Supplementary Table 3. Full list of proteins identified by mass spectrometry from SILAC experiment of wild type 3xMBT pulldown from WT (light) MEFs as compared to MLL1 KO (heavy) MEFs

Protein Id	**Gene Symb**	**Descriptio**	**Number of**	45331.0 **max_sn_heavy_median**	1.1 41553.3 **max_sn_light_median**	**Corrected_max_sn_light_median**	**Median Ratio_H_L**	**Corrected Median Ratio_H_L**	**Corrected Median Ratio_L_H**	1163763.1 **max_sn_heavy_sum**	1.2 956124.8 **max_sn_light_sum**	**Corrected_max_sn_light_sum**	**Sum Ratio_H_L**	**Corrected Sum Ratio_H_L**	**Corrected Sum Ratio_L_H (WT MET/KO MEF)_MBTWT pull down**
Q64487_PT	Ptprd	Receptor-ty	1	113.1	2.1	2.3	54.2	49.68	0.02	113.1	2.1	2.5	54.2	44.53	0.02
Q9ER72_SY	Cars	Cysteine--t	21	38.9	2.7	2.9	14.5	13.32	0.08	902.8	113.3	137.9	8.0	6.55	0.15
Q9DC23_D	Dnajc10	DnaJ homo	1	118.2	9.6	10.4	12.4	11.33	0.09	118.2	9.6	11.6	12.4	10.15	0.10
P24547_IM	Impdh2	Inosine-5'-r	1	31.5	2.9	3.1	11.0	10.10	0.10	31.5	2.9	3.5	11.0	9.05	0.11
P54775_PR	Psmc4	26S proteas	11	65.3	6.2	6.8	10.6	9.68	0.10	1034.0	194.5	236.7	5.3	4.37	0.23
P34022_RA	Ranbp1	Ran-specifi	1	14.7	1.4	1.5	10.5	9.58	0.10	14.7	1.4	1.7	10.5	8.59	0.12
Q99N15_Q	Hsd17b10	17beta-hyd	3	27.5	2.9	3.1	9.6	8.77	0.11	88.1	11.7	14.3	7.5	6.16	0.16
Q63844_M	Mapk3	Mitogen-ac	1	10.5	1.2	1.3	9.1	8.31	0.12	10.5	1.2	1.4	9.1	7.45	0.13
Q8BZ71_ST	Stac3	SH3 and cy	1	48.5	5.5	6.0	8.7	8.02	0.12	48.5	5.5	6.7	8.7	7.19	0.14
Q8CAY6_TH	Acat2	Acetyl-CoA	2	20.2	2.3	2.6	8.6	7.92	0.13	40.4	4.7	5.7	8.6	7.09	0.14
Q7TQK4_EX	Exosc3	Exosome co	1	10.4	1.2	1.3	8.4	7.74	0.13	10.4	1.2	1.5	8.4	6.94	0.14
O35098_DI	Dpysl4	Dihydropyr	1	70.7	8.4	9.2	8.4	7.67	0.13	70.7	8.4	10.3	8.4	6.88	0.15
Q9CRT8_XP	Xpot	Exportin-T	3	12.0	1.5	1.6	8.2	7.56	0.13	40.4	5.5	6.7	7.3	6.02	0.17
Q8BJY1_PS	Psmd5	26S proteas	5	18.2	2.3	2.5	8.1	7.39	0.14	93.8	14.1	17.1	6.7	5.47	0.18
Q71LX4_TL	Tln2	Talin-2 OS=	1	10.6	1.4	1.5	7.7	7.06	0.14	10.6	1.4	1.7	7.7	6.33	0.16
