

Accession	Gene Name	Description	Coverage	# Peptides	# PSMs	# Unique Peptides	# AAs	MW [kDa]	calc. pl	Abundances Control-2	Abundances Control-1	Abundances MYCT1-2	Abundances MYCT1-1	Average Control	Average MYCT1	MYCT1/Control	P value (Significance A)
F8W059	UNC13A	Protein unc-13 homolog A OS=Homo sapiens GN=UNC13A PE=1 SV=1	0.580720093	1	1	1	1722	195.007	5.38	27	23.8	168.1	181.1	25.4	174.6	6.87402	5.33E-48
Q9HD89	RETN	Resistin OS=Homo sapiens GN=RETN PE=1 SV=1	16.66666667	1	1	1	108	11.411	6.86	43.1	38	139.3	179.7	40.55	159.5	3.93342	6.72E-25
P05109	S100A8	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	23.65591398	2	2	2	93	10.828	7.03	61.1	58.6	72.7	207.6	59.85	140.15	2.34169	2.09E-10
B2RNT7	KLHDC5	Kelch domain containing 5 OS=Homo sapiens GN=KLHDC5 PE=2 SV=1	1.782178218	1	1	1	505	56.831	5.74	66.5	56	163.6	113.9	61.25	138.75	2.26531	1.05E-09
K7EQR9	ILF3	Interleukin enhancer-binding factor 3 (Fragment) OS=Homo sapiens GN=ILF3 PE=1 SV=1	51.66666667	8	23	1	180	19.576	8.27	66.9	60.8	148.6	123.7	63.85	136.15	2.13234	1.69E-08
Q5QJ74	TBCEL	Tubulin-specific chaperone cofactor E-like protein OS=Homo sapiens GN=TBCEL PE=1 SV=2	2.122641509	1	1	1	424	48.164	5.38	56.6	74.5	131.2	137.8	65.55	134.5	2.05187	8.87E-08
Q9NRD8	DUOX2	Dual oxidase 2 OS=Homo sapiens GN=DUOX2 PE=1 SV=2	0.452196382	1	1	1	1548	175.253	7.85	53.7	80.1	98.8	167.4	66.9	133.1	1.98954	3.16E-07
D6RB49	DTHD1	Death domain-containing protein 1 OS=Homo sapiens GN=DTHD1 PE=1 SV=1	0.852618758	1	1	1	821	92.739	7.05	70.5	63.6	151.9	113.9	67.05	132.9	1.9821	3.68E-07
B7Z8Q2		cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein OS=Homo sapiens PE=2 SV=1	1.616628176	1	2	1	433	46.597	6.28	45.6	90.5	102.5	161.4	68.05	131.95	1.93902	8.76E-07
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2	38.28715365	11	16	11	397	41.324	6.92	71.1	65.8	144	119.1	68.45	131.55	1.92184	1.24E-06
B2R4M6		Protein S100 OS=Homo sapiens PE=2 SV=1	7.01754386	1	2	1	114	13.202	6.13	66.9	70.6	85.8	176.7	68.75	131.25	1.90909	1.59E-06

O43677	NDUFC 1	NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial OS=Homo sapiens GN=NDUFC1 PE=3 SV=1	14.47368421	1	1	1	76	8.729	10.2	65.4	72.4	126	136.2	68.9	131.1	1.90276	1.81E-06
A1L497	ANKRD 26	ANKRD26 protein OS=Homo sapiens GN=ANKRD26 PE=2 SV=1	0.405561993	1	1	1	1726	198.09	5.68	54.5	83.4	100.6	161.6	68.95	131.1	1.90138	1.86E-06
B4DU44		Involucrin OS=Homo sapiens PE=2 SV=1	6.722689076	3	3	3	595	69.562	4.6	68.1	70.4	189	72.4	69.25	130.7	1.88736	2.45E-06
A0A024R AP2	HMGCR	3-hydroxy-3-methylglutaryl coenzyme A reductase OS=Homo sapiens GN=HMGCR PE=3 SV=1	9.797297297	7	9	7	888	97.413	6.74	70.8	69.4	109.5	150.3	70.1	129.9	1.85307	4.83E-06
A0A0A7K U15	TSC1- PDGFR B	TSC1-PDGFEF fusion protein (Fragment) OS=Homo sapiens GN=TSC1-PDGFRB fusion PE=2 SV=1	0.795947902	1	1	1	1382	154.474	6.04	65.1	75.2	135	124.7	70.15	129.85	1.85103	5.02E-06
I3L1P4	PELP1	Proline-, glutamic acid- and leucine-rich protein 1 (Fragment) OS=Homo sapiens GN=PELP1 PE=1 SV=1	44.59459459	4	12	1	148	15.056	10.68	74.2	66.2	141.4	118.2	70.2	129.8	1.849	5.23E-06
Q8NH19	OR10A G1	Olfactory receptor 10AG1 OS=Homo sapiens GN=OR10AG1 PE=2 SV=1	2.325581395	1	1	1	301	34.081	8.78	72.8	68.1	135.4	123.7	70.45	129.55	1.83889	6.37E-06
Q9UBW8	COPS7 A	COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1	12	3	5	3	275	30.258	8.22	64.6	76.6	105.4	153.4	70.6	129.4	1.83286	7.16E-06
Q6GMX4	IGL@	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	3.389830508	1	1	1	236	24.794	6.89	61	80.2	98.8	160	70.6	129.4	1.83286	7.16E-06
A0A024R9 44	SERPIN C1	Serpin peptidase inhibitor, clade C (Antithrombin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINC1 PE=3 SV=1	3.448275862	2	2	2	464	52.569	6.71	63.6	78	88.9	169.5	70.8	129.2	1.82486	8.37E-06

F5GXR3	PTMS	Parathyrosin OS=Homo sapiens GN=PTMS PE=1 SV=1	10.57692308	1	1	1	104	12.067	11	75.8	66.6	142.4	115.2	71.2	128.8	1.80899	1.14E-05
P14324	FDPS	Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4	16.70644391	7	13	7	419	48.245	6.15	73.1	69.7	140.1	117.2	71.4	128.65	1.80182	1.31E-05
O15040	TECPR2	Tectonin beta-propeller repeat- containing protein 2 OS=Homo sapiens GN=TECPR2 PE=1 SV=4	0.708717222	1	1	1	1411	153.751	5.55	78.1	65.2	145.1	111.6	71.65	128.35	1.79135	1.60E-05
P0CB47	UBTFL1	Upstream-binding factor 1-like protein 1 OS=Homo sapiens GN=UBTFL1 PE=3 SV=1	1.781170483	1	1	1	393	46.105	9.48	75.2	69.2	142.5	113.1	72.2	127.8	1.77008	2.41E-05
Q9H6M4		cDNA: FLJ22098 fis, clone HEP17040 (Fragment) OS=Homo sapiens PE=2 SV=1	7.418397626	4	4	1	674	75.246	9.52	76	68.7	136.9	118.4	72.35	127.65	1.76434	2.69E-05
D6RF35	GC	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	6.302521008	2	6	2	476	52.986	5.52	64.3	80.7	97.1	157.9	72.5	127.5	1.75862	3.00E-05
Q9ULC5	ACSL5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1	18.15519766	10	14	9	683	75.942	6.92	70.6	74.6	125.2	129.6	72.6	127.4	1.75482	3.22E-05
Q96RT7	TUBGC P6	Gamma-tubulin complex component 6 OS=Homo sapiens GN=TUBGCP6 PE=1 SV=3	1.539307312	1	1	1	1819	200.372	6.32	69.4	75.9	130.1	124.6	72.65	127.35	1.75293	3.34E-05
P42261	GRIA1	Glutamate receptor 1 OS=Homo sapiens GN=GRIA1 PE=1 SV=2	0.993377483	1	3	1	906	101.441	7.71	79	66.6	140.7	113.8	72.8	127.25	1.74794	3.67E-05
Q9NZJ4	SACS	Sacsin OS=Homo sapiens GN=SACS PE=1 SV=2	0.283904783	1	3	1	4579	520.795	7.05	78.4	67.5	155.7	98.4	72.95	127.05	1.7416	4.14E-05
Q6NSI1	ANKRD 26P1	Putative ankyrin repeat domain- containing protein 26-like protein OS=Homo sapiens GN=ANKRD26P1 PE=5 SV=2	3.115264798	1	1	1	321	35.415	5.39	80.1	66.1	140.9	112.9	73.1	126.9	1.73598	4.60E-05

Q99928	GABRG3	Gamma-aminobutyric acid receptor subunit gamma-3 OS=Homo sapiens GN=GABRG3 PE=2 SV=2	2.569593148	1	1	1	467	54.253	7.52	75.3	71	133.5	120.2	73.15	126.85	1.73411	4.76E-05
J3QS13	PSMD11	26S proteasome non-ATPase regulatory subunit 11 (Fragment) OS=Homo sapiens GN=PSMD11 PE=1 SV=1	48.88888889	4	8	1	90	10.074	8.43	76.4	70.5	138.1	115	73.45	126.55	1.72294	5.88E-05
Q01581	HMGCS1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2	10.96153846	5	5	5	520	57.257	5.41	74.3	72.6	123.3	129.8	73.45	126.55	1.72294	5.88E-05
Q86W25	NLRP13	NACHT, LRR and PYD domains-containing protein 13 OS=Homo sapiens GN=NLRP13 PE=2 SV=2	0.67114094	1	1	1	1043	118.807	5.66	82.3	65.2	140.2	112.3	73.75	126.25	1.71186	7.23E-05
A0A0S2Z3Z5	CASP10	Caspase 10 apoptosis-related cysteine peptidase isoform 1 (Fragment) OS=Homo sapiens GN=CASP10 PE=2 SV=1	3.0651341	1	1	1	522	58.956	6.62	75.4	72.9	122.6	129.1	74.15	125.85	1.69724	9.49E-05
A0A087WUG8	TTL11	Tubulin polyglutamylase TTL11 (Fragment) OS=Homo sapiens GN=TTL11 PE=4 SV=1	12.12121212	1	2	1	66	7.615	9.72	73.2	75.2	143	108.7	74.2	125.85	1.69609	9.70E-05
Q9H6X2	ANTXR1	Anthrax toxin receptor 1 OS=Homo sapiens GN=ANTXR1 PE=1 SV=2	12.41134752	6	7	6	564	62.749	7.61	78	70.9	124	127.1	74.45	125.55	1.68637	0.000116064
P63313	TMSB10	Thymosin beta-10 OS=Homo sapiens GN=TMSB10 PE=1 SV=2	31.81818182	1	4	1	44	5.023	5.36	59.6	90.4	137.5	112.4	75	124.95	1.666	0.000168728
O60658	PDE8A	High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A OS=Homo sapiens GN=PDE8A PE=1 SV=2	1.809408926	1	1	1	829	93.245	6.11	79.7	71.4	134.1	114.8	75.55	124.45	1.64725	0.000237322
H0Y948	AFDN	Protein AFDN (Fragment) OS=Homo sapiens GN=AFDN PE=1 SV=1	4.188481675	2	2	2	191	20.664	8.98	76	75.3	130.2	118.5	75.65	124.35	1.64375	0.000252836

Q8NDM7	CFAP43	Cilia- and flagella-associated protein 43 OS=Homo sapiens GN=CFAP43 PE=2 SV=3	0.42042042	1	2	1	1665	191.861	5.99	79.7	72	143.7	104.5	75.85	124.1	1.63612	0.000290156
I3L3A6	PRSS36	Polyserase-2 (Fragment) OS=Homo sapiens GN=PRSS36 PE=4 SV=1	28.57142857	1	1	1	28	2.989	7.25	86.2	65.7	136.3	111.8	75.95	124.05	1.63331	0.000305218
B4DPP6		cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1	10.03236246	7	41	7	618	70.317	6.09	72.5	79.8	101.6	146.1	76.15	123.85	1.6264	0.000345556
Q14512	FGFBP1	Fibroblast growth factor-binding protein 1 OS=Homo sapiens GN=FGFBP1 PE=1 SV=1	24.78632479	4	4	4	234	26.247	9.1	80	72.6	125.1	122.3	76.3	123.7	1.62123	0.000378994
Q14680	MELK	Maternal embryonic leucine zipper kinase OS=Homo sapiens GN=MELK PE=1 SV=3	3.533026114	2	2	2	651	74.594	8.72	75.4	78.3	128.6	117.7	76.85	123.15	1.60247	0.000528945
Q5TCU3	TPM2	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	33.09859155	10	21	1	284	32.795	4.68	73.4	80.4	115.7	130.5	76.9	123.1	1.60078	0.000544995
Q9GZM7	TINAGL1	Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1 PE=1 SV=1	2.141327623	1	1	1	467	52.353	6.99	76.4	77.6	131.8	114.2	77	123	1.5974	0.000578455
A0A024R577	TM7SF2	Transmembrane 7 superfamily member 2, isoform CRA_a OS=Homo sapiens GN=TM7SF2 PE=4 SV=1	4.306220096	2	3	2	418	46.375	8.87	79.8	74.4	123.9	121.9	77.1	122.9	1.59403	0.000613801
Q96F63	CCDC97	Coiled-coil domain-containing protein 97 OS=Homo sapiens GN=CCDC97 PE=1 SV=1	3.206997085	1	1	1	343	38.923	4.59	79.2	75.2	84.5	161.2	77.2	122.85	1.59132	0.00064377
B1N7B9		Cryocryoglobulin CC2 lambda light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	12.72727273	1	2	1	110	11.308	7.97	75.8	78.6	110.4	135.2	77.2	122.8	1.59067	0.000651131

A0A0U4B CF5		Complement factor I OS=Homo sapiens PE=2 SV=1	3.608247423	2	2	2	582	65.286	7.85	74.7	79.8	106.7	138.9	77.25	122.8	1.58964	0.000663002
D6RFG8	DCK	Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1	8.832807571	2	2	2	317	36.741	5.43	71.5	83	106.3	139.2	77.25	122.75	1.589	0.00067057
Q6MZX7	DKFZp6 86M242 18	Putative uncharacterized protein DKFZp686M24218 OS=Homo sapiens GN=DKFZp686M24218 PE=2 SV=1	5.25210084	1	5	1	476	52.387	7.77	56.7	98	83.7	161.7	77.35	122.7	1.5863	0.000703064
P49327	FASN	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	30.06770211	60	108	60	2511	273.254	6.44	79.7	75	130.6	114.7	77.35	122.65	1.58565	0.000711064
P31151	S100A7	Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	10.89108911	1	1	1	101	11.464	6.77	87.2	67.5	76.2	169.1	77.35	122.65	1.58565	0.000711064
B2R950		cDNA, FLJ94213, highly similar to Homo sapiens pregnancy-zone protein (PZP), mRNA OS=Homo sapiens PE=2 SV=1	2.834008097	4	12	2	1482	163.768	6.38	82.8	72.1	128.1	117	77.45	122.55	1.58231	0.000753798
Q969U7	PSMG2	Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 PE=1 SV=1	3.409090909	1	1	1	264	29.377	6.98	71.4	83.7	130.7	114.2	77.55	122.45	1.57898	0.000798885
H3BUA5		Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2	5	1	5	1	140	15.542	8.76	80.7	74.5	126.8	118	77.6	122.4	1.57732	0.000822346
Q4LE36	ACLY	ACLY variant protein (Fragment) OS=Homo sapiens GN=ACLY variant protein PE=2 SV=1	41.7766051	42	74	42	1137	124.477	8.03	82	74.1	127.5	116.4	78.05	121.95	1.56246	0.00106386
Q96GX5	MASTL	Serine/threonine-protein kinase greatwall OS=Homo sapiens GN=MASTL PE=1 SV=1	2.730375427	2	2	1	879	97.257	5.99	81.8	74.3	144.2	99.7	78.05	121.95	1.56246	0.00106386
O15554	KCNN4	Intermediate conductance calcium-activated potassium channel protein 4 OS=Homo sapiens GN=KCNN4 PE=1 SV=1	7.259953162	3	3	3	427	47.665	9.83	77.9	78.7	112.8	130.6	78.3	121.7	1.55428	0.00122461

P29401	TKT	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	52.32744783	27	95	27	623	67.835	7.66	80.1	76.5	128.9	114.4	78.3	121.65	1.55364	0.00123809
P01591	JCHAIN	Immunoglobulin J chain OS=Homo sapiens GN=JCHAIN PE=1 SV=4	6.289308176	1	2	1	159	18.087	5.24	69.3	87.5	104.1	139.1	78.4	121.6	1.55102	0.00129491
A0A024R1 A4	UBE2L3	Ubiquitin-conjugating enzyme E2L3, isoform CRA_a OS=Homo sapiens GN=UBE2L3 PE=3 SV=1	22.07792208	3	3	3	154	17.85	8.51	77.4	79.7	133.9	109.1	78.55	121.5	1.54679	0.00139211
Q01638	IL1RL1	Interleukin-1 receptor-like 1 OS=Homo sapiens GN=IL1RL1 PE=1 SV=4	1.258992806	1	2	1	556	63.317	8.35	82.4	74.8	124.8	118	78.6	121.4	1.54453	0.00144672
O75459	PAGE1	P antigen family member 1 OS=Homo sapiens GN=PAGE1 PE=1 SV=2	13.01369863	1	3	1	146	16.14	4.22	80.5	76.8	119.6	123.1	78.65	121.35	1.54291	0.00148713
BOYJ28	IL18	Interleukin-18 OS=Homo sapiens GN=IL18 PE=3 SV=1	41.4507772	6	10	6	193	22.293	4.84	75.9	81.5	130.1	112.5	78.7	121.3	1.5413	0.00152857
R9S3C3	p14ARF	p14ARF/p16INK4a fusion protein OS=Homo sapiens GN=p14ARF PE=2 SV=1	11.76470588	2	2	1	170	18.52	11.68	68.4	89	116.2	126.4	78.7	121.3	1.5413	0.00152857
A0A140V K56		Transaldolase OS=Homo sapiens PE=2 SV=1	43.91691395	17	24	17	337	37.516	6.81	85.1	72.5	130.7	111.7	78.8	121.2	1.53807	0.00161462
A0A024R0 L5	GSK3A	Glycogen synthase kinase 3 alpha, isoform CRA_a OS=Homo sapiens GN=GSK3A PE=3 SV=1	15.73498965	5	8	1	483	50.949	8.75	61.6	96.2	127.9	114.3	78.9	121.1	1.53485	0.00170508
Q6IAX1	FDFT1	FDFT1 protein OS=Homo sapiens GN=FDFT1 PE=2 SV=1	36.93045564	14	42	14	417	48.084	6.54	81.5	77	120.5	120.9	79.25	120.7	1.52303	0.00208117
Q16222	UAP1	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3	1.340996169	1	1	1	522	58.732	6.33	88.6	69.9	133.2	108.2	79.25	120.7	1.52303	0.00208117
P20073	ANXA7	Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3	25.40983607	11	20	11	488	52.706	5.68	86	72.6	128.6	112.9	79.3	120.75	1.5227	0.00209271
Q13907	IDI1	Isopentenyl-diphosphate Delta-isomerase 1 OS=Homo sapiens GN=IDI1 PE=1 SV=2	50.66079295	8	13	8	227	26.302	6.34	78.5	80.2	129.7	111.6	79.35	120.65	1.52048	0.00217206

G3V5L9	DLST	Dihydrolypoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=1	8.181818182	1	1	1	110	12.844	11.68	75.6	83.3	114	127	79.45	120.5	1.51668	0.00231467
Q8IZU8	DSEL	Dermatan-sulfate epimerase-like protein OS=Homo sapiens GN=DSEL PE=2 SV=2	1.155115512	1	1	1	1212	139.149	8.32	88.6	70.3	127.9	113.1	79.45	120.5	1.51668	0.00231467
D3DRR6	ITIH2	Inter-alpha (Globulin) inhibitor H2, isoform CRA_a OS=Homo sapiens GN=ITIH2 PE=4 SV=1	5.068637804	5	6	5	947	106.502	6.95	69.6	89.7	102.6	138.1	79.65	120.35	1.51099	0.00254501
Q8WXI2	CNKSR2	Connector enhancer of kinase suppressor of ras 2 OS=Homo sapiens GN=CNKSR2 PE=1 SV=1	0.773694391	1	1	1	1034	117.461	6.79	78	81.4	135.4	105.2	79.7	120.3	1.50941	0.00261254
H0Y300	HP	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4	6.561085973	3	3	3	442	49.074	6.64	72.2	87.2	97.1	143.5	79.7	120.3	1.50941	0.00261254
M0R2J8	DCDC1	Doublecortin domain-containing protein 1 OS=Homo sapiens GN=DCDC1 PE=1 SV=1	0.448681997	1	1	1	1783	200.465	8.9	82.6	76.9	124.5	116	79.75	120.25	1.50784	0.00268168
P02795	MT2A	Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1	65.57377049	3	5	3	61	6.037	7.83	68.6	91.2	122.6	117.6	79.9	120.1	1.50313	0.00289916
Q5T765	IFIT3	Interferon-induced protein with tetratricopeptide repeats 3, isoform CRA_a OS=Homo sapiens GN=IFIT3 PE=2 SV=1	7.142857143	3	4	3	490	55.95	5.2	80.4	79.7	125.6	114.3	80.05	119.95	1.49844	0.00313247
G9BZK0		Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens PE=2 SV=1	27.5	1	1	1	40	4.574	7.42	87.3	72.8	127.4	112.5	80.05	119.95	1.49844	0.00313247
V9HWD8	HEL-S-163pA	Epididymis secretory sperm binding protein Li 163pA OS=Homo sapiens GN=HEL-S-163pA PE=2 SV=1	1.414141414	1	1	1	495	54.22	5.86	78.6	81.5	103.6	136.3	80.05	119.95	1.49844	0.00313247

Q15800	MSMO1	Methylsterol monooxygenase 1 OS=Homo sapiens GN=MSMO1 PE=1 SV=1	15.01706485	4	8	4	293	35.193	7.23	92.6	67.9	123	116.6	80.25	119.8	1.49283	0.00343466
H0Y786	NEB	Nebulin (Fragment) OS=Homo sapiens GN=NEB PE=1 SV=1	0.29930163	1	1	1	3007	348.736	9.11	86.1	74.5	127	112.4	80.3	119.7	1.49066	0.00355926
P06733	ENO1	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	66.8202765	24	134	21	434	47.139	7.39	83	77.8	126.6	112.6	80.4	119.6	1.48756	0.00374418
Q9UGM1	CHRNA9	Neuronal acetylcholine receptor subunit alpha-9 OS=Homo sapiens GN=CHRNA9 PE=1 SV=2	1.461377871	1	1	1	479	54.772	6.47	100.1	60.8	143.2	95.9	80.45	119.55	1.48602	0.00383984
P31947	SFN	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	47.58064516	12	32	8	248	27.757	4.74	80.4	80.6	126.3	112.6	80.5	119.45	1.48385	0.00397773
V9HWA9	HEL-S-62p	Epididymis secretory sperm binding protein Li 62p OS=Homo sapiens GN=HEL-S-62p PE=2 SV=1	12.86831028	20	53	20	1663	187.03	6.4	72.2	88.9	99.5	139.4	80.55	119.45	1.48293	0.0040378
Q15813	TBCE	Tubulin-specific chaperone E OS=Homo sapiens GN=TBCE PE=1 SV=1	1.897533207	1	1	1	527	59.309	6.76	76.5	84.7	118.6	120.3	80.6	119.45	1.48201	0.00409866
A9UF07	BCR/ABL	BCR/ABL fusion protein isoform Y5 OS=Homo sapiens GN=BCR/ABL fusion PE=2 SV=1	1.061452514	1	1	1	1790	196.451	8.4	76.5	84.8	108.4	130.4	80.65	119.4	1.48047	0.0042024
A8K7T0	KYNU	Kynureninase OS=Homo sapiens GN=KYNU PE=2 SV=1	16.77419355	6	10	6	465	52.335	6.83	84.3	77.1	128.7	110	80.7	119.35	1.47893	0.00430849
Q5EBL4	RILPL1	RILP-like protein 1 OS=Homo sapiens GN=RILPL1 PE=1 SV=1	3.225806452	1	1	1	403	47.079	5.21	77.1	84.4	106	132.6	80.75	119.3	1.4774	0.00441699
Q0VDG5	SCRN3	SCRN3 protein OS=Homo sapiens GN=SCRN3 PE=2 SV=1	3.755868545	1	1	1	426	48.808	5.55	95.8	66.4	122.6	115.3	81.1	118.95	1.46671	0.00524772
Q53F11		tRNA isopentenyltransferase 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	2.355460385	1	1	1	467	52.695	8.03	81.6	80.6	119.9	117.9	81.1	118.9	1.46609	0.00529988
A8K9L8		cDNA FLJ76964, highly similar to Homo sapiens tropomodulin 2	1.994301994	1	2	1	351	39.585	5.27	68.7	93.7	104.9	132.7	81.2	118.8	1.46305	0.00556404

		(neuronal) (TMOD2), mRNA OS=Homo sapiens PE=2 SV=1																
A0A024QZ F8	EMP3	Epithelial membrane protein 3 OS=Homo sapiens GN=EMP3 PE=3 SV=1	8.588957055	1	2	1	163	18.417	7.96	79.7	83	114	123.3	81.35	118.65	1.45851	0.00598237	
HOYAH0	PCDH7	Protocadherin-7 (Fragment) OS=Homo sapiens GN=PCDH7 PE=1 SV=1	2.241195304	1	1	1	937	102.47	5.4	82.1	80.7	144.9	92.2	81.4	118.55	1.45639	0.00618808	
A0A0G2J PR0	C4A	Complement C4-A OS=Homo sapiens GN=C4A PE=4 SV=1	7.339449541	12	18	12	1744	192.754	7.03	78.6	84.3	101.1	136	81.45	118.55	1.45549	0.00627664	
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	29.60662526	13	18	13	483	53.106	7.23	81.7	81.3	124	112.9	81.5	118.45	1.45337	0.00649142	
A8K6N3		cDNA FLJ76886, highly similar to Homo sapiens loss of heterozygosity, 11, chromosomal region 2, gene A (LOH11CR2A), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	2.798982188	2	2	2	786	86.46	6.58	73.6	89.6	114.2	122.7	81.6	118.45	1.45159	0.00667721	
F4MH14	UTY	Ubiquitously transcribed tetratricopeptide repeat protein Y- linked transcript variant 205 OS=Homo sapiens GN=UTY PE=2 SV=1	1.166666667	2	2	2	600	67.254	7.43	83.7	79.5	127.6	109.2	81.6	118.4	1.45098	0.00674227	
Q8TBQ9	TMEM1 67A	Protein kish-A OS=Homo sapiens GN=TMEM167A PE=1 SV=1	12.5	1	1	1	72	8.054	8.95	77.6	85.9	129.5	106.9	81.75	118.2	1.44587	0.00730852	
V9HWC9	HEL-S- 44	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=HEL-S-44 PE=2 SV=1	13.63636364	2	9	2	154	15.926	6.13	83.6	80.1	126	110.3	81.85	118.15	1.44349	0.00758701	
A0A075B6 I0	IGLV8- 61	Protein IGLV8-61 (Fragment) OS=Homo sapiens GN=IGLV8-61 PE=1 SV=7	7.37704918	1	1	1	122	12.806	4.55	71.1	92.6	108.6	127.7	81.85	118.15	1.44349	0.00758701	

P02753	RBP4	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3	8.457711443	2	3	2	201	22.995	6.07	89.3	74.6	99.1	137	81.95	118.05	1.44051	0.00795041
A2VCK8	TMSB4X	Thymosin beta 4, X-linked OS=Homo sapiens GN=TMSB4X PE=2 SV=1	75	5	11	5	44	5.05	5.06	66.2	97.7	130.5	105.6	81.95	118.05	1.44051	0.00795041
Q6QNY5	GNE	UDP-N-acetylglucosamine-2- epimerase / N-acetylmannosamine kinase OS=Homo sapiens GN=GNE PE=2 SV=1	12.46537396	8	10	8	722	79.323	6.86	86.5	77.6	126.7	109.3	82.05	118	1.43815	0.00825024
P60891	PRPS1	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	39.3081761	10	18	5	318	34.812	6.98	86.7	77.7	120.2	115.4	82.2	117.8	1.43309	0.00892736
J3QLD6	UTP18	U3 small nucleolar RNA- associated protein 18 homolog (Fragment) OS=Homo sapiens GN=UTP18 PE=1 SV=1	22.60869565	2	3	1	115	12.665	9.04	87.4	77	128.2	107.4	82.2	117.8	1.43309	0.00892736
Q59GB4		Dihydropyrimidinase-like 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	28.82165605	13	21	4	628	68.142	6.24	81.7	82.8	118.8	116.6	82.25	117.7	1.431	0.00922169
A8K2T4		cDNA FLJ78207, highly similar to Human complement protein component C7 mRNA OS=Homo sapiens PE=2 SV=1	2.016607355	2	2	2	843	93.346	6.51	68	96.6	94.7	140.7	82.3	117.7	1.43013	0.00934696
B2RCY7		cDNA, FLJ96375, highly similar to Homo sapiens interleukin 1 receptor-like 2 (IL1RL2), mRNA OS=Homo sapiens PE=2 SV=1	1.217391304	1	1	1	575	65.348	7.46	90.4	74.3	125.2	110.1	82.35	117.65	1.42866	0.00956325
B4DUP2		cDNA FLJ56155, highly similar to UTP--glucose-1-phosphate uridylyltransferase 2 (EC 2.7.7.9) OS=Homo sapiens PE=2 SV=1	35.20309478	14	19	1	517	57.755	8.13	81	83.8	120.6	114.5	82.4	117.55	1.42658	0.00987616

A8KAJ3		cDNA FLJ77823, highly similar to Homo sapiens EGF-containing fibulin-like extracellular matrix protein 1, transcript variant 3, mRNA OS=Homo sapiens PE=2 SV=1	4.868154158	2	2	2	493	54.632	5.14	79.7	85.3	114.7	120.3	82.5	117.5	1.42424	0.0102388
D6R968	N4BP2L 2	NEDD4-binding protein 2-like 2 (Fragment) OS=Homo sapiens GN=N4BP2L2 PE=1 SV=1	1.692524683	1	1	1	709	82.316	6.38	81.6	83.5	115.6	119.3	82.55	117.45	1.42277	0.0104732
B7Z3K9		Fructose-bisphosphate aldolase OS=Homo sapiens PE=2 SV=1	31.92904656	13	62	7	451	48.378	8.07	84.5	80.6	126.3	108.6	82.55	117.45	1.42277	0.0104732
P51784	USP11	Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens GN=USP11 PE=1 SV=3	2.076843198	2	2	2	963	109.747	5.45	82.6	82.6	112.7	122.2	82.6	117.45	1.42191	0.010613
H3BNH8		Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2	12.76595745	1	1	1	94	10.371	9.29	63.1	102.1	99.3	135.6	82.6	117.45	1.42191	0.010613
Q5VT79	ANXA8L 1	Annexin A8-like protein 1 OS=Homo sapiens GN=ANXA8L1 PE=2 SV=2	16.20795107	5	6	5	327	36.856	5.78	83.8	81.5	122.7	112	82.65	117.35	1.41984	0.0109562
F8W809	TXNRD1	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=1	28.71485944	11	15	10	498	54.569	6.47	82.1	83.2	119.8	114.9	82.65	117.35	1.41984	0.0109562
P01611		Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1	16.66666667	1	1	1	108	11.601	7.28	91.7	73.6	123.9	110.8	82.65	117.35	1.41984	0.0109562
P61457	PCBD1	Pterin-4-alpha-carbinolamine dehydratase OS=Homo sapiens GN=PCBD1 PE=1 SV=2	16.34615385	2	2	2	104	11.992	6.8	86.6	78.8	125.5	109.2	82.7	117.35	1.41898	0.0111015
B4DHZ6	TF	Transferrin, isoform CRA_c OS=Homo sapiens GN=TF PE=2 SV=1	1.650943396	1	1	1	424	47.357	7.05	83.3	82.1	107.7	126.9	82.7	117.3	1.41838	0.0112049
Q7Z624	CAMKM T	Calmodulin-lysine N-methyltransferase OS=Homo	2.476780186	1	1	1	323	36.105	6.83	80.8	84.8	114.9	119.5	82.8	117.2	1.41546	0.0117174

		sapiens GN=CAMKMT PE=1 SV=2															
B3KM43		cDNA FLJ10228 fis, clone HEMBB1000119, highly similar to N-acetylserotonin O- methyltransferase-like protein OS=Homo sapiens PE=2 SV=1	6.280193237	3	3	1	621	68.754	6.13	75.4	90.2	110.3	124.1	82.8	117.2	1.41546	0.0117174
P01031	C5	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	3.341288783	6	6	6	1676	188.186	6.52	74.3	91.3	98	136.4	82.8	117.2	1.41546	0.0117174
Q6QNK2	ADGRD 1	Adhesion G-protein coupled receptor D1 OS=Homo sapiens GN=ADGRD1 PE=1 SV=1	3.318077803	1	3	1	874	96.468	7.88	71.6	94	89.4	145	82.8	117.2	1.41546	0.0117174
B2R7F8		Plasminogen OS=Homo sapiens PE=2 SV=1	3.827160494	3	4	1	810	90.48	7.24	80.9	84.8	100.3	133.9	82.85	117.1	1.4134	0.0120922
Q14781	CBX2	Chromobox protein homolog 2 OS=Homo sapiens GN=CBX2 PE=1 SV=2	1.879699248	1	1	1	532	56.046	10.01	81.9	84.1	125.5	108.5	83	117	1.40964	0.0128045
A0A090N7 T9	SCRN1	Secernin 1 OS=Homo sapiens GN=SCRN1 PE=4 SV=1	8.212560386	3	3	3	414	46.353	4.75	88.4	77.7	120	114	83.05	117	1.40879	0.0129707
H6VRG1	KRT1	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	31.1627907	22	76	15	645	66.086	8.12	79	87.1	136.4	97.6	83.05	117	1.40879	0.0129707
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	43.57798165	8	10	8	218	24.564	6.68	83.1	83	123.2	110.6	83.05	116.9	1.40759	0.0132098
Q9NZQ0	DNAJC2 7	DnaJ homolog subfamily C member 27 OS=Homo sapiens GN=DNAJC27 PE=1 SV=1	4.029304029	1	1	1	273	30.836	8.46	82.2	84.1	122.7	111.1	83.15	116.9	1.40589	0.013553
Q15819	UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4	22.75862069	3	4	3	145	16.352	8.09	77.8	88.6	122.5	111.1	83.2	116.8	1.40385	0.0139791
A0A0K0K 1L8	HEL-S- 129m	Epididymis secretory sperm binding protein Li 129m OS=Homo	31.3253012	9	13	9	249	28.705	6.02	89.3	77.1	125.3	108.2	83.2	116.75	1.40325	0.0141065

		sapiens GN=HEL-S-129m PE=2 SV=1																
H0YBS2	SLC36A 1	Proton-coupled amino acid transporter 1 (Fragment) OS=Homo sapiens GN=SLC36A1 PE=4 SV=1	11.23595506	1	1	1	89	9.739	8.28	120.7	45.8	137.3	96.3	83.25	116.8	1.403	0.0141582	
Q14997	PSME4	Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2	3.309820944	5	5	5	1843	211.199	6.9	86	80.5	125.9	107.6	83.25	116.75	1.4024	0.0142871	
Q96DC9	OTUB2	Ubiquitin thioesterase OTUB2 OS=Homo sapiens GN=OTUB2 PE=1 SV=2	2.991452991	1	2	1	234	27.196	6.23	94.6	72	132.5	100.9	83.3	116.7	1.40096	0.014601	
Q9UJ70	NAGK	N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4	9.593023256	2	2	2	344	37.352	6.24	87.9	78.7	123.9	109.5	83.3	116.7	1.40096	0.014601	
B2R983		cDNA, FLJ94267, highly similar to Homo sapiens glutathione S- transferase omega 1 (GSTO1), mRNA OS=Homo sapiens PE=2 SV=1	17.42738589	5	6	5	241	27.521	6.6	90.2	76.5	124.2	109.1	83.35	116.65	1.39952	0.0149209	
A8K6K2		cDNA FLJ75877, highly similar to Homo sapiens 5'-nucleotidase, cytosolic II (NT5C2), mRNA OS=Homo sapiens PE=2 SV=1	3.386809269	2	3	2	561	64.918	6.14	88.4	78.4	122.9	110.3	83.4	116.6	1.39808	0.0152468	
E7ER45	MGAM	Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=1 SV=2	1.452960407	3	3	3	2753	311.825	5.41	87.2	79.8	106.7	126.4	83.5	116.55	1.39581	0.0157755	
P30520	ADSS	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	27.85087719	9	13	9	456	50.066	6.55	84.3	82.7	117.6	115.4	83.5	116.5	1.39521	0.0159175	
P34949	MPI	Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=2	3.546099291	1	1	1	423	46.626	5.95	81.9	85.1	129.3	103.7	83.5	116.5	1.39521	0.0159175	

