 10708573]	
1461	0	0	0	0	0	0	0	0	Gtr1/RagA G protein	cytoplasm; nucleus	GTP binding; nucleotide
1462	0	0	0	0	0	0	0	0	VATPase_H, regulatory	hydrogen-transporting ATPase	ATP binding; ATPase activity
1463	0	0	0	0	0	0	0	0	SAP domain. The SAP	nucleus [pmid 1324173]	DNA binding; double-
1464	0	0	0	0	0	0	0	0			
1465	0	0	0	0	0	0	0	0	STAT protein, DNA binding	nucleus	calcium ion binding; signal
1466	0	0	0	0	0	0	0	0	Serine/Threonine protein	cytoplasm [pmid 11509566];	ATP binding [pmid
1467	0	0	0	0	0	0	0	0			
1468	0	0	0	0	0	0	0	0	LYAR-type C2HC zinc	nucleolus [pmid 11256614];	metal ion binding; zinc ion
1469	0	0	0	0	0	0	0	0	SAP domain. The SAP		DNA binding; nucleotide
1470	0	0	0	0	0	0	0	0	SWIRM domain. This	chromatin; nucleoplasm [pmid	chromatin binding; DNA
1471	0	0	0	0	0	0	0	0			
1472	0	0	0	0	0	0	0	0	Forkhead (FH), also known	intracellular; nucleus	metal ion binding; nucleic
1473	0	0	0	0	0	0	0	0			
1474	0	0	0	0	0	0	0	0	Rel homology domain	cytoplasm [pmid 8668213];	transcription factor activity
1475	0	0	0	0	0	0	1.45E-05	0		nucleus	DNA binding
1476	0	0	0	0	0	0	0	0			
1477	0	0	0	0	0	0	0	0	STAG domain. STAG	nucleus [pmid 9305759]	binding
1478	0	0	0	0	0	0	0	0			
1479	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding [pmid
1480	0	0	0	0	0	0	0	0	Trans-Isoprenyl		dimethylallyltranstransferase
1481	0	0	0	0	0	0	0	0	Fes/CIP4 homology	intracellular [pmid 12093360]	diacylglycerol binding; metal
1482	0	0	0	0	0	0	0	0			
1483	0	0	0	0	0	0	0	0	RecF/RecN/SMC N	exocyst [pmid 11406615]	
1484	0	0	0	0	0	0	0	0	DENN (AEX-3) domain.		
1485	0	0	0	0	0	0	0	0	RGS12 (regulator of G		GTPase activator activity
1486	0	0	0	0	0	0	0	0	Likely ribonuclease with	nucleus [pmid 8786132]	hydrolase activity, acting on
1487	0	0	0	0	0	0	0	0			
1488	0	0	0	0	0	0	0	0	TRX-like [2Fe-2S]	membrane fraction;	2 iron, 2 sulfur cluster
1489	0	0	0	0	0	0	0	0	D-isomer specific 2-	extracellular region	electron carrier activity [pmid
1490	0	0	0	0	0	0	0	0	Src homology 3 domains;	integral to membrane;	ATP binding; nucleotide
1491	0	0	0	0	0	0	0	0	Histidine kinase-like	mitochondrion [pmid 7499431]	ATP binding; kinase activity;
1492	0	0	0	0	0	0	0	0			
1493	0	0	0	0	0	0	0	0	Leo1-like protein. Members	nucleus	protein binding [pmid
1494	0	0	0	0	0	0	0	0	Tyrosyl-DNA	nucleus [pmid 10521354]	hydrolase activity;
1495	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus	
1496	0	0	0	0	0	0	0	0	Rok (Rho- associated	cytoskeleton; intracellular	ATP binding; diacylglycerol
1497	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus [pmid 9524131]	ATP binding [pmid 1825134];
1498	0	0	0	0	0	0	0	0	Kinesin motor domain,	kinesin complex [pmid	ATP binding; microtubule
1499	0	0	0	0	0	0	0	0	Band 4.1 homologues; Also	cytoskeleton	ATP binding; Janus kinase
1500	0	0	0	0	0	0	0	0	Double-stranded RNA	cytoplasm [pmid 11256614];	double-stranded RNA
1501	0	0	0	0	0	0	0	0	WD40 domain, found in a	small nucleolar	protein binding [pmid
1502	0	0	0	0	0	0	0	0	HEAT repeat. The HEAT	cytoplasm; nuclear pore [pmid	binding; protein transporter
1503	0	0	0	0	0	0	0	0	Spectrin repeats, found in	cell-cell adherens junction;	protein binding, bridging
1504	0	0	0	0	0	0	0	0	SH3 domain. SH3 (Src	cytoplasm [pmid 2821624];	GTPase binding [pmid
1505	0	0	0	0	0	0	0	0			
1506	0	0	0	0	0	0	0	0	Nucleoporin Nup153-like.	intracellular; nuclear pore	DNA binding; metal ion
1507	0	0	0	0	0	0	0	0			
1508	0	0	0	0	0	0	0	0	Chromosome condensation	nucleus [pmid 10910072]	binding
1509	0	0	0	0	0	0	0	0	Karyopherin (importin)		binding
1510	0	0	0	0	0	0	0	0			
1511	0	0	0	0	0	0	0	0			
1512	0	0	0	0	0	0	0	0			
1513	0	0	0	0	0	0	0	0			
1514	0	0	0	0	0	0	0	0			
1515	0	0	0	0	0	0	0	0		integrator complex [pmid	protein binding [pmid
1516	0	0	0	0	0	0	0	0	WD40 domain, found in a		isomerase activity; peptidyl-
1517	0	0	0	0	0	0	0	0	Ankyrin repeat. There's no		
1518	0	0	0	0	0	0	0	0	Formyltetrahydrofolate		ATP binding; catalytic
1519	0	0	0	0	0	0	0	0	NOT2 / NOT3 / NOT5	nucleus [pmid 10637334]	RNA polymerase II
1520	0	0	0	0	0	0	0	0	Centromere/kinetochore	endoplasmic reticulum [pmid	centromeric DNA binding
1521	0	0	0	0	0	0	0	0	Peptidase family M1.	cytosol [pmid 9048733];	aminopeptidase activity
1522	0	0	0	0	0	0	0	0	Polyribonucleotide	mitochondrion	3'-5'-exoribonuclease
1523	0	0	0	0	0	0	0	0	Glutaminyl-tRNA	cytoplasm; soluble fraction	ATP binding; glutamate-tRNA
1524	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus [pmid 14609955]	ATP binding; DNA binding;
1525	0	0	0	0	0	0	0	0	CAS/CSE protein involved	cytoplasm [pmid 11823430];	histone binding; protein
1526	0	0	0	0	0	0	0	0	Eps15 homology domain;		calcium ion binding
1527	0	0	0	0	0	0	0	0	ankyrin repeats; ankyrin		
1528	0	0	0	0	0	0	0	0	Transport protein Trs120.		
1529	0	0	0	0	0	0	0	0			
1530	0	0	0	0	0	0	0	0	TBC domain. Identification		GTPase activator activity
1531	0	0	0	0	0	0	0	0	RNA recognition motif.	intracellular [pmid 11256614];	nucleotide binding; RNA
1532	0	0	0	0	0	0	0	0	Threonyl-tRNA synthetase		ATP binding; electron carrier
1533	0	0	0	0	0	0	0	0			
1534	0	0	0	1.66E-05	0	0	0	0	Helicase superfamily c-	intracellular [pmid 11256614]	ATP binding; ATP-dependent
1535	0	0	0	0	0	0	0	0	glycine rich nucleic binding	intracellular; nucleus	metal ion binding; nucleic
1536	0	0	0	0	0	0	0	0	RING-finger (Really	chromosome; nucleus	ligase activity; metal ion
1537	0	0	0	0	0	0	0	0			
1538	0	0	0	0	0	0	0	0	N2,N2-dimethylguanosine	intracellular	methyltransferase activity;
1539	0	0	0	0	0	0	0	0			
1540	0	0	0	0	0	0	0	0	Apg7 is an E1-like protein,	cytoplasm [pmid 10233149]	catalytic activity; ubiquitin
1541	0	0	0	0	0	0	0	0	'SWI3, ADA2, N-CoR and	nucleus; spliceosome complex	DNA binding [pmid 8917598];
1542	0	0	0	0	0	0	0	0	Daxx Family. The Daxx	cytoplasm [pmid 15572661];	androgen receptor binding
1543	0	0	0	0	0	0	0	0	Fes/CIP4 homology		
1544	0	0	0	0	0	0	0	0	Sp100 domain. The	nuclear envelope [pmid	DNA binding; metal ion
1545	0	0	0	0	0	0	0	0			
1546	0	0	0	0	0	0	0	0	SAC3/GANP/Nin1/mts3/eIF-		protein binding [pmid
1547	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus [pmid 10395803]	
1548	0	0	0	0	0	0	0	0			
1549	0	0	0	0	0	0	0	0	Predicted hydrolases or	cytosol [pmid 10862610];	epoxide hydrolase activity
1550	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; ATP-dependent
1551	0	0	0	0	0	0	0	0	MIF4G domain. MIF4G is	cytoplasm; eukaryotic	protein binding [pmid
1552	0	0	0	0	0	0	0	0	CNH domain. Domain found		small GTPase regulator
1553	0	0	0	0	0	0	0	0	RUN domain. This domain	membrane	lipid binding; metal ion
1554	0	0	0	0	0	0	0	0	Leucine-rich repeats	membrane	protein binding [pmid
1555	0	0	0	0	0	0	0	0			
1556	0	0	0	0	0	0	0	0	autolysin; PRK06347		GTPase activator activity
1557	0	0	0	0	0	0	0	0	WD40 domain, found in a		
1558	0	0	0	0	0	0	0	0	CXXC zinc finger. This	nucleus [pmid 8940105]	DNA (cytosine-5-)-
1559	0	0	0	0	0	0	0	0			
1560	0	0	0	0	0	0	0	0			
1561	0	0	0	0	0	0	0	0	Sec24-like: Protein and	COPII vesicle coat [pmid	protein binding [pmid
1562	0	0	0	0	0	0	0	0			
1563	0	0	0	0	0	0	0	0	Helicase superfamily c-		ATP binding; ATP-dependent
1564	0	0	0	0	0	0	0	0	Phosphatidylinositol kinase	nucleus [pmid 9708738];	phosphotransferase activity,
1565	0	0	0	0	0	0	0	0	hypothetical protein;	integrator complex [pmid	protein binding [pmid
1566	0	0	0	0	0	0	0	0	MIT: domain contained	intracellular; nucleus	binding; calpain activity;
1567	0	0	0	0	0	0	0	0	ATPase family associated		ATP binding; nucleoside-
1568	0	0	0	0	0	0	0	0			

rk	NEs detected # out of 10 runs	NEs dNSAF_A VG	MMs detected # out of 8 runs	MMs dNSAF_A VG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP _HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_P OS	SIGNALP_HMM_S PROB	RESTING LYMPHOCYTES NEs: HsNoOH-NE_NT_lymphocytes_CNBr_TI_1_dNSAF	HsNoOH-NE_NT_lymphocytes_TI_1_dNSAF	HsNoOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_TI_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-nNEs dNSAF AVG	NT-bNEs dNSAF SDV	PHA-TREATED LYMPHOCYTES NEs: HsNoOH-NE_PHA_lymphocytes_CNBr_TI_1_dNSAF	HsNoOH-NE_PHA_lymphocytes_TI_1_dNSAF	HsNoOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_TI_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-nNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MMs: MmNoOH-MM_liver_CNBrTI_1_dNSAF	MmNoOH-MM_liver_CNBrTI_2_dNSAF	RnNoOH-MM_liver_TI_1_dNSAF	RnNoOH-MM_liver_TI_2_dNSAF	RnNoOH-MM_liver_TI_3_dNSAF	RnNoOH-MM_liver_TI_4_dNSAF	RnNoOH-MM_liver_PK_1_dNSAF	RnNoOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
1569	3	9.39E-06	0	0	NF		ENSG00000132153	DHX30			gi	20336290	ref	NP_	DEAH (Asp-Glu-Ala-His) box	1155	129438	8.2	0	O	O	0	0.004	0	4.04E-05	0	1.53E-05	0	2	1.39E-05	1.91E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Helicase superfamily c-	intracellular	ATP binding; ATP-dependent
1570	3	9.23E-06	0	0	NF		ENSG00000168488	ATXN2L			gi	32692640	ref	NP_	ataxin 2 related protein isofo	1062	111920	8.7	0	O	O	56	0.003	0	2.21E-05	0	2.69E-05	0	1	5.49E-06	1.1E-05	0	2.11E-05	1.55E-05	0	0	0	0	0	0	0	0	0	0	0	Ataxin-2 N-terminal region.	membrane	
1571	3	9.2E-06	0	0	NF		ENSG00000129355	CTDSPL			gi	32692640	ref	NP_	SR-related CTD-associated f	1312	139265	8.2	0	O	O	0	0	0	0	0	2.69E-05	0	1	6.73E-06	1.36E-05	0	3.42E-06	1.24E-05	0	0	0	0	0	0	0	0	0	0	0			
1572	3	9.19E-06	0	0	NF		ENSG00000113810	SMC4			gi|50658065|ref|NP_	SMC4 structural maintenance	1288	147182	6.8	0	O	O	0	0	0	1.81E-05	0	0	0	1	4.52E-06	9.05E-06	0	1.74E-05	3.8E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1573	3	9.02E-06	0	0	NF		ENSG00000135241	PNPLA8			gi|48525351|ref|NP_	patatin-like phospholipase do	782	88477	9.2	0	O	O	18	0.018	0	0	0	2.26E-05	0	1	5.65E-06	1.13E-05	0	2.87E-05	2.09E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1574	3	8.84E-06	0	0	NF		ENSG00000091009	RBM27			gi|16916834|ref|NP_	PREDICTED: similar to RNA	1060	118719	9.2	0	O	O	24	0.001	0	2.2E-05	0	3.33E-05	0	2	1.35E-05	1.66E-05	0	0	1.54E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1575	3	8.78E-06	0	0	NF		ENSG00000077235	GTF3C1			gi|10194324|ref|NP_	general transcription factor II	2109	238873	7.3	0	O	O	19	0.001	0	0	0	0	0	0	0	0	0	0	1.06E-05	2.32E-05	3.64E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1576	3	8.74E-06	0	0	NF		ENSG00000092098	RNF31			gi|19710543|ref|NP_	ring finger protein 31 [Homo	1072	119652	6.6	0	O	O	54	0	0	2.18E-05	0	3.3E-05	0	2	1.37E-05	1.64E-05	0	0	1.52E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1577	3	8.2E-06	0	0	NF		ENSG00000196604	KLOC653781			gi	11341320	ref	XP_	PREDICTED: similar to prote	1038	117390	6	0	O	O	40	0	0	0	0	6.03E-05	0	1	1.51E-05	3.02E-05	0	0	5.24E-06	0	0	0	0	0	0	0	0	0	0	0	0	Actin; An ubiquitous protein		
1578	3	8.12E-06	0	0	NF		ENSG00000112282	MED23			gi	28558969	ref	NP_	mediator complex subunit 23	1365	156193	7.4	0	O	O	16	0	0	0	0	1.29E-05	0	1	3.24E-06	6.47E-06	0	0	2.39E-05	2.81E-05	0	0	0	0	0	0	0	0	0	0	0		transcription factor complex	receptor activity;	
1579	3	7.91E-06	0	0	NF		ENSG00000196776	BMS1			gi	42281403	ref	NP_	BMS1-like, ribosome assembl	1282	146923	8.6	0	O	O	0	0	0	1.82E-05	0	2.76E-05	0	1	1.4E-05	1.37E-05	0	1.75E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	Bms1. Bms1 is an	nucleus	ATP binding; nucleotide
1580	3	7.39E-06	0	0	NF		ENSG00000198589	LRBA			gi|148233596|ref|NP_	LPS-responsive vesicle traffi	2863	319107	5.6	0	O	O	0	0	0	2.44E-05	0	0	0	1	6.11E-06	1.22E-05	0	7.84E-06	0	2.68E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1581	3	7.21E-06	0	0	NF		ENSG00000117713	ARID1A			gi	21264565	ref	NP_	AT rich interactive domain 1	2285	242042	6.7	0	O	O	15	0.096	0	0	0	0	0	0	0	0	0	0	9.82E-06	1.43E-05	3.39E-05	0	0	0	0	0	0	0	0	0	0	0	ARID/BRIGHT DNA binding	intracellular; nucleus;	binding; DNA binding [pmid
1582	3	6.99E-06	0	0	NF		ENSG00000132604	NUP42			gi	19923191	ref	NP_	nucleoporin 42 kDa [Homo	1980	240294	5.4	0	O	O	27	0.002	0	0	0	8.92E-06	0	1	2.23E-06	4.46E-06	0	0	8.24E-06	3.88E-05	0	0	0	0	0	0	0	0	0	0	0	0	Nuclear protein export	nucleus [pmid 9712826]	DNA binding [pmid 9712826]
1583	3	6.46E-06	0	0	NF		ENSG00000163029	SMC6			gi	13375848	ref	NP_	SMC6 protein [Homo sapiens]	1091	126325	7	0	O	O	0	0	0	0	0	1.62E-05	0	1	4.05E-06	8.1E-06	0	2.06E-05	1.5E-05	0	0	0	0	0	0	0	0	0	0	0	0	Eukaryotic SMC6 proteins;	chromosome; intracellular	ATP binding
1584	3	5.71E-06	0	0	NF		ENSG00000164366	NICTOR			gi	58914468	ref	NP_	apamycin-insensitive compa	1708	192215	7.5	0	O	O	0	0	1.37E-05	0	0	0	0	1	3.41E-06	8.83E-06	0	0	9.56E-06	2.26E-05	0	0	0	0	0	0	0	0	0	0	0	0			binding
1585	3	5.37E-06	0	0	NF		ENSG00000105357	NYH14			gi	16284304	ref	NP_	myosin , heavy chain 14 isofo	1905	227868	5.6	0	O	O	39	0.012	0	0	0	8.85E-06	0	1	2.21E-06	4.43E-06	0	1.12E-05	0	2.28E-05	0	0	0	0	0	0	0	0	0	0	0	0			
1586	3	5.09E-06	0	0	NF		ENSG00000184634	MED12			gi	10347429	ref	NP_	mediator of RNA polymerase	2177	243079	7.1	0	O	O	18	0	0	0	0	8.11E-06	0	1	2.03E-06	4.06E-06	0	0	1.5E-05	1.76E-05	0	0	0	0	0	0	0	0	0	0	0	0			
1587	3	4.91E-06	0	0	NF		ENSG00000135336	Magmas			gi	24767670	ref	NP_	hypothetical protein LOC228	1435	163920	8.8	0	O	O	29	0.007	0	0	0	1.22E-05	0	1	3.08E-06	6.15E-06	0	1.58E-05	1.14E-05	0	0	0	0	0	0	0	0	0	0	0	0		Golgi cis face	binding; intracellular	
1588	3	2.61E-06	0	0	NF		ENSG00000074755	ZZEF1			gi	73747881	ref	NP_	zinc finger, ZZ type with EF h	2961	331075	5.9	0	O	O	50	0	7.88E-06	0	0	0	0	1	1.97E-06	3.94E-06	0	0	0	1.3E-05	2	0.002036	0	0	0	0	0	0	0	0	0	0	Zinc finger, ZZ type. Zinc	anaphase-promoting complex	calcium ion binding; protein
1589	3	7.24E-07	0	0	NF		ENSG00000155657	TTN			gi	10349713	ref	NP_	titin isoform novex- 1 [Homo s	27051	3006786	5.8	0	O	O	24	0.116	0	4.31E-06	0	6.53E-07	0	2	1.24E-06	2.07E-06	0	9.29E-07	0	0	0	0	0	0	0	0	0	0	0	0	0			
1590	3	2.003302	0	0	NF		ENSG00000100097	LGALS1			gi	24504831	ref	NP_	beta-galactoside-binding lect	135	14716	5.5	0	O	O	18	0.027	0	0	0	0.005626	0	1	0.001402	0.002813	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Galectin/galactose-binding	cytoplasm [pmid 16130169]	signal transducer activity
1591	2	0.000959	0	0	NF		gi	169172248	refXP_	LOC100129427			gi	169172248	refXP_	PREDICTED: hypothetical p	79	8761	10.9	0	O	O	16	0	0.000053	0	0	0	0	1	0.000513	0.001026	0.005619	0	0	0	0	0	0	0	0	0	0	0	0	0			
1592	2	0.000848	0	0	NF		ENSG00000196154	S100A4			gi	88456516	ref	NP_	S100 calcium-binding protein	101	11728	8.1	0	O	O	22	0	0	0	0	0	0	1	0	0	0	0	0.000323	0.000645	0	0	0	0	0	0	0	0	0	0	0	S-100/CaBP-like domain;		calcium ion binding [pmid
1593	2	0.000628	0	0	NF		ENSG00000128803	HSPA2			gi	13676857	ref	NP_	heat shock 70kDa protein 2	639	70021	5.7	0	O	O	18	0.006	0	0.004998	0	0	0	1	0.00125	0.002499	0	0	2.56E-05	0	1	6.4E-06	1.28E-05	0	0	0	0	0	0	0	0	cell surface [pmid 12493773]	ATP binding; nucleotide	
1594	2	0.000559	1	3.51E-05	15.95551		ENSG00000124209	RAB22A			gi	10190714	ref	NP_	RAS-related protein RAB-22A	194	21655	8.2	0	O	O	18	0.003	0	0.000601	0.003874	0	0	1	0.001119	0.001858	0	0	0	0	0	0	0.00028	0	0	0	0	0	0	0	0	early endosome [pmid	GTP binding [pmid	
1595	2	0.000494	0	0	NF		ENSG00000169032	PRKAR2A			gi	4758790	ref	NP_	cAMP dependent protein kin	106	12517	9.1	0	O	O	0	0	0	0	0	0.000333	0	1	8.33E-05	0.000167	0	0	0	0.000362	0	0	0	0	0	0	0	0	0	0	0		membrane fraction;	NADH dehydrogenase	
1596	2	0.000471	0	0	NF		ENSG00000166710	B2M			gi	4757826	ref	NP_	beta-2-microglobulin precura	119	13715	6.5	0	O	O	21	-1	0	0	0	0.001188	0	1	0.000297	0.000594	0	0	0	0.002581	0	0	0	0	0	0	0	0	0	0	0	Immunoglobulin domain	extracellular region	MHC class I receptor activity
1597	2	0.000467	0	0	NF		ENSG00000156136	Magmas			gi	27363445	ref	NP_	mitochondrial-associated gra	125	13825	8.7	0	O	O	22	0.755	0	0.000187	0	0	0	1	4.66E-05	9.33E-05	0.003551	0	0	0	0	0	0	0	0	0	0	0	0	0	Pam16. The Pam16 protein	membrane; mitochondrion	heat shock protein binding
1598	2	0.000463	0	0	NF		ENSG00000100650	SRSF5			gi	8699144	ref	NP_	splicing factor, arginine/serine	272	31264	11.6	0	O	O	16	0	0	0	0.003454	0	0	1	0.000863	0.001727	0	0.000247	0	0	0	0	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus	nucleic acid binding;
1599	2	0.00041	0	0	NF		ENSG00000128609	NDUFA5			gi	4826848	ref	NP_	NADH dehydrogenase (ubiq	116	13459	6	0	O	O	20	0.031	0	0	0	0.002438	0	1	0.000609	0.001218	0	0	0.000844	0	0	0	0	0	0	0	0	0	0	0	0	ETC complex I subunit	mitochondrial inner	NADH dehydrogenase
1600	2	0.000276	0	0	NF		ENSG00000154148	KLOC284412			gi	19169255	ref	XP_	PREDICTED: similar to riboso	155	17138	10.6	0	O	O	0	0	0.000292	0	0	0	0	1	0.000146	0.000292	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1601	2	0.000267	0	0	NF		ENSG00000124767	GLO1			gi	11840258	ref	NP_	glyoxalase I [Homo sapiens]	184	20778	5.3	0	O	O	24	0.002	0	0	0	0.000672	0	1	0.000168	0.000336	0	0	0	0.00146	0	0	0	0	0	0	0	0	0	0	0			
1602	2	0.000259	0	0	NF		ENSG00000197956	S100A6			gi	7657532	ref	NP_	S100 calcium-binding protein	90	10180	5.5	0	O	O	22	0.116	0	0	0	0	0	1	0	0	0	0	0.000363	0.001706	0	0	0	0	0	0	0	0	0	0	0	S-100/CaBP-like domain;	cytoplasm [pmid 10913138]	calcium ion binding [pmid
1603	2	0.00024	0	0	NF		ENSG00000084388	PGLYRP1			gi	45270362	ref	NP_	peptidoglycan recognition pr	196	21731	8.6	0	O	O	22	0	0	0.001917	0	0	0.003317	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Animal peptidoglycan	extracellular region [pmid	bacterial binding [pmid
1604	2	0.000239	0	0	NF		ENSG00000122565	LOC653972			gi	89038889	ref	XP_	PREDICTED: similar to Chro	183	20811	5.3	0	O	O	0	0	0	0	0	0.001287	0	1	0.000322	0.000644	0	0	0.000624	0	0	0	0	0	0	0	0	0	0	0	0	Chromo Shadow Domain;		
1605	2	0.000236	0	0	NF		ENSG00000135333	HCLS1			gi	4885450	ref	NP_	hematopoietic cell-specific Ly	486	20258	4.8	0	O	O	0	0	0	0	0	7.27E-05	0	1	1.82E-05	3.63E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Src homology 3 domains;	cytoplasm; DNA-directed RNA	protein binding; transcription
1606	2	0.000221	0	0	NF		NA ENSMUSG00000	SNRPD2			gi	29294624	ref	NP_	small nuclear ribonucleoprot	118	13527	9.9	0	O	O	0	0.001374	0.000395	0	0	0	0	2	0.000442	0.000649	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus; ribonucleoprotein	protein binding [pmid
1607	2	0.000205	0	0	NF		ENSG00000156467	UQCRB			gi	54541152	ref	NP_	ubiquinol-cytochrome c redu	111	13530	8.8	0	O	O	17	0	0.00021	0	0.001432	0	0	2	0.000411	0.000688	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Ubiquinol-cytochrome C	membrane; mitochondrial	oxidoreductase activity;
1608	2	0.000203	0	0	NF		ENSG00000166908	SOD1			gi	40354420	ref	NP_	superoxide dismutase 1, soluble	148	16187	8.8	0	O	O	32	0	0	0	0	0	0	1	0	0	0.001333	0	0.001333	0	0	0	0	0	0	0	0	0	0	0	0	Nucleoside 2-	Nucleoside 2-	
1609	2	0.000203	0	0	NF		ENSG00000196656	KLOC644928			gi	148225456	ref	NP_	hypothetical protein LOC644	115	12977	11.2	0	O	O	30	0	0	0.000203	0	0	0	1	5.07E-05	0.000101	0	0	0.001419	0	0	0	0	0	0	0	0	0	0	0	0			
1610	2	0.000189	0	0	NF		ENSG00000185651	UBE2L3			gi|4507789|ref|NP_	ubiquitin-conjugating enzyme	154	17862	8.5	0	O	O	0	0	0	0	0	0.001262	0	1	0.000315	0.000631	0	0	0	0.000249	0	0	0	0	0	0	0	0	0	0	0	6.23E-05	0.000125		ubiquitin ligase complex [pmid	enzyme binding [pmid
1611	2	0.000178	0	0	NF		ENSG00000125306	RPS12			gi	14277700	ref	NP_	ribosomal protein S12 [Homo	132	14515	7.2	0	O	O	20	0.002	0	0	0	0	0	1	0.000917	0.001833	0	0	0	0.001229	0	0	0	0	0	0	0	0	0	0	0	0.000595	cytosolic small ribosomal	RNA binding [pmid 18619993]	
1612	2	0.000176	1	1.01E-06	174.4423		ENSG00000109061	MYH1			gi	11552082	ref	NP_	myosin, heavy chain 1, skele	1939	223143	5.7	0	O	O	14	0	0.000243	0.001163	0	0	0	2	0.000352	0.000553	0	0	0	0	0	0	0	0.06E-06	0	0	0	0	0	0	0			
1613	2	0.000176	0	0	NF		ENSG00000196367	LTAF			gi	55767250	ref	NP_	lipopolysaccharide-induced T	161	17103	10.6	0	O	O	19	0.003	0	0.001197	0	0	0	1	0.000299	0.000583	0	0	0	0.000203	0	1	5.96E-05	0.000119	0	0	0	0	0	0	0	Possible membrane-		RNA polymerase II
1614	2	0.000174	0	0	NF		ENSG00000109534	NOLA1			gi	15011916	ref	NP_	nucleolar protein family A, m	217	22348	10.9	0	O	O	27	0.000747	0.000645	0	0	0	0	2	0.000348	0.000404	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Gar1 protein RNA binding	membrane fraction; nucleus;	cation channel activity [pmid
1615	2	0.000171	0	0	NF		ENSG00000170430	MGMT			gi	4505177	ref	NP_	O-6-methylguanine-DNA met	207	21646	8.1	0	O	O	0	0	0	0	0	0.000256	0	1	6.4E-05	0.000128	0	0	0	0	0	0	0	0	0.000113	0	0.000278	0.000556	0	0	0	6-O-methylguanine DNA	nucleus [pmid 2188979]	DNA binding [pmid 2188979]
1616	2	0.000169	0	0	NF		ENSG00000111669	CC2D2B			gi	11340763	ref	XP_	PREDICTED: hypothetical p	249	26943	8.1	0	O	O	37	0	0	0	0	0	0	1	0.00027	0.00054	0	0	0	0	0	0	0	0	0.000219	0.000511	0	0.000397	0.000794	0	0	0	Trioisophosphate		
1617	2	0.000163	0	0	NF		ENSG00000171262	FAM98B			gi	10945258	ref	NP_	family with sequence similari	433	45547	8.7	0	O	O	0	0	0	0	0	0.000245	0	1	6.12E-05	0.000122	0	0	0.001065	0	0	0	0	0	0	0	0.000264	0.000528	0	0	0			
1618	2	0.000159	0	0	NF		ENSG00000145165	RPL42			gi	28667717	ref	NP_	ribosomal protein L42 [Homo	102	11634	10.9	0	O	O	0	0	0	0	0	0.000144	0	1	3.11E-05	6.22E-05	0	0	0.000149	0	0	0	0	0	0	0	0.000298	0.000596	0	0	0		mitochondrial small ribosomal	structural constituent of	
1619	2	0.000155	0	0	NF		ENSG00000125868	DSTN			gi	28209569	ref	NP_	destrin isoform a [Homo sapi	165	18506	7.9	0	O	O	0	0	0	0	0	0.000545	0	1	0.000136	0.000273	0	0	0.000692	0	0	0	0	0	0	0	0.000173	0.000346	0	0	0	Actin depolymerisation	intracellular	actin binding
1620	2	0.000146	0	0	NF		ENSG00000181594	LOC645870			gi	16164514	ref	XP_	PREDICTED: similar to barni	86	9740	6.1	0	O	O	32	0.001	0	0	0	0.000411	0	1	0.000103	0.000205	0	0	0.000759	0	0	0	0	0	0	0	0.00019	0.00038	0	0	0			
1621	2	0.000144	0	0	NF		ENSG00000116674	ENO2			gi	5803011	ref	NP_	enolase 2 [Homo sapiens]	434	47269	5.4	0	O	O	0	0	0	0	0	0.000138	0	1	3.45E-05	6.9E-05	0.001025	0	0	0	0	0	0	0	0.000208	0.000415	0	0	0	0	Enolase: Enolases are	phosphopyruvate hydratase	lyase activity; magnesium
1622	2	0.000145	0	0	NF		ENSG00000197045	GMFB			gi	47584442	ref	NP_	glia maturation factor, beta [H	142	16713	5.3	0	O	O	0	0	0.000164	0	0.000995	0	0	2	0.00029	0.000477	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Actin depolymerisation	intracellular	actin binding; growth factor
1623	2	0.000145	0	0	NF		ENSG00000156482	RPL30			gi	4509631	ref	NP_	ribosomal protein L30 [Homo	115	12784	9.6	0	O	O	31	0	0	0	0	0.000307	0	1	7.68E-05	0.000154	0	0	0.000851	0	0	0	0	0	0	0	0.000213	0.000426	0	0	0	Ribosomal protein L30E	intracellular; ribosome	structural constituent of
1624	2	0.000138	0	0	NF		ENSG00000185275	UBE2L6			gi	19854272	ref	NP_	ubiquitin-conjugating enzyme	153	17769	7.9	0	O	O	0	0	0	0	0	0.000808	0	1	0.000202	0.000404	0	0	0	0	0	0	0	0	0	0	0.000283	0.000147	0	0	0	Ubiquitin-conjugating	membrane	ligase activity; protein
1625	2	0.000133	0	0	NF		ENSG00000117280	RAB7L1			gi	4506375	ref	NP_	RAB7, member RAS oncoge	203	23155	7.2	0	O	O	20	0.037	0	0.000402	0	0	0	1	0.000101	0.000201	0	0.000663	0	0	0	0	0	0	0	0	0.000166	0.000332	0	0	0	Rab3B/Rab32 subfamily.		GTP binding; GTPase
1626	2	0.000126	0	0	NF		ENSG00000138398	CALM1			gi	14240545	ref	NP_	EF-hand calcium binding dor	355	45494	7.5	0	O	O	28	0	5.9E-05	0.000067	0	0	0	1	0.000295	0.000467	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	EF-hand, calcium binding	membrane	calcium ion binding
1627	2	0.000126	0	0	NF		ENSG00000102978	POLR2C			gi	14702171	ref	NP_	DNA directed RNA polymera	275	31441	4.9	0	O	O	0	0	0	0	0.00045	0	0	1	0.000112	0.000225	0	0	0.000558	0	0	0	0	0	0	0	0.00014	0.000279	0	0	0	RNA polymerases D; DNA-	DNA-directed RNA	DNA binding; DNA-directed
1628	2	0.000119	0	0	NF		ENSG00000124578	HIST1H4G			gi	4504319	ref	NP_	histone cluster 1, H4g [Homo	98	11009	11.1	0	O	O	25	0	0.000952	0	0	0	0	1	0.000238	0.000476	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Histone H4, one of the four	nucleosome; nucleus	
1629	2	0.000118	0	0	NF		ENSG00000196141	PSMD8			gi	15663100	ref	NP_	proteasome 26S non-ATPase	350	39612	9.7	0	O	O	35	0.035	0	0	0	0.000977	0	1	0.000244	0.000488	0.41E-05	0	0	0	0	0	0	0	0	0	0.000325	0.000429	0	0	0			