Q9D0R2_SY	Tars	Threonine--	24	27.3	3.7	4.0	7.5	6.86	0.15	873.8	122.7	149.4	7.1	5.85	0.17
O08553_DI	Dpysl2	Dihydropyr	18	36.5	4.9	5.3	7.5	6.85	0.15	751.4	90.1	109.6	8.3	6.86	0.15
Q9D1R2_K	Kti12	Protein KTI	1	8.1	1.1	1.2	7.5	6.85	0.15	8.1	1.1	1.3	7.5	6.14	0.16
Q68EF0_RA	Rab3ip	Rab-3A-inte	1	9.0	1.2	1.3	7.5	6.84	0.15	9.0	1.2	1.5	7.5	6.13	0.16
P97371_PS	Psme1	Proteasom	11	81.9	11.0	12.0	7.5	6.84	0.15	928.6	149.7	182.2	6.2	5.10	0.20
O70251_EF	Eef1b	Elongation	6	28.2	3.8	4.2	7.4	6.77	0.15	330.4	88.2	107.4	3.7	3.08	0.32
Q922W5_P	Pycr1	Pyrroline-5	1	92.0	13.0	14.1	7.1	6.50	0.15	92.0	13.0	15.8	7.1	5.83	0.17
A2A8Z1_OS	Osbpl9	Oxysterol-b	1	8.4	1.2	1.3	7.0	6.40	0.16	8.4	1.2	1.5	7.0	5.73	0.17
Q3UMR0_A	Ankrd27	Ankyrin rep	1	9.1	1.3	1.4	6.9	6.32	0.16	9.1	1.3	1.6	6.9	5.67	0.18
O88342_W	Wdr1	WD repeat-	28	63.1	9.2	10.0	6.9	6.29	0.16	1646.8	284.0	345.7	5.8	4.76	0.21
Q80SZ6_Q8	Nxf7	Nuclear RN	1	33.3	5.1	5.6	6.5	5.97	0.17	33.3	5.1	6.2	6.5	5.35	0.19
Q9CZD3_SY	Gars	Glycine--tR	8	29.1	4.5	4.9	6.5	5.94	0.17	228.4	43.0	52.4	5.3	4.36	0.23
Q8R459_IL	Il1f10	Interleukin	1	11.5	1.8	1.9	6.4	5.90	0.17	11.5	1.8	2.2	6.4	5.29	0.19
Q61035_SY	Hars	Histidine--t	1	9.2	1.4	1.6	6.4	5.84	0.17	9.2	1.4	1.8	6.4	5.23	0.19
Q5HZI1_MT	Mtus1	Microtubul	2	19.0	3.1	3.4	6.1	5.62	0.18	38.1	6.2	7.6	6.1	5.04	0.20
B2RY04_DO	Dock5	Dedicator c	2	25.0	4.1	4.5	6.1	5.58	0.18	50.0	8.2	10.0	6.1	5.00	0.20
P10126_EF	Eef1a1	Elongation	69	212.3	35.0	38.2	6.1	5.56	0.18	27286.9	5732.8	6977.8	4.8	3.91	0.26
Q3UQN2_F	Fcho2	F-BAR doma	1	11.1	1.8	2.0	6.1	5.55	0.18	11.1	1.8	2.2	6.1	4.97	0.20
Q91V64_IS	Isoc1	Isochorism	1	13.9	2.3	2.5	6.0	5.52	0.18	13.9	2.3	2.8	6.0	4.95	0.20
Q9CZ44_NS	Nsfl1c	NSFL1 cofa	4	20.8	3.5	3.8	5.9	5.39	0.19	77.6	16.9	20.6	4.6	3.76	0.27
P30416_FK	Fkbp4	Peptidyl-pr	3	20.2	3.4	3.8	5.9	5.37	0.19	60.9	21.8	26.5	2.8	2.30	0.44
A6PWE0_A	Gm15698	Protein Gm	1	28.7	4.9	5.4	5.9	5.37	0.19	28.7	4.9	6.0	5.9	4.81	0.21