Q9UNR6	ERG1	Squalene epoxidase OS=Homo sapiens GN=ERG1 PE=2 SV=1	30.83623693	13	22	13	574	63.882	8.63	84.9	82.2	114.1	118.9	83.55	116.5	1.39437	0.0161176
Q16853	AOC3	Membrane primary amine oxidase OS=Homo sapiens GN=AOC3 PE=1 SV=3	1.179554391	1	2	1	763	84.568	6.52	73.6	93.6	97.2	135.5	83.6	116.35	1.39175	0.0167627
P23381	WARS	Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	32.69639066	11	17	11	471	53.132	6.23	82.9	84.4	113.4	119.3	83.65	116.35	1.39091	0.0169717
Q9H2J4	PDCL3	Phosducin-like protein 3 OS=Homo sapiens GN=PDCL3 PE=1 SV=1	16.31799163	3	3	3	239	27.597	4.84	82.6	84.7	111.1	121.6	83.65	116.35	1.39091	0.0169717
O60271	SPAG9	C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4	2.119606359	3	3	3	1321	146.115	5.15	78.1	89.2	114.4	118.3	83.65	116.35	1.39091	0.0169717
Q5VXV3	SET	SET OS=Homo sapiens GN=SET PE=2 SV=1	34.13793103	8	24	8	290	33.469	4.32	91.6	75.8	126.4	106.2	83.7	116.3	1.38949	0.0173364
A8K103		cDNA FLJ75454, highly similar to Homo sapiens arrestin, beta 1 (ARRB1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	2.392344498	1	1	1	418	47.035	6.48	85.2	82.2	124.2	108.4	83.7	116.3	1.38949	0.0173364
Q96Q89	KIF20B	Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=1 SV=3	0.934065934	2	2	2	1820	210.5	5.67	88.2	79.3	123.7	108.8	83.75	116.25	1.38806	0.0177078
P16930	FAH	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2	2.14797136	1	1	1	419	46.344	6.95	79.8	87.7	127.3	105.1	83.75	116.2	1.38746	0.0178654
B1AKK2	DDAH1	Dimethylarginine dimethylaminohydrolase 1, isoform CRA_b OS=Homo sapiens GN=DDAH1 PE=2 SV=1	12.98245614	2	2	2	285	31.102	5.81	88.3	79.3	111.8	120.6	83.8	116.2	1.38663	0.0180862
Q9BRP1	PDCD2L	Programmed cell death protein 2-like OS=Homo sapiens GN=PDCD2L PE=1 SV=1	5.586592179	1	2	1	358	39.391	4.86	85.6	82.1	115.2	117.1	83.85	116.15	1.38521	0.0184715

B7ZKJ8	ITIH4	ITIH4 protein OS=Homo sapiens GN=ITIH4 PE=1 SV=1	3.101604278	3	13	3	935	103.816	6.89	75.2	92.5	102.6	129.7	83.85	116.15	1.38521	0.0184715
P31150	GDI1	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	20.80536913	8	12	4	447	50.55	5.14	84.4	83.3	122.5	109.7	83.85	116.1	1.38462	0.0186352
Q15555	MAPRE2	Microtubule-associated protein RP/EB family member 2 OS=Homo sapiens GN=MAPRE2 PE=1 SV=1	4.892966361	2	2	1	327	37.008	5.57	82.5	85.3	118	114.2	83.9	116.1	1.38379	0.0188639
Q6N097	DKFZp686H20196	Putative uncharacterized protein DKFZp686H20196 OS=Homo sapiens GN=DKFZp686H20196 PE=2 SV=1	7.484407484	2	2	2	481	52.725	8.48	103.2	64.6	109.1	123	83.9	116.05	1.38319	0.0190307
Q9NQ92	COPRS	Coordinator of PRMT5 and differentiation stimulator OS=Homo sapiens GN=COPRS PE=1 SV=3	6.52173913	1	1	1	184	20.054	4.18	78.9	89	115.5	116.6	83.95	116.05	1.38237	0.0192636
Q96GG9	DCUN1D1	DCN1-like protein 1 OS=Homo sapiens GN=DCUN1D1 PE=1 SV=1	21.23552124	4	4	4	259	30.105	5.34	85.5	82.6	123.1	108.8	84.05	115.95	1.37954	0.0200849
O00193	SMAP	Small acidic protein OS=Homo sapiens GN=SMAP PE=1 SV=1	25.68306011	4	10	4	183	20.32	4.72	86.5	81.7	122.1	109.7	84.1	115.9	1.37812	0.0205068
P12429	ANXA3	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3	29.41176471	9	10	9	323	36.353	5.92	86.3	81.9	120.7	111.1	84.1	115.9	1.37812	0.0205068
O95817	BAG3	BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3	19.82608696	9	13	9	575	61.557	6.95	82.8	85.4	117.9	113.9	84.1	115.9	1.37812	0.0205068
O43708	GSTZ1	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3	3.703703704	1	1	1	216	24.197	8.54	88.4	79.8	122.3	109.5	84.1	115.9	1.37812	0.0205068
B2R5R5		cDNA, FLJ92583, highly similar to Homo sapiens glycogenin (GYG), mRNA OS=Homo sapiens PE=2 SV=1	10.85714286	3	3	3	350	39.329	5.53	87.4	80.9	122.9	108.9	84.15	115.9	1.3773	0.0207547

B2RDF5		cDNA, FLJ96587, highly similar to Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA OS=Homo sapiens PE=2 SV=1	22.5	11	14	11	640	71.135	5.29	85.7	82.6	123.7	108	84.15	115.85	1.37671	0.0209363
B5BUB5	SSB	Autoantigen La (Fragment) OS=Homo sapiens GN=SSB PE=2 SV=1	30.88235294	15	22	15	408	46.838	7.12	89.7	78.7	127.4	104.2	84.2	115.8	1.3753	0.0213736
A0A024R2 G6	SH3BP5	SH3-domain binding protein 5 (BTK-associated), isoform CRA_b OS=Homo sapiens GN=SH3BP5 PE=4 SV=1	4.175824176	2	2	1	455	50.394	4.97	78	90.5	97.6	133.9	84.25	115.75	1.37389	0.0218187
P53602	MVD	Diphosphomevalonate decarboxylase OS=Homo sapiens GN=MVD PE=1 SV=1	15	5	6	5	400	43.377	7.23	82.3	86.2	123	108.4	84.25	115.7	1.37329	0.0220087
S4R435	RPS10- NUDT3	Protein RPS10-NUDT3 (Fragment) OS=Homo sapiens GN=RPS10-NUDT3 PE=4 SV=1	29.72027972	10	36	1	286	32.576	9.19	79	89.7	118.2	113.2	84.35	115.7	1.37167	0.0225376
B2RD51		Proteasome assembly chaperone 1 OS=Homo sapiens PE=2 SV=1	11.80555556	3	3	3	288	32.861	7.17	81.4	87.3	115.1	116.2	84.35	115.65	1.37107	0.022733
Q7Z4G4	TRMT11	tRNA (guanine(10)-N2)-methyltransferase homolog OS=Homo sapiens GN=TRMT11 PE=1 SV=1	2.591792657	1	2	1	463	53.387	7.78	85.3	83.5	121	110.2	84.4	115.6	1.36967	0.0232024
Q9H237	PORCN	Protein-serine O-palmitoleoyltransferase porcupine OS=Homo sapiens GN=PORCN PE=1 SV=2	2.169197397	1	1	1	461	52.283	8.84	79.5	89.3	114.3	116.9	84.4	115.6	1.36967	0.0232024
Q99471	PFDN5	Prefoldin subunit 5 OS=Homo sapiens GN=PFDN5 PE=1 SV=2	40.90909091	5	8	5	154	17.317	6.33	84.8	84	120.6	110.5	84.4	115.55	1.36908	0.0234031
Q6PD74	AAGAB	Alpha- and gamma-adaptin-binding protein p34 OS=Homo sapiens GN=AAGAB PE=1 SV=1	4.444444444	1	2	1	315	34.572	4.64	87	81.9	119.1	112	84.45	115.55	1.36827	0.0236801

P26038	MSN	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	53.55285962	40	93	26	577	67.778	6.4	83	85.9	113.5	117.6	84.45	115.55	1.36827	0.0236801
Q6ZS27	ZNF662	Zinc finger protein 662 OS=Homo sapiens GN=ZNF662 PE=1 SV=1	4.225352113	2	2	1	426	48.465	7.66	87	82.1	120	110.9	84.55	115.45	1.36546	0.024661
V9HWB8	HEL-S-30	Pyruvate kinase OS=Homo sapiens GN=HEL-S-30 PE=1 SV=1	74.38794727	33	150	33	531	57.9	7.84	84.9	84.2	119.2	111.7	84.55	115.45	1.36546	0.024661
Q9H6T0	ESRP2	Epithelial splicing regulatory protein 2 OS=Homo sapiens GN=ESRP2 PE=1 SV=1	1.5130674	1	1	1	727	78.351	6.71	79.5	89.6	102.7	128.2	84.55	115.45	1.36546	0.024661
O00622	CYR61	Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1	52.49343832	15	25	15	381	41.998	8.21	78.8	90.3	110.1	120.8	84.55	115.45	1.36546	0.024661
Q9Y2I7	PIKFYVE	1-phosphatidylinositol 3-phosphate 5-kinase OS=Homo sapiens GN=PIKFYVE PE=1 SV=3	0.333651096	1	1	1	2098	236.986	6.7	87.4	81.8	125.8	105	84.6	115.4	1.36407	0.0251643
Q96N23	CFAP54	Cilia- and flagella-associated protein 54 OS=Homo sapiens GN=CFAP54 PE=2 SV=3	0.226098191	1	1	1	3096	351.744	8.1	79.5	89.7	89.7	141	84.6	115.35	1.36348	0.0253799
Q93100	PHKB	Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB PE=1 SV=3	0.914913083	1	1	1	1093	124.805	6.95	85.8	83.5	122.9	107.8	84.65	115.35	1.36267	0.0256765
A0A024R0R4	SAE1	SUMO-1 activating enzyme subunit 1, isoform CRA_b OS=Homo sapiens GN=SAE1 PE=4 SV=1	28.03468208	8	11	8	346	38.426	5.3	83.2	86.1	124.9	105.8	84.65	115.35	1.36267	0.0256765
Q86UU0	BCL9L	B-cell CLL/lymphoma 9-like protein OS=Homo sapiens GN=BCL9L PE=1 SV=1	0.667111408	1	1	1	1499	157.027	8.63	87	82.5	118.9	111.6	84.75	115.25	1.35988	0.0267276
E9PQY2	PFDN4	Prefoldin subunit 4 OS=Homo sapiens GN=PFDN4 PE=1 SV=1	8.088235294	1	1	1	136	15.589	4.58	85.7	83.8	118.2	112.3	84.75	115.25	1.35988	0.0267276
Q05DJ2	MTAP	Purine nucleoside phosphorylase OS=Homo sapiens GN=MTAP PE=2 SV=1	25.61983471	5	7	5	242	26.773	6.84	84.8	84.7	118.9	111.6	84.75	115.25	1.35988	0.0267276

Q9NS93	TM7SF3	Transmembrane 7 superfamily member 3 OS=Homo sapiens GN=TM7SF3 PE=2 SV=1	1.578947368	1	1	1	570	64.125	7.01	73.5	96	125.2	105.3	84.75	115.25	1.35988	0.0267276
D3DSY9	FNTA	Farnesyltransferase, CAAX box, alpha, isoform CRA_a OS=Homo sapiens GN=FNTA PE=4 SV=1	2.188183807	1	1	1	457	52.577	5.57	87	82.5	123.9	106.5	84.75	115.2	1.35929	0.026955
P36871	PGM1	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	38.25622776	18	21	18	562	61.411	6.76	87	82.6	121.8	108.6	84.8	115.2	1.35849	0.0272668
A0A0A0MQR1	MAP4K5	Mitogen-activated protein kinase kinase kinase OS=Homo sapiens GN=MAP4K5 PE=1 SV=1	1.063829787	1	1	1	846	94.963	7.83	84.5	85.1	114.3	116.1	84.8	115.2	1.35849	0.0272668
O75663	TIPRL	TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2	4.411764706	1	1	1	272	31.424	5.91	82.7	86.9	118.9	111.4	84.8	115.15	1.3579	0.0274983
Q8IZP9	ADGRG2	Adhesion G-protein coupled receptor G2 OS=Homo sapiens GN=ADGRG2 PE=1 SV=2	3.638151426	3	3	3	1017	111.521	7.55	89	80.7	107.9	122.4	84.85	115.15	1.3571	0.0278154
P63104	YWHAZ	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	67.34693878	16	56	11	245	27.728	4.79	86.8	82.9	122.4	107.9	84.85	115.15	1.3571	0.0278154
A0A140VK83	PPP1R7	Protein phosphatase 1, regulatory subunit 7, isoform CRA_b OS=Homo sapiens GN=PPP1R7 PE=2 SV=1	10.27777778	4	4	4	360	41.539	4.91	89.6	80.2	118.3	111.9	84.9	115.1	1.35571	0.0283733
Q96AY4	TTC28	Tetratricopeptide repeat protein 28 OS=Homo sapiens GN=TTC28 PE=1 SV=4	1.088270859	2	2	2	2481	270.715	6.89	75.1	94.7	96.4	133.7	84.9	115.05	1.35512	0.0286131
A0A0A6Y92	ADSL	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=1	13.65461847	4	4	4	498	56.181	7.43	84.1	85.8	115.5	114.6	84.95	115.05	1.35433	0.0289407
B2R577		Protein S100 OS=Homo sapiens PE=2 SV=1	17.77777778	2	5	2	90	10.101	5.91	87.4	82.9	119.9	109.9	85.15	114.9	1.34938	0.0310488
A0A0K2BMD8	HBA2	Mutant hemoglobin alpha 2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	34.50704225	5	27	5	142	15.248	8.68	66.7	103.7	93.3	136.3	85.2	114.8	1.34742	0.0319253

P00558	PGK1	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	61.15107914	25	76	25	417	44.586	8.1	88.3	82.3	121.1	108.3	85.3	114.7	1.34467	0.0331903
A0A140VJ J2	ESD	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=2 SV=1	16.31205674	4	6	4	282	31.442	7.02	89	81.6	124.3	105	85.3	114.65	1.34408	0.0334655
Q43491	EPB41L 2	Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1	13.53233831	11	12	10	1005	112.519	5.44	83.7	87	108.5	120.8	85.35	114.65	1.34329	0.0338386
A0A140VJ P2		Testicular tissue protein Li 118 OS=Homo sapiens PE=2 SV=1	26.64670659	7	7	7	334	37.528	7.36	89.4	81.3	123	106.3	85.35	114.65	1.34329	0.0338386
Q8WTS6	SETD7	Histone-lysine N-methyltransferase SETD7 OS=Homo sapiens GN=SETD7 PE=1 SV=1	6.010928962	2	2	2	366	40.695	4.63	79.7	91	119	110.3	85.35	114.65	1.34329	0.0338386
P05546	SERPIN D1	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	2.404809619	1	3	1	499	57.034	6.9	78	92.7	91.7	137.6	85.35	114.65	1.34329	0.0338386
O75385	ULK1	Serine/threonine-protein kinase ULK1 OS=Homo sapiens GN=ULK1 PE=1 SV=2	0.666666667	1	1	1	1050	112.56	8.79	96.9	74.1	114.9	114.1	85.5	114.5	1.33918	0.0358481
Q9UK22	FBXO2	F-box only protein 2 OS=Homo sapiens GN=FBXO2 PE=1 SV=2	14.86486486	3	4	3	296	33.307	4.37	88.3	82.8	118.3	110.6	85.55	114.45	1.33781	0.03654
Q14019	COTL1	Coactosin-like protein OS=Homo sapiens GN=COTL1 PE=1 SV=3	28.16901408	5	5	5	142	15.935	5.67	82.1	89.1	119.6	109.3	85.6	114.45	1.33703	0.0369409
P52888	THOP1	Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2	9.869375907	6	7	6	689	78.789	6.05	84.1	87.1	115.7	113.1	85.6	114.4	1.33645	0.0372431
P60174	TPI1	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	69.58041958	17	43	17	286	30.772	5.92	87.7	83.6	120.3	108.4	85.65	114.35	1.33508	0.0379576
P04075	ALDOA	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	74.72527473	26	114	20	364	39.395	8.09	86.8	84.5	118	110.7	85.65	114.35	1.33508	0.0379576

P05161	ISG15	Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5	10.90909091	2	3	2	165	17.876	7.44	78.8	92.5	121.2	107.5	85.65	114.35	1.33508	0.0379576
O95833	CLIC3	Chloride intracellular channel protein 3 OS=Homo sapiens GN=CLIC3 PE=1 SV=2	6.779661017	2	2	2	236	26.632	6.43	83.8	87.6	120.3	108.3	85.7	114.3	1.33372	0.0386837
A0A024R DX3	ATP7B	ATPase, Cu++ transporting, beta polypeptide, isoform CRA_c OS=Homo sapiens GN=ATP7B PE=3 SV=1	0.4778157	1	2	1	1465	157.162	6.7	83.6	87.8	113.2	115.4	85.7	114.3	1.33372	0.0386837
Q86T29	ZNF605	Zinc finger protein 605 OS=Homo sapiens GN=ZNF605 PE=2 SV=1	1.092043682	1	1	1	641	74.328	9.11	79.7	91.8	118.8	109.7	85.75	114.25	1.33236	0.0394213
Q9BV57	ADI1	1,2-dihydroxy-3-keto-5- methylthiopentene dioxygenase OS=Homo sapiens GN=ADI1 PE=1 SV=1	7.82122905	1	1	1	179	21.485	5.68	74	97.5	113.5	114.9	85.75	114.2	1.33178	0.0397413
A0A024Q ZT9	NQO2	NAD(P)H dehydrogenase, quinone 2, isoform CRA_a OS=Homo sapiens GN=NQO2 PE=4 SV=1	24.24242424	3	4	3	231	25.936	6.29	89	82.6	120.5	107.9	85.8	114.2	1.331	0.0401708
B4DJW8		cDNA FLJ55697, highly similar to Protein transport protein Sec23B OS=Homo sapiens PE=2 SV=1	13.2176235	7	12	6	749	84.435	6.99	91.3	80.3	117	111.3	85.8	114.15	1.33042	0.040496
Q96TA1	FAM129 B	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3	17.69436997	12	16	12	746	84.085	6.19	83.9	87.7	114.6	113.7	85.8	114.15	1.33042	0.040496
Q69YJ7	DKFZp6 67H197	Putative uncharacterized protein DKFZp667H197 (Fragment) OS=Homo sapiens GN=DKFZp667H197 PE=2 SV=1	9.853249476	8	8	8	954	100.097	8.91	88.9	82.8	117.6	110.8	85.85	114.2	1.33023	0.040604
P62942	FKBP1A	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2	25	2	3	2	108	11.943	8.16	90.3	81.4	119.5	108.9	85.85	114.2	1.33023	0.040604

Q13642	FHL1	Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4	6.811145511	2	2	2	323	36.239	8.97	84.4	87.3	119.2	109.1	85.85	114.15	1.32964	0.0409322
Q6FHG5	SNCG	Gamma-synuclein OS=Homo sapiens GN=SNCG PE=2 SV=1	48.81889764	6	7	6	127	13.323	4.86	84.5	87.2	122.7	105.6	85.85	114.15	1.32964	0.0409322
Q92990	GLMN	Glomulin OS=Homo sapiens GN=GLMN PE=1 SV=2	4.713804714	3	3	3	594	68.165	5.33	83.3	88.5	120.1	108.1	85.9	114.1	1.32829	0.0417057
B2R9H3		cDNA, FLJ94391, highly similar to Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8 (SERPINB8), mRNA OS=Homo sapiens PE=2 SV=1	4.010695187	1	1	1	374	42.727	5.47	92.4	79.4	117.3	110.9	85.9	114.1	1.32829	0.0417057
Q03393	PTS	6-pyruvoyl tetrahydrobiopterin synthase OS=Homo sapiens GN=PTS PE=1 SV=1	15.17241379	2	2	2	145	16.375	6.68	85.6	86.2	120	108.1	85.9	114.05	1.32771	0.0420417
V9HWK2	HEL114	Epididymis luminal protein 114 OS=Homo sapiens GN=HEL114 PE=2 SV=1	40.12345679	42	67	42	1134	123.722	5.66	86.8	85.1	117.2	110.9	85.95	114.05	1.32693	0.0424914
Q59EF6		Calpain 2, large [catalytic] subunit variant (Fragment) OS=Homo sapiens PE=2 SV=1	16.32373114	11	12	11	729	83.056	5.06	84.1	87.8	118.2	109.9	85.95	114.05	1.32693	0.0424914
P81605	DCD	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	19.09090909	2	3	2	110	11.277	6.54	86.3	85.6	125.7	102.4	85.95	114.05	1.32693	0.0424914
P50991	CCT4	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	46.75324675	24	50	23	539	57.888	7.83	88.1	83.8	116.7	111.3	85.95	114	1.32635	0.0428329
H3BQK9	MACF1	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=1	5.597997893	38	41	1	7592	860.543	5.38	91.7	80.3	118.8	109.2	86	114	1.32558	0.0432894
A0A140V KG5	KIF2B	Kinesin-like protein OS=Homo sapiens GN=KIF2B PE=2 SV=1	5.349182764	3	6	1	673	76.206	8.65	72.2	99.8	90.9	137.1	86	114	1.32558	0.0432894

A0A024R DV8	TSC22D 1	TSC22 domain family, member 1, isoform CRA_a OS=Homo sapiens GN=TSC22D1 PE=4 SV=1	25.69444444	3	3	3	144	15.67	5.2	80.5	91.6	115.9	112.1	86.05	114	1.32481	0.0437499
Q8TCG2	PI4K2B	Phosphatidylinositol 4-kinase type 2-beta OS=Homo sapiens GN=PI4K2B PE=1 SV=1	5.405405405	2	3	2	481	54.71	5.97	89.7	82.4	110.4	117.4	86.05	113.9	1.32365	0.0444528
B4DLV7		cDNA FLJ60299, highly similar to Rab GDP dissociation inhibitor beta OS=Homo sapiens PE=2 SV=1	38.75278396	15	28	11	449	51.121	8.18	84.9	87.3	114.5	113.3	86.1	113.9	1.32288	0.0449233
A0A024R6 87	PLEKHC 1	Pleckstrin homology domain containing, family C (With FERM domain) member 1, isoform CRA_b OS=Homo sapiens GN=PLEKHC1 PE=4 SV=1	17.20588235	11	11	1	680	77.811	6.7	75.8	96.4	114.2	113.6	86.1	113.9	1.32288	0.0449233
Q9BYB4	GNB1L	Guanine nucleotide-binding protein subunit beta-like protein 1 OS=Homo sapiens GN=GNB1L PE=1 SV=2	7.033639144	1	1	1	327	35.595	7.97	83.4	88.8	115.7	112	86.1	113.85	1.3223	0.0452818
Q9NQ48	LZTFL1	Leucine zipper transcription factor- like protein 1 OS=Homo sapiens GN=LZTFL1 PE=1 SV=1	13.04347826	4	4	4	299	34.571	5.36	83.2	89.1	115.4	112.4	86.15	113.9	1.32211	0.0453978
P51157	RAB28	Ras-related protein Rab-28 OS=Homo sapiens GN=RAB28 PE=1 SV=2	4.977375566	1	1	1	221	24.826	5.97	88.4	83.9	118.2	109.5	86.15	113.85	1.32153	0.0457594
O60890	OPHN1	Oligophrenin-1 OS=Homo sapiens GN=OPHN1 PE=1 SV=1	1.87032419	1	1	1	802	91.583	7.96	99.3	73	130.6	97.1	86.15	113.85	1.32153	0.0457594
Q9BZD2	SLC29A 3	Equilibrative nucleoside transporter 3 OS=Homo sapiens GN=SLC29A3 PE=1 SV=3	1.894736842	1	1	1	475	51.781	7.78	89.1	83.2	122.1	105.6	86.15	113.85	1.32153	0.0457594
O00625	PIR	Pirin OS=Homo sapiens GN=PIR PE=1 SV=1	33.10344828	7	8	7	290	32.093	6.92	85.7	86.7	118.8	108.8	86.2	113.8	1.32019	0.0466084

B2R4U3		cDNA, FLJ92217, highly similar to Homo sapiens ubiquitin-conjugating enzyme E2C (UBE2C), mRNA OS=Homo sapiens PE=2 SV=1	11.73184358	2	2	2	179	19.606	7.37	85.8	86.6	99.5	128.1	86.2	113.8	1.32019	0.0466084
Q9UPZ3	HPS5	Hermansky-Pudlak syndrome 5 protein OS=Homo sapiens GN=HPS5 PE=1 SV=2	0.797165633	1	1	1	1129	127.368	5.54	71.1	101.3	116.7	110.9	86.2	113.8	1.32019	0.0466084
A0A024R B32	PTGES3	Prostaglandin E synthase 3 (Cytosolic), isoform CRA_a OS=Homo sapiens GN=PTGES3 PE=4 SV=1	38.75	6	18	6	160	18.685	4.54	89.3	83.1	115.4	112.1	86.2	113.75	1.31961	0.0469784
P15121	AKR1B1	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3	47.15189873	13	26	12	316	35.83	6.98	85.1	87.3	117.3	110.2	86.2	113.75	1.31961	0.0469784
P31153	MAT2A	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	39.74683544	14	20	14	395	43.633	6.48	88.6	83.9	118.4	109.1	86.25	113.75	1.31884	0.0474705
P50990	CCT8	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	59.12408759	28	76	28	548	59.583	5.6	85.9	86.6	118	109.5	86.25	113.75	1.31884	0.0474705
H0YB56	MTDH	Protein LYRIC (Fragment) OS=Homo sapiens GN=MTDH PE=1 SV=1	33.48214286	8	15	1	224	24.502	9.76	79.8	92.7	102.1	125.4	86.25	113.75	1.31884	0.0474705
A0A024R9 62	hCG_40 889	HCG40889, isoform CRA_b OS=Homo sapiens GN=hCG_40889 PE=4 SV=1	1.462225833	1	5	1	1231	138.979	6.62	79.5	93	78.4	149.1	86.25	113.75	1.31884	0.0474705
Q6FHV6	ENO2	ENO2 protein OS=Homo sapiens GN=ENO2 PE=1 SV=1	12.67281106	3	15	1	434	47.239	5.03	90.9	81.7	119.7	107.8	86.3	113.75	1.31808	0.0479666
Q496C9	DTD1	D-tyrosyl-tRNA(Tyr) deacylase OS=Homo sapiens GN=DTD1 PE=2 SV=1	7.177033493	1	1	1	209	23.469	8.35	93.1	79.5	117.5	109.9	86.3	113.7	1.3175	0.0483458

Q5STK2	PFDN6	Prefoldin subunit 6, isoform CRA_b OS=Homo sapiens GN=PFDN6 PE=2 SV=1	28.68217054	5	6	5	129	14.574	8.88	90	82.6	121.1	106.3	86.3	113.7	1.3175	0.0483458
O43157	PLXNB1	Plexin-B1 OS=Homo sapiens GN=PLXNB1 PE=1 SV=3	0.608899297	1	1	1	2135	232.151	5.49	93.6	79.1	118.8	108.5	86.35	113.65	1.31616	0.0492346
A0A140V KA6		Testis secretory sperm-binding protein Li 233m OS=Homo sapiens PE=2 SV=1	27.37127371	9	24	9	369	41.305	5.27	90.9	81.8	119.9	107.4	86.35	113.65	1.31616	0.0492346
A0A024R1 A3	UBE1	Testicular secretory protein Li 63 OS=Homo sapiens GN=UBE1 PE=2 SV=1	29.11153119	25	60	25	1058	117.774	5.76	90.7	82	121.1	106.2	86.35	113.65	1.31616	0.0492346
Q9Y2S0	POLR1D	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Homo sapiens GN=POLR1D PE=1 SV=1	8.270676692	1	1	1	133	15.227	5.8	110	108.2	93.4	88.4	109.1	90.9	0.83318 1	0.0423462
A8K778		cDNA FLJ76902, highly similar to Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1 (NFKBIL1), mRNA OS=Homo sapiens PE=2 SV=1	3.937007874	1	1	1	381	43.207	7.3	118	100.2	86.2	95.6	109.1	90.9	0.83318 1	0.0423462
A0A0G2J K44	BRD2	Bromodomain-containing protein 2 OS=Homo sapiens GN=BRD2 PE=1 SV=1	4.90430622	5	6	3	836	92.009	9.16	114.8	103.4	93.6	88.2	109.1	90.9	0.83318 1	0.0423462
A0A087W ZE9	HMG3	High mobility group nucleosome- binding domain-containing protein 3 OS=Homo sapiens GN=HMG3 PE=1 SV=1	14.61538462	2	3	2	130	13.948	9.91	108.8	109.5	89.1	92.6	109.15	90.85	0.83234 1	0.0413117
H7C1M2	SON	Protein SON (Fragment) OS=Homo sapiens GN=SON PE=1 SV=1	28.26685007	28	43	2	1454	159.92	9.13	108.5	109.8	90.5	91.2	109.15	90.85	0.83234 1	0.0413117
P26373	RPL13	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	42.65402844	10	37	10	211	24.247	11.65	109.4	108.9	84.4	97.3	109.15	90.85	0.83234 1	0.0413117