																					RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs										
rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
1716	2	4.64E-05	0	0	INF		ENSG00000128394:	APOBEC3F			gi|22907044|ref|NP_	apolipoprotein B mRNA editi	373	45020	7.2	0	o	Q	0	0	0	6.25E-05	0	0	0	1	1.56E-05	3.13E-05	0	0	0	0	0.000309	1	7.72E-05	0.000154	0	0	0	0	0	0	0	0	APOBEC-like C-terminal		hydrolase activity; hydrolase
1717	2	4.61E-05	0	0	INF		ENSG00000087157:	PGS1			gi|84508631|ref|NP_	phosphatidylglycerophospha	556	62730	8.9	0	o	S	64	0.962	0	0	0	0	0	0	0	0	0	0.000161	0	0	0.000207	2	9.21E-05	0.000108	0	0	0	0	0	0	0	0	Phospholipase D. Active	endoplasmic reticulum [pmid	catalytic activity; CDP-
1718	2	4.6E-05	0	0	INF		ENSG00000076053:	RBM7			gi|9994185|ref|NP_0	RNA binding motif protein 7 [	266	30503	9.6	0	o	Q	20	0	0	0	0	0.000199	0	1	4.98E-05	9.96E-05	0	0.000169	0	0	0	1	4.22E-05	8.43E-05	0	0	0	0	0	0	0	0	RNA recognition motif;		nucleic acid binding;
1719	2	4.57E-05	0	0	INF		ENSG00000165775:	FUNDC2			gi|24371248|ref|NP_	FUN14 domain containing 2	189	20676	9.7	0	o	Q	23	0.037	0	0.000247	0	0	0	1	6.17E-05	0.000123	0	0.000119	0	0	0	1	2.97E-05	5.94E-05	0	0	0	0	0	0	0	0	FUN14 family. This family		
1720	2	4.45E-05	0	0	INF		ENSG00000163636:	PSMD6			gi|7661914|ref|NP_0	proteasome (prosome, macro	389	45531	5.6	0	o	Q	36	0	0	6E-05	0	0	0	1	1.5E-05	3E-05	0	0	0	0	0.000296	1	7.4E-05	0.000148	0	0	0	0	0	0	0	0	26S proteasome regulatory	cytosol; proteasome complex	ATPase activity [pmid
1721	2	4.43E-05	0	0	INF		ENSG00000131966:	ACTR10			gi|8923712|ref|NP_0	uncharacterized hypothalamu	417	46307	7.4	0	o	Q	31	0	0	0	0	0	0	0	0	0	0	0	0	7.83E-05	0.000276	2	8.86E-05	0.00013	0	0	0	0	0	0	0	0	Actin; An ubiquitous protein	cytoskeleton	protein binding; structural
1722	2	4.41E-05	0	0	INF		ENSG00000116701:	NCF2			gi|67189970|ref|NP_	neutrophil cytosolic factor 2 [	526	59762	6.2	0	o	Q	17	0.183	0.000308	4.43E-05	0	0	0	2	8.82E-05	0.000148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	cytosol; soluble fraction	binding; electron carrier
1723	2	4.38E-05	0	0	INF		ENSG00000101898:	MCTS1			gi|169217217|ref|XP	PREDICTED: similar to Malig	156	17485	8.7	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000105	0.000246	2	8.77E-05	0.000117	0	0	0	0	0	0	0	0			
1724	2	4.37E-05	0	0	INF		ENSG00000076248:	UNG			gi|19718751|ref|NP_	uracil-DNA glycosylase isofo	313	34645	9.3	0	o	Q	17	0.001	0	0	0	0	0	0	0	0	0	0	0	0.000104	0.000245	2	8.74E-05	0.000116	0	0	0	0	0	0	0	0	uracil-DNA glycosylase;	mitochondrion; nucleus [pmid	hydrolase activity, acting on
1725	2	4.37E-05	0	0	INF		ENSG00000132581:	SDF2			gi|14141195|ref|NP_	stromal cell-derived factor 2	211	23026	7.3	0	o	S	19	1	0	0	0	0.000167	0	1	4.19E-05	8.37E-05	0	0	0	0	0.000182	1	4.55E-05	9.1E-05	0	0	0	0	0	0	0	0	Domain in ryanodine and	extracellular space [pmid	dolichyl-phosphate-mannose-
1726	2	4.36E-05	0	0	INF		ENSG00000084072:	PPIE			gi|45439316|ref|NP_	peptidylprolyl isomerase E is	296	33085	5.6	0	o	Q	25	0.002	0	0	0	0.000239	0	1	5.97E-05	0.000119	0	0	0	0.00011	0	1	2.76E-05	5.51E-05	0	0	0	0	0	0	0	0	cyclophilin_ABH_like:	nucleus [pmid 11313484]	cyclosporin A binding [pmid
1727	2	4.31E-05	0	0	INF		ENSG00000165416:	SUGT1			gi|5730041|ref|NP_0	suppressor of G2 allele of SK	333	37805	5.2	0	o	Q	22	0.031	0	0.00021	0	0	0	1	5.25E-05	0.000105	0	0.000135	0	0	0	1	3.37E-05	6.74E-05	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	kinetochore [pmid 10445024];	binding
1728	2	4.28E-05	0	0	INF		ENSG00000152700:	SAR1B			gi|75709204|ref|NP_	SAR1a gene homolog 2 [Hor	198	22410	6.1	0	o	Q	18	0.004	0	0.000236	0	0.000107	0	2	8.57E-05	0.000112	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Sar1 subfamily. Sar1 is an	endoplasmic reticulum;	GTP binding; magnesium ion
1729	2	4.25E-05	0	0	INF		ENSG00000185164:	NOMO2			gi|27734709|ref|NP_	nodal modulator 2 isoform 2	1222	134192	5.8	0	o	S	32	0.996	0	0	0	0.000101	0	1	2.53E-05	5.06E-05	0	0.000239	0	0	0	1	5.97E-05	0.000119	0	0	0	0	0	0	0	0	Predicted outer membrane	endoplasmic reticulum;	catalytic activity; ferric iron
1730	2	4.23E-05	0	0	INF		ENSG00000205405:	LOC389217			gi|169166302|ref|XP	PREDICTED: similar to temp	296	34331	4.6	0	o	Q	21	0.01	0	7.88E-05	0	0	0	1	1.97E-05	3.94E-05	0	0	0	0	0.000259	1	6.48E-05	0.00013	0	0	0	0	0	0	0	0			
1731	2	4.23E-05	0	0	INF		ENSG00000116747:	TROVE2			gi|108796056|ref|NP	TROVE domain family, mem	525	59270	8.5	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0.000214	0	0.000124	0	2	8.45E-05	0.000104	0	0	0	0	0	0	0	0			
1732	2	4.2E-05	0	0	INF		ENSG00000174740:	LOC100131622			gi|169217445|ref|XP	PREDICTED: hypothetical pr	382	43331	9.5	0	o	Q	28	0	0	0	0	0.000277	0	1	6.94E-05	0.000139	0	5.87E-05	0	0	0	1	1.47E-05	2.94E-05	0	0	0	0	0	0	0	0			
1733	2	4.19E-05	0	0	INF		ENSG00000146576:	C7orf26			gi|21362070|ref|NP_	hypothetical protein LOC790	449	50047	7.7	0	o	Q	35	0	0	0	0	7.87E-05	0	1	1.97E-05	3.93E-05	0	0	0	0	0.000256	1	6.41E-05	0.000128	0	0	0	0	0	0	0	0			
1734	2	4.18E-05	0	0	INF		ENSG00000163002:	NUP35			gi|31982904|ref|NP_	nucleoporin 35kDa [Homo sa	326	34774	9.1	0	o	Q	50	0.008	0	0	0	0.000217	0	1	5.42E-05	0.000108	0	0	0	0	0.000118	1	2.94E-05	5.89E-05	0	0	0	0	0	0	0	0	MPPN (rrm-like) domain.	nuclear pore; nucleus	
1735	2	4.13E-05	0	0	INF		ENSG00000144034:	TPRKB			gi|7705590|ref|NP_0	TP53RK binding protein [Hor	175	19661	6.8	0	o	Q	27	0	0	0	0	0.000202	0	1	5.05E-05	0.000101	0	0.000128	0	0	0	1	3.2E-05	6.41E-05	0	0	0	0	0	0	0	0	Kinase binding protein CGI-	cytosol [pmid 12659830]	protein binding [pmid
1736	2	4.12E-05	0	0	INF		ENSG00000116649:	SRM			gi|63253298|ref|NP_	spermidine synthase [Homo	302	33825	5.5	0	o	Q	35	0.001	0	0.000154	0	0.000175	0	2	8.25E-05	9.56E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Spermine/spermidine		spermidine synthase activity
1737	2	4.11E-05	0	0	INF		ENSG00000170619:	COMMD5			gi|154800418|ref|NP	COMM domain containing 5	224	24670	7	0	o	Q	20	0.079	0	0	0	0.000158	0	1	3.94E-05	7.89E-05	0	0	0	0	0.000171	1	4.28E-05	8.57E-05	0	0	0	0	0	0	0	0			
1738	2	4.11E-05	0	0	INF		ENSG00000115073:	ACTR1B			gi|11342680|ref|NP_	ARP1 actin-related protein 1	376	42293	6.4	0	o	Q	20	0	0	0	0	0	0	0	0	0	0	8.95E-05	0	0	0.000239	2	8.21E-05	0.000113	0	0	0	0	0	0	0	0	Actin; An ubiquitous protein	actin filament; cytoplasm	ATP binding; nucleotide
1739	2	4.04E-05	0	0	INF		ENSG00000101986:	ABCD1			gi|7262393|ref|NP_0	ATP-binding cassette, sub-fa	745	82937	8.9	0	o	S	35	0.952	0	0	0	0	0	0	0	0	0	0.000301	0	2.19E-05	0	2	8.08E-05	0.000147	0	0	0	0	0	0	0	0	ABC transporter	integral to membrane; integral	ATP binding; ATPase
1740	2	4.03E-05	0	0	INF		ENSG00000213024:	NUP62			gi|24497609|ref|NP_	nucleoporin 62kDa [Homo sa	522	53255	5.3	0	o	Q	27	0.045	0	0	0	0.000102	0	1	2.54E-05	5.08E-05	0	0	0	0	0.000221	1	5.52E-05	0.00011	0	0	0	0	0	0	0	0	Nsp1-like C-terminal region.	cytoplasm [pmid 10373430];	chromatin binding [pmid
1741	2	4E-05	0	0	INF		ENSG00000133275:	CSNK1G2			gi|153791733|ref|NP	casein kinase 1, gamma 2 [H	415	47457	9.1	0	o	Q	0	0	0	0	0	4.26E-05	0	1	1.06E-05	2.13E-05	0	0	0	0	0.000278	1	6.94E-05	0.000139	0	0	0	0	0	0	0	0			
1742	2	3.99E-05	0	0	INF		ENSG00000091732:	ZC3HC1			gi|66348045|ref|NP_	zinc finger, C3HC type 1 [Ho	502	55262	5.6	0	o	Q	20	0.003	0	0	0	0.000141	0	1	3.52E-05	7.04E-05	0	0.000179	0	0	0	1	4.47E-05	8.94E-05	0	0	0	0	0	0	0	0	C3HC zinc finger-like. This	nucleus	metal ion binding; protein
1743	2	3.97E-05	0	0	INF		ENSG00000136104:	RNASEH2B			gi|13375742|ref|NP_	ribonuclease H2, subunit B [	312	35105	9.1	0	o	Q	16	0	0	0	0	0	0	0	0	0	0	7.19E-05	0	0	0.000246	2	7.95E-05	0.000116	0	0	0	0	0	0	0	0		nucleus	
1744	2	3.92E-05	0	0	INF		ENSG00000197345:	MRPL21			gi|31652226|ref|NP_	mitochondrial ribosomal prote	205	22815	9.9	0	o	S	17	0.94	0	0.000228	0	8.62E-05	0	2	7.84E-05	0.000107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Ribosomal prokaryotic L21	intracellular; ribosome	RNA binding; structural
1745	2	3.89E-05	0	0	INF		ENSG00000117614:	SYF2			gi|46371998|ref|NP_	SYF2 homolog, RNA splicing	201	23568	8.1	0	o	Q	21	0.108	0	0	0	8.79E-05	0	1	2.2E-05	4.39E-05	0	0.000223	0	0	0	1	5.58E-05	0.000112	0	0	0	0	0	0	0	0	SYF2 splicing factor.	nucleus [pmid 11118353]	protein binding [pmid
1746	2	3.87E-05	0	0	INF		ENSG00000062582:	MRPS24			gi|15721937|ref|NP_	mitochondrial ribosomal prote	167	19015	9.4	0	o	S	17	0.836	0	0	0	0.000212	0	1	5.29E-05	0.000106	0	0	0	9.77E-05	0	1	2.44E-05	4.89E-05	0	0	0	0	0	0	0	0		mitochondrial small ribosomal	
1747	2	3.87E-05	0	0	INF		ENSG00000123908:	EIF2C2			gi|29171734|ref|NP_	eukaryotic translation initiatio	859	97208	9.2	0	o	Q	21	0.01	0	0	0	4.11E-05	0	1	1.03E-05	2.06E-05	0	0	0	0	0.000268	1	6.7E-05	0.000134	0	0	0	0	0	0	0	0	PAZ domain,		protein binding [pmid
1748	2	3.85E-05	0	0	INF		ENSG00000126088:	UROD			gi|71051616|ref|NP_	uroporphyrinogen decarboxy	367	40787	6.1	0	o	Q	0	0	0	6.36E-05	0	0	0	1	1.59E-05	3.18E-05	0	0.000245	0	0	0	1	6.11E-05	0.000122	0	0	0	0	0	0	0	0	Uroporphyrinogen		lyase activity;
1749	2	3.81E-05	0	0	INF		ENSG00000110871:	COQ5			gi|116063536|ref|NP	coenzyme Q5 homolog, meth	327	37140	6.9	0	o	S	19	0.67	0	0.000143	0	0.000162	0	2	7.62E-05	8.83E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1750	2	3.8E-05	0	0	INF		ENSG00000110619:	CARS			gi|10835051|ref|NP_	cysteinyl-tRNA synthetase is	748	85473	6.7	0	o	Q	30	0	0	0	0	4.72E-05	0	1	1.18E-05	2.36E-05	0	0	0	0	0.000257	1	6.42E-05	0.000128	0	0	0	0	0	0	0	0	This is the catalytic core	cytoplasm [pmid 7987009];	ATP binding; cysteine-tRNA
1751	2	3.76E-05	0	0	INF		ENSG00000102218:	RP2			gi|5902060|ref|NP_0	XRP2 protein [Homo sapiens	350	39642	5.1	0	o	Q	0	0	0	0.0002	0	0.000101	0	2	7.52E-05	9.58E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Nucleoside diphosphate		ATP binding; nucleoside
1752	2	3.74E-05	0	0	INF		ENSG00000135632:	SMYD5			gi|154689858|ref|NP	SMYD family member 5 [Hor	418	47341	5	0	o	Q	20	0.39	0	0	0	8.45E-05	0	1	2.11E-05	4.23E-05	0	0.000215	0	0	0	1	5.37E-05	0.000107	0	0	0	0	0	0	0	0			
1753	2	3.73E-05	1	4.61E-06	8.088435		ENSG00000102786:	INTS6			gi|11024694|ref|NP_	integrator complex subunit 6	887	100390	8.6	0	o	Q	21	0.067	0	0	0.000212	0	0	1	5.3E-05	0.000106	0	0	0	0	8.66E-05	1	2.16E-05	4.33E-05	0	0	0	0	0	0	3.69E-05	0	Von Willebrand factor type	integrator complex [pmid	helicase activity; peptidase
1754	2	3.68E-05	0	0	INF		ENSG00000092054:	MYH7			gi|115496169|ref|NP	myosin, heavy chain 7, cardi	1935	223095	5.8	0	o	Q	20	0	0	0.000272	0	0	0	1	6.79E-05	0.000136	0	2.32E-05	0	0	0	1	5.8E-06	1.16E-05	0	0	0	0	0	0	0	0			
1755	2	3.67E-05	0	0	INF		ENSG00000117906:	RCN2			gi|4506457|ref|NP_0	reticulocalbin 2, EF-hand cal	317	36876	4.4	0	o	S	26	1	0	0	0	0.000223	0	1	5.57E-05	0.000111	0	7.08E-05	0	0	0	1	1.77E-05	3.54E-05	0	0	0	0	0	0	0	0	EF-hand, calcium binding	endoplasmic reticulum [pmid	calcium ion binding [pmid
1756	2	3.64E-05	0	0	INF		ENSG00000172315:	TP53RK			gi|41327715|ref|NP_	p53-related protein kinase [H	253	28160	9.5	0	o	Q	46	0	0	0	0	0.00014	0	1	3.49E-05	6.98E-05	0	0	0	0	0.000152	1	3.79E-05	7.59E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	nucleus	ATP binding; nucleotide
1757	2	3.62E-05	0	0	INF		ENSG00000075188:	NUP37			gi|34222121|ref|NP_	nucleoporin 37kDa [Homo sa	326	36708	5.9	0	o	Q	0	0	0	0	0	5.42E-05	0	1	1.35E-05	2.71E-05	0	0	0	0	0.000236	1	5.89E-05	0.000118	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus	
1758	2	3.58E-05	0	0	INF		ENSG00000085377:	PREP			gi|41349456|ref|NP_	prolyl endopeptidase [Homo	710	80700	5.9	0	o	Q	0	0	0	0	0	0.000124	0	1	3.11E-05	6.22E-05	0	0	0	0	0.000162	1	4.06E-05	8.11E-05	0	0	0	0	0	0	0	0	Serine proteases of the	cytoplasm [pmid 9695945]	hydrolase activity; prolyl
1759	2	3.57E-05	0	0	INF		ENSG00000105373:	SNORD23			gi|7657130|ref|NP_0	glioma tumor suppressor can	478	54417	10.4	0	o	Q	33	0	0	9.76E-05	0	0	0	1	2.44E-05	4.88E-05	0	0.000188	0	0	0	1	4.69E-05	9.39E-05	0	0	0	0	0	0	0	0	Nop53 (60S ribosomal	intracellular [pmid 10196275];	
1760	2	3.52E-05	1	4.28E-06	8.235576		ENSG00000108344:	PSMD3			gi|25777612|ref|NP_	proteasome 26S non-ATPase	534	60978	8.4	0	o	Q	0	0	0	0	0	6.62E-05	0	1	1.65E-05	3.31E-05	0	0	0	0	0.000216	1	5.39E-05	0.000108	0	0	0	3.42E-05	0	0	0	0	Proteasome regulatory	cytosol; proteasome complex	binding
1761	2	3.44E-05	0	0	INF		ENSG00000152778:	IFIT5			gi|6912630|ref|NP_0	interferon-induced protein wit	482	55847	7.4	0	o	Q	26	0	0	0	0	3.66E-05	0	1	9.16E-06	1.83E-05	0	0	0	0	0.000239	1	5.97E-05	0.000119	0	0	0	0	0	0	0	0	Tetratricopeptide repeat		binding
1762	2	3.41E-05	0	0	INF		ENSG00000185115:	NDNL2			gi|20162572|ref|NP_	necdin-like 2 [Homo sapiens]	304	34308	9.3	0	o	Q	0	0	0	0	0	5.81E-05	0	1	1.45E-05	2.91E-05	0	0	0	0.000215	0	1	5.37E-05	0.000107	0	0	0	0	0	0	0	0	MAGE family. The MAGE	nucleus	
1763	2	3.4E-05	0	0	INF		ENSG00000153914:	SFRS12			gi|116089325|ref|NP	splicing factor, arginine/serin	624	71650	10.2	0	o	Q	23	0.308	0	0	0	0.000142	0	1	3.54E-05	7.08E-05	0	0	0	0.000131	0	1	3.27E-05	6.54E-05	0	0	0	0	0	0	0	0			
1764	2	3.4E-05	0	0	INF		ENSG00000115233:	PSMD14			gi|5031981|ref|NP_0	26S proteasome-associated	310	34577	6.5	0	o	Q	16	0.026	0	0	0	0.000114	0	1	2.85E-05	5.7E-05	0	0	0	0.000158	0	1	3.95E-05	7.9E-05	0	0	0	0	0	0	0	0	JAB/MPN domain; Domain	cytosol; proteasome complex	
1765	2	3.4E-05	0	0	INF		ENSG00000106305:	MCA2			gi|11125770|ref|NP_	JTV1 [Homo sapiens]	320	35349	8.2	0	o	Q	33	0	0	0	0	0.000221	0	1	5.52E-05	0.00011	0	0	0	0.000051	0	1	1.28E-05	2.55E-05	0	0	0	0	0	0	0	0	GST_C family, JTV-1		damaged DNA binding
1766	2	3.39E-05	0	0	INF		ENSG00000117308:	GALE			gi|56237023|ref|NP_	UDP-galactose-4-epimerase	348	38282	6.7	0	o	Q	26	0.014	0	0	0	5.08E-05	0	1	1.27E-05	2.54E-05	0	0	0	0	0.000221	1	5.52E-05	0.00011	0	0	0	0	0	0	0	0	UDP-glucose 4-epimerase		catalytic activity; coenzyme
1767	2	3.34E-05	0	0	INF		ENSG00000205302:	SNX2			gi|23111038|ref|NP_	sorting nexin 2 [Homo sapier	519	58471	5.1	0	o	Q	0	0	0	4.49E-05	0	0	0	1	1.12E-05	2.25E-05	0	0	0	0	0.000222	1	5.55E-05	0.000111	0	0	0	0	0	0	0	0	Sorting nexin, N-terminal		phosphoinositide binding;
1768	2	3.33E-05	0	0	INF		ENSG00000100462:	PRMT5			gi|20070220|ref|NP_	protein arginine methyltransf	637	72684	6.3	0	o	Q	18	0.139	0	0	0	0	0	0	0	0	0	0	0	2.56E-05	0.000241	2	6.67E-05	0.000117	0	0	0	0	0	0	0	0	PRMT5 arginine-N-	cytoplasm	histone-arginine N-
1769	2	3.26E-05	0	0	INF		ENSG00000169499:	PLEKHA2			gi|154146216|ref|NP	pleckstrin homology domain	425	47245	8.7	0	o	Q	0	0	0	0.00022	0	4.16E-05	0	2	6.53E-05	0.000105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1770	2	3.26E-05	0	0	INF		ENSG00000183093:	MRPL12			gi|27436901|ref|NP_	mitochondrial ribosomal prote	198	21348	8.9	0	o	S	21	0.861	0	0	0	0.000178	0	1	4.46E-05	8.92E-05	0	0	0	8.24E-05	0	1	2.06E-05	4.12E-05	0	0	0	0	0	0	0	0	50S ribosomal protein	intracellular; mitochondrial	RNA binding [pmid 8626705];
1771	2	3.23E-05	0	0	INF		ENSG00000081059:	TCF7			gi|42518080|ref|NP_	transcription factor 7 (T-cell s	384	41552	7.5	0	o	Q	19	0	0	0	0	4.6E-05	0	1	1.15E-05	2.3E-05	0	0	0	0.000213	0	1	5.31E-05	0.000106	0	0	0	0	0	0	0	0	N-terminal CTNNB1 binding	nucleus	DNA binding; RNA
1772	2	3.23E-05	0	0	INF		ENSG00000183386:	FHL3			gi|54112385|ref|NP_	four and a half LIM domains	280	31192	6.2	0	o	Q	0	0	0	8.33E-05	0	0	0	1	2.08E-05	4.17E-05	0	0	0	0.000175	0	1	4.37E-05	8.74E-05	0	0	0	0	0	0	0	0	Zinc-binding domain		metal ion binding; zinc ion
1773	2	3.22E-05	0	0	INF		ENSG00000185721:	DRG1			gi|4758796|ref|NP_0	developmentally regulated G	367	40542	8.9	0	o	Q	19	0	0	0	0	4.81E-05	0	1	1.2E-05	2.41E-05	0	0	0	0	0.000209	1	5.23E-05	0.000105	0	0	0	0	0	0	0	0	The developmentally	intracellular	GTP binding; nucleotide
1774	2	3.21E-05	0	0	INF		ENSG00000133731:	IMPA1			gi|5031789|ref|NP_0	inositol(myo)-1(or 4)-monoph	277	30189	5.3	0	o	Q	25	0.001	0	0	0	0	0	0	0	0	0	0	0	0.000118	0.000139	2	6.41E-05	7.45E-05	0	0	0	0	0	0	0	0	IMPase, inositol		hydrolase activity; inositol-
1775	2	3.2E-05	0	0	INF		ENSG00000139793:	MBNL2			gi|21464125|ref|NP_	muscleblind-like 2 isoform 1	367	39334	8.9	0	o	Q	29	0.001	0	6.36E-05	0	0.000193	0	2	6.4E-05	9.08E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	zinc finger; smart00356		nucleic acid binding; zinc ion
1776	2	3.19E-05	0	0	INF		ENSG00000108479:	GALK1			gi|4503895|ref|NP_0	galactokinase 1 [Homo sapie	392	42272	6.5	0	o	Q	20	0.005	0	5.95E-05	0	0	0	1	1.49E-05	2.98E-05	0	0	0	0	0.000196	1	4.9E-05	9.79E-05	0	0	0	0	0	0	0	0	GHMP kinases C terminal.	cytoplasm [pmid 8908517];	ATP binding [pmid
1777	2	3.15E-05	0	0	INF		ENSG00000038274:	MAT2B			gi|11034825|ref|NP_	methionine adenosyltransfera	334	37552	7.4	0	o	Q	20	0	0	0	0	0.000106	0	1	2.64E-05	5.29E-05	0	0	0	0.000147	0	1	3.66E-05	7.33E-05	0	0	0	0	0	0	0	0	RmlD substrate binding	intracellular [pmid 10644686];	dTDP-4-dehydrorhamnose
1778	2	3.13E-05	1	2.51E-06	12.46183		ENSG00000126216:	TUBGCP3			gi|5453660|ref|NP_0	tubulin, gamma complex ass	907	103571	8.1	0	o	Q	27	0.055	0	0	0	3.9E-05	0	1	9.74E-06	1.95E-05	0	0	0	0	0.000212	1	5.29E-05	0.000106	0	0	0	2.01E-05	0	0	0	0	Spc97 / Spc98 family. The	centriole [pmid 9566969];	gamma-tubulin binding [pmid
1779	2	3.13E-05	0	0	INF		ENSG00000167900:	TK1			gi|155969680|ref|NP	thymidine kinase 1, soluble [	276	29891	8.9	0	o	Q	54	0.005	0	0.000169	0	0	0	1	4.23E-05	8.45E-05	0	8.13E-05	0	0	0	1	2.03E-05	4.06E-05	0	0	0	0	0	0	0	0		cytoplasm	ATP binding; kinase activity;
1780	2	3.11E-05	0	0	INF		ENSG00000104081:	BMF			gi|51558688|ref|NP_	Bcl2 modifying factor isoform	184	20508	5	0	o	Q	0	0	0	0.000127	0	0	0	1	3.17E-05	6.34E-05	0	0.000122	0	0	0	1	3.05E-05	6.1E-05	0	0	0	0	0	0	0	0		myosin [pmid 11546872]	protein binding [pmid
1781	2	3.09E-05	0	0	INF		ENSG00000022267:	FHL1			gi|21361122|ref|NP_	four and a half LIM domains	280	31895	8.3	0	o	Q	0	0	0	0	0	0.000189	0	1	4.73E-05	9.46E-05	0	0	0	5.83E-05	0	1	1.46E-05	2.91E-05	0	0	0	0	0	0	0	0	Zinc-binding domain	nucleus	metal ion binding; zinc ion
1782	2	3.08E-05	0	0	INF		ENSG00000101346:	POFUT1			gi|27436889|ref|NP_	protein O-fucosyltransferase	388	43956	8.5	0	o	S	27	1	0	0.00012	0	0	0	1	3.01E-05	6.01E-05	0	0	0	0.000126	0	1	3.15E-05	6.31E-05	0	0	0	0	0	0	0	0		cytoplasm; endoplasmic	manganese ion binding;
1783	2	3.07E-05	0	0	INF		ENSG00000107672:	NSMCE4A			gi|8923009|ref|NP_0	non-SMC element 4 homolog	385	44286	5.3	0	o	Q	0	0	0	0	0	4.59E-05	0	1	1.15E-05	2.29E-05	0	0	0	0	0.000199	1	4.99E-05	9.97E-05	0	0	0	0	0	0	0	0	Nse4. Nse4 is a component		
1784	2	3.05E-05	0	0	INF		ENSG00000115234:	SNX17			gi|7661890|ref|NP_0	sorting nexin 17 [Homo sapie	470	52901	7.5	0	o	Q	30	0	0	0.000149	0	0	0	1	3.72E-05	7.44E-05	0	9.55E-05	0	0	0	1	2.39E-05	4.77E-05	0	0	0	0	0	0	0	0	Band 4.1 homologues; Also	early endosome [pmid	phosphoinositide binding;
1785	2	3.02E-05	0	0	INF		NA:ENSMUSG00000	LOC152663			gi|169166935|ref|XP	PREDICTED: similar to ribos	282	31661	10.2	0	o	Q	41	0	0	8.27E-05	0	0	0	1	2.07E-05	4.14E-05	0	0.000159	0	0	0	1	3.98E-05	7.96E-05	0	0	0	0	0	0	0	0			
1786	2	3.01E-05	1	5.85E-06	5.143564		ENSG00000090621:	PABPC4			gi|4504715|ref|NP_0	poly A binding protein, cytopl	644	70783	9.3	0	o	Q	21	0.047	0	0	0	0.000165	0	1	4.11E-05	8.23E-05	0	0	0	7.6E-05	0	1	1.9E-05	3.8E-05	0	0	0	0	0	0	0	4.68E-05	Poly-adenylate binding	cytoplasm [pmid 8524242]	nucleic acid binding;
1787	2	3E-05	0	0	INF		ENSG00000145388:	KIAA1627			gi|24308265|ref|NP_	hypothetical protein LOC577	456	52150	6.2	0	o	Q	31	0.002	0	0	0	0	0	0	0	0	0	0	0	7.16E-05	0.000168	2	6E-05	7.97E-05	0	0	0	0	0	0	0	0	MT-A70. MT-A70 is the S-	nucleus	methyltransferase activity
1788	2	2.98E-05	0	0	INF		ENSG00000204560:	DHX16			gi|4503293|ref|NP_0	DEAH (Asp-Glu-Ala-His) box	1041	119172	6.7	0	o	Q	40	0.004	0	0	0	1.7E-05	0	1	4.24E-06	8.48E-06	0	0	0	0	0.000221	1	5.53E-05	0.000111	0	0	0	0	0	0	0	0	DEXH-box helicases. A	nucleus [pmid 9547260]	ATP binding; ATP-dependent
1789	2	2.96E-05	0	0	INF		ENSG00000174840:	PDE12			gi|68051728|ref|NP_	phosphodiesterase 12 [Homo	609	67405	6.6	0	o	Q	17	0.06	0	0	0	0.000174	0	1	4.35E-05	8.7E-05	0	0	0	0	6.3E-05	1	1.58E-05	3.15E-05	0	0	0	0	0	0	0	0	mRNA deadenylase,		
1790	2	2.95E-05	0	0	INF		ENSG00000074201:	CLNS1A			gi|4502891|ref|NP_0	chloride channel, nucleotide-	237	26215	4.1	0	o	Q	16	0	0	9.84E-05	0	0	0	1	2.46E-05	4.92E-05	0	0	0	0.000138	0	1	3.44E-05	6.89E-05	0	0	0	0	0	0	0	0	Nucleotide-sensitive	nucleus; plasma membrane	auxiliary transport protein
1791	2	2.95E-05	0	0	INF		ENSG00000132676:	DAP3			gi|16905526|ref|NP_	death-associated protein 3 [H	398	45566	8.9	0	o	Q	34	0.001	0	5.86E-05	0	0.000178	0	2	5.9E-05	8.37E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		mitochondrial ribosome;	
1792	2	2.95E-05	0	0	INF		ENSG00000115761:	NOL10			gi|13430872|ref|NP_	nucleolar protein 10 [Homo s	638	74503	8.5	0	o	Q	22	0	0	0	0	5.54E-05	0	1	1.38E-05	2.77E-05	0	0	0	0	0.000181	1	4.51E-05	9.03E-05	0	0	0	0	0	0	0	0	NUC153 domain. This small	nucleus	
1793	2	2.94E-05	0	0	INF		ENSG00000176014:	TUBB6			gi|14210536|ref|NP_	tubulin, beta 6 [Homo sapien	446	49857	4.9	0	o	Q	16	0	0	0.000195	0	3.96E-05	0	2	5.87E-05	9.29E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	The tubulin superfamily	cytoplasm; microtubule;	GTP binding; GTPase
1794	2	2.93E-05	0	0	INF		ENSG00000123545:	C6orf66			gi|7661786|ref|NP_0	hormone-regulated proliferati	175	20266	8.8	0	o	Q	19	0	0	0.000133	0	0.000101	0	2	5.86E-05	6.89E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Uncharacterised protein		
1795	2	2.92E-05	0	0	INF		ENSG00000142186:	SCYL1			gi|115430241|ref|NP	SCY1-like 1 isoform A [Homo	808	89631	6.3	0	o	Q	27	0	0	0	0	0	0	0	0	0	0	0.000139	0	0	9.5E-05	2	5.85E-05	6.98E-05	0	0	0	0	0	0	0	0			
1796	2	2.88E-05	0	0	INF		ENSG00000114491:	UMPS			gi|4507835|ref|NP_0	uridine monophosphate synth	480	52222	7.2	0	o	S	21	0.845	0	0	0	0.000184	0	1	4.6E-05	9.2E-05	0	4.67E-05	0	0	0	1	1.17E-05	2.34E-05	0	0	0	0	0	0	0	0	Orotidine 5'-phosphate		lyase activity; orotate
1797	2	2.88E-05	0	0	INF		ENSG00000100380:	FAM10A7			gi|19923193|ref|NP_	heat shock 70kD protein bind	369	41332	5.3	0	o	Q	19	0	0	0	0	4.79E-05	0	1	1.2E-05	2.39E-05	0	0.000182	0	0	0	1	4.56E-05	9.12E-05	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	cytoplasm [pmid 8721986]	binding; protein binding,
1798	2	2.87E-05	0	0	INF		ENSG00000166181:	API5			gi|5729730|ref|NP_0	apoptosis inhibitor 5 [Homo s	504	56770	5.9	0	o	Q	0	0	0	0	0	0.00014	0	1	3.5E-05	7.01E-05	0	8.9E-05	0	0	0	1	2.23E-05	4.45E-05	0	0	0	0	0	0	0	0	Apoptosis inhibitory protein	cytoplasm [pmid 11075807];	binding; fibroblast growth
1799	2	2.86E-05	0	0	INF		ENSG00000198183:	PLUNC			gi|18765705|ref|NP_	palate, lung and nasal epithe	256	26713	5.7	0	o	S	20	0.99	0	9.11E-05	0	0.000138	0	2	5.73E-05	6.89E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	LBP / BPI / CETP family, N-	extracellular region [pmid	lipid binding
1800	2	2.84E-05	0	0	INF		ENSG00000101199:	ARFGAP1			gi|28416436|ref|NP_	ADP-ribosylation factor GTPa	414	45676	5.8	0	o	Q	48	0	0	5.63E-05	0	0.000171	0	2	5.68E-05	8.05E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Putative GTPase activating		GTPase activator activity;
1801	2	2.83E-05	0	0	INF		ENSG00000100796:	SMEK1			gi|31657117|ref|NP_	SMEK homolog 1, suppresso	820	93896	4.9	0	o	Q	0	0	0	0	0	8.62E-05	0	1	2.15E-05	4.31E-05	0	0	0	0	0.00014	1	3.51E-05	7.02E-05	0	0	0	0	0	0	0	0	Protein of unknown function		binding
1802	2	2.82E-05	0	0	INF		ENSG00000023909:	GCLM			gi|4504011|ref|NP_0	glutamate-cysteine ligase reg	274	30727	6	0	o	Q	26	0.008	0	8.51E-05	0	0	0	1	2.13E-05	4.26E-05	0	0	0	0	0.00014	1	3.5E-05	7.01E-05	0	0	0	0	0	0	0	0	Aldo/keto reductase family.		glutamate-cysteine ligase
1803	2	2.8E-05	0	0	INF		ENSG00000075142:	SRI			gi|38679884|ref|NP_	sorcin isoform b [Homo sapie	183	20345	5.3	0	o	Q	37	0.001	0	0.000127	0	9.65E-05	0	2	5.6E-05	6.59E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	EF-hand, calcium binding	cytoplasm [pmid 16130169]	calcium channel regulator
1804	2	2.8E-05	0	0	INF		ENSG00000120885:	CLU			gi|42716297|ref|NP_	clusterin isoform 1 [Homo sa	501	57833	6.7	0	o	Q	37	0	0	0	0	7.05E-05	0	1	1.76E-05	3.53E-05	0	0	0	0	0.000153	1	3.83E-05	7.66E-05	0	0	0	0	0	0	0	0	CLUSTERIN alpha chain;	extracellular space [pmid	
1805	2	2.75E-05	0	0	INF		ENSG00000183735:	TBK1			gi|7019547|ref|NP_0	TANK-binding kinase 1 [Hom	729	83642	6.8	0	o	Q	22	0.448	0	0.000128	0	0	0	1	3.2E-05	6.4E-05	0	9.23E-05	0	0	0	1	2.31E-05	4.62E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
1806	2	2.74E-05	0	0	INF		ENSG00000170854:	MINA			gi|110227621|ref|NP	MYC induced nuclear antiger	465	52800	6.7	0	o	Q	42	0	0	0	0	0.000114	0	1	2.85E-05	5.7E-05	0	0	0	0.000105	0	1	2.63E-05	5.26E-05	0	0	0	0	0	0	0	0			
1807	2	2.71E-05	0	0	INF		ENSG00000170748:	RBMXL2			gi|153252068|ref|NP	testes-specific heterogenous	392	42814	10.3	0	o	Q	27	0	0	0	0	4.51E-05	0	1	1.13E-05	2.25E-05	0	0.000172	0	0	0	1	4.29E-05	8.58E-05	0	0	0	0	0	0	0	0			
1808	2	2.71E-05	0	0	INF		ENSG00000169126:	ARMC4			gi|31657114|ref|NP_	armadillo repeat containing 4	1044	115679	7.8	0	o	Q	22	0.009	0	0	0.00018	0	0	1	4.5E-05	9E-05	0	0	0	0	3.68E-05	1	9.19E-06	1.84E-05	0	0	0	0	0	0	0	0	Armadillo/beta-catenin-like		binding
1809	2	2.7E-05	0	0	INF		ENSG00000166166:	C14orf172			gi|123173772|ref|NP	tRNA(m1A58)-methyltransfer	289	31382	7.4	0	o	Q	34	0	0	0	0	6.11E-05	0	1	1.53E-05	3.06E-05	0	0.000155	0	0	0	1	3.88E-05	7.76E-05	0	0	0	0	0	0	0	0			
1810	2	2.69E-05	0	0	INF		ENSG00000148341:	SH3GLB2			gi|9910352|ref|NP_0	SH3-domain GRB2-like endo	395	43974	6	0	o	Q	20	0.002	0	0.000118	0	0	0	1	2.95E-05	5.9E-05	0	0	0	0	9.72E-05	1	2.43E-05	4.86E-05	0	0	0	0	0	0	0	0	BAR domain; smart00721	cytoplasm	protein binding [pmid
1811	2	2.69E-05	0	0	INF		ENSG00000144893:	MED12L			gi|93277088|ref|NP_	mediator of RNA polymerase	2145	240117	7.8	0	o	Q	18	0	0	0	0	8.24E-06	0	1	2.06E-06	4.12E-06	0.000207	0	0	0	0	1	5.17E-05	0.000103	0	0	0	0	0	0	0	0			receptor activity
1812	2	2.69E-05	0	0	INF		ENSG00000167670:	CHAF1A			gi|50513245|ref|NP_	chromatin assembly factor 1,	956	106910	5.9	0	o	Q	18	0.001	0	0	0.000197	1.85E-05	0	2	5.38E-05	9.56E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		chromatin assembly complex	chromatin binding [pmid
1813	2	2.68E-05	0	0	INF		ENSG00000114767:	RRP9			gi|4759276|ref|NP_0	RNA, U3 small nucleolar inte	475	51841	7.9	0	o	Q	25	0.008	0	0	0	0.000112	0	1	2.79E-05	5.58E-05	0	0	0	0.000103	0	1	2.58E-05	5.15E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus; small nuclear	RNA binding
1814	2	2.68E-05	0	0	INF		ENSG00000176102:	CSTF3			gi|4557495|ref|NP_0	cleavage stimulation factor s	717	82922	8.1	0	o	Q	0	0	0	0	0	0.000123	0	1	3.08E-05	6.16E-05	0	0	0	9.1E-05	0	1	2.28E-05	4.55E-05	0	0	0	0	0	0	0	0	HAT (Half-A-TPR) repeats;	intracellular; nucleus [pmid	binding; RNA binding [pmid
1815	2	2.63E-05	0	0	INF		ENSG00000057663:	ATG5			gi|4757798|ref|NP_0	APG5 autophagy 5-like [Hom	275	32447	5.8	0	o	Q	33	0	0	0	0	0.000128	0	1	3.21E-05	6.42E-05	0	8.16E-05	0	0	0	1	2.04E-05	4.08E-05	0	0	0	0	0	0	0	0	Autophagy protein Apg5.	autophagic vacuole [pmid	
1816	2	2.62E-05	0	0	INF		ENSG00000138061:	CYP1B1			gi|4503203|ref|NP_0	cytochrome P450, family 1, s	543	60832	9	0	o	S	32	0.554	0	8.59E-05	0	0	0	1	2.15E-05	4.3E-05	0	0.000124	0	0	0	1	3.1E-05	6.2E-05	0	0	0	0	0	0	0	0	Cytochrome P450.	endoplasmic reticulum;	heme binding [pmid
1817	2	2.61E-05	0	0	INF		ENSG00000148290:	SURF1			gi|4507319|ref|NP_0	surfeit 1 [Homo sapiens]	300	33331	9.6	0	o	S	24	0.949	0	0	0	5.89E-05	0	1	1.47E-05	2.94E-05	0	0.00015	0	0	0	1	3.74E-05	7.48E-05	0	0	0	0	0	0	0	0	SURF1 family; pfam02104	integral to membrane;	cytochrome-c oxidase
1818	2	2.57E-05	0	0	INF		ENSG00000110711:	AIP			gi|4502009|ref|NP_0	aryl hydrocarbon receptor int	330	37664	6.5	0	o	Q	0	0	0	0	0	0.000107	0	1	2.68E-05	5.35E-05	0	0	0	9.89E-05	0	1	2.47E-05	4.95E-05	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	cytoplasm [pmid 8972861]	binding; signal transducer
1819	2	2.57E-05	0	0	INF		ENSG00000178896:	EXOSC4			gi|9506689|ref|NP_0	exosome component 4 [Hom	245	26383	6.5	0	o	Q	17	0	0	0	0	7.21E-05	0	1	1.8E-05	3.6E-05	0	0	0	0.000133	0	1	3.33E-05	6.66E-05	0	0	0	0	0	0	0	0	3' exoribonuclease family,	cytoplasm [pmid 11110791];	3'-5'-exoribonuclease activity
1820	2	2.54E-05	0	0	INF		ENSG00000114021:	NIT2			gi|9910460|ref|NP_0	nitrilase family, member 2 [H	276	30608	7.2	0	o	Q	19	0.444	0	0	0	6.4E-05	0	1	1.6E-05	3.2E-05	0	0	0	0	0.000139	1	3.48E-05	6.95E-05	0	0	0	0	0	0	0	0	Predicted amidohydrolase		hydrolase activity, acting on
1821	2	2.5E-05	0	0	INF		ENSG00000167363:	FN3K			gi|11545906|ref|NP_	fructosamine 3 kinase [Homo	309	35171	7.6	0	o	Q	31	0.032	0	7.55E-05	0	0	0	1	1.89E-05	3.77E-05	0	0	0	0	0.000124	1	3.11E-05	6.21E-05	0	0	0	0	0	0	0	0	Uncharacterized protein		fructosamine-3-kinase
1822	2	2.49E-05	0	0	INF		ENSG00000163938:	GNL3			gi|45593130|ref|NP_	guanine nucleotide binding p	549	61993	9.2	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	5.95E-05	0.00014	2	4.98E-05	6.62E-05	0	0	0	0	0	0	0	0	GNL3L/Grn1 putative	intracellular; nucleolus;	GTP binding; nucleotide
1823	2	2.48E-05	0	0	INF		ENSG00000070770:	CSNK2A2			gi|4503097|ref|NP_0	casein kinase 2, alpha prime	350	41213	8.6	0	o	Q	15	0	0	0	0	0.000151	0	1	3.79E-05	7.57E-05	0	0	0	4.66E-05	0	1	1.17E-05	2.33E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
1824	2	2.47E-05	0	0	INF		ENSG00000161618:	ALDH16A1			gi|23503239|ref|NP_	aldehyde dehydrogenase 16	802	85113	6.8	0	o	Q	42	0.014	0	8.72E-05	0	0.00011	0	2	4.93E-05	5.77E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Aldehyde dehydrogenase		oxidoreductase activity
1825	2	2.46E-05	0	0	INF		ENSG00000177646:	ACAD9			gi|21361497|ref|NP_	acyl-Coenzyme A dehydroge	621	68760	8	0	o	S	20	0.807	0	0	0	0.000171	0	1	4.27E-05	8.53E-05	0	0	0	2.63E-05	0	1	6.57E-06	1.31E-05	0	0	0	0	0	0	0	0	Very long chain acyl-CoA	mitochondrion	acyl-CoA dehydrogenase
1826	2	2.46E-05	0	0	INF		ENSG00000003402:	CFLAR			gi|21361769|ref|NP_	CASP8 and FADD-like apopt	480	55343	8.1	0	o	Q	0	0	0	0	0	3.68E-05	0	1	9.2E-06	1.84E-05	0	0	0	0	0.00016	1	4E-05	8E-05	0	0	0	0	0	0	0	0	Death effector domain.		caspase activity; protein
1827	2	2.43E-05	0	0	INF		ENSG00000151414:	NEK7			gi|19424132|ref|NP_	NIMA (never in mitosis gene	302	34551	8.3	0	o	Q	0	0	0	7.72E-05	0	0.000117	0	2	4.86E-05	5.84E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; magnesium ion
1828	2	2.42E-05	0	0	INF		ENSG00000067066:	SP100			gi|122939208|ref|NP	nuclear antigen Sp100 isofor	885	101575	7.4	0	o	Q	32	0	0	0	0	0.00012	0	1	2.99E-05	5.99E-05	0	0	0	7.38E-05	0	1	1.84E-05	3.69E-05	0	0	0	0	0	0	0	0			
1829	2	2.41E-05	0	0	INF		ENSG00000104129:	DNAJC17			gi|8922563|ref|NP_0	DnaJ (Hsp40) homolog, subf	304	34687	8.5	0	o	Q	24	0.002	0	7.67E-05	0	0.000116	0	2	4.82E-05	5.8E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	DnaJ domain. DnaJ		heat shock protein binding;
1830	2	2.39E-05	0	0	INF		ENSG00000160959:	LRRC14			gi|7661860|ref|NP_0	leucine rich repeat containing	493	54513	6.9	0	o	S	23	0.867	0	0	0	3.58E-05	0	1	8.96E-06	1.79E-05	0	0	0	0	0.000156	1	3.89E-05	7.79E-05	0	0	0	0	0	0	0	0	Leucine-rich repeats		transferase activity
1831	2	2.39E-05	0	0	INF		ENSG00000053372:	MRTO4			gi|18490987|ref|NP_	ribosomal protein P0-like pro	239	27560	8.3	0	o	Q	0	0	0	9.76E-05	0	0	0	1	2.44E-05	4.88E-05	0	9.39E-05	0	0	0	1	2.35E-05	4.69E-05	0	0	0	0	0	0	0	0	Ribosomal protein L10	intracellular; nucleus	
1832	2	2.39E-05	0	0	INF		ENSG00000157349:	DDX19B			gi|6005743|ref|NP_0	DEAD (Asp-Glu-Ala-As) box	479	53927	6.3	0	o	Q	18	0.003	0	9.74E-05	0	0	0	1	2.43E-05	4.87E-05	0	9.37E-05	0	0	0	1	2.34E-05	4.68E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	cytoplasm [pmid 10428971];	ATP binding; ATP-dependent
1833	2	2.38E-05	0	0	INF		ENSG00000124608:	AARS2			gi|38569417|ref|NP_	alanyl-tRNA synthetase like [	985	107326	6.3	0	o	Q	56	0.338	0	0.000118	0	7.17E-05	0	2	4.75E-05	5.81E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Alanyl-tRNA synthetase		alanine-tRNA ligase activity;
1834	2	2.35E-05	0	0	INF		ENSG00000065675:	PRKCQ			gi|5453976|ref|NP_0	protein kinase C, theta [Hom	706	81865	7.6	0	o	Q	18	0.071	0	0	0	2.5E-05	0	1	6.26E-06	1.25E-05	0	0	0	0	0.000163	1	4.08E-05	8.16E-05	0	0	0	0	0	0	0	0	Protein kinase C conserved	intracellular	ATP binding; diacylglycerol
1835	2	2.34E-05	0	0	INF		ENSG00000166200:	COPS2			gi|4759264|ref|NP_0	COP9 constitutive photomorp	443	51597	5.5	0	o	Q	0	0	0	0	0	3.99E-05	0	1	9.97E-06	1.99E-05	0	0	0	0.000147	0	1	3.68E-05	7.37E-05	0	0	0	0	0	0	0	0	26S proteasome regulatory	cytoplasm [pmid 9535219];	protein binding [pmid
1836	2	2.34E-05	0	0	INF		ENSG00000168884:	TNIP2			gi|34147370|ref|NP_	A20-binding inhibitor of NF-k	429	48728	6.4	0	o	Q	30	0.019	0	0	0	8.24E-05	0	1	2.06E-05	4.12E-05	0	0.000105	0	0	0	1	2.61E-05	5.23E-05	0	0	0	0	0	0	0	0	Chromosome segregation		
1837	2	2.33E-05	0	0	INF		ENSG00000142046:	BCKDHA			gi|11386135|ref|NP_	branched chain keto acid deh	445	50471	8.3	0	o	S	33	0.987	0	0	0	3.97E-05	0	1	9.92E-06	1.98E-05	0	0	0	0.000147	0	1	3.67E-05	7.33E-05	0	0	0	0	0	0	0	0	Thiamine pyrophosphate	alpha-ketoglutarate	3-methyl-2-oxobutanoate
1838	2	2.31E-05	0	0	INF		ENSG00000111716:	LDHB			gi|4557032|ref|NP_0	lactate dehydrogenase B [Ho	334	36639	6.1	0	o	Q	47	0	0	6.98E-05	0	0	0	1	1.75E-05	3.49E-05	0	0	0	0	0.000115	1	2.87E-05	5.75E-05	0	0	0	0	0	0	0	0	L-lactate dehydrogenases	cytoplasm [pmid 16130169]	L-lactate dehydrogenase
1839	2	2.3E-05	0	0	INF		ENSG00000136271:	DDX56			gi|9506931|ref|NP_0	DEAD (Asp-Glu-Ala-Asp) box	547	61590	9.3	0	o	Q	22	0	0	0	0	6.46E-05	0	1	1.61E-05	3.23E-05	0	0	0	0.000119	0	1	2.98E-05	5.97E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleolus [pmid 10749921];	ATP binding; ATP-dependent
1840	2	2.29E-05	0	0	INF		ENSG00000197498:	BXDC1			gi|39930469|ref|NP_	brix domain containing 1 [Ho	306	35583	10	0	o	Q	0	0	0	7.62E-05	0	0	0	1	1.91E-05	3.81E-05	0	0	0	0.000107	0	1	2.67E-05	5.33E-05	0	0	0	0	0	0	0	0	Uncharacterized conserved	nucleus	
1841	2	2.28E-05	0	0	INF		ENSG00000165806:	CASP7			gi|15718698|ref|NP_	caspase 7 isoform delta [Hor	336	37815	6.4	0	o	Q	34	0.001	0	0	0	0	0	0	0	0	0	0.000134	0	4.86E-05	0	2	4.55E-05	6.3E-05	0	0	0	0	0	0	0	0	Caspase, interleukin-1 beta	cytoplasm [pmid 8576161];	caspase activity; cysteine-
1842	2	2.26E-05	0	0	INF		ENSG00000116954:	RRAGC			gi|11995472|ref|NP_	Ras-related GTP binding C [	399	44224	5.1	0	o	Q	22	0	0	5.85E-05	0	0	0	1	1.46E-05	2.92E-05	0	0	0	0.000123	0	1	3.07E-05	6.14E-05	0	0	0	0	0	0	0	0	Gtr1/RagA G protein	cytoplasm [pmid 11073942];	GDP binding [pmid
1843	2	2.26E-05	0	0	INF		ENSG00000198130:	HIBCH			gi|37594469|ref|NP_	3-hydroxyisobutyryl-Coenzym	338	38012	8.5	0	o	Q	35	0.001	0	0	0	0	0	0	0	0	0	0.000133	0	4.83E-05	0	2	4.53E-05	6.26E-05	0	0	0	0	0	0	0	0	enoyl-CoA hydratase;		3-hydroxyisobutyryl-CoA
1844	2	2.26E-05	0	0	INF		ENSG00000142409:	ZNF787			gi|152963637|ref|NP	zinc finger protein 787 [Hom	382	40428	8	0	o	Q	0	0	0	0.000122	0	0	0	1	3.05E-05	6.11E-05	0	5.87E-05	0	0	0	1	1.47E-05	2.94E-05	0	0	0	0	0	0	0	0			
1845	2	2.26E-05	0	0	INF		ENSG00000114030:	KPNA1			gi|88758611|ref|NP_	karyopherin alpha 1 [Homo s	538	60249	5	0	o	Q	0	0	0	0	0	0.000109	0	1	2.74E-05	5.47E-05	0	0	0	0	7.14E-05	1	1.78E-05	3.57E-05	0	0	0	0	0	0	0	0	Importin beta binding	cytoplasm [pmid 7754385];	nuclear localization
1846	2	2.25E-05	0	0	INF		ENSG00000148334:	PTGES2			gi|13376617|ref|NP_	prostaglandin E synthase 2 is	377	41943	9.2	0	o	S	51	0.757	0	0	0	9.37E-05	0	1	2.34E-05	4.69E-05	0	0	0	8.66E-05	0	1	2.16E-05	4.33E-05	0	0	0	0	0	0	0	0	GST_N family; microsomal	integral to membrane;	electron carrier activity;
1847	2	2.23E-05	0	0	INF		ENSG00000166902:	MRPL16			gi|8923448|ref|NP_0	mitochondrial ribosomal prote	251	28449	10.1	0	o	S	29	0.949	0	0	0	0	0.001622	1	0	0	0	0.000179	0	0	0	1	4.47E-05	8.94E-05	0	0	0	0	0	0	0	0	50S ribosomal protein L16;	intracellular; mitochondrion;	structural constituent of
1848	2	2.22E-05	0	0	INF		ENSG00000071894:	CPSF1			gi|56676371|ref|NP_	cleavage and polyadenylatio	1443	160883	6.4	0	o	Q	34	0	0	0	0	9.79E-05	0	1	2.45E-05	4.9E-05	0	0	0	0	7.98E-05	1	2E-05	3.99E-05	0	0	0	0	0	0	0	0	CPSF A subunit region.	mRNA cleavage and	mRNA 3'-UTR binding [pmid
1849	2	2.21E-05	0	0	INF		ENSG00000109113:	RAB34			gi|31543537|ref|NP_	RAB39 [Homo sapiens]	259	29058	7.9	0	o	Q	25	0	0	9.01E-05	0	0	0	1	2.25E-05	4.5E-05	0	8.66E-05	0	0	0	1	2.17E-05	4.33E-05	0	0	0	0	0	0	0	0	Rab34/Rab36 subfamily.	membrane	GTP binding; nucleotide
1850	2	2.2E-05	0	0	INF		ENSG00000091542:	ALKBH5			gi|148539642|ref|NP	alkB, alkylation repair homolo	394	44256	9.1	0	o	S	49	0.953	0	0	0	0.000134	0	1	3.36E-05	6.72E-05	0	0	0	4.14E-05	0	1	1.04E-05	2.07E-05	0	0	0	0	0	0	0	0			
1851	2	2.19E-05	0	0	INF		ENSG00000163840:	DTX3L			gi|19923717|ref|NP_	deltex 3-like [Homo sapiens]	740	83554	8.1	0	o	Q	21	0	0	0	0	7.16E-05	0	1	1.79E-05	3.58E-05	0	0	0	0	0.000104	1	2.59E-05	5.19E-05	0	0	0	0	0	0	0	0	RING-finger (Really		metal ion binding; protein
1852	2	2.17E-05	0	0	INF		ENSG00000128050:	PAICS			gi|119220557|ref|NP	phosphoribosylaminoimidazo	425	47079	7.2	0	o	Q	0	0	0	0	0	8.31E-05	0	1	2.08E-05	4.16E-05	0	0	0	0	9.03E-05	1	2.26E-05	4.52E-05	0	0	0	0	0	0	0	0			
1853	2	2.16E-05	0	0	INF		ENSG00000148824:	MTG1			gi|93277113|ref|NP_	GTP_binding protein [Homo	334	37237	9.5	0	o	Q	15	0.138	0	0	0	0.000106	0	1	2.64E-05	5.29E-05	0	6.72E-05	0	0	0	1	1.68E-05	3.36E-05	0	0	0	0	0	0	0	0	YlqF. Proteins of the YlqF	intracellular	GTP binding
1854	2	2.15E-05	0	0	INF		ENSG00000145882:	PCYOX1L			gi|31543181|ref|NP_	prenylcysteine oxidase 1 like	494	54673	7.3	0	o	S	23	1	0	9.44E-05	0	0	0	1	2.36E-05	4.72E-05	0	0	0	0	7.77E-05	1	1.94E-05	3.89E-05	0	0	0	0	0	0	0	0	Prenylcysteine lyase. This		oxidoreductase activity
1855	2	2.13E-05	0	0	INF		ENSG00000197070:	ARRDC1			gi|22748653|ref|NP_	arrestin domain containing 1	433	45981	7	0	o	Q	15	0.013	0	0	0	8.16E-05	0	1	2.04E-05	4.08E-05	0	0	0	0	8.87E-05	1	2.22E-05	4.43E-05	0	0	0	0	0	0	0	0	Arrestin (or S-antigen), N-		
1856	2	2.12E-05	0	0	INF		ENSG00000100296:	THOC5			gi|50959115|ref|NP_	THO complex 5 [Homo sapie	683	78508	6.9	0	o	Q	0	0	0	0	0	2.59E-05	0	1	6.47E-06	1.29E-05	0	0	0	0.000143	0	1	3.58E-05	7.17E-05	0	0	0	0	0	0	0	0	RecF/RecN/SMC N		
1857	2	2.11E-05	0	0	INF		ENSG00000173145:	NOC3L			gi|20806097|ref|NP_	nucleolar complex associated	800	92548	9.2	0	o	Q	0	0	0	5.83E-05	0	0.00011	0	2	4.22E-05	5.31E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Nucleolar complex-	nucleus	
1858	2	2.1E-05	0	0	INF		ENSG00000138433:	CIR			gi|40068059|ref|NP_	CBF1 interacting corepresso	450	52313	9.9	0	o	Q	0	0	0	0	0	0.000118	0	1	2.94E-05	5.89E-05	0	4.99E-05	0	0	0	1	1.25E-05	2.49E-05	0	0	0	0	0	0	0	0		histone deacetylase complex	protein binding [pmid
1859	2	2.09E-05	0	0	INF		ENSG00000161011:	SQSTM1			gi|4505571|ref|NP_0	sequestosome 1 [Homo sapi	440	47687	5.2	0	o	Q	17	0.003	0	0	0	8.03E-05	0	1	2.01E-05	4.01E-05	0	0	0	0	8.72E-05	1	2.18E-05	4.36E-05	0	0	0	0	0	0	0	0	Zinc finger, ZZ type. Zinc	cytosol [pmid 8650207] [pmid	metal ion binding; protein
1860	2	2.09E-05	0	0	INF		ENSG00000138663:	COPS4			gi|38373690|ref|NP_	COP9 signalosome subunit 4	406	46269	5.8	0	o	Q	24	0	0	0	0	8.7E-05	0	1	2.18E-05	4.35E-05	0	0	0	8.04E-05	0	1	2.01E-05	4.02E-05	0	0	0	0	0	0	0	0	26S proteasome regulatory	nucleus; signalosome complex	protein binding [pmid
1861	2	2.09E-05	0	0	INF		ENSG00000116062:	MSH6			gi|4504191|ref|NP_0	mutS homolog 6 [Homo sapi	1360	152785	6.9	0	o	Q	21	0.029	0	0	0	2.6E-05	0	1	6.49E-06	1.3E-05	0	0	0	0	0.000141	1	3.53E-05	7.06E-05	0	0	0	0	0	0	0	0	MutS6 homolog in	nucleus [pmid 8942985]	ATP binding; damaged DNA
1862	2	2.09E-05	0	0	INF		ENSG00000006047:	YBX2			gi|156415990|ref|NP	Y box binding protein 2 [Hom	364	38518	10.8	0	o	S	28	0.886	0	0	0	0	0	0	0	0	0	6.16E-05	0	0	0.000105	2	4.18E-05	5.14E-05	0	0	0	0	0	0	0	0			

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_PROB	RESTING LYMPHOCYTES NEs: HsNaOH-NE_NT_lymphocytes_ChIBTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-nNEs AVG	NT-bNEs dNSAF SDV	PHA-TREATED LYMPHOCYTES NEs: HsNaOH-NE_PHA_lymphocytes_ChIBTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-nNEs AVG	PHA-bNEs dNSAF SDV	MMs: MmNaOH-MM_liver_ChIBTi_1_dNSAF	MmNaOH-MM_liver_ChIBTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
1863	2	2.07E-05	0	0	NF		ENSG00000076865	NTSC2			g	6591258	ref	NP_0	5'-nucleotidase, cytosolic II [	561	64970	8.1	0	o	G	0	0	0	0	0	0	0	0	0	0	0	0	0	2	4.15E-05	6.5E-05	0	0	0	0	0	0	0	0	5' nucleotidase family. This	cytosol	5'-nucleotidase activity [pmid
1864	2	2.07E-05	0	0	NF		ENSG00000005194	CIAPIN1			g	8927416	ref	NP_	cytokine induced apoptosis i	312	33582	5.6	0	o	S	25	0.038	0	0	0.000113	0	0	1	2.83E-05	5.66E-05	0	0	5.23E-05	0	0	1	1.31E-05	2.62E-05	0	0	0	0	0	0	0	0	Anamorsin family. This	cytoplasm [pmid 14970183]	
1865	2	2.05E-05	1	1.84E-06	11.11323		ENSG00000132535	ORC3L			g	32463367	ref	NP_	origin recognition complex	1	0	6.5E-05	0	0	G	0	0	0	0	9.94E-05	0	0	2	4.12E-05	4.96E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Origin recognition complex	chromatin; nucleus	DNA binding; DNA replicatio
1866	2	2.05E-05	1	1.84E-06	11.11323		ENSG00000170004	CHD3			g	52630320	ref	NP_	chromodomain helicase DNA	1966	222859	7.5	0	o	G	14	0.005	0	0	2.7E-05	0	0	1	6.74E-06	1.35E-05	0	0	0	0	0	1	3.42E-05	6.83E-05	0	0	0	0	0	1.47E-05	0	0	Helicase superfamily c-		ATP binding; ATP-dependent
1867	2	2.04E-05	0	0	NF		ENSG00000069998	CECR5			g	14861834	ref	NP_	cat eye syndrome chromoso	423	46321	8.1	0	o	S	16	0.994	0	0.00011	0	0	0	1	2.76E-05	5.51E-05	0	0.3E-05	0	0	0	1	1.33E-05	2.65E-05	0	0	0	0	0	0	0	0	Predicted sugar		hydrolase activity
1868	2	2.03E-05	0	0	NF		ENSG00000102974	CTCF			g	5729790	ref	NP_	CCCTC-binding factor (Homo	727	82785	7	0	o	G	0	0	0	0	7.29E-05	0	0	1	1.82E-05	3.64E-05	0	0	8.98E-05	0	0	1	2.24E-05	4.49E-05	0	0	0	0	0	0	0	0	Bacterial Peptidase A24 N-	intracellular; nucleus [pmid	metal ion binding; nucleic
1869	2	2.03E-05	0	0	NF		ENSG00000077168	FAFAH1B1			g	4557741	ref	NP_0	platelet-activating factor acet	410	46638	7.4	0	o	G	0	0	0	0	4.31E-05	0	0	1	1.08E-05	2.15E-05	0	0	0.000119	0	0	1	2.99E-05	5.97E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a	astral microtubule [pmid	dynein binding [pmid
1870	2	2.03E-05	0	0	NF		ENSG00000213380	CCG8			g	21166361	ref	NP_	component of oligomeric golg	612	68452	5.2	0	o	S	20	0.941	0	0	0	0	0	1	3.67E-05	7.34E-05	0	0.000125	0	0	0	1	4.05E-05	5.92E-05	0	0	0	0	0	0	0	0	Dor1-like family. Dor1 is	Golgi transport complex [pmid	
1871	2	2.02E-05	0	0	NF		ENSG00000100227	PDLIM7			g	2683765	ref	NP_0	DNA polymerase delta intera	421	46089	10	0	o	S	48	0	0	5.54E-05	0	0	0	1	1.39E-05	2.77E-05	0	0.000107	0	0	0	1	2.66E-05	5.32E-05	0	0	0	0	0	0	0	0	RNA-binding proteins (RRM)	nucleus	nucleotide binding; RNA
1872	2	2.02E-05	0	0	NF		ENSG00000130830	MPP1			g	4505237	ref	NP_0	palmitoylated membrane pro	466	52297	7.4	0	o	G	24	0	0	0	0.000114	0	0	1	2.84E-05	5.69E-05	0	4.81E-05	0	0	0	1	1.2E-05	2.41E-05	0	0	0	0	0	0	0	0	Src homology 3 domains;	integral to plasma membrane	guanylate kinase activity
1873	2	2.01E-05	0	0	NF		ENSG00000145425	RELB			g	2549000	ref	NP_0	reticuloendotheliosis viral on	579	62755	6.2	0	o	G	49	0.144	0	0	0.000122	0	0	1	3.05E-05	6.15E-05	0	3.87E-05	0	0	0	1	9.69E-06	1.94E-05	0	0	0	0	0	0	0	0	Rel homology domain	nucleus	protein binding [pmid
1874	2	2.01E-05	0	0	NF		ENSG00000113812	ACTR8			g	39812115	ref	NP_	actin-related protein 8 [Homo	624	70484	7.8	0	o	G	0	0	3.74E-05	0	0	0	0	1	9.34E-06	1.87E-05	0	0	0	0	0.000123	1	3.08E-05	6.15E-05	0	0	0	0	0	0	0	0	Actin; An ubiquitous protein	cytoskeleton	protein binding; structural
1875	2	2E-05	0	0	NF		ENSG00000160688	FLAD1			g	41872389	ref	NP_	flavin adenine dinucleotide s	587	65286	6.9	0	o	G	55	0.019	0	3.97E-05	0	0.00012	0	2	4E-05	5.67E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	This domain is found in		transferase activity
1876	2	2E-05	0	0	NF		ENSG00000132432	MAD3			g	51745131	ref	NP_	chromodomain helicase DNA	425	48481	7.2	0	o	G	18	0.005	0	0	8.31E-05	0	0	1	2.08E-05	4.16E-05	0	7.68E-05	0	0	0	1	1.92E-05	3.84E-05	0	0	0	0	0	0	0	0	MH2 domain; C terminal	intracellular [pmid 14612439]	protein binding [pmid
1877	2	1.99E-05	0	0	NF		ENSG00000116863	ADPRHL2			g	8923417	ref	NP_0	ADP-ribosylhydrolase like 2 [	363	38947	5.1	0	o	S	38	0.993	0	0	9.73E-05	0	0	1	2.43E-05	4.87E-05	0	6.18E-05	0	0	0	1	1.55E-05	3.09E-05	0	0	0	0	0	0	0	0	ADP-ribosylglycohydrolase;		hydrolase activity
1878	2	1.98E-05	0	0	NF		ENSG00000072518	MARK2			g	8699043	ref	NP_0	MAP/microtubule affinity-reg	724	81209	9.2	0	o	G	17	0	9.66E-05	0	0	0	0	1	2.42E-05	4.83E-05	0	6.2E-05	0	0	0	1	1.55E-05	3.1E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	membrane [pmid 14976552]	ATP binding [pmid
1879	2	1.98E-05	0	0	NF		ENSG00000191311	YARS2			g	34681057	ref	NP_	mitochondrial tyrosyl-RNA sy	477	53199	9	0	o	G	34	0.982	0	0.000111	0	0	0	1	2.76E-05	5.55E-05	0	4.75E-05	0	0	0	1	1.19E-05	2.35E-05	0	0	0	0	0	0	0	0	Tyrosyl-tRNA synthetase	mitochondrion [pmid	ATP binding; ligase activity;
1880	2	1.97E-05	0	0	NF		ENSG00000161204	ABCF3			g	14861283	ref	NP_	ATP-binding cassette, sub-fa	709	79745	6.3	0	o	G	18	0	3.29E-05	0	0.000125	0	0	2	3.94E-05	5.89E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
1881	2	1.95E-05	0	0	NF		ENSG00000150256	MORC3			g	28872812	ref	NP_	MORC family CW-type zinc f	939	107113	5.6	0	o	G	28	0.129	0	7.45E-05	0	0	0	1	1.86E-05	3.73E-05	0	8.18E-05	0	0	0	1	2.04E-05	4.09E-05	0	0	0	0	0	0	0	0	CW-type Zinc Finger. This	nucleus	ATP binding; metal ion
1882	2	1.95E-05	0	0	NF		ENSG00000154930	ACSS1			g	28416953	ref	NP_	acyl-CoA synthetase short-cl	689	74857	7.1	0	o	S	54	0.81	0	0	2.56E-05	0	0	1	6.41E-06	1.28E-05	0	0.00013	0	0	0	1	3.26E-05	6.51E-05	0	0	0	0	0	0	0	0	acetyl-coenzyme A	mitochondrion	acetate-CoA ligase activity;
1883	2	1.94E-05	0	0	NF		ENSG00000132109	TRIM21			g	15208660	ref	NP_	tripartite motif protein 21 [Ho	475	54170	6.4	0	o	G	17	0.011	0	0	7.44E-05	0	0	1	1.86E-05	3.72E-05	0	0	8.08E-05	0	0	1	2.02E-05	4.04E-05	0	0	0	0	0	0	0	0	RING-finger (Really	intracellular; ribonucleoprotein	DNA binding; metal ion
1884	2	1.94E-05	0	0	NF		ENSG00000008405	PDK5			g	31110047	ref	NP_0	pyruvate dehydrogenase kin	404	46928	8.8	0	o	G	0	0	4.37E-05	0	0	0	0	1	1.09E-05	2.19E-05	0	0.000111	0	0	0	1	2.78E-05	5.55E-05	0	0	0	0	0	0	0	0	Vps5 C terminal like. Vps5	cytosol; proteasome complex	phosphoinositide binding;
1885	2	1.92E-05	0	0	NF		ENSG00000159352	PSMD4			g	5292161	ref	NP_0	proteasome 26S non-ATPase	377	40737	4.8	0	o	G	14	0	9.37E-05	0	0	0	0	1	2.34E-05	4.69E-05	0	5.95E-05	0	0	0	1	1.49E-05	2.98E-05	0	0	0	0	0	0	0	0	26S proteasome plays a		DNA binding; hydrolase
1886	2	1.91E-05	0	0	NF		ENSG00000124523	SIRT5			g	13787215	ref	NP_0	sirtuin 5 isoform 2 [Homo sap	299	32674	8.8	0	o	G	26	0.014	7.8E-05	0	0	0	0	1	1.95E-05	3.9E-05	0	7.5E-05	0	0	0	1	1.88E-05	3.76E-05	0	0	0	0	0	0	0	0	SIRT5_AT1_CobB;	chromatin silencing complex	DNA binding; hydrolase
1887	2	1.91E-05	0	0	NF		ENSG00000167508	MVD			g|4505289|ref|NP_0	diphosphomevalonate decarl	400	43405	7.2	0	o	G	20	0.123	0	0	0	0	0	1	9.34E-06	1.87E-05	0	0	0	0	0.000112	1	4.08E-05	0	2	3.82E-05	5.29E-05	0	0	0	0	0	0	0	0	Mevalonate pyrophosphate		ATP binding [pmid
1888	2	1.88E-05	0	0	NF		ENSG00000081320	STK17B			g	4758194	ref	NP_0	serine/threonine kinase 17b [	372	42344	5.3	0	o	G	21	0.008	0	0	4.75E-05	0	0	1	1.19E-05	2.37E-05	0	0	0	0	0.000103	1	2.58E-05	5.16E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	nucleus [pmid 9786912]	ATP binding [pmid 9786912];
1889	2	1.87E-05	0	0	NF		ENSG00000133330	SCLY			g	15671344	ref	NP_0	selenocysteine lyase [Homo	445	48149	7.1	0	o	G	18	0.001	0	0	3.97E-05	0	0	1	9.92E-06	1.98E-05	0	0.00011	0	0	0	1	1.75E-05	5.5E-05	0	0	0	0	0	0	0	0			
1890	2	1.86E-05	0	0	NF		ENSG00000141480	ARRB2			g	39812055	ref	NP_0	arrestin, beta 2 isoform 2 [Ho	394	44392	7.9	0	o	G	51	0	5.92E-05	0	8.97E-05	0	0	2	3.72E-05	4.47E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Arrestin (or S-antigen), N-	cytoplasm [pmid 9346876];	
1891	2	1.86E-05	0	0	NF		ENSG00000184939	PNPO			g	8922488	ref	NP_0	pyridoxine 5'-phosphate oxid	261	29986	7.1	0	o	G	32	0.092	0	0	0	0	0	1	8.6E-06	1.72E-05	0	6.25E-05	0	0	0	1	3.71E-05	4.39E-05	0	0	0	0	0	0	0	0	Pyridoxamine-phosphate		FMN binding; oxidoreductase
1892	2	1.85E-05	0	0	NF		ENSG00000161956	ESENP3			g	21361499	ref	NP_0	SUMO/sentrin/SMT3 specif	574	65010	8.6	0	o	G	20	0	8.13E-05	0	0	0	0	1	2.03E-05	4.06E-05	0	0	6.69E-05	0	0	1	1.67E-05	3.34E-05	0	0	0	0	0	0	0	0	Ulp1 protease family, C-	nucleolus [pmid 11256614];	cysteine-type peptidase
1893	2	1.81E-05	0	0	NF		ENSG00000102030	ARD1A			g	10835057	ref	NP_0	N-acetyltransferase ARD1 [H	235	26458	5.6	0	o	G	24	0	0	0	7.52E-05	0	0	1	1.88E-05	3.76E-05	0	0	6.94E-05	0	0	1	1.74E-05	3.47E-05	0	0	0	0	0	0	0	0	Acetyltransferases	cytoplasm [pmid 15496142];	N-acetyltransferase activity;
1894	2	1.8E-05	0	0	NF		ENSG00000135336	ELAVL4			g	38605723	ref	NP_0	ELAV (embryonic lethal, abn	380	42151	5.6	0	o	G	34	0	0	0	0	0	0	1	4.29E-05	0.000101	0	0	0	0	0	1	3.6E-05	7.2E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a		protein activity
1895	2	1.8E-05	0	0	NF		ENSG00000164332	UBLCP1			g	21450802	ref	NP_0	ubiquitin-like domain contain	318	36733	6.7	0	o	G	21	0	7.33E-05	0	0	0	0	1	1.83E-05	3.67E-05	0	7.06E-05	0	0	0	1	1.76E-05	3.53E-05	0	0	0	0	0	0	0	0	The UBP (ubiquitin	nucleus	hydrolase activity;
1896	2	1.79E-05	0	0	NF		ENSG00000117408	IPO13			g	41281425	ref	NP_0	importin 13 [Homo sapiens]	963	108211	5.3	0	o	G	23	0	0	0	0	0	0	1	0	0	2.33E-05	0	0.00012	2	3.57E-05	5.7E-05	0	0	0	0	0	0	0	0	Exportin 1-like protein. The	cytoplasm; nuclear pore;	protein binding [pmid
1897	2	1.78E-05	0	0	NF		ENSG00000196954	CASP4			g	15451910	ref	NP_0	caspase 4 isoform gamma [	321	36705	5.7	0	o	G	29	0	7.27E-05	0	0	0	0	1	1.82E-05	3.63E-05	0	5.99E-05	0	0	0	1	1.75E-05	3.5E-05	0	0	0	0	0	0	0	0	Caspase. Interleukin-1 beta	cytoplasm; intracellular	cysteine-
1898	2	1.78E-05	0	0	NF		ENSG00000164024	METAP1			g	24308009	ref	NP_0	methionyl aminopeptidase 1	272	30369	6.6	0	o	G	0	0	0	0	0	0	0	1	0	0	8.25E-05	0.00006	0	0	0	2	3.56E-05	4.21E-05	0	0	0	0	0	0	0	0	Methionine Aminopeptidase	cytoplasm [pmid 14532271]	cobalt ion binding; metal ion
1899	2	1.78E-05	0	0	NF		ENSG00000157102	FLI1			g	7110593	ref	NP_0	Friend leukemia virus integrat	452	50982	7.5	0	o	G	25	0	0.000103	0	3.91E-05	0	0	2	3.56E-05	4.87E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	SAM / Pointed domain; A	nucleus	sequence-specific DNA
1900	2	1.78E-05	0	0	NF		ENSG00000198841	KTI12			g	19923939	ref	NP_	KTI12 homolog, chromatin as	354	38616	7	0	o	G	19	0.148	0	0	4.99E-05	0	0	1	1.25E-05	2.49E-05	0	0	9.22E-05	0	0	1	2.31E-05	4.61E-05	0	0	0	0	0	0	0	0	Chromatin associated		
1901	2	1.77E-05	0	0	NF		ENSG00000135387	CAPRIN1			g	42558250	ref	NP_	membrane component chrom	709	78366	5.2	0	o	G	41	0.122	0	0	4.98E-05	0	0	1	1.25E-05	2.49E-05	0	0	9.21E-05	0	0	1	2.3E-05	4.6E-05	0	0	0	0	0	0	0	0		integral to plasma membrane	GPI anchor binding	
1902	2	1.76E-05	0	0	NF		ENSG00000115689	INPP5J			g	45047031	ref	NP_0	5-phosphoinositol polyphosphate 1-pho	399	45398	5.3	0	o	G	22	0.001	0	0	4.43E-05	0	0	1	1.11E-05	2.21E-05	0	0	0.62E-05	0	0	1	2.41E-05	4.81E-05	0	0	0	0	0	0	0	0	IPPase; Inositol		hydrolase activity; inositol or
1903	2	1.76E-05	0	0	NF		ENSG00000112685	EXOC2			g	21361625	ref	NP_0	Sec5 protein [Homo sapiens]	924	104066	6.9	0	o	G	19	0.008	0	0	5.74E-05	0	0	1	1.43E-05	2.87E-05	0	0	8.31E-05	0	0	1	2.08E-05	4.15E-05	0	0	0	0	0	0	0	0	First repeat of the IPT		protein binding [pmid
1904	2	1.75E-05	0	0	NF		ENSG00000164134	NARG1			g	17149828	ref	NP_0	NMDA receptor regulated 1	866	101272	7.4	0	o	G	0	0	0	0	0.000102	0	0	1	2.55E-05	5.1E-05	0	3.77E-05	0	0	0	1	9.42E-06	1.88E-05	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	cytoplasm [pmid 12140756]	acetyltransferase activity
1905	2	1.74E-05	0	0	NF		ENSG00000250253				g	19923416	ref	NP_0	KIAA1008 [Homo sapiens]	958	105520	5.3	0	o	G	43	0.001	0	0	9.22E-05	0	0	1	2.31E-05	4.62E-05	0	4.68E-05	0	0	0	1	1.17E-05	2.34E-05	0	0	0	0	0	0	0	0	Large family of predicted	exosome (RNase complex)	5'-nucleotide activity; GDP-
1906	2	1.73E-05	0	0	NF		ENSG00000187994	RINL			g	38346206	ref	NP_0	hypothetical protein LOC126	452	50053	6.1	0	o	S	20	0.505	0	0	3.91E-05	0	0	1	9.77E-06	1.95E-05	0	9.93E-05	0	0	0	1	2.48E-05	4.96E-05	0	0	0	0	0	0	0	0	Vacuolar sorting protein 9		
1907	2	1.73E-05	0	0	NF		ENSG00000135330	RAVX1			g	11945639	ref	NP_0	ravin, gamma [Homo sapiens	331	38205	7.5	0	o	G	19	0	7.05E-05	0	0	0	0	1	1.76E-05	3.52E-05	0	6.78E-05	0	0	0	1	1.69E-05	3.39E-05	0	0	0	0	0	0	0	0	Calponin homology (CH)	cytoskeleton [pmid 11171322]	actin binding [pmid
1908	2	1.73E-05	0	0	NF		ENSG00000136653	RASSF5			g	32996731	ref	NP_0	Ras association (RalGDS/AF	418	47090	9.1	0	o	G	18	0	0	0	8.45E-05	0	0	1	2.11E-05	4.23E-05	0	5.37E-05	0	0	0	1	1.34E-05	2.68E-05	0	0	0	0	0	0	0	0	Protein kinase C conserved	microtubule	diacylglycerol binding; metal
1909	2	1.73E-05	0	0	NF		ENSG00000155903	RASA2			g	12545408	ref	NP_0	RAS p21 protein activator 2	849	96527	7.2	0	o	S	21	0.977	0	5.49E-05	8.32E-05	0	0	2	3.46E-05	4.15E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	BTK motif. Zinc-binding	intracellular	metal ion binding; Ras
1910	2	1.72E-05	0	0	NF		ENSG00000162619	FLIBP1			g	11405200	ref	NP_0	factor upstream element-binding	644	67980	7.6	0	o	S	25	0.001	0	3.62E-05	0	0	0	1	9.04E-06	1.81E-05	0	0.00010	0	0	0	1	2.53E-05	5.07E-05	0	0	0	0	0	0	0	0	K homology RNA-binding	nucleus	single stranded DNA binding
1911	2	1.72E-05	1	2.8E-06	6.149588		ENSG00000164922	COL1A2			g	48762934	ref	NP_0	alpha 2 type I collagen [Hom	1366	129314	9	0	o	G	25	0.997	0	0.000138	0	0	0.000138	2	3.44E-05	6.88E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.24E-05	Collagen triple helix repeat	collagen; collagen type I;	extracellular matrix structural
1912	2	1.71E-05	0	0	NF		ENSG00000123434	LANCL1			g	8923911	ref	NP_0	LanC lantibiotic synthetase c	450	50854	7.4	0	o	G	45	0	5.18E-05	0	0	0	0	1	1.3E-05	2.59E-05	0	8.53E-05	0	0	0	1	2.13E-05	4.27E-05	0	0	0	0	0	0	0	0	Lanthionine synthetase C-	cytosol [pmid 12566319]	ATP binding [pmid
1913	2	1.7E-05	0	0	NF		ENSG00000172673	C6orf190			g|55219189|ref|NP_0	hypothetical protein LOC387	440	73452	5.9	0	o	G	19	0	0	0	0	0	0	1	0	0	7.64E-05	5.99E-05	0	7.64E-05	0	0	0	1	2.41E-05	3.99E-05	0	0	0	0	0	0	0	0			
1914	2	1.7E-05	0	0	NF		ENSG00000168889	PATL1			g	22749427	ref	NP_0	protein associated with topoi	627	70639	9.7	0	o	G	17	0.001	0	7.44E-05	0	0	0	1	1.86E-05	3.72E-05	0	0	6.12E-05	0	0	1	1.53E-05	3.06E-05	0	0	0	0	0	0	0	0			
1915	2	1.69E-05	0	0	NF		ENSG00000179878	DPP7			g	24208889	ref	NP_0	dipeptidyl peptidase 7 prepro	492	54341	5.8	0	o	G	22	0	0	0	3.59E-05	0	0	1	8.98E-06	1.8E-05	0	9.95E-05	0	0	0	1	2.49E-05	4.98E-05	0	0	0	0	0	0	0	0	Serine carboxypeptidase	lysosome	aminopeptidase activity;
1916	2	1.69E-05	0	0	NF		ENSG00000138279	ANXA7			g	4502111	ref	NP_0	annexin VII isoform 1 [Homo	466	50316	6.6	0	o	G	0	0	0.0001	0	0	0	0	1	2.5E-05	5.01E-05	0	0	0	0	0	1	8.76E-06	1.75E-05	0	0	0	0	0	0	0	0	Annexin. This family of		calcium ion binding; calcium-
1917	2	1.69E-05	0	0	NF		ENSG00000110934	BIN2			g	44972835	ref	NP_0	bridging integrator 2 [Homo s	565	61874	5.1	0	o	G	25	0.001	0	4.13E-05	0	9.38E-05	0	1	2.38E-05	4.45E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	BAR domain. The BAR	cytoplasm	protein binding
1918	2	1.68E-05	0	0	NF		ENSG00000188488	FTO			g	12092726	ref	NP_0	fat mass and obesity associa	505	58282	5.2	0	o	G	0	0	0	0	7.56E-05	0	0	1	1.78E-05	3.56E-05	0	6.46E-05	0	0	0	1	1.62E-05	3.23E-05	0	0	0	0	0	0	0	0			
1919	2	1.68E-05	0	0	NF		ENSG00000142765	SYTL1			g	14249614	ref	NP_0	synaptotagmin-like 1 [Homo	550	60635	5.5	0	o	G	24	0.168	0	0	6.42E-05	0	0	1	1.61E-05	3.21E-05	0	0	6.98E-05	0	0	1	1.74E-05	3.49E-05	0	0	0	0	0	0	0	0	Protein kinase C conserved	extrinsic to plasma membrane	ATP binding; hydrogen-
1920	2	1.67E-05