P97807_FU	Fh	Fumarate h	5	15.7	2.7	2.9	5.8	5.34	0.19	110.9	15.0	18.3	7.4	6.06	0.17
Q8BGR9_U	Ublcp1	Ubiquitin-l	3	20.3	3.5	3.9	5.7	5.27	0.19	44.4	10.2	12.4	4.4	3.58	0.28
A2AAY5_SP	Sh3pxd2b	SH3 and PX	1	24.7	4.3	4.7	5.7	5.26	0.19	24.7	4.3	5.2	5.7	4.71	0.21
P09671_SO	Sod2	Superoxide	1	7.5	1.3	1.4	5.7	5.23	0.19	7.5	1.3	1.6	5.7	4.69	0.21
Q91ZJ5_UG	Ugp2	UTP--gluco	3	33.6	6.0	6.5	5.6	5.17	0.19	78.2	15.9	19.3	4.9	4.04	0.25
Q9CWY8_R	Rnaseh2a	Ribonuclea	3	18.9	3.4	3.7	5.6	5.10	0.20	58.7	11.8	14.3	5.0	4.10	0.24
Q61183_PA	Papola	Poly(A) pol	1	18.4	3.3	3.6	5.6	5.09	0.20	18.4	3.3	4.0	5.6	4.56	0.22
Q99JF8_PS	Psip1	PC4 and SF	1	5.7	1.0	1.1	5.4	4.97	0.20	5.7	1.0	1.3	5.4	4.45	0.22
Q9Z2I8_SU	Suclg2	Succinyl-Co	3	7.6	1.4	1.5	5.4	4.96	0.20	23.7	5.3	6.5	4.4	3.65	0.27
Q9ES00_UB	Ube4b	Ubiquitin c	2	21.1	4.0	4.3	5.3	4.89	0.20	42.2	7.9	9.6	5.3	4.38	0.23
Q9DAR7_D	Dcps	m7GpppX	3	25.3	4.7	5.2	5.3	4.89	0.20	66.5	20.0	24.4	3.3	2.73	0.37
P63005_LIS	Pafah1b1	Platelet-act	19	42.9	8.1	8.8	5.3	4.87	0.21	782.3	185.7	226.0	4.2	3.46	0.29
Q9CX11_UT	Utp23	rRNA-proce	1	7.2	1.4	1.5	5.3	4.86	0.21	7.2	1.4	1.7	5.3	4.35	0.23
P27612_PL	Plaa	Phospholip	5	14.5	2.8	3.0	5.2	4.79	0.21	78.4	14.9	18.1	5.3	4.32	0.23
Q9WUL7_A	Arl3	ADP-ribosy	1	19.6	3.8	4.1	5.2	4.78	0.21	19.6	3.8	4.6	5.2	4.28	0.23
P06745_G6	Gpi	Glucose-6-p	10	16.0	3.1	3.4	5.2	4.76	0.21	189.7	33.1	40.3	5.7	4.71	0.21
Q9WUM4_	Coro1c	Coronin-1C	3	9.1	1.8	1.9	5.2	4.74	0.21	25.5	6.9	8.4	3.7	3.04	0.33
Q91YS8_KC	Camk1	Calcium/ca	1	9.5	1.9	2.0	5.1	4.70	0.21	9.5	1.9	2.3	5.1	4.21	0.24
E9PYG6_E9	Rasa1	Protein Ras	1	6.8	1.3	1.5	5.1	4.69	0.21	6.8	1.3	1.6	5.1	4.21	0.24
Q8BV13_CS	Cops7b	COP9 signa	3	16.8	3.3	3.6	5.1	4.67	0.21	896.2	785.9	956.6	1.1	0.94	1.07
Q6P1B1_XP	Xpnpep1	Xaa-Pro am	3	14.9	2.9	3.2	5.1	4.65	0.21	40.5	10.4	12.6	3.9	3.21	0.31
P28660_NC	Nckap1	Nck-associa	7	22.6	4.5	4.9	5.0	4.60	0.22	159.3	37.8	46.0	4.2	3.46	0.29