Q01151	CD83	CD83 antigen OS=Homo sapiens GN=CD83 PE=1 SV=1	4.87804878	1	1	1	205	23.027	8.18	105.4	112.9	98.9	82.8	109.15	90.85	0.83234 1	0.0413117
P20674	COX5A	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2	38	8	39	8	150	16.752	6.79	111.5	106.9	91.2	90.5	109.2	90.85	0.83196	0.0408489
A0A024R BW9	CA5B	Carbonic anhydrase VB, mitochondrial, isoform CRA_c OS=Homo sapiens GN=CA5B PE=4 SV=1	17.35015773	4	4	4	317	36.41	7.81	112.6	105.8	85	96.7	109.2	90.85	0.83196	0.0408489
A0A024R2 Q4	RPL15	Ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=3 SV=1	50.49019608	12	57	12	204	24.131	11.62	103.7	114.6	85.5	96.1	109.15	90.8	0.83188 3	0.0407559
P63218	GNG5	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3	33.82352941	3	4	3	68	7.314	9.85	99	119.4	89.6	92	109.2	90.8	0.83150 2	0.0402985
A0A0J9YX F2	PON2	Paraoxonase 2, isoform CRA_a OS=Homo sapiens GN=PON2 PE=1 SV=1	37.86666667	10	29	6	375	41.501	5.72	111.6	106.9	95.5	85.9	109.25	90.7	0.83020 6	0.0387732
A0A0A0M S29	MFF	Mitochondrial fission factor OS=Homo sapiens GN=MFF PE=1 SV=1	42.53393665	8	28	1	221	25.286	8.76	101.4	117.1	91.8	89.6	109.25	90.7	0.83020 6	0.0387732
P23497	SP100	Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 PE=1 SV=3	10.80773606	9	19	6	879	100.354	8.22	111.6	107.1	93.6	87.7	109.35	90.65	0.82899	0.0373841
P17568	NDUFB7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Homo sapiens GN=NDUFB7 PE=1 SV=4	50.3649635	5	15	5	137	16.391	8.92	104.1	114.6	85.2	96.1	109.35	90.65	0.82899	0.0373841
P20645	M6PR	Cation-dependent mannose-6- phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	33.21299639	8	22	8	277	30.973	5.83	99.8	118.9	83.9	97.4	109.35	90.65	0.82899	0.0373841
Q8N5A5	ZGPAT	Zinc finger CCCH-type with G patch domain-containing protein	3.389830508	1	1	1	531	57.324	5.43	113	105.8	93.7	87.5	109.4	90.6	0.82815 4	0.0364532

		OS=Homo sapiens GN=ZGPAT PE=1 SV=3																
Q00597	FANCC	Fanconi anemia group C protein OS=Homo sapiens GN=FANCC PE=1 SV=1	1.433691756	1	1	1	558	63.388	6.15	103.1	115.7	89.7	91.5	109.4	90.6	0.828154	0.0364532	
Q14548	COX7A2L	Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Homo sapiens GN=COX7A2L PE=1 SV=2	41.22807018	5	6	5	114	12.607	9.42	84.6	134.2	90.6	90.6	109.4	90.6	0.828154	0.0364532	
Q02224	CENPE	Centromere-associated protein E OS=Homo sapiens GN=CENPE PE=1 SV=2	0.481303221	1	1	1	2701	316.219	5.64	116.6	102.3	90.4	90.7	109.45	90.55	0.827318	0.035542	
Q8WYQ5	DGCR8	Microprocessor complex subunit DGCR8 OS=Homo sapiens GN=DGCR8 PE=1 SV=1	2.457956016	1	1	1	773	85.991	5.95	104.7	114.2	83.9	97.2	109.45	90.55	0.827318	0.035542	
Q01196	RUNX1	Runt-related transcription factor 1 OS=Homo sapiens GN=RUNX1 PE=1 SV=3	3.090507726	1	1	1	453	48.706	9.35	115.5	103.4	85.1	95.9	109.45	90.5	0.826862	0.0350515	
A8KA68		cDNA FLJ75833, highly similar to Homo sapiens membrane-bound transcription factor peptidase, site 2 (MBTPS2), mRNA OS=Homo sapiens PE=2 SV=1	3.468208092	2	2	2	519	57.417	7.49	110.4	108.6	92.5	88.5	109.5	90.5	0.826484	0.0346503	
Q9BSK2	SLC25A33	Solute carrier family 25 member 33 OS=Homo sapiens GN=SLC25A33 PE=1 SV=1	6.230529595	2	2	1	321	35.352	9.6	109.4	109.7	86.2	94.7	109.55	90.45	0.82565	0.0337776	
A0A024R5H0	BANF1	Barrier to autointegration factor 1, isoform CRA_a OS=Homo sapiens GN=BANF1 PE=4 SV=1	79.7752809	7	33	7	89	10.052	6.09	107.9	111.2	89.7	91.2	109.55	90.45	0.82565	0.0337776	
P55317	FOXA1	Hepatocyte nuclear factor 3-alpha OS=Homo sapiens GN=FOXA1 PE=1 SV=2	11.65254237	2	2	2	472	49.116	8.82	106.2	113	89.7	91.2	109.6	90.45	0.825274	0.0333893	

A0A024QZ N7	C10orf7 0	Chromosome 10 open reading frame 70, isoform CRA_b OS=Homo sapiens GN=C10orf70 PE=4 SV=1	44.44444444	5	26	5	108	12.191	9.09	107	112.2	83.8	97.1	109.6	90.45	0.82527 4	0.0333893
P78386	KRT85	Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	5.128205128	3	11	2	507	55.766	6.55	100.9	118.3	90.3	90.6	109.6	90.45	0.82527 4	0.0333893
Q8N8J7	C4orf32	Uncharacterized protein C4orf32 OS=Homo sapiens GN=C4orf32 PE=2 SV=2	7.575757576	1	1	1	132	14.643	4.7	115.3	103.9	88.8	92	109.6	90.4	0.82481 8	0.0329238
O60476	MAN1A2	Mannosyl-oligosaccharide 1,2- alpha-mannosidase IB OS=Homo sapiens GN=MAN1A2 PE=1 SV=1	6.24024961	4	4	4	641	72.957	7.61	111.2	108	77.1	103.7	109.6	90.4	0.82481 8	0.0329238
A0A024R5 C4	RTN3	Reticulon OS=Homo sapiens GN=RTN3 PE=4 SV=1	28.38983051	4	11	1	236	25.593	8.51	106.6	112.6	82.8	98	109.6	90.4	0.82481 8	0.0329238
A0A024R3 J1	TRIM29	Tripartite motif-containing 29, isoform CRA_a OS=Homo sapiens GN=TRIM29 PE=4 SV=1	45.06802721	23	43	23	588	65.793	7.15	103.6	115.6	92	88.8	109.6	90.4	0.82481 8	0.0329238
Q68CP4	HGSNA T	Heparan-alpha-glucosaminide N- acetyltransferase OS=Homo sapiens GN=HGSNAT PE=1 SV=2	2.111613876	1	1	1	663	73.247	8.4	99.2	120	83.3	97.5	109.6	90.4	0.82481 8	0.0329238
B3KM74		cDNA FLJ10425 fis, clone NT2RP1000326, highly similar to Metaxin-2 OS=Homo sapiens PE=2 SV=1	28.13688213	7	20	7	263	29.614	6.77	107.3	112	80.5	100.2	109.65	90.35	0.82398 5	0.0320883
E7ESC7	MAEA	Macrophage erythroblast attacher OS=Homo sapiens GN=MAEA PE=1 SV=1	1.843317972	1	1	1	434	49.361	8.98	141.5	77.9	91.7	89	109.7	90.35	0.82361	0.031717
J3QLM1	STARD3	StAR-related lipid transfer protein 3 OS=Homo sapiens GN=STARD3 PE=1 SV=1	3.789473684	1	1	1	475	52.508	8.62	113	106.4	85.8	94.9	109.7	90.35	0.82361	0.031717

A0A024R466	ITM2C	Integral membrane protein 2C, isoform CRA_a OS=Homo sapiens GN=ITM2C PE=4 SV=1	7.490636704	1	1	1	267	30.204	8	121.2	98.2	94.2	86.4	109.7	90.3	0.823154	0.0312711
O94806	PRKD3	Serine/threonine-protein kinase D3 OS=Homo sapiens GN=PRKD3 PE=1 SV=1	1.011235955	1	1	1	890	100.406	6.87	115.7	103.8	88	92.6	109.75	90.3	0.822779	0.0309081
Q9BX26	SYCP2	Synaptonemal complex protein 2 OS=Homo sapiens GN=SYCP2 PE=2 SV=2	0.45751634	1	1	1	1530	175.529	8.85	104.3	115.1	77.6	102.9	109.7	90.25	0.822698	0.0308304
A8K0I8		cDNA FLJ76207, highly similar to Homo sapiens delta-notch-like EGF repeat-containing transmembrane (DNER), mRNA OS=Homo sapiens PE=2 SV=1	2.035278155	1	1	1	737	78.476	5.21	107.5	112	94.1	86.4	109.75	90.25	0.822323	0.0304717
Q9UJT1	TUBD1	Tubulin delta chain OS=Homo sapiens GN=TUBD1 PE=2 SV=2	3.752759382	1	1	1	453	51.001	6.83	118.8	100.7	84.7	95.8	109.75	90.25	0.822323	0.0304717
Q13488	TCIRG1	V-type proton ATPase 116 kDa subunit a isoform 3 OS=Homo sapiens GN=TCIRG1 PE=1 SV=3	17.8313253	12	14	12	830	92.908	7.12	115.3	104.2	94.3	86.2	109.75	90.25	0.822323	0.0304717
A0A024R3W2	TOMM20	Translocase of outer mitochondrial membrane 20 homolog (Yeast), isoform CRA_a OS=Homo sapiens GN=TOMM20 PE=3 SV=1	31.03448276	3	4	3	145	16.288	8.6	90.8	128.7	90	90.5	109.75	90.25	0.822323	0.0304717
Q9BY49	PECR	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2	10.56105611	3	3	3	303	32.524	8.81	106.4	113.2	92.4	88.1	109.8	90.25	0.821949	0.0301168
Q8IYL3	C1orf174	UPF0688 protein C1orf174 OS=Homo sapiens GN=C1orf174 PE=1 SV=2	5.761316872	1	1	1	243	25.961	6.9	114	105.6	84.9	95.5	109.8	90.2	0.821494	0.0296899
A0A140VJN5		Testicular tissue protein Li 111 OS=Homo sapiens PE=2 SV=1	0.580720093	1	2	1	1722	199.176	6.19	110.6	109.1	88	92.3	109.85	90.15	0.820665	0.0289252
A8K761	NDUFB1	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex,	56.97674419	10	33	10	172	20.763	8.48	104	115.7	89.2	91.1	109.85	90.15	0.820665	0.0289252

		10, 22kDa, isoform CRA_b OS=Homo sapiens GN=NDUFB10 PE=2 SV=1																
Q59EE7		Pro-alpha-1 type V collagen variant (Fragment) OS=Homo sapiens PE=2 SV=1	8.649553571	9	15	1	1792	178.407	5	119.8	100	91.8	88.4	109.9	90.1	0.81983 6	0.0281775	
Q9Y232	CDYL	Chromodomain Y-like protein OS=Homo sapiens GN=CDYL PE=1 SV=2	14.88294314	7	15	7	598	66.44	9.45	113.1	106.8	86.3	93.9	109.95	90.1	0.81946 3	0.0278462	
A0A0S2Z4 G7	NPM1	Nucleophosmin (Nucleolar phosphoprotein B23, numatrin), isoform CRA_f (Fragment) OS=Homo sapiens GN=NPM1 PE=2 SV=1	55.09433962	15	153	1	265	29.446	4.61	105.4	114.5	90.9	89.2	109.95	90.05	0.81900 9	0.0274465	
Q8WVX3	C4orf3	Uncharacterized protein C4orf3 OS=Homo sapiens GN=C4orf3 PE=1 SV=2	40.90909091	2	7	2	66	7.599	5.29	95.8	124.1	76.1	104	109.95	90.05	0.81900 9	0.0274465	
Q53HV5		Androgen-induced 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	5.042016807	1	2	1	238	27.426	7.17	80.7	139.2	90.4	89.7	109.95	90.05	0.81900 9	0.0274465	
A1A5C4	RRBP1	RRBP1 protein OS=Homo sapiens GN=RRBP1 PE=2 SV=1	52.03426124	50	111	2	934	102.763	5.38	118.3	101.7	79.1	101	110	90.05	0.81863 6	0.0271228	
P09669	COX6C	Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2	52	8	26	8	75	8.776	10.39	99.5	120.5	87.6	92.5	110	90.05	0.81863 6	0.0271228	
A0A024Q YW3	PLP2	Proteolipid protein 2 (Colonic epithelium-enriched), isoform CRA_a OS=Homo sapiens GN=PLP2 PE=4 SV=1	9.868421053	1	4	1	152	16.68	7.24	113.5	106.4	87.5	92.5	109.95	90	0.81855 4	0.0270515	
Q8N9T2	NKAPP1	Putative uncharacterized protein CXorf42 OS=Homo sapiens GN=NKAPP1 PE=5 SV=3	5.6	1	1	1	125	14.154	8.94	153.2	66.8	96.2	83.8	110	90	0.81818 2	0.0267318	

P18085	ARF4	ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	52.77777778	9	23	6	180	20.498	7.14	137.3	82.7	96.1	83.9	110	90	0.81818 2	0.0267318
Q96EL2	MRPS24	28S ribosomal protein S24, mitochondrial OS=Homo sapiens GN=MRPS24 PE=1 SV=1	5.389221557	1	1	1	167	19.003	9.38	116.1	103.9	72.2	107.7	110	89.95	0.81772 7	0.0263455
Q9H9Q4	NHEJ1	Non-homologous end-joining factor 1 OS=Homo sapiens GN=NHEJ1 PE=1 SV=1	8.361204013	2	3	2	299	33.316	5.97	114.8	105.2	88.4	91.5	110	89.95	0.81772 7	0.0263455
P27635	RPL10	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	45.79439252	9	41	1	214	24.588	10.08	110	110.1	81.1	98.8	110.05	89.95	0.81735 6	0.0260332
O75489	NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	44.31818182	10	29	10	264	30.223	7.5	107.5	112.6	82.9	97	110.05	89.95	0.81735 6	0.0260332
H0UI06	COX7A2	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=1 SV=1	20	2	9	2	115	12.836	9.13	106.3	113.9	93.6	86.2	110.1	89.9	0.81653	0.0253503
Q13948	CUX1	Protein CASP OS=Homo sapiens GN=CUX1 PE=1 SV=2	22.86135693	17	21	2	678	77.408	5.44	115.7	104.6	90.1	89.7	110.15	89.9	0.81616	0.0250485
A0A024R4 N0	hCG_16 40809	HCG1640809, isoform CRA_b OS=Homo sapiens GN=hCG_1640809 PE=4 SV=1	10.55900621	2	2	2	322	35.25	8.15	113.1	107.1	63.3	116.4	110.1	89.85	0.81607 6	0.0249809
Q8NBZ0	INO80E	INO80 complex subunit E OS=Homo sapiens GN=INO80E PE=1 SV=1	3.278688525	1	1	1	244	26.462	8.34	117.9	102.4	81.7	98	110.15	89.85	0.81570 6	0.024683
Q2KHT3	CLEC16 A	Protein CLEC16A OS=Homo sapiens GN=CLEC16A PE=1 SV=2	1.044634378	1	1	1	1053	117.64	5.86	112.7	107.7	78.3	101.4	110.2	89.85	0.81533 6	0.0243882
P27338	MAOB	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3	45.76923077	21	64	21	520	58.725	7.5	102.8	117.6	88.6	91.1	110.2	89.85	0.81533 6	0.0243882

P13010	XRCC5	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	39.07103825	30	86	30	732	82.652	5.81	115.9	104.5	92	87.6	110.2	89.8	0.814882	0.0240308
Q8NBU5	ATAD1	ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1	37.67313019	12	30	12	361	40.718	6.9	111	109.4	79.7	99.9	110.2	89.8	0.814882	0.0240308
Q9UKA4	AKAP11	A-kinase anchor protein 11 OS=Homo sapiens GN=AKAP11 PE=1 SV=1	0.368227249	1	1	1	1901	210.38	5.39	122.3	98.2	92	87.5	110.25	89.75	0.814059	0.0233936
I6L9F7	HIST1H2BM	Histone H2B (Fragment) OS=Homo sapiens GN=HIST1H2BM PE=2 SV=1	65.94202899	11	301	1	138	15.147	10.24	113.7	106.8	100.9	78.6	110.25	89.75	0.814059	0.0233936
A8K4V2		cDNA FLJ75930, highly similar to Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa (NDUFA9), mRNA OS=Homo sapiens PE=2 SV=1	38.46153846	13	36	13	377	42.425	9.86	111.3	109.2	83.6	95.9	110.25	89.75	0.814059	0.0233936
D3DU92	RNPS1	RNA binding protein S1 OS=Homo sapiens GN=RNPS1 PE=1 SV=1	29.18032787	8	29	8	305	34.188	11.84	114	106.7	75.9	103.4	110.35	89.65	0.812415	0.0221628
H0Y8C2	RPL22L1	60S ribosomal protein L22-like 1 (Fragment) OS=Homo sapiens GN=RPL22L1 PE=1 SV=1	19.01408451	2	3	2	142	16.89	9.25	107.5	113.3	90.6	88.7	110.4	89.65	0.812047	0.0218949
A0A059R2S3	COX1	Cytochrome c oxidase subunit 1 OS=Homo sapiens GN=COX1 PE=3 SV=1	6.04288499	1	1	1	513	56.984	6.8	118.3	102.5	83.7	95.6	110.4	89.65	0.812047	0.0218949
D3DSM6	SLC19A1	Solute carrier family 19 (Folate transporter), member 1, isoform CRA_f OS=Homo sapiens GN=SLC19A1 PE=4 SV=1	9.135399674	3	5	3	613	67.157	9.11	104	116.7	83.4	95.8	110.35	89.6	0.811962	0.0218332
Q6DD87	ZNF787	Zinc finger protein 787 OS=Homo sapiens GN=ZNF787 PE=1 SV=3	12.53263708	4	4	4	383	40.518	7.84	105.2	115.6	79.7	99.5	110.4	89.6	0.811594	0.0215687

A0A024R2 41	NFIL3	Nuclear factor interleukin-3- regulated protein OS=Homo sapiens GN=NFIL3 PE=3 SV=1	7.142857143	3	3	3	462	51.44	7.18	112.8	108.2	87.6	91.4	110.5	89.5	0.80995 5	0.0204219
P14854	COX6B1	Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2	66.27906977	5	32	5	86	10.186	7.05	109.9	111.1	91	88	110.5	89.5	0.80995 5	0.0204219
Q9NY64	SLC2A8	Solute carrier family 2, facilitated glucose transporter member 8 OS=Homo sapiens GN=SLC2A8 PE=1 SV=3	1.886792453	1	1	1	477	50.786	7.61	110.1	110.9	71.1	107.9	110.5	89.5	0.80995 5	0.0204219
P56524	HDAC4	Histone deacetylase 4 OS=Homo sapiens GN=HDAC4 PE=1 SV=3	0.73800738	1	1	1	1084	118.966	6.96	98.3	122.8	86.4	92.5	110.55	89.45	0.80913 6	0.0198686
A0A059R1 K5	COX2	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=COX2 PE=3 SV=1	30.83700441	6	28	1	227	25.543	4.89	104.2	117	93.3	85.6	110.6	89.45	0.80877	0.0196254
Q17RV3	LRRK2	Leucine-rich repeat kinase 2 OS=Homo sapiens GN=LRRK2 PE=2 SV=1	0.633161852	2	2	2	2527	285.884	6.79	94.1	127.1	86.4	92.3	110.6	89.35	0.80786 6	0.019035
P62854	RPS26	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	44.34782609	4	27	4	115	13.007	11	105.9	115.5	74.4	104.2	110.7	89.3	0.80668 5	0.0182861
B2R850		cDNA, FLJ93740, highly similar to Homo sapiens zinc finger protein 161 homolog (mouse) (ZFP161), mRNA OS=Homo sapiens PE=2 SV=1	2.227171492	1	1	1	449	50.894	6.04	114.1	107.4	94.7	83.8	110.75	89.25	0.80586 9	0.0177836
O95243	MBD4	Methyl-CpG-binding domain protein 4 OS=Homo sapiens GN=MBD4 PE=1 SV=1	1.379310345	1	1	1	580	66.009	8.82	104.3	117.4	69.3	109	110.85	89.15	0.80424	0.0168147
B4DL14		ATP synthase subunit gamma OS=Homo sapiens PE=2 SV=1	57.6	14	42	1	250	27.495	7.42	117.9	103.9	89.9	88.4	110.9	89.15	0.80387 7	0.0166051

J3KTC1	MSI2	RNA-binding protein Musashi homolog 2 (Fragment) OS=Homo sapiens GN=MSI2 PE=1 SV=8	49.28571429	5	6	1	140	15.45	9.5	115.7	106	92.3	85.9	110.85	89.1	0.803789	0.0165544
A0A024R8Z5	BRP44	Brain protein 44, isoform CRA_b OS=Homo sapiens GN=BRP44 PE=4 SV=1	9.448818898	1	2	1	127	14.27	10.43	125.4	96.4	90.1	88.1	110.9	89.1	0.803427	0.0163477
HOY7F4	GNAS	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short (Fragment) OS=Homo sapiens GN=GNAS PE=1 SV=1	19.59798995	3	6	1	199	22.776	8.78	108.8	113	71.7	106.5	110.9	89.1	0.803427	0.0163477
H9A532		BCL6 corepressor-cyclin B3 fusion protein OS=Homo sapiens PE=2 SV=1	1.481237656	3	3	3	3038	337.511	6.28	112.4	109.5	90.5	87.6	110.95	89.05	0.802614	0.0158921
P99999	CYCS	Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2	61.9047619	7	16	7	105	11.741	9.57	123.2	98.8	93.5	84.5	111	89	0.801802	0.0154477
P80723	BASP1	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	53.74449339	9	36	9	227	22.68	4.63	107.7	114.3	84.2	93.8	111	89	0.801802	0.0154477
Q16594	TAF9	Transcription initiation factor TFIID subunit 9 OS=Homo sapiens GN=TAF9 PE=1 SV=1	10.98484848	3	3	1	264	28.956	8.66	119.9	102.2	78.7	99.1	111.05	88.9	0.80054	0.0147781
P49006	MARCKSL1	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2	8.717948718	2	2	2	195	19.517	4.67	110.7	111.4	80.3	97.5	111.05	88.9	0.80054	0.0147781
B3KN59		cDNA FLJ13673 fis, clone PLACE1011858, highly similar to BAG family molecular chaperone regulator 2 OS=Homo sapiens PE=2 SV=1	50.71090047	9	40	9	211	23.733	6.57	108.4	113.9	83.9	93.9	111.15	88.9	0.79982	0.014407
S4R2Z7	MRPL42	39S ribosomal protein L42, mitochondrial OS=Homo sapiens GN=MRPL42 PE=1 SV=1	12.25806452	2	4	2	155	17.884	8.19	114.1	108.2	65.8	111.9	111.15	88.85	0.79937	0.0141792

P35680	HNF1B	Hepatocyte nuclear factor 1-beta OS=Homo sapiens GN=HNF1B PE=1 SV=1	2.513464991	1	1	1	557	61.285	7.77	107.4	115	90.4	87.3	111.2	88.85	0.79901 1	0.0139994
Q5TF85	FAM46A	Family with sequence similarity 46, member A, isoform CRA_a OS=Homo sapiens GN=FAM46A PE=1 SV=1	2.676864245	1	1	1	523	59.082	6.27	111.1	111.2	81.2	96.4	111.15	88.8	0.79892	0.0139545
Q86TW2	ADCK1	Uncharacterized aarF domain- containing protein kinase 1 OS=Homo sapiens GN=ADCK1 PE=2 SV=2	15.66037736	5	6	5	530	60.538	8.6	116.1	106.3	82.7	94.9	111.2	88.8	0.79856 1	0.0137772
A0A024R9 Y2	KIAA126 7	KIAA1267, isoform CRA_a OS=Homo sapiens GN=KIAA1267 PE=4 SV=1	1.447963801	1	1	1	1105	120.892	8.75	108.1	114.3	72.9	104.7	111.2	88.8	0.79856 1	0.0137772
E3SWF7	HLA-A	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1	34.80662983	8	29	3	181	20.907	6.7	108.7	113.8	76.6	100.9	111.25	88.75	0.79775 3	0.0133852
P29374	ARID4A	AT-rich interactive domain- containing protein 4A OS=Homo sapiens GN=ARID4A PE=1 SV=3	2.227525855	3	3	1	1257	142.664	5.1	113.4	109.1	74.6	102.8	111.25	88.7	0.79730 3	0.0131714
Q68DH5	LMBRD 2	LMBR1 domain-containing protein 2 OS=Homo sapiens GN=LMBRD2 PE=1 SV=1	5.755395683	4	5	4	695	81.12	7.5	110.3	112.2	75.3	102.1	111.25	88.7	0.79730 3	0.0131714
B3KM95		Phosphatidate cytidyltransferase OS=Homo sapiens PE=2 SV=1	4.269662921	1	3	1	445	51.326	7.09	107.9	114.7	85.2	92.2	111.3	88.7	0.79694 5	0.0130031
B7Z613	GPM6B	Neuronal membrane glycoprotein M6-b OS=Homo sapiens GN=GPM6B PE=1 SV=1	2.649006623	1	1	1	302	33.25	6.42	106.8	115.9	94.6	82.8	111.35	88.7	0.79658 7	0.0128367
O75475	PSIP1	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1	32.26415094	17	38	16	530	60.067	9.13	114.7	108	89.7	87.6	111.35	88.65	0.79613 8	0.0126306

B7Z946		Transmembrane channel-like protein OS=Homo sapiens PE=2 SV=1	1.689860835	1	1	1	1006	114.78	8.21	105.6	117.1	79.3	98	111.35	88.65	0.796138	0.0126306
Q8WUX1	SLC38A5	Sodium-coupled neutral amino acid transporter 5 OS=Homo sapiens GN=SLC38A5 PE=1 SV=1	2.966101695	1	1	1	472	51.423	8.21	118.2	104.6	86.3	90.9	111.4	88.6	0.795332	0.0122675
Q13151	HNRNP A0	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	39.01639344	11	51	9	305	30.822	9.29	108.6	114.2	74.9	102.2	111.4	88.55	0.794883	0.0120693
A0A024R A51	CDCA7L	Cell division cycle associated 7-like, isoform CRA_d OS=Homo sapiens GN=CDCA7L PE=4 SV=1	7.709251101	3	3	3	454	52.174	5.74	108	114.8	83.9	93.2	111.4	88.55	0.794883	0.0120693
Q9BUH6	C9orf142	Protein PAXX OS=Homo sapiens GN=C9orf142 PE=1 SV=2	15.19607843	2	2	2	204	21.626	5.48	119.5	103.4	91.2	85.9	111.45	88.55	0.794527	0.0119137
Q8NBQ5	HSD17B11	Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens GN=HSD17B11 PE=1 SV=3	27	7	9	7	300	32.915	9.07	110.9	112	81.3	95.7	111.45	88.5	0.794078	0.0117204
Q9H3R2	MUC13	Mucin-13 OS=Homo sapiens GN=MUC13 PE=1 SV=3	15.4296875	5	13	5	512	54.569	5.07	112.2	110.8	91.6	85.4	111.5	88.5	0.793722	0.011569
Q14103	HNRNP D	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	32.11267606	12	36	10	355	38.41	7.81	107	116	81.8	95.1	111.5	88.45	0.793274	0.0113806
Q04695	KRT17	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	69.21296296	38	283	21	432	48.076	5.02	101	122.2	89.8	87	111.6	88.4	0.792115	0.0109057
Q8N2U0	TMEM256	Transmembrane protein 256 OS=Homo sapiens GN=TMEM256 PE=3 SV=1	31.85840708	2	7	2	113	11.734	8.94	123.3	100.1	93	83.6	111.7	88.3	0.79051	0.0102764
B3KQU6		cDNA PSEC0207 fis, clone HEMBA1002981, highly similar to Homo sapiens nurim (nuclear envelope membrane protein)	19.46564885	4	5	4	262	29.37	8.63	124.8	98.7	86.7	89.8	111.75	88.25	0.789709	0.00997396

		(NRM), mRNA OS=Homo sapiens PE=2 SV=1																
E9PL71	EEF1D	Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=1 SV=1	49.73262032	10	20	1	187	20.806	5.01	88.8	135	72.3	103.9	111.9	88.1	0.78731	0.00911349	
O60248	SOX15	Protein SOX-15 OS=Homo sapiens GN=SOX15 PE=1 SV=1	13.30472103	2	2	2	233	25.236	9.76	107.8	116.2	88.8	87.2	112	88	0.785714	0.00857711	
Q8TAP8	PPP1R35	Protein phosphatase 1 regulatory subunit 35 OS=Homo sapiens GN=PPP1R35 PE=1 SV=1	4.347826087	1	1	1	253	27.936	8.68	105.6	118.4	84.7	91.2	112	87.95	0.785268	0.00843201	
G3V556	C14orf2	6.8 kDa mitochondrial proteolipid OS=Homo sapiens GN=C14orf2 PE=1 SV=1	12.12121212	1	6	1	99	11.274	9.16	141.4	82.7	92.5	83.4	112.05	87.95	0.784917	0.00831962	
Q96F25	ALG14	UDP-N-acetylglucosamine transferase subunit ALG14 homolog OS=Homo sapiens GN=ALG14 PE=1 SV=1	6.481481481	1	1	1	216	24.135	8.94	100.5	123.6	74	101.9	112.05	87.95	0.784917	0.00831962	
Q7L0Q8	RHOU	Rho-related GTP-binding protein RhoU OS=Homo sapiens GN=RHOU PE=1 SV=1	10.46511628	2	3	2	258	28.2	8.06	111	113.3	93.9	81.8	112.15	87.85	0.783326	0.00782518	
B4E2B5		MICOS complex subunit MIC60 OS=Homo sapiens PE=2 SV=1	48.76237624	18	50	1	404	43.194	9.2	117.2	107.1	70.6	105	112.15	87.8	0.78288	0.00769131	
H7BY36	EWSR1	RNA-binding protein EWS (Fragment) OS=Homo sapiens GN=EWSR1 PE=1 SV=1	21.42857143	4	10	1	308	32.16	9.82	137.2	87.6	94.2	81.1	112.4	87.65	0.779804	0.00682046	
B2R4S9	HIST1H2BE	Histone H2B OS=Homo sapiens GN=HIST1H2BE PE=2 SV=1	72.22222222	11	304	1	126	13.898	10.32	110.9	113.8	104.8	70.4	112.35	87.6	0.779706	0.00679418	
P16401	HIST1H1B	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	49.11504425	19	120	15	226	22.566	10.92	100.6	124.2	90	85.2	112.4	87.6	0.779359	0.00670187	
A4D1B1	CD36	CD36 antigen (Collagen type I receptor, thrombospondin receptor) OS=Homo sapiens GN=CD36 PE=2 SV=1	1.694915254	1	1	1	472	53.019	7.96	99.5	125.3	81.5	93.6	112.4	87.55	0.778915	0.00658505	

A0A024R CC6	FRAG1	FGF receptor activating protein 1, isoform CRA_d OS=Homo sapiens GN=FRAG1 PE=4 SV=1	3.492063492	1	1	1	315	36.392	7.9	104.7	120.2	77.3	97.8	112.45	87.55	0.77856 8	0.00649535
P49458	SRP9	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	53.48837209	5	11	5	86	10.105	7.97	111.2	113.8	78.6	96.4	112.5	87.5	0.77777 8	0.00629455
A0A0C4Z NA2	TRA	TRA protein (Fragment) OS=Homo sapiens GN=TRA PE=2 SV=1	5.303030303	1	1	1	132	14.605	7.08	105.7	119.4	81.3	93.6	112.55	87.45	0.77698 8	0.00609933
P16403	HIST1H 1C	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	52.58215962	19	183	7	213	21.352	10.93	101.6	123.5	87.7	87.2	112.55	87.45	0.77698 8	0.00609933
O00165	HAX1	HCLS1-associated protein X-1 OS=Homo sapiens GN=HAX1 PE=1 SV=2	37.27598566	7	12	7	279	31.601	4.92	108.4	116.8	72.2	102.6	112.6	87.4	0.77619 9	0.00590954
A8MTT3	CEBPZ OS	Protein CEBPZOS OS=Homo sapiens GN=CEBPZOS PE=1 SV=2	8.75	1	1	1	80	9.33	9.7	113	112.4	85.6	89	112.7	87.3	0.77462 3	0.00554582
A0A0S2Z4 91	NPM1	Nucleophosmin isoform 2 (Fragment) OS=Homo sapiens GN=NPM1 PE=2 SV=1	55.10204082	17	162	3	294	32.555	4.78	96	129.5	85.7	88.8	112.75	87.25	0.77383 6	0.0053716
P13073	COX41	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX41 PE=1 SV=1	37.86982249	8	45	8	169	19.564	9.51	105.3	120.2	77.5	96.9	112.75	87.2	0.77339 2	0.00527554
F8VS61	KRT77	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=1 SV=1	3.225806452	2	7	1	248	25.362	8.69	87.6	138.1	91.2	83.2	112.85	87.2	0.77270 7	0.00513004
A0A024R6 44	CLN5	Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN5 PE=1 SV=1	4.422604423	2	2	2	407	46.309	8.38	115.1	110.7	82.4	91.9	112.9	87.15	0.77192 2	0.00496768
Q8WXF1	PSPC1	Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1	28.48948375	15	24	14	523	58.706	6.67	116.9	108.9	88.7	85.5	112.9	87.1	0.77147 9	0.00487809