																					RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs										
rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
2010	2	1.13E-05	0	0	INF		ENSG00000204197:E	KIFC1			gi|28626498|ref|NP_	kinesin family member C1 [H	673	73744	9	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	3.33E-05	0	0	5.7E-05	2	2.26E-05	2.78E-05	0	0	0	0	0	0	0	0	Kinesin motor domain,	microtubule; microtubule	ATP binding [pmid 8276466];
2011	2	1.13E-05	0	0	INF		ENSG00000173575:N	CHD2			gi|118421089|ref|NP	chromodomain helicase DNA	1828	211342	8.1	0	o	Q	0	0	0	6.12E-05	0	2.9E-05	0	2	2.26E-05	2.92E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2012	2	1.13E-05	0	0	INF		ENSG00000084463:N	WBP11			gi|7706501|ref|NP_0	WW domain binding protein	641	69998	8.4	0	o	Q	0	0	0	0	0	5.51E-05	0	1	1.38E-05	2.76E-05	0	3.5E-05	0	0	0	1	8.75E-06	1.75E-05	0	0	0	0	0	0	0	0	V-type ATP synthase	nucleus [pmid 10593949]	protein binding [pmid
2013	2	1.12E-05	0	0	INF		ENSG00000105447:E	GRWD1			gi|31542862|ref|NP_	glutamate-rich WD repeat co	446	49346	4.9	0	o	Q	22	0	0	0	0	3.96E-05	0	1	9.9E-06	1.98E-05	0	5.03E-05	0	0	0	1	1.26E-05	2.52E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus	
2014	2	1.12E-05	0	0	INF		ENSG00000128191:E	DGCR8			gi|38488720|ref|NP_	DiGeorge syndrome critical r	773	86045	5.9	0	o	Q	25	0	0	0	0	6.86E-05	0	1	1.71E-05	3.43E-05	0	0	0	2.11E-05	0	1	5.28E-06	1.06E-05	0	0	0	0	0	0	0	0	Double-stranded RNA	cytoplasm [pmid 11256614];	double-stranded RNA
2015	2	1.11E-05	0	0	INF		ENSG00000080608:E	KIAA0020			gi|109948283|ref|NP	KIAA0020 protein [Homo sap	648	73584	9.6	0	o	Q	0	0	0	0	0	5.45E-05	0	1	1.36E-05	2.73E-05	0	3.46E-05	0	0	0	1	8.66E-06	1.73E-05	0	0	0	0	0	0	0	0			
2016	2	1.11E-05	0	0	INF		ENSG00000120800:E	UTP20			gi|120587023|ref|NP	down-regulated in metastasis	2785	318385	7.4	0	o	Q	25	0	0	0	0	6.34E-06	0	1	1.59E-06	3.17E-06	0	0	0	0	8.27E-05	1	2.07E-05	4.14E-05	0	0	0	0	0	0	0	0			
2017	2	1.11E-05	0	0	INF		ENSG00000065268:E	WDR18			gi|56243583|ref|NP_	WD repeat domain 18 [Homo	432	47405	6.7	0	o	Q	20	0.041	0	0	0	0	0.001885	1	0	0	0	0	0	0	8.89E-05	1	2.22E-05	4.44E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a		
2018	2	1.11E-05	0	0	INF		ENSG00000167483:E	FAM129C			gi|148664236|ref|NP	B-cell novel protein 1 isoform	651	72185	8.1	0	o	Q	25	0.001	0	0	0	5.43E-05	0	1	1.36E-05	2.71E-05	0	3.45E-05	0	0	0	1	8.62E-06	1.72E-05	0	0	0	0	0	0	0	0			
2019	2	1.11E-05	0	0	INF		ENSG00000129484:E	PARP2			gi|110825961|ref|NP	poly (ADP-ribose) polymeras	583	66206	8.9	0	o	Q	21	0	0	0	0	6.06E-05	0	1	1.51E-05	3.03E-05	0	0	0	2.8E-05	0	1	7E-06	1.4E-05	0	0	0	0	0	0	0	0			
2020	2	1.1E-05	0	0	INF		ENSG00000185215:E	TNFAIP2			gi|26051240|ref|NP_	tumor necrosis factor, alpha-	654	72661	6.5	0	o	Q	18	0	0	0	0	5.4E-05	0	1	1.35E-05	2.7E-05	0	3.43E-05	0	0	0	1	8.58E-06	1.72E-05	0	0	0	0	0	0	0	0	Exocyst complex	extracellular space [pmid	
2021	2	1.09E-05	0	0	INF		ENSG00000127586:E	CHTF18			gi|27501458|ref|NP_	CTF18, chromosome transm	975	107383	7.2	0	o	Q	0	0	0	4.78E-05	0	0	0	1	1.2E-05	2.39E-05	0	0	0	0	3.94E-05	1	9.84E-06	1.97E-05	0	0	0	0	0	0	0	0	AAA-superfamily of		ATP binding; helicase
2022	2	1.08E-05	0	0	INF		ENSG00000150990:E	DHX37			gi|29029601|ref|NP_	DEAH (Asp-Glu-Ala-His) box	1157	129545	8.1	0	o	Q	0	0	0	2.02E-05	0	0	0	1	5.04E-06	1.01E-05	0	0	0	0	6.64E-05	1	1.66E-05	3.32E-05	0	0	0	0	0	0	0	0	DEXH-box helicases. A		ATP binding; ATP-dependent
2023	2	1.08E-05	0	0	INF		ENSG00000182481:E	LOC728860			gi|169211157|ref|XP	PREDICTED: similar to Kary	529	57862	5.4	0	o	Q	0	0	0	4.41E-05	0	0	0	1	1.1E-05	2.2E-05	0	4.24E-05	0	0	0	1	1.06E-05	2.12E-05	0	0	0	0	0	0	0	0			
2024	2	1.08E-05	0	0	INF		ENSG00000137713:E	PPP2R1B			gi|32455244|ref|NP_	beta isoform of regulatory su	667	73585	5.1	0	o	Q	16	0.01	0	4.37E-05	0	4.27E-05	0	2	2.16E-05	2.49E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	HEAT repeat. The HEAT	cytosol; membrane;	antigen binding; binding;
2025	2	1.08E-05	0	0	INF		ENSG00000185246:E	PRPF39			gi|156938331|ref|NP	PRP39 pre-mRNA processin	669	78430	5.4	0	o	Q	0	0	0	0	0	5.28E-05	0	1	1.32E-05	2.64E-05	0	3.35E-05	0	0	0	1	8.38E-06	1.68E-05	0	0	0	0	0	0	0	0			
2026	2	1.08E-05	0	0	INF		ENSG00000042429:E	MED17			gi|28558975|ref|NP_	mediator complex subunit 17	651	72890	7.4	0	o	Q	16	0	0	0	0	2.71E-05	0	1	6.78E-06	1.36E-05	0	0	0	0	5.9E-05	1	1.47E-05	2.95E-05	0	0	0	0	0	0	0	0		mediator complex [pmid	ligand-dependent nuclear
2027	2	1.07E-05	0	0	INF		ENSG00000099917:E	MED15			gi|21312134|ref|NP_	mediator complex subunit 15	748	82581	9.3	0	o	Q	0	0	0	6.24E-05	0	2.36E-05	0	2	2.15E-05	2.94E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		nucleus	
2028	2	1.07E-05	0	0	INF		ENSG00000157212:E	PAXIP1			gi|93141033|ref|NP_	PAX interacting protein 1 [Ho	1069	121341	6.7	0	o	Q	0	0	0	4.36E-05	0	0	0	1	1.09E-05	2.18E-05	0	4.2E-05	0	0	0	1	1.05E-05	2.1E-05	0	0	0	0	0	0	0	0	Breast Cancer Suppressor	intracellular	
2029	2	1.04E-05	0	0	INF		ENSG00000154710:E	RABGEF1			gi|7657496|ref|NP_0	RAB guanine nucleotide exc	491	56891	7	0	o	Q	0	0	0	4.75E-05	0	3.6E-05	0	2	2.09E-05	2.46E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	A20-like zinc fingers; A20-		DNA binding; metal ion
2030	2	1.04E-05	0	0	INF		ENSG00000123213:E	NLN			gi|14149738|ref|NP_	neurolysin [Homo sapiens]	704	80652	6.6	0	o	Q	18	0.361	0	3.31E-05	0	5.02E-05	0	2	2.08E-05	2.5E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Peptidase family M3. This	mitochondrion	hydrolase activity; metal ion
2031	2	1.04E-05	0	0	INF		ENSG00000101126:E	ADNP			gi|31563503|ref|NP_	activity-dependent neuroprot	1102	123563	7.3	0	o	Q	16	0	0	4.23E-05	0	0	0	1	1.06E-05	2.12E-05	0	4.07E-05	0	0	0	1	1.02E-05	2.04E-05	0	0	0	0	0	0	0	0	Homeodomain; DNA binding	intracellular; nucleus	metal ion binding; sequence-
2032	2	1.04E-05	0	0	INF		ENSG00000112782:E	LOC100131610			gi|169169023|ref|XP	PREDICTED: similar to chlor	410	46503	4.8	0	o	Q	0	0	0	0	0	4.31E-05	0	1	1.08E-05	2.15E-05	0	0	0	3.98E-05	0	1	9.95E-06	1.99E-05	0	0	0	0	0	0	0	0			
2033	2	1.03E-05	0	0	INF		ENSG00000129347:E	KRI1			gi|145580615|ref|NP	KRI1 homolog [Homo sapien	709	83252	5.2	0	o	Q	24	0	0	3.29E-05	0	4.98E-05	0	2	2.07E-05	2.49E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2034	2	1.03E-05	0	0	INF		ENSG00000146085:E	MUT			gi|156105689|ref|NP	methylmalonyl Coenzyme A	750	83135	6.9	0	o	Q	25	0.016	0	3.11E-05	0	0	0	1	7.77E-06	1.55E-05	0	0	0	0	5.12E-05	1	1.28E-05	2.56E-05	0	0	0	0	0	0	0	0			
2035	2	1.03E-05	0	0	INF		ENSG00000159086:E	C21orf66			gi|22035565|ref|NP_	GC-rich sequence DNA-bind	917	104804	5.7	0	o	Q	0	0	0	0	0	5.78E-05	0	1	1.44E-05	2.89E-05	0	2.45E-05	0	0	0	1	6.12E-06	1.22E-05	0	0	0	0	0	0	0	0	GC-rich sequence DNA-	nucleus	transcription factor activity
2036	2	1.03E-05	0	0	INF		ENSG00000099308:E	MAST3			gi|150170729|ref|NP	microtubule associated serin	1309	143137	8.1	0	o	Q	44	0.002	0	0	0	1.35E-05	0	1	3.37E-06	6.75E-06	0	6.86E-05	0	0	0	1	1.71E-05	3.43E-05	0	0	0	0	0	0	0	0			
2037	2	1.02E-05	0	0	INF		ENSG00000187239:E	FNBP1			gi|38524622|ref|NP_	formin binding protein 1 [Hon	617	71307	5.7	0	o	Q	0	0	0	0	0	2.86E-05	0	1	7.16E-06	1.43E-05	0	0	0	5.29E-05	0	1	1.32E-05	2.65E-05	0	0	0	0	0	0	0	0	Src homology 3 domains;	intracellular; ribosome	RNA binding; structural
2038	2	1.02E-05	0	0	INF		ENSG00000130299:E	GTPBP3			gi|14249126|ref|NP_	GTP binding protein 3 (mitoc	492	52030	6.5	0	o	S	45	0.967	0	0	0	3.59E-05	0	1	8.98E-06	1.8E-05	0	4.56E-05	0	0	0	1	1.14E-05	2.28E-05	0	0	0	0	0	0	0	0	TrmE (MnmE, ThdF, MSS1)	intracellular	GTP binding; GTPase
2039	2	1.01E-05	0	0	INF		ENSG00000110075:E	SAPS3			gi|13489083|ref|NP_	SAPS domain family, membe	793	88952	4.6	0	o	Q	18	0	0	5.88E-05	0	2.23E-05	0	2	2.03E-05	2.78E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	SIT4 phosphatase-		binding
2040	2	1.01E-05	0	0	INF		ENSG00000138080:E	EMILIN1			gi|5901944|ref|NP_0	elastin microfibril interfacer 1	1016	106695	5.2	0	o	S	24	1	0	4.59E-05	0	3.48E-05	0	2	2.02E-05	2.37E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	EMI domain. The Pfam	cytoplasm; extracellular matrix	extracellular matrix structural
2041	2	1.01E-05	0	0	INF		ENSG00000171824:E	EXOSC10			gi|4505917|ref|NP_0	exosome component 10 isofo	860	98089	8.4	0	o	Q	23	0.013	0	0	0	6.16E-05	0	1	1.54E-05	3.08E-05	0	0	0	1.9E-05	0	1	4.74E-06	9.49E-06	0	0	0	0	0	0	0	0	3'-5' exonuclease. The	intracellular; nucleolus [pmid	3'-5' exonuclease activity;
2042	2	9.91E-06	0	0	INF		ENSG00000105819:E	PMPCB			gi|94538354|ref|NP_	mitochondrial processing pep	489	54366	6.8	0	o	S	33	0.923	0	0	0	0	0	0	0	0	0	4.59E-05	0	3.34E-05	0	2	1.98E-05	2.34E-05	0	0	0	0	0	0	0	0	Peptidase M16 inactive	mitochondrion	metal ion binding;
2043	2	9.9E-06	0	0	INF		ENSG00000113649:E	TCERG1			gi|21327715|ref|NP_	transcription elongation regu	1098	123901	8.6	0	o	Q	0	0	0	0	0	6.44E-05	0	1	1.61E-05	3.22E-05	0	0	0	1.49E-05	0	1	3.72E-06	7.43E-06	0	0	0	0	0	0	0	0	Two conserved tryptophans	nucleus [pmid 9315662]	protein binding [pmid
2044	2	9.87E-06	0	0	INF		ENSG00000179151:E	EDC3			gi|19923613|ref|NP_	enhancer of mRNA decappin	508	56078	7.1	0	o	Q	18	0.049	0	0	0	3.48E-05	0	1	8.69E-06	1.74E-05	0	4.42E-05	0	0	0	1	1.1E-05	2.21E-05	0	0	0	0	0	0	0	0	LSm16 belongs to a family		
2045	2	9.82E-06	0	0	INF		ENSG00000114857:E	NKTR			gi|6631100|ref|NP_0	natural killer-tumor recognitic	1462	165676	10	0	o	Q	0	0	0	4.79E-05	0	0	0	1	1.2E-05	2.39E-05	0	3.07E-05	0	0	0	1	7.67E-06	1.53E-05	0	0	0	0	0	0	0	0	cyclophilin_ABH_like:	plasma membrane	cyclosporin A binding [pmid
2046	2	9.81E-06	0	0	INF		ENSG00000136573:E	BLK			gi|33469982|ref|NP_	B lymphoid tyrosine kinase [H	505	57707	7.9	0	o	Q	0	0	0	4.62E-05	0	0	0	1	1.15E-05	2.31E-05	0	0	0	3.23E-05	0	1	8.08E-06	1.62E-05	0	0	0	0	0	0	0	0	Src homology 3 domains;		ATP binding; nucleotide
2047	2	9.61E-06	0	0	INF		ENSG00000020129:E	NCDN			gi|62526029|ref|NP_	neurochondrin isoform 1 [Ho	729	78864	5.5	0	o	Q	20	0.044	0	0	0	2.42E-05	0	1	6.06E-06	1.21E-05	0	0	0	0	5.27E-05	1	1.32E-05	2.63E-05	0	0	0	0	0	0	0	0	Neurochondrin. This family		
2048	2	9.53E-06	0	0	INF		ENSG00000111364:E	DDX55			gi|41327779|ref|NP_	DEAD (Asp-Glu-Ala-Asp) box	600	68547	9.2	0	o	Q	23	0.001	0	3.89E-05	0	0	0	1	9.72E-06	1.94E-05	0	3.74E-05	0	0	0	1	9.35E-06	1.87E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-		ATP binding; ATP-dependent
2049	2	9.46E-06	0	0	INF		ENSG00000124535:E	WRNIP1			gi|18426902|ref|NP_	Werner helicase interacting p	665	72133	6.1	0	o	Q	25	0	0	0	0	2.66E-05	0	1	6.64E-06	1.33E-05	0	0	0	4.91E-05	0	1	1.23E-05	2.45E-05	0	0	0	0	0	0	0	0	Rad18-like CCHC zinc	nucleus	ATP binding [pmid
2050	2	9.44E-06	0	0	INF		ENSG00000136152:E	COG3			gi|13899251|ref|NP_	component of golgi transport	828	94043	5.6	0	o	Q	15	0.324	0	0	0	2.13E-05	0	1	5.33E-06	1.07E-05	0	5.42E-05	0	0	0	1	1.35E-05	2.71E-05	0	0	0	0	0	0	0	0	Sec34-like family. Sec34	Golgi cis face; membrane	
2051	2	9.41E-06	0	0	INF		ENSG00000167984:E	NLRC3			gi|118918429|ref|NP	NOD3 protein [Homo sapiens	1065	114657	8.3	0	o	Q	40	0	0	0	0	3.32E-05	0	1	8.29E-06	1.66E-05	0	4.21E-05	0	0	0	1	1.05E-05	2.11E-05	0	0	0	0	0	0	0	0			
2052	2	9.26E-06	0	0	INF		ENSG00000146247:E	PHIP			gi|34996489|ref|NP_	pleckstrin homology domain	1821	206646	8.8	0	o	Q	31	0.003	0	2.56E-05	0	4.85E-05	0	2	1.85E-05	2.33E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	WD40 domain, found in a		insulin receptor binding [pmid
2053	2	9.23E-06	0	0	INF		ENSG00000115211:E	EIF2B4			gi|41281817|ref|NP_	eukaryotic translation initiatio	543	59630	9.4	0	o	S	34	0.858	0	0	0	3.25E-05	0	1	8.13E-06	1.63E-05	0	4.13E-05	0	0	0	1	1.03E-05	2.07E-05	0	0	0	0	0	0	0	0	Initiation factor 2 subunit	cytoplasm [pmid 11323413];	guanyl-nucleotide exchange
2054	2	9.21E-06	0	0	INF		ENSG00000119969:E	HELLS			gi|21914927|ref|NP_	helicase, lymphoid-specific [H	838	97074	7.9	0	o	Q	24	0	0	2.78E-05	0	0	0	1	6.96E-06	1.39E-05	0	0	0	0	4.58E-05	1	1.15E-05	2.29E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-		ATP binding; DNA binding;
2055	2	9.2E-06	0	0	INF		ENSG00000198730:E	CTR9			gi|7661950|ref|NP_0	SH2 domain binding protein	1173	133502	6.8	0	o	Q	0	0	0	5.97E-05	0	0	0	1	1.49E-05	2.98E-05	0	0	0	1.39E-05	0	1	3.48E-06	6.96E-06	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	nucleus	binding
2056	2	9.17E-06	0	0	INF		ENSG00000138801:E	PAPSS1			gi|46094058|ref|NP_	3'-phosphoadenosine 5'-phos	624	70833	6.9	0	o	Q	65	0	0	3.74E-05	0	0	0	1	9.34E-06	1.87E-05	0	3.6E-05	0	0	0	1	8.99E-06	1.8E-05	0	0	0	0	0	0	0	0	ATP-sulfurylase. This family	intracellular	adenylylsulfate kinase
2057	2	8.75E-06	0	0	INF		ENSG00000181192:E	DHTKD1			gi|38788380|ref|NP_	dehydrogenase E1 and trans	919	103043	6.9	0	o	Q	26	0.263	0	5.08E-05	0	1.92E-05	0	2	1.75E-05	2.4E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Thiamine pyrophosphate		oxoglutarate dehydrogenase
2058	2	8.71E-06	0	0	INF		ENSG00000100425:E	BRD1			gi|11321642|ref|NP_	bromodomain containing pro	1058	119520	8.6	0	o	Q	37	0	0	0	0	3.34E-05	0	1	8.35E-06	1.67E-05	0	0	0	0	3.63E-05	1	9.07E-06	1.81E-05	0	0	0	0	0	0	0	0	domain with conserved	nucleus [pmid 10602503]	metal ion binding; protein
2059	2	8.68E-06	0	0	INF		ENSG00000167202:E	TBC1D2B			gi|40353247|ref|NP_	TBC1 domain family, membe	788	90733	6.4	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	2.07E-05	4.87E-05	2	1.74E-05	2.31E-05	0	0	0	0	0	0	0	0	TBC domain. Identification		
2060	2	8.65E-06	0	0	INF		ENSG00000168944:E	CEP120			gi|96975038|ref|NP_	coiled-coil domain containing	986	112640	6.3	0	o	Q	18	0.032	0	2.37E-05	0	0	0	1	5.91E-06	1.18E-05	0	4.55E-05	0	0	0	1	1.14E-05	2.28E-05	0	0	0	0	0	0	0	0			
2061	2	8.49E-06	0	0	INF		ENSG00000105732:E	ZNF574			gi|154744870|ref|NP	zinc finger protein 574 [Homo	896	98900	8.1	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	2.5E-05	0	0	4.28E-05	2	1.7E-05	2.09E-05	0	0	0	0	0	0	0	0			
2062	2	8.47E-06	0	0	INF		ENSG00000172660:E	TAF15			gi|21327701|ref|NP_	TBP-associated factor 15 iso	592	61830	8	0	o	Q	0	0	0	0	0	2.98E-05	0	1	7.46E-06	1.49E-05	0	3.79E-05	0	0	0	1	9.47E-06	1.89E-05	0	0	0	0	0	0	0	0	Zn-finger in Ran binding	intracellular; nucleus;	DNA binding; metal ion
2063	2	8.4E-06	0	0	INF		ENSG00000007816:N	WDR46			gi|9954875|ref|NP_0	WD repeat domain 46 [Homo	610	68041	9.7	0	o	Q	0	0	0	3.82E-05	0	2.9E-05	0	2	1.68E-05	1.98E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	WD40 domain, found in a		
2064	2	8.38E-06	0	0	INF		ENSG00000135439:E	CENTG1			gi|7661962|ref|NP_0	centaurin, gamma 1 [Homo s	836	90537	8.8	0	o	Q	15	0.002	0	0	0	2.11E-05	0	1	5.28E-06	1.06E-05	0	0	0	0	4.59E-05	1	1.15E-05	2.3E-05	0	0	0	0	0	0	0	0	Putative GTPase activating	nucleus [pmid 11136977]	GTP binding; GTPase
2065	2	8.37E-06	0	0	INF		ENSG00000168438:E	CDC40			gi|7706657|ref|NP_0	cell division cycle 40 homolo	579	65521	7.1	0	o	S	18	0.964	0	0	0	0	0	0	0	0	0	3.87E-05	0	2.82E-05	0	2	1.67E-05	1.98E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a	nucleus; spliceosome complex	
2066	2	8.21E-06	0	0	INF		ENSG00000004534:E	RBM6			gi|5032033|ref|NP_0	RNA binding motif protein 6 [	1123	128644	6.3	0	o	Q	0	0	0	0	0	3.15E-05	0	1	7.86E-06	1.57E-05	0	0	0	0	3.42E-05	1	8.55E-06	1.71E-05	0	0	0	0	0	0	0	0	glycine rich nucleic binding	intracellular; nucleus [pmid	DNA binding [pmid
2067	2	8.2E-06	0	0	INF		ENSG00000009307:E	CSDE1			gi|56117850|ref|NP_	upstream of NRAS isoform 2	767	85747	6.2	0	o	Q	0	0	0	0	0	2.3E-05	0	1	5.76E-06	1.15E-05	0	0	0	4.26E-05	0	1	1.06E-05	2.13E-05	0	0	0	0	0	0	0	0	Cold shock protein domain;		DNA binding; RNA binding
2068	2	8.19E-06	0	0	INF		ENSG00000148308:E	GTF3C5			gi|6912402|ref|NP_0	general transcription factor II	519	59630	7.1	0	o	Q	19	0.008	0	0	0	3.4E-05	0	1	8.51E-06	1.7E-05	0	0	0	3.14E-05	0	1	7.86E-06	1.57E-05	0	0	0	0	0	0	0	0		nucleus; transcription factor	DNA binding; RNA
2069	2	8.18E-06	0	0	INF		ENSG00000074054:E	CLASP1			gi|31563537|ref|NP_	CLIP-associating protein 1 [H	1538	169450	9	0	o	Q	19	0	0	4.04E-05	0	0	0	1	1.01E-05	2.02E-05	0	0	0	0	2.5E-05	1	6.24E-06	1.25E-05	0	0	0	0	0	0	0	0	HEAT repeat. The HEAT	centrosome [pmid 12837247]	binding; kinetochore binding
2070	2	8.14E-06	0	0	INF		ENSG00000164430:E	C6orf150			gi|115511030|ref|NP	hypothetical protein LOC115	522	58815	9.5	0	o	Q	25	0.015	0	0	0	3.38E-05	0	1	8.46E-06	1.69E-05	0	0	0	3.13E-05	0	1	7.82E-06	1.56E-05	0	0	0	0	0	0	0	0			
2071	2	8.02E-06	0	0	INF		ENSG00000156931:E	VPS8			gi|57863275|ref|NP_	vacuolar protein sorting 8 ho	1426	161568	5.6	0	o	Q	0	0	0	3.27E-05	0	0	0	1	8.18E-06	1.64E-05	0	3.15E-05	0	0	0	1	7.87E-06	1.57E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a		metal ion binding; protein
2072	2	7.9E-06	0	0	INF		ENSG00000115816:E	CEBPZ			gi|42542392|ref|NP_	CCAAT/enhancer binding pro	1054	120974	5.9	0	o	Q	0	0	0	0	0	1.68E-05	0	1	4.19E-06	8.38E-06	0	0	0	4.65E-05	0	1	1.16E-05	2.32E-05	0	0	0	0	0	0	0	0	Nucleic-acid-binding protein	nucleus [pmid 2247079]	DNA binding [pmid 2247079]
2073	2	7.84E-06	0	0	INF		ENSG00000100523:E	DDHD1			gi|45120113|ref|NP_	DDHD domain containing 1 [	872	97069	5.7	0	o	Q	36	0	0	0	0	0	0	0	0	0	0	0	0	1.87E-05	4.4E-05	2	1.57E-05	2.09E-05	0	0	0	0	0	0	0	0	DDHD domain. The DDHD		hydrolase activity; metal ion
2074	2	7.8E-06	0	0	INF		ENSG00000114416:E	FXR1			gi|61835148|ref|NP_	fragile X mental retardation-r	621	69721	6.2	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	3.61E-05	0	2.63E-05	0	2	1.56E-05	1.85E-05	0	0	0	0	0	0	0	0	K homology RNA-binding	cytoplasm [pmid 7781595];	protein binding [pmid
2075	2	7.74E-06	0	0	INF		ENSG00000161905:E	ALOX15			gi|40316937|ref|NP_	arachidonate 15-lipoxygenas	662	74804	6.6	0	o	Q	25	0.01	0	3.52E-05	0	2.67E-05	0	2	1.55E-05	1.82E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	PLAT domain of 12/15-	plasma membrane	arachidonate 15-
2076	2	7.65E-06	0	0	INF		ENSG00000175595:E	ERCC4			gi|4885217|ref|NP_0	excision repair cross-comple	916	104486	6.9	0	o	Q	39	0	0	0	0	1.93E-05	0	1	4.82E-06	9.64E-06	0	0	0	0	4.19E-05	1	1.05E-05	2.1E-05	0	0	0	0	0	0	0	0	ERCC4-like helicases [DNA	nucleotide-excision repair	DNA binding;
2077	2	7.61E-06	0	0	INF		ENSG00000114316:E	USP4			gi|40795665|ref|NP_	ubiquitin specific protease, p	963	108565	5.7	0	o	Q	0	0	0	2.42E-05	0	3.67E-05	0	2	1.52E-05	1.83E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	A subfamily of Peptidase	lysosome [pmid 9827704];	cysteine-type endopeptidase
2078	2	7.58E-06	0	0	INF		ENSG00000158545:E	NHN1			gi|31377595|ref|NP_	zinc finger CCCH-type conta	953	106359	8.2	0	o	Q	0	0	0	0	0	3.71E-05	0	1	9.27E-06	1.85E-05	0	2.35E-05	0	0	0	1	5.89E-06	1.18E-05	0	0	0	0	0	0	0	0	AAA ATPase containing		nucleic acid binding; zinc ion
2079	2	7.54E-06	0	0	INF		ENSG00000174953:E	DHX36			gi|18497286|ref|NP_	DEAH (Asp-Glu-Ala-His) box	1008	114776	7.7	0	o	Q	32	0	0	0	0	0	0	0	0	0	0	2.23E-05	0	0	3.81E-05	2	1.51E-05	1.86E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; ATP-dependent
2080	2	7.54E-06	0	0	INF		ENSG00000143442:E	POGZ			gi|46397390|ref|NP_	pogo transposable element w	1410	155343	7.4	0	o	Q	0	0	0	3.31E-05	0	0	0	1	8.27E-06	1.65E-05	0	0	0	0	2.72E-05	1	6.81E-06	1.36E-05	0	0	0	0	0	0	0	0	DDE superfamily	intracellular; nucleus	DNA binding; metal ion
2081	2	7.53E-06	0	0	INF		ENSG00000185163:E	DDX51			gi|154759257|ref|NP	DEAD (Asp-Glu-Ala-Asp) box	666	72457	8.2	0	o	Q	18	0.022	0	0	0	2.65E-05	0	1	6.63E-06	1.33E-05	0	3.37E-05	0	0	0	1	8.42E-06	1.68E-05	0	0	0	0	0	0	0	0			
2082	2	7.5E-06	0	0	INF		ENSG00000159399:E	HK2			gi|15553127|ref|NP_	hexokinase 2 [Homo sapiens	917	102380	6.1	0	o	Q	15	0.005	0	0	0	1.93E-05	0	1	4.82E-06	9.63E-06	0	4.08E-05	0	0	0	1	1.02E-05	2.04E-05	0	0	0	0	0	0	0	0	Hexokinase. Hexokinase	membrane; mitochondrial	ATP binding; hexokinase
2083	2	7.49E-06	0	0	INF		ENSG00000056097:E	ZFR			gi|34101286|ref|NP_	zinc finger RNA binding prote	1074	117012	9	0	o	Q	19	0.057	0	4.34E-05	0	1.64E-05	0	2	1.5E-05	2.05E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	U1-like zinc finger; Family	intracellular; nucleus	nucleic acid binding; zinc ion
2084	2	7.48E-06	0	0	INF		ENSG00000070366:E	SMG6			gi|115511020|ref|NP	Smg-6 homolog, nonsense m	1419	160461	7	0	o	Q	29	0.013	0	0	0	1.24E-05	0	1	3.11E-06	6.22E-06	0	4.74E-05	0	0	0	1	1.19E-05	2.37E-05	0	0	0	0	0	0	0	0			
2085	2	7.39E-06	0	0	INF		ENSG00000125976:E	RBM12			gi|23510462|ref|NP_	RNA binding motif protein 12	932	97396	8.6	0	o	Q	16	0.052	0	0	0	0	0	0	0	0	0	2.41E-05	0	3.5E-05	0	2	1.48E-05	1.76E-05	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus	nucleotide binding; protein
2086	2	7.31E-06	0	0	INF		ENSG00000124181:E	PLCG1			gi|33598946|ref|NP_	phospholipase C gamma 1 is	1290	148532	6	0	o	Q	21	0.035	0	0	0	4.11E-05	0	1	1.03E-05	2.05E-05	0	1.74E-05	0	0	0	1	4.35E-06	8.7E-06	0	0	0	0	0	0	0	0	Src homology 3 domains;		calcium ion binding;
2087	2	7.28E-06	0	0	INF		ENSG00000119596:E	YLPM1			gi|146134388|ref|NP	YLP motif containing 1 [Hom	2146	241643	6.6	0	o	Q	38	0	0	0	0	1.65E-05	0	1	4.12E-06	8.23E-06	0	4.18E-05	0	0	0	1	1.05E-05	2.09E-05	0	0	0	0	0	0	0	0			
2088	2	7.19E-06	0	0	INF		ENSG00000135090:E	TAOK3			gi|148746218|ref|NP	TAO kinase 3 [Homo sapiens	898	105406	7.3	0	o	Q	0	0	0	0	0	3.93E-05	0	1	9.84E-06	1.97E-05	0	0	0	1.82E-05	0	1	4.54E-06	9.09E-06	0	0	0	0	0	0	0	0			
2089	2	7.19E-06	0	0	INF		ENSG00000164654:E	FLJ20323			gi|109150419|ref|NP	hypothetical protein FLJ2032	875	98584	6.7	0	o	Q	22	0	0	0	0	2.02E-05	0	1	5.05E-06	1.01E-05	0	0	0	3.73E-05	0	1	9.33E-06	1.87E-05	0	0	0	0	0	0	0	0			
2090	2	7.08E-06	0	0	INF		ENSG00000124126:E	PREX1			gi|34452732|ref|NP_	PREX1 protein [Homo sapien	1659	186203	6.4	0	o	Q	40	0	0	1.41E-05	0	4.26E-05	0	2	1.42E-05	2.01E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	PDZ domain, also called	cytosol [pmid 11955434];	enzyme binding; phospholipid
2091	2	6.91E-06	0	0	INF		ENSG00000080845:E	DLGAP4			gi|34335253|ref|NP_	disks large-associated protei	989	107567	7.3	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	1.65E-05	3.88E-05	2	1.38E-05	1.84E-05	0	0	0	0	0	0	0	0	Guanylate-kinase-	membrane	
2092	2	6.91E-06	0	0	INF		ENSG00000167107:E	ACSF2			gi|156151445|ref|NP	acyl-CoA synthetase family m	615	68125	7.6	0	o	S	29	0.888	0	0	0	2.87E-05	0	1	7.18E-06	1.44E-05	0	0	0	2.65E-05	0	1	6.63E-06	1.33E-05	0	0	0	0	0	0	0	0			
2093	2	6.9E-06	0	0	INF		ENSG00000163516:E	ANKZF1			gi|109150435|ref|NP	ankyrin repeat and zinc finge	726	80927	8.4	0	o	Q	42	0.186	0	0	0	2.43E-05	0	1	6.08E-06	1.22E-05	0	3.09E-05	0	0	0	1	7.73E-06	1.55E-05	0	0	0	0	0	0	0	0			
2094	2	6.83E-06	0	0	INF		ENSG00000049323:E	LTBP1			gi|46249412|ref|NP_	latent transforming growth fa	1396	152978	5.1	0	o	S	21	0.987	0	1.67E-05	0	3.8E-05	0	2	1.37E-05	1.8E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Plasmodium ookinete	extracellular matrix (sensu	calcium ion binding; growth
2095	2	6.78E-06	0	0	INF		ENSG00000187091:E	PLCD1			gi|90265805|ref|NP_	phospholipase C, delta 1 [Ho	756	85665	6.7	0	o	Q	22	0	0	3.09E-05	0	2.34E-05	0	2	1.36E-05	1.59E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Phospholipase C (PLC)		calcium ion binding;
2096	2	6.65E-06	0	0	INF		ENSG00000140694:E	PARN			gi|4505611|ref|NP_0	poly(A)-specific ribonuclease	639	73451	6.2	0	o	Q	0	0	0	0	0	2.76E-05	0	1	6.91E-06	1.38E-05	0	0	0	2.55E-05	0	1	6.38E-06	1.28E-05	0	0	0	0	0	0	0	0	R3H domain of Poly(A)-	cytoplasm [pmid 9736620];	exonuclease activity;
2097	2	6.57E-06	0	0	INF		ENSG00000140525:E	FANCI			gi|82830440|ref|NP_	Fanconi anemia, complemen	1268	142569	6.8	0	o	Q	15	0	0	0	0	1.39E-05	0	1	3.48E-06	6.97E-06	0	0	0	3.86E-05	0	1	9.65E-06	1.93E-05	0	0	0	0	0	0	0	0		integral to membrane;	
2098	2	6.53E-06	0	0	INF		ENSG00000213983:E	AP1G2			gi|18104996|ref|NP_	adaptor-related protein comp	785	87117	6.6	0	o	Q	18	0	0	2.97E-05	0	2.25E-05	0	2	1.31E-05	1.54E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Adaptin C-terminal domain.	AP-1 adaptor complex [pmid	protein binding
2099	2	6.5E-06	0	0	INF		ENSG00000108094:E	CUL2			gi|19482174|ref|NP_	cullin 2 [Homo sapiens]	745	86983	6.9	0	o	Q	28	0	0	0	0	0	0	0	0	0	0	3.01E-05	0	2.19E-05	0	2	1.3E-05	1.54E-05	0	0	0	0	0	0	0	0	Cullin, a subunit of E3		protein binding [pmid
2100	2	6.5E-06	0	0	INF		ENSG00000122257:E	RBBP6			gi|33620716|ref|NP_	retinoblastoma-binding prote	1758	197286	9.6	0	o	Q	28	0	0	0	0	3.01E-05	0	1	7.54E-06	1.51E-05	0	0	0	0	2.18E-05	1	5.46E-06	1.09E-05	0	0	0	0	0	0	0	0	RING-finger (Really	nucleus; ubiquitin ligase	metal ion binding; nucleic
2101	2	6.44E-06	0	0	INF		ENSG00000104880:E	LOC100134192			gi|169213714|ref|XP	PREDICTED: similar to hCG	796	89396	6.7	0	o	Q	40	0	0	2.93E-05	0	2.22E-05	0	2	1.29E-05	1.51E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2102	2	6.43E-06	0	0	INF		ENSG00000166266:E	CUL5			gi|40254446|ref|NP_	Vasopressin-activated calciu	780	90955	8	0	o	Q	0	0	0	0	0	2.26E-05	0	1	5.66E-06	1.13E-05	0	2.88E-05	0	0	0	1	7.19E-06	1.44E-05	0	0	0	0	0	0	0	0	Cullin, a subunit of E3		calcium channel activity
2103	2	6.37E-06	0	0	INF		ENSG00000133056:E	PIK3C2B			gi|15451926|ref|NP_	phosphoinositide-3-kinase, c	1634	184825	7.2	0	o	Q	28	0	0	0	0	0	0	0	0	0	0	2.75E-05	0	0	2.35E-05	2	1.27E-05	1.48E-05	0	0	0	0	0	0	0	0	Phosphoinositide 3-kinase	cytosol; microsome; nucleus;	inositol or
2104	2	6.27E-06	0	0	INF		ENSG00000170266:E	GLB1			gi|119372308|ref|NP	galactosidase, beta 1 isoform	677	76075	6.6	0	o	S	24	1	0	0	0	2.61E-05	0	1	6.52E-06	1.3E-05	0	0	0	2.41E-05	0	1	6.03E-06	1.21E-05	0	0	0	0	0	0	0	0			
2105	2	6.26E-06	0	0	INF		ENSG00000101191:E	DIDO1			gi|71044479|ref|NP_	death inducer-obliterator 1 is	2240	243840	7.9	0	o	Q	0	0	0	0	0	1.58E-05	0	1	3.94E-06	7.89E-06	0	0	0	0	3.43E-05	1	8.57E-06	1.71E-05	0	0	0	0	0	0	0	0	PHD-finger. PHD folds into	nucleus	metal ion binding; protein
2106	2	6.23E-06	0	0	INF		ENSG00000159842:E	ABR			gi|38679954|ref|NP_	active breakpoint cluster regi	822	93707	6.4	0	o	Q	0	0	0	2.84E-05	0	2.15E-05	0	2	1.25E-05	1.47E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RhoGAP_Bcr: RhoGAP	intracellular	GTPase activator activity
2107	2	6.19E-06	0	0	INF		ENSG00000058673:E	ZC3H11A			gi|114842410|ref|NP	zinc finger CCCH-type conta	810	89131	8.4	0	o	Q	20	0.001	0	0	0	2.18E-05	0	1	5.45E-06	1.09E-05	0	2.77E-05	0	0	0	1	6.92E-06	1.38E-05	0	0	0	0	0	0	0	0			
2108	2	6.1E-06	0	0	INF		ENSG00000185787:E	MORF4L1			gi|45643135|ref|NP_	MORF-related gene 15 isofo	362	41474	9.3	0	o	Q	31	0	0	0	0	4.88E-05	0.001125	2	1.22E-05	2.44E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MRG. This family consists	nucleus	
2109	2	6.08E-06	0	0	INF		ENSG00000169180:E	XPO6			gi|46049063|ref|NP_	exportin 6 [Homo sapiens]	1125	128883	6.4	0	o	Q	25	0	0	0	0	0	0	0	0	0	0	0	0	1.45E-05	3.41E-05	2	1.22E-05	1.62E-05	0	0	0	0	0	0	0	0	Exportin 1-like protein. The	cytoplasm [pmid 14592989];	protein binding [pmid
2110	2	6.01E-06	0	0	INF		ENSG00000178921:E	PFAS			gi|31657129|ref|NP_	phosphoribosylformylglycinar	1338	144734	5.8	0	o	Q	17	0.001	0	3.49E-05	0	1.32E-05	0	2	1.2E-05	1.65E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Formylglycinamide	cytoplasm	ATP binding; ligase activity;
2111	2	5.99E-06	0	0	INF		ENSG00000143093:E	FAM40A			gi|56790935|ref|NP_	hypothetical protein LOC853	837	95576	6.3	0	o	Q	19	0	0	0	0	2.11E-05	0	1	5.28E-06	1.06E-05	0	2.68E-05	0	0	0	1	6.7E-06	1.34E-05	0	0	0	0	0	0	0	0	N1221-like protein. The		
2112	2	5.95E-06	0	0	INF		ENSG00000060069:E	CTDP1			gi|67188445|ref|NP_	CTD (carboxy-terminal doma	961	104399	5.3	0	o	Q	59	0.307	0	2.43E-05	0	0	0	1	6.07E-06	1.21E-05	0	2.33E-05	0	0	0	1	5.84E-06	1.17E-05	0	0	0	0	0	0	0	0	FCP1, C-terminal. The C-	intracellular; nucleus	DNA-directed RNA
2113	2	5.95E-06	0	0	INF		ENSG00000018699:E	TTC27			gi|42476022|ref|NP_	tetratricopeptide repeat doma	843	96632	5.6	0	o	Q	17	0.013	0	0	0	2.1E-05	0	1	5.24E-06	1.05E-05	0	2.66E-05	0	0	0	1	6.65E-06	1.33E-05	0	0	0	0	0	0	0	0	Tetratricopeptide repeat		binding
2114	2	5.74E-06	0	0	INF		ENSG00000104133:E	SPG11			gi|93204888|ref|NP_	spastic paraplegia 11 (autos	2443	278866	6	0	o	S	40	0.748	0	0	0	1.45E-05	0	1	3.62E-06	7.23E-06	0	0	0	0	3.14E-05	1	7.86E-06	1.57E-05	0	0	0	0	0	0	0	0			catalytic activity; ferric iron
2115	2	5.67E-06	0	0	INF		ENSG00000154310:E	TNIK			gi|55741807|ref|NP_	TRAF2 and NCK interacting	1360	154943	7.2	0	o	Q	38	0	0	1.72E-05	0	0	0	1	4.29E-06	8.58E-06	0	0	0	0	2.82E-05	1	7.06E-06	1.41E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
2116	2	5.63E-06	0	0	INF		ENSG00000118960:E	HS1BP3			gi|68800430|ref|NP_	HCLS1 binding protein 3 [Ho	392	42780	5	0	o	Q	19	0.004	0	0	0	4.51E-05	0.001039	2	1.13E-05	2.25E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	PX domain. PX domains		phosphoinositide binding;
2117	2	5.53E-06	0	0	INF		ENSG00000175265:N	LOC390561			gi|169208144|ref|XP	PREDICTED: similar to hect	1394	149583	8.6	0	o	Q	22	0.001	0	1.67E-05	0	0	0	1	4.18E-06	8.37E-06	0	0	0	0	2.75E-05	1	6.88E-06	1.38E-05	0	0	0	0	0	0	0	0			
2118	2	5.25E-06	0	0	INF		ENSG00000140553:E	UNC45A			gi|29725607|ref|NP_	smooth muscle cell associate	944	103077	6.1	0	o	Q	50	0	0	2.47E-05	0	0	0	1	6.18E-06	1.24E-05	0	0	0	1.73E-05	0	1	4.32E-06	8.64E-06	0	0	0	0	0	0	0	0	Tetratricopeptide repeat		binding
2119	2	5.17E-06	0	0	INF		ENSG00000134900:E	TPP2			gi|4507657|ref|NP_0	tripeptidyl peptidase II [Homo	1249	138449	6.4	0	o	Q	24	0	0	0	0	2.83E-05	0	1	7.07E-06	1.41E-05	0	0	0	1.31E-05	0	1	3.27E-06	6.53E-06	0	0	0	0	0	0	0	0	Subtilase family. Subtilases	cytoplasm [pmid 9974389]	aminopeptidase activity; D-
2120	2	5.15E-06	0	0	INF		ENSG00000168071:E	CCDC88B			gi|88196790|ref|NP_	coiled-coil domain containing	1476	164764	5.1	0	o	S	32	0.732	0	0	0	0	0	0	0	0	0	1.52E-05	0	0	2.6E-05	2	1.03E-05	1.27E-05	0	0	0	0	0	0	0	0	Chromosome segregation		protein binding [pmid
2121	2	5.12E-06	0	0	INF		ENSG00000149091:E	DGKZ			gi|157688564|ref|NP	diacylglycerol kinase, zeta 1(	1117	124128	9	0	o	Q	65	0	0	2.09E-05	0	0	0	1	5.22E-06	1.04E-05	0	2.01E-05	0	0	0	1	5.02E-06	1E-05	0	0	0	0	0	0	0	0			
2122	2	5.1E-06	0	0	INF		ENSG00000114127:E	XRN1			gi|110624787|ref|NP	5'-3' exoribonuclease 1 isofor	1693	192713	7.3	0	o	Q	19	0	0	2.76E-05	0	0	0	1	6.89E-06	1.38E-05	0	1.33E-05	0	0	0	1	3.31E-06	6.63E-06	0	0	0	0	0	0	0	0			
2123	2	5.08E-06	0	0	INF		ENSG00000151503:E	NCAPD3			gi|45356151|ref|NP_	non-SMC condensin II compl	1498	168890	7.5	0	o	Q	22	0.007	0	0	0	0	0	0	0	0	0	1.5E-05	0	0	2.56E-05	2	1.02E-05	1.25E-05	0	0	0	0	0	0	0	0	Adaptin N terminal region.		binding
2124	2	5.06E-06	0	0	INF		ENSG00000080345:E	RIF1			gi|56676335|ref|NP_	RAP1 interacting factor 1 [Ho	2472	274464	5.5	0	o	Q	25	0.173	0	9.44E-06	0	0	0	1	2.36E-06	4.72E-06	0	0	0	0	3.11E-05	1	7.76E-06	1.55E-05	0	0	0	0	0	0	0	0		chromosome; chromosome,	binding
2125	2	4.96E-06	0	0	INF		ENSG00000166716:E	ZNF592			gi|108860697|ref|NP	zinc finger protein 592 [Homo	1267	137528	7.8	0	o	Q	27	0	0	0	0	1.39E-05	0	1	3.49E-06	6.97E-06	0	0	0	2.58E-05	0	1	6.44E-06	1.29E-05	0	0	0	0	0	0	0	0			
2126	2	4.96E-06	0	0	INF		ENSG00000104774:E	MAN2B1			gi|51873064|ref|NP_	mannosidase, alpha, class 2I	1011	113744	7.3	0	o	S	50	0.998	0	0	0	1.75E-05	0	1	4.37E-06	8.74E-06	0	2.22E-05	0	0	0	1	5.55E-06	1.11E-05	0	0	0	0	0	0	0	0	Alpha mannosidase, middle	lysosome	alpha-mannosidase activity
2127	2	4.82E-06	0	0	INF		ENSG00000198554:E	WDHD1			gi|56550086|ref|NP_	WD repeat and HMG-box DN	1006	112704	5.7	0	o	Q	32	0	0	0	0	0	0	0	0	0	0	2.23E-05	0	1.62E-05	0	2	9.63E-06	1.14E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a	cytoplasm [pmid 9175701];	DNA binding [pmid 9175701]
2128	2	4.74E-06	0	0	INF		ENSG00000064607:E	SFRS14			gi|62859987|ref|NP_	splicing factor, arginine/serin	1082	120237	7.3	0	o	Q	0	0	0	2.16E-05	0	1.63E-05	0	2	9.47E-06	1.11E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	glycine rich nucleic binding	intracellular; nucleus	RNA binding
2129	2	4.7E-06	0	0	INF		ENSG00000179832:N	KIAA1833			gi|113420243|ref|XP	PREDICTED: hypothetical pr	1218	134310	6.9	0	o	Q	20	0.211	0	1.91E-05	0	0	0	1	4.79E-06	9.57E-06	0	1.84E-05	0	0	0	1	4.6E-06	9.21E-06	0	0	0	0	0	0	0	0			
2130	2	4.52E-06	0	0	INF		ENSG00000092148:E	HECTD1			gi|118498337|ref|NP	HECT domain containing 1 [H	2610	289383	5.4	0	o	Q	19	0	0	0	0	6.77E-06	0	1	1.69E-06	3.38E-06	0	0	0	0	2.94E-05	1	7.35E-06	1.47E-05	0	0	0	0	0	0	0	0			
2131	2	4.47E-06	0	0	INF		ENSG00000156304:E	SFRS15			gi|40789229|ref|NP_	splicing factor, arginine/serin	1147	125869	9.6	0	o	Q	25	0	0	2.03E-05	0	1.54E-05	0	2	8.93E-06	1.05E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CID (CTD-Interacting	nucleus	nucleotide binding; RNA
2132	2	4.43E-06	0	0	INF		ENSG00000175931:E	UBE2O			gi|33636750|ref|NP_	ubiquitin-conjugating enzyme	1292	141383	5.1	0	o	Q	40	0.049	0	1.81E-05	0	0	0	1	4.51E-06	9.03E-06	0	1.74E-05	0	0	0	1	4.34E-06	8.68E-06	0	0	0	0	0	0	0	0	Ubiquitin-conjugating		ubiquitin-protein ligase
2133	2	4.41E-06	0	0	INF		ENSG00000173120:E	FBXL11			gi|16306580|ref|NP_	F-box and leucine-rich repea	1162	132793	7.6	0	o	Q	0	0	0	2.01E-05	0	1.52E-05	0	2	8.82E-06	1.04E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CXXC zinc finger. This	nucleus	DNA binding; iron ion binding
2134	2	4.39E-06	0	0	INF		ENSG00000146918:E	NCAPG2			gi|116812586|ref|NP	leucine zipper protein 5 [Hom	1143	130960	6.9	0	o	Q	18	0	0	0	0	1.55E-05	0	1	3.86E-06	7.73E-06	0	1.96E-05	0	0	0	1	4.91E-06	9.81E-06	0	0	0	0	0	0	0	0			
2135	2	4.23E-06	0	0	INF		ENSG00000095564:E	BTAF1			gi|27477070|ref|NP_	BTAF1 RNA polymerase II, E	1849	206886	6.5	0	o	Q	27	0.049	0	0	0	9.55E-06	0	1	2.39E-06	4.78E-06	0	2.43E-05	0	0	0	1	6.07E-06	1.21E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleus	ATP binding; helicase
2136	2	4.16E-06	0	0	INF		ENSG00000197442:E	MAP3K5			gi|5174547|ref|NP_0	mitogen-activated protein kin	1374	154536	5.8	0	o	Q	23	0.002	0	1.7E-05	0	0	0	1	4.24E-06	8.49E-06	0	1.63E-05	0	0	0	1	4.08E-06	8.16E-06	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; caspase
2137	2	4.16E-06	0	0	INF		ENSG00000141556:E	TBCD			gi|41350333|ref|NP_	beta-tubulin cofactor D [Hom	1192	132600	6.2	0	o	Q	32	0	0	1.96E-05	0	0	0	1	4.89E-06	9.78E-06	0	0	0	1.37E-05	0	1	3.42E-06	6.85E-06	0	0	0	0	0	0	0	0	Beta-tubulin folding cofactor		binding
2138	2	4.15E-06	0	0	INF		ENSG00000170776:N	AKAP13			gi|21493029|ref|NP_	A-kinase anchor protein 13 is	2813	307550	5.2	0	o	Q	27	0.01	0	3.32E-05	0	0	0.000145	2	8.29E-06	1.66E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Pleckstrin homology (PH)	intracellular; membrane	cAMP-dependent protein
2139	2	4.08E-06	0	0	INF		ENSG00000150347:E	ARID5B			gi|74136549|ref|NP_	AT rich interactive domain 5E	1188	132375	8.7	0	o	Q	18	0.001	0	0	0	0	0	0	0	0	0	1.89E-05	0	1.37E-05	0	2	8.16E-06	9.65E-06	0	0	0	0	0	0	0	0	BAH, or Bromo Adjacent	intracellular; nucleus [pmid	DNA binding [pmid
2140	2	4.05E-06	0	0	INF		ENSG00000165659:E	DACH1			gi|18375609|ref|NP_	dachshund homolog 1 isoforn	504	51891	8.8	0	o	Q	24	0.097	0	0	0	0	0	0	0	0	0	0	0.001387	3.24E-05	0	2	8.1E-06	1.62E-05	0	0	0	0	0	0	0	0	SKI/SNO/DAC family. This	nucleus	DNA binding; protein binding
2141	2	3.94E-06	0	0	INF		ENSG00000163539:E	CLASP2			gi|57863301|ref|NP_	CLIP-associating protein 2 [H	1506	164886	8.2	0	o	Q	40	0	0	2.06E-05	0	0	0	1	5.16E-06	1.03E-05	0	0	0	1.08E-05	0	1	2.71E-06	5.42E-06	0	0	0	0	0	0	0	0	HEAT repeat. The HEAT	cytoplasmic microtubule [pmid	binding; microtubule plus-end
2142	2	3.9E-06	0	0	INF		ENSG00000157654:E	PALM2-AKAP2			gi|22325356|ref|NP_	PALM2-AKAP2 protein isofor	1090	120630	5	0	o	Q	0	0	0	0	0	1.62E-05	0	1	4.05E-06	8.1E-06	0	0	0	1.5E-05	0	1	3.74E-06	7.49E-06	0	0	0	0	0	0	0	0			
2143	2	3.88E-06	0	0	INF		ENSG00000133858:E	CCDC131			gi|87116683|ref|NP_	proline/serine-rich coiled-coil	1989	226354	8.1	0	o	Q	17	0	0	1.17E-05	0	0	0	1	2.93E-06	5.86E-06	0	0	0	0	1.93E-05	1	4.82E-06	9.65E-06	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	intracellular	binding
2144	2	3.61E-06	0	0	INF		ENSG00000177409:E	SAMD9L			gi|51339291|ref|NP_	sterile alpha motif domain co	1584	184531	8	0	o	Q	0	0	0	1.47E-05	0	0	0	1	3.68E-06	7.36E-06	0	1.42E-05	0	0	0	1	3.54E-06	7.08E-06	0	0	0	0	0	0	0	0			
2145	2	3.57E-06	0	0	INF		ENSG00000158987:E	FNIP1			gi|54633319|ref|NP_	PDZ domain-containing guar	1601	179450	6.4	0	o	Q	0	0	0	1.46E-05	0	0	0	1	3.64E-06	7.28E-06	0	1.4E-05	0	0	0	1	3.5E-06	7.01E-06	0	0	0	0	0	0	0	0	effector domain of the CAP	intracellular; plasma	GTP-dependent protein
2146	2	3.42E-06	0	0	INF		ENSG00000198837:E	DENND4B			gi|148922920|ref|NP	DENN/MADD domain contai	1496	163846	7.2	0	o	Q	23	0.081	0	1.56E-05	0	1.18E-05	0	2	6.85E-06	8.06E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2147	2	3.41E-06	0	0	INF		ENSG00000204820:N	C12orf51			gi|157885806|ref|NP	chromosome 12 open readin	3996	439348	6.2	0	o	Q	18	0.012	0	0	0	1.77E-05	0	1	4.42E-06	8.84E-06	0	0	0	0	9.61E-06	1	2.4E-06	4.8E-06	0	0	0	0	0	0	0	0			
2148	2	3.11E-06	0	0	INF		ENSG00000064932:E	SBNO2			gi|154355002|ref|NP	strawberry notch homolog 2	1366	150274	6.5	0	o	Q	33	0	0	0	0	1.29E-05	0	1	3.23E-06	6.47E-06	0	0	0	1.19E-05	0	1	2.99E-06	5.97E-06	0	0	0	0	0	0	0	0			
2149	2	3.07E-06	0	0	INF		ENSG00000198399:E	ITSN2			gi|22325381|ref|NP_	intersectin 2 isoform 3 [Homo	1669	190364	8.2	0	o	Q	17	0	0	1.4E-05	0	1.06E-05	0	2	6.14E-06	7.22E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Src homology 3 domains;	intracellular	calcium ion binding; protein
2150	2	2.88E-06	0	0	INF		ENSG00000107290:E	SETX			gi|113722133|ref|NP	senataxin [Homo sapiens]	2677	302879	7.2	0	o	Q	15	0.008	0	8.71E-06	0	0	0	1	2.18E-06	4.36E-06	0	0	0	0	1.43E-05	1	3.58E-06	7.17E-06	0	0	0	0	0	0	0	0			
2151	2	2.76E-06	0	0	INF		ENSG00000197535:E	MYO5A			gi|115511014|ref|NP	myosin VA (heavy polypeptic	1855	215403	8.5	0	o	Q	17	0	0	1.26E-05	0	9.52E-06	0	2	5.52E-06	6.5E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2152	2	2.68E-06	0	0	INF		ENSG00000127616:E	SMARCA4			gi|21071056|ref|NP_	SWI/SNF-related matrix-ass	1647	184644	7.9	0	o	Q	40	0.002	0	0	0	2.15E-05	0	1	5.36E-06	1.07E-05	0	0	0.000425	0	0	1	0	0	0	0	0	0	0	0	0	0	Helicase superfamily c-	nucleoplasm [pmid 8208605];	ATP binding; DNA binding;
2153	2	2.65E-06	0	0	INF		ENSG00000125107:E	CNOT1			gi|42716275|ref|NP_	CCR4-NOT transcription com	2376	266937	7.1	0	o	Q	17	0.009	0	0	0	7.43E-06	0	1	1.86E-06	3.72E-06	0	0	0	1.37E-05	0	1	3.43E-06	6.87E-06	0	0	0	0	0	0	0	0	CCR4-Not complex		
2154	2	2.58E-06	0	0	INF		ENSG00000104517:E	LOC730429			gi|113420453|ref|XP	PREDICTED: similar to E3 u	2796	309192	6.1	0	o	Q	18	0	0	0	0	1.26E-05	0	1	3.16E-06	6.32E-06	0	8.02E-06	0	0	0	1	2.01E-06	4.01E-06	0	0	0	0	0	0	0	0	C-terminal domain of		
2155	2	2.3E-06	0	0	INF		ENSG00000204469:E	BAT2			gi|149158690|ref|NP	HLA-B associated transcript-	2157	228861	9.5	0	o	Q	0	0	0	1.08E-05	0	0	0	1	2.7E-06	5.41E-06	0	0	0	7.57E-06	0	1	1.89E-06	3.78E-06	0	0	0	0	0	0	0	0			
2156	2	2.13E-06	0	0	INF		ENSG00000005339:E	CREBBP			gi|119943102|ref|NP	CREB binding protein isoform	2404	260990	8.5	0	o	Q	0	0	0	9.7E-06	0	7.35E-06	0	2	4.26E-06	5.01E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs								Region_Note	GO_Component	GO_Function
																					HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF			
2157	2	2.11E-06	0	0	INF		ENSG00000137337:E	MDC1			gi|132626688|ref|NP	mediator of DNA damage ch	2089	226664	5.5	0	o	Q	0	0	0	0	0	1.69E-05	0.000195	2	4.23E-06	8.46E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2158	2	1.8E-06	0	0	INF		ENSG00000064999:E	ANKS1A			gi|140161500|ref|NP	ankyrin repeat and sterile alp	1134	123108	6.4	0	o	Q	42	0	0	0	0	0	0.000359	1	0	0	0	0	0	1.44E-05	0	1	3.6E-06	7.2E-06	0	0	0	0	0	0	0	0			
2159	2	1.66E-06	0	0	INF		ENSG00000172869:E	DMXL1			gi|148528998|ref|NP	Dmx-like 1 [Homo sapiens]	3027	337839	6.3	0	o	Q	18	0.004	0	0	0	5.84E-06	0	1	1.46E-06	2.92E-06	0	7.41E-06	0	0	0	1	1.85E-06	3.71E-06	0	0	0	0	0	0	0	0			
2160	2	1.37E-06	0	0	INF		ENSG00000065526:E	SPEN			gi|14790190|ref|NP_	spen homolog, transcriptiona	3664	402251	7.6	0	o	Q	0	0	0	0	0	4.82E-06	0	1	1.21E-06	2.41E-06	0	6.12E-06	0	0	0	1	1.53E-06	3.06E-06	0	0	0	0	0	0	0	0	SPOC domain. The SPOC	nucleus	DNA binding; nucleic acid
2161	2	1.31E-06	0	0	INF		ENSG00000127914:E	AKAP9			gi|22538387|ref|NP_	A-kinase anchor protein 9 isc	3907	452990	5	0	o	Q	0	0	0	5.97E-06	0	4.52E-06	0	2	2.62E-06	3.09E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RecF/RecN/SMC N	centrosome [pmid 10202149];	receptor binding [pmid
2162	2	1.17E-06	0	0	INF		ENSG00000168477:E	TNXB			gi|67782336|ref|NP_	tenascin XB isoform 1 [Homo	4289	464330	5.3	0	o	S	24	1	0	0	0	4.12E-06	0	1	1.03E-06	2.06E-06	0	5.23E-06	0	0	0	1	1.31E-06	2.62E-06	0	0	0	0	0	0	0	0	Fibronectin type 3 domain;	extracellular matrix (sensu	extracellular matrix structural
2163	2	1.1E-06	0	0	INF		ENSG00000072121:E	ZFYVE26			gi|38202205|ref|NP_	zinc finger, FYVE domain co	2539	284601	6.4	0	o	Q	35	0	0	0	0	0	0.00016	1	0	0	0	8.84E-06	0	0	0	1	2.21E-06	4.42E-06	0	0	0	0	0	0	0	0	FYVE domain; Zinc-binding		zinc ion binding
2164	2	0	0	0	INF		ENSG00000152767:E	FARP1			gi|5031633|ref|NP_0	FERM, RhoGEF, and pleckst	1045	118633	8.2	0	o	Q	0	0	0	0	0	0	0.00039	1	0	0	0	0	0.000669	0	0	1	0	0	0	0	0	0	0	0	0	0	Pleckstrin homology (PH)	cytoplasm; cytoskeleton [pmid	binding; cytoskeletal protein
2165	2	0	0	0	INF		ENSG00000157766:E	ACAN			gi|126090883|ref|NP	aggrecan isoform 1 precurso	2317	239432	4.1	0	o	S	17	0.998	0	0	0	0	0.000176	1	0	0	0	0	0.000302	0	0	1	0	0	0	0	0	0	0	0	0	0			
2166	1	0.000891	0	0	INF		ENSG00000127922:N	SHFM1			gi|5453640|ref|NP_0	candidate for split hand/foot	70	8278	4	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.007129	1	0.001782	0.003565	0	0	0	0	0	0	0	0		cytosol; integrator complex	peptidase activity [pmid
2167	1	0.000881	0	0	INF		ENSG00000132485:E	ZRANB2			gi|42741682|ref|NP_	zinc finger protein 265 isofor	320	36318	9.8	0	o	Q	0	0	0	0	0.007045	0	0	1	0.001761	0.003523	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Zinc finger domain; Zinc	intracellular; nucleus [pmid	metal ion binding; RNA
2168	1	0.000854	0	0	INF		ENSG00000182899:E	RPL35A			gi|16117791|ref|NP_	ribosomal protein L35a [Hom	110	12538	11.1	0	o	Q	18	0.003	0	0	0.006832	0	0	1	0.001708	0.003416	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Ribosomal protein L35Ae;	cytosolic large ribosomal	structural constituent of
2169	1	0.000713	0	0	INF		ENSG00000204983:E	LOC100134294			gi|169217813|ref|XP	PREDICTED: hypothetical pr	247	26539	6.5	0	o	S	16	0.997	0	0	0.005705	0	0	1	0.001426	0.002852	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2170	1	0.000425	0	0	INF		ENSG00000002834:E	LASP1			gi|5453710|ref|NP_0	LIM and SH3 protein 1 [Hom	261	29717	7	0	o	Q	21	0	0	0	0	0	0	0	0	0	0.003401	0	0	0	0	1	0.00085	0.001701	0	0	0	0	0	0	0	0	Src homology 3 domains;	cortical actin cytoskeleton;	actin binding; ion transporter
2171	1	0.0004	0	0	INF		ENSG00000175768:E	TOMM5			gi|49169828|ref|NP_	hypothetical protein LOC401	51	6035	9.7	0	o	Q	43	0	0	0.003201	0	0	0	1	0.0008	0.001601	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2172	1	0.000226	0	0	INF		ENSG00000102898:E	NUTF2			gi|5031985|ref|NP_0	nuclear transport factor 2 [Hc	127	14478	5.4	0	o	Q	0	0	0	0	0	0.001808	0	1	0.000452	0.000904	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Nuclear transport factor 2	intracellular	protein binding [pmid
2173	1	0.000188	0	0	INF		ENSG00000129455:E	KLK9			gi|29366812|ref|NP_	kallikrein-related peptidase 9	250	27513	7.4	0	o	S	20	1	0	0	0.001503	0	0	1	0.000376	0.000752	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Trypsin-like serine	extracellular region	peptidase activity; serine-
2174	1	0.000184	0	0	INF		ENSG00000173674:E	EIF1AY			gi|33356163|ref|NP_	eukaryotic translation initiatio	144	16442	5.2	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001473	0	1	0.000368	0.000737	0	0	0	0	0	0	0	0	eukaryotic translation		protein binding [pmid
2175	1	0.000183	0	0	INF		ENSG00000110025:E	ARL2			gi|148612885|ref|NP	ADP-ribosylation factor-like 2	184	20878	6.4	0	o	Q	28	0.001	0	0	0	0	0	0	0	0	0	0	0	0	0.00146	1	0.000365	0.00073	0	0	0	0	0	0	0	0			
2176	1	0.000173	0	0	INF		ENSG00000160075:E	SSU72			gi|7661832|ref|NP_0	Ssu72 RNA polymerase II CT	194	22574	5.3	0	o	Q	23	0.022	0	0	0	0	0	0	0	0	0	0	0	0	0.001385	1	0.000346	0.000693	0	0	0	0	0	0	0	0	Ssu72-like protein. The		
2177	1	0.000173	0	0	INF		ENSG00000163209:E	SPRR3			gi|148229144|ref|NP	small proline-rich protein 3 [H	169	18154	8.6	0	o	Q	0	0	0	0.00138	0	0	0	1	0.000345	0.00069	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2178	1	0.000159	0	0	INF		ENSG00000213145:E	CRIP1			gi|4503047|ref|NP_0	cysteine-rich protein 1 (intest	77	8533	8.8	0	i	Q	22	0	0	0	0	0	0	0	0	0	0	0	0	0.001272	0	1	0.000318	0.000636	0	0	0	0	0	0	0	0	LIM domain. This family	cytoplasm [pmid 9126610]	metal ion binding; zinc ion
2179	1	0.000158	0	0	INF		ENSG00000106355:N	LSM5			gi|6912488|ref|NP_0	LSM5 homolog, U6 small nuc	91	9937	4.5	0	o	Q	24	0.005	0	0	0	0	0	0	0	0	0	0	0	0	0.001266	1	0.000316	0.000633	0	0	0	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus [pmid 10369684];	protein binding [pmid
2180	1	0.00015	0	0	INF		ENSG00000154124:E	FAM105B			gi|115334675|ref|NP	hypothetical protein LOC902	352	40263	5.5	0	o	Q	18	0.008	0	0	0	0	0	0	0	0	0	0	0	0	0.0012	1	0.0003	0.0006	0	0	0	0	0	0	0	0			
2181	1	0.000147	0	0	INF		ENSG00000160213:E	CSTB			gi|4503117|ref|NP_0	cystatin B [Homo sapiens]	98	11140	7.6	0	o	Q	17	0.009	0	0	0	0	0	0	0	0	0	0	0	0	0.001175	1	0.000294	0.000588	0	0	0	0	0	0	0	0	Cystatin-like domain;	intracellular; nucleus	cysteine protease inhibitor
2182	1	0.000135	1	1.64E-05	8.249734		ENSG00000106682:E	EIF4H			gi|11559923|ref|NP_	eukaryotic translation initiatio	248	27385	7.2	0	o	Q	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001084	1	0.000271	0.000542	0	0	0	0	0	0	0.000131	0	RNA recognition motif;	eukaryotic translation	nucleic acid binding;
2183	1	0.000131	0	0	INF		ENSG00000167996:E	FTH1			gi|56682959|ref|NP_	ferritin, heavy polypeptide 1 [	183	21226	5.6	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001049	1	0.000262	0.000524	0	0	0	0	0	0	0	0	Eukaryotic Ferritin	ferritin complex [pmid	binding; ferric iron binding;
2184	1	0.000126	0	0	INF		ENSG00000158526:E	TSR2			gi|24308388|ref|NP_	TSR2, 20S rRNA accumulati	191	20894	4.4	0	o	Q	28	0.399	0	0	0	0	0	0	0	0	0	0	0	0	0.001005	1	0.000251	0.000502	0	0	0	0	0	0	0	0			
2185	1	0.000124	0	0	INF		ENSG00000100351:E	GRAP2			gi|4758476|ref|NP_0	GRB2-related adaptor protei	330	37909	7	0	o	Q	14	0	0	0	0	0	0	0	0	0	0	0	0	0.000989	0	1	0.000247	0.000495	0	0	0	0	0	0	0	0	Src homology 3 domains;	cytoplasm [pmid 9878555]	protein binding [pmid
2186	1	0.000123	0	0	INF		ENSG00000173465:E	SSSCA1			gi|5453838|ref|NP_0	Sjogren syndrome/scleroderr	199	21474	5.2	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000984	0	1	0.000246	0.000492	0	0	0	0	0	0	0	0	Sjogren's		
2187	1	0.000119	0	0	INF		ENSG00000099622:E	CIRBP			gi|4502847|ref|NP_0	cold inducible RNA binding p	172	18648	9.5	0	o	Q	21	0.001	0	0	0	0	0	0	0	0	0	0	0	0.000949	0	1	0.000237	0.000474	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus	nucleotide binding; RNA
2188	1	0.000118	0	0	INF		ENSG00000146386:E	C6orf115			gi|24308273|ref|NP_	hypothetical protein LOC585	81	9056	6.3	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000948	1	0.000237	0.000474	0	0	0	0	0	0	0	0			
2189	1	0.000112	0	0	INF		ENSG00000139343:E	SNRPF			gi|4507131|ref|NP_0	small nuclear ribonucleoprote	86	9725	4.7	0	o	Q	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000893	1	0.000223	0.000446	0	0	0	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus; ribonucleoprotein	RNA binding
2190	1	0.000111	0	0	INF		ENSG00000130255:E	RPL36			gi|16117796|ref|NP_	ribosomal protein L36 [Homo	105	12254	11.6	0	o	Q	15	0	0	0.000889	0	0	0	1	0.000222	0.000444	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Ribosomal protein L36e;	cytosolic large ribosomal	structural constituent of
2191	1	0.000107	0	0	INF		ENSG00000173598:E	NUDT4			gi|40317632|ref|NP_	nudix-type motif 4 isoform alp	180	20306	6.4	0	o	Q	37	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000853	1	0.000213	0.000427	0	0	0	0	0	0	0	0	Members of the Nudix	intracellular	diphosphoinositol-
2192	1	0.000101	0	0	INF		ENSG00000105205:N	CLC			gi|20357559|ref|NP_	Charcot-Leyden crystal prote	142	16453	7.4	0	o	Q	18	0.023	0	0	0	0	0	0	0	0	0	0	0	0	0.000811	1	0.000203	0.000406	0	0	0	0	0	0	0	0	Galectin/galactose-binding		hydrolase activity;
2193	1	0.000101	0	0	INF		ENSG00000150459:N	SAP18			gi|5032067|ref|NP_0	Sin3A-associated protein, 18	153	17561	9.4	0	o	Q	0	0	0	0	0	0.000808	0	1	0.000202	0.000404	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Sin3 associated	histone deacetylase complex	protein binding [pmid
2194	1	9.89E-05	0	0	INF		ENSG00000196754:N	S100A2			gi|5174661|ref|NP_0	S100 calcium binding protein	97	10986	4.8	0	o	Q	22	0.178	0	0	0	0	0	0	0	0	0	0	0	0	0.000791	1	0.000198	0.000396	0	0	0	0	0	0	0	0	S-100/ICaBP-like domain;		calcium ion binding [pmid
2195	1	9.6E-05	0	0	INF		ENSG00000163882:E	POLR2H			gi|14589953|ref|NP_	RNA polymerase II, polypept	150	17143	4.7	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000768	1	0.000192	0.000384	0	0	0	0	0	0	0	0	RNA polymerase Rpb8.	nucleus	DNA-directed RNA
2196	1	9.23E-05	0	0	INF		ENSG00000004779:E	NDUFAB1			gi|4826852|ref|NP_0	NADH dehydrogenase (ubiqu	156	17417	4.9	0	o	S	56	0.981	0	0	0	0	0	0	0	0	0	0	0	0	0.000738	1	0.000185	0.000369	0	0	0	0	0	0	0	0	acyl carrier protein;	membrane fraction;	acyl carrier activity; cofactor
2197	1	8.87E-05	0	0	INF		ENSG00000082701:E	GSK3B			gi|21361340|ref|NP_	glycogen synthase kinase 3 b	433	48034	8.8	0	o	Q	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000709	1	0.000177	0.000355	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; glycogen
2198	1	8.58E-05	0	0	INF		ENSG00000174021:E	GNG5			gi|4885287|ref|NP_0	guanine nucleotide binding p	68	7318	9.9	0	o	Q	16	0.001	0	0.000686	0	0	0	1	0.000172	0.000343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	G protein gamma subunit-	heterotrimeric G-protein	signal transducer activity
2199	1	8.57E-05	0	0	INF		ENSG00000132286:N	FXC1			gi|6912382|ref|NP_0	fractured callus expressed tra	103	11586	7.4	0	i	Q	31	0	0	0	0	0.000686	0	1	0.000171	0.000343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Tim10/DDP family zinc	membrane; mitochondrial	metal ion binding; zinc ion
2200	1	8.37E-05	0	0	INF		ENSG00000140990:E	NDUFB10			gi|4758774|ref|NP_0	NADH dehydrogenase (ubiqu	172	20777	8.5	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00067	1	0.000167	0.000335	0	0	0	0	0	0	0	0		membrane fraction;	NADH dehydrogenase
2201	1	8.24E-05	0	0	INF		ENSG00000130813:E	C19orf66			gi|154350198|ref|NP	hypothetical protein LOC553	291	33110	7.3	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00066	1	0.000165	0.00033	0	0	0	0	0	0	0	0			
2202	1	7.65E-05	0	0	INF		ENSG00000164167:E	LSM6			gi|5901998|ref|NP_0	Sm protein F [Homo sapiens]	80	9128	9.6	0	i	Q	28	0	0	0	0	0	0	0	0	0	0	0	0	0.000612	0	1	0.000153	0.000306	0	0	0	0	0	0	0	0	The eukaryotic Sm and Sm-	nucleus; small nuclear	protein binding [pmid
2203	1	7.59E-05	0	0	INF		ENSG00000204435:E	CSNK2B			gi|23503295|ref|NP_	casein kinase 2, beta polype	215	24942	5.6	0	o	Q	19	0.02	0	0	0	0	0	0	0	0	0	0	0	0.000607	0	1	0.000152	0.000304	0	0	0	0	0	0	0	0	Casein kinase II regulatory	protein kinase CK2 complex	identical protein binding
2204	1	7.44E-05	0	0	INF		ENSG00000088986:N	DYNLL1			gi|83267868|ref|NP_	dynein light chain 1 [Homo sa	89	10366	7.4	0	i	Q	0	0	0	0	0	0.000595	0	1	0.000149	0.000298	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Dynein light chain type 1;	dynein complex; microtubule	microtubule motor activity
2205	1	7.08E-05	0	0	INF		ENSG00000106636:E	YKT6			gi|5730120|ref|NP_0	YKT6 v-SNARE protein [Hom	198	22418	6.9	0	o	Q	15	0.027	0	0	0	0	0	0	0	0	0	0.000567	0	0	0	1	0.000142	0.000283	0	0	0	0	0	0	0	0	Synaptobrevin/VAMP-like	endoplasmic reticulum [pmid	protein binding [pmid
2206	1	6.83E-05	0	0	INF		ENSG00000125877:E	ITPA			gi|15626999|ref|NP_	inosine triphosphatase isofor	194	21446	5.6	0	o	Q	18	0.002	0	0	0	0.000546	0	1	0.000137	0.000273	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NTPase/HAM1. This family		hydrolase activity;
2207	1	6.74E-05	0	0	INF		ENSG00000142252:E	GEMIN7			gi|55953074|ref|NP_	gemin 7 [Homo sapiens]	131	14537	7.4	0	o	Q	21	0	0	0	0	0.000539	0	1	0.000135	0.00027	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		cytoplasm [pmid 12065586];	protein binding [pmid
2208	1	6.73E-05	0	0	INF		ENSG00000067955:E	CBFB			gi|13124873|ref|NP_	core-binding factor, beta sub	182	21508	6.6	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000538	0	1	0.000135	0.000269	0	0	0	0	0	0	0	0	Core binding factor beta	nucleus	protein binding [pmid
2209	1	6.54E-05	0	0	INF		ENSG00000189227:N	LOC145853			gi|169208955|ref|XP	PREDICTED: similar to hCG	223	24767	10.5	0	o	Q	37	0.023	0	0.000523	0	0	0	1	0.000131	0.000261	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2210	1	6.45E-05	0	0	INF		ENSG00000198780:E	FAM169A			gi|153792633|ref|NP	hypothetical protein LOC260	670	74955	4.6	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000516	1	0.000129	0.000258	0	0	0	0	0	0	0	0			
2211	1	6.42E-05	0	0	INF		ENSG00000133112:E	TPT1			gi|4507669|ref|NP_0	tumor protein, translationally-	172	19595	4.9	0	o	Q	0	0	0	0	0	0.000513	0	1	0.000128	0.000257	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Translationally controlled	cytoplasm [pmid 15162379]	calcium ion binding [pmid
2212	1	6.38E-05	0	0	INF		ENSG00000130640:E	TUBGCP2			gi|5729840|ref|NP_0	tubulin, gamma complex ass	902	102534	6.8	0	o	Q	25	0.004	0	0	0	0	0	0	0	0	0	0	0	0	0.000511	1	0.000128	0.000255	0	0	0	0	0	0	0	0	Spc97 / Spc98 family. The	cytoplasmic microtubule [pmid	
2213	1	6.25E-05	1	1.02E-05	6.102401		ENSG00000155906:E	RMND1			gi|157388927|ref|NP	required for meiotic nuclear c	449	51604	8.7	0	o	Q	20	0.029	0	0	0	0	0	0	0	0	0	0.0005	0	0	0	1	0.000125	0.00025	0	0	0	8.19E-05	0	0	0	0			
2214	1	6.21E-05	0	0	INF		ENSG00000142002:E	DPP9			gi|51988902|ref|NP_	dipeptidylpeptidase 9 [Homo	850	96613	6.5	0	o	Q	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000497	1	0.000124	0.000248	0	0	0	0	0	0	0	0	Dipeptidyl peptidase IV	membrane	aminopeptidase activity;
2215	1	6.09E-05	0	0	INF		ENSG00000177700:E	POLR2L			gi|10863925|ref|NP_	DNA directed RNA polymera	67	7645	7.8	0	o	Q	33	0.002	0	0	0	0	0	0	0	0	0	0	0	0.000487	0	1	0.000122	0.000244	0	0	0	0	0	0	0	0	DNA-directed RNA	nucleus	DNA binding; DNA-directed
2216	1	5.88E-05	0	0	INF		ENSG00000196976:E	LAGE3			gi|24430137|ref|NP_	L antigen family, member 3 [	143	14804	8.6	0	o	Q	43	0	0	0	0	0	0	0	0	0	0	0.000471	0	0	0	1	0.000118	0.000235	0	0	0	0	0	0	0	0	Transcription factor Pcc1.		
2217	1	5.87E-05	0	0	INF		ENSG00000122958:E	VPS26A			gi|17978519|ref|NP_	vacuolar protein sorting 26 A	327	38170	6.5	0	o	Q	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00047	1	0.000117	0.000235	0	0	0	0	0	0	0	0	Vacuolar protein sorting-	cytosol [pmid 11102511];	protein binding [pmid
2218	1	5.72E-05	0	0	INF		ENSG00000173141:E	MRP63			gi|13128970|ref|NP_	mitochondrial ribosomal prote	102	12266	11.5	0	o	Q	15	0.002	0	0.000457	0	0	0	1	0.000114	0.000229	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2219	1	5.63E-05	0	0	INF		ENSG00000102317:E	RBM3			gi|5803137|ref|NP_0	RNA binding motif protein 3 [	157	17170	8.9	0	o	Q	21	0	0	0	0	0.00045	0	1	0.000113	0.000225	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RNA recognition motif;		nucleic acid binding;
2220	1	5.58E-05	0	0	INF		ENSG00000112664:E	NUDT3			gi|5729804|ref|NP_0	nudix-type motif 3 [Homo sap	172	19471	6.4	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000446	1	0.000112	0.000223	0	0	0	0	0	0	0	0	Members of the Nudix	intracellular	diphosphoinositol-
2221	1	5.57E-05	0	0	INF		ENSG00000128524:E	ATP6V1F			gi|20357547|ref|NP_	ATPase, H+ transporting, lys	119	13370	5.5	0	o	Q	20	0.002	0	0	0	0.000445	0	1	0.000111	0.000223	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ATP synthase (F/14-kDa)	membrane fraction [pmid	hydrogen-transporting ATP
2222	1	5.55E-05	0	0	INF		ENSG00000134058:E	CDK7			gi|4502743|ref|NP_0	cyclin-dependent kinase 7 [H	346	39038	8.5	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000444	1	0.000111	0.000222	0	0	0	0	0	0	0	0	Serine/Threonine protein	nucleus [pmid 7936635]	androgen receptor binding
2223	1	5.53E-05	0	0	INF		ENSG00000197451:E	HNRPAB			gi|55956919|ref|NP_	heterogeneous nuclear ribon	332	35968	6.9	0	o	Q	46	0	0	0	0	0	0	0	0	0	0	0	0	0.000442	0	1	0.000111	0.000221	0	0	0	0	0	0	0	0	RNA recognition motif.	nucleus	mRNA binding [pmid
2224	1	5.49E-05	0	0	INF		ENSG00000103363:E	TCEB2			gi|46276893|ref|NP_	elongin B isoform b [Homo sa	161	17911	6.1	0	o	Q	0	0	0	0	0	0.000439	0	1	0.00011	0.000219	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Elongin B is part of an E3	nucleus	protein binding [pmid
2225	1	5.36E-05	0	0	INF		ENSG00000176261:E	ZBTB8OS			gi|30425510|ref|NP_	zinc finger and BTB domain c	179	20675	4.6	0	o	Q	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000429	1	0.000107	0.000214	0	0	0	0	0	0	0	0	Protein of unknown function		
2226	1	5.24E-05	0	0	INF		ENSG00000130725:E	UBE2M			gi|4507791|ref|NP_0	ubiquitin-conjugating enzyme	183	20900	7.7	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00042	1	0.000105	0.00021	0	0	0	0	0	0	0	0	Ubiquitin-conjugating		ligase activity; ubiquitin-
2227	1	5.16E-05	0	0	INF		ENSG00000132376:E	SKIP			gi|18765707|ref|NP_	skeletal muscle and kidney e	372	42784	6.5	0	o	Q	27	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0.000413	1	0.000103	0.000206	0	0	0	0	0	0	0	0	Calcium binding and coiled-		
2228	1	5.16E-05	0	0	INF		ENSG00000153487:E	ING1			gi|38201667|ref|NP_	inhibitor of growth family, me	279	31864	7.1	0	o	Q	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000413	1	0.000103	0.000206	0	0	0	0	0	0	0	0	PHD-finger. PHD folds into	nucleus [pmid 10866301]	metal ion binding; protein
2229	1	5.15E-05	0	0	INF		ENSG00000119705:E	C14orf156			gi|13654278|ref|NP_	SRA stem-loop-interacting R	109	12349	10.2	0	o	Q	32	0.045	0	0	0	0	0	0	0	0	0	0.000412	0	0	0	1	0.000103	0.000206	0	0	0	0	0	0	0	0	RNA recognition motif;	mitochondrion; nucleus	nucleotide binding; RNA
2230	1	5.05E-05	0	0	INF		ENSG00000198904:N	APOBEC3D			gi|22907039|ref|NP_	apolipoprotein B mRNA editi	190	22826	7.6	0	o	Q	28	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000404	1	0.000101	0.000202	0	0	0	0	0	0	0	0	APOBEC-like C-terminal		hydrolase activity; hydrolase
2231	1	5.04E-05	0	0	INF		ENSG00000129559:E	NEDD8			gi|5453760|ref|NP_0	neural precursor cell express	81	9072	8.4	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000403	0	1	0.000101	0.000201	0	0	0	0	0	0	0	0	Nedd8 (also known as	nucleus [pmid 9353319]	ubiquitin conjugating enzyme
2232	1	5E-05	0	0	INF		ENSG00000069424:E	KCNAB2			gi|27436969|ref|NP_	potassium voltage-gated cha	353	39287	8.6	0	o	Q	48	0.008	0	0	0	0.0004	0	1	0.0001	0.0002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Predicted oxidoreductases	cytoplasm; integral to	ion channel activity;
2233	1	5E-05	0	0	INF		ENSG00000132953:E	XPO4			gi|148886661|ref|NP	exportin 4 [Homo sapiens]	1151	130139	5	0	o	Q	19	0.003	0	0	0	0	0	0	0	0	0	0	0	0	0.0004	1	0.0001	0.0002	0	0	0	0	0	0	0	0			
2234	1	4.88E-05	0	0	INF		ENSG00000099964:E	MIF			gi|4505185|ref|NP_0	macrophage migration inhibit	115	12476	7.9	0	o	Q	33	0.002	0	0	0	0	0	0	0	0	0	0.00039	0	0	0	1	9.75E-05	0.000195	0	0	0	0	0	0	0	0	Macrophage migration	extracellular region [pmid	cytokine activity [pmid
2235	1	4.81E-05	0	0	INF		gi|169201473|ref|XP_	LOC100131133			gi|169201473|ref|XP	PREDICTED: similar to hCG	299	32030	6.2	0	o	Q	44	0.046	0	0	0	0	0	0	0	0	0	0	0	0	0.000385	1	9.63E-05	0.000193	0	0	0	0	0	0	0	0			
2236	1	4.8E-05	0	0	INF		ENSG00000146833:N	TRIM4			gi|14670266|ref|NP_	tripartite motif protein TRIM4	500	57401	8.1	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000384	1	9.6E-05	0.000192	0	0	0	0	0	0	0	0	RING-finger (Really	intracellular	metal ion binding; protein
2237	1	4.75E-05	0	0	INF		ENSG00000166289:E	PLEKHF1			gi|153791377|ref|NP	apoptosis-inducing protein D	279	31195	8.2	0	o	Q	27	0.001	0	0	0	0.00038	0	1	9.5E-05	0.00019	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2238	1	4.58E-05	0	0	INF		ENSG00000100575:E	TIMM9			gi|6912714|ref|NP_0	translocase of inner mitochor	89	10378	7.2	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000367	0	1	9.17E-05	0.000183	0	0	0	0	0	0	0	0	Tim10/DDP family zinc	membrane; mitochondrial	metal ion binding; zinc ion
2239	1	4.56E-05	0	0	INF		ENSG00000085063:E	CD59			gi|42761474|ref|NP_	CD59 antigen p18-20 [Homo	128	14177	6.5	0	o	S	26	0.997	0	0.000364	0	0	0	1	9.11E-05	0.000182	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Ly-6 antigen / uPA receptor	membrane fraction [pmid	GPI anchor binding; protein
2240	1	4.51E-05	0	0	INF		ENSG00000172183:E	ISG20			gi|6857800|ref|NP_0	interferon stimulated exonucl	181	20363	8.9	0	o	Q	36	0	0	0	0	0	0	0	0	0	0	0	0	0.000361	0	1	9.02E-05	0.00018	0	0	0	0	0	0	0	0	exonuclease domain in	intracellular; nucleoplasm	3'-5'-exoribonuclease activity
2241	1	4.48E-05	0	0	INF		ENSG00000150456:E	N6AMT2			gi|28372547|ref|NP_	N-6 adenine-specific DNA m	214	24506	4.5	0	o	Q	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000359	1	8.97E-05	0.000179	0	0	0	0	0	0	0	0			
2242	1	4.42E-05	0	0	INF		ENSG00000124107:E	SLPI			gi|4507065|ref|NP_0	secretory leukocyte peptidas	132	14326	8.7	0	o	S	26	0.999	0	0.000353	0	0	0	1	8.83E-05	0.000177	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Four-disulfide core		serine-type endopeptidase
2243	1	4.33E-05	0	0	INF		ENSG00000148362:E	C9orf142			gi|39930541|ref|NP_	hypothetical protein LOC286	204	21640	5.5	0	o	Q	16	0	0	0	0	0.000346	0	1	8.66E-05	0.000173	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2244	1	4.31E-05	0	0	INF		ENSG00000115523:N	GNLY			gi|157502222|ref|NP	granulysin isoform 519 [Hom	130	14853	9	0	o	Q	20	0.001	0	0	0	0	0	0	0	0	0	0.000345	0	0	0	1	8.63E-05	0.000173	0	0	0	0	0	0	0	0			
2245	1	4.28E-05	0	0	INF		ENSG00000101421:E	CHMP4B			gi|28827795|ref|NP_	chromatin modifying protein 4	224	24950	4.8	0	o	Q	16	0.013	0	0	0	0	0	0	0	0	0	0	0	0	0.000343	1	8.57E-05	0.000171	0	0	0	0	0	0	0	0	Snf7. This family of proteins		
2246	1	4.22E-05	0	0	INF		ENSG00000169217:E	CD2BP2			gi|5174409|ref|NP_0	CD2 antigen (cytoplasmic tai	341	37646	4.6	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000338	1	8.44E-05	0.000169	0	0	0	0	0	0	0	0	GYF domain: contains	cytoplasm [pmid 9843987]	
2247	1	4.16E-05	0	0	INF		ENSG00000153048:E	CARHSP1			gi|109715858|ref|NP	calcium-regulated heat-stable	147	15892	8.2	0	o	Q	27	0	0	0	0	0	0	0	0	0	0	0	0	0.000333	0	1	8.33E-05	0.000167	0	0	0	0	0	0	0	0			
2248	1	4.09E-05	0	0	INF		ENSG00000135002:E	RFK			gi|19923525|ref|NP_	riboflavin kinase [Homo sapie	162	18410	8	0	o	Q	18	0.001	0	0	0	0.000327	0	1	8.18E-05	0.000164	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Riboflavin kinase. This	cytoplasm [pmid 12623014]	ATP binding; magnesium ion
2249	1	4.01E-05	0	0	INF		ENSG00000183291:E	SEPT15			gi|42741648|ref|NP_	15 kDa selenoprotein isoform	165	17942	5	0	o	S	32	0.998	0	0	0	0.000321	0	1	8.03E-05	0.000161	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Sep15/SelM redox domain.	endoplasmic reticulum;	protein binding [pmid
2250	1	4.01E-05	0	0	INF		ENSG00000136522:E	MRPL47			gi|29826285|ref|NP_	mitochondrial ribosomal prote	140	16991	10.7	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0.00032	0	0	0	1	8.01E-05	0.00016	0	0	0	0	0	0	0	0	Mitochondrial 39-S	mitochondrial ribosome;	structural constituent of
2251	1	0.00004	0	0	INF		ENSG00000163634:E	THOC7			gi|156151381|ref|NP	Ngg1 interacting factor 3 like	204	23743	5.7	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00032	0	1	0.00008	0.00016	0	0	0	0	0	0	0	0			
2252	1	3.94E-05	0	0	INF		ENSG00000154582:E	TCEB1			gi|5032161|ref|NP_0	elongin C [Homo sapiens]	112	12473	4.8	0	o	Q	0	0	0	0	0	0.000315	0	1	7.89E-05	0.000158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Found in Skp1 protein	nucleus	protein binding [pmid
2253	1	3.92E-05	0	0	INF		ENSG00000137364:E	TPMT			gi|4507653|ref|NP_0	thiopurine S-methyltransfera	245	28180	6.2	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000313	1	7.83E-05	0.000157	0	0	0	0	0	0	0	0	Thiopurine S-	cytoplasm	methyltransferase activity;
2254	1	3.9E-05	0	0	INF		ENSG00000165512:E	ZNF22			gi|42714596|ref|NP_	zinc finger protein 22 (KOX 1	224	25915	10	0	o	Q	20	0	0	0.000312	0	0	0	1	7.81E-05	0.000156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	FOG: Zn-finger [General	intracellular; nucleus	DNA binding; metal ion
2255	1	3.88E-05	0	0	INF		ENSG00000171700:E	RGS19			gi|86990435|ref|NP_	G protein signalling regulator	217	24636	5.6	0	o	Q	50	0	0	0	0	0	0	0	0	0	0	0.00031	0	0	0	1	7.75E-05	0.000155	0	0	0	0	0	0	0	0	Regulator of G protein	Golgi apparatus [pmid	GTPase activator activity;
2256	1	3.85E-05	0	0	INF		ENSG00000161939:E	C17orf49			gi|52856421|ref|NP_	hypothetical protein LOC124	172	17900	7.3	0	o	Q	24	0.038	0	0	0	0.000308	0	1	7.7E-05	0.000154	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		nucleus	DNA binding
2257	1	3.81E-05	0	0	INF		ENSG00000076242:E	MLH1			gi|4557757|ref|NP_0	MutL protein homolog 1 [Hon	756	84601	5.7	0	o	Q	32	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000305	1	7.62E-05	0.000152	0	0	0	0	0	0	0	0	Histidine kinase-like	nucleus	ATP binding; protein binding
2258	1	3.79E-05	0	0	INF		ENSG00000108465:E	CDK5RAP3			gi|28872792|ref|NP_	CDK5 regulatory subunit ass	506	56921	4.8	0	o	Q	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000303	1	7.59E-05	0.000152	0	0	0	0	0	0	0	0	Protein of unknown function		neuronal Cdc2-like kinase
2259	1	3.74E-05	0	0	INF		ENSG00000119559:E	C19orf25			gi|154240706|ref|NP	hypothetical protein LOC148	118	12878	5.1	0	o	Q	23	0.003	0	0	0	0.000299	0	1	7.48E-05	0.00015	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2260	1	3.72E-05	0	0	INF		ENSG00000151876:E	FBXO4			gi|15834619|ref|NP_	F-box only protein 4 isoform	387	44136	6.2	0	o	Q	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000298	1	7.44E-05	0.000149	0	0	0	0	0	0	0	0	F-box domain. This domain	ubiquitin ligase complex [pmid	ubiquitin-protein ligase
2261	1	3.68E-05	0	0	INF		ENSG00000145293:E	ENOPH1			gi|10864017|ref|NP_	enolase-phosphatase 1 [Hom	261	28933	4.8	0	o	Q	20	0.065	0	0	0	0	0	0	0	0	0	0	0	0	0.000294	1	7.35E-05	0.000147	0	0	0	0	0	0	0	0	Predicted enolase-		hydrolase activity;
2262	1	3.62E-05	0	0	INF		ENSG00000100931:N	CHMP4A			gi|40548422|ref|NP_	chromatin modifying protein 4	265	29804	5.1	0	o	Q	28	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00029	1	7.24E-05	0.000145	0	0	0	0	0	0	0	0	Snf7. This family of proteins	membrane	lipid binding
2263	1	3.62E-05	0	0	INF		ENSG00000133119:E	RFC3			gi|108773789|ref|NP	replication factor C 3 isoform	305	34756	8.4	0	o	Q	0	0	0	0	0	0.00029	0	1	7.24E-05	0.000145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2264	1	3.53E-05	0	0	INF		ENSG00000115128:E	SF3B14			gi|7706326|ref|NP_0	splicing factor 3B, 14 kDa su	125	14585	9.4	0	i	Q	33	0	0	0	0	0.000283	0	1	7.07E-05	0.000141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus	nucleotide binding; RNA
2265	1	3.51E-05	0	0	INF		ENSG00000020633:E	RUNX3			gi|4757918|ref|NP_0	runt-related transcription fact	415	44356	9.5	0	o	Q	49	0.008	0	0.000281	0	0	0	1	7.03E-05	0.000141	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Runx inhibition domain. This	nucleus	ATP binding [pmid 7835892];
2266	1	3.48E-05	0	0	INF		ENSG00000167196:E	FBXO22			gi|13443000|ref|NP_	F-box only protein 22 isoform	276	30589	6.8	0	o	Q	36	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000278	1	6.95E-05	0.000139	0	0	0	0	0	0	0	0	F-box domain. This domain		
2267	1	3.47E-05	0	0	INF		ENSG00000159840:E	ZYX			gi|58530845|ref|NP_	zyxin [Homo sapiens]	572	61277	6.7	0	o	Q	19	0.122	0	0	0	0.000278	0	1	6.95E-05	0.000139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Zinc-binding domain	cell-cell adherens junction	metal ion binding; protein
2268	1	3.46E-05	0	0	INF		ENSG00000108679:E	LOC100133842			gi|169211543|ref|XP	PREDICTED: similar to lectin	554	61645	5.5	0	o	Q	46	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0.000277	1	6.93E-05	0.000139	0	0	0	0	0	0	0	0			
2269	1	3.46E-05	0	0	INF		ENSG00000011052:N	NME1-NME2			gi|38045913|ref|NP_	non-metastatic cells 1, protei	177	19654	5.6	0	o	S	22	0.649	0	0	0	0	0	0	0	0	0	0	0	0.000277	0	1	6.92E-05	0.000138	0	0	0	0	0	0	0	0	Nucleoside diphosphate	cytoplasm [pmid 16130169];	ATP binding;
2270	1	3.44E-05	0	0	INF		ENSG00000140450:E	ARRDC4			gi|34419647|ref|NP_	arrestin domain containing 4	418	45449	6.2	0	o	Q	16	0.036	0	0	0	0	0	0	0	0	0	0	0	0	0.000276	1	6.89E-05	0.000138	0	0	0	0	0	0	0	0	Arrestin (or S-antigen), N-		
2271	1	3.41E-05	0	0	INF		ENSG00000101019:E	UQCC			gi|41327685|ref|NP_	basic FGF-repressed Zic bin	299	34600	8.9	0	o	Q	33	0.08	0	0	0	0	0	0	0	0	0	0	0	0.000273	0	1	6.82E-05	0.000136	0	0	0	0	0	0	0	0	Ubiquinol-cytochrome C		
2272	1	3.4E-05	0	0	INF		ENSG00000172062:E	LOC100133835			gi|169167322|ref|XP	PREDICTED: hypothetical pr	282	30450	5.5	0	o	Q	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000272	1	6.81E-05	0.000136	0	0	0	0	0	0	0	0			
2273	1	3.39E-05	0	0	INF		ENSG00000160679:E	C1orf77			gi|28875797|ref|NP_	hypothetical protein LOC260	248	26397	12.2	0	o	Q	16	0	0	0	0	0	0	0	0	0	0	0.000271	0	0	0	1	6.78E-05	0.000136	0	0	0	0	0	0	0	0			protein binding [pmid
2274	1	3.38E-05	0	0	INF		ENSG00000159111:E	MRPL10			gi|22547114|ref|NP_	mitochondrial ribosomal prote	261	29283	9.6	0	o	Q	16	0.113	0	0	0	0.000271	0	1	6.77E-05	0.000135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50S ribosomal protein L10;		
2275	1	3.38E-05	0	0	INF		ENSG00000117543:E	DPH5			gi|117190324|ref|NP	diphthine synthase isoform b	284	31580	5.3	0	o	Q	13	0.002	0	0	0	0	0	0	0	0	0	0	0	0	0.00027	1	6.76E-05	0.000135	0	0	0	0	0	0	0	0			
2276	1	3.37E-05	0	0	INF		ENSG00000131368:E	MRPS25			gi|14028877|ref|NP_	mitochondrial ribosomal prote	173	20116	8.8	0	o	Q	20	0	0	0.00027	0	0	0	1	6.74E-05	0.000135	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Mitochondrial ribosomal	mitochondrial small ribosomal	nucleic acid binding;
2277	1	3.34E-05	0	0	INF		ENSG00000136147:E	PHF11			gi|94681065|ref|NP_	PHD finger protein 11 isoform	331	37582	7.7	0	o	Q	38	0.004	0	0	0	0.000267	0	1	6.67E-05	0.000133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			metal ion binding; protein
2278	1	3.29E-05	0	0	INF		ENSG00000145494:E	NDUFS6			gi|4758792|ref|NP_0	NADH dehydrogenase (ubiqu	124	13712	8.3	0	o	Q	18	0.215	0	0	0	0	0	0	0	0	0	0	0	0.000263	0	1	6.58E-05	0.000132	0	0	0	0	0	0	0	0	Uncharacterized protein	mitochondrion	NADH dehydrogenase
2279	1	3.14E-05	0	0	INF		ENSG00000103510:E	MYST1			gi|14149875|ref|NP_	MYST histone acetyltransfera	458	52378	8.3	0	o	S	20	0.979	0	0	0	0	0	0	0	0	0	0	0	0	0.000251	1	6.29E-05	0.000126	0	0	0	0	0	0	0	0	Chromatin organization	chromatin; nucleus [pmid	acetyltransferase activity
2280	1	3.13E-05	0	0	INF		ENSG00000070010:E	UFD1L			gi|29501813|ref|NP_	ubiquitin fusion degradation 1	307	34500	6.7	0	o	Q	39	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00025	1	6.25E-05	0.000125	0	0	0	0	0	0	0	0	Ubiquitin fusion degradation		ubiquitin-specific protease
2281	1	3.11E-05	0	0	INF		ENSG00000144231:E	POLR2D			gi|4758574|ref|NP_0	DNA directed RNA polymera	142	16311	4.8	0	o	Q	0	0	0	0	0	0.000249	0	1	6.22E-05	0.000124	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	DNA-directed RNA-	DNA-directed RNA	DNA-directed RNA
2282	1	3.11E-05	0	0	INF		ENSG00000141560:E	FN3KRP			gi|20149680|ref|NP_	fructosamine-3-kinase-relate	309	34412	7.3	0	o	Q	27	0.002	0	0	0	0	0	0	0	0	0	0	0	0	0.000248	1	6.21E-05	0.000124	0	0	0	0	0	0	0	0	Uncharacterized protein		kinase activity; transferase
2283	1	3.09E-05	0	0	INF		ENSG00000070423:E	RNF126			gi|37622894|ref|NP_	ring finger protein 126 [Homo	311	33862	5.5	0	o	Q	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000247	1	6.17E-05	0.000123	0	0	0	0	0	0	0	0	RING-finger (Really		metal ion binding; protein
2284	1	3.05E-05	0	0	INF		ENSG00000172081:E	MOBKL2A			gi|18677731|ref|NP_	MOB-LAK [Homo sapiens]	217	25464	8.6	0	o	Q	49	0	0	0	0	0.000244	0	1	6.11E-05	0.000122	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Mob1/phocein family. Mob1	intracellular [pmid 11256614]	metal ion binding; zinc ion
2285	1	3.02E-05	0	0	INF		ENSG00000166899:N	FABP5L7			gi|169202850|ref|XP	PREDICTED: hypothetical pr	135	15164	7	0	o	Q	40	0	0	0	0	0	0	0	0	0	0	0	0	0.000242	0	1	6.04E-05	0.000121	0	0	0	0	0	0	0	0			
2286	1	3.02E-05	0	0	INF		ENSG00000023697:E	DERA			gi|116063554|ref|NP	deoxyribose-phosphate aldol	318	35231	8.9	0	o	Q	62	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000241	1	6.04E-05	0.000121	0	0	0	0	0	0	0	0			
2287	1	2.98E-05	1	5.72E-06	5.213184		ENSG00000136485:E	WDR68			gi|108936958|ref|NP	WD-repeat protein [Homo sa	342	38926	5.5	0	o	Q	29	0	0	0	0	0	0	0	0	0	0	0	0	0.000239	0	1	5.96E-05	0.000119	0	0	0	0	0	4.58E-05	0	0			
2288	1	2.98E-05	0	0	INF		ENSG00000179295:E	PTPN11			gi|33356177|ref|NP_	protein tyrosine phosphatase	593	68011	7.3	0	o	Q	28	0.002	0	0	0	0.000238	0	1	5.96E-05	0.000119	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Protein tyrosine		hydrolase activity; non-
2289	1	2.98E-05	0	0	INF		ENSG00000126254:E	RBM42			gi|21359951|ref|NP_	RNA binding motif protein 42	480	50414	9.6	0	o	Q	25	0.053	0	0	0	0	0	0	0	0	0	0	0	0.000238	0	1	5.95E-05	0.000119	0	0	0	0	0	0	0	0	RNA recognition motif.		nucleotide binding; RNA
2290	1	2.94E-05	0	0	INF		ENSG00000185127:E	C6orf120			gi|71143156|ref|NP_	hypothetical protein LOC387	191	20772	4.8	0	o	S	31	1	0	0	0	0	0	0	0	0	0	0.000235	0	0	0	1	5.87E-05	0.000117	0	0	0	0	0	0	0	0			
2291	1	2.89E-05	0	0	INF		ENSG00000189114:E	BLOC1S3			gi|47086495|ref|NP_	biogenesis of lysosome-relat	202	21256	5.1	0	o	Q	28	0	0	0.000231	0	0	0	1	5.77E-05	0.000115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			identical protein binding
2292	1	2.89E-05	0	0	INF		ENSG00000205751:N	MRPL23			gi|27436904|ref|NP_	mitochondrial ribosomal prote	153	17811	9.7	0	o	Q	35	0.028	0	0	0	0.000231	0	1	5.77E-05	0.000115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50S ribosomal protein L23;	mitochondrial large ribosomal	nucleotide binding; RNA
2293	1	2.87E-05	0	0	INF		ENSG00000122694:E	C9orf19			gi|11641247|ref|NP_	chromosome 9 open reading	154	17218	9.4	0	o	Q	0	0	0	0	0	0.000229	0	1	5.74E-05	0.000115	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	SCP / Tpx-1 / Ag5 / PR-1 /	extracellular region;	
2294	1	2.86E-05	0	0	INF		ENSG00000130731:E	C16orf13			gi|93102387|ref|NP_	hypothetical protein LOC843	204	22578	7.8	0	o	Q	49	0	0	0.000229	0	0	0	1	5.72E-05	0.000114	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Protein of unknown function		
2295	1	2.83E-05	0	0	INF		ENSG00000071539:E	TRIP13			gi|11321607|ref|NP_	thyroid hormone receptor inte	432	48551	6.1	0	o	Q	17	0	0	0	0	0	0	0	0	0	0	0	0	0.000227	0	1	5.67E-05	0.000113	0	0	0	0	0	0	0	0	ATPases associated with a	nucleus [pmid 7776974]	ATP binding; nucleoside-
2296	1	2.81E-05	0	0	INF		ENSG00000144840:E	RABL3			gi|62751417|ref|NP_	RAB, member of RAS oncog	236	26423	7.1	0	o	Q	34	0.018	0	0	0	0.000225	0	1	5.61E-05	0.000112	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RabL3 (Rab-like3)	intracellular	ATP binding; GTP binding;
2297	1	2.76E-05	0	0	INF		ENSG00000168101:E	NUDT16L1			gi|14150147|ref|NP_	syndesmos [Homo sapiens]	211	23338	8.9	0	o	Q	43	0.004	0	0.000221	0	0	0	1	5.53E-05	0.000111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2298	1	2.73E-05	0	0	INF		ENSG00000047579:E	DTNBP1			gi|19549327|ref|NP_	dystrobrevin binding protein 1	351	39493	4.7	0	o	Q	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000219	1	5.47E-05	0.000109	0	0	0	0	0	0	0	0	Dysbindin (Dystrobrevin	axon; cytoplasm; nucleus;	identical protein binding
2299	1	2.73E-05	0	0	INF		ENSG00000198585:E	NUDT16			gi|24308370|ref|NP_	nudix-type motif 16 [Homo sa	162	17830	6.7	0	o	Q	24	0.012	0	0	0	0.000218	0	1	5.45E-05	0.000109	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			hydrolase activity;
2300	1	2.71E-05	0	0	INF		ENSG00000108179:E	PPIF			gi|5031987|ref|NP_0	peptidylprolyl isomerase F pr	207	22040	9.4	0	o	S	30	0.711	0	0	0	0	0	0	0	0	0	0.000217	0	0	0	1	5.42E-05	0.000108	0	0	0	0	0	0	0	0	cyclophilin_ABH_like:	membrane fraction [pmid	isomerase activity; peptide
2301	1	2.7E-05	0	0	INF		ENSG00000101843:E	PSMD10			gi|28605137|ref|NP_	proteasome 26S non-ATPase	151	16137	6	0	o	Q	17	0.066	0	0	0	0	0	0	0	0	0	0	0	0.000216	0	1	5.4E-05	0.000108	0	0	0	0	0	0	0	0	ankyrin repeats; ankyrin	cytosol; proteasome	
2302	1	2.66E-05	0	0	INF		ENSG00000118939:E	UCHL3			gi|5174741|ref|NP_0	ubiquitin carboxyl-terminal es	230	26183	4.9	0	o	Q	19	0	0	0	0	0	0	0	0	0	0	0	0	0.000213	0	1	5.32E-05	0.000106	0	0	0	0	0	0	0	0	Ubiquitin carboxyl-terminal	cytoplasm; intracellular	cysteine-type peptidase
2303	1	2.65E-05	0	0	INF		ENSG00000126524:E	SBDS			gi|28416940|ref|NP_	Shwachman-Bodian-Diamon	250	28764	8.7	0	o	Q	24	0	0	0	0	0.000212	0	1	5.3E-05	0.000106	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Shwachman-Bodian-		