Q60967_PA	Papss1	Bifunctiona	1	12.2	2.4	2.7	5.0	4.56	0.22	12.2	2.4	3.0	5.0	4.09	0.24
Q8CI95_OS	Osbpl11	Oxysterol-b	9	26.4	5.3	5.8	5.0	4.56	0.22	240.2	69.8	84.9	3.4	2.83	0.35
Q9EPK7_XP	Xpo7	Exportin-7	7	25.3	5.1	5.6	4.9	4.51	0.22	174.3	44.2	53.8	3.9	3.24	0.31
Q8R010_AI	Aimp2	Aminoacyl	7	36.2	7.4	8.0	4.9	4.51	0.22	237.3	82.6	100.6	2.9	2.36	0.42
Q8BMP6_G	Acbd3	Golgi reside	1	9.4	1.9	2.1	4.9	4.48	0.22	9.4	1.9	2.3	4.9	4.02	0.25
Q99L47_F1	St13	Hsc70-inter	2	24.3	5.0	5.4	4.9	4.48	0.22	48.5	9.9	12.1	4.9	4.02	0.25
Q6PB66_LP	Lrpprc	Leucine-ric	5	14.0	2.9	3.1	4.9	4.48	0.22	69.0	14.2	17.3	4.9	3.99	0.25
Q78PY7_SN	Snd1	Staphyloco	13	17.5	3.6	3.9	4.9	4.47	0.22	240.1	90.4	110.0	2.7	2.18	0.46
Q80UG5_SE	9-Sep	Septin-9 OS	14	53.2	10.9	11.9	4.9	4.46	0.22	697.3	154.4	188.0	4.5	3.71	0.27
Q8CG76_AI	Akr7a2	Aflatoxin B	1	26.0	5.4	5.9	4.8	4.43	0.23	26.0	5.4	6.6	4.8	3.97	0.25
Q8BML9_Q	Qars	Glutaminyl	13	20.7	4.3	4.7	4.8	4.41	0.23	316.1	92.7	112.8	3.4	2.80	0.36
Q99J09_MI	Wdr77	Methylosor	1	19.9	4.1	4.5	4.8	4.39	0.23	19.9	4.1	5.0	4.8	3.94	0.25
Q9D8N0_EI	Eef1g	Elongation	13	43.8	9.1	10.0	4.8	4.39	0.23	700.4	139.3	169.5	5.0	4.13	0.24
Q9JMD0_ZI	Znf207	BUB3-inter	1	22.4	4.8	5.2	4.7	4.30	0.23	22.4	4.8	5.8	4.7	3.85	0.26
Q64737_PU	Gart	Trifunction	8	25.6	5.5	6.0	4.7	4.29	0.23	193.8	49.6	60.4	3.9	3.21	0.31
Q8K2L8_TP	Trappc12	Trafficking	1	16.3	3.5	3.8	4.7	4.28	0.23	16.3	3.5	4.2	4.7	3.84	0.26
Q62189_SN	Snrpa	U1 small nu	3	43.5	9.3	10.2	4.7	4.28	0.23	130.4	34.1	41.5	3.8	3.14	0.32
Q99MD9_N	Nasp	Nuclear aut	2	23.2	5.0	5.4	4.7	4.28	0.23	46.3	9.9	12.1	4.7	3.83	0.26
P53395_OI	Dbt	Lipoamide	1	15.0	3.2	3.5	4.7	4.26	0.23	15.0	3.2	3.9	4.7	3.82	0.26
P23506_PI	Pcmt1	Protein-L-is	1	27.8	6.0	6.5	4.6	4.24	0.24	27.8	6.0	7.3	4.6	3.80	0.26
P61202_CS	Cops2	COP9 signa	18	20.5	4.4	4.8	4.6	4.23	0.24	463.6	143.3	174.5	3.2	2.66	0.38
Q3TIR3_RIC	Ric8a	Synembryn	1	14.6	3.2	3.5	4.6	4.23	0.24	14.6	3.2	3.9	4.6	3.79	0.26