P23511	NFYA	Nuclear transcription factor Y subunit alpha OS=Homo sapiens GN=NFYA PE=1 SV=2	5.475504323	1	1	1	347	36.854	8.94	125.2	100.6	82.7	91.4	112.9	87.05	0.771036	0.00478991
V9GYT7	PSIP1	PC4 and SFRS1-interacting protein (Fragment) OS=Homo sapiens GN=PSIP1 PE=1 SV=1	26.15384615	1	1	1	65	7.783	7.52	114.6	111.3	85.8	88.3	112.95	87.05	0.770695	0.00472289
A0A024R4A8	BOK	BCL2-related ovarian killer, isoform CRA_a OS=Homo sapiens GN=BOK PE=4 SV=1	13.20754717	2	4	2	212	23.265	9.11	110.7	115.2	86.4	87.7	112.95	87.05	0.770695	0.00472289
P35659	DEK	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1	36.8	17	46	17	375	42.648	8.56	123.4	102.5	84.6	89.5	112.95	87.05	0.770695	0.00472289
Q8TE01	derp12	DERP12 (Dermal papilla derived protein 12) OS=Homo sapiens GN=derp12 PE=2 SV=1	35.86005831	12	21	12	343	38.169	6.58	102.1	123.8	86.6	87.5	112.95	87.05	0.770695	0.00472289
P46776	RPL27A	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	21.62162162	4	15	4	148	16.551	11	113.2	113.1	63.5	110.2	113.15	86.85	0.767565	0.00414565
Q99595	TIMM17A	Mitochondrial import inner membrane translocase subunit Tim17-A OS=Homo sapiens GN=TIMM17A PE=1 SV=1	28.65497076	3	5	3	171	18.012	7.87	96.9	129.5	76.7	96.9	113.2	86.8	0.766784	0.00401166
Q9NRP2	CMC2	COX assembly mitochondrial protein 2 homolog OS=Homo sapiens GN=CMC2 PE=1 SV=1	54.43037975	4	17	4	79	9.454	7.87	108.9	117.6	81.7	91.8	113.25	86.75	0.766004	0.00388162
Q92570	NR4A3	Nuclear receptor subfamily 4 group A member 3 OS=Homo sapiens GN=NR4A3 PE=1 SV=3	1.277955272	1	1	1	626	68.186	7.81	113.2	113.6	91.8	81.4	113.4	86.6	0.763668	0.00351402
Q86WA6	BPHL	Valacyclovir hydrolase OS=Homo sapiens GN=BPHL PE=1 SV=1	27.83505155	8	13	8	291	32.522	9.14	119.7	107.1	78.7	94.5	113.4	86.6	0.763668	0.00351402
A0A024R1X0	CASC3	Cancer susceptibility candidate 3, isoform CRA_a OS=Homo sapiens GN=CASC3 PE=4 SV=1	1.214574899	1	1	1	741	80.426	7.17	94.6	132.3	78.6	94.5	113.45	86.55	0.762891	0.00339868

O95562	SFT2D2	Vesicle transport protein SFT2B OS=Homo sapiens GN=SFT2D2 PE=1 SV=1	17.5	2	5	2	160	17.767	9.13	107.9	119.3	84.7	88.2	113.6	86.45	0.761003	0.00313235
Q8WV99	ZFAND2B	AN1-type zinc finger protein 2B OS=Homo sapiens GN=ZFAND2B PE=1 SV=1	9.338521401	1	1	1	257	28.004	6.92	117.6	109.6	86.1	86.7	113.6	86.4	0.760563	0.00307296
A8K8Q0		cDNA FLJ78753, highly similar to Homo sapiens zinc fingers and homeoboxes 3 (ZHX3), mRNA OS=Homo sapiens PE=2 SV=1	2.30125523	1	1	1	956	104.618	6.07	134.4	93	72.8	99.8	113.7	86.3	0.759015	0.00287184
A0A024R118	METTL7A	Methyltransferase like 7A, isoform CRA_a OS=Homo sapiens GN=METTL7A PE=4 SV=1	22.13114754	4	11	4	244	28.301	8.38	113.3	114.1	95.6	77	113.7	86.3	0.759015	0.00287184
Q9P2N2	ARHGA28	Rho GTPase-activating protein 28 OS=Homo sapiens GN=ARHGAP28 PE=1 SV=3	1.09739369	1	1	1	729	82.008	7.75	110.8	116.9	84	88.2	113.85	86.1	0.756258	0.00254239
E7ETY2	TCOF1	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=1	26.74731183	35	55	2	1488	152.213	8.85	115.6	112.6	74.8	97.1	114.1	85.95	0.753287	0.00222513
B4E1H4		cDNA FLJ54226, highly similar to Transmembrane protein 9 OS=Homo sapiens PE=2 SV=1	6.25	1	1	1	208	23.372	6.7	108.9	119.3	77.9	93.9	114.1	85.9	0.752848	0.00218144
A0A024R2L0	UBP1	Upstream binding protein 1 (LBP-1a), isoform CRA_a OS=Homo sapiens GN=UBP1 PE=4 SV=1	2.592592593	1	1	1	540	60.453	6.35	95.6	132.6	81.2	90.6	114.1	85.9	0.752848	0.00218144
A3R0T8	HIST1H1E	Histone 1, H1e OS=Homo sapiens GN=HIST1H1E PE=2 SV=1	50.2283105	18	150	6	219	21.852	11.03	96.6	131.8	84.9	86.7	114.2	85.8	0.751314	0.00203438
A0A024RBH7	TMPO	Thymopoietin, isoform CRA_a OS=Homo sapiens GN=TMPO PE=4 SV=1	51.30434783	14	65	2	345	38.714	9.16	107.5	121.1	79.1	92.4	114.3	85.75	0.750219	0.00193493
P11474	ESRRA	Steroid hormone receptor ERR1 OS=Homo sapiens GN=ESRRA PE=1 SV=3	3.073286052	1	1	1	423	45.481	6.38	129.8	99.1	77.2	93.9	114.45	85.55	0.747488	0.00170545

A0A0S2Z3 H3	SLC25A 4	Solute carrier family 25 member 4 isoform 1 (Fragment) OS=Homo sapiens GN=SLC25A4 PE=2 SV=1	47.65100671	17	71	4	298	33.043	9.76	122.4	106.7	73.7	97.1	114.55	85.4	0.74552 6	0.00155589
P39059	COL15A 1	Collagen alpha-1(XV) chain OS=Homo sapiens GN=COL15A1 PE=1 SV=2	5.403458213	6	6	6	1388	141.632	5	118.1	111.1	88.7	82.1	114.6	85.4	0.74520 1	0.00153225
A0A024R4 Z1	hCG_20 42749	HCG2042749, isoform CRA_b OS=Homo sapiens GN=hCG_2042749 PE=4 SV=1	1.578947368	1	1	1	570	63.406	7.36	122.2	107	89.7	81.1	114.6	85.4	0.74520 1	0.00153225
Q68D09	DKFZp6 86D196 8	Putative uncharacterized protein DKFZp686D1968 (Fragment) OS=Homo sapiens GN=DKFZp686D1968 PE=2 SV=1	10.69518717	6	11	1	561	62.203	6.73	110.1	119.2	90.5	80.2	114.65	85.35	0.74444	0.00147821
Q6VMQ6	ATF7IP	Activating transcription factor 7- interacting protein 1 OS=Homo sapiens GN=ATF7IP PE=1 SV=3	0.866141732	1	1	1	1270	136.31	4.7	149	80.4	87.6	82.9	114.7	85.25	0.74324 3	0.00139668
A8MWD9	SNRPG P15	Putative small nuclear ribonucleoprotein G-like protein 15 OS=Homo sapiens GN=SNRPGP15 PE=5 SV=2	25	2	13	2	76	8.538	8.84	122.1	107.6	61.9	108.3	114.85	85.1	0.74096 6	0.00125257
A0A0G2J NU3	BDP1	Transcription factor TFIIIB component B'' homolog OS=Homo sapiens GN=BDP1 PE=1 SV=1	0.952743902	1	1	1	2624	293.719	5.11	137.3	92.7	89.6	80.4	115	85	0.73913	0.0011462
B4E0X1		Beta-2-microglobulin OS=Homo sapiens PE=2 SV=1	34.42622951	3	14	3	122	13.937	7.44	100.4	130.1	53	116.6	115.25	84.8	0.73579 2	0.000973334
Q7Z7H8	MRPL10	39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3	26.43678161	4	6	4	261	29.264	9.58	151.7	78.9	85.9	83.5	115.3	84.7	0.73460 5	0.000917795
A0A059Q FD5	COX2	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=COX2 PE=3 SV=1	18.94273128	4	16	1	227	25.625	4.84	141.6	89.1	86.1	83.2	115.35	84.65	0.73385 3	0.000884087
U3KQK5		Uncharacterized protein OS=Homo sapiens PE=4 SV=1	5.487804878	1	8	1	164	17.002	10.8	107.3	123.5	64.1	105.2	115.4	84.65	0.73353 6	0.000870173

A8K9F5		cDNA FLJ77771, highly similar to Homo sapiens replication initiator 1, mRNA OS=Homo sapiens PE=2 SV=1	12.52204586	5	6	5	567	63.576	9.98	114.6	116.4	73.9	95.2	115.5	84.55	0.73203 5	0.000807109
P25490	YY1	Transcriptional repressor protein YY1 OS=Homo sapiens GN=YY1 PE=1 SV=2	27.53623188	9	10	9	414	44.685	6.25	114.9	116.1	69.1	99.9	115.5	84.5	0.73160 2	0.0007897
F1D8R0	NR2F2	Nuclear receptor subfamily 2, group F, member 2, isoform CRA_a OS=Homo sapiens GN=NR2F2 PE=2 SV=1	13.04347826	5	5	1	414	45.542	8.28	104.3	126.7	85.9	83.1	115.5	84.5	0.73160 2	0.0007897
Q9NX76	CMTM6	CKLF-like MARVEL transmembrane domain-containing protein 6 OS=Homo sapiens GN=CMTM6 PE=1 SV=1	5.464480874	1	1	1	183	20.406	5.29	109.4	121.7	85.5	83.5	115.55	84.5	0.73128 5	0.000777186
B7Z213		cDNA FLJ50130, highly similar to Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens PE=2 SV=1	33.203125	7	20	2	256	28.561	9.17	104.6	126.6	84.6	84.3	115.6	84.45	0.73053 6	0.000748291
Q86V81	ALYREF	THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3	43.19066148	9	38	1	257	26.872	11.15	72	159.3	79.3	89.5	115.65	84.4	0.72978 8	0.00072039
Q02086	SP2	Transcription factor Sp2 OS=Homo sapiens GN=SP2 PE=1 SV=3	2.610114192	1	1	1	613	64.86	9.92	110.6	121.1	85	83.4	115.85	84.2	0.72680 2	0.000618142
P68431	HIST1H3A	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	55.88235294	8	96	1	136	15.394	11.12	123.5	108.3	85.1	83.2	115.9	84.15	0.72605 7	0.000594771
A0A024QZZ7	HIST1H2BD	Histone H2B OS=Homo sapiens GN=HIST1H2BD PE=3 SV=1	72.22222222	11	301	1	126	13.928	10.32	116.2	115.6	96.4	71.7	115.9	84.05	0.72519 4	0.000568705
Q9HD51		Uncharacterized gastric protein YC12P (Fragment) OS=Homo sapiens PE=2 SV=1	19.04761905	1	1	1	84	9.609	8.1	147	85.3	82	85.7	116.15	83.85	0.72191 1	0.000478701
A0A024R0B8	FLJ21657	Uncharacterized protein OS=Homo sapiens GN=FLJ21657 PE=4 SV=1	6.511627907	1	1	1	215	24.201	8.59	144.4	88.1	83.6	83.8	116.25	83.7	0.72	0.000432453

Q9Y623	MYH4	Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2	1.031459515	2	2	1	1939	222.932	5.85	101.5	131.1	79.2	88.2	116.3	83.7	0.71969	0.000425356
O43715	TRIAP1	TP53-regulated inhibitor of apoptosis 1 OS=Homo sapiens GN=TRIAP1 PE=1 SV=1	10.52631579	1	1	1	76	8.78	5.48	113.4	119.4	82.6	84.6	116.4	83.6	0.71821 3	0.000392922
O75298	RTN2	Reticulon-2 OS=Homo sapiens GN=RTN2 PE=1 SV=1	3.302752294	1	1	1	545	59.228	5.31	127.2	105.8	74	93	116.5	83.5	0.71673 8	0.0003628
I3L0U2	PRSS21	Testisin (Fragment) OS=Homo sapiens GN=PRSS21 PE=1 SV=1	36.69724771	7	11	1	218	24.8	8.31	170.7	62.5	79.5	87.3	116.6	83.4	0.71526 6	0.000334839
P07305	H1F0	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	36.08247423	10	27	10	194	20.85	10.84	106.6	127	78.7	87.7	116.8	83.2	0.71232 9	0.000284837
J3KPT4	TRABD	TraB domain-containing protein OS=Homo sapiens GN=TRABD PE=1 SV=1	10.55408971	3	7	3	379	42.665	8	121	112.7	61	105.2	116.85	83.1	0.71116 8	0.00026703
HOY322	LIN9	Protein lin-9 homolog (Fragment) OS=Homo sapiens GN=LIN9 PE=1 SV=1	1.794453507	1	1	1	613	69.705	9.7	87.7	146.1	75.9	90.3	116.9	83.1	0.71086 4	0.000262535
Q59H39		Signal transducer and activator of transcription (Fragment) OS=Homo sapiens PE=2 SV=1	8.121827411	5	6	2	788	89.91	6.2	110.8	123.1	82.5	83.6	116.95	83.05	0.71013 3	0.000252005
P42568	MLLT3	Protein AF-9 OS=Homo sapiens GN=MLLT3 PE=1 SV=2	7.570422535	4	4	4	568	63.313	8.63	108.8	125.6	85.1	80.4	117.2	82.75	0.70605 8	0.000200082
Q5TD94	RSPH4A	Radial spoke head protein 4 homolog A OS=Homo sapiens GN=RSPH4A PE=1 SV=1	5.30726257	1	2	1	716	80.684	4.44	131.4	103.7	74.4	90.5	117.55	82.45	0.70140 4	0.000152857
B3KRJ9		cDNA FLJ34439 fis, clone HLUNG2001146, highly similar to Splicing factor, arginine/serine-rich 12 OS=Homo sapiens PE=2 SV=1	9.53307393	4	6	1	514	58.167	9.92	121.1	114.5	83.9	80.5	117.8	82.2	0.69779 3	0.000123521
Q86X19	TMEM1 7	Transmembrane protein 17 OS=Homo sapiens GN=TMEM17 PE=1 SV=2	4.04040404	1	1	1	198	23.031	6.79	110.3	125.4	51.5	112.8	117.85	82.15	0.69707 3	0.000118327

B9TX04	MED16	Mediator complex subunit MED16 variant MED16_i11 (Fragment) OS=Homo sapiens GN=MED16 PE=2 SV=1	18.18181818	2	2	1	165	18.648	7.87	130	106.2	89	74.8	118.1	81.9	0.69348	9.53E-05
A0A024R608	RPLP1	Ribosomal protein, large, P1, isoform CRA_a OS=Homo sapiens GN=RPLP1 PE=3 SV=1	28.94736842	2	7	1	114	11.507	4.32	144.7	92.2	81.4	81.7	118.45	81.55	0.688476	7.00E-05
Q96ET8	TVP23C	Golgi apparatus membrane protein TVP23 homolog C OS=Homo sapiens GN=TVP23C PE=1 SV=3	12.68115942	2	4	2	276	31.085	9.29	121.9	115.5	46.3	116.3	118.7	81.3	0.68492	5.60E-05
Q3MIH3	UBA52	Ubiquitin A-52 residue ribosomal protein fusion product 1 OS=Homo sapiens GN=UBA52 PE=2 SV=1	45.3125	7	112	2	128	14.719	9.83	105.5	132.8	62.8	99	119.15	80.9	0.678976	3.82E-05
Q96HP0	DOCK6	Dedicator of cytokinesis protein 6 OS=Homo sapiens GN=DOCK6 PE=1 SV=3	0.537371764	1	1	1	2047	229.414	6.74	112.2	126.5	82.2	79.2	119.35	80.7	0.676163	3.18E-05
A0A087WYC6	DNAH11	Dynein heavy chain 11, axonemal OS=Homo sapiens GN=DNAH11 PE=1 SV=1	0.154764537	1	1	1	4523	520.724	6.44	95.3	144	79.1	81.7	119.65	80.4	0.67196	2.40E-05
Q6N075	MFSD5	Molybdate-anion transporter OS=Homo sapiens GN=MFSD5 PE=1 SV=2	6.444444444	2	3	2	450	49.732	7.8	162.4	77.1	77.6	82.9	119.75	80.25	0.670146	2.12E-05
O60303	KIAA0556	Protein KIAA0556 OS=Homo sapiens GN=KIAA0556 PE=1 SV=4	0.43263288	1	1	1	1618	180.806	5.87	110	130.1	77	82.9	120.05	79.95	0.665973	1.59E-05
A8K517	RPS23	Ribosomal protein S23, isoform CRA_a OS=Homo sapiens GN=RPS23 PE=2 SV=1	22.37762238	5	25	5	143	15.798	10.49	110.2	130.3	47.7	111.9	120.25	79.8	0.663617	1.35E-05
A0A024R4A2	ALPI	Alkaline phosphatase OS=Homo sapiens GN=ALPI PE=3 SV=1	46.21212121	18	146	14	528	56.776	5.86	126.8	113.8	84.8	74.6	120.3	79.7	0.66251	1.25E-05
P12532	CKMT1A	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1	2.398081535	1	1	1	417	47.007	8.34	135.5	106.4	82.3	75.8	120.95	79.05	0.653576	6.58E-06

B4DZC6		cDNA FLJ60989, highly similar to Bardet-Biedl syndrome 5 protein OS=Homo sapiens PE=2 SV=1	2.573529412	2	2	1	544	60.952	6.64	107.6	137.3	77.7	77.5	122.45	77.6	0.633728	1.43E-06
Q71MF9	FP6679	Putative uncharacterized protein FP6679 OS=Homo sapiens GN=FP6679 PE=2 SV=1	7.446808511	1	1	1	94	10.827	9.51	116.3	128.7	76.4	78.6	122.5	77.5	0.632653	1.31E-06
Q9P0M6	H2AFY2	Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3	9.139784946	3	14	1	372	40.033	9.69	131.3	114.6	40.1	114	122.95	77.05	0.626678	7.99E-07
O43506	ADAM20	Disintegrin and metalloproteinase domain-containing protein 20 OS=Homo sapiens GN=ADAM20 PE=2 SV=2	4.958677686	1	1	1	726	81.548	6.48	152.9	94.4	79.3	73.4	123.65	76.35	0.617469	3.65E-07
Q92482	AQP3	Aquaporin-3 OS=Homo sapiens GN=AQP3 PE=2 SV=2	2.739726027	1	1	1	292	31.523	7.23	103.9	143.5	74.2	78.5	123.7	76.35	0.617219	3.57E-07
Q05CW7	NAT10	NAT10 protein (Fragment) OS=Homo sapiens GN=NAT10 PE=2 SV=1	28.70036101	14	21	1	554	62.345	9.26	119.9	127.6	49.5	103.1	123.75	76.3	0.616566	3.37E-07
B4DJS6		cDNA FLJ51221, highly similar to Ubiquitin-protein ligase RMA1 (EC 6.3.2.-) OS=Homo sapiens PE=2 SV=1	4.945054945	1	1	1	182	20.241	8.21	115.5	134.4	78.4	71.7	124.95	75.05	0.60064	7.94E-08
B2R6H6		cDNA, FLJ92954, highly similar to Homo sapiens TAF9-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa (TAF9L), mRNA OS=Homo sapiens PE=2 SV=1	11.55378486	3	3	1	251	27.572	9.55	122.4	127.9	75.7	74	125.15	74.85	0.598082	6.23E-08
Q6XD76	ASCL4	Achaete-scute homolog 4 OS=Homo sapiens GN=ASCL4 PE=1 SV=1	4.651162791	1	2	1	172	19.241	9.03	124.7	127.1	77.4	70.8	125.9	74.1	0.588562	2.47E-08

Q9Y2D2	SLC35A3	UDP-N-acetylglucosamine transporter OS=Homo sapiens GN=SLC35A3 PE=1 SV=1	4.615384615	1	1	1	325	35.961	9.16	122.6	131.1	35.6	110.8	126.85	73.2	0.57706	7.60E-09
L0R6G9	FUNDC2	Alternative protein FUNDC2 OS=Homo sapiens GN=FUNDC2 PE=4 SV=1	14.49275362	1	2	1	69	7.963	6.49	151.5	103.7	69.7	75	127.6	72.35	0.567006	2.58E-09
P30536	TSPO	Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3	4.733727811	1	4	1	169	18.816	9.36	122.3	134.8	30.3	112.5	128.55	71.4	0.555426	6.97E-10
B2R5B3		Histone H2A OS=Homo sapiens PE=2 SV=1	40.76923077	6	105	2	130	14.102	11.06	96.5	163.5	70.4	69.6	130	70	0.538462	8.98E-11
B2RB90		cDNA, FLJ95375, highly similar to Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA OS=Homo sapiens PE=2 SV=1	9.090909091	5	6	1	682	76.91	7.25	117.7	142.7	77.1	62.5	130.2	69.8	0.536098	6.66E-11
Q16466		Non-histone chromosomal protein (Fragment) OS=Homo sapiens PE=2 SV=1	47.70642202	6	19	1	109	12.563	9.76	157.2	104.8	37.3	100.7	131	69	0.526718	1.97E-11
Q4G010	CCSMS T1	Protein CCSMST1 OS=Homo sapiens GN=CCSMST1 PE=2 SV=1	15.90909091	1	1	1	132	14.994	7.02	133.1	132.2	30.4	104.3	132.65	67.35	0.507727	1.41E-12
Q9HC85	MB2	Metastasis related protein (Fragment) OS=Homo sapiens GN=MB2 PE=2 SV=1	28.26086957	2	3	2	92	10.414	5.48	123.1	153	67.7	56.1	138.05	61.9	0.448388	6.79E-17
Q6ZRZ8		cDNA FLJ45949 fis, clone PLACE7007973 OS=Homo sapiens PE=2 SV=1	1.449275362	1	1	1	483	54.35	8.38	161.1	122.8	63.9	52.2	141.95	58.05	0.408947	1.55E-20
A0A126GW78	OR5AC2	Olfactory receptor OS=Homo sapiens GN=OR5AC2 PE=3 SV=1	2.265372168	1	1	1	309	35.263	8.94	148.1	163.3	44.6	43.9	155.7	44.25	0.2842	1.19E-38
E9PR30	FAU	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1	10.20408163	1	1	1	98	10.898	11.56	117.6	99.9	90.3	92.1	108.75	91.2	0.838621	0.0495635

P78545	ELF3	ETS-related transcription factor Elf-3 OS=Homo sapiens GN=ELF3 PE=1 SV=1	7.277628032	2	2	2	371	41.428	5.77	111.9	105.6	91.3	91.1	108.75	91.2	0.838621	0.0495635
P23246	SFPQ	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	44.83734088	27	104	26	707	76.102	9.44	108.2	109.4	87.3	95.1	108.8	91.2	0.838235	0.0490219
B7Z537		cDNA FLJ59580, highly similar to Cell division protein kinase 10 (EC 2.7.11.22) OS=Homo sapiens PE=2 SV=1	1.813471503	1	1	1	386	43.793	8.95	111.7	106	93.5	88.9	108.85	91.2	0.83785	0.0484856
Q9H9L3	ISG20L2	Interferon-stimulated 20 kDa exonuclease-like 2 OS=Homo sapiens GN=ISG20L2 PE=1 SV=1	12.74787535	4	5	4	353	39.13	9.94	105.3	112.4	84.9	97.5	108.85	91.2	0.83785	0.0484856
Q86YS6	RAB43	Ras-related protein Rab-43 OS=Homo sapiens GN=RAB43 PE=1 SV=1	20.28301887	3	5	2	212	23.325	5.64	91	126.7	91.4	91	108.85	91.2	0.83785	0.0484856
P54709	ATP1B3	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	48.74551971	12	53	12	279	31.492	8.35	111.6	106	97.2	85.1	108.8	91.15	0.837776	0.0483822
Q9P0B6	CCDC167	Coiled-coil domain-containing protein 167 OS=Homo sapiens GN=CCDC167 PE=1 SV=2	15.46391753	1	2	1	97	11.452	9.5	112.3	105.4	89.9	92.4	108.85	91.15	0.837391	0.0478518
O75340	PDCD6	Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	50.78534031	10	38	10	191	21.855	5.4	105.4	112.3	89	93.3	108.85	91.15	0.837391	0.0478518
A0A024R0Z5	TEGT	Testis enhanced gene transcript (BAX inhibitor 1), isoform CRA_a OS=Homo sapiens GN=TEGT PE=3 SV=1	3.797468354	2	3	2	237	26.52	8.54	109.7	108	98.2	84	108.85	91.1	0.836932	0.0472247
A6NFM0	POLR2J2	DNA-directed RNA polymerase II subunit RPB11-b1 OS=Homo sapiens GN=POLR2J2 PE=1 SV=1	26.58227848	3	4	3	158	17.193	5.82	121.8	96	88.1	94.1	108.9	91.1	0.836547	0.0467052

E7EQY1	FAM136 A	Protein FAM136A OS=Homo sapiens GN=FAM136A PE=1 SV=1	17.55102041	4	7	4	245	26.758	8.24	108.1	109.7	88.2	94	108.9	91.1	0.83654 7	0.0467052
P32189	GK	Glycerol kinase OS=Homo sapiens GN=GK PE=1 SV=3	28.80143113	14	17	14	559	61.205	6.54	108	109.8	92.3	89.9	108.9	91.1	0.83654 7	0.0467052
Q06787	FMR1	Synaptic functional regulator FMR1 OS=Homo sapiens GN=FMR1 PE=1 SV=1	16.13924051	8	14	5	632	71.131	7.42	107.3	110.5	81.6	100.6	108.9	91.1	0.83654 7	0.0467052
A0A1B0G UR5	CHRNA 7	Neuronal acetylcholine receptor subunit alpha-7 (Fragment) OS=Homo sapiens GN=CHRNA7 PE=4 SV=1	15.58441558	1	1	1	231	26.058	8.22	127.9	90	96.8	85.3	108.95	91.05	0.83570 4	0.0455816
Q9GZN2	TGIF2	Homeobox protein TGIF2 OS=Homo sapiens GN=TGIF2 PE=1 SV=1	7.172995781	1	1	1	237	25.862	7.99	121	96.9	98.1	84	108.95	91.05	0.83570 4	0.0455816
Q53H12	AGK	Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=1 SV=2	37.44075829	14	28	14	422	47.107	8.09	109.4	108.6	82.9	99.1	109	91	0.83486 2	0.0444809
A4D0S4	LAMB4	Laminin subunit beta-4 OS=Homo sapiens GN=LAMB4 PE=2 SV=1	0.567859171	1	1	1	1761	193.413	6.35	103.4	114.6	90.1	91.9	109	91	0.83486 2	0.0444809
H0Y886	NDUFB5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial (Fragment) OS=Homo sapiens GN=NDUFB5 PE=1 SV=1	26.69902913	7	13	7	206	23.529	9.6	108.8	109.2	92.1	89.8	109	90.95	0.83440 4	0.0438903
A0A024R1 N4	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_a OS=Homo sapiens GN=XRCC6 PE=4 SV=1	51.55993432	31	98	31	609	69.799	6.64	110.4	107.7	91.8	90.1	109.05	90.95	0.83402 1	0.0434025
P58107	EPPK1	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	47.68172888	91	227	5	5090	555.279	5.6	109.5	108.7	97.5	84.4	109.1	90.95	0.83363 9	0.0429195

Q4J6C6	PREPL	Prolyl endopeptidase-like OS=Homo sapiens GN=PREPL PE=1 SV=1	4.264099037	3	3	3	727	83.873	6.38	90.6	82.2	115.7	111.5	86.4	113.6	1.31481	0.0501369
H0YCJ8	RHCE	Blood group Rh(CE) polypeptide (Fragment) OS=Homo sapiens GN=RHCE PE=4 SV=1	9.090909091	1	1	1	77	8.388	7.44	87.8	85	118	109.2	86.4	113.6	1.31481	0.0501369
O75832	PSMD10	26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens GN=PSMD10 PE=1 SV=1	28.76106195	4	5	4	226	24.412	6.1	88.5	84.3	121.2	105.9	86.4	113.55	1.31424	0.0505309
V9HWEO	HEL-S-7	Annexin OS=Homo sapiens GN=HEL-S-7 PE=2 SV=1	45.9375	13	23	12	320	35.914	5.05	93.5	79.4	118.3	108.8	86.45	113.55	1.31348	0.0510529
Q7Z2Z4	DKFZp68614200	Putative uncharacterized protein DKFZp68614200 (Fragment) OS=Homo sapiens GN=DKFZp68614200 PE=2 SV=1	2.234636872	1	1	1	358	40.704	5.38	85.8	87.1	122.4	104.7	86.45	113.55	1.31348	0.0510529
A0A024R7 B7	CDC37	CDC37 cell division cycle 37 homolog (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=CDC37 PE=4 SV=1	15.07936508	4	7	4	378	44.44	5.25	88.6	84.4	119.4	107.7	86.5	113.55	1.31272	0.0515789
P00966	ASS1	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	23.78640777	10	14	10	412	46.501	8.02	87.1	85.9	120	107.1	86.5	113.55	1.31272	0.0515789
A0A024R5 S9	NEDD4	Neural cell expressed, developmentally down-regulated 4, isoform CRA_b OS=Homo sapiens GN=NEDD4 PE=4 SV=1	12	8	10	6	900	104.095	5.92	89.1	83.9	115.3	111.7	86.5	113.5	1.31214	0.0519827
B7Z6L7		cDNA FLJ61737, moderately similar to Adrenodoxin-like protein OS=Homo sapiens PE=2 SV=1	16.66666667	2	2	2	186	19.89	5.54	85.6	87.5	99.3	127.7	86.55	113.5	1.31138	0.0525164
P52788	SMS	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	25.95628415	8	10	8	366	41.242	5.02	91.8	81.3	123.1	103.8	86.55	113.45	1.3108	0.0529264

Q96RS6	NUDCD 1	NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2	10.80617496	6	7	6	583	66.713	5.11	89.4	83.7	119.8	107.1	86.55	113.45	1.3108	0.0529264
P23526	AHCY	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	34.25925926	14	22	13	432	47.685	6.34	90.3	82.8	120.8	106	86.55	113.4	1.31023	0.0533394
Q5GLZ8	HERC4	Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens GN=HERC4 PE=1 SV=1	1.135288553	1	1	1	1057	118.487	6.19	81.7	91.5	116.8	110	86.6	113.4	1.30947	0.0538844
Q9H993	ARMT1	Protein-glutamate O- methyltransferase OS=Homo sapiens GN=ARMT1 PE=1 SV=1	5.215419501	2	2	2	441	51.14	5.76	94.8	78.4	117.6	109.2	86.6	113.4	1.30947	0.0538844
V9HWJ1	HEL-S- 64p	Glutathione synthetase OS=Homo sapiens GN=HEL-S-64p PE=2 SV=1	9.493670886	4	4	4	474	52.352	5.92	88.3	85	116.8	109.9	86.65	113.35	1.30814	0.0548566
O60701	UGDH	UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	32.59109312	12	17	12	494	54.989	7.12	92.2	81.1	119.9	106.8	86.65	113.35	1.30814	0.0548566
Q9H074	PAIP1	Polyadenylate-binding protein- interacting protein 1 OS=Homo sapiens GN=PAIP1 PE=1 SV=1	11.27348643	5	7	1	479	53.491	4.81	91.8	81.5	118.1	108.6	86.65	113.35	1.30814	0.0548566
P13645	KRT10	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	33.90410959	18	44	15	584	58.792	5.21	83.1	90.2	124	102.7	86.65	113.35	1.30814	0.0548566
P42229	STAT5A	Signal transducer and activator of transcription 5A OS=Homo sapiens GN=STAT5A PE=1 SV=1	6.297229219	4	5	1	794	90.59	6.39	79.1	94.2	119.7	107	86.65	113.35	1.30814	0.0548566
P34932	HSPA4	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	42.26190476	29	51	26	840	94.271	5.19	90.2	83.3	118.4	108.1	86.75	113.25	1.30548	0.0568447
P62633	CNBP	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	35.59322034	5	15	5	177	19.45	7.71	84.3	89.2	112.3	114.1	86.75	113.2	1.3049	0.0572837

Q5T5C7	SARS	Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1	19.7761194	9	14	9	536	61.274	7.06	90.9	82.7	113.7	112.7	86.8	113.2	1.30415	0.0578607
A0A096LP 25	AAK1	AP2-associated protein kinase 1 (Fragment) OS=Homo sapiens GN=AAK1 PE=1 SV=1	7.632093933	3	4	2	511	54.415	5.12	87	86.6	107.2	119.2	86.8	113.2	1.30415	0.0578607
A0A0B4J2 C3	TPT1	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	22.33502538	4	9	4	197	22.559	5.24	86.3	87.3	118.9	107.5	86.8	113.2	1.30415	0.0578607
Q7L2H7	EIF3M	Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1	29.67914439	8	16	8	374	42.476	5.63	93.5	80.1	117.9	108.5	86.8	113.2	1.30415	0.0578607
P49643	PRIM2	DNA primase large subunit OS=Homo sapiens GN=PRIM2 PE=1 SV=2	13.55599214	5	6	5	509	58.769	7.91	89.2	84.4	131	95.4	86.8	113.2	1.30415	0.0578607
A8K070	GPS1	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=1	8.745247148	4	4	4	526	58.885	6.32	88	85.6	124.8	101.6	86.8	113.2	1.30415	0.0578607
A0A140V K69		Aspartate aminotransferase OS=Homo sapiens PE=2 SV=1	29.78208232	10	11	10	413	46.219	7.01	84.8	88.9	115.5	110.8	86.85	113.15	1.30282	0.0588917
A0A140V K27		Leukotriene A(4) hydrolase OS=Homo sapiens PE=2 SV=1	21.44026187	11	16	11	611	69.241	6.18	89.5	84.2	121	105.3	86.85	113.15	1.30282	0.0588917
P61981	YWHAG	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	58.70445344	15	39	10	247	28.285	4.89	89.3	84.5	116	110.3	86.9	113.15	1.30207	0.0594815
Q96KP4	CNDP2	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	13.68421053	4	5	4	475	52.845	5.97	89.8	84	117.4	108.8	86.9	113.1	1.3015	0.0599377
A0A024R1 K7	YWHAH	Tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, eta polypeptide, isoform CRA_b OS=Homo sapiens GN=YWHAH PE=3 SV=1	51.62601626	12	28	8	246	28.201	4.84	87.5	86.3	114.8	111.4	86.9	113.1	1.3015	0.0599377