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S=signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_PROB	RESTING LYMPHOCYTES NEs: HsNaOH-NE_NT_lymphocytes_Tl_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Tl_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Tl_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-dNEs AVG	NT-bNEs SDV	PHA-TREATED LYMPHOCYTES NEs: HsNaOH-NE_PHA_lymphocytes_Tl_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Tl_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Tl_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-dNEs AVG	PHA-bNEs SDV	MMs: MmNaOH-MM_liver_CNBrTl_1_dNSAF	MmNaOH-MM_liver_CNBrTl_2_dNSAF	RnNaOH-MM_liver_Tl_1_dNSAF	RnNaOH-MM_liver_Tl_2_dNSAF	RnNaOH-MM_liver_Tl_3_dNSAF	RnNaOH-MM_liver_Tl_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
2304	1	2.63E-05	0	0	INF		ENSG00000171115	GMAPR			gi	28416956	ref	NP_	GTPase, IMAP family membe	665	74890	8.3	0	O	Q	22	0.008	0	0.00023	0	0	0	1	5.26E-05	0.000105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	AAX1 (arrf8p2-induced		GTP binding
2305	1	2.62E-05	0	0	INF		ENSG00000126698	DNAJC8			gi	11229327	ref	NP	DnaJ (Hsp40) homolog, subf	253	29842	9.1	0	O	Q	17	0	0	0	0.000209	1	5.24E-05	0.000105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2306	1	2.61E-05	0	0	INF		ENSG00000164132	NDUFA12L			gi	27894809	ref	NP_	NADH dehydrogenase (ubiq	169	19427	9.6	0	O	Q	17	0.001	0	0	0.000209	1	5.23E-05	0.000105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NADH ubiquinone	membrane; mitochondrion	electron carrier activity;
2307	1	2.55E-05	0	0	INF		ENSG00000182307	C8orf33			gi	12751401	ref	NP_	hypothetical protein LOC852	229	24992	10	0	O	Q	19	0.173	0	0.000204	0	0	0	1	5.09E-05	0.000102	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2308	1	2.48E-05	0	0	INF		ENSG00000173540	GMPPB			gi	11761619	ref	NP_	GDP-mannose pyrophospho	387	42650	6.4	0	O	Q	21	0.304	0	0	0	0	0	0	0.000198	1	4.96E-05	0.992E-05	0	0	0	0	0	0	0	0	0	0	0	0	Left-Handed Parallel beta-		acyltransferase activity;
2309	1	2.45E-05	0	0	INF		ENSG00000083123	BCKDHB			gi|34101272|ref|NP_	branched chain keto acid de	392	43123	6	0	O	S	20	0.994	0	0	0	0	0	0	0.000196	1	4.9E-05	9.79E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Transketolase, pyrimidine	alpha-ketoglutarate	3-methyl-2-oxobutanoate
2310	1	2.44E-05	0	0	INF		ENSG00000163320	CCGBP1			gi	56550055	ref	NP_	CGG triplet repeat binding pr	167	18820	9	0	O	Q	18	0	0	0	0	0	0	1	4.89E-05	0.000195	0	0	0	0	0	0	0	0	0	0	0	0	0	0		nucleus [pmid 11256614]	
2311	1	2.43E-05	0	0	INF		ENSG00000205220	PSMB10			gi	4506191	ref	NP_	proteasome beta 10 subunit	273	28936	7.8	0	O	Q	55	0.001	0	0	0.000194	1	4.85E-05	9.71E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	proteasome beta type-7	cytosol; proteasome core	threonine endopeptidase
2312	1	2.41E-05	0	0	INF		ENSG00000128928	EVD			gi	4504799	ref	NP_	isovaleryl Coenzyme A dehy	423	46319	8.2	0	O	S	32	0.748	0	0	0	0	0	0	0.000193	1	4.82E-05	9.65E-05	0	0	0	0	0	0	0	0	0	0	0	0	isovaleryl-CoA	mitochondrial matrix [pmid	FAD binding; isovaleryl-CoA
2313	1	2.4E-05	0	0	INF		ENSG00000120699	EXOSC8			gi	31415882	ref	NP_	exosome component 8 [Hom	276	30040	5.3	0	O	Q	0	0	0	0	0.000192	1	4.8E-05	9.6E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3'-exoribonuclease family,	exosome (RNase complex);	3'-5'-exoribonuclease
2314	1	2.38E-05	0	0	INF		ENSG00000182093	CCDC7			gi	50401407	ref	NP_	coiled-coil domain containing	278	31863	5.5	0	O	Q	21	0	0	0	0.000191	1	4.77E-05	9.53E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		microtubule	
2315	1	2.37E-05	0	0	INF		ENSG00000131193	EFAM104A			gi	15435022	ref	NP	hypothetical protein LOC849	186	19484	11.3	0	O	Q	20	0.001	0	0	0.00019	1	4.75E-05	9.5E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2316	1	2.34E-05	0	0	INF		ENSG00000124802	EEF1E1			gi	4758862	ref	NP_0	eukaryotic translation elonga	174	19811	8.6	0	O	Q	16	0.117	0	0	0	0	0	0	0.000188	1	4.69E-05	9.38E-05	0	0	0	0	0	0	0	0	0	0	0	0	GST_C family, Gamma	aminoacyl-tRNA synthetase	protein binding
2317	1	2.34E-05	0	0	INF		ENSG00000165101	ANAPC7			gi	7705334	ref	NP_0	anaphase promoting complex	565	65177	5.8	0	O	S	31	0.002	0	0	0.000187	1	4.69E-05	9.38E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	anaphase-promoting complex	binding
2318	1	2.34E-05	0	0	INF		ENSG00000998101	MTAP			gi	47132622	ref	NP_	5'-methylthioadenosine phos	283	31236	7.2	0	O	Q	20	0.01	0	0	0.000187	1	4.68E-05	9.36E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Phosphorylase family 2;		Phosphorylase activity [pmid
2319	1	2.32E-05	0	0	INF		ENSG00000164077	KCMF1			gi	4882178	ref	NP_0	potassium channel modulato	381	41945	5.7	0	O	Q	20	0	0	0	0.000185	1	4.64E-05	9.27E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Drought induced 19 protein	intracellular; nucleus	ion channel activity; metal
2320	1	2.31E-05	0	0	INF		ENSG00000158019	BRK			gi	13617110	ref	NP_	hypothetical protein LOC52	415	45974	6.1	0	O	Q	26	0.002	0	0	0	0	0	0	0.000185	1	4.63E-05	9.25E-05	0	0	0	0	0	0	0	0	0	0	0	0	Brain and reproductive	cytoplasm [pmid 15465831];	peroxisome targeting
2321	1	2.31E-05	0	0	INF		ENSG00000056558	TRAF1			gi	5032193	ref	NP_0	TNF receptor-associated fact	416	46164	6.1	0	O	Q	28	0	0	0	0	0	0	0	0.000185	1	4.61E-05	9.23E-05	0	0	0	0	0	0	0	0	0	0	0	0	Tumor Necrosis Factor	cytoplasm [pmid 8069916]	protein binding [pmid
2322	1	2.3E-05	0	0	INF		ENSG00000014401	MPA2			gi	7657236	ref	NP_0	inositol(myo)-1(or 4)-monopt	288	31321	8.6	0	O	Q	22	0.006	0	0	0.000184	1	4.6E-05	9.2E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	MPase, inositol		hydrolase activity; inositol or
2323	1	2.29E-05	0	0	INF		ENSG00000172172	MRPL13			gi	14165270	ref	NP_	mitochondrial ribosomal prot	178	20692	9.1	0	O	Q	24	0.012	0	0	0	0	0	0	0.000183	1	4.58E-05	9.17E-05	0	0	0	0	0	0	0	0	0	0	0	0	50S ribosomal protein L13;	intracellular; mitochondrial	structural constituent of
2324	1	2.29E-05	0	0	INF		ENSG00000128708	HAT1			gi	4504341	ref	NP_	histone acetyltransferase 1 is	419	49513	5.7	0	O	Q	18	0	0	0	0	0	0	0	0.000183	1	4.58E-05	9.16E-05	0	0	0	0	0	0	0	0	0	0	0	0	Outer membrane protein	nucleus [pmid 9427644]	acyltransferase activity;
2325	1	2.28E-05	0	0	INF		ENSG00000160049	CFA			gi	4713200	ref	NP_0	complement factor, 4B [Hom	268	29411	4.6	0	O	S	21	0	0	0	0	0	0	0	0	0	4.57E-05	9.15E-05	0	0	0	0	0	0	0	0	0	0	0	0	CIDE-N domain. This	cytosol [pmid 9109473];	caspase-activated
2326	1	2.28E-05	0	0	INF		ENSG00000168530	MYL1			gi	17986273	ref	NP_	fast skeletal myosin alkali ligh	194	21145	5	0	O	Q	32	0.44	0	0	0.000182	1	4.55E-05	9.11E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	EF-hand, calcium binding	muscle myosin; myosin	calcium ion binding; motor
2327	1	2.27E-05	0	0	INF		ENSG00000115725	PRKAR1			gi	19923359	ref	NP_	IMAP-associated protein kinase	270	30382	6.4	0	O	Q	21	0	0	0	0.000181	1	4.54E-05	9.07E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5'-AMP-activated protein		hydrolase activity,
2328	1	2.26E-05	0	0	INF		ENSG00000103490	PYCARD			gi	10835256	ref	NP_	PYD and CARD domain cont	195	21627	6.4	0	O	Q	18	0	0	0	0.000181	1	4.53E-05	9.06E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	PAAD/DAPIN/Pyrin domain	cytoplasm [pmid 12019269];	caspase activator activity
2329	1	2.25E-05	0	0	INF		ENSG00000196502	SULT1A1			gi	29540539	ref	NP_	sulfotransferase family, cytos	295	34165	6.6	0	O	Q	37	0	0	0	0.00018	1	4.49E-05	8.98E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Sulfotransferase domain.		aryl sulfotransferase activity;
2330	1	2.23E-05	0	0	INF		ENSG00000157870	C1orf93			gi	27487990	ref	NP_	hypothetical protein LOC127	198	21223	6.7	0	O	Q	21	0.064	0	0	0.000178	1	4.46E-05	8.92E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Peroxisodon (PRX)-like 2		
2331	1	2.23E-05	0	0	INF		gi|169172079|ref|XP_	LOC100134165			gi|169172079|ref|XP	PREDICTED: hypothetical pr	393	42353	11.5	0	O	Q	18	0.255	0	0.000178	0	0	0	1	4.45E-05	8.9E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2332	1	2.2E-05	0	0	INF		ENSG00000169479	MED6			gi	15502019	ref	NP_	mediator complex subunit 6 [	301	33969	9.1	0	O	Q	23	0.001	0	0	0.000176	1	4.4E-05	8.8E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2333	1	2.2E-05	0	0	INF		ENSG00000120314	WDR55			gi	38327642	ref	NP_	WD repeat domain 55 [Hom	383	42123	4.9	0	O	Q	0	0	0	0	0	0	0	0	0.000176	1	4.39E-05	8.79E-05	0	0	0	0	0	0	0	0	0	0	0	0	WD40 domain, found in a		
2334	1	2.19E-05	0	0	INF		ENSG00000130489	SCO2			gi	15379313	ref	NP	cytochrome oxidase deficient	266	29810	8.9	0	O	Q	40	0.298	0	0.000175	0	0	0	1	4.38E-05	8.77E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2335	1	2.17E-05	0	0	INF		ENSG00000103723	AP3B2			gi	34482047	ref	NP_	adaptor-related protein comp	1082	119050	5.6	0	O	Q	16	0	0	0	0.000174	1	4.34E-05	8.68E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Adaptin N terminal region.	coated pit; COPI-coated	binding; transporter activity
2336	1	2.16E-05	0	0	INF		ENSG00000108836	PABPN1			gi	4758876	ref	NP_0	poly(A) binding protein, nucle	306	32749	5.1	0	O	S	19	0.994	0	0	0.000173	1	4.33E-05	8.66E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RNA recognition motif;	nucleus	nucleotide binding; protein
2337	1	2.16E-05	0	0	INF		ENSG00000102837	OLFM4			gi	32113593	ref	NP_0	olfactomedin 4 precursor [Ho	510	57280	5.7	0	O	S	21	1	0	0	0.000173	1	4.33E-05	8.66E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Recf/RecN/SMC N	membrane	latrotoxin receptor activity
2338	1	2.15E-05	0	0	INF		ENSG00000133742	CA1			gi	34520517	ref	NP_0	carbonic anhydrase I [Homo	261	28870	7.1	0	O	S	0	0	0	0	0	0	0	0	0.000172	1	4.3E-05	8.6E-05	0	0	0	0	0	0	0	0	0	0	0	0	Carbonic anhydrase alpha,	cytoplasm	carbonate dehydratase
2339	1	2.15E-05	0	0	INF		ENSG00000116096	SPR			gi	4507185	ref	NP_0	sepiapterin reductase (7,8-dih	261	28048	6	0	O	S	41	0.924	0	0	0	0	0	0	0.000172	1	4.3E-05	8.6E-05	0	0	0	0	0	0	0	0	0	0	0	0	short chain dehydrogenase		aldo-keto reductase activity
2340	1	2.15E-05	0	0	INF		ENSG00000229223	WDR26			gi	55743153	ref	NP_0	WD repeat domain 26 [Homo	514	58682	6.2	0	O	Q	0	0	0	0	0.000172	1	4.3E-05	8.59E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	WD40 domain, found in a		
2341	1	2.11E-05	0	0	INF		ENSG00000196212	COPS8			gi	5729779	ref	NP_0	COPS signalosome subunit 8	209	23226	5.4	0	O	Q	18	0.001	0	0	0.000169	1	4.23E-05	8.45E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		nucleus [pmid 8689678];	racemase and epimerase
2342	1	2.07E-05	0	0	INF		ENSG00000174425	ZNF581			gi	7705495	ref	NP_0	zinc finger protein 581 [Hom	197	22010	8.8	0	O	Q	20	0.028	0	0	0	0	0	0	0.000166	1	4.14E-05	8.28E-05	0	0	0	0	0	0	0	0	0	0	0	0		intracellular; nucleus	DNA binding; metal ion
2343	1	2.06E-05	0	0	INF		ENSG00000178115	PEDX2			gi	32189302	ref	NP_	peroxiredoxin 2 isoform a [Ho	198	21892	6.7	0	O	Q	31	0	0	0	0	0	0	0	0.000161	1	4.12E-05	8.24E-05	0	0	0	0	0	0	0	0	0	0	0	0	Peroxiredoxin (PRX) family,	cytoplasm [pmid 16130169]	peroxiredoxine activity;
2344	1	2.04E-05	0	0	INF		ENSG00000078140	HIP2			gi	4885417	ref	NP_0	ubiquitin-conjugating enzyme	200	22407	5.4	0	O	Q	0	0	0	0	0	0	0	0	0.000163	1	4.08E-05	8.16E-05	0	0	0	0	0	0	0	0	0	0	0	0	Ubiquitin Associated	nucleus	ligase activity; transcription
2345	1	0.00002	0	0	INF		ENSG00000222277	C20orf43			gi	7705483	ref	NP_0	hypothetical protein LOC519	306	33823	8.6	0	O	Q	0	0	0	0	0	0	0	0	0.00016	1	0.00004	0.00008	0	0	0	0	0	0	0	0	0	0	0	0	Protein of unknown		
2346	1	2E-05	0	0	INF		ENSG00000142208	AKT1			gi	22241015	ref	NP_	v-akt murine thymoma viral o	480	55686	6.1	0	O	S	0	0	0	0	0	0	0	0	0	0.00016	1	4E-05	8E-05	0	0	0	0	0	0	0	0	0	0	0	AKt pleckstrin homology	cytoplasm; nucleus	ATP binding; identical protein
2347	1	1.99E-05	0	0	INF		ENSG00000107362	EAM108B1			gi	7105160	ref	NP_	family with sequence similari	293	32823	6.8	0	O	S	21	0.528	0	0.000159	0	0	0	1	3.98E-05	7.96E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Hydrolases of the		
2348	1	1.96E-05	0	0	INF		ENSG00000167525	EAX2			gi	5031653	ref	NP_0	breast carcinoma amplified s	225	26131	8.8	0	O	S	16	0.074	0	0	0.000157	1	3.93E-05	7.86E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Breast carcinoma amplified	nucleus; spliceosome complex	RNA splicing factor activity,
2349	1	1.96E-05	0	0	INF		ENSG00000134202	GSTM3			gi	23065552	ref	NP_	glutathione S-transferase M3	225	26560	5.5	0	O	S	21	0.008	0	0	0.000157	1	3.93E-05	7.85E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	GST_N family, Class Mu		glutathione transferase
2350	1	1.96E-05	0	0	INF		ENSG00000163960	UBXN7			gi	14994446	ref	NP_	UBX domain containing 7 [Ho	489	54862	5.2	0	O	Q	26	0.142	0	0	0	0	0	0	0.000157	1	3.93E-05	7.85E-05	0	0	0	0	0	0	0	0	0	0	0	0			
2351	1	1.96E-05	0	0	INF		ENSG00000137342	C4orf108			gi	21367776	ref	NP_0	hypothetical protein LOC557	490	54739	8.6	0	O	Q	0	0	0	0	0	0	0	0	0.000157	1	3.92E-05	7.85E-05	0	0	0	0	0	0	0	0	0	0	0	0	Adaptor complexes medium	clathrin vesicle coat	
2352	1	1.94E-05	0	0	INF		ENSG00000131462	TUBG1			gi	31543831	ref	NP_0	tubulin, gamma 1 [Homo sap	451	51170	6.1	0	O	Q	17	0.001	0	0.000155	0	0	0	1	3.88E-05	7.76E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Gamma-tubulin is a	centrosome [pmid 9566969];	GTP binding; GTPase
2353	1	1.94E-05	0	0	INF		ENSG00000193235	C9orf11			gi	89235579	ref	NP_0	chromosome 20 open readin	228	28740	5	0	O	S	0	0	0	0	0.000155	1	3.87E-05	7.75E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	LisH. The LisH (lis	nucleus	
2354	1	1.92E-05	0	0	INF		ENSG00000105298	C10orf29			gi	28272314	ref	NP	chromosome 19 open readin	758	88702	9.1	0	O	Q	0	0	0	0.000154	0	0	0	1	3.85E-05	7.69E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2355	1	1.92E-05	0	0	INF		ENSG00000111731	KIAA0528			gi	29789060	ref	NP_0	hypothetical protein LOC984	1000	110447	5.7	0	O	Q	22	0	0	0	0.000154	1	3.84E-05	7.68E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Protein kinase C conserved	membrane; synaptic vesicle	transporter activity
2356	1	1.91E-05	0	0	INF		ENSG00000167106	CAMK1G			gi	30387611	ref	NP_0	cell division cycle 2-like 6 (CT	502	56802	8.5	0	O	Q	0	0	0	0	0	0	0	0	0	0	3.82E-05	7.65E-05	0	0	0	0	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
2357	1	1.91E-05	0	0	INF		ENSG00000160741	CRTC2			gi	32171215	ref	NP_0	CREB regulated transcription	693	73302	7.1	0	O	Q	17	0.005	0	0	0.000153	1	3.82E-05	7.65E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2358	1	1.91E-05	0	0	INF		ENSG00000131238	PPT1			gi	4506031	ref	NP_0	palmitoyl-protein thioesterase	306	34193	6.5	0	O	S	21	1	0	0.000152	0	0	0	1	3.81E-05	7.62E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Palmitoyl protein	lysosome	hydrolase activity; palmitoyl-
2359	1	1.89E-05	0	0	INF		ENSG00000198828	KIAA0586			gi	21068329	ref	NP_	small and compound eye	741	83533	6.7	0	O	Q	18	0	0	0	0	0	0	0	0.000151	1	3.78E-05	7.57E-05	0	0	0	0	0	0	0	0	0	0	0	0	Ankyrin repeats, ankyrin		ATP binding;
2360	1	1.89E-05	0	0	INF		ENSG00000173542	MOBKL1A			gi	27735029	ref	NP_	MOB1, Mps One Binder kina	216	25091	6.7	0	O	Q	0	0	0	0	0	0	0	0	0.000151	1	3.78E-05	7.56E-05	0	0	0	0	0	0	0	0	0	0	0	0	Mob1/phocein family. Mob1	cytoplasm [pmid 15067004];	kinase activator activity
2361	1	1.88E-05	0	0	INF		ENSG00000166543	THUMPD1			gi	34276024	ref	NP_	THUMP domain containing 1	353	39315	7.8	0	O	S	34	1	0	0.000151	0	0	0	1	3.75E-05	7.51E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	THUMP domain. The		
2362	1	1.87E-05	0	0	INF		ENSG00000139496	NUPL1			gi	30102928	ref	NP_	nucleoporin like 1 isoform a [	599	60897	9.3	0	O	S	20	0.758	0	0	0	0	0	0	0.000151	1	3.75E-05	7.49E-05	0	0	0	0	0	0	0	0	0	0	0	0	PBC domain. The PBC	integral to membrane;	porin activity; serine-type
2363	1	1.86E-05	0	0	INF		ENSG00000181873	C1orf59			gi	58197556	ref	NP_	hypothetical protein LOC200	356	38155	9.8	0	O	S	16	0.567	0	0	0.000149	1	3.72E-05	7.44E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Glycine cleavage T-protein	cytoplasm	aminomethyltransferase
2364	1	1.86E-05	0	0	INF		ENSG00000167582	UCHL5			gi	7706753	ref	NP_0	ubiquitin C-terminal hydrolas	329	37607	5.3	0	O	Q	20	0	0	0	0	0	0	0	0.000149	1	3.72E-05	7.44E-05	0	0	0	0	0	0	0	0	0	0	0	0	Ubiquitin carboxyl-terminal	cytosol; intracellular; protein	cysteine peptidase
2365	1	1.86E-05	0	0	INF		ENSG00000041802	LSG1			gi	14149720	ref	NP_0	large subunit GTPase 1 hom	658	75226	6.3	0	O	Q	27	0.009	0	0	0	0	0	0	0.000149	1	3.72E-05	7.44E-05	0	0	0	0	0	0	0	0	0	0	0	0	HSR1/MMR1. Human	endoplasmic reticulum [pmid	GTP binding
2366	1	1.86E-05	0	0	INF		ENSG00000143383	PRUNE			gi	24309263	ref	NP_0	prune homolog [Homo sapiens	453	50200	5.5	0	O	Q	49	0.001	0	0	0	0	0	0	0.000149	1	3.71E-05	7.42E-05	0	0	0	0	0	0	0	0	0	0	0	0	DHHA2 domain. This	cytoplasm	pyrophosphatase activity
2367	1	1.84E-05