Q4KWH5_P	Plch1	1-phosphat	1	43.1	9.4	10.2	4.6	4.22	0.24	43.1	9.4	11.4	4.6	3.78	0.26
Q9ES46_PA	Parvb	Beta-parvin	1	13.5	2.9	3.2	4.6	4.21	0.24	13.5	2.9	3.6	4.6	3.77	0.27
P46471_PR	Psmc2	26S proteas	19	23.4	5.2	5.7	4.5	4.14	0.24	975.1	186.5	227.0	5.2	4.30	0.23
O08848_RO	Trove2	60 kDa SS-A	1	9.2	2.0	2.2	4.5	4.13	0.24	9.2	2.0	2.5	4.5	3.70	0.27
Q80Y81_RN	Elac2	Zinc phospl	2	9.0	2.0	2.2	4.5	4.13	0.24	18.0	4.0	4.9	4.5	3.70	0.27
O35593_PS	Psmd14	26S proteas	6	31.0	6.9	7.6	4.5	4.11	0.24	320.1	63.0	76.6	5.1	4.18	0.24
Q8BH69_SE	Sephs1	Selenide, w	2	13.9	3.1	3.4	4.5	4.11	0.24	27.8	6.2	7.5	4.5	3.68	0.27
Q9CQR4_A	Acot13	Acyl-coenzy	2	15.0	3.3	3.7	4.5	4.10	0.24	30.0	6.7	8.1	4.5	3.68	0.27
Q60770_ST	Stxbp3	Syntaxin-bi	1	17.4	3.9	4.3	4.5	4.09	0.24	17.4	3.9	4.7	4.5	3.67	0.27
O35864_CS	Cops5	COP9 signa	16	17.4	3.9	4.3	4.5	4.08	0.25	388.1	114.6	139.5	3.4	2.78	0.36
Q99KD5_U	Unc45a	Protein unc	5	12.0	2.7	3.0	4.4	4.08	0.25	70.9	17.1	20.8	4.2	3.41	0.29
Q99K85_SE	Psat1	Phosphoser	31	58.9	13.3	14.5	4.4	4.07	0.25	2267.1	645.6	785.9	3.5	2.88	0.35
Q7TMB8_C	Cyfip1	Cytoplasmi	9	27.8	6.3	6.8	4.4	4.07	0.25	241.1	83.7	101.9	2.9	2.37	0.42
Q2LKV8_Q2	Nlrp1b	NACHT-, LR	1	18.8	4.3	4.7	4.4	4.04	0.25	18.8	4.3	5.2	4.4	3.62	0.28
Q9WUA3_P	Pfkp	ATP-depend	11	19.2	4.4	4.8	4.4	4.03	0.25	222.7	56.3	68.5	4.0	3.25	0.31
Q91V92_AC	Acly	ATP-citrate	17	19.8	4.5	5.0	4.4	3.99	0.25	377.7	75.5	91.9	5.0	4.11	0.24
Q9D1M4_M	Eef1e1	Eukaryotic	4	27.3	6.3	6.9	4.3	3.98	0.25	109.6	38.5	46.9	2.8	2.34	0.43
Q8BG32_PS	Psmd11	26S proteas	29	28.9	6.7	7.3	4.3	3.98	0.25	1342.4	271.5	330.5	4.9	4.06	0.25
E9PUD1_E9	Spag9	C-Jun-amin	14	16.5	3.8	4.2	4.3	3.98	0.25	225.1	54.3	66.1	4.1	3.40	0.29
Q8VCG1_Q	Dut	Deoxyuridi	2	24.9	5.7	6.3	4.3	3.98	0.25	49.8	11.5	14.0	4.3	3.56	0.28
Q9JKR6_HY	Hyou1	Hypoxia up	26	13.7	3.2	3.5	4.3	3.97	0.25	532.4	106.7	129.9	5.0	4.10	0.24
Q8CGC7_SY	Eprs	Bifunctiona	44	40.9	9.5	10.3	4.3	3.96	0.25	2761.8	802.8	977.1	3.4	2.83	0.35