B3KN49		cDNA FLJ13562 fis, clone PLACE1008080, highly similar to Homo sapiens hexamethylene bis- acetamide inducible 1 (HEXIM1), mRNA OS=Homo sapiens PE=2 SV=1	4.735376045	1	1	1	359	40.582	4.89	95.1	78.7	119.4	106.8	86.9	113.1	1.3015	0.0599377
A0A0C4D FL7	CYP51A 1	Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1 PE=1 SV=1	36.54223969	16	38	16	509	57.242	8.53	88.2	85.6	105.2	121	86.9	113.1	1.3015	0.0599377
P15509	CSF2RA	Granulocyte-macrophage colony- stimulating factor receptor subunit alpha OS=Homo sapiens GN=CSF2RA PE=1 SV=1	2.75	1	1	1	400	46.177	7.75	79.6	94.2	101.1	125	86.9	113.05	1.30092	0.0603971
O43765	SGTA	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1	14.37699681	4	6	4	313	34.042	4.87	90.2	83.7	116.7	109.4	86.95	113.05	1.30017	0.0609989
Q9NR45	NANS	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2	32.31197772	8	12	8	359	40.281	6.74	88.5	85.4	117.7	108.4	86.95	113.05	1.30017	0.0609989
A0A024R5 F7	DHCR7	7-dehydrocholesterol reductase isoform 1 OS=Homo sapiens GN=DHCR7 PE=2 SV=1	20	9	25	9	475	54.454	8.7	88.1	85.8	114.1	112	86.95	113.05	1.30017	0.0609989
A0A087W UF6	FGF2	Fibroblast growth factor OS=Homo sapiens GN=FGF2 PE=1 SV=1	10.06944444	3	3	3	288	30.733	11.18	83.9	90	109.4	116.7	86.95	113.05	1.30017	0.0609989
Q9BRQ0	PYGO2	Pygopus homolog 2 OS=Homo sapiens GN=PYGO2 PE=1 SV=2	1.97044335	1	1	1	406	41.218	7.28	92.4	81.5	117.7	108.4	86.95	113.05	1.30017	0.0609989
V9HWC7	HEL-S- 128m	Epididymis secretory sperm binding protein Li 128m OS=Homo sapiens GN=HEL-S-128m PE=2 SV=1	51.78571429	11	23	11	224	25.019	6.38	87.5	86.4	119.4	106.7	86.95	113.05	1.30017	0.0609989
A0A140VJ T8		Testicular tissue protein Li 164 OS=Homo sapiens PE=2 SV=1	43.81778742	14	20	14	461	49.941	4.82	84.7	89.3	118.9	107.1	87	113	1.29885	0.0620757

Q68D85	NCR3L G1	Natural cytotoxicity triggering receptor 3 ligand 1 OS=Homo sapiens GN=NCR3LG1 PE=1 SV=1	1.982378855	1	1	1	454	50.795	5.59	80.4	93.6	110.2	115.8	87	113	1.29885	0.0620757
Q5JSZ5	PRRC2 B	Protein PRRC2B OS=Homo sapiens GN=PRRC2B PE=1 SV=2	1.076716016	2	2	2	2229	242.817	8.34	89.7	84.4	116.9	109	87.05	112.95	1.29753	0.0631678
P21291	CSRP1	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3	63.21243523	10	27	10	193	20.554	8.57	82.7	91.5	114.1	111.8	87.1	112.95	1.29679	0.0637913
P08238	HSP90A B1	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	53.17679558	38	207	8	724	83.212	5.03	88.2	86	115.8	110	87.1	112.9	1.29621	0.0642756
Q8IWW6	ARHGA P12	Rho GTPase-activating protein 12 OS=Homo sapiens GN=ARHGAP12 PE=1 SV=1	2.836879433	2	2	2	846	96.196	7.61	85.3	88.9	109.7	116.1	87.1	112.9	1.29621	0.0642756
A8K4M1		cDNA FLJ75033, highly similar to Homo sapiens RAS and EF-hand domain containing (RASEF), mRNA OS=Homo sapiens PE=2 SV=1	1.486486486	1	2	1	740	82.805	5.08	84.6	89.6	117.2	108.6	87.1	112.9	1.29621	0.0642756
P80217	IFI35	Interferon-induced 35 kDa protein OS=Homo sapiens GN=IFI35 PE=1 SV=5	3.146853147	1	1	1	286	31.527	6.09	87.1	87.1	111.3	114.4	87.1	112.85	1.29564	0.0647631
J3KMZ9	LDLR	Low-density lipoprotein receptor (Fragment) OS=Homo sapiens GN=LDLR PE=1 SV=1	21.37566138	17	32	16	945	104.605	5.27	86.1	88.2	110.4	115.3	87.15	112.85	1.29489	0.0653993
Q05655	PRKCD	Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2	1.035502959	1	1	1	676	77.455	7.75	93.7	80.6	123.9	101.8	87.15	112.85	1.29489	0.0653993
B2R9G9		cDNA, FLJ94385, highly similar to Homo sapiens cofactor required for Sp1 transcriptional activation,	4.333333333	2	2	2	600	65.348	9.23	88	86.3	106.8	118.8	87.15	112.8	1.29432	0.0658941

		subunit 7, 70kDa (CRSP7), mRNA OS=Homo sapiens PE=2 SV=1															
P60983	GMFB	Glia maturation factor beta OS=Homo sapiens GN=GMFB PE=1 SV=2	18.30985915	2	3	2	142	16.702	5.29	80.4	94	114.5	111.2	87.2	112.85	1.29415	0.0660402
P11216	PYGB	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	12.33689205	8	14	6	843	96.635	6.86	90.9	83.5	117.1	108.5	87.2	112.8	1.29358	0.066539
Q5U043		S-(hydroxymethyl)glutathione dehydrogenase OS=Homo sapiens PE=2 SV=1	22.99465241	10	12	10	374	39.664	7.49	86.7	87.8	115.7	109.8	87.25	112.75	1.29226	0.0676948
P42224	STAT1	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	30	20	24	20	750	87.28	6.05	87.1	87.4	120.2	105.3	87.25	112.75	1.29226	0.0676948
A0A024R7 I5	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae), isoform CRA_c OS=Homo sapiens GN=TRMT1 PE=4 SV=1	8.042488619	4	4	4	659	72.188	7.64	91.8	82.8	115.8	109.6	87.3	112.7	1.29095	0.068867
A0A024R DS1	HSPH1	Heat shock 105kDa/110kDa protein 1, isoform CRA_c OS=Homo sapiens GN=HSPH1 PE=3 SV=1	35.1981352	26	40	22	858	96.804	5.39	87.2	87.4	113.8	111.6	87.3	112.7	1.29095	0.068867
A0A0A0M TS2	GPI	Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens GN=GPI PE=1 SV=1	39.44153578	19	57	19	573	64.784	9.04	89.5	85.1	118.4	107	87.3	112.7	1.29095	0.068867
Q14914	PTGR1	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2	31.91489362	10	13	10	329	35.847	8.29	86.4	88.3	120.1	105.2	87.35	112.65	1.28964	0.0700556
V9HW87	HEL-S- 299	Abhydrolase domain containing 14B, isoform CRA_a OS=Homo sapiens GN=HEL-S-299 PE=2 SV=1	15.23809524	2	7	2	210	22.332	6.4	86	88.7	119	106.3	87.35	112.65	1.28964	0.0700556

P48449	LSS	Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1	28.68852459	18	32	18	732	83.255	6.61	89.3	85.5	114.8	110.4	87.4	112.6	1.28833	0.0712609
Q16512	PKN1	Serine/threonine-protein kinase N1 OS=Homo sapiens GN=PKN1 PE=1 SV=2	2.229299363	2	2	1	942	103.868	6.37	83	91.8	113.6	111.6	87.4	112.6	1.28833	0.0712609
O94855	SEC24D	Protein transport protein Sec24D OS=Homo sapiens GN=SEC24D PE=1 SV=2	5.910852713	6	6	5	1032	112.936	7.25	88.6	86.2	121.1	104.1	87.4	112.6	1.28833	0.0712609
P35908	KRT2	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	35.05477308	23	41	12	639	65.393	8	85.3	89.5	129.5	95.7	87.4	112.6	1.28833	0.0712609
A0A024R AF1	BIN1	Bridging integrator 1, isoform CRA_k OS=Homo sapiens GN=BIN1 PE=4 SV=1	5.227655987	3	4	3	593	64.659	5.06	81.4	93.4	116.4	108.8	87.4	112.6	1.28833	0.0712609
Q02790	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	48.583878	19	31	19	459	51.772	5.43	86.3	88.6	116	109.1	87.45	112.55	1.28702	0.0724829
Q86VX2	COMMD 7	COMM domain-containing protein 7 OS=Homo sapiens GN=COMMD7 PE=1 SV=2	6	1	1	1	200	22.526	5.92	84.4	90.5	121.3	103.8	87.45	112.55	1.28702	0.0724829
B2R825		Alpha-1,4 glucan phosphorylase OS=Homo sapiens PE=2 SV=1	29.39787485	21	31	19	847	97.006	7.3	92.3	82.6	117.9	107.1	87.45	112.5	1.28645	0.0730227
A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1	5.038022814	5	5	5	1052	117.895	6.14	88.5	86.4	118.9	106.1	87.45	112.5	1.28645	0.0730227
A8K586		AP-3 complex subunit beta OS=Homo sapiens PE=2 SV=1	12.88848263	14	16	4	1094	121.214	5.97	86.9	88.1	117.2	107.9	87.5	112.55	1.28629	0.0731778
O14732	IMPA2	Inositol monophosphatase 2 OS=Homo sapiens GN=IMPA2 PE=1 SV=1	7.291666667	2	2	2	288	31.301	6.61	87.9	87.1	117.4	107.6	87.5	112.5	1.28571	0.0737219
P07900	HSP90A A1	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	47.67759563	36	189	23	732	84.607	5.02	87.4	87.6	114.4	110.6	87.5	112.5	1.28571	0.0737219

B4DHQ3		Phosphoserine aminotransferase OS=Homo sapiens PE=2 SV=1	25.30120482	9	17	9	415	45.326	9.03	86.6	88.4	114.2	110.8	87.5	112.5	1.28571	0.0737219
P21333	FLNA	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	53.07895731	103	253	2	2647	280.564	6.06	86.1	88.9	108.7	116.3	87.5	112.5	1.28571	0.0737219
Q9BYV7	BCO2	Beta,beta-carotene 9',10'- oxygenase OS=Homo sapiens GN=BCO2 PE=1 SV=5	7.944732297	4	4	4	579	65.632	8.41	88.3	86.7	120.2	104.8	87.5	112.5	1.28571	0.0737219
A8K5D4	MPZL1	Myelin protein zero-like 1, isoform CRA_b OS=Homo sapiens GN=MPZL1 PE=2 SV=1	13.38289963	3	6	3	269	29.064	8.72	83.9	91.1	107.1	117.9	87.5	112.5	1.28571	0.0737219
Q6FIC5	CLIC4	Chloride intracellular channel protein OS=Homo sapiens GN=CLIC4 PE=2 SV=1	7.114624506	2	3	2	253	28.754	5.59	89	86.1	118.4	106.6	87.55	112.5	1.28498	0.0744261
Q9HAW7	UGT1A7	UDP-glucuronosyltransferase 1-7 OS=Homo sapiens GN=UGT1A7 PE=1 SV=2	16.41509434	7	8	7	530	59.779	7.78	86.6	88.5	116.1	108.8	87.55	112.45	1.28441	0.0749779
A0A024R9 22	C1orf11 2	Chromosome 1 open reading frame 112, isoform CRA_a OS=Homo sapiens GN=C1orf112 PE=4 SV=1	1.289566237	1	1	1	853	96.492	6	86.5	88.6	113.2	111.6	87.55	112.4	1.28384	0.0755334
A0A087X1 Z3	PSME2	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1	23.22834646	6	8	6	254	29.108	6.71	90.9	84.2	120.8	104	87.55	112.4	1.28384	0.0755334
Q8N122	RPTOR	Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1	6.217228464	5	6	5	1335	148.942	6.89	89.7	85.4	120.4	104.4	87.55	112.4	1.28384	0.0755334
Q5T5H1	ENSA	Alpha-endosulfine OS=Homo sapiens GN=ENSA PE=1 SV=1	12.8342246	2	3	2	187	20.981	7.87	87.7	87.5	113.8	111	87.6	112.4	1.28311	0.0762513
A0A024R2 03	PSME3	Proteasome (Prosome, macropain) activator subunit 3 (PA28 gamma Ki), isoform CRA_a OS=Homo sapiens GN=PSME3 PE=4 SV=1	30.18867925	7	10	7	265	30.87	6.71	92.1	83.1	119.5	105.3	87.6	112.4	1.28311	0.0762513

Q8N7G1		Purine nucleoside phosphorylase OS=Homo sapiens PE=2 SV=1	48.12286689	12	17	12	293	32.53	7.21	92.5	82.7	111.9	112.8	87.6	112.35	1.28253	0.0768147
B2R6J2		cDNA, FLJ92973, highly similar to Homo sapiens villin 2 (ezrin) (VIL2), mRNA OS=Homo sapiens PE=2 SV=1	50.34129693	35	67	20	586	69.358	6.27	84.3	91	111	113.8	87.65	112.4	1.28237	0.0769744
V9HW12	HEL-S- 2a	Epididymis secretory sperm binding protein Li 2a OS=Homo sapiens GN=HEL-S-2a PE=2 SV=1	40.90909091	10	27	9	198	21.878	5.97	84	91.3	118	106.7	87.65	112.35	1.2818	0.0775421
A8K180		cDNA FLJ76749, highly similar to Homo sapiens Wiskott-Aldrich syndrome-like (WASL), mRNA OS=Homo sapiens PE=2 SV=1	2.772277228	1	1	1	505	54.735	8.12	83	92.3	107.4	117.3	87.65	112.35	1.2818	0.0775421
Q13158	FADD	FAS-associated death domain protein OS=Homo sapiens GN=FADD PE=1 SV=1	8.653846154	1	2	1	208	23.265	5.69	90.1	85.2	107.6	117	87.65	112.3	1.28123	0.0781135
A0A024R3 E3	APOA1	Apolipoprotein A-I, isoform CRA_a OS=Homo sapiens GN=APOA1 PE=3 SV=1	5.992509363	1	11	1	267	30.759	5.76	90.4	85	107.2	117.4	87.7	112.3	1.2805	0.0788504
P40763	STAT3	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	19.61038961	13	20	13	770	88.011	6.3	86.9	88.5	118.4	106.2	87.7	112.3	1.2805	0.0788504
Q13325	IFIT5	Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 PE=1 SV=1	3.319502075	1	2	1	482	55.812	7.4	92.9	82.6	114.5	110	87.75	112.25	1.2792	0.0801766
A8KA19		cDNA FLJ75831, highly similar to Homo sapiens exportin, tRNA (nuclear export receptor for tRNAs) (XPOT), mRNA OS=Homo sapiens PE=2 SV=1	4.885654886	4	6	4	962	109.849	5.39	96.1	79.4	118.6	105.9	87.75	112.25	1.2792	0.0801766

A0A024R4 R3	CNOT3	CCR4-NOT transcription complex, subunit 3, isoform CRA_a OS=Homo sapiens GN=CNOT3 PE=4 SV=1	0.929614874	1	1	1	753	81.822	6.2	90.7	84.9	116.7	107.8	87.8	112.25	1.27847	0.0809284
Q32Q10	RSU1	RSU1 protein (Fragment) OS=Homo sapiens GN=RSU1 PE=2 SV=1	5.714285714	2	2	2	280	31.34	9.09	89.8	85.8	116.4	108	87.8	112.2	1.2779	0.0815206
A8K168		Malic enzyme OS=Homo sapiens PE=2 SV=1	9.79020979	4	4	4	572	64.095	6.13	85.1	90.5	115.3	109.1	87.8	112.2	1.2779	0.0815206
V9HWA6	HEL32	Epididymis luminal protein 32 OS=Homo sapiens GN=HEL32 PE=2 SV=1	42.42424242	8	19	7	165	18.493	7.85	84.6	91	113.7	110.7	87.8	112.2	1.2779	0.0815206
B3KNU3		cDNA FLJ30480 fis, clone BRAWH1000174, moderately similar to Rho-GTPase-activating protein 8 OS=Homo sapiens PE=2 SV=1	3.804347826	1	1	1	368	40.872	6.73	109	66.6	124.4	100	87.8	112.2	1.2779	0.0815206
Q9BTT0	ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1	13.80597015	3	6	3	268	30.674	3.85	96.7	78.9	124.1	100.3	87.8	112.2	1.2779	0.0815206
Q9BS40	LXN	Latexin OS=Homo sapiens GN=LXN PE=1 SV=2	17.56756757	3	4	3	222	25.734	5.78	78.8	96.8	121.4	103	87.8	112.2	1.2779	0.0815206
A0A140VJ R2		Testicular tissue protein Li 138 OS=Homo sapiens PE=2 SV=1	3.245436105	1	1	1	493	54.513	6	101.7	74	112.3	112	87.85	112.15	1.27661	0.0828825
D3DWY7	VBP1	von Hippel-Lindau binding protein 1, isoform CRA_b OS=Homo sapiens GN=VBP1 PE=4 SV=1	12.01716738	3	3	3	233	26.519	9.01	91.4	84.3	116.2	108	87.85	112.1	1.27604	0.0834868
Q9NPF4	OSGEP	Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens GN=OSGEP PE=1 SV=1	12.53731343	3	3	3	335	36.403	6.35	88.7	87	116.1	108.1	87.85	112.1	1.27604	0.0834868

Q9NQW7	XPNPE P1	Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3	15.24879615	7	9	1	623	69.873	5.67	92	83.8	119.4	104.9	87.9	112.15	1.27588	0.0836541
Q9H6Z4	RANBP3	Ran-binding protein 3 OS=Homo sapiens GN=RANBP3 PE=1 SV=1	14.99118166	6	8	6	567	60.173	4.78	89.9	85.9	121.5	102.8	87.9	112.15	1.27588	0.0836541
HOYL70	TLE3	Transducin-like enhancer protein 3 OS=Homo sapiens GN=TLE3 PE=1 SV=1	4.603580563	3	3	3	782	84.425	7.27	83.2	92.6	123.6	100.7	87.9	112.15	1.27588	0.0836541
Q99497	PARK7	Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	61.9047619	10	24	10	189	19.878	6.79	86.8	89	116.3	107.9	87.9	112.1	1.27531	0.0842627
P49321	NASP	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	18.65482234	12	16	12	788	85.186	4.3	92.7	83.1	122.1	102.1	87.9	112.1	1.27531	0.0842627
Q9BV73	CEP250	Centrosome-associated protein CEP250 OS=Homo sapiens GN=CEP250 PE=1 SV=2	1.31040131	3	3	3	2442	280.967	5.02	88.6	87.3	112.8	111.3	87.95	112.05	1.27402	0.0856614
A8K690		cDNA FLJ76863, highly similar to Homo sapiens stress-induced- phosphoprotein 1 (Hsp70/Hsp90- organizing protein) (STIP1), mRNA OS=Homo sapiens PE=2 SV=1	58.93186004	39	67	39	543	62.615	6.8	91.4	84.5	116.7	107.4	87.95	112.05	1.27402	0.0856614
B4DNW0		cDNA FLJ60317, highly similar to Aminoacylase-1 (EC 3.5.1.14) OS=Homo sapiens PE=2 SV=1	14.45783133	5	5	5	498	55.959	7.03	87.6	88.3	119.1	104.9	87.95	112	1.27345	0.0862824
A0A024R0 36	DAB2	Disabled homolog 2, mitogen- responsive phosphoprotein (Drosophila), isoform CRA_a OS=Homo sapiens GN=DAB2 PE=4 SV=1	29.61038961	17	29	17	770	82.397	5.53	90.3	85.7	116.7	107.3	88	112	1.27273	0.0870786
Q15738	NSDHL	Sterol-4-alpha-carboxylate 3- dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2	48.52546917	16	65	16	373	41.874	8.06	86.6	89.4	112.5	111.5	88	112	1.27273	0.0870786

Q8TDH9	BLOC1S5	Biogenesis of lysosome-related organelles complex 1 subunit 5 OS=Homo sapiens GN=BLOC1S5 PE=1 SV=1	5.347593583	1	1	1	187	21.596	7.59	84.6	91.4	110.2	113.8	88	112	1.27273	0.0870786
Q5U0F4	EIF3S2	Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3S2 PE=2 SV=1	17.53846154	5	7	5	325	36.479	5.64	89.3	86.7	119.4	104.6	88	112	1.27273	0.0870786
B3KMQ6		cDNA FLJ12172 fis, clone MAMMA1000684, highly similar to Opioid growth factor receptor OS=Homo sapiens PE=2 SV=1	2.363367799	1	2	1	677	73.324	4.84	90.2	85.8	120.3	103.6	88	111.95	1.27216	0.0877082
B4E1C2	KNG1	Kininogen 1, isoform CRA_b OS=Homo sapiens GN=KNG1 PE=2 SV=1	1.397515528	1	1	1	644	71.87	6.81	83.9	92.2	90.8	133.2	88.05	112	1.272	0.0878802
Q9H974	QTRTD1	Queuine tRNA-ribosyltransferase accessory subunit OS=Homo sapiens GN=QTRTD1 PE=1 SV=1	15.6626506	4	4	4	415	46.683	6.81	93.1	83	113.6	110.3	88.05	111.95	1.27144	0.0885144
P49588	AARS	Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	41.52892562	33	53	33	968	106.743	5.53	88.2	87.9	114.5	109.4	88.05	111.95	1.27144	0.0885144
Q12841	FSTL1	Follistatin-related protein 1 OS=Homo sapiens GN=FSTL1 PE=1 SV=1	16.55844156	5	6	5	308	34.963	5.52	87.6	88.5	115.3	108.6	88.05	111.95	1.27144	0.0885144
P58546	MTPN	Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2	41.52542373	4	5	4	118	12.887	5.52	83.7	92.4	114	109.9	88.05	111.95	1.27144	0.0885144
B4E2P4		cDNA FLJ58474, highly similar to Xaa-Pro aminopeptidase 1 (EC 3.4.11.9) OS=Homo sapiens PE=2 SV=1	23.63636364	7	8	1	440	49.564	6.3	82.7	93.4	110.9	113	88.05	111.95	1.27144	0.0885144
Q8N6L1	KRTCA P2	Keratinocyte-associated protein 2 OS=Homo sapiens GN=KRTCAP2 PE=1 SV=2	12.5	1	2	1	136	14.669	9.61	78.5	97.6	105.8	118.1	88.05	111.95	1.27144	0.0885144

G3V5T9	CDK2	Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=1	30.92485549	8	11	6	346	39.153	8.62	88	88.2	112.5	111.4	88.1	111.95	1.27072	0.0893261
Q14558	PRPSA P1	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSA1 PE=1 SV=2	17.41573034	5	5	2	356	39.369	7.2	88.8	87.4	117.5	106.4	88.1	111.95	1.27072	0.0893261
P19623	SRM	Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1	35.43046358	6	11	6	302	33.803	5.49	93.6	82.6	114	109.8	88.1	111.9	1.27015	0.089969
B2RE43		cDNA, FLJ96916, highly similar to Homo sapiens netrin 4 (NTN4), mRNA OS=Homo sapiens PE=2 SV=1	2.388535032	1	1	1	628	70.027	8	86	90.2	97.2	126.6	88.1	111.9	1.27015	0.089969
A0A087X0 N3	NOL4L	Nucleolar protein 4-like OS=Homo sapiens GN=NOL4L PE=1 SV=1	2.352941176	1	1	1	680	74.178	5.77	90.6	85.7	113.3	110.5	88.15	111.9	1.26943	0.0907911
A0A0K0K 1K7	HEL-S- 304	6-phosphogluconolactonase, isoform CRA_b OS=Homo sapiens GN=HEL-S-304 PE=2 SV=1	44.96124031	9	12	9	258	27.53	6.05	86.1	90.2	118.1	105.6	88.15	111.85	1.26886	0.0914428
O43653	PSCA	Prostate stem cell antigen OS=Homo sapiens GN=PSCA PE=1 SV=1	22.76422764	3	8	3	123	12.903	5.29	83.3	93	124.7	99	88.15	111.85	1.26886	0.0914428
A0A024R3 V8	TSNAX	Translin-associated factor X, isoform CRA_c OS=Homo sapiens GN=TSNAX PE=4 SV=1	23.44827586	6	8	6	290	33.092	6.55	88.2	88.2	114.8	108.8	88.2	111.8	1.26757	0.0929355
A0A0A0M TQ8	CCDC17 5	Coiled-coil domain-containing protein 175 OS=Homo sapiens GN=CCDC175 PE=1 SV=1	1.086956522	1	1	1	828	97.353	5.99	82.1	94.3	117	106.6	88.2	111.8	1.26757	0.0929355
I3L0W4	SAT2	Diamine acetyltransferase 2 OS=Homo sapiens GN=SAT2 PE=1 SV=1	6.617647059	1	1	1	136	15.047	6.01	92.2	84.2	114.5	109	88.2	111.75	1.26701	0.0936002
A8K486		Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1	70.90909091	12	78	11	165	18.002	6.9	91.1	85.4	115	108.5	88.25	111.75	1.26629	0.0944477

P13797	PLS3	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	38.25396825	23	43	19	630	70.766	5.6	88.2	88.3	114.2	109.3	88.25	111.75	1.26629	0.0944477
Q13433	SLC39A6	Zinc transporter ZIP6 OS=Homo sapiens GN=SLC39A6 PE=1 SV=3	2.649006623	2	2	2	755	84.993	6.95	91.1	85.4	103	120.5	88.25	111.75	1.26629	0.0944477
A0A024R0L6	PAFAH1B3	Platelet-activating factor acetylhydrolase, isoform lb, gamma subunit 29kDa, isoform CRA_a OS=Homo sapiens GN=PAFAH1B3 PE=4 SV=1	27.27272727	5	5	5	231	25.718	6.84	87.1	89.4	118	105.5	88.25	111.75	1.26629	0.0944477
P13647	KRT5	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	24.40677966	18	60	7	590	62.34	7.74	83	93.5	120.3	103.2	88.25	111.75	1.26629	0.0944477
O75822	EIF3J	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2	36.04651163	8	14	8	258	29.045	4.83	88.4	88.2	113.3	110.1	88.3	111.7	1.26501	0.0959793
P21399	ACO1	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	20.80989876	13	15	13	889	98.337	6.68	91.1	85.5	116.7	106.7	88.3	111.7	1.26501	0.0959793
O75223	GGCT	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1	17.55319149	3	6	3	188	20.994	5.14	87.9	88.7	117.7	105.7	88.3	111.7	1.26501	0.0959793
Q9NRR3	CDC42SE2	CDC42 small effector protein 2 OS=Homo sapiens GN=CDC42SE2 PE=1 SV=1	22.61904762	1	2	1	84	9.217	8.35	83.6	93	105.5	117.9	88.3	111.7	1.26501	0.0959793
P49368	CCT3	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	58.71559633	32	73	32	545	60.495	6.49	91.8	84.9	114.3	109.1	88.35	111.7	1.26429	0.0968431
Q16775	HAGH	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2	23.7012987	6	7	6	308	33.784	8.12	86.5	90.2	116.7	106.7	88.35	111.7	1.26429	0.0968431
B5BU38	ANXA1	Annexin OS=Homo sapiens GN=ANXA1 PE=2 SV=1	50.57803468	16	41	16	346	38.656	7.02	92	84.7	118.7	104.7	88.35	111.7	1.26429	0.0968431

P04259	KRT6B	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	18.08510638	14	74	1	564	60.03	8	82.3	94.4	82.2	141.2	88.35	111.7	1.26429	0.0968431
A0A024R DY0	RANBP5	RAN binding protein 5, isoform CRA_d OS=Homo sapiens GN=RANBP5 PE=4 SV=1	28.62351869	24	42	23	1097	123.55	4.94	90.8	85.9	115.3	108	88.35	111.65	1.26372	0.0975305
Q13363	CTBP1	C-terminal-binding protein 1 OS=Homo sapiens GN=CTBP1 PE=1 SV=2	8.181818182	4	4	1	440	47.505	6.77	90.8	85.9	125	98.3	88.35	111.65	1.26372	0.0975305
B2RDY9		Adenylyl cyclase-associated protein OS=Homo sapiens PE=2 SV=1	36.84210526	15	22	15	475	51.583	8.22	87.5	89.2	114.5	108.7	88.35	111.6	1.26316	0.0982224
Q96C23	GALM	Aldose 1-epimerase OS=Homo sapiens GN=GALM PE=1 SV=1	4.093567251	1	2	1	342	37.742	6.65	88.9	87.8	118.7	104.5	88.35	111.6	1.26316	0.0982224
A0A024R2 Q7	CLEC3B	C-type lectin domain family 3, member B, isoform CRA_a OS=Homo sapiens GN=CLEC3B PE=4 SV=1	35.64356436	5	11	5	202	22.522	5.67	85.9	90.8	91.3	131.9	88.35	111.6	1.26316	0.0982224
A0A0A0M RJ7	F5	Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=1	2.1982952	4	4	4	2229	252.078	6.05	74.9	101.8	101.4	121.8	88.35	111.6	1.26316	0.0982224
V9HWD6	HEL-S-1	Epididymis secretory protein Li 1 OS=Homo sapiens GN=HEL-S-1 PE=2 SV=1	52.03252033	11	33	5	246	28.065	4.83	90.5	86.3	113.6	109.6	88.4	111.6	1.26244	0.0991016
B4DWB5		cDNA FLJ53931, highly similar to Bifunctional 3'- phosphoadenosine5'- phosphosulfate synthetase 2 OS=Homo sapiens PE=2 SV=1	22.16828479	12	19	12	618	69.988	7.33	90	86.8	112.2	111	88.4	111.6	1.26244	0.0991016
A4D0Z4	GCC1	GRIP and coiled-coil domain containing 1 OS=Homo sapiens GN=GCC1 PE=4 SV=1	2.193548387	2	2	2	775	87.757	5.45	95.1	81.7	117.6	105.6	88.4	111.6	1.26244	0.0991016
A0A024R5 29	DAK	Dihydroxyacetone kinase 2 homolog (Yeast), isoform CRA_a	12.69565217	5	6	5	575	58.94	7.49	90.3	86.6	109.9	113.2	88.45	111.55	1.26116	0.100693

		OS=Homo sapiens GN=DAK PE=4 SV=1															
Q05CP8	CCDC6	CCDC6 protein (Fragment) OS=Homo sapiens GN=CCDC6 PE=2 SV=1	33.23353293	12	18	10	334	38.14	9.39	86.2	90.7	114.5	108.6	88.45	111.55	1.26116	0.100693
P61956	SUMO2	Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=3	10.52631579	1	2	1	95	10.864	5.5	93.7	83.2	114.5	108.6	88.45	111.55	1.26116	0.100693
P40925	MDH1	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	35.02994012	9	22	9	334	36.403	7.36	91	85.9	118.8	104.3	88.45	111.55	1.26116	0.100693
Q9UBB4	ATXN10	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1	28.63157895	13	15	13	475	53.455	5.25	85.5	91.4	119	104.1	88.45	111.55	1.26116	0.100693
A0A0U1R QMO		Uncharacterized protein OS=Homo sapiens PE=4 SV=1	16.37931034	1	1	1	116	12.657	10.24	86.9	90	107.8	115.2	88.45	111.5	1.2606	0.101403
A0A0D9S G79	UBAP1	Ubiquitin-associated protein 1 (Fragment) OS=Homo sapiens GN=UBAP1 PE=1 SV=1	3.409090909	1	1	1	528	57.818	5.57	83.7	93.3	109.6	113.4	88.5	111.5	1.25989	0.102304
B3KS98	EIF3H	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1	16.12021858	5	7	5	366	41.555	7.33	95.5	81.5	114.8	108.2	88.5	111.5	1.25989	0.102304
Q53GG0		Epithelial protein lost in neoplasm beta variant (Fragment) OS=Homo sapiens PE=2 SV=1	31.75230567	24	42	24	759	85.201	6.84	93.3	83.7	116.8	106.2	88.5	111.5	1.25989	0.102304
D6W5V3	hCG_20 24112	HCG2024112, isoform CRA_c (Fragment) OS=Homo sapiens GN=hCG_2024112 PE=4 SV=1	2.671755725	1	1	1	262	28.888	8.07	74.3	102.7	112.1	110.9	88.5	111.5	1.25989	0.102304
Q06830	PRDX1	Peroxisiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	78.3919598	14	44	11	199	22.096	8.13	87.7	89.4	109.7	113.3	88.55	111.5	1.25918	0.10321
Q969F9	HPS3	Hermansky-Pudlak syndrome 3 protein OS=Homo sapiens GN=HPS3 PE=1 SV=1	2.788844622	2	2	2	1004	113.662	6.43	84.8	92.3	117.4	105.5	88.55	111.45	1.25861	0.103935