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB
2451	1	1.13E-05	0	0	INF		ENSG00000129465:E	RIPK3			gi|40254844|ref|NP_	receptor-interacting serine-th	518	56887	6.5	0	o	Q	18	0.002
2452	1	1.12E-05	0	0	INF		ENSG00000106348:E	IMPDH1			gi|156616279|ref|NP	inosine monophosphate deh	589	63253	6.8	0	o	Q	18	0.017
2453	1	1.12E-05	0	0	INF		ENSG00000198945:E	L3MBTL3			gi|55770870|ref|NP_	l(3)mbt-like 3 isoform a [Hom	780	88337	6.5	0	o	Q	0	0
2454	1	1.11E-05	0	0	INF		ENSG00000102172:E	SMS			gi|21264341|ref|NP_	spermine synthase [Homo sa	366	41268	5	0	o	Q	20	0.064
2455	1	1.1E-05	0	0	INF		ENSG00000164068:E	RNF123			gi|37588869|ref|NP_	ring finger protein 123 [Homo	1314	148514	6.7	0	o	Q	22	0
2456	1	1.09E-05	0	0	INF		ENSG00000135341:E	MAP3K7			gi|21735562|ref|NP_	mitogen-activated protein kin	606	67196	7.1	0	o	Q	16	0.239
2457	1	1.09E-05	0	0	INF		ENSG00000111641:E	NOL1			gi|76150625|ref|NP_	nucleolar protein 1, 120kDa [	808	88973	9.2	0	o	Q	37	0
2458	1	1.07E-05	0	0	INF		ENSG00000097021:E	ACOT7			gi|32528282|ref|NP_	acyl-CoA thioesterase 7 isofo	380	41796	8.5	0	o	Q	37	0.301
2459	1	1.06E-05	0	0	INF		ENSG00000136100:E	VPS36			gi|71051598|ref|NP_	vacuolar protein sorting 36 [H	386	43817	7.2	0	o	Q	17	0.017
2460	1	1.05E-05	0	0	INF		ENSG00000141376:E	BCAS3			gi|153218595|ref|NP	breast carcinoma amplified s	913	99681	6.6	0	o	Q	29	0
2461	1	1.05E-05	0	0	INF		ENSG00000125149:E	C16orf70			gi|21361956|ref|NP_	lin-10 [Homo sapiens]	422	47525	7.7	0	o	Q	33	0
2462	1	1.04E-05	0	0	INF		ENSG00000116221:E	MRPL37			gi|22547134|ref|NP_	mitochondrial ribosomal prote	423	48118	8.6	0	o	S	25	0.687
2463	1	1.04E-05	0	0	INF		ENSG00000136560:E	TANK			gi|19743569|ref|NP_	TRAF interacting protein TAN	425	47816	5.7	0	o	Q	0	0
2464	1	1.01E-05	0	0	INF		ENSG00000146826:E	C7orf43			gi|27363480|ref|NP_	hypothetical protein LOC552	580	62597	8.9	0	o	Q	23	0.001
2465	1	1E-05	0	0	INF		ENSG00000093000:E	NUP50			gi|24497447|ref|NP_	nucleoporin 50kDa isoform a	440	46863	8.3	0	o	Q	55	0
2466	1	1E-05	0	0	INF		ENSG00000106524:E	ANKMY2			gi|28461129|ref|NP_	ankyrin repeat and MYND do	441	49299	6.3	0	o	Q	0	0
2467	1	9.93E-06	0	0	INF		ENSG00000136877:E	FPGS			gi|66932984|ref|NP_	folylpolyglutamate synthase i	587	64609	7.9	0	o	S	22	0.999
2468	1	9.9E-06	0	0	INF		ENSG00000141101:E	NOB1			gi|7661532|ref|NP_0	nin one binding protein [Hom	412	46675	7.2	0	o	Q	21	0.023
2469	1	9.89E-06	0	0	INF		ENSG00000141252:E	VPS53			gi|21361728|ref|NP_	vacuolar protein sorting 53 [H	670	76352	6	0	o	Q	26	0
2470	1	9.82E-06	0	0	INF		ENSG00000174842:E	GLMN			gi|16933537|ref|NP_	glomulin [Homo sapiens]	594	68208	5.3	0	o	Q	0	0
2471	1	9.8E-06	0	0	INF		ENSG00000132005:E	RFX1			gi|52486543|ref|NP_	regulatory factor X1 [Homo s	979	104728	6.3	0	o	Q	28	0
2472	1	9.71E-06	0	0	INF		ENSG00000108578:E	BLMH			gi|4557367|ref|NP_0	bleomycin hydrolase [Homo	455	52562	6.3	0	o	Q	28	0.017
2473	1	9.68E-06	0	0	INF		ENSG00000035687:E	ADSS			gi|34577063|ref|NP_	adenylosuccinate synthase [	456	50097	6.6	0	o	Q	19	0.003
2474	1	9.61E-06	0	0	INF		ENSG00000172009:E	THOP1			gi|4507491|ref|NP_0	thimet oligopeptidase 1 [Hom	689	78840	6	0	o	Q	18	0.008
2475	1	9.59E-06	0	0	INF		ENSG00000154822:E	PLCL2			gi|24308011|ref|NP_	phospholipase C-like 2 [Hom	1001	113749	6.3	0	o	Q	21	0
2476	1	9.58E-06	0	0	INF		ENSG00000198087:E	CD2AP			gi|11321634|ref|NP_	CD2-associated protein [Hon	639	71451	6.4	0	o	Q	0	0
2477	1	9.47E-06	0	0	INF		ENSG00000135686:E	C16orf44			gi|31542246|ref|NP_	hypothetical protein LOC797	616	69896	6.2	0	o	Q	0	0
2478	1	9.45E-06	0	0	INF		ENSG00000175216:E	CKAP5			gi|57164942|ref|NP_	colonic and hepatic tumor ov	2032	225493	7.8	0	o	Q	0	0
2479	1	9.4E-06	0	0	INF		ENSG00000033800:E	PIAS1			gi|7706637|ref|NP_0	protein inhibitor of activated	651	71836	7.3	0	o	Q	27	0.001
2480	1	9.28E-06	0	0	INF		ENSG00000135655:E	USP15			gi|14149627|ref|NP_	ubiquitin specific peptidase 1	952	109297	5.2	0	o	Q	30	0
2481	1	9.21E-06	0	0	INF		ENSG00000089336:E	KIAA0841			gi|149944680|ref|NP	hypothetical protein LOC233	633	71683	8.5	0	o	Q	25	0.001
2482	1	9.19E-06	0	0	INF		ENSG00000115977:E	AAK1			gi|148277037|ref|NP	AP2 associated kinase 1 [Ho	961	103885	6.5	0	o	Q	30	0.003
2483	1	9.18E-06	0	0	INF		ENSG00000113240:E	CLK4			gi|10190706|ref|NP_	CDC-like kinase 4 [Homo sa	481	57492	8.7	0	o	Q	0	0
2484	1	8.97E-06	0	0	INF		ENSG00000113282:E	CLINT1			gi|7661968|ref|NP_0	epsin 4 [Homo sapiens]	625	68259	6.4	0	o	Q	0	0
2485	1	8.83E-06	0	0	INF		ENSG00000166037:E	CEP57			gi|45430055|ref|NP_	translokin [Homo sapiens]	500	57089	9.3	0	o	S	20	0.669
2486	1	8.8E-06	0	0	INF		ENSG00000165006:E	UBAP1			gi|8394499|ref|NP_0	ubiquitin associated protein 1	502	55084	5.1	0	o	Q	18	0
2487	1	8.79E-06	0	0	INF		ENSG00000146376:E	ARHGAP18			gi|39932589|ref|NP_	Rho GTPase activating prote	663	74977	6.4	0	o	Q	15	0.035
2488	1	8.77E-06	0	0	INF		ENSG00000103047:E	TMCO7			gi|153791502|ref|NP	transmembrane and coiled-c	1094	120747	6.1	0	o	Q	36	0.01
2489	1	8.67E-06	0	0	INF		ENSG00000106683:E	LIMK1			gi|4505001|ref|NP_0	LIM domain kinase 1 [Homo	647	72585	7	0	o	Q	17	0.055
2490	1	8.57E-06	0	0	INF		ENSG00000101654:E	RNMT			gi|4506567|ref|NP_0	RNA (guanine-7-) methyltran	476	54844	6.6	0	o	Q	0	0
2491	1	8.57E-06	0	0	INF		ENSG00000068394:E	GPKOW			gi|15811782|ref|NP_	G patch domain and KOW m	476	52229	6.2	0	o	Q	23	0.316
2492	1	8.54E-06	0	0	INF		ENSG00000138646:N	HERC5			gi|110825982|ref|NP	hect domain and RLD 5 [Hon	1024	116852	7.6	0	o	S	48	0.84
2493	1	8.51E-06	0	0	INF		ENSG00000130935:E	NOL11			gi|21361468|ref|NP_	nucleolar protein 11 [Homo s	719	81124	6.1	0	o	Q	25	0.201
2494	1	8.47E-06	0	0	INF		ENSG00000103043:E	VAC14			gi|39780552|ref|NP_	Vac14 homolog [Homo sapie	782	87973	6.1	0	o	Q	18	0
2495	1	8.35E-06	0	0	INF		ENSG00000072803:E	FBXW11			gi|48928046|ref|NP_	F-box and WD repeat domai	529	60898	6.7	0	o	Q	0	0
2496	1	8.31E-06	0	0	INF		ENSG00000147324:E	MFHAS1			gi|110825984|ref|NP	malignant fibrous histiocytom	1052	116950	7.9	0	o	S	46	0.892
2497	1	8.26E-06	0	0	INF		ENSG00000100784:E	RPS6KA5			gi|32528295|ref|NP_	ribosomal protein S6 kinase,	802	89865	7.1	0	o	Q	19	0.001
2498	1	8.24E-06	0	0	INF		ENSG00000124383:E	MPHOSPH10			gi|31317305|ref|NP_	M-phase phosphoprotein 10	681	78864	4.9	0	o	Q	24	0.003
2499	1	8.24E-06	0	0	INF		ENSG00000070367:E	EXOC5			gi|5730037|ref|NP_0	SEC10 protein [Homo sapien	708	81853	6.7	0	o	Q	0	0
2500	1	8.22E-06	0	0	INF		ENSG00000164951:E	PPM2C			gi|45439339|ref|NP_	pyruvate dehydrogenase pho	537	61054	6.7	0	o	Q	18	0.025
2501	1	8.12E-06	0	0	INF		ENSG00000155034:E	FBXL18			gi|157426875|ref|NP	F-box and leucine-rich repea	718	78919	8.3	0	o	Q	0	0
2502	1	8.05E-06	0	0	INF		ENSG00000004139:E	SARM1			gi|154090976|ref|NP	sterile alpha and TIR motif co	724	79388	6.6	0	o	Q	20	0.282
2503	1	7.98E-06	0	0	INF		ENSG00000140848:E	CPNE2			gi|30181236|ref|NP_	copine II [Homo sapiens]	548	61190	6.1	0	o	Q	25	0.041
2504	1	7.86E-06	0	0	INF		ENSG00000127804:E	METT10D			gi|122114654|ref|NP	methyltransferase 10 domain	562	63621	7.9	0	o	Q	0	0
2505	1	7.83E-06	0	0	INF		ENSG00000075651:E	PLD1			gi|4505873|ref|NP_0	phospholipase D1, phosphatic	1074	124184	8.8	0	o	Q	20	0
2506	1	7.83E-06	0	0	INF		ENSG00000039650:E	PNKP			gi|31543419|ref|NP_	polynucleotide kinase 3'-phos	521	57076	8.5	0	o	Q	31	0.002
2507	1	7.82E-06	0	0	INF		ENSG00000138399:E	FASTKD1			gi|31377837|ref|NP_	FAST kinase domains 1 [Hor	847	97367	7.7	0	o	Q	21	0.085
2508	1	7.75E-06	0	0	INF		ENSG00000124570:E	SERPINB6			gi|41152086|ref|NP_	serine (or cysteine) proteinas	376	42622	5.3	0	o	Q	21	0.004
2509	1	7.73E-06	0	0	INF		ENSG00000015171:E	ZMYND11			gi|47078243|ref|NP_	zinc finger, MYND domain co	528	61830	8.3	0	o	Q	39	0.001
2510	1	7.64E-06	0	0	INF		ENSG00000168297:E	PXK			gi|31543452|ref|NP_	PX domain containing serine	578	64950	9.3	0	o	Q	30	0.004
2511	1	7.6E-06	0	0	INF		ENSG00000065883:E	CDC2L5			gi|145309300|ref|NP	cell division cycle 2-like 5 iso	1452	158434	9.7	0	o	Q	19	0.014
2512	1	7.56E-06	0	0	INF		ENSG00000156697:E	UTP14A			gi|21361348|ref|NP_	UTP14, U3 small nucleolar ri	771	87978	7.9	0	o	Q	17	0.072
2513	1	7.5E-06	0	0	INF		ENSG00000178252:E	WDR6			gi|11072093|ref|NP_	WD repeat domain 6 protein	1121	121724	6.9	0	o	Q	29	0.017
2514	1	7.5E-06	0	0	INF		ENSG00000149231:E	CCDC82			gi|19923844|ref|NP_	coiled-coil domain containing	544	64002	5	0	o	Q	0	0
2515	1	7.46E-06	0	0	INF		ENSG00000170242:E	USP47			gi|71774197|ref|NP_	ubiquitin specific protease 47	1287	147222	5.1	0	o	Q	0	0
2516	1	7.43E-06	0	0	INF		ENSG00000196843:E	ARID5A			gi|47078224|ref|NP_	AT rich interactive domain 5A	594	64074	9.2	0	o	Q	0	0
2517	1	7.34E-06	0	0	INF		ENSG00000066557:E	LRRC40			gi|21361633|ref|NP_	leucine rich repeat containing	602	68250	6.4	0	o	Q	21	0
2518	1	7.29E-06	0	0	INF		ENSG00000164306:E	CCDC111			gi|22749373|ref|NP_	coiled-coil domain containing	560	64412	5.3	0	o	Q	0	0
2519	1	7.25E-06	0	0	INF		ENSG00000167721:E	TSR1			gi|39780588|ref|NP_	TSR1, 20S rRNA accumulati	804	91810	7.4	0	o	Q	0	0
2520	1	7.2E-06	0	0	INF		ENSG00000198522:E	ZNF512			gi|40217790|ref|NP_	zinc finger protein 512 [Hom	567	64682	9.8	0	o	Q	23	0.002
2521	1	7.2E-06	0	0	INF		ENSG00000100949:E	RABGGTA			gi|53828918|ref|NP_	Rab geranylgeranyltransfera	567	65072	5.7	0	o	Q	0	0
2522	1	7.03E-06	0	0	INF		ENSG00000165819:E	METTL3			gi|21361827|ref|NP_	methyltransferase like 3 [Hor	580	64474	6.4	0	o	Q	0	0
2523	1	7.03E-06	0	0	INF		ENSG00000129691:E	ASH2L			gi|157412280|ref|NP	ash2-like isoform a [Homo sa	628	68723	5.7	0	o	Q	28	0.011
2524	1	7.03E-06	0	0	INF		ENSG00000178996:E	SNX18			gi|157057543|ref|NP	sorting nexin associated golg	628	68895	5.7	0	o	Q	0	0
2525	1	6.88E-06	0	0	INF		ENSG00000149262:E	INTS4			gi|50086624|ref|NP_	integrator complex subunit 4	963	108171	6.4	0	o	Q	0	0
2526	1	6.82E-06	0	0	INF		ENSG00000182511:E	FES			gi|4503687|ref|NP_0	V-FES feline sarcoma viral/V	822	93497	6.7	0	o	Q	18	0.001
2527	1	6.73E-06	0	0	INF		ENSG00000204120:E	GIGYF2			gi|156766043|ref|NP	trinucleotide repeat containin	1299	150070	5.5	0	o	Q	33	0.009
2528	1	6.64E-06	0	0	INF		ENSG00000118898:E	PPL			gi|45439327|ref|NP_	periplakin [Homo sapiens]	1756	204676	5.6	0	o	Q	0	0
2529	1	6.64E-06	0	0	INF		ENSG00000164169:E	PRMT10			gi|40538772|ref|NP_	protein arginine methyltransf	845	94501	5.2	0	o	Q	47	0
2530	1	6.6E-06	0	0	INF		ENSG00000100226:E	GTPBP1			gi|82546879|ref|NP_	GTP binding protein 1 [Homo	669	72454	8.3	0	o	Q	32	0.012
2531	1	6.59E-06	0	0	INF		ENSG00000167674:E	AC011498.7-2			gi|14249158|ref|NP_	hepatoma-derived growth fac	670	74230	7.5	0	o	Q	18	0
2532	1	6.58E-06	0	0	INF		ENSG00000119778:E	ATAD2B			gi|153792536|ref|NP	ATPase family, AAA domain	1458	164913	6.8	0	o	Q	27	0.002
2533	1	6.56E-06	0	0	INF		ENSG00000162227:E	TAF6L			gi|5453844|ref|NP_0	TAF6-like RNA polymerase I	622	67814	9	0	o	Q	38	0
2534	1	6.46E-06	0	0	INF		ENSG00000119203:E	CPSF3			gi|7706427|ref|NP_0	cleavage and polyadenylatio	684	77486	5.6	0	o	Q	21	0
2535	1	6.44E-06	0	0	INF		ENSG00000196642:E	C9orf86			gi|38201704|ref|NP_	Rab-like GTP-binding protein	686	74831	5.1	0	o	Q	23	0
2536	1	6.41E-06	0	0	INF		ENSG00000173020:E	ADRBK1			gi|148539876|ref|NP	beta adrenergic receptor kina	689	79574	7.3	0	o	Q	23	0.005
2537	1	6.31E-06	0	0	INF		ENSG00000148634:E	HERC4			gi|37620181|ref|NP_	hect domain and RLD 4 isofo	1049	117697	6.3	0	o	Q	16	0.014
2538	1	6.31E-06	0	0	INF		ENSG00000095787:E	WAC			gi|18379328|ref|NP_	WW domain-containing adap	647	70724	9.5	0	o	Q	0	0
2539	1	6.2E-06	0	0	INF		ENSG00000163507:E	KIAA1524			gi|24308239|ref|NP_	p90 autoantigen [Homo sapie	905	102201	6.2	0	o	Q	17	0.048
2540	1	6.19E-06	0	0	INF		ENSG00000196792:E	STRN3			gi|142976675|ref|NP	nuclear autoantigen isoform	713	77745	5.3	0	o	Q	16	0.003
2541	1	6.12E-06	0	0	INF		ENSG00000095383:E	TBC1D2			gi|62198225|ref|NP_	TBC1 domain family, membe	917	104165	6.5	0	o	Q	0	0
2542	1	6.09E-06	0	0	INF		ENSG00000100106:E	TRIOBP			gi|88501738|ref|NP_	TRIO and F-actin binding pro	2365	261373	8.5	0	o	Q	0	0
2543	1	6.08E-06	0	0	INF		ENSG00000196865:E	NHLRC2			gi|42476013|ref|NP_	NHL repeat containing 2 [Ho	726	79444	5.6	0	o	Q	27	0.495
2544	1	6.07E-06	0	0	INF		ENSG00000164308:N	ERAP2			gi|11641261|ref|NP_	endoplasmic reticulum amino	960	110462	6.7	0	o	Q	38	0.212
2545	1	6.04E-06	0	0	INF		ENSG00000110514:E	MADD			gi|18860862|ref|NP_	MAP-kinase activating death	1588	176586	6.1	0	o	Q	30	0.029
2546	1	6.01E-06	0	0	INF		ENSG00000122299:E	ZC3H7A			gi|27414497|ref|NP_	zinc finger CCCH-type conta	971	110538	7.3	0	o	Q	0	0
2547	1	5.78E-06	0	0	INF		ENSG00000005156:E	LIG3			gi|73747829|ref|NP_	ligase III, DNA, ATP-depende	1009	112907	9	0	o	Q	16	0.035
2548	1	5.77E-06	0	0	INF		ENSG00000033030:E	ZCCHC8			gi|38044290|ref|NP_	zinc finger, CCHC domain co	707	78577	4.9	0	o	Q	0	0
2549	1	5.71E-06	0	0	INF		ENSG00000138758:E	SEPT11			gi|8922712|ref|NP_0	septin 11 [Homo sapiens]	429	49398	6.8	0	o	Q	29	0
2550	1	5.66E-06	0	0	INF		ENSG00000167447:E	C17orf71			gi|47777319|ref|NP_	hypothetical protein LOC551	991	109684	7.7	0	o	Q	25	0.232
2551	1	5.57E-06	0	0	INF		ENSG00000112297:E	AIM1			gi|62988361|ref|NP_	absent in melanoma 1 [Homo	1723	188616	5.9	0	o	Q	28	0
2552	1	5.56E-06	0	0	INF		ENSG00000011451:E	WIZ			gi|151301215|ref|NP	widely-interspaced zinc finge	794	85380	9.1	0	o	Q	16	0.009
2553	1	5.54E-06	0	0	INF		ENSG00000117859:E	OSBPL9			gi|20070331|ref|NP_	oxysterol-binding protein-like	736	83185	6.2	0	o	Q	35	0
2554	1	5.51E-06	0	0	INF		ENSG00000067646:E	LOC100130829			gi|169216333|ref|XP	PREDICTED: hypothetical pr	801	90505	6.1	0	o	Q	0	0
2555	1	5.49E-06	0	0	INF		ENSG00000159459:E	UBR1			gi|28372497|ref|NP_	ubiquitin protein ligase E3 co	1749	200209	6	0	o	Q	0	0
2556	1	5.48E-06	0	0	INF		ENSG00000034063:E	UHRF1			gi|115430233|ref|NP	ubiquitin-like, containing PHD	806	91100	7.4	0	o	Q	21	0.016
2557	1	5.46E-06	0	0	INF		ENSG00000130787:E	HIP1R			gi|48762942|ref|NP_	huntingtin interacting protein-	1068	119388	6.7	0	o	Q	20	0
2558	1	5.44E-06	0	0	INF		ENSG00000198824:E	C13orf8			gi|41281612|ref|NP_	hypothetical protein LOC283	812	89099	8.4	0	o	Q	0	0
2559	1	5.42E-06	0	0	INF		ENSG00000003756:E	RBM5			gi|5032031|ref|NP_0	RNA binding motif protein 5 [	815	92154	6.3	0	o	Q	0	0
2560	1	5.41E-06	0	0	INF		ENSG00000165458:E	INPPL1			gi|4755142|ref|NP_0	inositol polyphosphate phosp	1258	138585	6.5	0	o	Q	16	0.049
2561	1	5.41E-06	0	0	INF		ENSG00000133704:E	IPO8			gi|53759103|ref|NP_	importin 8 [Homo sapiens]	1037	119938	5.2	0	o	Q	22	0
2562	1	5.25E-06	0	0	INF		ENSG00000151148:E	UBE3B			gi|35493959|ref|NP_	ubiquitin protein ligase E3B [	1068	123098	8.2	0	o	Q	19	0.002
2563	1	5.2E-06	0	0	INF		ENSG00000065534:E	MYLK			gi|116008188|ref|NP	myosin light chain kinase iso	1845	203054	6.2	0	o	Q	19	0.013
2564	1	5.09E-06	0	0	INF		ENSG00000147854:E	UHRF2			gi|23312364|ref|NP_	Np95-like ring finger protein [	802	89985	8.2	0	o	Q	0	0
2565	1	5.03E-06	0	0	INF		ENSG00000143631:N	FLG			gi|60097902|ref|NP_	filaggrin [Homo sapiens]	4061	435180	9.2	0	o	Q	20	0
2566	1	4.94E-06	0	0	INF		ENSG00000153107:E	ANAPC1			gi|12056971|ref|NP_	anaphase promoting comple	1944	216498	6.3	0	o	Q	0	0
2567	1	4.79E-06	0	0	INF		ENSG00000184863:E	RBM33			gi|151301053|ref|NP	RNA binding motif protein 33	1170	129986	6.9	0	o	Q	15	0.071
2568	1	4.68E-06	0	0	INF		ENSG00000120685:N	C13orf23			gi|125656155|ref|NP	hypothetical protein LOC802	944	95698	8.9	0	o	Q	0	0
2569	1	4.63E-06	0	0	INF		ENSG00000083799:E	CYLD			gi|109637776|ref|NP	ubiquitin carboxyl-terminal hy	953	107044	5.6	0	o	Q	32	0
2570	1	4.44E-06	0	0	INF		ENSG00000173889:E	PHC3			gi|148612879|ref|NP	polyhomeotic like 3 [Homo sa	995	107480	6.5	0	o	Q	0	0
2571	1	4.34E-06	0	0	INF		ENSG00000090920:E	FCGBP			gi|154146262|ref|NP	Fc fragment of IgG binding p	5405	572021	5.3	0	o	S	22	0.993
2572	1	4.33E-06	0	0	INF		ENSG00000157483:E	MYO1E			gi|55956916|ref|NP_	myosin IE [Homo sapiens]	1108	127062	8.9	0	o	Q	0	0
2573	1	4.22E-06	0	0	INF		ENSG00000171634:N	BPTF			gi|38788260|ref|NP_	bromodomain PHD finger tra	2903	322217	6.4	0	o	Q	23	0.003
2574	1	4.1E-06	0	0	INF		ENSG00000152465:E	NMT2			gi|4758816|ref|NP_0	N-myristoyltransferase 2 [Ho	498	56980	7.6	0	o	Q	0	0
2575	1	3.95E-06	0	0	INF		ENSG00000172716:E	SLFN11			gi|157388965|ref|NP	schlafen family member 11 [H	901	102836	7.8	0	o	Q	16	0
2576	1	3.92E-06	0	0	INF		ENSG00000197323:E	TRIM33			gi|74027249|ref|NP_	tripartite motif-containing 33	1127	122533	6.7	0	o	Q	35	0.001
2577	1	3.69E-06	0	0	INF		ENSG00000144550:E	CPNE9			gi|88703066|ref|NP_	copine-like protein [Homo sa	553	61864	5.3	0	o	Q	35	0
2578	1	3.59E-06	0	0	INF		ENSG00000113318:E	MSH3			gi|68303635|ref|NP_	mutS homolog 3 [Homo sapie	1137	127440	8.1	0	o	S	22	0.876
2579	1	3.59E-06	0	0	INF		ENSG00000197299:E	BLM			gi|4557365|ref|NP_0	Bloom syndrome protein [Ho	1417	159000	7.5	0	o	Q	0	0
2580	1	3.58E-06	0	0	INF		ENSG00000126001:E	CEP250			gi|21735548|ref|NP_	centrosomal protein 2 isoform	2442	281134	5	0	o	Q	27	0.002
2581	1	3.58E-06	0	0	INF		ENSG00000171467:E	ZNF318			gi|120587019|ref|NP	zinc finger protein 318 [Homo	2279	251110	7.2	0	o	Q	0	0
2582	1	3.52E-06	0	0	INF		ENSG00000188994:E	ZNF292			gi|150170718|ref|NP	zinc finger protein 292 [Homo	2723	304815	7.4	0	o	Q	0	0
2583	1	3.47E-06	0	0	INF		ENSG00000213079:E	RBM16			gi|62460633|ref|NP_	RNA-binding motif protein 16	1271	140519	8.3	0	o	Q	0	0
2584	1	2.95E-06	0	0	INF		ENSG00000083223:E	ZCCHC6			gi|58331272|ref|NP_	zinc finger, CCHC domain co	1495	171228	6.8	0	o	Q	0	0
2585	1	2.95E-06	0	0	INF		ENSG00000090615:E	GOLGA3			gi|30089940|ref|NP_	Golgi autoantigen, golgin sub	1498	167354	5.4	0	o	Q	0	0
2586	1	2.94E-06	0	0	INF		ENSG00000186566:E	GPATCH8			gi|50962882|ref|NP_	G patch domain containing 8	1502	164197	8.7	0	o	Q	0	0
2587	1	2.85E-06	0	0	INF		ENSG00000173473:E	SMARCC1			gi|21237802|ref|NP_	SWI/SNF-related matrix-asso	1105	122721	5.8	0	o	S	30	0.806
2588	1	2.74E-06	0	0	INF		ENSG00000167258:E	CRKRS			gi|157817023|ref|NP	Cdc2-related kinase, arginine	1490	164154	9.4	0	o	Q	27	0.001
2589	1	2.47E-06	0	0	INF		ENSG00000187908:E	DMBT1			gi|148539840|ref|NP	deleted in malignant brain tu	1785	193970	5.4	0	o	S	20	0.902
2590	1	2.17E-06	0	0	INF		ENSG00000152223:E	KIAA1632			gi|93204865|ref|NP_	hypothetical protein LOC577	2579	292479	6.4	0	o	Q	0	0
2591	1	1.99E-06	0	0	INF		ENSG00000198734:E	F5			gi|105990535|ref|NP	coagulation factor V precurso	2224	251701	6	0	o	S	29	0.98
2592	1	1.69E-06	0	0	INF		ENSG00000131503:E	MASK-BP3			gi|37620163|ref|NP_	ANKHD1-EIF4EBP3 protein	2617	277173	5.9	0	o	Q	0	0
2593	1	1.11E-06	0	0	INF		ENSG00000118058:E	MLL			gi|56550039|ref|NP_	myeloid/lymphoid or mixed-li	3969	431768	9.1	0	o	Q	49	0.279
2594	10	0.003425	7	0.000842	4.066459		ENSG00000139641:E	FAM62A			gi|14149680|ref|NP_	family with sequence similari	1104	122856	5.8	2	o68-90i241	Q	0	0
2595	10	0.001218	6	0.000855	1.424603		ENSG00000089597:E	GANAB			gi|38202257|ref|NP_	alpha glucosidase II alpha su	944	106874	6.1	1	i13-32o	S	33	0.996
2596	10	0.000909	6	0.000398	2.281314		ENSG00000112992:E	NNT			gi|122939155|ref|NP	nicotinamide nucleotide trans	1086	113895	8.1	12	o476-498i5	S	24	0.535

rk	RESTING LYMPHOCYTES NEs: HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	PHA-TREATED LYMPHOCYTES NEs: HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MMs: MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
2451	0	9.01E-05	0	0	0	1	2.25E-05	4.5E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
2452	0	0	0	9E-05	0	1	2.25E-05	4.5E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2453	0	8.97E-05	0	0	0	1	2.24E-05	4.49E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Present in Drosophila Scm,	nucleus	
2454	0	0	0	0	0	0	0	0	0	0	0	8.92E-05	0	1	2.23E-05	4.46E-05	0	0	0	0	0	0	0	0	Spermine/spermidine		spermidine synthase activity
2455	0	0	0	0	0	0	0	0	0	0	0	0	8.76E-05	1	2.19E-05	4.38E-05	0	0	0	0	0	0	0	0	RING-finger (Really	cytoplasm [pmid 11256614]	ligase activity; metal ion
2456	0	0	0	8.74E-05	0	1	2.19E-05	4.37E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; magnesium ion
2457	0	0	0	8.74E-05	0	1	2.19E-05	4.37E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Protein-L-isoaspartate	nucleolus [pmid 1394192];	methyltransferase activity;
2458	0	0	0	0	0	0	0	0	0	0	0	8.59E-05	0	1	2.15E-05	4.29E-05	0	0	0	0	0	0	0	0	Brown fat-inducible	cytoplasm [pmid 10578051];	acyl-CoA binding [pmid
2459	0	0	0	0	0	0	0	0	0	0	0	8.46E-05	0	1	2.11E-05	4.23E-05	0	0	0	0	0	0	0	0	Vacuolar protein sorting 36.	nucleus	lipid binding
2460	0	0	0	0	0	0	0	0	0	0	0	0	8.41E-05	1	2.1E-05	4.2E-05	0	0	0	0	0	0	0	0			
2461	0	0	0	8.37E-05	0	1	2.09E-05	4.19E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Uncharacterised protein		protein binding [pmid
2462	0	0	0	8.35E-05	0	1	2.09E-05	4.18E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Mitochondrial 28S	mitochondrial ribosome [pmid	structural constituent of
2463	0	0	0	8.31E-05	0	1	2.08E-05	4.16E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	V-type ATPase 116kDa		metal ion binding; protein
2464	0	8.04E-05	0	0	0	1	2.01E-05	4.02E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		cytoplasm [pmid 11256614]	catalytic activity
2465	0	0	0	8.03E-05	0	1	2.01E-05	4.01E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	NUP50 (Nucleoporin 50	integral to membrane; nuclear	porin activity
2466	0	0	0	8.01E-05	0	1	2E-05	4.01E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ankyrin repeats; ankyrin		metal ion binding; zinc ion
2467	0	7.95E-05	0	0	0	1	1.99E-05	3.97E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Folylpolyglutamate	cytoplasm [pmid 1409616];	ATP binding; ligase activity;
2468	0	0	0	0	0	0	0	0	0	0	0	7.92E-05	0	1	1.98E-05	3.96E-05	0	0	0	0	0	0	0	0	Nin one binding (NOB1) Zn-	nucleus	metal ion binding; zinc ion
2469	0	0	0	7.91E-05	0	1	1.98E-05	3.95E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Vps53-like, N-terminal.	membrane	
2470	0	7.85E-05	0	0	0	1	1.96E-05	3.93E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		intracellular [pmid 12604780]	hepatocyte growth factor
2471	0	0	0	0	0	0	0	0	0	0	0	0	7.84E-05	1	1.96E-05	3.92E-05	0	0	0	0	0	0	0	0	RFX DNA-binding domain.	nucleus	DNA binding; RNA
2472	0	0	0	7.76E-05	0	1	1.94E-05	3.88E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Peptidase C1B subfamily	cytoplasm [pmid 8639621];	aminopeptidase activity
2473	0	0	0	7.75E-05	0	1	1.94E-05	3.87E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Adenylosuccinate		adenylosuccinate synthase
2474	0	0	0	7.69E-05	0	1	1.92E-05	3.85E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Peptidase family M3. This		metal ion binding;
2475	0	0	0	0	0	0	0	0	0	0	0	0	7.67E-05	1	1.92E-05	3.83E-05	0	0	0	0	0	0	0	0	Phospholipase C (PLC)		calcium ion binding;
2476	0	0	0	0	0	0	0	0	0	0	0	7.66E-05	0	1	1.92E-05	3.83E-05	0	0	0	0	0	0	0	0	Src homology 3 domains;	actin cytoskeleton [pmid	protein binding [pmid
2477	0	7.57E-05	0	0	0	1	1.89E-05	3.79E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Kelch motif. The kelch motif		protein binding
2478	0	0	0	0	0	0	0	0	0	0	0	0	7.56E-05	1	1.89E-05	3.78E-05	0	0	0	0	0	0	0	0		centrosome [pmid 14718566];	binding; protein binding [pmid
2479	0	0	0	0	0	0	0	0	0	0	0	7.52E-05	0	1	1.88E-05	3.76E-05	0	0	0	0	0	0	0	0	MIZ/SP-RING zinc finger.	nucleus [pmid 9724754]	androgen receptor binding
2480	0	0	0	7.42E-05	0	1	1.86E-05	3.71E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	A subfamily of Peptidase		cysteine-type endopeptidase
2481	0	7.37E-05	0	0	0	1	1.84E-05	3.68E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2482	0	0	0	7.35E-05	0	1	1.84E-05	3.68E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2483	0	0	0	7.34E-05	0	1	1.84E-05	3.67E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Serine/Threonine protein	nucleus	ATP binding; nucleotide
2484	0	0	0	0	0	0	0	0	0	7.18E-05	0	0	0	1	1.79E-05	3.59E-05	0	0	0	0	0	0	0	0	ENTH domain, Epsin family;	Golgi apparatus [pmid	lipid binding
2485	0	0	0	7.07E-05	0	1	1.77E-05	3.53E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Protein of unknown function	centrosome [pmid 14654843];	fibroblast growth factor
2486	0	0	0	7.04E-05	0	1	1.76E-05	3.52E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Helix-turn-helix (HTH)	cytoplasm [pmid 11256614]	
2487	0	7.04E-05	0	0	0	1	1.76E-05	3.52E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RhoGAP_ARHGAP18:	intracellular	GTPase activator activity;
2488	0	0	0	0	0	0	0	0	0	0	0	0	7.02E-05	1	1.75E-05	3.51E-05	0	0	0	0	0	0	0	0			
2489	0	0	0	0	0	0	0	0	0	6.94E-05	0	0	0	1	1.73E-05	3.47E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein	cytoplasm [pmid 8537403]	ATP binding; metal ion
2490	0	0	0	0	0	0	0	0	0	0	0	6.86E-05	0	1	1.71E-05	3.43E-05	0	0	0	0	0	0	0	0	mRNA capping enzyme.	nucleus [pmid 9705270]	methyltransferase activity;
2491	0	0	0	0	0	0	0	0	0	0	0	6.86E-05	0	1	1.71E-05	3.43E-05	0	0	0	0	0	0	0	0	glycine rich nucleic binding	intracellular	nucleic acid binding
2492	0	6.83E-05	0	0	0	1	1.71E-05	3.42E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2493	0	0	0	0	0	0	0	0	0	0	0	6.81E-05	0	1	1.7E-05	3.4E-05	0	0	0	0	0	0	0	0	NUC205 domain. This	nucleus	
2494	0	0	0	6.78E-05	0	1	1.69E-05	3.39E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			binding; receptor activity
2495	0	0	0	6.68E-05	0	1	1.67E-05	3.34E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	WD40 domain, found in a	ubiquitin ligase complex [pmid	protein binding [pmid
2496	0	6.65E-05	0	0	0	1	1.66E-05	3.33E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2497	0	0	0	6.61E-05	0	1	1.65E-05	3.3E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Serine/Threonine protein	nucleus [pmid 9687510]	ATP binding [pmid 9687510];
2498	0	0	0	0	0	0	0	0	0	6.59E-05	0	0	0	1	1.65E-05	3.29E-05	0	0	0	0	0	0	0	0	Mpp10 protein. This family	nucleolus [pmid 9450966];	protein binding [pmid
2499	0	6.59E-05	0	0	0	1	1.65E-05	3.29E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Exocyst complex	cytoplasm [pmid 9119050]	
2500	0	0	0	6.58E-05	0	1	1.64E-05	3.29E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Serine/threonine	mitochondrion; protein	calcium ion binding; catalytic
2501	0	6.5E-05	0	0	0	1	1.62E-05	3.25E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2502	0	6.44E-05	0	0	0	1	1.61E-05	3.22E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2503	0	6.38E-05	0	0	0	1	1.6E-05	3.19E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	VWA Copine: Copines are		
2504	0	0	0	6.29E-05	0	1	1.57E-05	3.14E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2505	0	0	0	0	0	0	0	0	0	6.27E-05	0	0	0	1	1.57E-05	3.13E-05	0	0	0	0	0	0	0	0	Phospholipase D (PLD)	endoplasmic reticulum;	hydrolase activity;
2506	0	0	0	0	0	0	0	0	0	0	0	6.26E-05	0	1	1.57E-05	3.13E-05	0	0	0	0	0	0	0	0	Polynucleotide kinase 3	nucleus [pmid 10446193]	ATP binding [pmid
2507	0	0	0	6.26E-05	0	1	1.56E-05	3.13E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RAP domain. This domain		ATP binding; protein kinase
2508	0	6.2E-05	0	0	0	1	1.55E-05	3.1E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Plasminogen Activator	cytosol [pmid 8415716]	protein binding [pmid
2509	0	0	0	0	0	0	0	0	0	0	0	6.18E-05	0	1	1.55E-05	3.09E-05	0	0	0	0	0	0	0	0	PWWP domain. The	nucleus [pmid 7621829]	DNA binding; metal ion
2510	0	0	0	6.11E-05	0	1	1.53E-05	3.06E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Serine/Threonine protein	cytoplasm [pmid 16142408]	actin binding; ATP binding
2511	0	0	0	6.08E-05	0	1	1.52E-05	3.04E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2512	0	6.05E-05	0	0	0	1	1.51E-05	3.03E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Utp14 protein. This protein	nucleus	protein binding [pmid
2513	0	0	0	0	0	0	0	0	0	6E-05	0	0	0	1	1.5E-05	3E-05	0	0	0	0	0	0	0	0	WD40 domain, found in a		
2514	0	0	0	0	0	0	0	0	0	0	0	0.00006	0	1	0.000015	0.00003	0	0	0	0	0	0	0	0			
2515	0	0	0	0	0	0	0	0	0	0	0	0	5.97E-05	1	1.49E-05	2.98E-05	0	0	0	0	0	0	0	0	A subfamily of Peptidase		cysteine-type endopeptidase
2516	0	0	0	5.95E-05	0	1	1.49E-05	2.97E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	BRIGHT, ARID (A/T-rich	intracellular; nucleus [pmid	DNA binding [pmid
2517	0	0	0	5.87E-05	0	1	1.47E-05	2.93E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Leucine-rich repeats		transferase activity
2518	0	0	0	0	0	0	0	0	0	0	0	5.83E-05	0	1	1.46E-05	2.91E-05	0	0	0	0	0	0	0	0	Herpesviridae UL52/UL70		
2519	0	5.8E-05	0	0	0	1	1.45E-05	2.9E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Bms1. Bms1 is an		
2520	0	0	0	0	0	0	0	0	0	0	0	5.76E-05	0	1	1.44E-05	2.88E-05	0	0	0	0	0	0	0	0	Putative transcriptional	intracellular; nucleus	DNA binding; metal ion
2521	0	0	0	0	0	0	0	0	0	0	0	5.76E-05	0	1	1.44E-05	2.88E-05	0	0	0	0	0	0	0	0	Rab geranylgeranyl		metal ion binding; protein
2522	0	0	0	0	0	0	0	0	0	0	0	5.63E-05	0	1	1.41E-05	2.81E-05	0	0	0	0	0	0	0	0	MT-A70. MT-A70 is the S-	nucleus [pmid 9409616]	methyltransferase activity;
2523	0	0	0	5.63E-05	0	1	1.41E-05	2.81E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2524	0	0	0	5.63E-05	0	1	1.41E-05	2.81E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2525	0	0	0	5.5E-05	0	1	1.38E-05	2.75E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Adaptin N terminal region.	integrator complex [pmid	binding; protein binding [pmid
2526	0	0	0	0	0	0	0	0	0	5.46E-05	0	0	0	1	1.36E-05	2.73E-05	0	0	0	0	0	0	0	0	Serine/Threonine protein		ATP binding; nucleotide
2527	0	5.39E-05	0	0	0	1	1.35E-05	2.69E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2528	0	5.31E-05	0	0	0	1	1.33E-05	2.66E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Spectrin repeats, found in	cytoskeleton [pmid 9521878]	protein binding [pmid
2529	0	0	0	0	0	0	0	0	0	5.31E-05	0	0	0	1	1.33E-05	2.66E-05	0	0	0	0	0	0	0	0	Tetratricopeptide repeat		methyltransferase activity;
2530	0	0	0	5.28E-05	0	1	1.32E-05	2.64E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Domain III of the GP-1		electron carrier activity; GTP
2531	0	0	0	5.27E-05	0	1	1.32E-05	2.64E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	PWWP domain. The		
2532	0	0	0	0	0	0	0	0	0	0	0	0	5.27E-05	1	1.32E-05	2.63E-05	0	0	0	0	0	0	0	0			
2533	0	0	0	0	0	0	0	0	0	0	0	5.25E-05	0	1	1.31E-05	2.62E-05	0	0	0	0	0	0	0	0	Protein of unknown function	histone deacetylase complex	DNA binding [pmid 9674425];
2534	0	0	0	5.16E-05	0	1	1.29E-05	2.58E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RNA-metabolising metallo-	nucleoplasm [pmid 7969155];	RNA binding
2535	0	0	0	5.15E-05	0	1	1.29E-05	2.57E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Rab family. Rab GTPases		GTP binding; nucleotide
2536	0	0	0	5.13E-05	0	1	1.28E-05	2.56E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2537	0	0	0	5.05E-05	0	1	1.26E-05	2.53E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Domain Homologous to E6-	intracellular	ubiquitin-protein ligase
2538	0	0	0	0	0	0	0	0	0	0	0	5.04E-05	0	1	1.26E-05	2.52E-05	0	0	0	0	0	0	0	0	Two conserved tryptophans		glucan 1,4-alpha-glucosidase
2539	0	0	0	0	0	0	0	0	0	4.96E-05	0	0	0	1	1.24E-05	2.48E-05	0	0	0	0	0	0	0	0	Chromosome segregation	cytoplasm [pmid 11256614]	binding
2540	0	0	0	4.95E-05	0	1	1.24E-05	2.48E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2541	0	0	0	0	0	0	0	0	0	4.89E-05	0	0	0	1	1.22E-05	2.45E-05	0	0	0	0	0	0	0	0	PARIS-1 pleckstrin		GTPase activator activity
2542	0	0	0	0	0	0	0	0	0	0	0	0	4.87E-05	1	1.22E-05	2.43E-05	0	0	0	0	0	0	0	0	Pleckstrin homology (PH)	actin cytoskeleton [pmid	actin binding; GTP-Rho
2543	0	0	0	4.87E-05	0	1	1.22E-05	2.43E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	TlpA-like family, DipZ-like		electron carrier activity
2544	0	4.86E-05	0	0	0	1	1.21E-05	2.43E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Peptidase family M1.	endoplasmic reticulum lumen	aminopeptidase activity
2545	0	0	0	0	0	0	0	0	0	0	0	0	4.83E-05	1	1.21E-05	2.42E-05	0	0	0	0	0	0	0	0	DENN (AEX-3) domain.	cytoplasm [pmid 8988362];	death receptor binding [pmid
2546	0	4.8E-05	0	0	0	1	1.2E-05	2.4E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Tetratricopeptide repeat	intracellular; nucleus	metal ion binding; nucleic
2547	0	4.62E-05	0	0	0	1	1.16E-05	2.31E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ATP dependent DNA ligase	intracellular; nucleus [pmid	ATP binding; DNA binding
2548	0	0	0	0	0	0	0	0	0	0	0	4.62E-05	0	1	1.15E-05	2.31E-05	0	0	0	0	0	0	0	0	Zinc knuckle. The zinc		metal ion binding; nucleic
2549	0	0	0	0	0	0	0	0	0	0	0	4.57E-05	0	1	1.14E-05	2.28E-05	0	0	0	0	0	0	0	0	CDC/Septin. Septins are a	stress fiber [pmid 15485874]	GTP binding; nucleotide
2550	0	0	0	0	0	0	0	0	0	4.53E-05	0	0	0	1	1.13E-05	2.26E-05	0	0	0	0	0	0	0	0			
2551	0	0	0	0	0	0	0	0	0	0	0	0	4.46E-05	1	1.11E-05	2.23E-05	0	0	0	0	0	0	0	0	Ricin-type beta-trefoil;		sugar binding
2552	0	0	0	4.45E-05	0	1	1.11E-05	2.22E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2553	0	0	0	0	0	0	0	0	0	0	0	4.43E-05	0	1	1.11E-05	2.22E-05	0	0	0	0	0	0	0	0	Oxysterol binding protein		
2554	0	0	0	4.41E-05	0	1	1.1E-05	2.21E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2555	0	0	0	0	0	0	0	0	0	0	0	0	4.39E-05	1	1.1E-05	2.19E-05	0	0	0	0	0	0	0	0	ATP-dependent Clp		ligase activity; metal ion
2556	0	0	0	4.38E-05	0	1	1.1E-05	2.19E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2557	0	4.37E-05	0	0	0	1	1.09E-05	2.18E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	ANTH domain. AP180 is an	clathrin-coated vesicle;	actin binding; phospholipid
2558	0	0	0	4.35E-05	0	1	1.09E-05	2.18E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	preprotein translocase	intracellular	metal ion binding; nucleic
2559	0	0	0	4.33E-05	0	1	1.08E-05	2.17E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	glycine rich nucleic binding	intracellular; nucleus [pmid	DNA binding [pmid
2560	0	0	0	0	0	0	0	0	0	4.33E-05	0	0	0	1	1.08E-05	2.17E-05	0	0	0	0	0	0	0	0	Inositol polyphosphate		inositol or
2561	0	0	0	0	0	0	0	0	0	4.33E-05	0	0	0	1	1.08E-05	2.16E-05	0	0	0	0	0	0	0	0	Importin, protein involved in	cytoplasm; nuclear pore;	binding; protein transporter
2562	0	0	0	0	0	0	0	0	0	4.2E-05	0	0	0	1	1.05E-05	2.1E-05	0	0	0	0	0	0	0	0	Domain Homologous to E6-	intracellular	ubiquitin-protein ligase
2563	0	0	0	0	0	0	0	0	0	0	0	0	4.16E-05	1	1.04E-05	2.08E-05	0	0	0	0	0	0	0	0			
2564	0	0	0	0	0	0	0	0	0	0	0	4.07E-05	0	1	1.02E-05	2.03E-05	0	0	0	0	0	0	0	0	RING-finger (Really	nucleus [pmid 12176013]	DNA binding; ligase activity;
2565	0	4.02E-05	0	0	0	1	1.01E-05	2.01E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	S-100/ICaBP-like domain;	cytoplasmic membrane-bound	calcium ion binding [pmid
2566	0	0	0	0	0	0	0	0	0	0	0	0	3.95E-05	1	9.87E-06	1.97E-05	0	0	0	0	0	0	0	0			
2567	0	0	0	0	0	0	0	0	0	3.84E-05	0	0	0	1	9.59E-06	1.92E-05	0	0	0	0	0	0	0	0			
2568	0	0	0	3.74E-05	0	1	9.36E-06	1.87E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2569	0	0	0	3.71E-05	0	1	9.27E-06	1.85E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2570	0	0	0	3.55E-05	0	1	8.88E-06	1.78E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2571	0	0	3.48E-05	0	0	1	8.69E-06	1.74E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2572	0	0	0	0	0	0	0	0	0	0	0	0	3.46E-05	1	8.66E-06	1.73E-05	0	0	0	0	0	0	0	0	Src homology 3 domains;	myosin	actin binding; ATP binding;
2573	0	0	0	0	0	0	0	0	0	0	0	3.37E-05	0	1	8.43E-06	1.69E-05	0	0	0	0	0	0	0	0	DDT domain. This domain	cytoplasm [pmid 7621746];	DNA-dependent ATPase
2574	0	0	0	0	0	0	0	0	0	0	0	3.28E-05	0	1	8.19E-06	1.64E-05	0	0	0	0	0	0	0	0	Myristoyl-CoA:protein N-		acyltransferase activity;
2575	0	3.16E-05	0	0	0	1	7.91E-06	1.58E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2576	0	0	0	3.13E-05	0	1	7.84E-06	1.57E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	B-Box-type zinc finger; zinc	intracellular; nucleus	DNA binding; metal ion
2577	0	0	0	0	0	0	0	0	0	0	0	2.95E-05	0	1	7.38E-06	1.48E-05	0	0	0	0	0	0	0	0	VWA Copine: Copines are		
2578	0	0	0	0	0	0	0	0	0	0	0	2.87E-05	0	1	7.18E-06	1.44E-05	0	0	0	0	0	0	0	0	MutS3 homolog in	nucleus [pmid 8942985]	ATP binding; damaged DNA
2579	0	0	0	0	0	0	0	0	0	0	0	0	2.87E-05	1	7.17E-06	1.43E-05	0	0	0	0	0	0	0	0	Helicase superfamily c-	intracellular; nucleus	ATP binding; ATP-dependent
2580	0	2.87E-05	0	0	0	1	7.16E-06	1.43E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	RecF/RecN/SMC N	centrosome [pmid 9647649]	protein kinase binding [pmid
2581	0	0	0	0	0	0	0	0	0	0	0	2.86E-05	0	1	7.16E-06	1.43E-05	0	0	0	0	0	0	0	0			
2582	0	0	0	0	0	0	0	0	0	0	0	0	2.82E-05	1	7.05E-06	1.41E-05	0	0	0	0	0	0	0	0			
2583	0	0	0	2.78E-05	0	1	6.95E-06	1.39E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CID (CTD-Interacting		nucleotide binding; RNA
2584	0	0	0	2.36E-05	0	1	5.91E-06	1.18E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Zinc knuckle. The zinc		metal ion binding; nucleic
2585	0	0	0	2.36E-05	0	1	5.9E-06	1.18E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Chromosome segregation	Golgi apparatus [pmid	transporter activity [pmid
2586	0	0	0	2.35E-05	0	1	5.88E-06	1.18E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Spectrin repeats, found in		
2587	0	0	0	2.28E-05	0	1	5.71E-06	1.14E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	SWIRM domain. This	chromatin; nucleoplasm [pmid	chromatin binding; DNA
2588	0	0	0	0	0	0	0	0	0	0	0	2.19E-05	0	1	5.48E-06	1.1E-05	0	0	0	0	0	0	0	0			
2589	0	0	0	1.98E-05	0	1	4.95E-06	9.9E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2590	0	0	0	0	0	0	0	0	0	1.74E-05	0	0	0	1	4.35E-06	8.7E-06	0	0	0	0	0	0	0	0			
2591	0	0	0	1.59E-05	0	1	3.97E-06	7.94E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
2592	0	0	0	1.35E-05	0	1	3.37E-06	6.75E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Ankyrin repeat. There's no		RNA binding
2593	0	0	0	8.9E-06	0	1	2.23E-06	4.45E-06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CXXC zinc finger. This	nucleus [pmid 11313484]	ATP binding; DNA binding;
2594	0.005435	0.003739	0.006126	0.000832	0.000369	5	0.004033	0.002358	0.006433	0.002682	0.0038	0.00034	0.001808	5	0.002816	0.002598	0	0.000846	0.000893	0.0012	0.001503	0.000575	0.000958	0.000761	Protein kinase C conserved	integral to membrane;	
2595	0.001203	0.001557	0.002189	0.000505	0.002588	5	0.001363	0.000703	0.00047	0.00183	0.000741	0.000571	0.001423	5	0.001073	0.000661	0	0	0.001197	0.001615	0.001544	0.000907	0.000944	0.000635	Glycosyl hydrolases family	endoplasmic reticulum	hydrolase activity; hydrolase
2596	0.001941	0.001224	0.000173	0.000472	0.00075	5	0.000953	0.000794	0.001635	0.001384	0.003219	9.02E-05	0.000353	5	0.000866	0.000758	0	0	0.000341	0.000668	0.00093	0.000404	0.00045	0.000396			