Q8C1A5_TI	Thop1	Thimet olig	4	11.0	2.5	2.8	4.3	3.95	0.25	45.7	11.4	13.9	4.0	3.30	0.30
Q8VDM4_P	Psmd2	26S protea	28	45.0	10.5	11.5	4.3	3.93	0.25	1777.7	435.3	529.8	4.1	3.36	0.30
Q8QZZ7_TP	Tprkb	EKC/KEOPS	3	21.0	4.9	5.3	4.3	3.92	0.25	51.3	12.7	15.5	4.0	3.31	0.30
Q3UJK4_G	Gtpbp2	GTP-bindin	1	12.9	3.0	3.3	4.3	3.92	0.26	12.9	3.0	3.7	4.3	3.51	0.28
Q91YR1_TV	Twf1	Twinfilin-1	1	24.5	5.8	6.3	4.3	3.90	0.26	24.5	5.8	7.0	4.3	3.49	0.29
Q9R112_SC	Sqrdl	Sulfide:qui	1	6.9	1.6	1.8	4.2	3.88	0.26	6.9	1.6	2.0	4.2	3.48	0.29
Q61151_2A	Ppp2r5e	Serine/thre	1	8.4	2.0	2.2	4.2	3.88	0.26	8.4	2.0	2.4	4.2	3.47	0.29
Q8BJW6_EI	Eif2a	Eukaryotic	24	24.6	5.8	6.3	4.2	3.87	0.26	777.4	191.9	233.5	4.1	3.33	0.30
Q3TXS7_PS	Psmd1	26S protea	30	30.3	7.2	7.8	4.2	3.87	0.26	1363.2	303.6	369.5	4.5	3.69	0.27
P09602_HI	Hmgn2	Non-histon	1	10.6	2.5	2.8	4.2	3.85	0.26	10.6	2.5	3.1	4.2	3.45	0.29
Q60864_ST	Stip1	Stress-indu	6	16.5	3.9	4.3	4.2	3.83	0.26	128.1	27.3	33.3	4.7	3.85	0.26
P40124_CA	Cap1	Adenylyl cy	7	36.0	8.6	9.4	4.2	3.83	0.26	237.0	86.5	105.3	2.7	2.25	0.44
P47809_M	Map2k4	Dual specifi	3	13.0	3.1	3.4	4.2	3.83	0.26	42.4	9.8	11.9	4.3	3.56	0.28
P57759_EF	Erp29	Endoplasm	1	8.1	2.0	2.1	4.2	3.82	0.26	8.1	2.0	2.4	4.2	3.42	0.29
Q69Z37_SA	Samd9l	Sterile alph	18	35.3	8.5	9.3	4.2	3.81	0.26	698.1	198.7	241.8	3.5	2.89	0.35
Q99J83_AT	Atg5	Autophagy	1	14.7	3.6	3.9	4.1	3.80	0.26	14.7	3.6	4.3	4.1	3.40	0.29
P24527_LK	Lta4h	Leukotrien	6	8.8	2.1	2.3	4.1	3.79	0.26	61.6	14.4	17.6	4.3	3.51	0.28
Q921I9_EX	Exosc4	Exosome cc	1	5.4	1.3	1.4	4.1	3.77	0.27	5.4	1.3	1.6	4.1	3.38	0.30
Q9D8W5_P	Psmd12	26S protea	27	25.8	6.3	6.8	4.1	3.77	0.27	1066.1	305.4	371.7	3.5	2.87	0.35
Q9CQC6_B	Bzw1	Basic leucir	4	24.2	5.9	6.4	4.1	3.77	0.27	97.0	23.5	28.6	4.1	3.39	0.29
P62192_PF	Psmc1	26S protea	22	28.2	6.9	7.5	4.1	3.75	0.27	1239.3	287.0	349.3	4.3	3.55	0.28
Q99J77_Q9	Nans	N-acetylneu	2	10.6	2.6	2.8	4.1	3.75	0.27	21.3	5.2	6.3	4.1	3.36	0.30