Q96KB5	PBK	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3	12.11180124	3	4	3	322	36.062	5.12	82.2	94.9	114.5	108.4	88.55	111.45	1.25861	0.103935
A0A024R001	TMEM14C	Transmembrane protein 14C, isoform CRA_a OS=Homo sapiens GN=TMEM14C PE=4 SV=1	8.928571429	1	2	1	112	11.557	9.88	64.7	112.4	107	115.8	88.55	111.4	1.25805	0.104664
A0A024R9Y7	MAGED2	Melanoma antigen family D, 2, isoform CRA_a OS=Homo sapiens GN=MAGED2 PE=4 SV=1	21.12211221	14	18	14	606	64.914	9.32	88.9	88.3	122.8	100.1	88.6	111.45	1.2579	0.104853
A4D1L5	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) OS=Homo sapiens GN=UBE2H PE=2 SV=1	17.4863388	3	4	3	183	20.642	4.67	86.7	90.5	114.2	108.6	88.6	111.4	1.25734	0.105587
Q9BTE1	DCTN5	Dynactin subunit 5 OS=Homo sapiens GN=DCTN5 PE=1 SV=1	5.494505495	1	1	1	182	20.113	8.02	94.3	82.9	110.6	112.2	88.6	111.4	1.25734	0.105587
P25789	PSMA4	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	48.27586207	11	23	11	261	29.465	7.72	93.9	83.3	117.4	105.4	88.6	111.4	1.25734	0.105587
A8KA30		Oxysterol-binding protein OS=Homo sapiens PE=2 SV=1	1.789473684	1	1	1	950	108.37	6.33	92.7	84.5	117.4	105.4	88.6	111.4	1.25734	0.105587
Q9H6T3	RPAP3	RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 PE=1 SV=2	8.721804511	4	4	4	665	75.672	6.84	92.3	84.9	115.4	107.4	88.6	111.4	1.25734	0.105587
B1Q2B0	URCC5	URCC5 OS=Homo sapiens GN=URCC5 PE=2 SV=1	15.80680571	11	13	11	911	101.244	8.43	83.2	94	110.7	112.1	88.6	111.4	1.25734	0.105587
P56937	HSD17B7	3-keto-steroid reductase OS=Homo sapiens GN=HSD17B7 PE=1 SV=1	20.82111437	6	13	6	341	38.182	8.1	91.1	86.1	112.8	109.9	88.6	111.35	1.25677	0.106325
Q9HAB3	SLC52A2	Solute carrier family 52, riboflavin transporter, member 2 OS=Homo sapiens GN=SLC52A2 PE=1 SV=1	1.797752809	1	1	1	445	45.747	7.15	95.9	81.4	114.5	108.3	88.65	111.4	1.25663	0.106515
Q9HD26	GOPC	Golgi-associated PDZ and coiled-coil motif-containing protein	4.329004329	2	2	2	462	50.489	5.92	84.9	92.4	115.8	107	88.65	111.4	1.25663	0.106515

		OS=Homo sapiens GN=GOPC PE=1 SV=1																
O60925	PFDN1	Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2	22.13114754	3	3	3	122	14.202	6.81	91.8	85.5	114.6	108.1	88.65	111.35	1.25606	0.107259	
Q15075	EEA1	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	17.00921332	20	24	20	1411	162.367	5.68	90.6	86.7	115.7	107	88.65	111.35	1.25606	0.107259	
Q8N543	OGFOD1	Prolyl 3-hydroxylase OGFOD1 OS=Homo sapiens GN=OGFOD1 PE=1 SV=1	9.778597786	4	4	4	542	63.206	5.11	88.3	89	114.6	108.1	88.65	111.35	1.25606	0.107259	
Q53G42		mRNA decapping enzyme variant (Fragment) OS=Homo sapiens PE=2 SV=1	18.99109792	5	6	5	337	38.586	6.38	94.5	82.8	116.3	106.4	88.65	111.35	1.25606	0.107259	
Q6P996	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1 SV=2	18.90862944	11	17	11	788	86.652	5.38	89.7	87.6	117.5	105.2	88.65	111.35	1.25606	0.107259	
P02751	FN1	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	6.621961442	12	17	12	2386	262.46	5.71	85.5	91.8	100	122.7	88.65	111.35	1.25606	0.107259	
A0A140V KF3		Testis tissue sperm-binding protein Li 70n OS=Homo sapiens PE=2 SV=1	7.894736842	3	4	3	418	46.283	6.38	84.1	93.2	100.2	122.5	88.65	111.35	1.25606	0.107259	
O60825	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 PE=1 SV=2	9.702970297	4	7	4	505	58.44	8.38	90.3	87	117.4	105.2	88.65	111.3	1.2555	0.108007	
Q5T040	FAM120AOS	Uncharacterized protein FAM120AOS (Fragment) OS=Homo sapiens GN=FAM120AOS PE=4 SV=1	10.60606061	1	1	1	66	7.1	10.7	84.4	92.9	122.7	99.9	88.65	111.3	1.2555	0.108007	
P55786	NPEPPS	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	19.26006529	14	20	14	919	103.211	5.72	94.5	82.9	119.2	103.4	88.7	111.3	1.25479	0.108952	

A4D2M9	INSIG1	Insulin-induced gene protein OS=Homo sapiens GN=INSIG1 PE=3 SV=1	2.121212121	1	1	1	330	36.429	9.04	93.9	83.5	106.9	115.7	88.7	111.3	1.25479	0.108952
Q8TF05	PPP4R1	Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens GN=PPP4R1 PE=1 SV=1	0.736842105	1	1	1	950	106.936	4.77	91.6	85.8	118.2	104.4	88.7	111.3	1.25479	0.108952
A0A024Q YX0	EBP	Emopamil binding protein OS=Homo sapiens GN=EBP PE=2 SV=1	16.95652174	4	19	4	230	26.336	7.9	82.6	94.8	117.5	105.1	88.7	111.3	1.25479	0.108952
Q14240	EIF4A2	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2	25.06142506	11	22	3	407	46.373	5.48	89.1	88.3	119.8	102.7	88.7	111.25	1.25423	0.10971
A0A024R0 D2	hCG_38 636	AP complex subunit beta OS=Homo sapiens GN=hCG_38636 PE=3 SV=1	2.165087957	1	1	1	739	83.206	5.86	86.6	90.9	109.4	113.2	88.75	111.3	1.25408	0.109903
B2RE31		cDNA, FLJ96896 OS=Homo sapiens PE=2 SV=1	2.976190476	1	2	1	504	56.41	8.81	93.4	84.1	110.7	111.8	88.75	111.25	1.25352	0.110666
B2R8K8		cDNA, FLJ93949, highly similar to Homo sapiens NIMA (never in mitosis gene a)-related kinase 7 (NEK7), mRNA OS=Homo sapiens PE=2 SV=1	3.311258278	1	1	1	302	34.514	8.25	93.2	84.3	113.2	109.3	88.75	111.25	1.25352	0.110666
P48507	GCLM	Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1	18.61313869	4	4	4	274	30.708	6.02	87.7	89.8	110.5	112	88.75	111.25	1.25352	0.110666
Q68CZ1	RPGRIP 1L	Protein fantom OS=Homo sapiens GN=RPGRIP1L PE=1 SV=2	0.532319392	1	1	1	1315	151.107	5.35	97.2	80.3	124.1	98.4	88.75	111.25	1.25352	0.110666
A0A024R7 55	CALU	Calumenin, isoform CRA_a OS=Homo sapiens GN=CALU PE=4 SV=1	54.28571429	16	50	2	315	37.111	4.59	89.3	88.2	118.7	103.8	88.75	111.25	1.25352	0.110666

P35527	KRT9	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	32.58426966	17	28	16	623	62.027	5.24	81.6	95.9	127.6	94.9	88.75	111.25	1.25352	0.110666
A0A0S2Z4 55	SERPINI 1	Serpin peptidase inhibitor clade I member 1 isoform 1 (Fragment) OS=Homo sapiens GN=SERPINI1 PE=2 SV=1	2.926829268	1	1	1	410	46.397	4.91	88.5	89.1	107.3	115.1	88.8	111.2	1.25225	0.112401
Q7Z4Q2	HEATR3	HEAT repeat-containing protein 3 OS=Homo sapiens GN=HEATR3 PE=1 SV=2	6.617647059	4	4	4	680	74.535	5.11	95.4	82.2	103.2	119.2	88.8	111.2	1.25225	0.112401
Q6XQN6	NAPRT	Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT PE=1 SV=2	7.620817844	3	4	3	538	57.542	5.68	89.9	87.7	119.6	102.8	88.8	111.2	1.25225	0.112401
Q9UJY1	HSPB8	Heat shock protein beta-8 OS=Homo sapiens GN=HSPB8 PE=1 SV=1	12.24489796	3	5	3	196	21.591	5.12	78.3	99.3	108.2	114.2	88.8	111.2	1.25225	0.112401
Q16658	FSCN1	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	42.39350913	17	33	17	493	54.496	7.24	91.2	86.5	106.7	115.7	88.85	111.2	1.25155	0.113374
P39687	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1	31.3253012	9	20	4	249	28.568	4.09	88.2	89.5	119.5	102.9	88.85	111.2	1.25155	0.113374
Q9NWW4	C1orf12 3	UPF0587 protein C1orf123 OS=Homo sapiens GN=C1orf123 PE=1 SV=1	10	2	2	2	160	18.037	5.01	87	90.7	117.1	105.2	88.85	111.15	1.25098	0.114157
Q07889	SOS1	Son of sevenless homolog 1 OS=Homo sapiens GN=SOS1 PE=1 SV=1	0.525131283	1	1	1	1333	152.368	6.84	80.3	97.4	89.3	133	88.85	111.15	1.25098	0.114157
P57081	WDR4	tRNA (guanine-N(7)-) methyltransferase non-catalytic subunit WDR4 OS=Homo sapiens GN=WDR4 PE=1 SV=2	6.796116505	2	5	2	412	45.461	7.11	88.2	89.5	114.9	107.3	88.85	111.1	1.25042	0.114944

Q96L92	SNX27	Sorting nexin-27 OS=Homo sapiens GN=SNX27 PE=1 SV=2	3.512014787	2	3	2	541	61.226	6.49	100.1	77.7	115.6	106.7	88.9	111.15	1.25028	0.115142
B2R665		cDNA, FLJ92810, highly similar to Homo sapiens protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform (PPM1G), mRNA OS=Homo sapiens PE=2 SV=1	28.38827839	11	15	11	546	59.205	4.36	92.2	85.6	117.8	104.5	88.9	111.15	1.25028	0.115142
P26639	TARS	Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	41.35546335	29	53	29	723	83.382	6.67	91.9	85.9	113.6	108.6	88.9	111.1	1.24972	0.115934
A0A140VJ F4		Biliverdin reductase A OS=Homo sapiens PE=2 SV=1	14.52702703	4	6	4	296	33.407	6.44	88.7	89.1	111.1	111.1	88.9	111.1	1.24972	0.115934
O00273	DFFA	DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA PE=1 SV=1	16.918429	4	4	4	331	36.5	4.79	88.2	89.6	111.3	110.9	88.9	111.1	1.24972	0.115934
J3QLU8	PEMT	Phosphatidylethanolamine N-methyltransferase OS=Homo sapiens GN=PEMT PE=4 SV=1	9.278350515	1	1	1	97	10.228	5.94	82.2	95.6	106	116.2	88.9	111.1	1.24972	0.115934
Q53HV2		Chaperonin containing TCP1, subunit 7 (Eta) variant (Fragment) OS=Homo sapiens PE=2 SV=1	46.40883978	21	55	21	543	59.303	7.65	91.8	86.1	113.6	108.6	88.95	111.1	1.24902	0.116931
Q96D71	REPS1	RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens GN=REPS1 PE=1 SV=3	3.391959799	2	2	2	796	86.609	5.69	87.3	90.6	110.1	112.1	88.95	111.1	1.24902	0.116931
Q9HCN4	GPN1	GPN-loop GTPase 1 OS=Homo sapiens GN=GPN1 PE=1 SV=1	7.754010695	2	2	2	374	41.714	4.92	88.7	89.2	95.8	126.4	88.95	111.1	1.24902	0.116931
K7EM18	EIF1	Eukaryotic translation initiation factor 1 OS=Homo sapiens GN=EIF1 PE=1 SV=1	59.50413223	5	13	1	121	13.599	7.9	99.2	78.7	105.8	116.3	88.95	111.05	1.24845	0.117733
A0A024R9 K2	BAHD1	Bromo adjacent homology domain containing 1, isoform CRA_a	1.153846154	1	1	1	780	84.599	9.07	93.1	84.8	126.6	95.5	88.95	111.05	1.24845	0.117733

		OS=Homo sapiens GN=BAHD1 PE=4 SV=1															
P49137	MAPKA PK2	MAP kinase-activated protein kinase 2 OS=Homo sapiens GN=MAPKAPK2 PE=1 SV=1	7.75	3	3	3	400	45.538	8.68	86.4	91.5	112.4	109.6	88.95	111	1.24789	0.118541
B2R6D4		Phosphomannomutase OS=Homo sapiens PE=2 SV=1	19.91869919	4	4	4	246	28.036	6.77	89.1	88.9	115	107	89	111	1.24719	0.119554
A8K7U3		cDNA FLJ77788 OS=Homo sapiens PE=2 SV=1	3.685503686	1	1	1	407	46.973	8.91	95	83	115.6	106.4	89	111	1.24719	0.119554
P49915	GMPS	GMP synthase [glutamine- hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1	35.4978355	21	31	21	693	76.667	6.87	93.5	84.5	115.9	106.1	89	111	1.24719	0.119554
A0A140VJ Z4		Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	10	2	2	2	230	26.166	4.92	89.4	88.6	116.6	105.4	89	111	1.24719	0.119554
Q05209	PTPN12	Tyrosine-protein phosphatase non- receptor type 12 OS=Homo sapiens GN=PTPN12 PE=1 SV=3	3.333333333	2	2	2	780	88.051	5.62	86.7	91.3	117.4	104.6	89	111	1.24719	0.119554
Q15785	TOMM3 4	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2	20.38834951	5	5	5	309	34.538	8.98	85.5	92.5	118.5	103.5	89	111	1.24719	0.119554
B2R5M8		Isocitrate dehydrogenase [NADP] OS=Homo sapiens PE=2 SV=1	44.20289855	17	27	16	414	46.619	7.01	92.4	85.6	115.9	106	89	110.95	1.24663	0.120371
O95861	BPNT1	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1	11.68831169	3	4	3	308	33.371	5.69	85.4	92.6	117.2	104.7	89	110.95	1.24663	0.120371
Q86SZ2	TRAPP C6B	Trafficking protein particle complex subunit 6B OS=Homo sapiens GN=TRAPPC6B PE=1 SV=1	8.860759494	1	1	1	158	17.971	8.68	84.3	93.7	107.2	114.7	89	110.95	1.24663	0.120371
Q9BY32	ITPA	Inosine triphosphate pyrophosphatase OS=Homo sapiens GN=ITPA PE=1 SV=2	12.37113402	2	2	2	194	21.432	5.66	92.9	85.2	120.5	101.5	89.05	111	1.24649	0.120573

P46926	GNPDA 1	Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1	16.60899654	4	6	4	289	32.648	6.92	91.4	86.7	112.4	109.5	89.05	110.95	1.24593	0.121396
Q9HBM1	SPC25	Kinetochores protein Spc25 OS=Homo sapiens GN=SPC25 PE=1 SV=1	4.910714286	1	1	1	224	26.137	8	92.4	85.7	117	104.9	89.05	110.95	1.24593	0.121396
Q9UHV9	PFDN2	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=1 SV=1	29.22077922	4	5	4	154	16.638	6.58	91.2	86.9	119	102.9	89.05	110.95	1.24593	0.121396
P09758	TACSTD 2	Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3	11.14551084	3	3	3	323	35.687	8.87	86.4	91.7	116.2	105.7	89.05	110.95	1.24593	0.121396
Q8N2H3	PYROX D2	Pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2 OS=Homo sapiens GN=PYROXD2 PE=1 SV=2	4.475043029	2	2	2	581	63.027	6.95	93.8	84.3	120.1	101.7	89.05	110.9	1.24537	0.122224
O15371	EIF3D	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	39.7810219	14	23	14	548	63.932	6.05	93.2	85	112	109.8	89.1	110.9	1.24467	0.12326
Q8IZ83	ALDH16 A1	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2	10.8478803	7	9	7	802	85.074	6.79	92.3	85.9	114.5	107.3	89.1	110.9	1.24467	0.12326
O75146	HIP1R	Huntingtin-interacting protein 1- related protein OS=Homo sapiens GN=HIP1R PE=1 SV=2	6.27340824	6	7	6	1068	119.315	6.67	92.1	86.1	111.9	109.9	89.1	110.9	1.24467	0.12326
Q96IZ0	PAWR	PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1	12.94117647	3	5	3	340	36.545	5.41	87.7	90.5	110.6	111.2	89.1	110.9	1.24467	0.12326
D6W4Z6	hCG_23 833	HCG23833, isoform CRA_b OS=Homo sapiens GN=hCG_23833 PE=4 SV=1	22.27171492	7	10	7	449	51.044	6.57	84.6	93.6	116.3	105.5	89.1	110.9	1.24467	0.12326
Q14232	EIF2B1	Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=1 SV=1	27.21311475	7	8	7	305	33.691	7.33	89.3	88.9	109.3	112.4	89.1	110.85	1.24411	0.124098

Q6MZT3	DKFZp686C1054	Putative uncharacterized protein DKFZp686C1054 OS=Homo sapiens GN=DKFZp686C1054 PE=2 SV=1	13.2118451	5	5	5	439	48.46	8.92	94.8	83.5	113.2	108.6	89.15	110.9	1.24397	0.124303
P14735	IDE	Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	17.66437684	16	22	16	1019	117.893	6.61	92.3	86	114.4	107.3	89.15	110.85	1.24341	0.125147
Q13596	SNX1	Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3	20.30651341	9	12	7	522	59.033	5.15	88.6	89.7	113.7	108	89.15	110.85	1.24341	0.125147
A0A0J9YXC7	LIMS4	LIM and senescent cell antigen-like-containing domain protein 3 OS=Homo sapiens GN=LIMS4 PE=1 SV=1	3.015075377	1	2	1	398	45.694	7.88	92.2	86.1	118.5	103.2	89.15	110.85	1.24341	0.125147
Q8WUP2	FBLIM1	Filamin-binding LIM protein 1 OS=Homo sapiens GN=FBLIM1 PE=1 SV=2	2.680965147	1	1	1	373	40.643	6.02	82.1	96.2	114.8	106.9	89.15	110.85	1.24341	0.125147
H7BY58	PCMT1	Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=1	31.11888112	7	8	7	286	30.339	6.73	85.8	92.6	112.3	109.4	89.2	110.85	1.24271	0.126201
A8K7F6		cDNA FLJ78244, highly similar to Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA OS=Homo sapiens PE=2 SV=1	43.10344828	16	40	8	406	46.093	5.48	92.2	86.2	116.5	105.2	89.2	110.85	1.24271	0.126201
P55263	ADK	Adenosine kinase OS=Homo sapiens GN=ADK PE=1 SV=2	9.392265193	3	3	3	362	40.52	6.7	91.9	86.5	115.2	106.4	89.2	110.8	1.24215	0.127055
Q59FI4		Importin 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	9.57278481	10	12	10	1264	138.112	5.25	91	87.4	106	115.6	89.2	110.8	1.24215	0.127055
O96007	MOCS2	Molybdopterin synthase catalytic subunit OS=Homo sapiens GN=MOCS2 PE=1 SV=1	7.978723404	1	2	1	188	20.931	5.44	86.3	92.1	118	103.6	89.2	110.8	1.24215	0.127055
A0A087WY96	SLC6A6	Transporter OS=Homo sapiens GN=SLC6A6 PE=1 SV=1	1.248266297	1	1	1	721	81.286	8.78	93.9	84.5	104.3	117.2	89.2	110.75	1.24159	0.127914

Q9H1E3	NUCKS 1	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens GN=NUCKS1 PE=1 SV=1	14.81481481	4	9	4	243	27.28	5.08	96.9	81.6	113.4	108.2	89.25	110.8	1.24146	0.128122
A9UFC0	CASP14	Caspase 14 OS=Homo sapiens GN=CASP14 PE=2 SV=1	6.198347107	1	1	1	242	27.649	5.34	92.3	86.2	97.4	124.2	89.25	110.8	1.24146	0.128122
Q9P2S2	NRXN2	Neurexin-2 OS=Homo sapiens GN=NRXN2 PE=2 SV=1	0.408878505	1	1	1	1712	184.865	5.92	86.6	91.9	111.1	110.4	89.25	110.75	1.2409	0.128986
A0A024Q YW6	WDR45	WD repeat domain 45, isoform CRA_c OS=Homo sapiens GN=WDR45 PE=4 SV=1	2.69541779	1	1	1	371	41.018	7.24	85.2	93.3	111.4	110.1	89.25	110.75	1.2409	0.128986
Q9BW83	IFT27	Intraflagellar transport protein 27 homolog OS=Homo sapiens GN=IFT27 PE=1 SV=1	8.602150538	1	1	1	186	20.467	5.41	91.2	87.3	116.3	105.2	89.25	110.75	1.2409	0.128986
A8K9A5		cDNA FLJ78114, highly similar to Homo sapiens thymidylate synthetase, mRNA OS=Homo sapiens PE=2 SV=1	12.4600639	3	3	3	313	35.792	7.24	83.5	95	113.1	108.4	89.25	110.75	1.2409	0.128986
Q53G35		Phosphoglycerate mutase (Fragment) OS=Homo sapiens PE=2 SV=1	53.1496063	10	29	10	254	28.814	7.18	86.1	92.4	110.6	110.8	89.25	110.7	1.24034	0.129855
B0YIW6	ARCN1	Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=1 SV=1	29.71014493	15	23	15	552	61.587	5.85	91.6	87	111.9	109.5	89.3	110.7	1.23964	0.130939
P53041	PPP5C	Serine/threonine-protein phosphatase 5 OS=Homo sapiens GN=PPP5C PE=1 SV=1	12.8256513	5	7	5	499	56.842	6.28	89.9	88.7	114.6	106.8	89.3	110.7	1.23964	0.130939
B2RA10	HOMER 3	Homer homolog 3 (Drosophila), isoform CRA_b OS=Homo sapiens GN=HOMER3 PE=1 SV=1	12.46537396	3	3	3	361	39.881	5.55	89.1	89.5	113.4	108	89.3	110.7	1.23964	0.130939
O95373	IPO7	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	11.65703276	10	20	10	1038	119.44	4.82	95.4	83.2	115.8	105.6	89.3	110.7	1.23964	0.130939

B7ZKN5	UTX	UTX protein OS=Homo sapiens GN=UTX PE=2 SV=1	1.445285616	2	2	2	1453	159.714	7.68	91	87.6	94.2	127.2	89.3	110.7	1.23964	0.130939
A0A024R9 G4	FAM49B	Family with sequence similarity 49, member B, isoform CRA_a OS=Homo sapiens GN=FAM49B PE=4 SV=1	25.30864198	6	8	6	324	36.725	6.06	88.7	89.9	105.2	116.2	89.3	110.7	1.23964	0.130939
F5H1S1	PIGB	Mannosyltransferase OS=Homo sapiens GN=PIGB PE=1 SV=2	3.423423423	2	2	2	555	65.128	9.29	84.4	94.2	125.9	95.5	89.3	110.7	1.23964	0.130939
Q2QL34	MPV17L	Mpv17-like protein OS=Homo sapiens GN=MPV17L PE=1 SV=1	5.102040816	1	1	1	196	22.101	9.89	83.1	95.5	110.3	111.1	89.3	110.7	1.23964	0.130939
Q9Y4A1		Talin-related protein (Fragment) OS=Homo sapiens PE=2 SV=1	7.179487179	2	3	1	195	20.157	4.81	87.4	91.3	113.3	108.1	89.35	110.7	1.23895	0.13203
A0A0S2Z3 81	ADA	Adenosine deaminase isoform 1 (Fragment) OS=Homo sapiens GN=ADA PE=2 SV=1	4.132231405	2	2	2	363	40.739	5.95	93.9	84.8	112.6	108.7	89.35	110.65	1.23839	0.132915
Q15181	PPA1	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	32.1799308	8	15	7	289	32.639	5.86	92.4	86.3	114.4	106.9	89.35	110.65	1.23839	0.132915
A0A0S2Z4 97	PEX19	Peroxisomal biogenesis factor 19 isoform 1 (Fragment) OS=Homo sapiens GN=PEX19 PE=2 SV=1	16.72240803	4	6	3	299	32.786	4.34	87.7	91	113.7	107.6	89.35	110.65	1.23839	0.132915
Q8WV60	PTCD2	Pentatricopeptide repeat- containing protein 2, mitochondrial OS=Homo sapiens GN=PTCD2 PE=1 SV=3	5.412371134	2	2	2	388	43.939	9.23	90.9	87.8	104.3	117	89.35	110.65	1.23839	0.132915
H0YNJ6	GMPR2	GMP reductase OS=Homo sapiens GN=GMPR2 PE=1 SV=1	6.791569087	3	3	3	427	46.908	8.51	90	88.7	116.6	104.7	89.35	110.65	1.23839	0.132915
Q06124	PTPN11	Tyrosine-protein phosphatase non- receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2	5.862646566	3	4	3	597	68.393	7.3	86	92.7	119.4	101.9	89.35	110.65	1.23839	0.132915
E9PGC5	PTPRK	Receptor-type tyrosine-protein phosphatase kappa OS=Homo sapiens GN=PTPRK PE=1 SV=1	2.921195652	4	4	4	1472	165.922	5.91	84.2	94.5	106.5	114.8	89.35	110.65	1.23839	0.132915

P06454	PTMA	Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2	12.61261261	1	5	1	111	12.196	3.78	87.9	90.9	111.6	109.5	89.4	110.55	1.23658	0.135815
Q9BTE3	MCMBP	Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2	10.28037383	5	5	5	642	72.934	5.87	90.8	88.1	115.7	105.5	89.45	110.6	1.23644	0.136029
Q9NRY2	INIP	SOSS complex subunit C OS=Homo sapiens GN=INIP PE=1 SV=1	11.53846154	1	1	1	104	11.418	9.25	86.3	92.6	104.3	116.9	89.45	110.6	1.23644	0.136029
P04424	ASL	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4	4.310344828	1	1	1	464	51.625	6.48	93.6	85.3	111.4	109.7	89.45	110.55	1.23589	0.136936
Q9BQ61	C19orf43	Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=1 SV=1	13.63636364	3	4	3	176	18.408	9.44	92.7	86.2	112.2	108.9	89.45	110.55	1.23589	0.136936
B2RDE8		cDNA, FLJ96580, highly similar to Homo sapiens hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA OS=Homo sapiens PE=2 SV=1	38.33333333	9	17	8	240	26.789	4.67	100.5	78.4	116.2	104.9	89.45	110.55	1.23589	0.136936
Q9NR19	ACSS2	Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens GN=ACSS2 PE=1 SV=1	7.132667618	3	4	3	701	78.529	6.46	96.5	82.4	116.1	105	89.45	110.55	1.23589	0.136936
V9HW62	HEL-S-74	Lactoylglutathione lyase OS=Homo sapiens GN=HEL-S-74 PE=2 SV=1	50	9	11	9	184	20.706	5.47	92.4	86.5	115.4	105.6	89.45	110.5	1.23533	0.137848
Q13829	TNFAIP1	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 2 OS=Homo sapiens GN=TNFAIP1 PE=1 SV=1	15.18987342	3	4	2	316	36.181	8.03	95.7	83.3	116.4	104.7	89.5	110.55	1.2352	0.138063
A0A024RDE8	PDLIM5	PDZ and LIM domain 5, isoform CRA_c OS=Homo sapiens GN=PDLIM5 PE=4 SV=1	26.84563758	12	17	12	596	63.935	8.21	89.6	89.4	112.6	108.4	89.5	110.5	1.23464	0.138981

Q7Z4G1	COMMD6	COMM domain-containing protein 6 OS=Homo sapiens GN=COMMD6 PE=1 SV=1	38.82352941	3	3	3	85	9.632	6	87.1	91.9	108.7	112.3	89.5	110.5	1.23464	0.138981
Q9UP83	COG5	Conserved oligomeric Golgi complex subunit 5 OS=Homo sapiens GN=COG5 PE=1 SV=3	2.026221692	2	2	2	839	92.685	6.6	94.9	84.1	120.4	100.6	89.5	110.5	1.23464	0.138981
Q9Y3B8	REXO2	Oligoribonuclease, mitochondrial OS=Homo sapiens GN=REXO2 PE=1 SV=3	34.17721519	6	6	6	237	26.816	6.87	87.7	91.3	117.9	103.1	89.5	110.5	1.23464	0.138981
A0A024R DG1	VDP	Vesicle docking protein p115, isoform CRA_a OS=Homo sapiens GN=VDP PE=4 SV=1	20.89397089	17	28	17	962	107.828	4.91	90.2	88.8	111.8	109.1	89.5	110.45	1.23408	0.139904
G1JTE6	MICA	MHC class I chain-related protein A (Fragment) OS=Homo sapiens GN=MICA PE=4 SV=1	12.5	5	7	5	384	42.94	6.76	87.2	91.8	107.7	113.2	89.5	110.45	1.23408	0.139904
Q7Z2Z2	EFL1	Elongation factor-like GTPase 1 OS=Homo sapiens GN=EFL1 PE=1 SV=2	5.446428571	6	6	6	1120	125.35	5.91	91.5	87.6	116.7	104.3	89.55	110.5	1.23395	0.14012
Q59ER5		WD repeat-containing protein 1 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	30.28846154	11	14	11	624	68.128	7.23	92	87.1	112	108.9	89.55	110.45	1.23339	0.141049
V9HW37	HEL-S- 69	Epididymis secretory protein Li 69 OS=Homo sapiens GN=HEL-S-69 PE=1 SV=1	44.36229205	20	42	19	541	59.633	5.66	90.8	88.3	108.4	112.5	89.55	110.45	1.23339	0.141049
Q86UA3	C12orf1 0	Chromosome 12 open reading frame 10 OS=Homo sapiens GN=C12orf10 PE=1 SV=1	18.88297872	6	6	6	376	42.482	6.84	88.9	90.2	112.7	108.2	89.55	110.45	1.23339	0.141049
A0A024R5 71	EHD1	EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=1	37.04379562	16	19	14	548	61.888	6.71	86.4	92.7	112.2	108.7	89.55	110.45	1.23339	0.141049
Q15942	ZYX	Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1	11.71328671	6	8	6	572	61.238	6.67	84.8	94.3	110.3	110.6	89.55	110.45	1.23339	0.141049

Q86X55	CARM1	Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=3	4.934210526	3	3	3	608	65.811	6.73	85.3	93.8	120.1	100.8	89.55	110.45	1.23339	0.141049
A4D0U5	TES	Testis derived transcript (3 LIM domains) OS=Homo sapiens GN=TES PE=4 SV=1	38.47980998	12	18	12	421	47.964	7.68	84.6	94.5	112.6	108.3	89.55	110.45	1.23339	0.141049
Q9Y547	HSPB11	Intraflagellar transport protein 25 homolog OS=Homo sapiens GN=HSPB11 PE=1 SV=1	27.77777778	3	5	3	144	16.287	5.03	93.8	85.3	115.7	105.1	89.55	110.4	1.23283	0.141983
J3KQ32	OLA1	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=1	19.95192308	8	11	8	416	46.908	8.06	91.5	87.7	109.4	111.5	89.6	110.45	1.2327	0.1422
B2R9K8		cDNA, FLJ94440, highly similar to Homo sapiens chaperonin containing TCP1, subunit 6A (zeta 1)(CCT6A), mRNA OS=Homo sapiens PE=2 SV=1	36.15819209	18	29	18	531	57.93	6.8	90.9	88.3	112.1	108.7	89.6	110.4	1.23214	0.14314
Q99615	DNAJC7	DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7 PE=1 SV=2	32.59109312	15	19	15	494	56.405	6.96	85.5	93.7	111.4	109.4	89.6	110.4	1.23214	0.14314
A0A0F7G 8J1	PLG	Plasminogen OS=Homo sapiens GN=PLG PE=2 SV=1	4.57354759	4	7	2	809	90.569	7.36	89.7	89.5	104	116.8	89.6	110.4	1.23214	0.14314
Q9BVG3	TRIM62	E3 ubiquitin-protein ligase TRIM62 OS=Homo sapiens GN=TRIM62 PE=1 SV=1	1.473684211	1	1	1	475	54.233	6.62	96	83.3	115	105.8	89.65	110.4	1.23146	0.144304
P28325	CST5	Cystatin-D OS=Homo sapiens GN=CST5 PE=1 SV=1	4.929577465	1	2	1	142	16.07	7.17	90.7	88.6	117.9	102.9	89.65	110.4	1.23146	0.144304
P23528	CFL1	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	63.85542169	10	28	8	166	18.491	8.09	90.4	88.9	113.4	107.3	89.65	110.35	1.2309	0.145255
Q15417	CNN3	Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1	11.55015198	3	3	2	329	36.391	6.05	89.8	89.5	106.5	114.2	89.65	110.35	1.2309	0.145255
Q9NZ63	C9orf78	Uncharacterized protein C9orf78 OS=Homo sapiens GN=C9orf78 PE=1 SV=1	17.64705882	5	5	5	289	33.667	6.74	93.5	85.8	116.9	103.8	89.65	110.35	1.2309	0.145255