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel
2597	9	0.00407	7	0.004424	0.919853		ENSG00000118705:E	RPN2			gi|35493916|ref|NP_	ribophorin II precursor [Homo	631	69284	5.7	4
2598	9	0.003376	7	0.002292	1.473132		ENSG00000117242:E	DDOST			gi|20070197|ref|NP_	dolichyl-diphosphooligosacch	456	50702	6.4	2
2599	9	0.003289	7	0.004089	0.804313		ENSG00000127022:E	CANX			gi|66933005|ref|NP_	calnexin precursor [Homo sa	592	67568	4.6	1
2600	9	0.003267	8	0.003386	0.964865		ENSG00000163902:E	RPN1			gi|4506675|ref|NP_0	ribophorin I precursor [Homo	607	68569	6.4	1
2601	9	0.000984	8	0.003631	0.270981		ENSG00000115275:E	GCS1			gi|149999606|ref|NP	mannosyl-oligosaccharide gl	837	91918	8.9	1
2602	8	0.003807	8	0.002361	1.612516		ENSG00000148248:E	SURF4			gi|19557691|ref|NP_	surfeit 4 [Homo sapiens]	269	30394	7.8	5
2603	8	0.001644	7	0.012806	0.128383		ENSG00000004939:E	SLC4A1			gi|4507021|ref|NP_0	solute carrier family 4, anion	911	101792	5.2	11
2604	8	0.000812	8	0.008862	0.091681		ENSG00000127948:E	POR			gi|127139033|ref|NP	cytochrome P450 reductase	680	77048	5.6	1
2605	8	0.000453	6	0.001644	0.275677		ENSG00000110090:E	CPT1A			gi|73623028|ref|NP_	carnitine palmitoyltransferase	756	86239	8.4	2
2606	7	0.001687	6	0.001346	1.253351		NA:ENSMUSG00000	SEC22B			gi|94429050|ref|NP_	SEC22 vesicle trafficking pro	215	24593	6.9	1
2607	7	0.001601	7	0.001253	1.277655		ENSG00000058262:E	SEC61A1			gi|7019415|ref|NP_0	Sec61 alpha 1 subunit [Homo	476	52265	8.1	10
2608	7	0.001438	7	0.001112	1.293369		ENSG00000198171:E	C20orf116			gi|13027602|ref|NP_	hypothetical protein LOC659	314	35611	5.1	1
2609	7	0.00135	6	0.001852	0.728832		ENSG00000149084:E	HSD17B12			gi|7705855|ref|NP_0	hydroxysteroid (17-beta) deh	312	34324	9.3	3
2610	7	0.00109	6	0.000312	3.497465		ENSG00000204267:E	TAP2			gi|73747915|ref|NP_	transporter 2, ATP-binding ca	703	77695	7.9	6
2611	7	0.000914	6	0.000224	4.083687		ENSG00000101290:E	CDS2			gi|20143480|ref|NP_	phosphatidate cytidylyltransfe	445	51418	7.1	8
2612	7	0.000796	7	0.00096	0.829292		ENSG00000211456:E	SACM1L			gi|41281579|ref|NP_	suppressor of actin 1 [Homo	587	66979	7.3	2
2613	7	0.000724	6	0.000502	1.443314		ENSG00000174437:E	ATP2A2			gi|24638454|ref|NP_	ATPase, Ca++ transporting,	1042	114757	5.3	8
2614	7	0.000497	8	0.000538	0.925305		ENSG00000110719:E	TCIRG1			gi|19924145|ref|NP_	T-cell, immune regulator 1 is	830	92968	7.1	8
2615	7	0.000477	8	0.00049	0.973038		ENSG00000147649:E	MTDH			gi|30520310|ref|NP_	metadherin [Homo sapiens]	582	63823	9.3	1
2616	7	8.45E-05	6	0.000175	0.482079		ENSG00000135636:E	DYSF			gi|4503431|ref|NP_0	dysferlin [Homo sapiens]	2080	237293	5.6	1
2617	6	0.003332	6	0.00205	1.625166		ENSG00000171557:E	FGG			gi|70906437|ref|NP_	fibrinogen, gamma chain isof	437	49497	6.1	1
2618	6	0.002939	7	0.03209	0.091597		ENSG00000103018:E	CYB5B			gi|83921614|ref|NP_	cytochrome b5 outer mitocho	150	16695	5	1
2619	6	0.002389	7	0.001072	2.22908		ENSG00000164040:E	PGRMC2			gi|5453916|ref|NP_0	progesterone receptor memb	223	23818	4.9	1
2620	6	0.001615	4	0.000794	2.033751		ENSG00000144746:E	ARL6IP5			gi|5453704|ref|NP_0	ADP-ribosylation-like factor 6	188	21615	9.8	3
2621	6	0.001312	2	0.000528	2.484284		ENSG00000169223:E	LMAN2			gi|5803023|ref|NP_0	lectin, mannose-binding 2 [H	356	40229	7	1
2622	6	0.000912	5	0.001007	0.90505		ENSG00000170348:E	TMED10			gi|98986464|ref|NP_	transmembrane emp24 doma	219	24976	7.5	2
2623	6	0.000843	5	0.000813	1.036601		ENSG00000103415:E	HMOX2			gi|8051608|ref|NP_0	heme oxygenase (decyclizing	316	36033	5.4	1
2624	6	0.000738	8	0.002732	0.270227		ENSG00000184743:E	ATLA3			gi|45827806|ref|NP_	atlastin 3 [Homo sapiens]	541	60542	5.7	2
2625	6	0.000721	8	0.0029	0.248733		ENSG00000074695:E	LMAN1			gi|5031873|ref|NP_0	lectin, mannose-binding, 1 pr	510	57549	6.8	1
2626	6	0.000594	1	0.000337	1.764567		ENSG00000138073:E	PREB			gi|7019503|ref|NP_0	prolactin regulatory element	417	45468	7.9	2
2627	6	0.000516	4	0.000209	2.471704		ENSG00000115310:E	RTN4			gi|24431933|ref|NP_	reticulon 4 isoform B [Homo	373	40318	4.8	2
2628	6	0.000438	2	0.000413	1.059677		ENSG00000163399:E	ATP1A1			gi|21361181|ref|NP_	Na+/K+ -ATPase alpha 1 sub	1023	112896	5.5	10
2629	6	0.000374	5	0.000339	1.104376		ENSG00000168003:E	SLC3A2			gi|61744475|ref|NP_	solute carrier family 3 (activa	661	71123	5	1
2630	6	0.000268	3	0.000105	2.559167		ENSG00000100258:E	TMEM112B			gi|24308356|ref|NP_	lipase maturation factor 2 [H	682	76915	10	6
2631	6	0.000223	4	6.24E-05	3.58053		ENSG00000149428:E	HYOU1			gi|5453832|ref|NP_0	hypoxia up-regulated 1 precu	999	111335	5.2	1
2632	6	0.000176	5	0.000178	0.989877		ENSG00000105726:E	ATP13A1			gi|9966897|ref|NP_0	ATPase type 13A1 [Homo sa	1086	121110	7.8	6
2633	6	0.000171	6	0.000267	0.64182		ENSG00000025796:E	SEC63			gi|6005872|ref|NP_0	SEC63-like protein [Homo sa	760	87997	5.3	3
2634	5	0.001648	6	0.001415	1.164339		ENSG00000147955:E	OPRS1			gi|5032117|ref|NP_0	opioid receptor, sigma 1 isof	223	25128	6	1
2635	5	0.001237	8	0.010376	0.119229		ENSG00000093010:E	COMT			gi|4502969|ref|NP_0	catechol-O-methyltransferase	271	30037	5.5	1
2636	5	0.001115	6	0.000715	1.559526		ENSG00000110917:E	MLEC; KIAA0152			gi|7661948|ref|NP_0	malectin precursor ; hypothet	292	32234	5.4	1
2637	5	0.000906	6	0.002711	0.334294		ENSG00000101558:E	VAPA			gi|94721252|ref|NP_	vesicle-associated membran	249	27893	8.6	1
2638	5	0.000625	5	0.00018	3.474205		ENSG00000005961:E	ITGA2B			gi|88758615|ref|NP_	integrin alpha 2b preproprote	1039	113377	5.4	1
2639	5	0.000583	7	0.004092	0.14252		ENSG00000099797:E	GPSN2			gi|24475816|ref|NP_	glycoprotein, synaptic 2 [Hom	308	36034	9.4	4
2640	5	0.000551	4	0.000719	0.766853		ENSG00000124783:E	SSR1			gi|4507237|ref|NP_0	signal sequence receptor, alp	286	32183	4.5	1
2641	5	0.000441	4	0.000155	2.850312		ENSG00000095303:E	PTGS1			gi|18104967|ref|NP_	prostaglandin-endoperoxide	599	68686	7.2	1
2642	5	0.000409	7	0.001662	0.246047		ENSG00000074696:E	PTPLAD1			gi|117168248|ref|NP	protein tyrosine phosphatase	362	43160	8.9	5
2643	5	0.000355	7	0.001696	0.209505		ENSG00000108829:E	LRRC59			gi|40254924|ref|NP_	leucine rich repeat containing	307	34930	9.6	1
2644	5	0.000353	6	0.000443	0.797513		ENSG00000116521:E	SCAMP3			gi|16445419|ref|NP_	secretory carrier membrane	347	38287	7.6	4
2645	5	0.000353	6	0.000391	0.900559		ENSG00000125505:E	LENG4			gi|23308572|ref|NP_	leukocyte receptor cluster (L	472	52775	9	5
2646	5	0.000344	6	0.000905	0.380336		ENSG00000150093:E	ITGB1			gi|19743815|ref|NP_	integrin beta 1 isoform 1B pr	789	87446	5.5	1
2647	5	0.000327	6	0.000434	0.754431		ENSG00000185187:E	SIGIRR			gi|11141877|ref|NP_	single Ig IL-1R-related molec	410	45707	6.6	1
2648	5	0.000327	6	0.000374	0.872997		ENSG00000198363:E	ASPH			gi|14589866|ref|NP_	aspartate beta-hydroxylase is	758	85863	5	1
2649	5	0.000279	6	0.000285	0.979674		ENSG00000104853:E	CLPTM1			gi|4502897|ref|NP_0	cleft lip and palate associated	669	76097	6.3	5
2650	5	0.000253	3	6.14E-05	4.118586		ENSG00000101294:E	HM13			gi|23308607|ref|NP_	minor histocompatibility antig	377	41488	6.4	7
2651	5	0.000246	3	8.17E-05	3.011292		ENSG00000072274:E	TFRC			gi|4507457|ref|NP_0	transferrin receptor [Homo sa	760	84901	6.6	1
2652	5	0.000235	5	7.41E-05	3.168642		ENSG00000084073:E	ZMPSTE24			gi|18379366|ref|NP_	zinc metalloproteinase STE2	475	54813	7.5	7
2653	5	0.000199	6	0.001488	0.133613		ENSG00000185825:E	BCAP31			gi|32171186|ref|NP_	B-cell receptor-associated pr	246	27992	8.4	3
2654	5	0.000127	2	3.56E-05	3.575722		ENSG00000091039:E	OSBPL8			gi|18079218|ref|NP_	oxysterol-binding protein-like	889	101196	7	1
2655	5	0.000126	4	0.000133	0.940279		ENSG00000090863:E	GLG1			gi|54633312|ref|NP_	golgi apparatus protein 1 [Ho	1203	137222	6.9	1
2656	5	0.000103	3	0.000115	0.897763		ENSG00000143641:E	GALNT2			gi|4758412|ref|NP_0	polypeptide N-acetylgalactos	571	64733	8.4	1
2657	5	9.8E-05	3	2.06E-05	4.74781		ENSG00000126777:E	KTN1			gi|118498356|ref|NP	kinectin 1 isoform a [Homo s	1357	156275	5.6	1
2658	5	8.22E-05	8	0.01996	0.004121		ENSG00000143819:E	EPHX1			gi|4503583|ref|NP_0	epoxide hydrolase 1, microso	455	52949	7.3	0
2659	5	6.78E-05	5	0.000202	0.33573		ENSG00000099219:E	ERMP1			gi|55749804|ref|NP_	aminopeptidase Fxna [Homo	904	100231	7.5	8
2660	5	6.59E-05	3	2.23E-05	2.950422		ENSG00000123104:E	ITPR2			gi|95147335|ref|NP_	inositol 1,4,5-triphosphate re	2701	308062	6.4	6
2661	4	0.001231	4	0.001981	0.621465		ENSG00000189043:E	NDUFA4			gi|4505357|ref|NP_0	NADH dehydrogenase (ubiqu	81	9370	9.4	1
2662	4	0.001171	7	0.000606	1.932896		ENSG00000124222:E	STX16			gi|34447229|ref|NP_	syntaxin 16 isoform b [Homo	304	34813	6.2	1
2663	4	0.000888	3	0.000246	3.606555		ENSG00000143198:E	MGST3			gi|4758714|ref|NP_0	microsomal glutathione S-tra	152	16516	9.4	4
2664	4	0.000779	4	0.000374	2.083714		ENSG00000100216:E	TOMM22			gi|9910382|ref|NP_0	mitochondrial import receptor	142	15522	4.3	1
2665	4	0.000649	2	0.000326	1.989144		ENSG00000129128:E	SPCS3			gi|11345462|ref|NP_	signal peptidase complex sub	180	20313	8.6	1
2666	4	0.000645	5	0.000301	2.146339		ENSG00000118363:E	SPCS2			gi|7661908|ref|NP_0	signal peptidase complex sub	123	14268	8.6	1
2667	4	0.000493	6	0.001509	0.327028		ENSG00000184840:E	TMED9			gi|39725636|ref|NP_	transmembrane emp24 prote	235	27277	8	2
2668	4	0.000366	2	7.42E-05	4.930377		ENSG00000103502:E	CDIPT			gi|5453906|ref|NP_0	CDP-diacylglycerol--inositol 3	213	23539	8	4
2669	4	0.000364	6	0.010092	0.036111		ENSG00000105518:E	TMEM205			gi|63055043|ref|NP_	transmembrane protein 205	189	21198	8.6	4
2670	4	0.000347	3	0.00054	0.641858		ENSG00000165644:E	COMTD1			gi|31542747|ref|NP_	catechol-O-methyltransferase	262	28809	8.4	1
2671	4	0.000323	2	6.58E-05	4.905199		ENSG00000100997:E	ABHD12			gi|109689718|ref|NP	abhydrolase domain containi	398	45097	8.6	1
2672	4	0.000299	6	0.001099	0.272128		ENSG00000112473:E	SLC39A7			gi|117553619|ref|NP	solute carrier family 39, mem	469	50118	6.9	7
2673	4	0.000295	2	0.000202	1.463268		ENSG00000101152:E	DNAJC5			gi|45504382|ref|NP_	DnaJ (Hsp40) homolog, subf	198	22149	5.1	1
2674	4	0.000292	4	6.64E-05	4.400476		ENSG00000008952:E	TLOC1			gi|4507525|ref|NP_0	translocation protein 1 [Homo	399	45862	7.1	2
2675	4	0.00025	6	0.001376	0.181441		ENSG00000105135:E	OR10B1P			gi|21361361|ref|NP_	ilvB (bacterial acetolactate sy	632	67868	8.1	1
2676	4	0.000225	1	0.00019	1.18494		ENSG00000168958:E	C2orf33			gi|31377607|ref|NP_	hypothetical protein LOC569	342	38465	9	1
2677	4	0.000216	5	0.000352	0.613387		ENSG00000109133:E	TMEM33			gi|8922491|ref|NP_0	transmembrane protein 33 [H	247	27951	9.7	3
2678	4	0.0002	6	0.000439	0.456227		ENSG00000131446:E	MGAT1			gi|4505161|ref|NP_0	mannosyl (alpha-1,3-)-glycop	445	50862	9.2	1
2679	4	0.000183	5	0.0001	1.830458		ENSG00000087111:E	PIGS			gi|15088795|ref|NP_	phosphatidylinositol glycan a	555	61656	6.5	2
2680	4	0.000181	7	0.000457	0.396301		ENSG00000115307:E	AUP1			gi|31712030|ref|NP_	ancient ubiquitous protein 1 [	410	45787	8.6	1
2681	4	0.00018	2	0.000111	1.616275		ENSG00000179820:E	MYADM			gi|66932929|ref|NP_	myeloid-associated differenti	322	35274	8.2	8
2682	4	0.000142	4	5.03E-05	2.822885		ENSG00000058668:E	ATP2B4			gi|48255957|ref|NP_	plasma membrane calcium A	1205	133930	6.4	8
2683	4	0.000141	5	8.65E-05	1.624856		ENSG00000141458:E	NPC1			gi|4557803|ref|NP_0	Niemann-Pick disease, type	1278	142148	5.4	12
2684	4	0.000121	6	0.001738	0.069812		ENSG00000125304:E	TM9SF2			gi|4758874|ref|NP_0	transmembrane 9 superfamil	663	75776	7.4	9
2685	4	0.000117	2	2.6E-05	4.512137		ENSG00000165282:E	PIGO			gi|23397648|ref|NP_	phosphatidylinositol glycan a	1089	118699	8.1	14
2686	4	0.000116	2	3.49E-05	3.326494		ENSG00000162736:E	NCSTN			gi|24638433|ref|NP_	nicastrin precursor [Homo sa	709	78411	6	1
2687	4	0.000104	8	0.008475	0.012294		ENSG00000140284:E	SLC27A2			gi|4503653|ref|NP_0	solute carrier family 27 (fatty	620	70312	8.4	3
2688	4	9.71E-05	1	0.000102	0.952342		ENSG00000119777:E	TMEM214			gi|134152721|ref|NP	hypothetical protein LOC548	689	77151	9.1	0
2689	4	9.63E-05	6	0.010192	0.009451		ENSG00000072210:E	ALDH3A2			gi|4557303|ref|NP_0	aldehyde dehydrogenase 3A	485	54848	7.9	1
2690	4	9.51E-05	2	5.09E-05	1.868626		ENSG00000156026:E	CCDC109A; LOC294560			gi|24308400|ref|NP_	coiled-coil domain containing	350	39758	8.6	3
2691	4	8.84E-05	7	0.000759	0.116469		ENSG00000150527:E	CTAGE5			gi|42740897|ref|NP_	CTAGE family, member 5 iso	804	90996	5.2	1
2692	4	8.58E-05	7	0.003154	0.027197		ENSG00000117528:E	ABCD3			gi|4506341|ref|NP_0	ATP-binding cassette, sub-fa	659	75476	9.4	3
2693	4	6.85E-05	4	9.33E-05	0.733917		ENSG00000173852:E	DPY19L1			gi|148839335|ref|NP	dpy-19-like 1 [Homo sapiens]	675	77319	9	10
2694	4	5.31E-05	6	0.000494	0.107352		ENSG00000077147:E	TM9SF3			gi|33859833|ref|NP_	transmembrane 9 superfamil	721	81802	8.4	9
2695	4	4.12E-05	5	3.26E-05	1.261922		ENSG00000198802:E	PECAM1			gi|110347451|ref|NP	platelet/endothelial cell adhe	738	82536	7	1
2696	4	3.93E-05	4	2.04E-05	1.923214		ENSG00000138119:E	FER1L3			gi|19718759|ref|NP_	myoferlin isoform b [Homo sa	2048	233474	6.2	1
2697	3	0.000784	5	0.001229	0.638038		ENSG00000117500:E	TMED5			gi|19923442|ref|NP_	transmembrane emp24 prote	229	26017	4.8	2
2698	3	0.000501	5	0.000462	1.083533		ENSG00000143183:E	TMCO1			gi|24308133|ref|NP_	transmembrane and coiled-c	188	21175	9.7	2
2699	3	0.000321	5	0.000424	0.758577		ENSG00000125037:E	TMEM111			gi|8923857|ref|NP_0	transmembrane protein 111 [	261	29952	6.8	2
2700	3	0.00029	4	0.000258	1.123202		ENSG00000079950:E	STX7			gi|4507295|ref|NP_0	syntaxin 7 [Homo sapiens]	261	29846	5.6	1
2701	3	0.000276	3	5.67E-05	4.871041		ENSG00000170540:E	ARL6IP1			gi|24308007|ref|NP_	ADP-ribosylation factor-like 6	203	23363	9.3	4
2702	3	0.000267	1	6.57E-05	4.05695		ENSG00000130193:E	C8orf55			gi|7706200|ref|NP_0	mesenchymal stem cell prote	208	23865	9.6	1
2703	3	0.000248	7	0.000898	0.275993		ENSG00000116133:E	DHCR24			gi|13375618|ref|NP_	24-dehydrocholesterol reduc	516	60101	8.2	2
2704	3	0.000246	4	0.000658	0.373591		ENSG00000110651:E	CD81			gi|4757944|ref|NP_0	CD81 antigen [Homo sapiens	236	25809	5.3	4
2705	3	0.000234	4	0.000445	0.524528		ENSG00000167130:E	DOLPP1			gi|30794376|ref|NP_	dolichyl pyrophosphate phos	238	27031	9.4	4
2706	3	0.000204	5	0.000404	0.503913		ENSG00000172954:E	LYCAT			gi|42558246|ref|NP_	lysocardiolipin acyltransferas	414	48920	8.6	3
2707	3	0.000187	4	0.000118	1.579581		ENSG00000049656:E	CLPTM1L			gi|21359965|ref|NP_	CLPTM1-like [Homo sapiens	538	62229	8.6	6
2708	3	0.000185	2	4.38E-05	4.234505		ENSG00000075790:E	BCAP29			gi|56549091|ref|NP_	B-cell receptor-associated pr	241	28320	9.5	3
2709	3	0.000185	4	0.000192	0.960156		ENSG00000178537:E	SLC25A20			gi|4557403|ref|NP_0	carnitine/acylcarnitine translo	301	32944	9.4	3
2710	3	0.00017	3	0.000468	0.363993		ENSG00000102050:E	PRAF2			gi|6005794|ref|NP_0	PRA1 domain family, membe	178	19258	9.2	4
2711	3	0.000159	4	0.000112	1.422766		ENSG00000116685:E	KIAA2013			gi|25286703|ref|NP_	hypothetical protein LOC902	634	69157	8.2	2
2712	3	0.000143	3	0.000126	1.131858		ENSG00000179036:E	VAMP2			gi|7657675|ref|NP_0	vesicle-associated membran	116	12649	8.1	1
2713	3	0.000139	3	0.000114	1.22424		ENSG00000138617:E	PARP16			gi|46195794|ref|NP_	poly (ADP-ribose) polymeras	323	36470	9	1
2714	3	0.000139	4	6.43E-05	2.157366		ENSG00000099968:E	BCL2L13			gi|45243501|ref|NP_	BCL2-like 13 (apoptosis facil	485	52723	4.4	1
2715	3	0.00012	4	4.24E-05	2.832422		ENSG00000116688:E	MFN2			gi|7662004|ref|NP_0	mitofusin 2 [Homo sapiens]	757	86402	7	1
2716	3	0.000119	1	0.0002	0.594213		ENSG00000141699:E	FAM134C			gi|30023820|ref|NP_	hypothetical protein LOC162	466	51396	5	3
2717	3	0.000115	5	0.000424	0.271877		ENSG00000166794:E	PPIB			gi|4758950|ref|NP_0	peptidylprolyl isomerase B pr	216	23743	9.4	1
2718	3	0.000103	4	0.000126	0.818546		ENSG00000169682:E	SPNS1			gi|14042968|ref|NP_	spinster homolog 1 [Homo sa	528	56630	6.6	11
2719	3	9.72E-05	5	0.000939	0.103579		ENSG00000137824:E	FAM82C			gi|8922532|ref|NP_0	family with sequence similari	470	52118	5.1	1
2720	3	9.44E-05	4	0.000167	0.563629		ENSG00000100292:E	HMOX1			gi|4504437|ref|NP_0	heme oxygenase (decyclizing	288	32819	8.2	1
2721	3	9.39E-05	2	0.000158	0.594558		ENSG00000185000:E	LOC727765			gi|169172688|ref|XP	PREDICTED: hypothetical pr	488	55278	9.3	9
2722	3	9.25E-05	6	0.001166	0.079345		ENSG00000101337:E	TM9SF4			gi|7662028|ref|NP_0	transmembrane 9 superfamil	625	72541	6.7	9
2723	3	9.02E-05	5	0.000681	0.132558		ENSG00000135218:E	CD36			gi|48375180|ref|NP_	CD36 antigen [Homo sapiens	472	53053	8	2
2724	3	8.9E-05	6	0.001285	0.069216		ENSG00000112697:E	TMEM30A			gi|8922720|ref|NP_0	transmembrane protein 30A	361	40684	8.6	2
2725	3	8.67E-05	4	5.01E-05	1.729503		ENSG00000160216:E	AGPAT3			gi|83267874|ref|NP_	1-acylglycerol-3-phosphate O	376	43381	8.7	3
2726	3	8.54E-05	5	0.000243	0.351189		ENSG00000120697:E	ALG5			gi|7019323|ref|NP_0	asparagine-linked glycosylati	324	36946	9.3	1
2727	3	8.15E-05	4	8.54E-05	0.954136		ENSG00000168818:E	STX18			gi|8394376|ref|NP_0	syntaxin 18 [Homo sapiens]	335	38674	5.5	1
2728	3	7.8E-05	6	0.000665	0.117157		ENSG00000105701:E	FKBP8			gi|52630440|ref|NP_	FK506-binding protein 8 [Hor	413	44649	4.8	1
2729	3	7.76E-05	4	0.00057	0.13613		ENSG00000164897:E	TMUB1			gi|13899257|ref|NP_	transmembrane and ubiquitir	246	26261	5.7	3
2730	3	7.74E-05	3	5.22E-05	1.481736		ENSG00000178732:E	GP5			gi|4758460|ref|NP_0	glycoprotein V (platelet) [Hor	560	60959	9.6	1
2731	3	7.23E-05	6	0.001067	0.067691		ENSG00000143418:E	LASS2			gi|32455256|ref|NP_	LAG1 longevity assurance 2	380	44876	9	5
2732	3	7.01E-05	5	0.000139	0.504088		ENSG00000125844:E	RRBP1			gi|110611220|ref|NP	ribosome binding protein 1 [H	977	108655	5.5	1
2733	3	6.79E-05	6	0.000714	0.095056		ENSG00000172893:E	DHCR7			gi|119943112|ref|NP	7-dehydrocholesterol reducta	475	54489	8.7	6
2734	3	6.21E-05	7	0.004408	0.014082		ENSG00000138760:E	SCARB2			gi|5031631|ref|NP_0	scavenger receptor class B,	478	54290	5.1	2
2735	3	5.97E-05	3	2.45E-05	2.434015		ENSG00000137845:E	ADAM10			gi|4557251|ref|NP_0	ADAM metallopeptidase dom	748	84142	7.8	1
2736	3	5.57E-05	2	3.13E-05	1.780649		ENSG00000080815:E	PSEN1			gi|4506163|ref|NP_0	presenilin 1 [Homo sapiens]	467	52668	5.3	9
2737	3	5.44E-05	3	0.000309	0.176143		ENSG00000108587:E	GOSR1			gi|4758456|ref|NP_0	golgi SNAP receptor complex	250	28613	9.4	1
2738	3	5.12E-05	2	7.66E-05	0.668412		ENSG00000071553:E	ATP6AP1			gi|17136148|ref|NP_	ATPase, H+ transporting, lys	470	52026	6.1	2
2739	3	4.71E-05	5	2.71E-05	1.735649		ENSG00000157637:E	SLC38A10			gi|83921602|ref|NP_	solute carrier family 38, mem	1119	119762	5.7	9
2740	3	4.65E-05	6	0.000432	0.107553		ENSG00000198162:E	MAN1A2			gi|5729913|ref|NP_0	mannosidase, alpha, class 1	641	73004	7.6	1
2741	3	4.54E-05	5	0.000139	0.326631		ENSG00000160746:E	TMEM16K			gi|94536803|ref|NP_	transmembrane protein 16K	660	76329	7.4	8
2742	3	4.38E-05	1	1.25E-05	3.502346		ENSG00000121542:E	SEC22A			gi|14591919|ref|NP_	SEC22 vesicle trafficking pro	307	34948	8.2	4
2743	3	3.76E-05	5	0.000339	0.11099		ENSG00000165782:E	TMEM55B			gi|154816184|ref|NP	transmembrane protein 55B	277	29470	8.9	2

rk	NEs detected # out of 10 runs	NEs dNSAF_A VG	MMs detected # out of 8 runs	MMs dNSAF_A VG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	SIGNALP_HMM_TMHMM_TYPE (S=signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_PROB	RESTING LYMPHOCYTES NEs: HsNaOH-NE_NT_lymphocytes_CNBr_T1_1_dNSAF	HsNaOH-NE_NT_lymphocytes_T1_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_T1_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-dNEs Detected # Out of 5	NT-dNSAF AVG	NT-dNSAF SDV	PHA-TREATED LYMPHOCYTES NEs: HsNaOH-NE_PHA_lymphocytes_CNBr_T1_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_T1_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_T1_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-dNEs Detected # Out of 5	PHA-dNSAF AVG	PHA-dNSAF SDV	MMs: MmNaOH-MM_liver_CNBrT1_1_dNSAF	MmNaOH-MM_liver_CNBrT1_2_dNSAF	RnNaOH-MM_liver_T1_1_dNSAF	RnNaOH-MM_liver_T1_2_dNSAF	RnNaOH-MM_liver_T1_3_dNSAF	RnNaOH-MM_liver_T1_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
2744	3	3.47E-05	2	2.67E-05	1.300175			ENSGO00000004693	PEX3			4505727(ref)NP_0	peroxisomal biogenesis facto	373	42140	8.2		0	o	A	31	0.043	0	6.25E-05	0	9.47E-05	0	2	3.93E-05	4.73E-05	0	0	0.000122	0	0	0	0	0	0.000128	8.42E-05	0	Peroxin-3. Peroxin-3 is a	integral to peroxisomal	protein binding [pmid
2745	3	3.39E-05	4	6.27E-05	0.539995			ENSGO00000135048	ETMEM2			gi	7019555	ref	NP_	transmembrane protein 2 [H	365	39783	8.3		1	83-105o	Q	22	0	0	5.06E-05	0	2.55E-05	0	2	1.9E-05	2.42E-05	0	0	0.000195	0	0	0	0	0	0.000268	0.000131	0	7.92E-05	2.36E-05	0		integral to membrane;	
2746	3	3.37E-05	3	7.76E-05	0.434741			ENSGO00000170557	DPP4			gi	7185694	ref	NP_	dipeptidyl peptidase IV [Homo	766	88531	6.2		1	27-29o	A	23	0.622	0	2.31E-05	0	0.0001	0	2	1.57E-05	1.99E-05	0	0	0.000582	0	0	0	0	0	0.000843	0.00577	0.004578	0.005265	0.005478	0.005367	Dipeptidyl peptidase IV	integral to membrane;	aminopeptidase activity;
2747	3	3.22E-05	3	7.76E-05	0.414741			ENSGO00000130150	MOSPD2			gi	22749197	ref	NP_	motile sperm domain contain	519	59746	6		1	o403-515	Q	0	0	0	3.41E-05	0	0	0	2	3.56E-05	4.31E-05	0	0	0.000195	0	0	0	0	0	0.000236	0.000134	0	0.000231		0		Sec14p-like lipid-binding	structural molecule activity
2748	3	3.16E-05	3	0.000199	0.158744			ENSGO00000116199	FAM20B			gi	7662150	ref	NP_	hypothetical protein LOC991	409	48433	6.9		1	7-25o	S	25	0.537	0	5.7E-05	0	8.64E-05	0	2	3.59E-05	4.31E-05	0	0	0.000111	0.00031	0	0	0	0	0.000173	0.00031	0	0.000153		0		Protein of unknown function	
2749	3	2.68E-05	3	0.000465	0.057588			ENSGO00000100926	ETMB7			gi	21361315	ref	NP_	transmembrane 9 superfamil	606	68981	7.2		9	o236-258S	S	28	0.99	0	7.7E-05	0	6.33E-05	0	2	1.92E-05	3.85E-05	0	0	0.000157	0.000308	0.00408	0.00283	0.00425	0.00426	Endomembrane protein 70.	integral to membrane [pmid	transporter activity
2750	3	1.34E-05	5	0.000302	0.044429			ENSGO00000119787	ARL6IP2			gi	11641303	ref	NP_	ADP-ribosylation factor-like 6	579	66159	6		1	o475-497d	Q	41	0.025	0	4.03E-05	0	0	0	1	1.01E-05	2.01E-05	2.82E-05	0	0.000792	0.00059	0.000165	0.000843	0.000223	0		Guanylate-binding protein		GTP binding; GTPase
2751	3	1.33E-05	1	5.51E-06	2.421633			ENSGO00000164889	SLC4A2			gi	15607147	ref	NP_	solute carrier family 4, anion	1241	137009	6.3		11	o709-731i	Q	0	0	0	5.64E-05	0	1.42E-05	0	2	1.77E-05	2.67E-05	0	0	0	0	0	0	0	0	9.04E-06	1.81E-05	0				
2752	3	1.3E-05	2	0.003606	0.003606			ENSGO00000242445	RETSAT			gi	31377748	ref	NP_	all-trans-13,14-dihydroretinol	610	66793	8.3		1	12-24o	S	19	0	0	3.68E-05	0	2.9E-05	0	2	1.68E-05	1.98E-05	0	0	0.000521	0.004702	0.00271	0.005924	0.003932	0.003316	0.002721	Phytoene dehydrogenase	endoplasmic reticulum;	all-trans-retinol 13,14-
2753	3	6.69E-06	3	1.78E-05	0.375569			ENSGO00000075568	ETMEM131			gi|150456424|ref|NP	RW1 protein [Homo sapiens]	1883	205137	8.6		2	o1083-1101	S	60	0.988	0	1.24E-05	0	0	0	1	3.1E-06	6.19E-06	1.73E-05	0	0	0	0	0	0	0	2.03E-05	1.22E-05	0	1.74E-05		0				
2754	3	0.000525	4	0.000259	2.15133			ENSGO00000132591	CSTC			gi	24306477	ref	NP	DC2 protein [Homo sapiens]	149	16933	9.1		1	132-154S	S	41	0.008	0.003265	0.00039	0	0	0	1	0.000117	0.00154	0	0	0.000101	0.000101	0.00009	0.000333	0	0.000659	0.000206					
2755	2	0.00043	4	0.001843	0.233469			ENSGO00000136986	DERL1			gi|13236510|ref|NP	Der1-like domain family, mer	251	28801	9.5		5	20-42o57-Q	Q	33	0.065	0	0.001208	0	0	0	1	0.000302	0.000604	0	0	0.000359	0.000101	0	0	0	0	0.000599	0.001117	0.005284	0.007441	0.001659	0.003361		Der1-like family. The	endoplasmic reticulum [pmid	ubiquitin ligase activity
2756	2	0.000414	3	0.00028	1.478182			ENSGO00000158604	ETMED4			gi|33457308|ref|NP_	transmembrane emp24 prote	227	25943	8.3		2	o215-341i9S	S	30	1	0	0.001632	0	0	0	1	0.000408	0.000816	0	0	0.000408	0.000816	0	0	0	0	0.000842	0.00084	0	0.000824		0		emp24/gp25L/p24	endoplasmic reticulum;	signal transducer activity
2757	2	0.000288	2	0.000157	1.837037			ENSGO00000147314	ECD			gi|27268193|ref|NP_	ecdysone receptor binding p	230	26553	7.9		2	o29-51i64-A	A	54	0.011	0.00141	0.000075	0	0	0	1	0.000305	0.000705	0	0	0.000305	0.000705	0	0	0	0	0.000489	0.000488	0	0.000489		0		Ecdysone receptor binding protein.	endoplasmic reticulum [pmid	cholesterol delta-isomerase
2758	2	0.00026	3	5.71E-05	4.549354			ENSGO00000145354	CISD2			gi|56605994|ref|NP	CDGSH iron sulfur domain 2	135	15278	9.6		1	o38-60i	A	59	0.012	0	0.001555	0	0.000523	0	2	0.00052	0.000733	0	0	0	0	0	0	0	0	0.000127	0.000255	0	0.000127		0		CDGSH-type zinc finger.	protein complex [pmid	
2759	2	0.00025	3	7.66E-05	3.267974			ENSGO00000164308	ALG11			gi|58892492|ref|NP	asparagine-linked glycosylat	492	55693	8.5		2	o240-252A	A	42	0.002	0	0	0.001909	0	0	0	1	0.000477	0.000955	0	0	0.000477	0.000955	0	0	0	0	0.000221	0.000198	0.000199		0		Glycosyl transferases		
2760	2	0.000198	3	0.002605	0.075959			ENSGO00000147383	NSDHL			gi	30305160	ref	NP_	NADH dehydrogenase(ubiqui	373	41900	8.1		2	o296-318i	Q	0	0	0	0.000561	0	0	0	1	0.000141	0.000281	0	0	0.000123	0	0	0	0	0	0.000256	0.000511	0.001221	0.001548	0.004068	0.002906	0.004119	0.003243	0.00171	0.002034	Male sterility protein. This	endoplasmic reticulum [pmid	3-beta-hydroxy-delta5-
2761	2	0.000122	5	0.001104	0.110221			ENSGO00000728491	DERL2			gi|31455614|ref|NP	Der1-like domain family, mer	239	27567	7.3		4	i57-79o99i	Q	34	0.039	0	0.000786	0	0	0	1	0.000197	0.000393	0	0	0.000188	0	0	0	0	0	1.69E-05	9.39E-05	0.0037	0	0	0	0	0	0	0	1.69E-05	0.000146		Der1-like family. The	endoplasmic reticulum [pmid	protein binding [pmid
2762	2	0.00011	4	0.000468	0.219988			ENSGO00000169446	ETMEM32			gi|27334000|ref|NP	transmembrane protein 32 [H	131	14989	6.9		1	7-25o	S	26	0.039	0	0.000534	0	0	0	1	0.000134	0.000267	0	0	0.000134	0.000267	0	0	0	0	9.56E-05	0.000171	0	0.000203		0			endoplasmic reticulum [pmid	
2763	2	0.000108	4	8.17E-05	1.320962			ENSGO00000119004	CYP20A1			gi|29171730|ref|NP_	cytochrome P450, family 20,	462	52432	6.2		1	6-24o	S	30	0.919	0	5.05E-05	0.000833	0	0	0	2.000216	0.000399	0	0	0	0	0	0	0	0	0.0002	7.85E-05	0.000104	0.000271		0		Cytochrome P450.	membrane	heme binding; iron ion
2764	2	0.000105	3	8.73E-05	1.201949			ENSGO00000105409	ATP1A3			gi|22748667|ref|NP_	Na+/K+ -ATPase alpha 3 isoft	1013	111748	5.4		8	i88-110o12	Q	0	0	0.0008	3.95E-05	0	0	0	2	0.00021	0.000394	0	0	0.000243	0.00023	6.15E-05	0	0	0	0.000394	0.00243	0	0.000117		0		haloacid dehalogenase-like	membrane; sodium;potassium	ATP binding; hydrolase
2765	2	9.46E-05	2	0.000629	0.188601			ENSGO00000146162	ECM1L			gi|56750000|ref|NP	BEC11-like 1 [Homo sapiens	179	20625	9.5		1	i21-43s	Q	33	0	0	0.000425	0	0	0	1	0.000622	0.000622	0	0	0.000622	0.000622	0	0	0	0	0.000177	0.000313	0.00247	0	0	0	0	0	0	0	0.000177	0.000312		Signal peptidase I		serine-type peptidase
2766	2	8.42E-05	6	0.00564	0.014937			ENSGO00000172270	BSG			gi|38372923|ref|NP	basigin isoform 4 [Homo sapi	205	22764	5.5		1	o143-165i	Q	0	0	0	0.000455	0	0	0	1	0.000114	0.000228	0	0	0.000219	0	0	0	0	0	5.47E-05	0.000109	0	0.000219		0		Immunoglobulin V-set	integral to membrane;	immunoglobulin;
2767	2	8.38E-05	2	0.000255	0.329153			ENSGO00000106638	TBL2			gi	75497939	ref	NP_	transducin (beta)-like 2 [Hom	447	49798	9.4		1	i9-31s	S	29	0.985	0	0.00047	0	0	0	1	0.000117	0.000235	0	0	0.000201	0	0	0	0	0	5.02E-05	2.00E-05	0.005001	0.001268	0.001505	0.000369	0.001415	0.000348	0	0	WD40 domain, found in a		
2768	2	8.2E-05	5	0.000211	0.388963			ENSGO00000134153	C15orf24			gi	39910346	ref	NP_	chromosome 15 open readin	242	26471	9.2		1	o160-182i	S	24	1	0	0.000193	0	0	0	1	4.82E-05	9.64E-05	0	0	0.000464	0	0	0	0	0	0.000116	0.000232	0	0.000384	0.000452	0.0002	0	0.00027	0.000382			cytoplasm [pmid 10873569];	purine nucleotide binding	
2769	2	8.13E-05	2	0.000113	0.7186			ENSGO00000175274	TP53I11			gi	11564870	ref	NP	p53-induced protein [Homo s	189	21054	9.6		1	i61-83o10Q	Q	0	0	0	0.00037	0	0.00028	0	1	0.000163	0.000191	0	0	0	0	0	0	0	0	0.000267	0	0	0.000267		0.000639	0				
2770	2	7.52E-05	2	2.97E-05	2.531676			ENSGO00000134255	CEPT1			gi|56116223|ref|NP	choline/ethanolamineprosph	416	45554	8.2		1	i83-105o11	Q	38	0	0	0.000226	0	0	0	1	5.61E-05	0.000112	0	0	0.000378	0	0	0	0	0	9.44E-05	0.000189	0	0.000151		0		CEPT family.	integral to membrane [pmid	ethanolaminephosphotransfe
2771	2	7.19E-05	2	9.38E-05	0.7661			ENSGO00000886488	EALN2			gi|118026921|ref|NP	asparagine-linked glycosylat	618	70787	8.7		6	i136-158o	Q	24	0.001	0	0.000113	0	0	0	1	2.83E-05	5.66E-05	0	0.26E-05	0	0	0	0	0	1.000115	0.000192	0.000721	0	0	0	0	0	0	0	0.000721	0.000192		A subgroup of the band 7		
2772	2	6.95E-05	4	0.000153	0.522556			ENSGO00000107959	ENPP5			gi	54537092	ref	NP	ER lipid raft associated 1 [H	413	45846	8.9		1	i73-90o	Q	51	0.209	0.000393	0	0	0	0	1	9.82E-05	0.000393	0	0	0.000393	0	0	0	0	0	4.07E-05	8.15E-05	0	0.000615		7.58E-05	0	0.000140			
2773	2	6.76E-05	4	0.000457	0.147965			ENSGO00000103466	STX4			gi	24149560	ref	NP	syntaxin 4 [Homo sapiens]	297	34180	6.3		1	i274-296o	Q	0	0	0	0.000314	0	0	0	1	7.85E-05	0.000157	0	0	0.000227	0	0	0	0	0	0.000134	0.000365	0	5.25E-05		0.000103	Syntaxin N-terminus	integral to membrane;	protein binding [pmid
2774	2	6.02E-05	6	0.000906	0.066431			ENSGO00000124164	VAPB			gi|47590302|ref|NP	VAMP-associated protein B/	243	27228	7.3		1	o220-242i	Q	17	0	0	0.000297	0	0	0	1	7.42E-05	0.000148	0	0	0.000185	0	0	0	0	0	0.001142	0.001717	0.002178	0.00058	0.001243	0.000391		Immunoglobulin V-set	integral to plasma membrane	structural molecule activity
2775	2	5.86E-05	2	7.02E-05	0.835822			ENSGO00000170961	CD48			gi	21361757	ref	NP	CD48 molecule [Homo sapie	229	25925	5.2		1	o225-242i	S	29	0.994	0	0.000158	0	0	0	1	0.000227	0.000227	0	0	0.000227	0	0	0	0	0	9.92E-05	0.000139	0	0.000427		0.000402			Immunoglobulin V-set	integral to plasma membrane	GPI anchor binding; protein
2776	2	5.71E-05	2	2.95E-05	1.933309			ENSGO00000182544	MFSD5			gi	31543150	ref	NP	major facilitator superfamily	450	49737	7.8		10	o45-64r77i	S	27	0	0	0.000207	0	0	0	1	5.18E-05	0.000104	0	0	0.000249	0	0	0	0	0	6.23E-05	0.000125	0	0					Protein of unknown function		
2777	2	5.54E-05	2	0.000105	0.527206			ENSGO00000213463	SYNJ2BP			gi	157388993	ref	NP	synaptojanin 2 binding protein	145	15928	6.3		1	o117-139i	Q	0	0	0	0.000322	0	0.000122	0	2	0.000111	0.000152	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2778	2	5.52E-05	1	2.16E-05	1.183324			ENSGO00000184702	UBA2			gi|20986388|ref|NP	UBA domain containing 2 [H	309	34876	9		2	i93-115o11	Q	51	0.113	0	0.000151	0	0	0	1	3.77E-05	7.55E-05	0	0	0	0	0	0	0	0	7.26E-05	0.000145	0	0.000202		0		Ubiquitin Associated		
2779	2	5.49E-05	2	0.000292	0.187803			ENSGO00000140688	C16orf58			gi|12232403|ref|NP	hypothetical protein LOC847	468	50960	7.2		2	i248-270i	Q	22	0.001	0	0.000199	0	0	0	1	4.98E-05	9.97E-05	0	0	0.000024	0	0	0	0	0	5.99E-05	0.00012	0.001897	0	0	0	0	0	0	0	0.001897	0		Protein of unknown		
2780	2	4.88E-05	2	5.4E-05	0.905106			ENSGO00000159399	HAPR1			gi	21071001	ref	NP	autocrine motility factor recep	643	70980	6.8		2	i83-102i12	S	38	0.631	0	0.000181	0	0	0	1	4.53E-05	9.23E-05	0	0	0	0	0	0	0	0	9.23E-05	0.000138	4.14E-05	3.90E-05	RING finger (Really	endoplasmic reticulum;	ligase activity; metal ion
2781	2	4.82E-05	6	0.00069	0.06981			ENSGO00000058931	LAMP2			gi	4504957	ref	NP	lysosomal-associated membra	410	44961	5.6		1	o378-400i	S	29	0.991	0	5.69E-05	0	0	0	1	1.42E-05	8.55E-05	0	0	0.000328	0	0	0	0	0	1.82E-05	0.000164	0	0.000113	0.000971	0.000484	0.001098	0.001724	0.001194	0.001195	Lysosome-associated	integrate; late	
2782	2	4.77E-05	6	0.000246	0.19361			ENSGO00000168763	CNNM3			gi	40068047	ref	NP	cyclin M3 isoform 2 [Homo s	659	70632	7.1		1	i190-212o2	S	28	0.017	0	0.000177	0	0	0	1	4.42E-05	8.85E-05	0	0	0.000204	0	0	0	0	0	5.11E-05	0.000102	0	0.000249	0.000565	0.000136	0.000268	0.000369	0.000174	This cd contains two		DNA binding; DNA-directed
2783	2	3.02E-05	4	4.48E-05	0.674295			ENSGO00000131469	UBE2J1			gi	37577122	ref	NP	ubiquitin-conjugating enzyme	318	35190	8.6		1	i128-308o	Q	38	0.631	0	0.000181	0	0	0	1	3.62E-05	7.24E-05	0	0	0.000181	0	0	0	0	0	3.62E-05	7.24E-05	0	0.000181		7.95E-05	0	0.000104	ubiquitin-conjugating	endoplasmic reticulum;	ligase activity; ubiquitin-
2784	2	4.18E-05	2	0.000198	0.211182			ENSGO00000070961	ATP2B1			gi	48255945	ref	NP	plasma membrane calcium A	1220	134685	5.9		7	o377-399w	Q	0	0	0	2.68E-05	0.000308	0	0	0	2.83E-05	0.000015	0	0	0.000286	0.000306	0.000341	0.000235	haloacid dehalogenase-like	integral to plasma membrane	ATP binding; calcium ion
2785	2	4.18E-05	2	0.000338	0.124638			ENSGO00000137414	FAMBA1			gi|7705268|ref|NP	family with sequence similari	413	44123	7.2		1	o255-277i	Q	0	0	0	0.000228	0	0	0	1	5.65E-05	0.000113	0	0	0.000109	0	0	0	0	0	1.22E-05	5.43E-05	0.002216	0.000468	0	0	0	0	0	0	0.002216	0		RDD family. This family of		
2786	2	4.11E-05	3	0.000243	0.345515			ENSGO00000135821	PIKFYVE			gi|28826997|ref|NP	kiphosphoinositide phosphoryl	1423	137480	6.2		1	i9-112-134d	Q	19	0.006	0	0.000275	0	0	0	1	6.86E-05	0.000138	0	0	0.000275	0	0	0	0	0	1.33E-05	2.66E-05	0	0.000877	4.35E-05	0.304	3.71E-05	0	0	0	0.000877		Endonuclease/Exonuclease/	integral to membrane	hydrolase activity;
2787	2	3.76E-05	4	2.9E-05	1.294621			ENSGO00000172601	ATP2C1			gi	48762685	ref	NP	calcium-transporting ATPase	919	100577	6.7		8	i83-100o11	Q	0	0	0	0.000203	0	0	0	1	5.08E-05	0.000102	0	0	0.000146	0	0	0	0	0	2.44E-05	4.88E-05	0	0.000117	7.89E-05	0.515	6.68E-05	0.000152	0.000117		ATP binding; calcium ion	integral to membrane [pmid	metal ion transporter activity
2788	2	3.73E-05	3	3.45E-05	0.687753			ENSGO00000100292	CHPF			gi	40254000	ref	NP	soluble carrier family 39 (zinc	323	36497	8.6		7	i5-27o37-A	A	23	0.469	0	0.000275	0	0	0	1	6.86E-05	0.000137	0	0	0.000137	0	0	0	0	0	1.95E-05	3.91E-05	0	0.000109	0.000192	0.000192	0.000192	0.000192	0.000192		Predicted divalent heavy-		
2789	2	3.64E-05	2	5.19E-05	0.701782			ENSGO00000125991	EROG13			gi	38327615	ref	NP	serologically defined breast c	388	43772	6		1	o20-42i34	A	47	0.001	0	6.01E-05	0	0	0	1	1.5E-05	3.01E-05	0	0	0.000231	0	0	0	0	0	5.78E-05	0.000116	0	0.000104	0.000164		0	0.000147			Protein of unknown function	endoplasmic reticulum; ER-	protein binding [pmid
2790	2	3.58E-05	2	4.64E-05	0.771744			ENSGO00000082821	SYPL1			gi|33239443|ref|NP	synaptophysin-like 1 isoform	241	26412	7.2		3	i69-121o11	Q	36	0.036	0	0.000194	0	0	0	1	4.84E-05	9.68E-05	0	0	9.31E-05	0	0	0	0	0	1.23E-05	4.65E-05	0	0	0	0	0	0	0	0				Membrane-associating	integrate to plasma membrane	transporter activity
2791	2	3.55E-05	2	8.88E-05	0.400234			ENSGO00000109616	ERG27B			gi|21469199|ref|NP	LBA domain containing 2 [H	325	36916	9.6		1	i21-43o	S	47	0.531	0	0.000253	0	0	0	1	6.32E-05	0.000126	0	0	6.96E-05	0	0	0	0	0	1.58E-05	3.16E-05	0	0.000126	0.000279	0	0.000253	0	0	0			Dehydrogenases with		oxidoreductase activity
2792	2	3.42E-05	2	3.7E-05	0.923403			ENSGO00000121940	CLCC1			gi|15270970|ref|NP	Mid-1-related chloride chann	551	62023	5.6		1	o185-207d	S	19	0.999	0	0	0	0	0	1	0	0	0.97E-05	0	0.000204	0	0	0	0	0	6.83E-05	9.6E-05	0	0.000171	6.7E-05	0	5.79E-05	0	0	0						
2793	2	3.33E-05	2	1.5E-05	2.222619			ENSGO00000159184	NINS			gi|23809351|ref|NP	kidneifowin 5 [Homo sapiens	340	37124	9.3		1	i109-131o11	S	24	0.194	0	6.86E-05	0	0	0	1	1.72E-05	3.43E-05	0	0	0.000168	0	0	0	0	0	1.45E-05	9.9E-05	0	0	0	0	0	0	0	0				Tricarboxylate carrier;	integrate to membrane;	cation transportor activity;
2794	2	3.31E-05	2	2.58E-05	1.286043			ENSGO00000196715	VKORC1L1			gi	46309463	ref	NP	vitamin K epoxide reductase	176	19836	9.1		2	i92-114o12	S	34	0.724	0	0.000265	0	0	0	1	6.63E-05	0.000133	0	0	0	0	0	0	0	0	0	0	0	0	0	0				Vitamin K epoxide		
2795	2	3.18E-05	3	8.59E-05	0.370035			ENSGO00000130303	BST2			4757876(ref)NP_0	bone marrow stromal cell ant	180	19769	5.6		1	122-44o	A	39	0	0	0.00013	0	0	0	1	3.24E-05	6.48E-05	0	0	0.000125	0	0	0	0	0	3.12E-05	6.23E-05	0	0	0.000316	0.00028	9.1E-05	0	0	0						
2796	2	3.03E-05	2	1.06E-05	2.86128			ENSGO00000159110	IFI16			gi	21361315	ref	NP	Ifi/p1 interacting factor homo	283	31175	7.4		1	i125-145o12	S	35	0.967	0	8.81E-05	0	0	0	1	1.76E-05	3.52E-05	0	0	0.000588	0	0	0	0	0	7.93E-05	0.000106	0	0.000588	0.000619		0.000619				YIF1. YIF1 (Yip1	integrate to membrane;	
2797	2	2.96E-05	2	3.23E-05	0.918321			ENSGO00000140199	SLC12A5			gi|11022444|ref|NP	solute carrier family 12, mem	150	127617	7.1		12	o186-208d	Q	21	0	0	8.11E-05	0	0	0	1	2.03E-05	4.06E-05	0	0	0.000159	0	0	0	0	0	1.39E-05	7.8E-05	0	5.07E-05	0.000139	0	8.11E-05	0	0	0						
2798	2	2.92E-05	2	6.87E-05	0.424432			ENSGO00000154122	ANKH			gi	16905507	ref	NP	progressive ankylosis protein	492	54241	7.9		7	i86-105o11	Q	27	0.062	0	0.000142	0	0	0	1	3.56E-05	7.11E-05	0	0	9.12E-05	0	0	0	0	0	2.28E-05	4.56E-05	0	0.000186	0.000364		0				Progressive ankylosis	integrate to membrane [pmid	inorganic diphosphate
2799	2	2.84E-05	2	0.000861	0