Q6NXL1_Q	Sec24d	Protein Sec	7	38.4	9.4	10.3	4.1	3.74	0.27	212.5	67.2	81.7	3.2	2.60	0.38
Q8VI75_IP	Ipo4	Importin-4	4	30.0	7.4	8.0	4.1	3.74	0.27	114.4	29.1	35.4	3.9	3.24	0.31
Q61081_CI	Cdc37	Hsp90 co-c	5	22.3	5.5	6.0	4.1	3.73	0.27	125.7	32.1	39.1	3.9	3.21	0.31
Q9R1K9_CI	Cetn2	Centrin-2 C	3	18.4	4.6	5.0	4.0	3.71	0.27	49.2	23.7	28.8	2.1	1.71	0.59
Q8CD10_M	Micu2	Calcium up	1	5.9	1.5	1.6	4.0	3.70	0.27	5.9	1.5	1.8	4.0	3.32	0.30
Q01730_RS	Rsu1	Ras suppres	5	24.3	6.1	6.6	4.0	3.66	0.27	98.0	26.3	32.0	3.7	3.06	0.33
P17427_AP	Ap2a2	AP-2 compl	12	21.3	5.3	5.8	4.0	3.66	0.27	297.6	88.0	107.1	3.4	2.78	0.36
G5E8S8_G5	Mpp7	MAGUK p5	3	9.3	2.3	2.6	4.0	3.65	0.27	29.9	7.3	8.9	4.1	3.36	0.30
Q99JI4_PSI	Psmd6	26S protea	8	20.2	5.1	5.5	4.0	3.65	0.27	179.8	48.7	59.2	3.7	3.04	0.33
Q61171_PI	Prdx2	Peroxiredo	3	28.5	7.2	7.8	4.0	3.64	0.27	66.9	17.7	21.5	3.8	3.11	0.32
Q62465_VA	Vat1	Synaptic ve	28	40.2	10.2	11.1	3.9	3.61	0.28	1434.3	346.6	421.9	4.1	3.40	0.29
Q9Z1F9_SA	Uba2	SUMO-activ	3	25.0	6.4	7.0	3.9	3.57	0.28	83.4	25.5	31.0	3.3	2.69	0.37
P47915_RL	Rpl29	60S ribosor	8	167.7	43.1	47.0	3.9	3.57	0.28	3275.7	993.8	1209.6	3.3	2.71	0.37
Q9DBL1_AC	Acadsb	Short/bran	1	6.1	1.6	1.7	3.9	3.56	0.28	6.1	1.6	1.9	3.9	3.19	0.31
Q6ZQB6_VI	Ppip5k2	Inositol hex	1	6.8	1.8	1.9	3.9	3.56	0.28	6.8	1.8	2.1	3.9	3.19	0.31
Q2NL51_G	Gsk3a	Glycogen sy	1	15.7	4.1	4.4	3.9	3.54	0.28	15.7	4.1	5.0	3.9	3.17	0.32
Q9D172_ES	D10Jhu81e	ES1 protein	2	14.2	3.7	4.0	3.9	3.54	0.28	28.5	7.4	9.0	3.9	3.17	0.32
P45591_CC	Cfl2	Cofilin-2 OS	3	10.7	2.8	3.0	3.8	3.53	0.28	31.2	7.9	9.6	4.0	3.26	0.31
P97372_PS	Psme2	Proteasom	17	34.5	9.0	9.8	3.8	3.50	0.29	794.5	174.3	212.2	4.6	3.75	0.27
P05132_KA	Prkaca	cAMP-depe	3	25.4	6.7	7.3	3.8	3.48	0.29	76.3	20.7	25.2	3.7	3.03	0.33
Q5SUQ9_C	Ctc1	CST comple	2	17.2	4.5	5.0	3.8	3.48	0.29	34.5	9.1	11.1	3.8	3.12	0.32
Q99LD4_CS	Gps1	COP9 signa	8	36.7	9.7	10.6	3.8	3.47	0.29	319.7	79.3	96.5	4.0	3.31	0.30