A8K8U1		cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens PE=2 SV=1	26.58536585	29	37	27	1230	136.231	5.83	92.1	87.2	117	103.7	89.65	110.35	1.2309	0.145255
O95999	BCL10	B-cell lymphoma/leukemia 10 OS=Homo sapiens GN=BCL10 PE=1 SV=1	7.725321888	2	2	2	233	26.235	5.74	89	90.3	100.5	120.2	89.65	110.35	1.2309	0.145255
B5BUC0	GSK3B	Glycogen synthase kinase-3 beta (Fragment) OS=Homo sapiens GN=GSK3B PE=2 SV=1	15	5	5	1	420	46.669	8.87	84.9	94.4	111.9	108.7	89.65	110.3	1.23034	0.146211
P12004	PCNA	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	52.87356322	12	29	12	261	28.75	4.69	97	82.4	117	103.7	89.7	110.35	1.23021	0.146432
B0YIW2	APOC3	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1	13.67521368	1	2	1	117	12.807	8.18	78.1	101.3	101.2	119.5	89.7	110.35	1.23021	0.146432
O75369	FLNB	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	53.72790161	104	230	97	2602	277.99	5.73	92.1	87.3	112.4	108.2	89.7	110.3	1.22965	0.147393
Q9NZN4	EHD2	EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	17.86372007	9	11	8	543	61.123	6.46	92.2	87.2	115.6	105	89.7	110.3	1.22965	0.147393
Q96LW7	CARD19	Caspase recruitment domain-containing protein 19 OS=Homo sapiens GN=CARD19 PE=1 SV=1	10.0877193	2	2	2	228	25.573	9.2	89.8	89.6	129.6	91	89.7	110.3	1.22965	0.147393
A0A0S2Z4 B5	PPP3CA	Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP3CA PE=2 SV=1	11.93737769	6	6	6	511	57.622	6.3	92.9	86.6	113.4	107.1	89.75	110.25	1.22841	0.149556
Q8TE77	SSH3	Protein phosphatase Slingshot homolog 3 OS=Homo sapiens GN=SSH3 PE=1 SV=2	1.820940819	1	1	1	659	72.951	5.3	86.6	92.9	116.1	104.4	89.75	110.25	1.22841	0.149556

P36507	MAP2K2	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	15	6	8	3	400	44.396	6.55	84.9	94.6	114.7	105.8	89.75	110.25	1.22841	0.149556
Q99426	TBCB	Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2	9.016393443	2	2	2	244	27.308	5.15	82.2	97.3	115	105.5	89.75	110.25	1.22841	0.149556
P05362	ICAM1	Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=1 SV=2	16.35338346	6	8	6	532	57.789	7.99	91.1	88.4	105.7	114.7	89.75	110.2	1.22786	0.150534
A8K3B6		Tyrosine-protein kinase OS=Homo sapiens PE=2 SV=1	7.555555556	4	4	4	450	50.67	7.06	90.6	88.9	112.8	107.6	89.75	110.2	1.22786	0.150534
A0AVF1	TTC26	Intraflagellar transport protein 56 OS=Homo sapiens GN=TTC26 PE=2 SV=1	3.610108303	1	1	1	554	64.136	6.93	90.5	89.1	115.5	105	89.8	110.25	1.22773	0.150758
Q7L9L4	MOB1B	MOB kinase activator 1B OS=Homo sapiens GN=MOB1B PE=1 SV=3	8.796296296	2	2	2	216	25.075	6.73	81.1	98.5	107.2	113.3	89.8	110.25	1.22773	0.150758
P34896	SHMT1	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1	12.42236025	4	8	4	483	53.049	7.71	95.2	84.4	113.1	107.3	89.8	110.2	1.22717	0.151742
P67775	PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1	51.45631068	11	19	2	309	35.571	5.54	92.3	87.3	115.4	105	89.8	110.2	1.22717	0.151742
A0A0A0M SG2	FHL2	Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=1	41.26582278	14	20	14	395	44.808	8.06	85.4	94.2	103.3	117.1	89.8	110.2	1.22717	0.151742
Q6AI08	HEATR6	HEAT repeat-containing protein 6 OS=Homo sapiens GN=HEATR6 PE=1 SV=1	0.931414056	1	1	1	1181	128.699	7.03	83.8	95.8	115.5	104.9	89.8	110.2	1.22717	0.151742
Q5T4S7	UBR4	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	6.463438163	25	35	25	5183	573.476	6.04	88.9	90.7	114.2	106.1	89.8	110.15	1.22661	0.152731

P62258	YWHAE	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	74.50980392	18	64	16	255	29.155	4.74	91.5	88.2	113.8	106.6	89.85	110.2	1.22649	0.152956
Q96Q05	TRAPP C9	Trafficking protein particle complex subunit 9 OS=Homo sapiens GN=TRAPPC9 PE=1 SV=2	2.613240418	2	2	2	1148	128.449	6.62	85.3	94.4	106.4	114	89.85	110.2	1.22649	0.152956
Q9H4A4	RNPEP	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2	25.53846154	15	20	15	650	72.549	5.74	94.1	85.6	116.7	103.6	89.85	110.15	1.22593	0.153952
Q8TDJ5	TFG/ALK	Tyrosine-protein kinase receptor OS=Homo sapiens GN=TFG/ALK fusion PE=2 SV=1	15.06849315	9	16	9	803	88.615	6.33	93.6	86.1	117.8	102.5	89.85	110.15	1.22593	0.153952
A8K7Z3		cDNA FLJ77229, highly similar to Homo sapiens GRIP1 associated protein 1 (GRIPAP1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	11.77170036	8	10	8	841	95.932	5.07	92.3	87.4	119.3	101	89.85	110.15	1.22593	0.153952
E9PSG9	POLR2M	DNA-directed RNA polymerase II subunit GRINL1A, isoforms 4/5 OS=Homo sapiens GN=POLR2M PE=4 SV=1	8.176100629	1	1	1	159	16.161	8.21	86.4	93.3	115	105.3	89.85	110.15	1.22593	0.153952
A0A024R1X5	BECN1	Beclin 1 (Coiled-coil, myosin-like BCL2 interacting protein), isoform CRA_b OS=Homo sapiens GN=BECN1 PE=2 SV=1	2.222222222	1	1	1	450	51.863	4.89	87.4	92.3	106.6	113.6	89.85	110.1	1.22538	0.154953
A8K0G7		cDNA FLJ78425, highly similar to Homo sapiens zinc fingers and homeoboxes 1 (ZHX1), mRNA OS=Homo sapiens PE=2 SV=1	1.26002291	1	1	1	873	98.012	5.91	99.2	80.6	118.9	101.4	89.9	110.15	1.22525	0.155179
Q9P1Z2	CALCO CO1	Calcium-binding and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=CALCOCO1 PE=1 SV=2	2.170767004	1	2	1	691	77.289	4.82	70.7	109.1	99.3	121	89.9	110.15	1.22525	0.155179
Q6PIJ6	FBXO38	F-box only protein 38 OS=Homo sapiens GN=FBXO38 PE=1 SV=3	2.525252525	2	2	2	1188	133.858	6.33	94	85.8	109.6	110.6	89.9	110.1	1.22469	0.156186

Q8NBP7	PCSK9	Proprotein convertase subtilisin/kexin type 9 OS=Homo sapiens GN=PCSK9 PE=1 SV=3	15.31791908	9	10	9	692	74.239	6.61	93.9	85.9	111.2	109	89.9	110.1	1.22469	0.156186
Q9Y5B8	NME7	Nucleoside diphosphate kinase 7 OS=Homo sapiens GN=NME7 PE=1 SV=1	6.382978723	2	2	2	376	42.464	6.47	91.6	88.2	110.8	109.4	89.9	110.1	1.22469	0.156186
Q53FE8		cDNA FLJ36526 fis, clone TRACH2003347, highly similar to NSFL1 cofactor p47 (Fragment) OS=Homo sapiens PE=2 SV=1	25.94594595	7	9	7	370	40.547	5.14	87.8	92	113.7	106.5	89.9	110.1	1.22469	0.156186
Q7L5N1	COPS6	COP9 signalosome complex subunit 6 OS=Homo sapiens GN=COPS6 PE=1 SV=1	36.39143731	9	12	9	327	36.14	5.73	93.8	86	114.5	105.7	89.9	110.1	1.22469	0.156186
Q9NP77	SSU72	RNA polymerase II subunit A C-terminal domain phosphatase SSU72 OS=Homo sapiens GN=SSU72 PE=1 SV=1	5.154639175	1	1	1	194	22.56	5.33	93.7	86.1	127.6	92.6	89.9	110.1	1.22469	0.156186
P51797	CLCN6	Chloride transport protein 6 OS=Homo sapiens GN=CLCN6 PE=1 SV=2	1.726121979	1	1	1	869	97.225	6.81	88.9	90.9	120.3	99.9	89.9	110.1	1.22469	0.156186
E9PL57	NEDD8-MDP1	Protein NEDD8-MDP1 (Fragment) OS=Homo sapiens GN=NEDD8-MDP1 PE=4 SV=1	6.470588235	1	1	1	170	19.524	7.43	100.8	79	115.6	104.5	89.9	110.05	1.22414	0.157199
O14929	HAT1	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1	19.80906921	7	11	7	419	49.481	5.69	89.5	90.3	118.2	101.9	89.9	110.05	1.22414	0.157199
A0A0B4J1R4	HPD	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=1	13.99491094	4	4	4	393	44.936	7.01	88.6	91.3	109.8	110.4	89.95	110.1	1.22401	0.157426
B0QY89	EIF3L	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	17.79242175	11	17	11	607	70.857	6.65	95	84.9	112.4	107.8	89.95	110.1	1.22401	0.157426

A0A161I202	LTF	Lactoferrin OS=Homo sapiens GN=LTF PE=2 SV=1	2.953586498	2	5	2	711	78.288	8.18	88.3	91.6	103.8	116.4	89.95	110.1	1.22401	0.157426
Q9Y3D8	AK6	Adenylate kinase isoenzyme 6 OS=Homo sapiens GN=AK6 PE=1 SV=1	5.23255814	1	1	1	172	20.049	4.58	89.6	90.3	114.6	105.5	89.95	110.05	1.22346	0.158445
Q13439	GOLGA4	Golgin subfamily A member 4 OS=Homo sapiens GN=GOLGA4 PE=1 SV=1	16.50224215	34	40	34	2230	260.98	5.39	88.9	91	111.4	108.7	89.95	110.05	1.22346	0.158445
A0A0K1H1B1	DDX60L	Putative ATP-dependent RNA helicase DDX60 OS=Homo sapiens GN=DDX60L PE=2 SV=1	1.348182884	2	2	2	1706	197.569	8.29	87.1	92.8	113.5	106.6	89.95	110.05	1.22346	0.158445
A0A0U1R6	ENAH	Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=1	5.36159601	3	4	3	802	87.346	7.77	97.9	82	113.4	106.7	89.95	110.05	1.22346	0.158445
Q5T9B7	AK1	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=1	8.571428571	2	2	2	210	23.396	8.6	84.5	95.4	111.4	108.7	89.95	110.05	1.22346	0.158445
Q9NRN7	AASDH PPT	L-aminoadipate-semialdehyde dehydrogenase- phosphopantetheinyl transferase OS=Homo sapiens GN=AASDH PPT PE=1 SV=2	9.061488673	2	2	2	309	35.753	6.8	88.9	91.1	112.6	107.4	90	110	1.22222	0.160728
B4E0Y9	STK26	Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=1	31.27853881	11	14	5	438	49.153	5.68	90.9	89.1	117.2	102.8	90	110	1.22222	0.160728
B8ZWD9	DBI	Diazepam binding inhibitor, splice form 1D(2) OS=Homo sapiens GN=DBI PE=2 SV=1	38.19444444	5	11	5	144	16.1	5.05	82.7	97.3	114.5	105.4	90	109.95	1.22167	0.161763
A0A024R718	PBEF1	Pre-B-cell colony enhancing factor 1, isoform CRA_a OS=Homo sapiens GN=PBEF1 PE=4 SV=1	20.97759674	8	8	8	491	55.487	7.15	96.6	83.5	113.4	106.6	90.05	110	1.22154	0.161994
A0A024R3L9	VPS26B	Vacuolar protein sorting 26 homolog B (Yeast), isoform CRA_a	5.952380952	2	2	1	336	39.13	7.36	93.8	86.3	115	105	90.05	110	1.22154	0.161994

		OS=Homo sapiens GN=VPS26B PE=4 SV=1																
Q8TEY7	USP33	Ubiquitin carboxyl-terminal hydrolase 33 OS=Homo sapiens GN=USP33 PE=1 SV=2	6.794055202	4	5	4	942	106.659	6.02	92.6	87.5	109.5	110.4	90.05	109.95	1.22099	0.163035	
Q5VYK3	ECM29	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	14.09214092	19	23	19	1845	204.16	7.12	97	83.1	114	105.9	90.05	109.95	1.22099	0.163035	
O15357	INPPL1	Phosphatidylinositol 3,4,5- trisphosphate 5-phosphatase 2 OS=Homo sapiens GN=INPPL1 PE=1 SV=2	8.585055644	9	9	9	1258	138.513	6.54	90.3	89.8	115	104.9	90.05	109.95	1.22099	0.163035	
Q9Y244	POMP	Proteasome maturation protein OS=Homo sapiens GN=POMP PE=1 SV=1	5.673758865	1	1	1	141	15.779	5.11	86.5	93.6	114.4	105.4	90.05	109.9	1.22043	0.164083	
K7EQB2	GLYR1	Putative oxidoreductase GLYR1 (Fragment) OS=Homo sapiens GN=GLYR1 PE=1 SV=8	24.32432432	4	6	1	185	20.46	9.54	83.7	96.5	111.4	108.5	90.1	109.95	1.22031	0.164314	
Q96T51	RUFY1	RUN and FYVE domain-containing protein 1 OS=Homo sapiens GN=RUFY1 PE=1 SV=2	25.70621469	15	18	15	708	79.767	5.74	86.8	93.4	112.1	107.7	90.1	109.9	1.21976	0.165368	
A0A024R A80	TXNDC3	Thioredoxin domain containing 3 (Spermatozoa), isoform CRA_a OS=Homo sapiens GN=TXNDC3 PE=4 SV=1	1.19047619	1	1	1	588	67.199	4.97	101.6	78.6	116.9	102.9	90.1	109.9	1.21976	0.165368	
Q13643	FHL3	Four and a half LIM domains protein 3 OS=Homo sapiens GN=FHL3 PE=1 SV=4	13.21428571	2	3	2	280	31.171	6.2	94.7	85.5	111.2	108.6	90.1	109.9	1.21976	0.165368	
Q16186	ADRM1	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2	16.46191646	5	6	5	407	42.127	5.07	93.2	87	114	105.8	90.1	109.9	1.21976	0.165368	
B2R9W9		Craniofacial development protein 1 OS=Homo sapiens PE=2 SV=1	2.675585284	1	1	1	299	33.587	4.81	92.2	88	116.9	102.9	90.1	109.9	1.21976	0.165368	

E7EWW0	C16orf6 2	UPF0505 protein C16orf62 OS=Homo sapiens GN=C16orf62 PE=1 SV=2	1.140684411	1	1	1	1052	118.537	7.84	83.7	96.5	111.7	108.1	90.1	109.9	1.21976	0.165368
A0A024R9 30	PRG4	Proteoglycan 4, isoform CRA_a OS=Homo sapiens GN=PRG4 PE=4 SV=1	0.783475783	1	1	1	1404	150.984	9.5	82.6	97.6	91.5	128.3	90.1	109.9	1.21976	0.165368
A0A024R8 06	MGC109 11	Uncharacterized protein OS=Homo sapiens GN=MGC10911 PE=4 SV=1	18.85245902	2	2	2	122	13.096	7.88	92.1	88.1	113.9	105.8	90.1	109.85	1.2192	0.166427
P40261	NNMT	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	20.83333333	4	6	4	264	29.555	5.74	84.7	95.6	112.4	107.4	90.15	109.9	1.21908	0.166659
D6REX3	SEC31A	Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=1	13.7490008	16	20	16	1251	136.141	6.98	91.9	88.4	113.7	106	90.15	109.85	1.21852	0.167725
Q15057	ACAP2	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ACAP2 PE=1 SV=3	10.41131105	7	7	7	778	87.973	6.8	90.3	90	113.4	106.3	90.15	109.85	1.21852	0.167725
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	80.59701493	24	214	24	335	36.03	8.46	87.9	92.4	113.2	106.5	90.15	109.85	1.21852	0.167725
A0A0C4D GB5	CAST	Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=1	32.75862069	19	38	1	754	80.95	5.1	91.1	89.2	114.7	105	90.15	109.85	1.21852	0.167725
Q8N4V1	MMGT1	Membrane magnesium transporter 1 OS=Homo sapiens GN=MMGT1 PE=1 SV=1	23.66412214	2	6	2	131	14.677	9.16	73.2	107.1	108.1	111.6	90.15	109.85	1.21852	0.167725
A8K8N7	PFAS	Phosphoribosylformylglycinamide synthase (FGAR amidotransferase), isoform CRA_b OS=Homo sapiens GN=PFAS PE=2 SV=1	12.63079223	13	13	13	1338	144.633	5.76	92.8	87.5	112	107.6	90.15	109.8	1.21797	0.168796

Q9Y4E8	USP15	Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 PE=1 SV=3	8.76656473	7	7	7	981	112.348	5.22	89.1	91.2	113.2	106.4	90.15	109.8	1.21797	0.168796
A8K2Z3		cDNA FLJ76092, highly similar to Homo sapiens 5'-nucleotidase, cytosolic II-like 1 (NT5C2L1), mRNA OS=Homo sapiens PE=2 SV=1	2.417582418	1	1	1	455	51.826	6.35	85.8	94.5	113.9	105.7	90.15	109.8	1.21797	0.168796
Q12929	EPS8	Epidermal growth factor receptor kinase substrate 8 OS=Homo sapiens GN=EPS8 PE=1 SV=1	4.622871046	3	3	3	822	91.824	7.5	86.3	94.1	108.3	111.3	90.2	109.8	1.21729	0.170106
O14737	PDCD5	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3	40	5	6	5	125	14.276	6.04	99.6	80.8	114	105.6	90.2	109.8	1.21729	0.170106
B4DRM3		cDNA FLJ54492, highly similar to Eukaryotic translation initiation factor 4B OS=Homo sapiens PE=2 SV=1	21.26623377	12	18	12	616	69.685	5.67	95	85.4	110.9	108.7	90.2	109.8	1.21729	0.170106
A0A024R3Z6	BZW1	Basic leucine zipper and W2 domains 1, isoform CRA_a OS=Homo sapiens GN=BZW1 PE=4 SV=1	30.7875895	15	32	12	419	48.013	5.92	94.2	86.2	117.3	102.3	90.2	109.8	1.21729	0.170106
Q0IIN1	KRT77	Keratin 77 OS=Homo sapiens GN=KRT77 PE=1 SV=1	11.5916955	7	17	2	578	61.764	5.85	83.7	96.7	122.3	97.3	90.2	109.8	1.21729	0.170106
F5H265	UBC	Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=1 SV=1	64.4295302	6	104	1	149	16.831	6.58	82.4	98	97.1	122.5	90.2	109.8	1.21729	0.170106
Q9Y490	TLN1	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	30.3030303	62	105	53	2541	269.599	6.07	90.1	90.4	111.7	107.9	90.25	109.8	1.21662	0.171425
A0A024RD93	PAICS	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase,	32.47058824	12	25	12	425	47.049	7.23	90.7	89.8	112.9	106.6	90.25	109.75	1.21607	0.172513

		isoform CRA_c OS=Homo sapiens GN=PAICS PE=3 SV=1																
Q53GE7		Tetratricopeptide repeat domain 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	23.63013699	6	8	6	292	33.574	4.88	89.6	90.9	112.5	107	90.25	109.75	1.21607	0.172513	
Q15642	TRIP10	Cdc42-interacting protein 4 OS=Homo sapiens GN=TRIP10 PE=1 SV=3	9.816971714	6	6	6	601	68.31	5.73	87.8	92.7	112.2	107.3	90.25	109.75	1.21607	0.172513	
A0A0S2Z4 89	PSMD12	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12, isoform CRA_a (Fragment) OS=Homo sapiens GN=PSMD12 PE=2 SV=1	32.01754386	11	18	11	456	52.871	7.65	95.5	85	114.3	105.2	90.25	109.75	1.21607	0.172513	
P61024	CKS1B	Cyclin-dependent kinases regulatory subunit 1 OS=Homo sapiens GN=CKS1B PE=1 SV=1	32.91139241	2	3	2	79	9.654	8.94	90.4	90.1	89.2	130.3	90.25	109.75	1.21607	0.172513	
Q12792	TWF1	Twinfilin-1 OS=Homo sapiens GN=TWF1 PE=1 SV=3	16.28571429	5	5	4	350	40.258	6.96	87.2	93.3	114	105.5	90.25	109.75	1.21607	0.172513	
A0A1B0G TU4	PXN	Paxillin OS=Homo sapiens GN=PXN PE=4 SV=1	3.977798335	2	3	2	1081	115.832	5.64	89.7	90.8	108.9	110.5	90.25	109.7	1.21551	0.173608	
O43707	ACTN4	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	60.59275521	49	166	34	911	104.788	5.44	97.4	83.2	109.7	109.8	90.3	109.75	1.21539	0.173844	
Q9Y3E8		CGI-150 protein OS=Homo sapiens PE=2 SV=1	17.26190476	7	9	7	504	54.977	8.7	92.4	88.2	113.9	105.6	90.3	109.75	1.21539	0.173844	
Q5SQP8	CTBP2	C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1	10.72124756	5	6	2	513	56.066	6.96	96.8	83.8	117.7	101.7	90.3	109.7	1.21484	0.174945	
H9ZYJ2	TXN	Thioredoxin OS=Homo sapiens GN=TXN PE=2 SV=1	40	5	15	5	105	11.73	4.92	86.8	93.8	111.7	107.6	90.3	109.65	1.21429	0.176052	
Q9Y4C2	TCAF1	TRPM8 channel-associated factor 1 OS=Homo sapiens GN=TCAF1 PE=1 SV=3	5.754614549	5	6	5	921	102.061	6.54	94	86.6	114.1	105.2	90.3	109.65	1.21429	0.176052	

A0A024R0 Q5	PPP1R1 3L	Protein phosphatase 1, regulatory (Inhibitor) subunit 13 like, isoform CRA_a OS=Homo sapiens GN=PPP1R13L PE=4 SV=1	11.11111111	8	8	8	828	89.036	6.81	85.2	95.4	110.9	108.4	90.3	109.65	1.21429	0.176052
A0A024R8 A9	USP20	Ubiquitin specific peptidase 20, isoform CRA_a OS=Homo sapiens GN=USP20 PE=3 SV=1	0.982532751	1	1	1	916	102.181	6.21	87.4	93.3	112.6	106.7	90.35	109.65	1.21361	0.177403
Q53EY9		F-box only protein 22 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	5.70719603	2	3	2	403	44.45	7.03	98.4	82.3	116	103.3	90.35	109.65	1.21361	0.177403
Q53Y51	DDT	D-dopachrome tautomerase OS=Homo sapiens GN=DDT PE=2 SV=1	38.98305085	4	7	4	118	12.704	7.3	96.4	84.3	119	100.3	90.35	109.65	1.21361	0.177403
F5H039	GPHN	Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1	6.393861893	3	3	3	782	84.681	5.73	95.8	84.9	111.8	107.5	90.35	109.65	1.21361	0.177403
Q9Y3P9	RABGA P1	Rab GTPase-activating protein 1 OS=Homo sapiens GN=RABGAP1 PE=1 SV=3	7.296538821	6	6	6	1069	121.66	5.25	90.8	89.9	118.9	100.4	90.35	109.65	1.21361	0.177403
A8KAM7		cDNA FLJ75421, highly similar to Homo sapiens lung seven transmembrane receptor 1 (LUSTR1) mRNA OS=Homo sapiens PE=2 SV=1	4.891304348	2	2	1	552	61.892	7.2	88.2	92.5	116.8	102.5	90.35	109.65	1.21361	0.177403
B5BU16	MAP2K6	Mitogen-activated protein kinase kinase 6 OS=Homo sapiens GN=MAP2K6 PE=2 SV=1	17.06586826	5	5	4	334	37.44	7.06	86.5	94.2	117.2	102.1	90.35	109.65	1.21361	0.177403
A0A087W TY1	POLR1D	DNA-directed RNA polymerases I and III subunit RPAC2 OS=Homo sapiens GN=POLR1D PE=1 SV=1	7.446808511	1	1	1	94	11.012	10.24	96.1	84.6	107.6	111.6	90.35	109.6	1.21306	0.178521
Q9Y4X5	ARIH1	E3 ubiquitin-protein ligase ARIH1 OS=Homo sapiens GN=ARIH1 PE=1 SV=2	12.38779174	6	6	6	557	64.076	5.08	88	92.8	106.3	113	90.4	109.65	1.21294	0.17876

A0A024R A52	PSMA2	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA2 PE=1 SV=1	43.16239316	7	12	7	234	25.882	7.43	97.4	83.4	114.6	104.7	90.4	109.65	1.21294	0.17876
Q13085	ACACA	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	12.36146633	23	26	23	2346	265.385	6.37	92.6	88.2	114.9	104.4	90.4	109.65	1.21294	0.17876
A0A024R3 94	CHORD C1	Cysteine and histidine-rich domain (CHORD)-containing 1, isoform CRA_c OS=Homo sapiens GN=CHORDC1 PE=4 SV=1	32.8313253	9	14	9	332	37.51	7.72	89.8	91	105.2	114	90.4	109.6	1.21239	0.179885
A0A109N GN6		Proteasome subunit alpha type OS=Homo sapiens PE=2 SV=1	51.0373444	8	19	8	241	26.394	4.79	98.2	82.6	113.7	105.5	90.4	109.6	1.21239	0.179885
Q9Y6Y0	IVNS1A BP	Influenza virus NS1A-binding protein OS=Homo sapiens GN=IVNS1ABP PE=1 SV=3	1.713395639	1	1	1	642	71.683	5.53	97.3	83.5	116.2	103	90.4	109.6	1.21239	0.179885
B0YJ89	RIOK3	RIO kinase 3 (Yeast), isoform CRA_a OS=Homo sapiens GN=RIOK3 PE=2 SV=1	6.358381503	2	2	2	519	59.055	5.76	96.5	84.3	113.7	105.5	90.4	109.6	1.21239	0.179885
Q59EB2		Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	4.756980352	4	4	4	967	109.498	7.33	90.5	90.3	110.3	108.8	90.4	109.55	1.21184	0.181016
Q92963	RIT1	GTP-binding protein Rit1 OS=Homo sapiens GN=RIT1 PE=1 SV=1	10.0456621	2	2	2	219	25.129	9.1	85.5	95.3	113.2	105.9	90.4	109.55	1.21184	0.181016
P08243	ASNS	Asparagine synthetase [glutamine- hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4	17.11229947	8	10	2	561	64.329	6.86	88.1	92.8	109.6	109.6	90.45	109.6	1.21172	0.181256
B2R6H7		cDNA, FLJ92955, highly similar to Homo sapiens transportin-SR (TRN-SR), mRNA OS=Homo sapiens PE=2 SV=1	7.908992416	6	9	6	923	104.164	5.57	92.9	88	112	107.1	90.45	109.55	1.21117	0.182394

Q9UBQ5	EIF3K	Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=1 SV=1	17.88990826	3	6	3	218	25.043	4.93	90	90.9	111.4	107.7	90.45	109.55	1.21117	0.182394
A8K5T7		cDNA FLJ75365, highly similar to Homo sapiens SUGT1B (SUGT1) mRNA OS=Homo sapiens PE=2 SV=1	29.04109589	8	9	8	365	41.026	5.16	89.9	91	109.8	109.3	90.45	109.55	1.21117	0.182394
Q02952	AKAP12	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	0.673400673	1	1	1	1782	191.367	4.41	89.9	91	109.3	109.8	90.45	109.55	1.21117	0.182394
A0A0K0K110	HEL-S-265	Epididymis secretory protein Li 265 OS=Homo sapiens GN=HEL-S-265 PE=2 SV=1	31.33802817	10	16	4	284	32.846	4.77	97.1	83.8	117.1	102	90.45	109.55	1.21117	0.182394
Q5T4F4	ZFYVE27	Protrudin OS=Homo sapiens GN=ZFYVE27 PE=1 SV=1	8.759124088	2	2	2	411	45.814	5.15	95.7	85.2	119.4	99.7	90.45	109.55	1.21117	0.182394
P30711	GSTT1	Glutathione S-transferase theta-1 OS=Homo sapiens GN=GSTT1 PE=1 SV=4	8.333333333	2	2	2	240	27.318	7.49	94.8	86.1	116	103.1	90.45	109.55	1.21117	0.182394
B7ZAC7		cDNA, FLJ79141, highly similar to Nucleosome assembly protein 1-like 4 OS=Homo sapiens PE=2 SV=1	27.97927461	8	14	7	386	44.157	4.7	94	86.9	114.3	104.8	90.45	109.55	1.21117	0.182394
U6EG95	HLA-B	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1	43.09392265	7	14	1	181	21.052	5.49	92.7	88.2	132.3	86.8	90.45	109.55	1.21117	0.182394
Q8WVY7	UBLCP1	Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens GN=UBLCP1 PE=1 SV=2	2.830188679	1	1	1	318	36.781	6.46	88.5	92.4	116.3	102.8	90.45	109.55	1.21117	0.182394
A4D198	LOC392647	Similar to mKIAA0038 protein OS=Homo sapiens GN=LOC392647 PE=4 SV=1	9.523809524	3	6	3	294	32.584	8.87	86.8	94.1	114.7	104.4	90.45	109.55	1.21117	0.182394
A8K6S3		cDNA FLJ77570, highly similar to Homo sapiens pleckstrin homology	17.20588235	11	11	1	680	77.827	6.7	85.7	95.2	117	102.1	90.45	109.55	1.21117	0.182394

		domain containing, family C (with FERM domain) member 1 (PLEKHC1), mRNA OS=Homo sapiens PE=2 SV=1																
Q4LE65	PIK3C2B	PIK3C2B variant protein (Fragment) OS=Homo sapiens GN=PIK3C2B variant protein PE=2 SV=1	1.580547112	2	2	2	1645	185.814	7.24	85.4	95.5	110.5	108.5	90.45	109.5	1.21061	0.183537	
H9NL12	IFITM3	IFITM3 OS=Homo sapiens GN=IFITM3 PE=4 SV=1	30.82706767	3	16	1	133	14.654	7.01	106.1	74.9	110	109.1	90.5	109.55	1.2105	0.183778	
Q641Q2	FAM21A	WASH complex subunit FAM21A OS=Homo sapiens GN=FAM21A PE=1 SV=3	6.263982103	5	7	5	1341	147.095	4.81	86.7	94.3	114.1	105	90.5	109.55	1.2105	0.183778	
A0A0S2Z4G4	TPM3	Tropomyosin 3 isoform 1 (Fragment) OS=Homo sapiens GN=TPM3 PE=2 SV=1	48.38709677	15	25	11	248	29.015	4.78	93.9	87.1	110.3	108.7	90.5	109.5	1.20994	0.184927	
P23193	TCEA1	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2	22.59136213	5	7	5	301	33.948	8.38	91.6	89.4	112.9	106.1	90.5	109.5	1.20994	0.184927	
Q13867	BLMH	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	18.02197802	7	8	7	455	52.528	6.27	91.3	89.7	112.3	106.7	90.5	109.5	1.20994	0.184927	
O15397	IPO8	Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	2.121504339	2	2	2	1037	119.861	5.16	89.9	91.1	113	106	90.5	109.5	1.20994	0.184927	
P27348	YWHAQ	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	57.55102041	15	41	10	245	27.747	4.78	99.5	81.5	113.3	105.7	90.5	109.5	1.20994	0.184927	
P25788	PSMA3	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	39.60784314	9	14	9	255	28.415	5.33	98.3	82.7	114.4	104.6	90.5	109.5	1.20994	0.184927	
A8K8Z3		cDNA FLJ77613, highly similar to Homo sapiens tousled-like kinase 1 (TLK1), mRNA OS=Homo sapiens PE=2 SV=1	2.219321149	2	2	1	766	86.616	8.72	91.7	89.3	116	103	90.5	109.5	1.20994	0.184927	