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	ORTHO_GROUP	GENE_NAME
2890	8	0.000938	6	0.00024	3.905729	ENSG00000167004:E	PDIA3
2891	8	0.000684	6	0.000221	3.092866	ENSG00000188229:E	TUBB2C
2892	8	0.000244	6	0.000113	2.161875	ENSG00000197102:E	DYNC1H1
2893	7	0.002217	5	0.001774	1.249955	ENSG00000174903:E	RAB1C
2894	7	0.000748	6	0.001016	0.736069	ENSG00000197043:E	ANXA6
2895	7	0.000748	6	0.001779	0.420218	ENSG00000141367:E	CLTC
2896	7	0.000661	2	0.000243	2.715493	ENSG00000174444:E	RPL4
2897	7	0.000608	6	0.000755	0.80573	ENSG00000116459:E	ATP5F1
2898	7	0.000465	3	0.000207	2.247132	ENSG00000115840:E	SLC25A12
2899	7	0.000401	6	0.000264	1.518697	ENSG00000165280:E	VCP
2900	7	0.000292	7	0.000616	0.473194	ENSG00000127463:E	KIAA0090
2901	6	0.002009	1	0.000564	3.562584	ENSG00000075785:N	RAB7A
2902	6	0.001673	6	0.001172	1.427326	ENSG00000070831:E	CDC42
2903	6	0.001161	6	0.002287	0.507923	ENSG00000149273:E	RPS3
2904	6	0.000849	3	0.000172	4.935098	ENSG00000180879:E	SSR4
2905	6	0.000766	5	0.000733	1.045552	ENSG00000119396:E	RAB14
2906	6	0.000758	5	0.000199	3.804482	ENSG00000171560:E	FGA
2907	6	0.000608	4	0.000294	2.067803	ENSG00000159251:E	ACTC1
2908	6	0.000443	5	0.000287	1.545134	ENSG00000113194:E	UBXD8
2909	6	0.000427	4	0.000247	1.730655	ENSG00000170889:E	RPS9
2910	6	0.000407	3	9.33E-05	4.35747	ENSG00000130402:E	ACTN4
2911	6	0.000395	6	0.000242	1.633538	ENSG00000007923:E	DNAJC11
2912	6	0.000354	3	0.000152	2.333601	ENSG00000147403:E	RPL10
2913	6	0.000353	6	0.001287	0.274159	ENSG00000185624:E	P4HB
2914	6	0.000286	4	9.13E-05	3.135216	ENSG00000215301:E	DDX3X
2915	6	0.000283	4	0.000117	2.431656	ENSG00000172354:E	GNB2
2916	6	0.000265	6	0.00014	1.887388	ENSG00000143149:E	ALDH9A1
2917	6	0.000182	4	0.000147	1.242427	ENSG00000197157:E	SND1
2918	6	0.000181	5	0.000385	0.469384	ENSG00000107581:E	EIF3A
2919	6	0.000168	4	3.67E-05	4.564441	ENSG00000089154:E	GCN1L1
2920	6	0.000113	6	0.000268	0.421488	ENSG00000169710:E	FASN
2921	6	6.29E-05	2	1.31E-05	4.806003	ENSG00000101310:E	SEC23B
2922	6	6.22E-05	4	3.04E-05	2.045429	ENSG00000115306:E	SPTBN1
2923	5	0.001212	6	0.002751	0.440532	NA:ENSMUSG00000	RPL15
2924	5	0.000997	6	0.000483	2.065604	ENSG00000179218:E	CALR
2925	5	0.000907	4	0.00036	2.519409	ENSG00000185236:E	RAB11B
2926	5	0.000906	5	0.000226	4.013467	ENSG00000083845:E	RPS5
2927	5	0.000743	4	0.000335	2.215737	ENSG00000104388:E	RAB2A
2928	5	0.000714	6	0.000899	0.793926	ENSG00000168374:E	ARF4
2929	5	0.00069	4	0.000226	3.049607	ENSG00000204628:E	GNB2L1
2930	5	0.000623	6	0.000829	0.750765	ENSG00000171564:E	FGB
2931	5	0.000549	5	0.000151	3.627084	ENSG00000186676:E	EEF1G
2932	5	0.000437	6	0.000762	0.573242	ENSG00000100316:E	RPL3
2933	5	0.000428	6	0.000171	2.499664	ENSG00000148303:N	RPL7A
2934	5	0.000313	1	0.000898	0.348854	ENSG00000112081:E	SFRS3
2935	5	0.00028	4	0.000104	2.701848	ENSG00000159322:E	ADPGK
2936	5	0.000271	6	0.000908	0.298968	ENSG00000161016:E	RPL8
2937	5	0.000263	3	0.000121	2.178562	ENSG00000175390:E	EIF3F
2938	5	0.000233	4	0.000263	0.884215	ENSG00000110700:E	RPS13
2939	5	0.000196	5	0.000138	1.425584	ENSG00000129083:E	COPB1
2940	5	0.000186	1	3.76E-05	4.954721	ENSG00000120805:E	ARL1
2941	5	0.000186	7	0.000603	0.308701	ENSG00000143870:E	PDIA6
2942	5	0.000162	5	0.000127	1.279888	ENSG00000085719:E	CPNE3
2943	5	0.000159	5	0.000387	0.410921	ENSG00000120063:E	GNA13
2944	5	0.000144	6	0.001879	0.076453	ENSG00000018510:E	AGPS
2945	5	0.000136	3	5.67E-05	2.393371	ENSG00000147065:E	MSN
2946	5	0.000136	3	3.26E-05	4.160518	ENSG00000122218:E	COPA
2947	5	0.00013	2	5.3E-05	2.461691	ENSG00000164111:E	ANXA5
2948	5	0.00013	5	0.000155	0.837525	ENSG00000166224:E	SGPL1
2949	5	0.000117	3	0.000148	0.788599	ENSG00000182934:E	SRPR
2950	5	9.96E-05	6	0.000474	0.210357	ENSG00000108828:E	VAT1
2951	5	9.43E-05	3	9.79E-05	0.963017	ENSG00000131473:E	ACLY
2952	5	9.16E-05	2	3.33E-05	2.751799	ENSG00000173786:E	CNP
2953	5	8.16E-05	2	5.91E-05	1.381784	ENSG00000198356:E	ASNA1
2954	5	8.15E-05	5	0.000114	0.712433	ENSG00000079805:E	DNM2
2955	5	8.05E-05	4	0.000173	0.46571	ENSG00000166333:E	ILK
2956	5	6.27E-05	6	7.98E-05	0.785848	ENSG00000073969:E	NSF
2957	5	5.43E-05	3	5.79E-05	0.93798	ENSG00000167881:E	SRP68
2958	5	2.76E-05	2	1.26E-05	2.198345	ENSG00000204843:E	DCTN1
2959	5	2.08E-05	2	1.39E-05	1.497049	ENSG00000198793:E	FRAP1
2960	5	1.72E-05	3	1.54E-05	1.11428	ENSG00000162688:E	AGL
2961	5	1.16E-05	1	3.88E-06	2.99428	ENSG00000124942:E	AHNAK
2962	4	0.000641	3	0.000214	2.996937	ENSG00000178741:E	COX5A
2963	4	0.000584	6	0.001399	0.417375	ENSG00000138326:E	RPS24
2964	4	0.00044	3	0.00017	2.590413	ENSG00000142534:E	RPS11
2965	4	0.000292	5	0.000195	1.49351	ENSG00000089009:E	RPL6
2966	4	0.000277	6	0.004841	0.057236	ENSG00000198189:E	HSD17B11
2967	4	0.000233	6	0.00189	0.123339	ENSG00000072042:E	RDH11
2968	4	0.000208	6	0.000316	0.659179	ENSG00000138138:E	ATAD1
2969	4	0.00019	4	0.000156	1.214935	ENSG00000130313:E	PGLS
2970	4	0.000173	5	0.000262	0.658161	ENSG00000100280:E	AP1B1
2971	4	0.000171	3	6.03E-05	2.843419	ENSG00000173801:E	JUP
2972	4	0.000167	3	5.93E-05	2.819877	ENSG00000169738:E	DCXR
2973	4	0.000141	6	0.000522	0.270647	ENSG00000087008:E	ACOX3
2974	4	0.000136	5	0.00027	0.506069	ENSG00000122359:E	ANXA11
2975	4	0.000133	3	0.000364	0.364522	ENSG00000136238:E	RAC1
2976	4	0.000115	2	2.46E-05	4.651978	ENSG00000082153:E	BZW1
2977	4	9.84E-05	4	0.000172	0.57279	ENSG00000006125:E	AP2B1
2978	4	9.01E-05	4	0.000118	0.761851	ENSG00000108588:E	CCDC47
2979	4	8.7E-05	4	0.000109	0.8005	ENSG00000184640:E	SEPT9
2980	4	8.03E-05	3	9.45E-05	0.850152	ENSG00000092108:E	SCFD1
2981	4	7.88E-05	5	7.69E-05	1.024256	ENSG00000160703:E	NLRX1
2982	4	7.87E-05	3	0.000116	0.676941	ENSG00000116005:E	PCYOX1
2983	4	6.17E-05	1	1.94E-05	3.174798	ENSG00000132394:E	EEFSEC
2984	4	6.14E-05	3	1.72E-05	3.566071	ENSG00000198959:E	TGM2
2985	4	5.95E-05	5	0.000157	0.379281	ENSG00000136051:E	KIAA1033
2986	4	5.62E-05	4	2.96E-05	1.899124	ENSG00000164307:E	ERAP1
2987	4	5.42E-05	3	3.42E-05	1.583641	ENSG00000184178:E	SCFD2
2988	4	5.34E-05	2	3.78E-05	1.413953	ENSG00000136827:E	TOR1A
2989	4	5.34E-05	2	1.79E-05	2.981573	ENSG00000092964:E	DPYSL2
2990	4	5.08E-05	1	1.15E-05	4.432192	ENSG00000100883:E	SRP54
2991	4	4.57E-05	2	1.17E-05	3.92235	ENSG00000167986:E	DDB1
2992	4	4.38E-05	1	1.14E-05	3.847659	ENSG00000065000:E	AP3D1
2993	4	4.35E-05	2	2.38E-05	1.826484	ENSG00000105220:E	GPI
2994	4	4.21E-05	3	1.17E-05	3.598922	ENSG00000132842:E	AP3B1
2995	4	4.06E-05	3	3.71E-05	1.09237	ENSG00000147507:E	LYN
2996	4	4E-05	1	9.3E-06	4.304156	ENSG00000008128:E	CDC2L2
2997	4	3.7E-05	2	1.25E-05	2.966642	ENSG00000135249:E	RINT1
2998	4	3.19E-05	1	1.25E-05	2.552058	ENSG00000164961:E	KIAA0196
2999	4	2.88E-05	6	0.000418	0.068894	ENSG00000100934:E	SEC23A
3000	4	2.84E-05	4	7.58E-05	0.373976	ENSG00000198211:E	TUBB3
3001	4	2.58E-05	4	6.11E-05	0.421586	ENSG00000113615:E	SEC24A
3002	4	2.31E-05	6	7.84E-05	0.294945	ENSG00000138674:E	SEC31A
3003	4	2.29E-05	2	2.73E-05	0.836177	ENSG00000185722:E	ANKFY1
3004	4	2.19E-05	6	0.000159	0.137873	ENSG00000136731:E	UGCGL1
3005	4	2.14E-05	2	1.72E-05	1.24626	ENSG00000122729:E	ACO1
3006	4	1.88E-05	4	3.58E-05	0.526664	ENSG00000138246:E	DNAJC13
3007	4	1.82E-05	1	3.65E-06	4.975066	ENSG00000204351:E	SKIV2L
3008	4	1.77E-05	4	2.94E-05	0.601986	ENSG00000107862:E	GBF1
3009	4	1.07E-05	2	9.83E-06	1.093328	ENSG00000100241:E	SBF1
3010	3	0.000443	4	0.00026	1.701996	ENSG00000000419:E	DPM1
3011	3	0.000263	4	0.000251	1.047965	ENSG00000167863:E	ATP5H
3012	3	0.000239	3	0.000109	2.194691	ENSG00000198755:E	RPL10A
3013	3	0.000215	4	0.000263	0.81626	ENSG00000134108:E	ARL8B
3014	3	0.00021	2	7.82E-05	2.680762	ENSG00000177889:E	UBE2N
3015	3	0.000197	5	0.000121	1.627782	ENSG00000170638:E	TRABD
3016	3	0.000184	6	0.002561	0.071938	ENSG00000130203:E	APOE
3017	3	0.000181	2	5.65E-05	3.207164	ENSG00000103035:E	PSMD7
3018	3	0.000172	5	0.00103	0.167006	ENSG00000108298:E	RPL19
3019	3	0.000133	3	9.07E-05	1.467353	ENSG00000135924:E	DNAJB2
3020	3	0.000133	3	0.000156	0.852752	ENSG00000105372:E	RPS19
3021	3	0.000125	6	0.001399	0.089145	ENSG00000126458:E	RRAS
3022	3	0.000124	3	0.000201	0.61494	ENSG00000123595:E	RAB9A
3023	3	0.000117	4	0.000594	0.196265	ENSG00000159186:E	ATP5O
3024	3	0.000108	3	0.000284	0.380572	ENSG00000177350:E	LOC728658
3025	3	9.67E-05	3	0.000222	0.435722	ENSG00000111540:E	RAB5B
3026	3	9.55E-05	1	2.41E-05	3.95949	ENSG00000133703:E	KRAS
3027	3	8.8E-05	3	0.000176	0.49903	ENSG00000060971:E	ACAA1
3028	3	7.83E-05	4	0.000413	0.18959	ENSG00000137154:N	RPS6
3029	3	7.49E-05	3	2.5E-05	2.992215	ENSG00000043822:E	PI4K2A
3030	3	7.32E-05	4	0.000106	0.687956	ENSG00000167925:E	GHDC
3031	3	6.91E-05	2	1.66E-05	4.158659	ENSG00000047056:E	WDR37
3032	3	6.73E-05	3	0.000132	0.5083	ENSG00000181524:E	RPL24
3033	3	6.19E-05	2	2.04E-05	3.032951	ENSG00000116906:E	GNPAT
3034	3	5.34E-05	1	1.53E-05	3.487158	ENSG00000169228:E	RAB24
3035	3	4.76E-05	3	0.000132	0.359891	ENSG00000079739:E	PGM1
3036	3	4.63E-05	2	6.43E-05	0.719734	ENSG00000154229:E	PRKCA

rk	NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)
3037	3	4.45E-05	1	1.54E-05	2.895044		ENSG00000105402:E	NAPA			gi|47933379|ref|NP_	N-ethylmaleimide-sensitive fa	295	33233	5.4	0	o	Q
3038	3	4.05E-05	1	1.26E-05	3.205343		ENSG00000147813:E	NAPRT1			gi|40255089|ref|NP_	nicotinate phosphoribosyltran	466	49577	5.5	0	o	Q
3039	3	3.85E-05	5	0.000158	0.244368		ENSG00000049239:E	H6PD			gi|52145310|ref|NP_	hexose-6-phosphate dehydro	791	88893	7.3	0	o	S
3040	3	3.72E-05	4	0.000189	0.197123		ENSG00000108433:E	GOSR2			gi|16905520|ref|NP_	golgi SNAP receptor complex	213	24584	8.5	0	o	Q
3041	3	3.66E-05	3	1.98E-05	1.849546		ENSG00000078061:E	ARAF			gi|4502193|ref|NP_0	v-raf murine sarcoma 3611 v	606	67585	9	0	o	Q
3042	3	3.66E-05	4	0.000114	0.321697		ENSG00000196961:E	AP2A1			gi|19913414|ref|NP_	adaptor-related protein comp	977	107546	7	0	o	Q
3043	3	3.57E-05	2	2.55E-05	1.400839		ENSG00000105379:E	ETFB			gi|4503609|ref|NP_0	electron-transfer-flavoprotein	255	27844	8.1	0	o	Q
3044	3	3.47E-05	1	1.29E-05	2.687925		ENSG00000204590:E	GNL1			gi|38788319|ref|NP_	guanine nucleotide binding p	607	68661	5.8	0	o	Q
3045	3	3.3E-05	2	1.06E-05	3.110752		ENSG00000139842:E	CUL4A			gi|57165424|ref|NP_	cullin 4A isoform 1 [Homo sa	759	87680	8.1	0	o	Q
3046	3	3.26E-05	2	1.29E-05	2.529495		ENSG00000068793:E	CYFIP1			gi|24307969|ref|NP_	cytoplasmic FMR1 interacting	1253	145182	6.9	0	o	Q
3047	3	3.25E-05	2	8.76E-06	3.70736		ENSG00000171109:E	MFN1			gi|45269137|ref|NP_	mitofusin 1 [Homo sapiens]	741	84159	6.3	0	o	Q
3048	3	3.24E-05	5	0.000272	0.119034		ENSG00000144224:E	UBXD2			gi|24307965|ref|NP_	UBX domain containing 2 [Ho	508	56778	6.4	0	o	S
3049	3	3.19E-05	1	1.39E-05	2.291151		ENSG00000170581:E	STAT2			gi|4885615|ref|NP_0	signal transducer and activat	851	97916	5.5	0	o	Q
3050	3	2.97E-05	5	0.000226	0.131221		ENSG00000197879:E	MYO1C			gi|124494238|ref|NP	myosin IC isoform a [Homo s	1063	121682	9.4	0	o	Q
3051	3	2.4E-05	5	2.43E-05	0.989591		ENSG00000196535:E	MYO18A			gi|28416946|ref|NP_	myosin 18A isoform a [Homo	2054	233113	6.3	0	o	Q
3052	3	2.3E-05	1	6.66E-06	3.447982		ENSG00000198380:E	GFPT1			gi|4503981|ref|NP_0	glucosamine-fructose-6-phos	681	76747	6.9	0	o	Q
3053	3	2.03E-05	3	4.98E-05	0.407309		ENSG00000109689:E	STIM2			gi|41349446|ref|NP_	stromal interaction molecule	833	93025	7.5	0	o	Q
3054	3	2.01E-05	1	4.04E-06	4.963003		ENSG00000172725:E	CORO1B			gi|65787364|ref|NP_	coronin, actin binding protein	489	54235	5.9	0	o	Q
3055	3	1.95E-05	1	1.7E-05	1.149537		ENSG00000112851:E	ERBB2IP			gi|55770895|ref|NP_	ERBB2 interacting protein iso	1302	146086	5.3	0	o	Q
3056	3	1.9E-05	5	0.000383	0.049507		ENSG00000164209:E	SLC25A46			gi|20270311|ref|NP_	solute carrier family 25, mem	418	46174	7.4	0	o	Q
3057	3	1.78E-05	6	0.000589	0.030261		ENSG00000029534:E	ANK1			gi|70780353|ref|NP_	ankyrin 1 isoform 4 [Homo sa	1856	203403	6.1	0	o	Q
3058	3	1.73E-05	1	6.09E-06	2.834961		ENSG00000160220:E	PWP2			gi|48762926|ref|NP_	PWP2 periodic tryptophan pr	919	102452	6.1	0	o	Q
3059	3	1.67E-05	2	4.21E-06	3.975199		ENSG00000203485:E	INF2			gi|149999378|ref|NP	inverted formin 2 isoform 2 [H	1240	134617	5.5	0	o	Q
3060	3	1.66E-05	1	1.6E-05	1.039307		ENSG00000112478:E	VPS52			gi|73747799|ref|NP_	vacuolar protein sorting 52 [H	723	82221	6	0	o	Q
3061	3	1.64E-05	3	4.72E-05	0.346827		ENSG00000162434:E	JAK1			gi|102469034|ref|NP	janus kinase 1 [Homo sapien	1154	133277	7.5	0	o	Q
3062	3	1.62E-05	2	8.55E-06	1.888717		ENSG00000160695:E	VPS11			gi|17978477|ref|NP_	vacuolar protein sorting 11 [H	941	107809	7.1	0	o	Q
3063	3	1.54E-05	6	0.000124	0.124125		ENSG00000013364:E	MVP			gi|19913412|ref|NP_	major vault protein [Homo sa	893	99327	5.5	0	o	Q
3064	3	1.51E-05	1	1.35E-05	1.115394		ENSG00000099381:E	SETD1A			gi|55741677|ref|NP_	SET domain containing 1A [H	1707	186033	5.1	0	o	Q
3065	3	1.43E-05	2	1.19E-05	1.203335		ENSG00000100592:E	DAAM1			gi|21071077|ref|NP_	dishevelled-associated activa	1078	123473	7.2	0	o	Q
3066	3	1.41E-05	1	4.46E-06	3.15985		ENSG00000179115:E	FARSA			gi|4758340|ref|NP_0	phenylalanyl-tRNA synthetas	508	57564	7.8	0	o	Q
3067	3	1.07E-05	1	4.31E-06	2.473426		ENSG00000004487:E	AOF2			gi|58761546|ref|NP_	amine oxidase (flavin contain	852	92903	6.5	0	o	S
3068	3	5.61E-06	2	1.97E-06	2.853066		ENSG00000115760:E	BIRC6			gi|153792694|ref|NP	baculoviral IAP repeat-contai	4857	530274	6	0	o	S
3069	3	2.18E-06	1	7.88E-07	2.770681		ENSG00000005810:E	MYCBP2			gi|126116565|ref|NP	MYC binding protein 2 [Homo	4640	510091	7	0	o	S
3070	2	0.000167	4	0.000154	1.085617		ENSG00000187838:E	PLSCR3			gi|31543417|ref|NP_	phospholipid scramblase 3 [H	295	31648	6.7	0	o	Q
3071	2	0.000139	5	0.000646	0.214528		ENSG00000103769:E	RAB11A			gi|4758984|ref|NP_0	Ras-related protein Rab-11A	216	24394	6.5	0	o	Q
3072	2	0.000137	6	0.002975	0.045929		ENSG00000181035:E	SLC25A42			gi|60460887|ref|NP_	solute carrier family 25, mem	318	35437	10.1	0	o	Q
3073	2	0.000109	1	5.45E-05	1.994303		ENSG00000110717:E	NDUFS8			gi|4505371|ref|NP_0	NADH dehydrogenase (ubiqu	210	23705	6.3	0	o	S
3074	2	9.48E-05	2	1.98E-05	4.779363		ENSG00000147654:E	EBAG9			gi|37694065|ref|NP_	estrogen receptor binding site	213	24377	6.3	0	o	S
3075	2	8.5E-05	4	0.00061	0.139509		ENSG00000129472:E	RAB2B			gi|21361884|ref|NP_	RAB2B protein [Homo sapien	216	24214	7.8	0	o	Q
3076	2	8.08E-05	5	0.000481	0.168205		ENSG00000156052:E	GNAQ			gi|40254462|ref|NP_	guanine nucleotide binding p	359	42142	5.7	0	o	Q
3077	2	7.7E-05	3	3.87E-05	1.990979		ENSG00000163050:E	CABC1			gi|34147522|ref|NP_	chaperone, ABC1 activity of	647	71950	7	0	o	Q
3078	2	7.65E-05	3	0.000121	0.630248		ENSG00000131469:E	RPL27			gi|4506623|ref|NP_0	ribosomal protein L27 [Homo	136	15798	10.6	0	o	Q
3079	2	7.11E-05	5	0.000375	0.189471		ENSG00000198843:E	SELT			gi|42789380|ref|NP_	selenoprotein T [Homo sapie	195	22174	8.6	0	o	S
3080	2	6.38E-05	3	9.89E-05	0.644923		ENSG00000086061:E	DNAJA1			gi|4504511|ref|NP_0	DnaJ (Hsp40) homolog, subf	397	44868	7.1	0	o	Q
3081	2	5.98E-05	6	0.00078	0.076653		ENSG00000071082:N	RPL31			gi|148746199|ref|NP	ribosomal protein L31 isoform	128	14632	10.8	0	o	Q
3082	2	5.55E-05	5	0.000303	0.183514		ENSG00000006451:E	RALA			gi|33946329|ref|NP_	ras related v-ral simian leuke	206	23567	7.1	0	o	Q
3083	2	4.88E-05	4	0.000258	0.189033		ENSG00000197582:E	GPX1			gi|41406084|ref|NP_	glutathione peroxidase 1 isof	203	21938	6.5	0	o	S
3084	2	4.82E-05	1	1.84E-05	2.624848		ENSG00000109180:E	OCIAD1			gi|119874205|ref|NP	OCIA domain containing 1 is	245	27626	7.5	0	o	Q
3085	2	4.77E-05	1	1.54E-05	3.108054		ENSG00000164244:E	PRRC1			gi|18677735|ref|NP_	proline-rich coiled-coil 1 [Hon	445	46701	5.8	0	o	Q
3086	2	4.62E-05	4	0.000146	0.317414		ENSG00000095139:E	ARCN1			gi|11863154|ref|NP_	archain [Homo sapiens]	511	57210	6.2	0	o	S
3087	2	4.62E-05	4	0.000128	0.361978		ENSG00000072958:E	AP1M1			gi|14210504|ref|NP_	adaptor-related protein comp	423	48587	7.3	0	o	Q
3088	2	4.23E-05	4	0.000546	0.077504		ENSG00000133818:E	RRAS2			gi|21361416|ref|NP_	related RAS viral (r-ras) onco	204	23400	6	0	o	Q
3089	2	4.08E-05	4	7.96E-05	0.512472		ENSG00000115806:E	GORASP2			gi|29826294|ref|NP_	golgi reassembly stacking pr	452	47145	4.8	0	o	Q
3090	2	3.83E-05	2	3.86E-05	0.992498		ENSG00000149257:E	SERPINH1			gi|32454741|ref|NP_	serine (or cysteine) proteinas	418	46441	8.7	0	o	S
3091	2	3.81E-05	5	0.000359	0.106106		ENSG00000142655:E	PEX14			gi|4758896|ref|NP_0	peroxisomal biogenesis facto	377	41237	4.9	0	o	Q
3092	2	3.6E-05	5	0.000165	0.218351		ENSG00000087460:E	GNAS			gi|117938762|ref|NP	GNAS complex locus isoform	395	45752	5.8	0	o	Q
3093	2	3.16E-05	3	3.94E-05	0.802169		ENSG00000168385:E	SEPT2			gi|56549640|ref|NP_	septin 2 [Homo sapiens]	361	41487	6.6	0	o	Q
3094	2	2.93E-05	1	7.23E-06	4.045665		ENSG00000101997:E	CCDC22			gi|7661844|ref|NP_0	coiled-coil domain containing	627	70756	6.8	0	o	Q
3095	2	2.91E-05	2	4.21E-05	0.691125		ENSG00000198898:E	CAPZA2			gi|5453599|ref|NP_0	capping protein (actin filamen	286	32949	5.8	0	o	Q
3096	2	2.75E-05	6	0.000329	0.083495		ENSG00000161267:E	BDH1			gi|44680136|ref|NP_	3-hydroxybutyrate dehydroge	343	38157	9	0	o	Q
3097	2	2.74E-05	1	6.6E-06	4.148873		ENSG00000132300:E	PTCD3			gi|38683855|ref|NP_	Pentatricopeptide repeat dom	689	78550	6.4	0	o	Q
3098	2	2.71E-05	2	1.62E-05	1.675206		ENSG00000114302:E	PRKAR2A			gi|4758958|ref|NP_0	cAMP-dependent protein kin	404	45518	5.1	0	o	Q
3099	2	2.69E-05	1	1.56E-05	1.725565		ENSG00000185515:E	BRCC3			gi|13236583|ref|NP_	BRCA1/BRCA2-containing c	316	36072	5.9	0	o	Q
3100	2	2.45E-05	3	0.000144	0.170441		ENSG00000196975:E	ANXA4			gi|4502105|ref|NP_0	annexin IV [Homo sapiens]	321	36085	6.1	0	o	Q
3101	2	2.4E-05	1	7.23E-06	3.316582		ENSG00000033050:E	ABCF2			gi|10947137|ref|NP_	ATP-binding cassette, sub-fa	634	72444	7.5	0	o	Q
3102	2	2.15E-05	1	1.29E-05	1.662076		ENSG00000141858:E	SAMD1			gi|39930517|ref|NP_	sterile alpha motif domain co	538	56052	7.6	0	o	S
3103	2	2.03E-05	1	4.43E-06	4.569317		ENSG00000130749:E	ZC3H4			gi|126723060|ref|NP	zinc finger CCCH-type conta	1303	140256	6.3	0	o	Q
3104	2	1.89E-05	1	7.27E-06	2.606598		ENSG00000013563:E	DNASE1L1			gi|58430946|ref|NP_	deoxyribonuclease I-like 1 pr	302	33893	5.7	0	o	S
3105	2	1.87E-05	2	1.86E-05	1.004619		ENSG00000127359:E	KIAA1147			gi|122937185|ref|NP	hypothetical protein LOC571	455	51446	5.3	0	o	Q
3106	2	1.87E-05	1	5.46E-06	3.423364		ENSG00000119318:E	RAD23B			gi|4506387|ref|NP_0	UV excision repair protein RA	409	43171	4.8	0	o	Q
3107	2	1.82E-05	2	5.12E-06	3.554107		ENSG00000138802:E	SEC24B			gi|112382212|ref|NP	SEC24 (S. cerevisiae) homol	1268	137417	6.7	0	o	S
3108	2	1.74E-05	3	2.39E-05	0.728268		ENSG00000157184:E	CPT2			gi|4503023|ref|NP_0	carnitine palmitoyltransferase	658	73777	8.2	0	o	Q
3109	2	1.51E-05	2	5.18E-06	2.907436		ENSG00000120008:E	BRWD2			gi|13324688|ref|NP_	bromodomain and WD repea	1224	136685	6.9	0	o	Q
3110	2	1.39E-05	1	9.92E-06	1.402216		ENSG00000167378:E	IRGQ			gi|56090582|ref|NP_	immunity-related GTPase far	623	62717	4.9	0	o	Q
3111	2	1.28E-05	2	4.23E-06	3.034435		ENSG00000107651:E	SEC23IP			gi|6005824|ref|NP_0	Sec23-interacting protein p12	1000	111076	5.5	0	o	Q
3112	2	1.22E-05	1	2.77E-05	0.441896		ENSG00000137486:E	ARRB1			gi|10880134|ref|NP_	arrestin beta 1 isoform B [Ho	410	46309	6.3	0	o	Q
3113	2	1.16E-05	4	2.25E-05	0.517003		ENSG00000133392:E	MYH11			gi|13124875|ref|NP_	smooth muscle myosin heav	1938	223575	5.5	0	o	Q
3114	2	1.16E-05	4	3.83E-05	0.302959		ENSG00000166747:E	AP1G1			gi|71772942|ref|NP_	adaptor-related protein comp	822	91351	6.8	0	o	Q
3115	2	1.03E-05	6	3.88E-05	0.265121		ENSG00000115414:E	FN1			gi|16933542|ref|NP_	fibronectin 1 isoform 3 prepro	2355	259223	5.7	0	o	S
3116	2	9.66E-06	3	3.82E-05	0.252662		ENSG00000116266:E	STXBP3			gi|118600975|ref|NP	syntaxin binding protein 3 [Ho	592	67764	7.8	0	o	Q
3117	2	9.55E-06	1	7.98E-06	1.196856		ENSG00000138750:E	NUP54			gi|26051237|ref|NP_	nucleoporin 54kDa [Homo sa	507	55436	7	0	o	S
3118	2	8.54E-06	3	7.98E-06	1.069886		ENSG00000167716:E	WDR81			gi|116256466|ref|NP	WD repeat domain 81 [Homo	890	95676	5.1	0	o	Q
3119	2	8.4E-06	1	4.2E-06	2.00064		ENSG00000146909:E	NOM1			gi|61097912|ref|NP_	nucleolar protein with MIF4G	860	96257	8.1	0	o	Q
3120	2	7.63E-06	1	3.11E-06	2.451471		ENSG00000197226:E	TBC1D9B			gi|45597175|ref|NP_	TBC1 domain family, membe	1250	140525	5.3	0	o	Q
3121	2	7.44E-06	1	5.53E-06	1.343517		ENSG00000146834:E	MEPCE			gi|47271406|ref|NP_	bin3, bicoid-interacting 3 [Ho	689	74355	9.6	0	o	Q
3122	2	7.23E-06	1	2.53E-06	2.854119		ENSG00000124198:E	ARFGEF2			gi|150417986|ref|NP	ADP-ribosylation factor guan	1785	202037	6.3	0	o	Q
3123	2	7.11E-06	2	8.53E-06	0.832739		ENSG00000155629:E	PIK3AP1			gi|45505139|ref|NP_	phosphoinositide-3-kinase ad	805	90398	5.4	0	o	Q
3124	2	6.9E-06	1	1.61E-05	0.427371		ENSG00000114480:E	GBE1			gi|119393897|ref|NP	glucan (1,4-alpha-), branchin	702	80474	6.3	0	o	Q
3125	2	6.71E-06	1	2.02E-06	3.32727		ENSG00000155506:E	LARP1			gi|39725634|ref|NP_	la related protein isoform 1 [H	1019	116465	9.1	0	o	Q
3126	2	6.27E-06	1	1.55E-06	4.031523		ENSG00000141027:E	NCOR1			gi|22538461|ref|NP_	nuclear receptor co-represso	2440	270207	7.1	0	o	Q
3127	2	6.01E-06	1	4.37E-06	1.37502		ENSG00000156983:E	BRPF1			gi|51173720|ref|NP_	bromodomain and PHD finge	1220	138185	7.7	0	o	Q
3128	2	5.74E-06	2	8.31E-06	0.690806		ENSG00000119321:E	FKBP15			gi|150010552|ref|NP	FK506 binding protein 15, 13	1219	133630	5.2	0	o	Q
3129	2	5.66E-06	1	5.94E-06	0.953931		ENSG00000146872:E	TLK2			gi|45643117|ref|NP_	tousled-like kinase 2 isoform	750	85444	8.4	0	o	Q
3130	2	5.53E-06	3	1.33E-05	0.416881		ENSG00000115677:E	HDLBP			gi|42716280|ref|NP_	high density lipoprotein bindi	1268	141439	6.9	0	o	Q
3131	2	5.28E-06	1	4.13E-06	1.27956		ENSG00000198231:E	DDX42			gi|45446747|ref|NP_	DEAD box polypeptide 42 pr	938	102975	7	0	o	Q
3132	2	3.41E-06	4	3.25E-05	0.105052		ENSG00000148396:E	SEC16A			gi|124378039|ref|NP	SEC16 homolog A [Homo sa	2357	251891	5.8	0	o	Q
3133	2	3.31E-06	2	1.09E-05	0.302289		ENSG00000142197:E	DOPEY2			gi|45827701|ref|NP_	pad-1-like [Homo sapiens]	2298	258227	6.3	0	o	Q
3134	2	2.92E-06	3	1.96E-05	0.149305		ENSG00000061987:E	MON2			gi|114326552|ref|NP	MON2 homolog [Homo sapie	1717	190357	6.1	0	o	Q
3135	2	2.55E-06	1	4.36E-06	0.584539		ENSG00000160299:E	PCNT			gi|81295809|ref|NP_	pericentrin [Homo sapiens]	3336	378039	5.6	0	o	Q
3136	2	2.11E-06	1	5.06E-06	0.417739		ENSG00000143669:E	LYST			gi|54292123|ref|NP_	lysosomal trafficking regulato	3801	429141	6.6	0	o	Q
3137	1	0.000817	2	0.000178	4.60063		ENSG00000145287:E	PLAC8			gi|7706158|ref|NP_0	placenta-specific 8 [Homo sa	115	12507	7.6	0	i	Q
3138	1	0.000164	2	0.000138	1.188105		NA:ENSMUSG00000	RPS16			gi|4506691|ref|NP_0	ribosomal protein S16 [Homo	146	16445	10.2	0	o	Q
3139	1	0.000128	2	0.000113	1.13066		ENSG00000204444:E	APOM			gi|22091452|ref|NP_	apolipoprotein M [Homo sapi	188	21253	6	0	o	S
3140	1	0.000121	1	2.7E-05	4.499252		ENSG00000168035:N	LOC100131572			gi|169161552|ref|XP	PREDICTED: similar to hCG	84	9461	9.5	0	o	Q
3141	1	5.98E-05	1	0.001197	0.04995		ENSG00000187446:E	CHP			gi|6005731|ref|NP_0	calcium binding protein P22 [	195	22456	5.1	0	o	Q
3142	1	5.61E-05	4	0.00039	0.14368		ENSG00000175582:E	RAB6A			gi|19923231|ref|NP_	RAB6A, member RAS oncog	208	23549	5.5	0	o	Q
3143	1	5.32E-05	2	3.02E-05	1.765874		ENSG00000110880:E	CORO1C			gi|7656991|ref|NP_0	coronin, actin binding protein	474	53249	7.1	0	o	Q
3144	1	4.18E-05	2	6.53E-05	0.639712		ENSG00000176055:E	MBLAC2			gi|42822880|ref|NP_	similar to metallo-beta-lactam	279	31341	6.9	0	o	Q
3145	1	3.79E-05	6	9.06E-05	0.418711		ENSG00000070182:E	SPTB			gi|67782319|ref|NP_	spectrin beta isoform b [Hom	2137	246466	5.3	0	o	Q
3146	1	3.05E-05	3	3.64E-05	0.83778		ENSG00000109854:E	HTATIP2			gi|148728166|ref|NP	HIV-1 Tat interactive protein	276	30131	8.4	0	o	S
3147	1	2.76E-05	1	1.3E-05	2.132771		ENSG00000137502:E	RAB30			gi|21361418|ref|NP_	RAB30, member RAS oncog	203	23058	5	0	o	Q
3148	1	2.72E-05	2	5.15E-05	0.527358		ENSG00000155744:E	FAM126B			gi|28376658|ref|NP_	hypothetical protein LOC285	530	58647	7.9	0	o	Q
3149	1	2.58E-05	5	0.000199	0.129861		ENSG00000131100:E	ATP6V1E1			gi|4502317|ref|NP_0	vacuolar H+ ATPase E1 isofo	226	26145	8	0	o	Q
3150	1	2.47E-05	7	0.001106	0.022331		ENSG00000105854:E	PON2			gi|66529294|ref|NP_	paraoxonase 2 isoform 1 [Ho	354	39381	5.6	0	o	S
3151	1	2.41E-05	1	6.91E-06	3.488225		ENSG00000135919:E	SERPINE2			gi|24307907|ref|NP_	plasminogen activator inhibito	398	44002	9.3	0	o	S
3152	1	2.23E-05	1	0.000124	0.179693		ENSG00000167536:E	DHRS13			gi|146231950|ref|NP	dehydrogenase/reductase (S	377	40849	7.7	0	o	S
3153	1	2.19E-05	2	2.89E-05	0.756369		ENSG00000074416:E	MGLL			gi|51242953|ref|NP_	monoglyceride lipase isoform	303	33261	7	0	o	Q
3154	1	2.03E-05	3	3.53E-05	0.576666		ENSG00000181744:E	C3orf58			gi|27734895|ref|NP_	hypothetical protein LOC205	430	49482	8.5	0	o	S
3155	1	1.76E-05	1	1.37E-05	1.282147		ENSG00000181929:E	PRKAG1			gi|4506061|ref|NP_0	AMP-activated protein kinase	331	37579	6.9	0	o	Q
3156	1	1.31E-05	4	0.0001	0.131079		ENSG00000160285:E	LSS			gi|47933397|ref|NP_	lanosterol synthase [Homo sa	732	83309	6.6	0	o	Q
3157	1	1.27E-05	1	4.66E-06	2.721893		ENSG00000149187:E	CUGBP1			gi|38570081|ref|NP_	CUG triplet repeat, RNA-bind	483	51617	8.5	0	o	Q
3158	1	1.21E-05	3	2.08E-05	0.582624		ENSG00000173933:E	RBM4			gi|93277122|ref|NP_	RNA binding motif protein 4 [	364	40314	7.1	0	o	Q
3159	1	1.17E-05	1	5.1E-06	2.299566		ENSG00000090372:E	STRN4			gi|89886477|ref|NP_	zinedin isoform 1 [Homo sap	753	80596	5.4	0	o	S
3160	1	1.16E-05	1	4.66E-06	2.4901		ENSG00000135457:E	TFCP2			gi|21361278|ref|NP_	transcription factor CP2 [Hom	502	57256	5.8	0	o	Q
3161	1	1.02E-05	6	0.000106	0.096222		ENSG00000143627:E	PKLR			gi|10835121|ref|NP_	pyruvate kinase, liver and RB	574	61830	7.8	0	o	Q
3162	1	9.88E-06	4	0.00015	0.065871		ENSG00000182484:E	LOC376475			gi|169216741|ref|XP	PREDICTED: hypothetical pr	447	47990	5.7	0	o	Q
3163	1	9.57E-06	6	0.00366	0.002616		ENSG00000163631:E	ALB			gi|4502027|ref|NP_0	albumin precursor [Homo sap	609	69367	6.3	0	o	S
3164	1	9.53E-06	1	5.76E-06	1.654348		ENSG00000169299:E	PGM2			gi|63055049|ref|NP_	phosphoglucomutase 2 [Hom	612	68283	6.7	0	o	Q
3165	1	6.88E-06	1	2.76E-06	2.491046		ENSG00000132334:E	PTPRE			gi|18860859|ref|NP_	protein tyrosine phosphatase	642	74595	7.5	0	o	Q
3166	1	5.99E-06	1	6.17E-06	0.971322		ENSG00000087274:E	ADD1			gi|29826319|ref|NP_	adducin 1 (alpha) isoform a [	737	80955	5.8	0	o	Q
3167	1	5.97E-06	3	6.89E-05	0.08673		ENSG00000176658:E	MYO1D			gi|51100974|ref|NP_	myosin ID [Homo sapiens]	1006	116202	9.4	0	o	Q
3168	1	5.8E-06	3	2.28E-05	0.254178		ENSG00000133026:E	MYH10			gi|41406064|ref|NP_	myosin, heavy polypeptide 1	1976	228997	5.5	0	o	Q
3169	1	5.21E-06	6	0.00034	0.015329		ENSG00000100504:E	PYGL			gi|71037379|ref|NP_	glycogen phosphorylase, live	847	97149	7.2	0	o	Q
3170	1	4.64E-06	4	4.85E-05	0.095607		ENSG00000163554:E	SPTA1			gi|115298659|ref|NP	spectrin, alpha, erythrocytic 1	2419	280013	5	0	o	Q
3171	1	3.14E-06	6	0.000526	0.005955		ENSG00000183020:E	AP2A2			gi|27477041|ref|NP_	adaptor-related protein comp	939	103960	7	0	o	Q
3172	1	2.8E-06	1	1.25E-06	2.237958		ENSG00000183495:E	EP400			gi|56549696|ref|NP_	E1A binding protein p400 [Ho	3122	339693	9.2	0	o	Q
3173	1	2.77E-06	1	4.83E-06	0.57277		ENSG00000103194:E	USP10			gi|119220605|ref|NP	ubiquitin specific protease 10	798	87134	5.3	0	o	Q
3174	1	1.94E-06	2	2.93E-06	0.660465		ENSG00000197969:E	VPS13A			gi|15619008|ref|NP_	vacuolar protein sorting 13A	3095	350903	6	0	o	Q
3175	10	0.003719	4	0.001109	3.35322	Y	ENSG00000212874:E	MT-CO2			gi|17981856|ref|NP_	cytochrome c oxidase subun	227	25565	4.8	2	i26-48o63-	A
3176	8	0.002791	6	0.000561	4.979252	Y	ENSG00000075415:E	SLC25A3			gi|47132595|ref|NP_	solute carrier family 25 memb	361	39959	9.4	2	o261-283i3	Q
3177	8	0.002315	4	0.000473	4.898439	Y	ENSG00000164466:E	SFXN1			gi|23618867|ref|NP_	sideroflexin 1 [Homo sapiens	322	35619	9.1	3	o174-196i2	Q
3178	7	0.000759	6	0.000207	3.658171	Y	ENSG00000154174:E	TOMM70A			gi|54607135|ref|NP_	translocase of outer mitochon	608	67455	7.1	2	i7-29o39-6	S
3179	7	0.00026	8	0.008389	0.031	Y	ENSG00000151726:E	ACSL1			gi|40807491|ref|NP_	acyl-CoA synthetase long-ch	698	77943	7.1	1	i21-43o	A
3180	6	0.00215	5	0.000502	4.280603	Y	ENSG00000131143:E	COX4I1			gi|4502981|ref|NP_0	cytochrome c oxidase subun	169	19577	9.5	1	i103-120o	Q
3181	6	0.000185	0	0	INF	Y	ENSG00000115159:E	GPD2			gi|133908616|ref|NP	glycerol-3-phosphate dehydro	727	80834	7.5	1	i7-29o	S
3182	5	0.001119	0	0	INF	Y	ENSG00000087088:E	BAX			gi|20631958|ref|NP_	BCL2-associated X protein is	192	21184	5.2	1	o169-188i	Q

rk			RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs							
	SIGNALP_HMM_POS	SIGNALP_HMM_SPROB	HsNaOH-NE_NT_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Ti_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTi_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Ti_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Ti_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV
3037	18	0	0	0	0	5.99E-05	0	1	1.5E-05	2.99E-05	0	0	0	0.000166	0.00013	2	7.4E-05	8.67E-05
3038	46	0.159	0	0.0002	0	7.58E-05	0	2	6.9E-05	9.45E-05	0	4.81E-05	0	0	0	1	1.2E-05	2.41E-05
3039	20	1	0	5.9E-05	0	2.23E-05	0	2	2.03E-05	2.78E-05	0	0.000227	0	0	0	1	5.67E-05	0.000113
3040	0	0	0	0.00011	0	8.29E-05	0	2	4.81E-05	5.66E-05	0	0.000105	0	0	0	1	2.63E-05	5.27E-05
3041	18	0	0	0.000154	0	5.83E-05	0	2	5.31E-05	7.27E-05	0	0	0	8.08E-05	0	1	2.02E-05	4.04E-05
3042	26	0.001	0	4.77E-05	0	4.82E-05	0	2	2.4E-05	2.77E-05	0	0	0	0	0.000196	1	4.91E-05	9.82E-05
3043	18	0	0	0	0	6.93E-05	0	1	1.73E-05	3.46E-05	0	8.8E-05	0	0.000128	0	2	5.4E-05	6.45E-05
3044	0	0	0	7.69E-05	0	0	0	1	1.92E-05	3.84E-05	0	7.39E-05	0	0	0.000126	2	5.01E-05	6.17E-05
3045	38	0.019	0	3.07E-05	0	8.15E-05	0	2	2.8E-05	3.84E-05	0	0	0	0	0.000152	1	3.79E-05	7.59E-05
3046	17	0	0.000129	6.2E-05	0	0	0	2	4.79E-05	6.17E-05	0	0	0	0	6.89E-05	1	1.72E-05	3.45E-05
3047	33	0.002	0	0.000126	0	0	0	1	3.15E-05	6.3E-05	0	3.03E-05	0	0	0.000104	2	3.35E-05	4.89E-05
3048	29	0.671	0	9.18E-05	0	3.48E-05	0	2	3.16E-05	4.33E-05	0	0.000132	0	0	0	1	3.31E-05	6.62E-05
3049	0	0	0	8.22E-05	0	4.15E-05	0	2	3.09E-05	3.94E-05	0	0.000132	0	0	0	1	3.3E-05	6.59E-05
3050	20	0.003	0	4.39E-05	0.000177	1.66E-05	0	3	5.93E-05	8.04E-05	0	0	0	0	0	0	0	0
3051	0	0	0	6.81E-05	0	2.58E-05	0	2	2.35E-05	3.22E-05	0	9.83E-05	0	0	0	1	2.46E-05	4.92E-05
3052	16	0	0	0	0	5.19E-05	0.000598	2	1.3E-05	2.59E-05	0	0.000132	0	0	0	1	3.29E-05	6.59E-05
3053	52	0.001	0	3.5E-05	0	0	0	1	8.75E-06	1.75E-05	0	0.000108	0	1.96E-05	0	2	3.18E-05	5.14E-05
3054	18	0	0	0	0	3.61E-05	0	1	9.03E-06	1.81E-05	0	4.59E-05	0	0	7.85E-05	2	3.11E-05	3.83E-05
3055	20	0.366	0	5.37E-05	0	6.78E-05	0	2	3.04E-05	3.56E-05	0	3.45E-05	0	0	0	1	8.62E-06	1.72E-05
3056	37	0	0	5.58E-05	0	4.23E-05	0	2	2.45E-05	2.88E-05	0	5.37E-05	0	0	0	1	1.34E-05	2.68E-05
3057	23	0.005	8.74E-05	0	0	1.9E-05	0	2	2.66E-05	4.15E-05	0	3.63E-05	0	0	0	1	9.07E-06	1.81E-05
3058	21	0.002	0	5.08E-05	0	3.84E-05	0	2	2.23E-05	2.62E-05	0	4.88E-05	0	0	0	1	1.22E-05	2.44E-05
3059	0	0	0	1.88E-05	0	4.27E-05	0	2	1.54E-05	2.03E-05	0	7.24E-05	0	0	0	1	1.81E-05	3.62E-05
3060	19	0.326	0	0	0	4.89E-05	0	1	1.22E-05	2.44E-05	0	3.1E-05	0	0	5.31E-05	2	2.1E-05	2.59E-05
3061	23	0	0	8.08E-05	0	3.06E-05	0	2	2.79E-05	3.82E-05	0	1.94E-05	0	0	0	1	4.86E-06	9.72E-06
3062	58	0.001	0	7.44E-05	0	3.75E-05	0	2	2.8E-05	3.56E-05	0	0	0	1.73E-05	0	1	4.34E-06	8.67E-06
3063	0	0	0	2.61E-05	0	7.91E-05	0	2	2.63E-05	3.73E-05	0	0	0	1.83E-05	0	1	4.57E-06	9.14E-06
3064	0	0	0	1.37E-05	0	2.07E-05	0	2	8.59E-06	1.03E-05	0	0	0	8.6E-05	0	1	2.15E-05	4.3E-05
3065	25	0.008	0	0	0	1.64E-05	0	1	4.1E-06	8.19E-06	0	6.24E-05	0	0	3.56E-05	2	2.45E-05	3.03E-05
3066	17	0.01	0	4.59E-05	0	3.48E-05	0	2	2.02E-05	2.37E-05	0	0	0	3.21E-05	0	1	8.03E-06	1.61E-05
3067	24	1	0	0	0	2.07E-05	0	1	5.18E-06	1.04E-05	0	2.63E-05	0	3.83E-05	0	2	1.62E-05	1.93E-05
3068	45	0.599	0	9.6E-06	0	3.64E-06	0	2	3.31E-06	4.53E-06	0	0	0	0	3.16E-05	1	7.9E-06	1.58E-05
3069	23	0.806	0	5.03E-06	0	7.61E-06	0	2	3.16E-06	3.8E-06	0	4.84E-06	0	0	0	1	1.21E-06	2.42E-06
3070	64	0	0.001099	0.000237	0	0	0	2	0.000334	0.000522	0	0	0	0	0	0	0	0
3071	24	0	0	0.000239	0.00087	0	0	2	0.000277	0.000411	0	0	0	0	0	0	0	0
3072	48	0.011	0.00102	7.33E-05	0	0	0	2	0.000273	0.000499	0	0	0	0	0	0	0	0
3073	20	0.994	0	0	0	0.000505	0	1	0.000126	0.000252	0	0	0	0	0.000366	1	9.14E-05	0.000183
3074	28	0.677	0	0.000548	0	0	0	1	0.000137	0.000274	0	0.000211	0	0	0	1	5.27E-05	0.000105
3075	19	0.001	0	0.000605	0	0	0	1	0.000151	0.000302	0	0	0	7.56E-05	0	1	1.89E-05	3.78E-05
3076	19	0.005	0.000452	0.000195	0	0	0	2	0.000162	0.000214	0	0	0	0	0	0	0	0
3077	22	0.055	0	0	0	8.19E-05	0	1	2.05E-05	4.1E-05	0	0	0	0	0.000534	1	0.000133	0.000267
3078	24	0.029	0	0	0	0	0	0	0	0	0	0.00033	0	0	0.000282	2	0.000153	0.000178
3079	20	1	0	0.000478	0	9.06E-05	0	2	0.000142	0.000228	0	0	0	0	0	0	0	0
3080	0	0	0	0	0	0.000222	0	1	5.56E-05	0.000111	0	0	0	0.000288	0	1	7.19E-05	0.000144
3081	0	0	0	0	0	0	0	0	0	0	0	0.000351	0	0.000128	0	2	0.00012	0.000165
3082	30	0.012	0	0.000226	0	0	0	1	5.66E-05	0.000113	0	0.000218	0	0	0	1	5.45E-05	0.000109
3083	19	0.998	0	0.00023	0	0	0	1	5.74E-05	0.000115	0	0	0	0.000161	0	1	4.02E-05	8.04E-05
3084	0	0	0	0	0	7.21E-05	0	1	1.8E-05	3.6E-05	0	0	0	0	0.000313	1	7.83E-05	0.000157
3085	37	0.008	0	0	0	0	0	0	0	0	0	0	0	3.67E-05	0.000345	2	9.54E-05	0.000167
3086	16	0.622	0	0	0	6.91E-05	0	1	1.73E-05	3.46E-05	0	0	0	0	0.0003	1	7.51E-05	0.00015
3087	19	0	0	0	0	0.000292	0	1	7.31E-05	0.000146	0	0	0	7.72E-05	0	1	1.93E-05	3.86E-05
3088	30	0.01	0	0.000229	0	0	0	1	5.72E-05	0.000114	0	0.00011	0	0	0	1	2.75E-05	5.5E-05
3089	17	0	0	0	0	0.000156	0	1	3.91E-05	7.82E-05	0	0	0	0	0.00017	1	4.25E-05	8.49E-05
3090	19	1	0	0	0	0	0	0	0	0	0	0.000215	0	0	9.18E-05	2	7.66E-05	0.000102
3091	0	0	0	0.000186	0	0	0	1	4.64E-05	9.28E-05	0	0.000119	0	0	0	1	2.98E-05	5.95E-05
3092	0	0	0	0.000247	0	0	0	1	6.17E-05	0.000123	0	0	0	4.13E-05	0	1	1.03E-05	2.07E-05
3093	0	0	0	0	0	0.000147	0	1	3.67E-05	7.34E-05	0	0	0	0	0.000106	1	2.66E-05	5.32E-05
3094	19	0.001	0	0.000112	0	0	0	1	2.79E-05	5.58E-05	0	0	0	0	0.000122	1	3.06E-05	6.12E-05
3095	0	0	0	0	0	6.18E-05	0	1	1.54E-05	3.09E-05	0	0	0	0.000171	0	1	4.28E-05	8.56E-05
3096	50	0.197	0	0	0	0.000154	0	1	3.86E-05	7.72E-05	0	6.54E-05	0	0	0	1	1.64E-05	3.27E-05
3097	18	0.406	0	0	0	0	0	0	0	0	0	0.000195	0	2.37E-05	0	2	5.48E-05	9.44E-05
3098	17	0.002	0	0.000173	0	4.37E-05	0	2	5.42E-05	8.19E-05	0	0	0	0	0	0	0	0
3099	19	0.039	0	0	0	0.000112	0	1	2.79E-05	5.59E-05	0	0	0	0.000103	0	1	2.58E-05	5.16E-05
3100	16	0.001	0	0.000145	0	0	0	1	3.63E-05	7.27E-05	0	0	0	5.08E-05	0	1	1.27E-05	2.54E-05
3101	0	0	0	0	0	0	0	0	0	0	0	7.08E-05	0	0	0.000121	2	4.8E-05	5.91E-05
3102	27	0.982	0	0.00013	0	0	0	1	3.25E-05	6.5E-05	0	4.17E-05	0	0	0	1	1.04E-05	2.09E-05
3103	16	0	0	1.79E-05	0.000144	0	0	2	4.05E-05	6.96E-05	0	0	0	0	0	0	0	0
3104	19	1	0	7.72E-05	0	0	0	1	1.93E-05	3.86E-05	0	7.43E-05	0	0	0	1	1.86E-05	3.71E-05
3105	23	0.004	0	5.13E-05	0	0	0	1	1.28E-05	2.56E-05	0	9.86E-05	0	0	0	1	2.47E-05	4.93E-05
3106	0	0	0	0	0	0	0	0	0	0	0	0.00011	0	3.99E-05	0	2	3.74E-05	5.17E-05
3107	39	0.734	0.000128	0	0	0	0	1	3.2E-05	6.39E-05	0	1.77E-05	0	0	0	1	4.42E-06	8.85E-06
3108	28	0.092	0	7.09E-05	0	0	0	1	1.77E-05	3.54E-05	0	6.82E-05	0	0	0	1	1.7E-05	3.41E-05
3109	52	0.014	0	0	0	5.77E-05	0	1	1.44E-05	2.89E-05	0	0	0	0	6.27E-05	1	1.57E-05	3.14E-05
3110	20	0.136	0	0	0	8.51E-05	0	1	2.13E-05	4.25E-05	0	0	0	2.62E-05	0	1	6.55E-06	1.31E-05
3111	29	0.024	0	0	0	3.53E-05	0	1	8.83E-06	1.77E-05	0	6.73E-05	0	0	0	1	1.68E-05	3.37E-05
3112	0	0	0	0	0	4.31E-05	0	1	1.08E-05	2.15E-05	0	5.47E-05	0	0	0	1	1.37E-05	2.74E-05
3113	0	0	8.37E-05	0	0	9.29E-06	0	2	2.32E-05	4.05E-05	0	0	0	0	0	0	0	0
3114	22	0.001	0	2.84E-05	0	6.45E-05	0	2	2.32E-05	3.06E-05	0	0	0	0	0	0	0	0
3115	26	0.997	0	2.97E-05	0	5.25E-05	0	2	2.06E-05	2.55E-05	0	0	0	0	0	0	0	0
3116	21	0	0	3.94E-05	0	0	0	1	9.85E-06	1.97E-05	0	3.79E-05	0	0	0	1	9.47E-06	1.89E-05
3117	27	0.592	0	0	0	0	0	0	0	0	0	4.43E-05	0	3.22E-05	0	2	1.91E-05	2.26E-05
3118	20	0.003	0	0	0	0	0	0	0	0	0	2.52E-05	0	0	4.31E-05	2	1.71E-05	2.1E-05
3119	18	0.001	0	0	0	4.11E-05	0	1	1.03E-05	2.05E-05	0	2.61E-05	0	0	0	1	6.52E-06	1.3E-05
3120	23	0.08	0	1.87E-05	0	4.24E-05	0	2	1.53E-05	2.01E-05	0	0	0	0	0	0	0	0
3121	0	0	0	3.39E-05	0	2.56E-05	0	2	1.49E-05	1.75E-05	0	0	0	0	0	0	0	0
3122	21	0.001	0	3.27E-05	0	0	0	1	8.17E-06	1.63E-05	0	2.51E-05	0	0	0	1	6.28E-06	1.26E-05
3123	21	0.001	0	2.9E-05	0	0	0	1	7.24E-06	1.45E-05	0	2.79E-05	0	0	0	1	6.97E-06	1.39E-05
3124	32	0.002	0	0	0	0	0	0	0	0	0	3.2E-05	0	2.32E-05	0	2	1.38E-05	1.63E-05
3125	31	0	0	0	0	0	0	0	0	0	0	0	0	1.6E-05	3.77E-05	2	1.34E-05	1.78E-05
3126	0	0	0	0	0	4.34E-05	0	1	1.09E-05	2.17E-05	0	0	0	6.69E-06	0	1	1.67E-06	3.34E-06
3127	17	0	0	1.91E-05	0	2.9E-05	0	2	1.2E-05	1.44E-05	0	0	0	0	0	0	0	0
3128	33	0.001	0	1.91E-05	0	0	0	1	4.78E-06	9.57E-06	0	0	0	2.68E-05	0	1	6.69E-06	1.34E-05
3129	0	0	0	0	0	2.36E-05	0	1	5.89E-06	1.18E-05	0	0	0	2.18E-05	0	1	5.44E-06	1.09E-05
3130	19	0.005	0	0	0	1.39E-05	0	1	3.48E-06	6.97E-06	0	0	0	0	3.03E-05	1	7.57E-06	1.51E-05
3131	25	0.006	0	2.49E-05	0	0	0	1	6.22E-06	1.24E-05	0	0	0	1.74E-05	0	1	4.35E-06	8.7E-06
3132	22	0.001	0	1.98E-05	0	7.49E-06	0	2	6.82E-06	9.34E-06	0	0	0	0	0	0	0	0
3133	0	0	0	0	0	0	0	0	0	0	0	9.76E-06	0	0	1.67E-05	2	6.62E-06	8.15E-06
3134	0	0	0	0	0	1.03E-05	0	1	2.57E-06	5.14E-06	0	1.31E-05	0	0	0	1	3.27E-06	6.53E-06
3135	0	0	0	0	0	1.06E-05	0	1	2.65E-06	5.3E-06	0	0	0	9.78E-06	0	1	2.45E-06	4.89E-06
3136	30	0	0	1.23E-05	0	4.65E-06	0	2	4.23E-06	5.79E-06	0	0	0	0	0	0	0	0
3137	18	0.058	0	0	0.006535	0	0	1	0.001634	0.003267	0	0	0	0	0	0	0	0
3138	22	0.003	0	0	0	0	0	0	0	0	0	0	0	0	0.001315	1	0.000329	0.000657
3139	23	0.637	0	0	0	0	0	0	0	0	0	0	0	0	0.001021	1	0.000255	0.00051
3140	65	0	0	0	0	0	0	0	0	0	0	0	0	0.000971	0	1	0.000243	0.000486
3141	0	0	0	0.000478	0	0	0	1	0.00012	0.000239	0	0	0	0	0	0	0	0
3142	30	0	0	0.000449	0	0	0	1	0.000112	0.000224	0	0	0	0	0	0	0	0
3143	24	0	0	0	0	0	0	0	0	0	0	0.000426	0	0	0	1	0.000106	0.000213
3144	16	0	0	0.000334	0	0	0	1	8.36E-05	0.000167	0	0	0	0	0	0	0	0
3145	0	0	0.000304	0	0	0	0	1	7.59E-05	0.000152	0	0	0	0	0	0	0	0
3146	19	0.993	0	0	0	0	0	0	0	0	0	0.000244	0	0	0	1	6.1E-05	0.000122
3147	22	0.001	0	0	0	0	0	0	0	0	0	0.000221	0	0	0	1	5.53E-05	0.000111
3148	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000217	1	5.43E-05	0.000109
3149	0	0	0	0.000206	0	0	0	1	5.16E-05	0.000103	0	0	0	0	0	0	0	0
3150	24	0.997	0	0.000198	0	0	0	1	4.94E-05	9.88E-05	0	0	0	0	0	0	0	0
3151	21	0.995	0	0	0	0	0	0	0	0	0	0	0	0	0.000193	1	4.82E-05	9.65E-05
3152	26	0.762	0	0	0	0	0	0	0	0	0	0.000179	0	0	0	1	4.46E-05	8.93E-05
3153	26	0	0	0	0	0.000175	0	1	4.37E-05	8.74E-05	0	0	0	0	0	0	0	0
3154	38	0.993	0	0.000163	0	0	0	1	4.07E-05	8.14E-05	0	0	0	0	0	0	0	0
3155	0	0	0	0.000141	0	0	0	1	3.52E-05	7.05E-05	0	0	0	0	0	0	0	0
3156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000105	1	2.62E-05	5.24E-05
3157	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000101	0	1	2.53E-05	5.07E-05
3158	17	0	0	0	0	9.71E-05	0	1	2.43E-05	4.85E-05	0	0	0	0	0	0	0	0
3159	24	0.962	0	0	0	9.38E-05	0	1	2.35E-05	4.69E-05	0	0	0	0	0	0	0	0
3160	17	0.002	0	9.29E-05	0	0	0	1	2.32E-05	4.65E-05	0	0	0	0	0	0	0	0
3161	37	0	0	8.13E-05	0	0	0	1	2.03E-05	4.06E-05	0	0	0	0	0	0	0	0
3162	22	0	0	0	0	7.9E-05	0	1	1.98E-05	3.95E-05	0	0	0	0	0	0	0	0
3163	19	1	0	7.66E-05	0	0	0	1	1.91E-05	3.83E-05	0	0	0	0	0	0	0	0
3164	16	0	0	7.62E-05	0	0	0	1	1.91E-05	3.81E-05	0	0	0	0	0	0	0	0
3165	20	0	0	0	0	5.5E-05	0	1	1.38E-05	2.75E-05	0	0	0	0	0	0	0	0
3166	20	0.002	0	0	0	4.79E-05	0	1	1.2E-05	2.4E-05	0	0	0	0	0	0	0	0
3167	0	0	0	4.78E-05	0	0	0	1	1.19E-05	2.39E-05	0	0	0	0	0	0	0	0
3168	29	0	0	0	0	0	0	0	0	0	0	0	0	0	4.64E-05	1	1.16E-05	2.32E-05
3169	0	0	0	0	0	4.17E-05	0	1	1.04E-05	2.09E-05	0	0	0	0	0	0	0	0
3170	0	0	0	0	0	0	0	0	0	0	0	3.71E-05	0	0	0	1	9.27E-06	1.85E-05
3171	26	0.001	0	0	0	2.51E-05	0	1	6.27E-06	1.25E-05	0	0	0	0	0	0	0	0
3172	20	0	0	2.24E-05	0	0	0	1	5.6E-06	1.12E-05	0	0	0	0	0	0	0	0
3173	16	0	0	0	0	2.21E-05	0	1	5.53E-06	1.11E-05	0	0	0	0	0	0	0	0
3174	17	0	0	0	0	0	0	0	0	0	0	0	0	0	1.55E-05	1	3.88E-06	7.75E-06
3175	48	0.001	0.003572	0.001747	0.011587	0.001012	0.005381	5	0.004479	0.004859	0.003911	0.00336	0.030802	0.000503	0.004059	5	0.002958	0.001664
3176	28	0.001	0.002695	0.002972	0.004684	0.001957	0	4	0.003077	0.001154	0.003689	0.004226	0	0.000723	0.001382	4	0.002505	0.001712
3177	0	0	0.002518	0.000685	0	0.000549	0.001264	4	0.000938	0.001094	0.011028	0.002021	0	5.07E-05	0.001669	4	0.003692	0.004965
3178	21	0.936	0.002667	0.001266	0.000618	0.00032	0	4	0.001218	0.001044	0	0.000812	0	0.000134	0.000253	3	0.0003	0.000357
3179	49	0.002	0.000929	6.68E-05	0	2.53E-05	0	3	0.000255	0.00045	0.000636	0.000321	0	4.68E-05	5.5E-05	4	0.000265	0.000278
3180	24	0.106	0	0.00069	0.003335	0.000209	0	3	0.001059	0.001545	0.010506	0.001328	0	0	0.001136	3	0.003242	0.004878
3181	24	0.858	0.000446	0.00016	0	0.000146	0	3	0.000188	0.000187	0.000611	9.26E-05	0	2.24E-05	0	3	0.000181	0.000289
3182	36	0	0	0.001093	0.005871	0	0	2	0.001741	0.002801	0	0.000701	0	0.000085	0.0012	3	0.000496	0.000563