A0A059S4 M9	ATP8	ATP synthase protein 8 OS=Homo sapiens GN=ATP8 PE=3 SV=1	39.70588235	3	20	1	68	7.916	9.91	85.8	95.2	114.4	104.6	90.5	109.5	1.20994	0.184927
Q8IZ03	IFIT2	Interferon-induced protein with tetratricopeptide repeats 2 OS=Homo sapiens GN=IFIT2 PE=1 SV=2	4.958677686	2	2	2	484	56.177	6.76	90.7	90.3	110.2	108.7	90.5	109.45	1.20939	0.186082
Q4LE38	IKBKAP	IKBKAP variant protein (Fragment) OS=Homo sapiens GN=IKBKAP variant protein PE=2 SV=1	12.44411326	12	12	12	1342	151.36	6	90.4	90.7	107	111.9	90.55	109.45	1.20872	0.187487
Q9UNS2	COPS3	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3	15.13002364	5	6	5	423	47.842	6.65	94.2	86.9	116.8	102.1	90.55	109.45	1.20872	0.187487
D3DPK5	SH3BGRL3	SH3 domain binding glutamic acid-rich protein like 3, isoform CRA_a (Fragment) OS=Homo sapiens GN=SH3BGRL3 PE=4 SV=1	11.28404669	3	4	3	257	26.803	8.38	93.4	87.7	115.3	103.6	90.55	109.45	1.20872	0.187487
Q6YP21	KYAT3	Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens GN=KYAT3 PE=1 SV=1	24.00881057	9	12	9	454	51.368	8.19	93.3	87.8	115.7	103.2	90.55	109.45	1.20872	0.187487
Q96IR7	HPDL	4-hydroxyphenylpyruvate dioxygenase-like protein OS=Homo sapiens GN=HPDL PE=1 SV=1	12.12938005	3	4	3	371	39.361	7.03	90.4	90.7	120.3	98.6	90.55	109.45	1.20872	0.187487
Q5BJF2	TMEM97	Transmembrane protein 97 OS=Homo sapiens GN=TMEM97 PE=1 SV=1	18.75	3	22	3	176	20.834	9.38	96.5	84.6	112.4	106.4	90.55	109.4	1.20817	0.188654
O60232	SSSCA1	Sjoegren syndrome/scleroderma autoantigen 1 OS=Homo sapiens GN=SSSCA1 PE=1 SV=1	18.09045226	3	4	3	199	21.461	5.24	92.5	88.7	114.4	104.5	90.6	109.45	1.20806	0.188898
V9HWG3	HEL-S-45	Epididymis secretory protein Li 45 OS=Homo sapiens GN=HEL-S-45 PE=2 SV=1	13.5371179	9	12	9	687	77.28	5.22	91.6	89.6	115.1	103.8	90.6	109.45	1.20806	0.188898

Q9P2J9	PDP2	[Pyruvate dehydrogenase [acetyl- transferring]]-phosphatase 2, mitochondrial OS=Homo sapiens GN=PDP2 PE=2 SV=2	1.512287335	1	1	1	529	59.94	6.07	94.4	86.8	109.5	109.3	90.6	109.4	1.20751	0.190072
P30622	CLIP1	CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1 PE=1 SV=2	13.69958275	19	20	18	1438	162.147	5.36	91.3	89.9	111.2	107.6	90.6	109.4	1.20751	0.190072
P61221	ABCE1	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1	17.86310518	10	14	10	599	67.271	8.34	88.5	92.7	110.1	108.7	90.6	109.4	1.20751	0.190072
Q9UI26	IPO11	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1	3.179487179	2	2	2	975	112.463	5.25	99.2	82	116.8	102	90.6	109.4	1.20751	0.190072
Q5H924	HUWE1	HECT, UBA and WWE domain containing 1 (Fragment) OS=Homo sapiens GN=HUWE1 PE=4 SV=1	12.18080423	31	44	1	3407	373.963	5.1	98.2	83	118.5	100.3	90.6	109.4	1.20751	0.190072
Q5VWZ2	LYPLAL 1	Lysophospholipase-like protein 1 OS=Homo sapiens GN=LYPLAL1 PE=1 SV=3	4.219409283	1	1	1	237	26.299	7.84	94.2	87	119.2	99.6	90.6	109.4	1.20751	0.190072
X6R8F3	LCN2	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=1	8.5	1	1	1	200	22.774	8.5	88.9	92.3	90.6	128.2	90.6	109.4	1.20751	0.190072
O60826	CCDC22	Coiled-coil domain-containing protein 22 OS=Homo sapiens GN=CCDC22 PE=1 SV=1	5.582137161	3	4	3	627	70.712	6.74	87.2	94	106.2	112.6	90.6	109.4	1.20751	0.190072
P19827	ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	1.427003293	1	2	1	911	101.326	6.79	81.8	99.4	96.6	122.2	90.6	109.4	1.20751	0.190072
A0A087W UB1	CCDC12 9	Coiled-coil domain-containing protein 129 OS=Homo sapiens GN=CCDC129 PE=4 SV=1	1.518026565	1	1	1	1054	116.436	5.31	77.2	104	110.7	108.1	90.6	109.4	1.20751	0.190072
Q14520	HABP2	Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1	4.107142857	2	2	2	560	62.63	6.54	81.2	100	93.5	125.2	90.6	109.35	1.20695	0.191252

A0A140V KE9		Testis tissue sperm-binding protein Li 66n OS=Homo sapiens PE=2 SV=1	4.545454545	2	2	2	638	71.412	5.2	90.1	91.2	117.2	101.6	90.65	109.4	1.20684	0.191497
Q9Y2V2	CARHS P1	Calcium-regulated heat-stable protein 1 OS=Homo sapiens GN=CARHSP1 PE=1 SV=2	23.80952381	3	6	3	147	15.882	8.21	88.4	92.9	117	101.8	90.65	109.4	1.20684	0.191497
Q9H3F6	KCTD10	BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 3 OS=Homo sapiens GN=KCTD10 PE=1 SV=1	13.09904153	4	5	3	313	35.41	6.34	94.6	86.7	112.6	106.1	90.65	109.35	1.20629	0.192683
O00154	ACOT7	Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3	19.47368421	5	6	5	380	41.769	8.54	94.1	87.2	112.7	106	90.65	109.35	1.20629	0.192683
I3L0M9	TCEB2	Transcription elongation factor B polypeptide 2 (Fragment) OS=Homo sapiens GN=TCEB2 PE=1 SV=1	29.28571429	3	3	3	140	15.592	5.17	91	90.3	114.2	104.5	90.65	109.35	1.20629	0.192683
A0A024R1 S8	LASP1	LIM and SH3 protein 1, isoform CRA_b OS=Homo sapiens GN=LASP1 PE=4 SV=1	28.35249042	7	14	7	261	29.698	7.05	86	95.3	112.3	106.4	90.65	109.35	1.20629	0.192683
P49773	HINT1	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2	42.85714286	4	6	4	126	13.793	6.95	81.8	99.5	111.6	107.1	90.65	109.35	1.20629	0.192683
Q9H773	DCTPP1	dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1	31.76470588	3	3	3	170	18.669	5.03	96.9	84.4	113.8	104.8	90.65	109.3	1.20574	0.193875
A0A024R9 15	ACBD6	Acyl-Coenzyme A binding domain containing 6, isoform CRA_a OS=Homo sapiens GN=ACBD6 PE=4 SV=1	4.255319149	1	1	1	282	31.131	5.11	84.9	96.4	112	106.6	90.65	109.3	1.20574	0.193875
B7ZMD7	AMY1A	Alpha-amylase OS=Homo sapiens GN=AMY1A PE=2 SV=1	6.849315068	3	3	3	511	57.717	6.93	81	100.3	96	122.6	90.65	109.3	1.20574	0.193875

Q92905	COPS5	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	29.04191617	8	12	8	334	37.555	6.54	92.3	89.1	114.7	104	90.7	109.35	1.20562	0.194122
P41236	PPP1R2	Protein phosphatase inhibitor 2 OS=Homo sapiens GN=PPP1R2 PE=1 SV=2	17.56097561	3	3	3	205	23.001	4.74	89.5	91.9	108.6	110	90.7	109.3	1.20507	0.19532
Q6IN84	MRM1	rRNA methyltransferase 1, mitochondrial OS=Homo sapiens GN=MRM1 PE=1 SV=1	10.19830028	3	6	3	353	38.614	7.94	92.4	89	127.1	91.5	90.7	109.3	1.20507	0.19532
Q96RR1	PEO1	Twinkle protein, mitochondrial OS=Homo sapiens GN=PEO1 PE=1 SV=1	1.461988304	1	1	1	684	77.106	8.98	87.7	93.7	93.6	125	90.7	109.3	1.20507	0.19532
A6NMQ1	POLA1	DNA polymerase OS=Homo sapiens GN=POLA1 PE=1 SV=1	6.471389646	9	11	9	1468	166.351	5.81	91.8	89.6	114	104.5	90.7	109.25	1.20452	0.196525
P17812	CTPS1	CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2	22.67343486	12	15	10	591	66.648	6.46	95.3	86.2	111.8	106.8	90.75	109.3	1.20441	0.196772
Q9Y266	NUDC	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	40.18126888	14	27	14	331	38.219	5.38	85.4	96.1	109.2	109.4	90.75	109.3	1.20441	0.196772
Q5VW32	BROX	BRO1 domain-containing protein BROX OS=Homo sapiens GN=BROX PE=1 SV=1	5.839416058	2	3	2	411	46.447	7.65	91.1	90.4	113.3	105.2	90.75	109.25	1.20386	0.197984
O14562	UBFD1	Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens GN=UBFD1 PE=1 SV=2	3.55987055	1	1	1	309	33.361	5.77	96.9	84.6	110.3	108.2	90.75	109.25	1.20386	0.197984
Q05932	FPGS	Folypolyglutamate synthase, mitochondrial OS=Homo sapiens GN=FPGS PE=1 SV=3	4.429301533	2	2	2	587	64.568	7.94	87.2	94.3	105.3	113.2	90.75	109.25	1.20386	0.197984
P02533	KRT14	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	32.41525424	21	76	1	472	51.529	5.16	79.4	102.1	112.1	106.4	90.75	109.25	1.20386	0.197984

Q53HB3		Proteasome 26S ATPase subunit 1 variant (Fragment) OS=Homo sapiens PE=1 SV=1	47.27272727	18	31	17	440	49.182	6.21	93.2	88.3	113.5	104.9	90.75	109.2	1.20331	0.199201
Q5U077	LDHB	L-lactate dehydrogenase OS=Homo sapiens GN=LDHB PE=2 SV=1	42.21556886	13	47	12	334	36.615	6.05	92.3	89.3	109.4	109.1	90.8	109.25	1.20319	0.199449
Q5T1V6	DDX59	Probable ATP-dependent RNA helicase DDX59 OS=Homo sapiens GN=DDX59 PE=1 SV=1	1.938610662	1	2	1	619	68.766	7.44	89.3	92.3	105.5	112.9	90.8	109.2	1.20264	0.200673
A0A024R B62	METTL1	tRNA (guanine-N(7)-methyltransferase OS=Homo sapiens GN=METTL1 PE=3 SV=1	12.95681063	2	2	2	301	34.071	7.9	97.4	84.2	108.4	110	90.8	109.2	1.20264	0.200673
E5KNQ5	TK2	Mitochondrial thymidine kinase 2 OS=Homo sapiens GN=TK2 PE=1 SV=1	7.166123779	2	2	2	307	35.39	9.5	96	85.6	113.4	105	90.8	109.2	1.20264	0.200673
Q96DM3	C18orf8	Uncharacterized protein C18orf8 OS=Homo sapiens GN=C18orf8 PE=1 SV=2	3.652968037	2	2	2	657	74.927	7.83	92.4	89.2	123.3	95.1	90.8	109.2	1.20264	0.200673
K7EIK7	EML2	Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2 PE=1 SV=1	12.93661061	9	10	3	773	84.676	6.87	91.9	89.7	115.6	102.8	90.8	109.2	1.20264	0.200673
Q6AW98	DKFZp686P13170	Putative uncharacterized protein DKFZp686P13170 OS=Homo sapiens GN=DKFZp686P13170 PE=2 SV=1	1.741293532	1	1	1	402	45.998	9.88	90.4	91.2	116.8	101.6	90.8	109.2	1.20264	0.200673
P20618	PSMB1	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2	22.82157676	4	6	4	241	26.472	8.13	87.6	94	104.9	113.5	90.8	109.2	1.20264	0.200673
A8K5M4		cDNA FLJ75088, highly similar to Homo sapiens p21 (CDKN1A)-activated kinase 2 (PAK2), mRNA OS=Homo sapiens PE=2 SV=1	38.35877863	15	20	15	524	58.007	5.85	85.3	96.3	110.5	107.9	90.8	109.2	1.20264	0.200673

A0A059QB80	ATP6	ATP synthase subunit a OS=Homo sapiens GN=ATP6 PE=4 SV=1	4.424778761	1	1	1	226	24.744	10.1	84.5	97.1	99.4	119	90.8	109.2	1.20264	0.200673
B4DPQ0	C1R	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=1	1.112656467	1	1	1	719	81.837	6.37	80	101.6	99.4	119	90.8	109.2	1.20264	0.200673
Q96EK6	GNPNA T1	Glucosamine 6-phosphate N-acetyltransferase OS=Homo sapiens GN=GNPNAT1 PE=1 SV=1	24.45652174	3	4	3	184	20.736	7.99	95.1	86.6	116.4	102	90.85	109.2	1.20198	0.202152
Q9H1B7	IRF2BPL	Interferon regulatory factor 2-binding protein-like OS=Homo sapiens GN=IRF2BPL PE=1 SV=1	2.386934673	2	2	1	796	82.607	8.24	96.3	85.4	110.2	108.1	90.85	109.15	1.20143	0.203389
B4DZK0		cDNA FLJ56391, highly similar to Cysteine protease ATG4B (EC 3.4.22.-) OS=Homo sapiens PE=2 SV=1	3.333333333	1	1	1	510	57.284	8.53	83.4	98.3	104.7	113.6	90.85	109.15	1.20143	0.203389
Q06609	RAD51	DNA repair protein RAD51 homolog 1 OS=Homo sapiens GN=RAD51 PE=1 SV=1	6.784660767	2	2	2	339	36.943	5.6	91.6	90.1	115.3	102.9	90.85	109.1	1.20088	0.204632
K7PML8	CDKN2A	Cyclin-dependent kinase inhibitor 2A OS=Homo sapiens GN=CDKN2A PE=2 SV=1	32.69230769	3	4	2	156	16.522	5.81	89	92.7	104.3	113.9	90.85	109.1	1.20088	0.204632
H3BM91	COMMD4	COMM domain-containing protein 4 (Fragment) OS=Homo sapiens GN=COMMD4 PE=1 SV=1	3.317535545	1	1	1	211	22.749	7.9	89.6	92.2	111.9	106.4	90.9	109.15	1.20077	0.204882
B4DF04		cDNA FLJ55807, highly similar to Neurogenic locus notch homolog protein 2 OS=Homo sapiens PE=2 SV=1	8.641975309	2	3	1	243	26.448	5.94	74.5	107.3	77.8	140.5	90.9	109.15	1.20077	0.204882
D3DND1	CDV3	CDV3 homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=CDV3 PE=4 SV=1	33.72093023	6	9	6	258	28.581	9.44	93.6	88.2	111.1	107.1	90.9	109.1	1.20022	0.206131

P78371	CCT2	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	61.4953271	29	65	29	535	57.452	6.46	91	90.8	108.6	109.6	90.9	109.1	1.20022	0.206131
A0A140V KC8		Testis tissue sperm-binding protein Li 45a OS=Homo sapiens PE=2 SV=1	14.01869159	3	3	3	321	35.87	6.6	93.5	88.3	113.7	104.5	90.9	109.1	1.20022	0.206131
P23921	RRM1	Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1	48.61111111	32	107	32	792	90.013	7.15	91.2	90.6	114.2	104	90.9	109.1	1.20022	0.206131
Q06210	GFPT1	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	28.46924177	16	20	12	699	78.756	7.11	89.6	92.2	111.5	106.6	90.9	109.05	1.19967	0.207387
Q59EE8		Nuclear receptor coactivator 3 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	1.331464611	1	1	1	1427	155.558	7.56	93.5	88.4	112.2	105.9	90.95	109.05	1.19901	0.2089
P36954	POLR2I	DNA-directed RNA polymerase II subunit RPB9 OS=Homo sapiens GN=POLR2I PE=1 SV=1	8.8	1	1	1	125	14.514	5.14	93	88.9	112.2	105.9	90.95	109.05	1.19901	0.2089
O00151	PDLIM1	PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	56.83890578	14	19	14	329	36.049	7.02	91.8	90.1	108.9	109.2	90.95	109.05	1.19901	0.2089
P49662	CASP4	Caspase-4 OS=Homo sapiens GN=CASP4 PE=1 SV=1	4.24403183	2	2	2	377	43.235	6	90.6	91.3	115.1	103	90.95	109.05	1.19901	0.2089
P07737	PFN1	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	78.57142857	10	41	10	140	15.045	8.27	87	94.9	111.8	106.3	90.95	109.05	1.19901	0.2089
B2RBY4		DNA primase OS=Homo sapiens PE=2 SV=1	12.38095238	5	7	5	420	49.924	8.38	97.2	84.7	125.1	92.9	90.95	109	1.19846	0.210168
Q9H649	NSUN3	Putative methyltransferase NSUN3 OS=Homo sapiens GN=NSUN3 PE=2 SV=1	6.176470588	2	2	2	340	38.22	8.87	93.4	88.5	111	107	90.95	109	1.19846	0.210168
O00767	SCD	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2	17.54874652	5	9	5	359	41.496	9	82.4	99.5	95.9	122.1	90.95	109	1.19846	0.210168

Q14376	GALE	UDP-glucose 4-epimerase OS=Homo sapiens GN=GALE PE=1 SV=2	10.34482759	2	4	2	348	38.257	6.73	99.5	82.5	111.5	106.6	91	109.05	1.19835	0.210421
O14980	XPO1	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	20.35480859	18	30	18	1071	123.306	6.06	98.3	83.7	112.9	105.1	91	109	1.1978	0.211695
Q9P2K8	EIF2AK4	eIF-2-alpha kinase GCN2 OS=Homo sapiens GN=EIF2AK4 PE=1 SV=3	1.394784718	2	2	2	1649	186.794	6.28	94.7	87.3	111.3	106.7	91	109	1.1978	0.211695
Q59EV7		Transporter (Fragment) OS=Homo sapiens PE=2 SV=1	2.01863354	1	1	1	644	71.382	6.99	88.5	93.5	110	108	91	109	1.1978	0.211695
A0A024R A11	ACTR3	ARP3 actin-related protein 3 homolog (Yeast), isoform CRA_a OS=Homo sapiens GN=ACTR3 PE=3 SV=1	30.86124402	9	16	2	418	47.341	5.88	91.7	90.3	115.9	102	91	108.95	1.19725	0.212976
A0A0S2Z5 00	OPTN	Optineurin isoform 1 (Fragment) OS=Homo sapiens GN=OPTN PE=2 SV=1	4.506065858	3	3	3	577	65.88	5.24	86.4	95.6	114.8	103.1	91	108.95	1.19725	0.212976
G3V5Z7	PSMA6	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1	43.25396825	10	25	10	252	28.129	6.76	95.6	86.5	114.8	103.2	91.05	109	1.19714	0.21323
Q14222	EEF1A	EEF1A protein (Fragment) OS=Homo sapiens GN=EEF1A PE=2 SV=1	31.71806167	4	40	1	227	24.181	9.58	95.6	86.5	113.4	104.5	91.05	108.95	1.1966	0.214517
V9HW90	HEL-75	Epididymis luminal protein 75 OS=Homo sapiens GN=HEL-75 PE=2 SV=1	17.04980843	5	7	5	522	56.221	8.5	94.3	87.8	112.1	105.8	91.05	108.95	1.1966	0.214517
B2R7P8		cDNA, FLJ93545, highly similar to Homo sapiens 5-aminoimidazole- 4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (ATIC), mRNA OS=Homo sapiens PE=2 SV=1	46.4527027	20	32	20	592	64.594	6.8	94.2	87.9	110.3	107.6	91.05	108.95	1.1966	0.214517

O00764	PDXK	Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1	18.26923077	5	6	5	312	35.08	6.13	92.6	89.5	107	110.9	91.05	108.95	1.1966	0.214517
Q9NS87	KIF15	Kinesin-like protein KIF15 OS=Homo sapiens GN=KIF15 PE=1 SV=1	0.936599424	1	1	1	1388	160.061	6	91.2	90.9	110.4	107.5	91.05	108.95	1.1966	0.214517
Q4LE43	PLCG1	Phosphoinositide phospholipase C (Fragment) OS=Homo sapiens GN=PLCG1 variant protein PE=2 SV=1	0.920679887	1	1	1	1412	161.201	7.18	89.5	92.6	103.6	114.3	91.05	108.95	1.1966	0.214517
P61086	UBE2K	Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3	15.5	3	5	3	200	22.393	5.44	87.6	94.5	111.2	106.7	91.05	108.95	1.1966	0.214517
A0A024R5 Q1	hCG_20 03792	HCG2003792, isoform CRA_b OS=Homo sapiens GN=hCG_2003792 PE=4 SV=1	19.37984496	2	2	2	129	14.656	4.93	103.4	78.7	108.7	109.1	91.05	108.9	1.19605	0.215811
A8K7H4		Origin recognition complex subunit 4 OS=Homo sapiens PE=2 SV=1	12.8440367	5	7	5	436	50.361	7.96	94.1	88	108.4	109.4	91.05	108.9	1.19605	0.215811
A8K8D2		cDNA FLJ77371, highly similar to Homo sapiens MLF1 interacting protein (MLF1IP), mRNA OS=Homo sapiens PE=2 SV=1	2.392344498	1	1	1	418	47.539	9.13	93.3	88.8	106.7	111.1	91.05	108.9	1.19605	0.215811
P55060	CSE1L	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	26.26158599	22	33	22	971	110.346	5.77	93	89.1	107	110.8	91.05	108.9	1.19605	0.215811
D9IAI1	PEBP1	Epididymis secretory protein Li 34 OS=Homo sapiens GN=PEBP1 PE=2 SV=1	58.28877005	7	15	7	187	21.044	7.53	88.7	93.4	109.9	107.9	91.05	108.9	1.19605	0.215811
E9PK54	HSPA8	Heat shock cognate 71 kDa protein (Fragment) OS=Homo sapiens GN=HSPA8 PE=1 SV=8	93.44262295	15	135	1	183	19.943	7.33	96.6	85.6	113	104.9	91.1	108.95	1.19594	0.216065
J3QQX2	ARHGDI A	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI A PE=1 SV=1	31.91489362	5	7	5	235	25.815	7.44	96	86.2	113.2	104.6	91.1	108.9	1.19539	0.217366

A0A024R4 U3	TTLL12	Tubulin tyrosine ligase-like family, member 12, isoform CRA_a OS=Homo sapiens GN=TTLL12 PE=4 SV=1	24.53416149	12	14	12	644	74.356	5.53	93	89.2	110.7	107.1	91.1	108.9	1.19539	0.217366
Q8N3F8	MICALL 1	MICAL-like protein 1 OS=Homo sapiens GN=MICALL1 PE=1 SV=2	1.622247972	1	1	1	863	93.383	7.25	87.7	94.5	110.9	106.9	91.1	108.9	1.19539	0.217366
B1AHB0	MCM5	DNA helicase OS=Homo sapiens GN=MCM5 PE=2 SV=1	44.95912807	28	44	28	734	82.233	8.37	93.4	88.8	112.6	105.1	91.1	108.85	1.19484	0.218673
M0R2C6		Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1	33.50340136	14	22	1	588	65.718	6.54	90.5	91.7	103.3	114.4	91.1	108.85	1.19484	0.218673
H0YBH7	SARAF	Store-operated calcium entry- associated regulatory factor (Fragment) OS=Homo sapiens GN=SARAF PE=1 SV=1	14.98559078	4	4	4	347	37.854	5.34	89.1	93.1	110.2	107.5	91.1	108.85	1.19484	0.218673
A8K9D8		cDNA FLJ78129, highly similar to Homo sapiens reversion-inducing- cysteine-rich protein with kazal motifs (RECK), mRNA OS=Homo sapiens PE=2 SV=1	0.926879506	1	1	1	971	106.387	6.68	88.3	94	110.1	107.7	91.15	108.9	1.19473	0.218928
V9HW41	HEL-S- 71	Epididymis secretory protein Li 71 OS=Homo sapiens GN=HEL-S-71 PE=2 SV=1	31.57894737	5	7	5	152	17.127	6.57	92.2	90.1	115.1	102.6	91.15	108.85	1.19419	0.220242
Q9Y5X3	SNX5	Sorting nexin-5 OS=Homo sapiens GN=SNX5 PE=1 SV=1	28.71287129	10	12	9	404	46.787	6.76	90.1	92.2	111.3	106.4	91.15	108.85	1.19419	0.220242
B3KUL5		Oxysterol-binding protein OS=Homo sapiens PE=2 SV=1	4.842931937	3	4	2	764	83.89	8.31	84.1	98.2	113.1	104.6	91.15	108.85	1.19419	0.220242
Q96K49	TMEM8 7B	Transmembrane protein 87B OS=Homo sapiens GN=TMEM87B PE=1 SV=1	2.162162162	1	2	1	555	63.495	7.44	99.5	82.9	111.3	106.4	91.2	108.85	1.19353	0.221818
A0A140V K41		Testicular secretory protein Li 41 OS=Homo sapiens PE=2 SV=1	44.23676012	11	20	6	321	35.032	6.46	96.8	85.6	115.2	102.4	91.2	108.8	1.19298	0.223144

J9R021	eIF3a	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=eIF3a PE=2 SV=1	17.87264834	25	37	25	1382	166.381	6.79	95.6	86.8	111.5	106.1	91.2	108.8	1.19298	0.223144
P36639	NUDT1	7,8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens GN=NUDT1 PE=1 SV=3	7.614213198	1	1	1	197	22.505	5.27	91.7	90.7	117.5	100.1	91.2	108.8	1.19298	0.223144
A0A024R7I0	GIPC1	GIPC PDZ domain containing family, member 1, isoform CRA_a OS=Homo sapiens GN=GIPC1 PE=4 SV=1	11.71171171	3	4	3	333	36.027	6.28	90	92.4	105.9	111.7	91.2	108.8	1.19298	0.223144
Q8WXE0	CASKIN2	Caskin-2 OS=Homo sapiens GN=CASKIN2 PE=1 SV=2	2.662229617	2	2	2	1202	126.705	7.09	89.1	93.3	115.6	102	91.2	108.8	1.19298	0.223144
Q9BVG4	PBDC1	Protein PBDC1 OS=Homo sapiens GN=PBDC1 PE=1 SV=1	5.579399142	1	1	1	233	26.041	4.79	86.2	96.2	110.4	107.2	91.2	108.8	1.19298	0.223144
B2R932		cDNA, FLJ94187, highly similar to Homo sapiens CD99 antigen (CD99), mRNA OS=Homo sapiens PE=2 SV=1	9.72972973	1	1	1	185	18.935	4.82	89.6	92.9	106.5	111.1	91.25	108.8	1.19233	0.224734
H7C1D1		Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2	6.18556701	1	1	1	291	31.291	4.94	88.9	93.6	102.4	115.2	91.25	108.8	1.19233	0.224734
Q13136	PPFIA1	Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1 PE=1 SV=1	14.22628952	11	16	11	1202	135.695	6.29	88.6	93.9	103.8	113.8	91.25	108.8	1.19233	0.224734
P07996	THBS1	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	16.15384615	15	22	15	1170	129.3	4.94	80.3	102.2	96.1	121.5	91.25	108.8	1.19233	0.224734
Q92688	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	27.88844622	8	21	3	251	28.77	4.06	108.8	73.7	117.2	100.3	91.25	108.75	1.19178	0.226074
A2N0T1	VH6DJ	VH6DJ protein (Fragment) OS=Homo sapiens GN=VH6DJ PE=2 SV=1	5.882352941	2	2	2	119	13.012	8.47	100.4	82.1	97.7	119.8	91.25	108.75	1.19178	0.226074

A0A024R7 M1	RFXAN K	Regulatory factor X-associated ankyrin-containing protein, isoform CRA_a OS=Homo sapiens GN=RFXANK PE=4 SV=1	4.615384615	1	1	1	260	28.085	4.55	94	88.5	108.2	109.3	91.25	108.75	1.19178	0.226074
C9JIF9	APEH	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=1	9.090909091	5	5	5	737	81.622	5.54	89.6	92.9	112.1	105.4	91.25	108.75	1.19178	0.226074
O43414	ERI3	ERI1 exoribonuclease 3 OS=Homo sapiens GN=ERI3 PE=1 SV=2	6.231454006	2	3	2	337	37.214	8.07	96.2	86.4	115	102.5	91.3	108.75	1.19113	0.227678
B1ALK7	ARHGE F7	Rho guanine nucleotide exchange factor 7 OS=Homo sapiens GN=ARHGEF7 PE=1 SV=1	9.787234043	6	7	6	705	79.782	6.67	90.2	92.4	112.6	104.9	91.3	108.75	1.19113	0.227678
O00299	CLIC1	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	53.94190871	9	21	9	241	26.906	5.17	97.7	84.9	108.9	108.5	91.3	108.7	1.19058	0.229031
P17980	PSMC3	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	40.77448747	15	23	15	439	49.172	5.24	97.4	85.2	114.6	102.8	91.3	108.7	1.19058	0.229031
P60228	EIF3E	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	25.61797753	9	12	9	445	52.187	6.04	96.6	86	110.4	107	91.3	108.7	1.19058	0.229031
Q9BXV9	C14orf1 42	Uncharacterized protein C14orf142 OS=Homo sapiens GN=C14orf142 PE=1 SV=2	41	2	2	2	100	10.852	4.27	95	87.6	107.6	109.8	91.3	108.7	1.19058	0.229031
P14174	MIF	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	27.82608696	2	7	2	115	12.468	7.88	94.6	88	115.3	102.1	91.3	108.7	1.19058	0.229031
Q9Y263	PLAA	Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2	18.86792453	9	13	9	795	87.101	6.37	90.8	91.8	111.9	105.5	91.3	108.7	1.19058	0.229031
E9PD50	SMG7	Protein SMG7 OS=Homo sapiens GN=SMG7 PE=1 SV=1	1.452991453	2	3	2	1170	130.777	7.88	88.1	94.5	121.7	95.6	91.3	108.65	1.19003	0.23039

A0A0S2Z4 A5	MCM7	DNA helicase (Fragment) OS=Homo sapiens GN=MCM7 PE=2 SV=1	36.02225313	22	34	22	719	81.257	6.46	96	86.7	114.7	102.6	91.35	108.65	1.18938	0.232014
L0R5C8	SKA1	Alternative protein SKA1 OS=Homo sapiens GN=SKA1 PE=4 SV=1	8.235294118	1	1	1	85	9.445	7.31	95.1	87.6	115.3	102	91.35	108.65	1.18938	0.232014
A0A024R CZ8	KLC4	Kinesin light chain 4, isoform CRA_a OS=Homo sapiens GN=KLC4 PE=4 SV=1	5.654281099	3	3	1	619	68.598	6.18	91.8	90.9	112.6	104.7	91.35	108.65	1.18938	0.232014
Q9BXP2	SLC12A 9	Solute carrier family 12 member 9 OS=Homo sapiens GN=SLC12A9 PE=1 SV=1	9.628008753	6	8	6	914	96.049	8.07	90.3	92.4	114	103.3	91.35	108.65	1.18938	0.232014
Q9UBK8	MTRR	Methionine synthase reductase OS=Homo sapiens GN=MTRR PE=1 SV=3	16.13793103	8	8	8	725	80.359	6.49	89.8	92.9	109.7	107.6	91.35	108.65	1.18938	0.232014
A0A0U1R RB6	EXOC6 B	Exocyst complex component 6B OS=Homo sapiens GN=EXOC6B PE=1 SV=1	6.380368098	4	4	4	815	94.626	6.46	88.9	93.8	109.2	108.1	91.35	108.65	1.18938	0.232014
Q9H9S5	FKRP	Fukutin-related protein OS=Homo sapiens GN=FKRP PE=1 SV=1	4.242424242	2	2	2	495	54.533	7.4	88.6	94.1	87.1	130.2	91.35	108.65	1.18938	0.232014
B3KQY7		cDNA FLJ33305 fis, clone BNGH42003529, highly similar to E3 ubiquitin protein ligase TRAF7 (EC 6.3.2.-) OS=Homo sapiens PE=2 SV=1	5.820895522	4	4	4	670	74.545	7.15	86.3	96.4	106	111.3	91.35	108.65	1.18938	0.232014
Q9NP79	VTA1	Vacuolar protein sorting- associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1	28.01302932	6	11	6	307	33.858	6.29	86.1	96.6	108.6	108.7	91.35	108.65	1.18938	0.232014
A0A140VJ T2		Testicular tissue protein Li 158 OS=Homo sapiens PE=2 SV=1	5.535055351	1	1	1	271	29.798	5.74	84.9	97.8	109.2	108.1	91.35	108.65	1.18938	0.232014

B5BUi8	DUSP3	Dual specificity phosphatase 3 (Fragment) OS=Homo sapiens GN=DUSP3 PE=2 SV=1	21.62162162	3	3	3	185	20.564	8.15	88.7	94	109.1	108.1	91.35	108.6	1.18883	0.233387
A0A140VJ M4	KCTD12	Potassium channel tetramerisation domain containing 12 OS=Homo sapiens GN=KCTD12 PE=2 SV=1	8.307692308	2	2	2	325	35.679	5.64	93.1	89.7	115.5	101.8	91.4	108.65	1.18873	0.233646
A0A140VJ E6		Guanylate cyclase OS=Homo sapiens PE=2 SV=1	10.74458058	9	9	9	1061	118.844	6.64	91.1	91.7	105.8	111.5	91.4	108.65	1.18873	0.233646
P13929	ENO3	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5	14.51612903	4	19	1	434	46.957	7.71	98.6	84.2	106.4	110.8	91.4	108.6	1.18818	0.235025
A0A0K0K 1K4	HEL-S- 276	Proteasome subunit alpha type OS=Homo sapiens GN=HEL-S- 276 PE=2 SV=1	56.0483871	12	22	12	248	27.87	8.46	96.9	85.9	115.5	101.7	91.4	108.6	1.18818	0.235025