rk	MMs										
	MmNaOH-MM_liver_CNBrTi_1_dNSAF	MmNaOH-MM_liver_CNBrTi_2_dNSAF	RnNaOH-MM_liver_Ti_1_dNSAF	RnNaOH-MM_liver_Ti_2_dNSAF	RnNaOH-MM_liver_Ti_3_dNSAF	RnNaOH-MM_liver_Ti_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
3037	0	0	0	0.000123	0	0	0	0		endoplasmic reticulum; Golgi	binding; intracellular
3038	0	0	0	0.000101	0	0	0	0	Nicotinate		nicotinate
3039	0	0	0.000232	0.000205	0	7.86E-05	0.000245	0.000501	6PGL: 6-	endoplasmic reticulum	6-phosphogluconolactonase
3040	0	0	0.000873	0.000257	0	7.38E-05	0.000307	0	Vesicle transport v-SNARE	integral to membrane;	receptor activity; transporter
3041	0	0	7.66E-05	3E-05	0	5.18E-05	0	0	Protein kinase C conserved		ATP binding; diacylglycerol
3042	0	0	0.000534	0.000154	0	5.05E-05	0.000171	0	Alpha adaptin AP2, C-	AP-2 adaptor complex [pmid	binding; structural molecule
3043	0	0	0	0.000142	0	6.14E-05	0	0	The electron transfer	mitochondrial matrix [pmid	electron carrier activity [pmid
3044	0	0	0	0	0	0.000103	0	0	HSR1/MMR1. Human	intracellular	GTP binding [pmid 8180467];
3045	0	0	6.09E-05	2.39E-05	0	0	0	0	Cullin, a subunit of E3		protein binding [pmid
3046	0	0	7.4E-05	2.9E-05	0	0	0	0	Cytoplasmic Fragile-X		
3047	0	0	0	4.9E-05	0	2.11E-05	0	0	fzo-like conserved region.	integral to membrane;	GTP binding; GTPase
3048	0	0.001477	0	0.000323	0	0.000124	0.000193	6.06E-05	UAS family; UAS is a		
3049	0	0	0	0	0	0.000112	0	0	STAT protein, DNA binding	nucleus	calcium ion binding;
3050	0	0	0.00054	0.0003	0.000421	0.000487	0	5.97E-05			
3051	0	0	6.76E-05	1.77E-05	4.68E-05	3.05E-05	3.17E-05	0	B-cell receptor-associated	myosin	ATP binding; DNA binding;
3052	0	0	0	5.33E-05	0	0	0	0	Glutamine	cytoplasm	glutamine-fructose-6-
3053	0	0	0	2.24E-05	0.000357	1.93E-05	0	0	Sterile alpha motif.;	integral to membrane [pmid	calcium ion binding; protein
3054	0	0	0	0	0	3.23E-05	0	0	WD40 domain, found in a		actin binding
3055	0	0.000136	0	0	0	0	0	0	Leucine-rich repeats	cytoplasm [pmid 11375975]	ErbB-2 class receptor
3056	0.002115	0	0.000443	8.68E-05	0.000345	7.49E-05	0	0	Mitochondrial carrier	integral to membrane;	binding
3057	0	0	0.001004	0.001133	0.001324	0.00087	0.000172	0.000211	DEATH domain, found in	actin cytoskeleton;	cytoskeletal adaptor activity
3058	0	0	0	0	4.87E-05	0	0	0	WD40 domain, found in a	nucleus	signal transducer activity
3059	0	0	0	1.81E-05	0	1.56E-05	0	0			
3060	0	0	0.000128	0	0	0	0	0	Vps52 / Sac2 family. Vps52	membrane	
3061	0	0	0.000193	0.000106	0	7.84E-05	0	0			
3062	0	0	4.92E-05	1.93E-05	0	0	0	0	RING-finger (Really	membrane	ATP binding; metal ion
3063	0	0	0.000322	0.000232	0.000168	0.0002	3.78E-05	3.56E-05	Major Vault Protein repeat.	cytoplasm [pmid 7585126];	
3064	0	0	0	0	0	0.000108	0	0	SET domain. SET domains	nucleus	histone-lysine N-
3065	0	0	0	5.05E-05	4.46E-05	0	0	0	Diaphanous GTPase-		actin binding; binding; Rho
3066	0	0	0	3.57E-05	0	0	0	0	Phenylalanyl-tRNA	cytoplasm [pmid 9177188];	ATP binding; ligase activity;
3067	0	0	0	0	0	0	0	3.45E-05	Flavin containing amine	nucleus	oxidoreductase activity;
3068	0	0	9.23E-06	0	0	0	6.5E-06	0			
3069	0	0	0	0	0	0	0	6.31E-06			
3070	0	0	0	0.000123	0	5.29E-05	0.00033	0.000726	Scramblase. Scramblase is	integral to membrane; plasma	calcium ion binding [pmid
3071	0	0	0.001713	0.000756	0.000445	0.001686	0	0.000568	Rab11-like. Rab11a,	Golgi trans face [pmid	GTP binding; GTPase
3072	0.00278	0.01997	0.000255	0.00045	0.000133	0.000216	0	0	Mitochondrial carrier	integral to membrane;	binding
3073	0	0	0.000436	0	0	0	0	0	4Fe-4S binding domain.	membrane fraction;	4 iron, 4 sulfur cluster
3074	0	0	0	8.51E-05	0	7.35E-05	0	0	Protein of unknown function	integral to membrane;	apoptotic protease activator
3075	0	0	0.000215	0.000938	0.002237	0.001486	0	0	Rab2 subfamily. Rab2 is	endoplasmic reticulum;	GTP binding; nucleotide
3076	0.002463	0	0.00029	0.000303	0	0.000698	9.07E-05	0	G-protein alpha subunit. G	cytoplasm [pmid 9175863];	GTP binding; GTPase
3077	0	0	0.000214	0	0	4.82E-05	0	4.73E-05	ABC1 family. This family	mitochondrion	
3078	0	0	0	0.000267	0	0	0.000479	0.000226	Ribosomal L27e protein	intracellular; ribosome [pmid	structural constituent of
3079	0	0	0	0.000794	0.001404	0.000343	0.000238	0.000224			selenium binding [pmid
3080	0	0	0.000117	0.00032	0	0.000355	0	0	DnaJ central domain (4		heat shock protein binding;
3081	0	0	0.00111	0.001016	0.001154	0.000626	0.002085	0.000245			
3082	0	0	0.000449	0.000205	0	0.00038	0.000791	0.000596	RalA/RalB subfamily. The	intracellular; membrane	GTP binding [pmid 2550440];
3083	0	0	0.00046	0.000271	0.000479	0.000857	0	0	Glutathione (GSH)		glutathione peroxidase
3084	0	0	0	0.000147	0	0	0	0			
3085	0	0	0	0.000123	0	0	0	0	Inosine/xanthosine		
3086	0	0	0.000453	0.000177	0.000471	0	6.37E-05	0	Adaptor complexes medium	clathrin vesicle coat; COPI	
3087	0	0	0.000709	6.95E-05	0	0.00018	6.24E-05	0	Adaptor complexes medium	clathrin vesicle coat; coated	protein binding [pmid
3088	0	0	0	0.0008	0.000236	0.000175	0	0.003159	M-Ras/R-Ras-like	intracellular; membrane	GTP binding; nucleotide
3089	0	0	0.000306	0.00016	0	0.000103	0	6.76E-05	GRASP55/65 family.	membrane	protein binding
3090	0	0	0.000222	8.7E-05	0	0	0	0	Heat shock protein 47	endoplasmic reticulum [pmid	collagen binding [pmid
3091	0	0.000994	0.001107	0.000434	0.000128	0.000208	0	0	Peroxisomal membrane	integral to peroxisomal	protein binding [pmid
3092	0	0	0.000235	0.00035	0	0.000171	0.000331	0.000234			
3093	0	0	0	0.0001	0	0.00013	0	8.50E-05	CDC/Septin. Septins are a	contractile ring [pmid	GTP binding; GTPase
3094	0	0	0	5.79E-05	0	0	0	0	Protein of unknown function		
3095	0	0	0	6.34E-05	0	0.000274	0	0	F-actin capping protein	F-actin capping protein	actin binding
3096	0	0	0.000269	0.000527	0.00042	0.000683	0.000379	0.000357	short chain dehydrogenase;	mitochondrial matrix;	3-hydroxybutyrate
3097	0	0	0	5.28E-05	0	0	0	0			
3098	0	0	0	9.05E-05	0	3.9E-05	0	0	effector domain of the CAP	cAMP-dependent protein	cAMP binding; cAMP-
3099	0	0	0	0.000125	0	0	0	0	JAB/MPN domain; Domain	nuclear ubiquitin ligase	enzyme regulator activity
3100	0	0	0.00058	0.000227	0	0.000343	0	0	Annexin. This family of	cytoplasm [pmid 16130169]	calcium ion binding; calcium-
3101	0	0	0	5.79E-05	0	0	0	0	ABC Carbohydrate and	ATP-binding cassette (ABC)	ATP binding [pmid 9878413];
3102	0	0	0	0.000103	0	0	0	0	Sterile alpha motif.;		
3103	0	0	3.55E-05	0	0	0	0	0			
3104	0	0	0	5.81E-05	0	0	0	0	deoxyribonuclease I;	endoplasmic reticulum	deoxyribonuclease activity
3105	0	0	0	4.08E-05	0.000108	0	0	0			
3106	0	0	0	4.37E-05	0	0	0	0	XPC-binding domain.	nucleus [pmid 8168482]	single-stranded DNA binding
3107	0	0	0	1.5E-05	0	2.59E-05	0	0			
3108	0	0	7.03E-05	0	7.31E-05	4.76E-05	0	0	Choline/Carnitine o-	membrane; mitochondrial	acyltransferase activity;
3109	0	0	0	1.48E-05	0	0	2.66E-05	0	WD40 domain, found in a	integral to membrane;	
3110	0	0	7.93E-05	0	0	0	0	0			
3111	0	0	0	1.82E-05	0	1.57E-05	0	0	DDHD domain. The DDHD	cytoplasm [pmid 10400679];	metal ion binding; protein
3112	0	0	0.000221	0	0	0	0	0	Arrestin (or S-antigen), N-	cytoplasm [pmid 10823817];	enzyme inhibitor activity
3113	0	0	0	4.67E-05	0	9.42E-05	2.23E-05	1.67E-05	Myosin motor domain, type	muscle myosin [pmid	actin binding; ATP binding;
3114	0	0	0	0.000154	0	7.59E-05	3.95E-05	3.72E-05	Adaptin C-terminal domain.	clathrin coat of trans-Golgi	binding; transporter activity
3115	0	0	5.6E-05	0.000124	3.88E-05	1.26E-05	6.57E-05	1.24E-05	Fibronectin type 3 domain;	ER-Golgi intermediate	collagen binding [pmid
3116	0	0	7.8E-05	0.000122	0	0.000106	0	0			
3117	0	0	0	0	0	0	6.39E-05	0		cytoplasm [pmid 8707840];	
3118	0	0	2.4E-05	0	0	8.11E-06	0	3.18E-05			
3119	0	0	0	0	0	0	0	3.36E-05	MIF4G domain. MIF4G is		RNA binding
3120	0	0	0	0	0	2.49E-05	0	0	TBC domain. Identification		calcium ion binding
3121	0	0	0	0	0	0	0	4.43E-05	Bicoid-interacting protein 3		methyltransferase activity;
3122	0	0	0	2.03E-05	0	0	0	0			
3123	0	0	0	0	5.15E-05	1.68E-05	0	0			kinase activity
3124	0	0	0	0.000129	0	0	0	0			
3125	0	0	0	1.61E-05	0	0	0	0	La protein, small RNA-		RNA binding
3126	0	0	0	0	0	0	0	1.24E-05	'SWI3, ADA2, N-CoR and	nucleus	DNA binding; protein binding
3127	0	0	3.5E-05	0	0	0	0	0	Putative transcriptional	intracellular; nucleus [pmid	DNA binding; metal ion
3128	0	0	0	1.49E-05	0	5.15E-05	0	0			
3129	0	0	0	0	0	0	0	4.75E-05	Serine/Threonine protein	nucleus [pmid 9427565] [pmid	ATP binding [pmid
3130	0	0	3.65E-05	5.72E-05	0	1.23E-05	0	0	K homology RNA-binding	nucleus; plasma membrane	lipid binding [pmid 1318310];
3131	0	0	0	0	0	0	0	3.30E-05	Helicase superfamily c-		ATP binding; ATP-dependent
3132	0	0	3.35E-05	0.000157	3.48E-05	3.4E-05	0	0			
3133	0	0	6.03E-05	0	0	2.72E-05	0	0	Dopey, N-terminal. DopA is	Golgi membrane [pmid	
3134	0	0	0.000108	2.12E-05	0	2.74E-05	0	0			
3135	0	0	0	3.49E-05	0	0	0	0	Membrane-bound		calmodulin binding
3136	0	0	0	0	0	0	0	4.05E-05	WD40 domain, found in a	endosome [pmid 9606205];	
3137	0	0	0	0	0	0	0.000872	0.000548	PLAC8 family. This family		
3138	0	0	0.000925	0.000181	0	0	0	0	Ribosomal protein S9/S16.	cytosolic small ribosomal	structural constituent of
3139	0	0	0	9.55E-05	0	0	0	0.000808		integral to plasma membrane	binding; lipid transporter
3140	0	0	0	0.000216	0	0	0	0			
3141	0	0.009578	0	0	0	0	0	0	EF-hand, calcium binding		calcium ion binding;
3142	0	0	0.000667	0.001482	0	0.000677	0	0.000295	Rab6 subfamily. Rab6 is	Golgi apparatus [pmid	GTP binding; GTPase
3143	0	0	0	3.83E-05	0.000203	0	0	0	WD40 domain, found in a	actin cytoskeleton [pmid	actin binding
3144	0	0	0	0.00013	0	0.000393	0	0	Zn-dependent hydrolases,		
3145	0	0	0.000156	0.000258	2.25E-05	0.000245	1.52E-05	2.87E-05	Spectrin repeats, found in	cytoskeleton; membrane;	actin binding; actin filament
3146	0	0	0.000168	6.6E-05	0	5.69E-05	0	0			
3147	0	0	0	0.000104	0	0	0	0	Rab30 subfamily. Rab30	Golgi stack [pmid 9792283];	GTP binding; GTPase
3148	0	0	0	0	0	0	0.000143	0.000269		intracellular [pmid 11256614]	
3149	0	0	0	0.000401	0.000213	0.000416	0.000288	0.000272	ATP synthase (E/31 kDa)	plasma membrane; proton-	hydrogen-transporting ATP
3150	0.001249	0	0.001045	0.001383	0.000272	0.00115	0.001932	0.00182	Arylesterase. This family	extracellular region;	aryldialkylphosphatase
3151	0	0	0	0	0	0	5.53E-05	0	Plasminogen activator	extracellular region [pmid	heparin binding [pmid
3152	0	0.000994	0	0	0	0	0	0			
3153	0	0	0	0.00018	0	5.17E-05	0	0	alpha/beta hydrolase fold.		acylglycerol lipase activity;
3154	0	0	0.000151	2.95E-05	0	0.000102	0	0			
3155	0	0	0	0.00011	0	0	0	0	This cd contains two		cAMP-dependent protein
3156	0	0	6.31E-05	0.000173	0	0.000342	0.000222	0	Squalene cyclase (SQCY)		isomerase activity;
3157	0	0	0	3.72E-05	0	0	0	0	RNA recognition motif;	nucleus [pmid 10893231];	BRE binding [pmid
3158	0	0	0	3.77E-05	0	6.51E-05	0	6.38E-05	Zinc knuckle. The zinc	nucleus	metal ion binding; nucleotide
3159	0	0	0	0	0	0	0	4.08E-05	WD40 domain, found in a	cytoplasm [pmid 10748158];	calmodulin binding [pmid
3160	0	0	0	3.73E-05	0	0	0	0	CP2 transcription factor.	nucleus	transcription factor activity
3161	0	0	8.52E-05	0.000267	8.86E-05	0.000231	6E-05	0.000113	Pyruvate kinase, barrel		magnesium ion binding;
3162	0	0	0.00039	0.000344	0	0.00033	0.000137	0			
3163	0	0	0.004717	0.005429	0.00538	0.004814	0.00591	0.003028		extracellular region [pmid	antioxidant activity [pmid
3164	0	0	0	0	0	0	0	4.61E-05	Phosphoglucomutase/phos		isomerase activity;
3165	0	0	0	2.21E-05	0	0	0	0	Protein tyrosine	cytoplasm; integral to plasma	hydrolase activity; protein
3166	0	0	0	4.94E-05	0	0	0	0	Class II Aldolase and	actin cytoskeleton; membrane	actin binding [pmid
3167	0	0	0	0.000126	0.000191	0.000233	0	0	Myosin motor domain, type	myosin	actin binding; ATP binding;
3168	0	0	0	2.91E-05	0	0	0.000137	1.67E-05	Myosin motor domain, type	myosin [pmid 7499478]	actin binding [pmid
3169	0	0	0.000707	0.00032	0.001358	0.000184	0.000115	3.61E-05	Carbohydrate		glycogen phosphorylase
3170	0	0	0.000175	0.000114	4.03E-05	5.91E-05	0	0			
3171	0	0	0.00133	0.001042	0.000462	0.0009	0.000347	0.000131	Alpha adaptin AP2, C-	AP-2 adaptor complex;	binding; lipid binding;
3172	0	0	0	0	0	0	0	1.00E-05	Helicase superfamily c-	nucleus	ATP binding; DNA binding;
3173	0	0	0	0	0	0	0	3.86E-05			
3174	0	0	0	5.35E-06	0	0	0	1.81E-05	Protein of unknown function	intracellular [pmid 11381254]	intracellular transporter
3175	0	0	0	0.000559	0	0.000138	0.003444	0.004731	Cytochrome C oxidase		
3176	0	0	0.00039	0.000917	0.001216	0.000616	0.000915	0.000431	Mitochondrial carrier	integral to plasma membrane	binding; phosphate carrier
3177	0	0	0.002155	0.000169	0	0.000243	0.001214	0	Tricarboxylate carrier;	integral to membrane;	cation transporter activity;
3178	0	0	0.000758	0.000149	0.000158	0.00018	0.000214	0.000201	Tetratricopeptide repeat	integral to membrane;	protein binding [pmid
3179	0.000949	0.008603	0.007147	0.010428	0.010541	0.009853	0.008239	0.011355	Long-chain acyl-CoA	integral to membrane;	ligase activity; long-chain-
3180	0	0	0.000274	0.000429	0.000285	0.001297	0.001735	0	Cytochrome c oxidase	membrane; mitochondrion	cytochrome-c oxidase
3181	0	0	0	0	0	0	0	0			
3182	0	0	0	0	0	0	0	0	Apoptosis regulator	integral to membrane;	protein binding [pmid

rk	NEs detected # out of 10 runs	NEs dNSAF_A VG	MMs detected # out of 8 runs	MMs dNSAF_A VG	NEs:MMs	Detected in Mito	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP _HMM_P OS	SIGNALP _HMM_S PROB	RESTING LYMPHOCYTES NEs HsNaOH-NE_NT_lymphocytes_CNBrTl_1_dNSAF	HsNaOH-NE_NT_lymphocytes_Tl_1_dNSAF	HsSD-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_Tl_1_dNSAF	NT-dNEs Detected # Out of 5	NT-dNEs dNSAF AVG	NT-dNEs dNSAF SDV	PHA-TREATED LYMPHOCYTES NEs HsNaOH-NE_PHA_lymphocytes_CNBrTl_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_Tl_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_Tl_1_dNSAF	PHA-NEs Detected # Out of 5	PHA-NEs dNSAF AVG	PHA-NEs dNSAF SDV	MMs MmNaOH-MM_liver_CNBrTl_1_dNSAF	MmNaOH-MM_liver_Tl_2_dNSAF	RnNaOH-MM_liver_Tl_1_dNSAF	RnNaOH-MM_liver_Tl_2_dNSAF	RnNaOH-MM_liver_Tl_3_dNSAF	RnNaOH-MM_liver_Tl_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
3183	5	0.000872	0	0	INF	Y	ENSG00000212875:ENPF	MT-CO1			ENSG00000198804:MT-CO1	cytochrome c oxidase subun	513	57041	6.7	12	20-42c57-A	31	0.208	0	0.000136	0.005226	3.44E-05	3	0.001596	0.003085	0	0.000131	0	0.000449	3	0.000145	0.000212	0	0	0	0	0	0	0	0	Cytochrome C oxidase	Cytochrome c	
3184	5	0.000181	1	0.000364	0.497365	Y	ENSG00000212870:MT-ND5	MT-ND5			ENSG00000198786:MT-ND5	NADH dehydrogenase subun	603	67013	9	15	35-57c85-S	22	0.789	0	0.000851	0	8.79E-05	2	0.000235	0.000413	0	0.000846	0	6.37E-05	3	0.000128	0.000215	0.002913	0	0	0	0	0	0	0	NADH-		
3185	5	0.000259	1	5.04E-05	5.144779	Y	ENSG00000198763:MT-ND4	MT-ND4			ENSG00000198886:MT-ND4	NADH dehydrogenase subun	459	51681	9.4	10	23-45c105-S	18	0.797	0.000707	0.00065	0	3.85E-05	3	0.000339	0.000271	0	0.000463	0	8.36E-05	3	0.000208	0.000327	0	0.000463	0	0	0	0	0	0	NADH-		
3186	5	0.000153	0	0	INF	Y	ENSG00000173371:MTK1	MTK1			ENSG00000198763:MTK1	mitochondrial tRNA methyl	396	45477	9.8	1	42c1-443-G	37	0.955	0	0.000604	0	0	1	0.000119	0.000191	0	0.000481	0.000105	0.000165	3	0.000188	0.000207	0	0	0	0	0.000505	0	0	GST_C family, Metaxin	integral to membrane [pmid	
3187	4	0.000322	3	0.000236	1.361875	Y	ENSG00000166136:NDUFB8	NDUFB8			ENSG00000166136:NDUFB8	NADH dehydrogenase (ubiq	186	21766	6.8	1	124-146c-Q	19	0.107	0	0.000878	0	0.00038	2	0.000314	0.000416	0	0.000965	0	0.00351	2	0.000329	0.000455	0	0	0	0.000505	0	0	NADH dehydrogenase	endoplasmic reticulum [pmid	NADH dehydrogenase
3188	4	0.000101	2	2.22E-05	4.54737	Y	ENSG00000131269:ABCB7	ABCB7			ENSG00000131269:ABCB7	ATP-binding cassette, sub-fa	753	82769	9.3	5	143-165c-F	37	0.924	0.000247	0.000181	0	0.000779	1	0.000147	0.000181	0	0.000779	0	4.33E-05	2	5.55E-05	8.47E-05	0	0	0	0	0	0	0	ABC transporter	integral to membrane;	ATP binding [pmid 9621516];
3189	4	9.89E-05	0	0.006014	0.016445	Y	ENSG00000197142:ACSL5	ACSL5			ENSG00000197142:ACSL5	acyl-CoA synthetase long-ch	739	82263	7.4	0	43-65721-	0	0	0	0.00041	0	7.17E-05	2	0.000121	0.000196	0	0.000243	0	6.63E-05	0	0	0	0	0	0	0	0	Long-chain acyl-CoA	integral to membrane;	catalytic activity; ligase
3190	4	7.95E-05	6	0.000271	0.29373	Y	ENSG00000156709:AFM1	AFM1			ENSG00000156709:AFM1	programmed cell death 8 isof	609	66295	8.9	1	62-81c	23	0.031	0	0.000306	0	5.8E-05	2	9.11E-05	0.000146	0	0.000111	0	0.00161	0	0	0	0	0	0	0	0	Pyridine nucleotide-	mitochondrion [pmid	disulfide oxidoreductase
3191	3	0.000387	6	0.002158	0.17957	Y	ENSG00000111775:COX6A1	COX6A1			ENSG00000111775:COX6A1	mitochondrial ribosomal pro	109	12155	9.5	1	c40-59	54	0.131	0	0.000851	0	0.00132	1	0.000377	0.00113	0	0.000377	0	0.002396	0.00074	0	0.000775	0.00113	0	0.00049	0.000847	0.002538	0.003815	0.001659	Cytochrome c oxidase	membrane; mitochondrial	cytochrome-c oxidase
3192	3	0.0001	8	0.020355	0.004922	Y	ENSG00000166347:CYBSA	CYBSA			ENSG00000166347:CYBSA	cytochrome b-5 isoform 1 [H	134	15330	5	1	109-131c	0	0	0	0	0	0.000132	1	3.3E-05	6.59E-05	0	0.00067	0	0.005218	0	0.000167	0.000335	0.016496	0.01812	0.004833	0.010828	0.023334	0.016587	0.040351	0.032288	Cytochrome b5-like	endoplasmic reticulum;	cytochrome-c oxidase
3193	3	0.000188	2	3.9E-05	4.824212	Y	ENSG00000213398:SLC25A22	SLC25A22	NET44		ENSG00000213398:SLC25A22	mitochondrial carrier protei	323	34000	8.3	1	112-31c	0	0.059	0	0.000361	0	0.000656	1	0.000206	0.000317	0	0.000496	0	0.000317	0	0.000245	0.000168	0	0	0	0	0	0	0	Mitochondrial carrier	integral to membrane;	binding; carrier activity [pmid
3194	3	0.000165	4	0.000421	0.391562	Y	ENSG00000198888:MT-ND1	MT-ND1			ENSG00000198888:MT-ND1	NADH dehydrogenase subun	318	35661	6.5	8	34-2368-B	19	0.94	0	0.000513	0	0	1	0.000128	0.000257	0	0.000584	0	0.000241	2	0.000201	0.000267	0	0	0	0	0	0	0	NADH dehydrogenase;		
3195	3	0.000107	1	7.68E-06	13.94085	Y	ENSG00000126821:SGPP1	SGPP1			ENSG00000126821:SGPP1	sphingosine-1-phosphate phi	441	49108	8.8	7	131-153c	22	0.001	0	0.00037	0	8.01E-05	2	0.000113	0.000176	0	0.000407	0	0	0	0	0	0	0	0	0	6.15E-05	0	0	PAP2_like proteins,	endoplasmic reticulum;	hydrolase activity
3196	3	9.69E-05	0	0	INF	Y	ENSG00000198712:MTND2	MT-ND2			ENSG00000198712:MTND2	mitochondrial ribosomal pro	347	38961	9.8	6	67-29c69-A	24	0.372	0	0.000388	0	5.09E-05	2	0.000161	0.000288	0	0.000388	0	0	0	0	0	0	0	0	0	0	0	0	NADH-		
3197	3	0.00011	5	0.000129	0.858222	Y	ENSG00000168924:LETM1	LETM1			ENSG00000168924:LETM1	leucine zipper-EF-hand conta	739	83354	6.7	1	206-228c	43	0.036	0	0.0006	0	7.17E-05	2	0.000168	0.00029	0	0.000213	0	0	0	0	0	0	0	0	0	6.26E-05	0.000344	0	0.000191	0.000309	0.000125	LETM1 protein	integral to plasma membrane	calcium ion binding [pmid
3198	3	4.55E-05	2	2.49E-05	1.826464	Y	ENSG00000144919:COX15	COX15			ENSG00000144919:COX15	COX15 homolog isoform 1 p	320	36422	9.2	3	68-90c15-E	32	0.44	0	0.000114	0	8.62E-05	2	5E-05	5.88E-05	0	0.000164	0	0	0	0	0	0	0	0	0	0.000112	8.78E-05	0	0	Uncharacterized protein	integral to membrane;	cytochrome-c oxidase
3199	3	3.72E-05	0	0	INF	Y	ENSG00000119711:ALDH6A1	ALDH6A1			ENSG00000119711:ALDH6A1	methylmalonate-semialdeh	535	57840	8.5	1	174-196c	5	0.81	0	0	0	0.000165	1	4.13E-05	8.25E-05	0	0	0	6.1E-05	7.18E-05	0	3.32E-05	3.86E-05	0	0	0	0	0	0	0	Aldehyde dehydrogenase	mitochondrion [pmid 15270993]	acyl-CoA binding; malonate-
3200	3	4.11E-05	2	4.63E-05	0.88606	Y	ENSG00000136521:NDUFB5	NDUFB5			ENSG00000136521:NDUFB5	NADH dehydrogenase (ubiq	189	21750	9.6	1	70-92c	35	0.916	0	0.000123	0	0	1	3.09E-05	6.17E-05	0	0.000119	0	8.63E-05	0	0	0	0	0	0	0	0	0	0	Cytochrome c1 [Energy	mitochondrion	NADH dehydrogenase
3201	2	0.00015	8	0.028343	0.005284	Y	ENSG00000008394:MGST1	MGST1			ENSG00000008394:MGST1	microsomal glutathione S-tra	155	17599	9.4	1	c15-37	0	0.36	0	0.001053	0	0	1	0.000353	0.000527	0	0.000145	0	0	0	0	0	0	0	0	0	0	0	0	0	MAPEG family. This family	membrane;	glutathione transferase
3202	2	6.33E-05	0	0	INF	Y	ENSG00000115944:COX7A2L	COX7A2L			ENSG00000115944:COX7A2L	cytochrome c oxidase subun	114	12615	9.4	1	i86-108c	0	0.18	0	0.016	0	0.00031	1	7.75E-05	0.000155	0	0.000197	0	0	0	0	0	0	0	0	0	0	0	0	0	Cytochrome c oxidase	mitochondrial electron	cytochrome-c oxidase
3203	2	6.23E-05	0	0	INF	Y	ENSG00000156398:SFXN2	SFXN2			ENSG00000156398:SFXN2	sideroflexin 2 [Homo sapiens	322	36232	9.4	5	c100-122c	0	0	0	0.00029	0	0	1	7.24E-05	0.000145	0	0.000209	0	0	0	0	0	0	0	0	0	0	0	0	0	Tricarboxylate carrier;	integral to membrane;	
3204	2	5.89E-05	2	4.09E-05	1.438975	Y	ENSG00000188603:LZIKN3	LZIKN3			ENSG00000188603:LZIKN3	zeinoid lipofuscinoids, neuron	438	47923	6.4	1	i38-60c99-G	59	0	0	0.00029	0	0	1	0.000133	0.000205	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
3205	2	9.89E-05	0	0	INF	Y	ENSG00000112695:CCDC72A2	CCDC72A2			ENSG00000112695:CCDC72A2	cytochrome c oxidase subun	83	9396	9.7	1	i53-75c	20	0.013	0	0.000562	0	0.000213	1	0.000194	0.000265	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Cytochrome c oxidase	membrane; mitochondrial	cytochrome-c oxidase
3206	2	2.55E-05	6	0.000993	0.258069	Y	ENSG00000170031:KNX0	KNX0			ENSG00000170031:KNX0	dynamitin-like 2 [Homo sapiens	486	55757	8.9	1	c385-404c	25	0.198	0	9.9E-05	0	0	1	2.4E-05	4.8E-05	0	9.23E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	2-polyprenyl-6-	integral to membrane;	electron carrier activity [pmid
3207	2	4.37E-05	0	0	INF	Y	ENSG00000212869:MT-ND6	MT-ND6			ENSG00000212869:MT-ND6	NADH dehydrogenase subun	174	18622	4.2	6	i2-21c46-A	16	0.315	0	0	0	0	1	0.000121	0	0	0.000129	0	0	0	0.000221	2	8.74E-05	0.000108	0	0	0	0	0	0	0			
3208	2	1.66E-05	3	2.73E-05	0.609151	Y	ENSG00000197912:SPG7	SPG7			ENSG00000197912:SPG7	spastic paraplegia 7 isoform	795	88235	8.7	2	c145-167c	17	0.674	0	8.8E-05	0	4.44E-05	2	3.31E-05	4.22E-05	0	0	0	0	0	0	0	0	0	0.000124	7.31E-05	0	2.1E-05	0	0	FtsH Extracellular. This	extracellular matrix (sensu	ATP binding; metal ion
3209	2	0.000107	4	4.22E-05	2.54265	Y	ENSG00000128868:CYB	CYB			ENSG00000128868:CYB	cytochrome b [Homo sapiens	378	42442	9	6	c333-357c	49	0.041	0.000858	0	0	0	1	0.000215	0.000429	0	0	0	0	0	0	0	0	0	0.000122	4.77E-05	0.000127	4.12E-05	0	0	Cytochrome b [N-		
3210	1	9.79E-05	0	0	INF	Y	ENSG00000119013:NDUFB3	NDUFB3			ENSG00000119013:NDUFB3	NADH dehydrogenase (ubiq	98	11402	9.2	1	c66-88i	0	0	0	0	0	0	1	0	0	0	0.000783	1	0	0	0	0	0	0	0	0	0	0	0	0	0	NADH dehydrogenase	mitochondrion	NADH dehydrogenase
3211	1	9.3E-05	3	0.000275	0.338095	Y	ENSG00000147678:ATPS12	ATPS12			ENSG00000147678:ATPS12	ATP synthase, H+ transporti	94	10518	8.7	0	c63-82i	43	0	0	0.000744	0	0	1	0.000198	0.000372	0	0	0	0	0	0	0	0	0	0.000206	0.00164	0.000356	0	0	0	0	mitochondrion; protein-	mitochondrion [pmid	hydrogen ion transporter
3212	1	1.97E-05	0	0	INF	Y	ENSG00000131748:STARD3	STARD3			ENSG00000131748:STARD3	START-related lipid transfer (S	340	50516	8.4	1	i52-74c04-	30	0.055	0	0.000157	0	0	1	3.93E-05	7.86E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	START(Steroidogenic	cytoplasm [pmid 9139840];	cholesterol binding [pmid
3213	1	1.13E-05	1	9.9E-06	1.141636	Y	ENSG00000115317:HTRA2	HTRA2			ENSG00000115317:HTRA2	HtrA serine peptidase 2 isofo	361	38493	10.7	1	i105-124c	35	0.598	0	0	0	0	1	0	0	0	9.04E-05	0	0	0	0	0	0	0	0	0	7.92E-05	0	0	0	0	PDZ domain of bacterial	endoplasmic reticulum [pmid	serine-type endopeptidase
3214	1	6.46E-06	2	9.35E-06	0.690649	Y	ENSG00000121057:AAAP1	AAAP1			ENSG00000121057:AAAP1	A-kinase anchor protein 1 pm	903	97342	4.9	1	i7-26c	53	0.727	0	5.17E-05	0	0	1	1.29E-05	2.58E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	3.67E-05	3.81E-05	0	0	K homology RNA-binding	integral to membrane;	RNA binding [pmid 8769136]
3215	10	0.003776	8	0.001189	3.175385	Y	ENSG00000110955:ATP5B	ATP5B			ENSG00000110955:ATP5B	ATP synthase, H+ transporti	529	56560	5.4	0	o	S	43	0.797	0.003066	0.002028	0.00071	0.008916	5	0.00368	0.003621	0.005117	0.003435	0.007651	0.001887	5	0.003873	0.002598	0.001671	0.001765	0.001487	0.001509	0.000727	0.001568	0.000554	0.000232	F1 ATP synthase beta	mitochondrion; proton-	ATP binding; hydrogen-
3216	9	0.003603	8	0.001104	3.26311	Y	ENSG00000152234:ATP5A1	ATP5A1			ENSG00000152234:ATP5A1	ATP synthase, H+ transporti	553	59751	9.1	0	o	S	39	0.48	0.002002	0.001858	0.000679	0.008613	5	0.003416	0.003271	0.005119	0.003398	0.005459	0.001319	5	0.003398	0.00212	0.000759	0.000676	0.001556	0.001574	0.001044	0.001968	0.000585	0.000777	F1 ATP synthase alpha.	membrane fraction;	ATP binding; hydrogen-
3217	8	0.005034	1	1.83E-05	275.5807	Y	ENSG00000067225:PKM2	PKM2			ENSG00000067225:PKM2	pyruvate kinase, muscle isofo	531	57937	7.6	0	o	S	24	0.089	0.008551	0.00245	0	0.007917	5	0.004732	0.004175	0.001672	0.004014	0.014353	0.001301	5	0.005335	0.006131	0	0	0	0	0	0	0.000146	0	Pyruvate kinase (PK):	cytoplasm [pmid 11256614];	magnesium ion binding;
3218	8	0.00378	0	0	INF	Y	ENSG00000167055:FHB	FHB			ENSG00000167055:FHB	fibrinogen beta chain precur	272	29294	5.8	0	o	S	26	0.848	0.003577	0.006003	0.004835	0.05578	5	0.005449	0.004104	0	0.005479	0	0.003	0	0.002371	0.002409	0	0	0	0	0	0	0	Band_7_prohibitin. A	integral to plasma membrane	protein binding [pmid
3219	8	0.003923	6	0.002047	1.916287	Y	ENSG00000179091:CYC1	CYC1			ENSG00000179091:CYC1	cytochrome c-1 [Homo sapie	325	35390	9	0	o	S	20	0.741	0.010977	0.001507	0.000578	0.00761	5	0.004366	0.00503	0.015023	0.002002	0.00302	0.000306	5	0.004391	0.007135	0.013603	0	0.000851	0.001057	0.002295	0.000384	0	0.000188	Cytochrome c1 [Energy	mitochondrion	cytochrome c-type
3220	8	0.001597	6	0.000329	4.855454	Y	ENSG00000167553:TUBA1C	TUBA1C			ENSG00000167553:TUBA1C	tubulin alpha 6 [Homo sapier	449	49895	5.1	0	o	S	20	0.005	0.002956	0	0.004324	0.000341	5	0.001905	0.002084	0.003295	0.001332	0.000528	0	0.001289	0.001446	0	0	0	0	0	0	0	6.83E-05	0	The tubulin superfamily	microtubule; protein complex	GTP binding; GTPase
3221	8	0.001633	5	5.45E-05	29.94052	Y	ENSG00000213671:CAC1	CAC1			ENSG00000213671:CAC1	aldehyde dehydrogenase 2 [H	124	13611	6.9	0	o	S	12	0.107	0.000576	0.002268	0	0.000394	5	0.001237	0.002574	0	0.000537	0.000576	0.001168	5	0.000577	0.000376	0	0	0	0	0	0	0	9.77E-05	0	Mitochondrial carrier	integral to plasma membrane	oxoglutarate/malate
3222	7	0.00204	0	0.000333	6.120539	Y	ENSG00000078668:VDAC3	VDAC3			ENSG00000078668:VDAC3	voltage-dependent anion cha	283	30659	8.6	0	o	S	0	0.000573	0.002837	0.004487	0.002115	0.000247	5	0.002511	0.001677	0	0.000312	0.000196	0.002137	5	0.00157	0.001308	0	0	0	0	0	0	0	0.000115	0.000217	Eukaryotic porin;	cytoplasm [pmid 9207238];	voltage-gated anion channel
3223	7	0.001295	8	0.011895	6.108904	Y	ENSG00000100243:CYB5R3	CYB5R3			ENSG00000100243:CYB5R3	cytochrome b5 reductase 3e	301	34235	7.6	0	o	S	33	0.681	0.003233	0.002092	0.001248	0.002093	5	0.001717	0.00125	0	0.001714	0.00038	0.001403	5	0.000874	0.000815	0.01175	0.001241	0.005532	0.010062	0.011686	0.013157	0.022076	0.019675	Oxidoreductase NAD-	cytoplasm [pmid 9207238];	cytochrome-b5 reductase
3224	7	0.000824	0	0.000842	0.979804	Y	ENSG00000139180:NDUFA9	NDUFA9			ENSG00000139180:NDUFA9	NADH dehydrogenase (ubiq	377	41920	8.4	1	o	S	31	0.783	0.003611	0.000687	0	0.000938	5	0.001177	0.000776	0.001177	0.000273	0.002374	0.000204	5	0.000911	0.000627	0	0	0	0	0	0	0	0.000204	0	Predicted nucleotide-	mitochondrion [pmid	NADH/
3225	7	0.000148	2	3.06E-06	48.5062	Y	ENSG00000167978:SRRM2	SRRM2			ENSG00000167978:SRRM2	splicing coactivator subunit 3	2752	299616	12.1	0	o	S	18	0	0.000178	0.000478	3.21E-05	0.000194	5	0.000172	0.000218	0.000423	0.000207	0.000423	0.000207	5	0.000425	0.000359	0	0	0.6TE-06	1.78E-05	0	0	0	0	0	0	0			
3226	6	0.002143	0	0	INF	Y	ENSG00000127184:COX7C	COX7C			ENSG00000127184:COX7C	cytochrome c oxidase subun	63	8000	9.6	0	o	S	51	0.001	0	0.000444	0	0.001122	5	0.000398	0.000273	0.000206	0.000273	0.000206	0.000273	5	0.000398	0.000359	0	0	0	0	0	0	0	0	0	Cytochrome c oxidase	membrane;	cytochrome-c oxidase
3227	6	0.00549	3	0.000302	18.17435	Y	ENSG00000213585:VDAC4	VDAC4			ENSG00000213585:VDAC4	voltage-dependent anion cha	283	30773	8.5	0	o	S	0	0	0.009148	0.002656	0.008364	0	0.005042	0.004435	0	0.010861	0	0.006113	0.006782	5	0.005994	0.004481	0	0	0	0	0	0	0	0	0	Eukaryotic porin;	integral to membrane;	
3228	6	0.002876	0	0	INF	Y	ENSG00000172974:LOC729317	LOC729317			ENSG00000172974:LOC729317	PREDICTED: similar to volta	293	31479	7.6	0	o	S	20	0.008	0	0.005254	0.000641	0.004823	5	0.00268	0.002742	0	0.005743	0	0.00078	0.005765	5	0.003072	0.003113	0	0	0	0	0	0	0	0	0	Eukaryotic porin;		
3229	6	0.001087	6	0.000142	7.65472	Y	ENSG00000164024:YWHAZ	YWHAZ			ENSG00000164024:YWHAZ	tyrosine 3-monooxygenase/	245	27745	4.8	0	o	S	0	0	0.000815	0	0.000841	5	0.000841	0.000511	0	0.002864	0	0.000711	0.000511	5	0.001421	0.01327	0	0	0	0	0	0	0	0	0	14-3-3 protein; gi	gen0244		protein domain specific
3230	6	0.001237	0	0	INF	Y	ENSG00000025708:ECGF1	ECGF1			ENSG00000025708:ECGF1	endothelial cell growth factor	482	49955	5.5	0	o	S	14	0.043	0.003364	0.00229	0	0.000183	5	0.00096	0.001608	0.005525	0.003972	0	0.000159	5	0.001514	0.002678	0	0	0	0	0	0	0	0	0	Glycosyl transferase family	extracellular space; soluble	growth factor activity;
3231	6	0.001214	0	0	INF	Y	ENSG00000172977:HPD1	HPD1			ENSG00000172977:HPD1	chaperonin [Homo sapiens]	573	61355	5.9	0	o	S	28	0.175	0.002283	0.000325	0	0.000288	5	0.000377	0.001355	0	0.000401	0	0.00042	0	0	0	0	0	0	0	0	0	0	0	0	CrdS_like type I	cytoplasm [pmid 16130169];	ATP binding; chaperone
3232	6	0.000427	6	0.000407	1.04999	Y	ENSG00000088475:HADHA	HADHA			ENSG00000088475:HADHA	mitochondrial trifunctional pr	763	82933	9.2	0	o	S	24	0.108	0	0.000343	0	0.00081	5	0.00031	0.00039	0	0.000544	0.00064	0	0.001476	0.000201	5	0.00039	0.000384	8.04E-05	0.001394	0.000856	0.001899	0.000349	0.000384	8.04E-05	3-hydroxyacyl-CoA	fatty acid oxidation	3-hydroxyacyl-CoA
3233	6	0.000408	0	0	INF	Y	ENSG00000182054:IDH2	IDH2			ENSG00000182054:IDH2	isocitrate dehydrogenase 2 (	452	50909	8.7	0	o	S	33	0.429	0.000359	0.001032	0	0.000703	5	0.000524	0.000444	0	0.000447	0	0.000469	0.000255	5	0.000293	0.000218	0	0	0	0	0	0	0	0	0	isocitrate dehydrogenase;	mitochondrion [pmid 8707889]	isocitrate dehydrogenase
3234	6	0.000244	3	3.84E-05	6.183993	Y	ENSG00000164252:MDH2	MDH2			ENSG00000164252:MDH2	malate dehydrogenase [Hom	338	36496	8.9	0	o	S	0.38	0.006096	0.002087	0.000261	0	0.000341	5	0.000241	0.000184	0	0.000451	0	0.000215	0	0	0	0	0	0	0	0	0	0	0	0	malate dehydrogenase	mitochondrion	L-lactate dehydrogenase
3235	6	0.000939	0	0	INF	Y	ENSG00000015475:BID	BID			ENSG00000015475:BID	BH3 interacting domain death	241	26836	7.1	0	o	S	0.451	0.002692	0.00029	0	0.00066	5	0.00091	0.001218	0.003684	0.000188	0	0	0	0	0	0	0	0	0	0	0	0	0	0	BH3 interacting domain	cytoplasm; cytosol [pmid	death receptor binding [pmid
3236	5	0.001098	0	0	INF	Y	ENSG00000163541:SUCLG1	SUCLG1			ENSG00000163541:SUCLG1	succinate-CoA ligase, GDP-l	346	36250	8.8	0	o	S	25	0.778	0	0	0.001086	0.000153	5	0.00031	0.000522	0	8.48E-05	0	4.72E-05	0.007433	5	0.000381	0.000639	0	0	0	0	0	0	0	0	0			
3237	5	0.000865	1	0.003007	0.280207	Y	ENSG00000106119:SCS	SCS			ENSG00000106119:SCS	succinyl-CoA synthetase horm	303	33331	6	0	o	S	19	0.468	0.001067	0.001694	0	0.000175	5	0.000368	0.000905	0	0.000929	0	0.00152	5	0.000388	0.001008	0.002918	0	0	0	0	0	0	0	0	0	Mitochondrial carrier	integral to membrane;	binding
3238	5	0.00023	3	8.81E-05	2.604223	Y	ENSG00000158864:NDUFS2	NDUFS2			ENSG00000158864:NDUF

																							RESTING LYMPHOCYTES NEs								PHA-TREATED LYMPHOCYTES NEs								MMs										
rk		NEs detected # out of 10 runs	NEs dNSAF_AVG	MMs detected # out of 8 runs	MMs dNSAF_AVG	NEs:MMs	Detected in Mitochondria	ORTHO_GROUP	GENE_NAME	NET_NAME	Location & Gene Expression Data	Locus	Description	Length	MW	pI	PredHel	TMHMM_Topology	SIGNALP_HMM_TYPE (S= signal; A= Anchor; Q= none)	SIGNALP_HMM_POS	SIGNALP_HMM_PROB	HsNaOH-NE_NT_lymphocytes_CNBrTI_1_dNSAF	HsNaOH-NE_NT_lymphocytes_TI_1_dNSAF	HsNaOH-NE_NT_lymphocytes_PK_1_dNSAF	HsSD-NE_NT_lymphocytes_TI_1_dNSAF	RnNaOH-NE_NT_lymphocytes_PK_1_dNSAF	NT-bNEs Detected # Out of 5	NT-bNEs dNSAF AVG	NT-bNEs dNSAF SDV	HsNaOH-NE_PHA_lymphocytes_CNBrTI_1_dNSAF	HsNaOH-NE_PHA_lymphocytes_TI_1_dNSAF	RnNaOH-NE_PHA_lymphocytes_PK_1_dNSAF	HsSD-NE_PHA_lymphocytes_TI_1_dNSAF	HsSD-NE_PHA_lymphocytes_PK_1_dNSAF	PHA-bNEs Detected # Out of 5	PHA-bNEs dNSAF AVG	PHA-bNEs dNSAF SDV	MmNaOH-MM_liver_CNBrTI_1_dNSAF	MmNaOH-MM_liver_CNBrTI_2_dNSAF	RnNaOH-MM_liver_TI_1_dNSAF	RnNaOH-MM_liver_TI_2_dNSAF	RnNaOH-MM_liver_TI_3_dNSAF	RnNaOH-MM_liver_TI_4_dNSAF	RnNaOH-MM_liver_PK_1_dNSAF	RnNaOH-MM_liver_PK_2_dNSAF	Region_Note	GO_Component	GO_Function
3329		2	9.18E-06	0	0	INF	Y	ENSG00000136143	SUCLA2			gi|11321583|ref|NP_	succinate-CoA ligase, ADP-fo	463	50317	7.4	0	o	Q	30	0.097	0	0	0	3.82E-05	-	1	9.54E-06	1.91E-05	0	0	-	3.52E-05	0	1	9.81E-06	1.76E-05	0	0	0	0	0	0	0	0	CoA-ligase. This family	mitochondrion [pmid	ATP binding; ligase activity;
3330		2	1.47E-05	0	0	INF	Y	ENSG00000112294	ALDH5A1			gi|25777721|ref|NP_	aldehyde dehydrogenase 5A	548	58653	8.1	0	o	S	64	0.531	0	8.51E-05	0	3.22E-05	-	2	2.93E-05	4.02E-05	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	0	NAD-dependent aldehyde	mitochondrion [pmid 9683595]	oxidoreductase activity;
3331		2	1.44E-05	1	8.91E-06	1.616985	Y	ENSG00000091140	DLD			gi|9199540|ref|NP_	dihydrolipoamide dehydroge	509	54177	7.9	0	o	Q	37	0.039	0	4.58E-05	0	6.94E-05	-	2	2.88E-05	3.46E-05	0	0	-	0	0	0	0	7.13E-05	0	0	0	0	0	0	0	0	Pyridine nucleotide-	cytoplasm; mitochondrion	dihydrolipoyl dehydrogenase
3332		1	0.00042	0	0	INF	Y	ENSG00000131174	COX7B			gi|4502991|ref|NP_0	cytochrome c oxidase subun	80	9160	10.3	0	o	Q	23	0.002	0	0	0	0	-	0	0	0	0	0	0	-	0	0.003359	0	1	0.00084	0.001679	0	0	0	0	0	0	0	Cytochrome C oxidase	Integral to membrane;	cytochrome-c oxidase
3333		1	8.29E-05	3	0.000322	0.257452	Y	ENSG00000115286	NDUFS7			gi|38524585|ref|NP_	NADH-ubiquinone oxidoredu	213	23580	10	0	o	S	28	0.771	0	0	0	0.000663	-	1	0.000166	0.000332	0	0	-	0	0	0	0	0	8.32E-05	0.002207	0.000287	0	0	0	0	0	0	NADH dehydrogenase	mitochondrion	4 iron, 4 sulfur cluster
3334		1	4.49E-05	0	0	INF	Y	ENSG00000154999	MRPS17			gi|7705425|ref|NP_	mitochondrial ribosomal prot	130	14502	9.6	0	o	Q	20	0.006	0	0.000359	0	0	-	1	8.97E-05	0.000179	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	0	30S ribosomal protein S17,	intracellular; membrane;	nucleic acid binding; rRNA
3335		1	4.25E-05	3	4.27E-05	0.995519	Y	ENSG00000164733	CTSB			gi|22538437|ref|NP_	cathepsin B preproprotein [H	339	37822	6.3	0	o	S	20	1	0	0	0	0	-	0	0	0	0	0	0	-	0	0.00034	0	1	8.49E-05	0.00017	0	0	0	0	0	0	0	Cathepsin B activity [pmid	intracellular [pmid 1645961];	cathepsin B activity [pmid
3336		1	3.79E-05	0	0	INF	Y	ENSG00000164258	NDUFS4			gi|4505369|ref|NP_0	NADH dehydrogenase (ubiq	175	20108	10.3	0	o	S	33	0.967	0	0	0	0.000303	-	1	7.57E-05	0.000151	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	0	ETC complex I subunit	membrane fraction [pmid	NADH dehydrogenase
3337		1	3.31E-05	6	0.00047	0.07042	Y	ENSG00000161203	AP2M1			gi|14917109|ref|NP_	adaptor-related protein comp	435	49655	9.5	0	o	Q	0	0	0	0	0	0	-	0	0	0	0	0	0	-	0	0.000265	0	1	6.62E-05	0.000132	0	0	0.000106	0.000876	0.000221	0.001979	0.000225	0.000353	Adaptor complexes medium	clathrin vesicle coat; coated	lipid binding; protein binding
3338		1	2.79E-05	0	0	INF	Y	ENSG00000136897	MRPL50			gi|21265096|ref|NP_	mitochondrial ribosomal prot	158	18325	7.9	0	o	Q	21	0.069	0	0	0	0.000224	-	1	5.59E-05	0.000112	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	0		mitochondrion	
3339		1	2.29E-05	4	3.27E-05	0.698725	Y	ENSG00000176974	SHMT1			gi|22547186|ref|NP_	serine hydroxymethyltransfer	483	53083	7.7	0	o	Q	0	0	0	0	0	0.000183	-	1	4.57E-05	9.14E-05	0	0	-	0	0	0	0	2.66E-05	0.000141	4.6E-05	4.78E-05	0	0	0	0	0	Serine	cytosol [pmid 8505317]	glycine
3340		1	2.21E-05	7	0.001037	0.021336	Y	ENSG00000121691	CAT			gi|4557014|ref|NP_0	catalase [Homo sapiens]	527	59756	7.4	0	o	Q	0	0	0	0.000177	0	0	-	1	4.43E-05	8.85E-05	0	0	-	0	0	0	0	0.001418	0.000878	0.000826	0.001552	0.000772	0.000989	0.001863	Catalase. Catalase is an	peroxisome	catalase activity [pmid
3341		1	1.97E-05	0	0	INF	Y	ENSG00000106049	HIBADH			gi|23308751|ref|NP_	3-hydroxyisobutyrate dehydr	336	35329	8.1	0	o	S	38	0.993	0	0	0	0.000158	-	1	3.94E-05	7.89E-05	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	NAD binding domain of 6-	mitochondrion	3-hydroxyisobutyrate
3342		1	1.96E-05	3	6.45E-05	0.304209	Y	ENSG00000128311	TST			gi|17402865|ref|NP_	thiosulfate sulfurtransferase [	297	33429	7.3	0	o	Q	18	0.026	0	0.000157	0	0	-	1	3.93E-05	7.85E-05	0	0	-	0	0	0	0	0.000244	0	5.27E-05	0.000219	0	0	0	0	0	Thiosulfate	mitochondrial matrix [pmid	thiosulfate sulfurtransferase
3343		1	1.95E-05	0	0	INF	Y	ENSG00000147853	AK3			gi|19923437|ref|NP_	adenylate kinase 3 [Homo sa	227	25565	9.2	0	o	S	20	0.657	0	0	0	0.000156	-	1	3.89E-05	7.78E-05	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	Adenylate kinase (ADK)	mitochondrion	adenylate kinase activity;
3344		1	1.92E-05	0	0	INF	Y	ENSG00000103707	MTFMT			gi|21245130|ref|NP_	mitochondrial methionyl-tRN	304	33833	9.5	0	o	Q	32	0.001	0	0.000153	0	0	-	1	3.84E-05	7.67E-05	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	Formyl transferase. This	mitochondrion	methionyl-tRNA
3345		1	1.91E-05	0	0	INF	Y	ENSG00000123297	TFSFM			gi|21361280|ref|NP_	Ts translation elongation fact	346	37658	7.7	0	o	Q	18	0.472	0	0	0	0.000153	-	1	3.83E-05	7.66E-05	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	UBA/TS-N domain. This	mitochondrion [pmid 7615523]	transcriptional elongation
3346		1	1.58E-05	1	1.63E-05	0.97047	Y	ENSG00000143575	HAX1			gi|13435366|ref|NP_	HCLS1 associated protein X-	279	31621	4.9	0	o	Q	19	0.005	0	0	0	0.000127	-	1	3.17E-05	6.33E-05	0	0	-	0	0	0	0	0.00013	0	0	0	0	0	0	0		actin cytoskeleton [pmid	interleukin-1 binding [pmid
3347		1	1.23E-05	0	0	INF	Y	ENSG00000175110	MRPS22			gi|9910244|ref|NP_0	mitochondrial ribosomal prot	360	41280	7.0	0	o	S	20	0.985	0	0	0	9.81E-05	-	1	2.45E-05	4.91E-05	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0		mitochondrial ribosome [pmid	
3348		1	1.22E-05	0	0	INF	Y	ENSG00000011376	LARS2			gi|7661872|ref|NP_0	leucyl-tRNA synthetase 2, mi	903	101976	8.2	0	o	Q	22	0.094	0	0	0	9.78E-05	-	1	2.45E-05	4.89E-05	0	0	-	0	0	0	0	0	0	0	0	0	0	0	0	This is the catalytic core	mitochondrion	ATP binding; leucine-tRNA
3349		1	1.07E-05	5	0.00021	0.051033	Y	ENSG00000117984	CTSD			gi|4503143|ref|NP_0	cathepsin D preproprotein [H	412	44552	6.5	0	o	S	21	1	0	0	0	8.57E-05	-	1	2.14E-05	4.29E-05	0	0	-	0	0	0	0	0.000114	0.000624	0.000236	0	0.00048	0.000226	Eukaryotic aspartyl	extracellular region [pmid	cathepsin D activity [pmid
3350		1	8.05E-06	0	0	INF	Y	ENSG00000196236	XPNPEP3			gi|11559925|ref|NP_	X-prolyl aminopeptidase (am	507	57034	6.8	0	o	S	23	0.604	0	0	0	0	-	0	0	0	6.44E-05	0	0	-	0	0	0	1	1.61E-05	3.22E-05	0	0	0	0	0	0	Prolidase. E.C. 3.4.13.9.		metallooxopeptidase activity;
3351		1	0.000008	1	3.86E-06	2.073002	Y	ENSG00000091483	FH			gi|19743875|ref|NP_	fumarate hydratase precurso	510	54637	8.8	0	o	S	32	0.992	0	0	0	0	-	0	0	0	0.000064	0	0	-	0	0	0	1	0.000016	0.00003	0	0	0	0	3.09E-05	0	0	Class II fumarases. This	cytoplasm [pmid 8200987];	fumarate hydratase activity