Q9WUP7_U	Uchl5	Ubiquitin c	9	17.0	4.5	4.9	3.8	3.46	0.29	186.2	53.1	64.6	3.5	2.88	0.35
Q9QXL2_KI	Kif21a	Kinesin-like	1	5.9	1.6	1.7	3.8	3.46	0.29	5.9	1.6	1.9	3.8	3.10	0.32
Q99J45_NF	Nrbp1	Nuclear rec	1	21.2	5.6	6.1	3.8	3.44	0.29	21.2	5.6	6.9	3.8	3.09	0.32
P31750_AK	Akt1	RAC-alpha s	2	13.7	3.6	4.0	3.8	3.44	0.29	27.3	7.3	8.9	3.8	3.09	0.32
Q9JMA1_U	Usp14	Ubiquitin c	9	11.5	3.1	3.3	3.8	3.44	0.29	91.4	46.1	56.2	2.0	1.63	0.61
Q05920_PY	Pc	Pyruvate ca	2	11.8	3.1	3.4	3.7	3.43	0.29	23.5	6.3	7.7	3.7	3.07	0.33
Q99LP6_GI	Grpel1	GrpE protei	2	9.6	2.6	2.8	3.7	3.42	0.29	19.2	5.2	6.3	3.7	3.07	0.33
Q9CQK7_R	Rwdd1	RWD doma	3	66.4	17.8	19.4	3.7	3.41	0.29	215.6	59.6	72.6	3.6	2.97	0.34
Q78ZA7_NI	Nap1l4	Nucleosom	3	13.1	3.5	3.8	3.7	3.41	0.29	36.0	10.8	13.2	3.3	2.73	0.37
Q99JY9_AR	Actr3	Actin-relate	5	17.1	4.6	5.0	3.7	3.40	0.29	91.5	31.7	38.6	2.9	2.37	0.42
A2AF47_DC	Dock11	Dedicator c	6	27.0	7.3	8.0	3.7	3.39	0.29	160.3	45.9	55.8	3.5	2.87	0.35
Q9D906_A	Atg7	Ubiquitin-l	5	9.7	2.6	2.8	3.7	3.39	0.29	48.1	18.0	21.9	2.7	2.20	0.45
Q8VI93_OA	Oas3	2'-5'-oligoa	11	27.1	7.3	8.0	3.7	3.39	0.29	426.2	115.3	140.3	3.7	3.04	0.33
P50431_GI	Shmt1	Serine hydr	5	21.7	5.9	6.4	3.7	3.39	0.29	212.8	52.0	63.3	4.1	3.36	0.30
O54781_SF	Srpk2	SRSF protei	3	31.4	8.5	9.3	3.7	3.39	0.29	79.6	24.3	29.5	3.3	2.70	0.37
Q8BY87_UI	Usp47	Ubiquitin c	2	16.3	4.4	4.8	3.7	3.39	0.29	32.7	8.8	10.8	3.7	3.04	0.33
Q9WUM5_	Suclg1	Succinyl-Co	2	22.9	6.2	6.8	3.7	3.39	0.29	45.9	12.4	15.1	3.7	3.04	0.33
Q99MN1_S	Kars	Lysine--tRN	20	28.0	7.6	8.3	3.7	3.38	0.30	555.3	198.9	242.1	2.8	2.29	0.44
Q61699_HS	Hsph1	Heat shock	3	15.2	4.1	4.5	3.7	3.38	0.30	57.3	12.3	15.0	4.6	3.82	0.26
A2CG63_AI	Arid4b	AT-rich inte	1	9.2	2.5	2.7	3.7	3.36	0.30	9.2	2.5	3.1	3.7	3.01	0.33
Q8C0L8_CC	Cog5	Conserved	1	6.4	1.8	1.9	3.6	3.34	0.30	6.4	1.8	2.1	3.6	3.00	0.33
O88271_CI	Cfdp1	Craniofacia	1	18.4	5.1	5.5	3.6	3.33	0.30	18.4	5.1	6.2	3.6	2.98	0.34
P14685_PS	Psmd3	26S protea	25	40.8	11.3	12.3	3.6	3.31	0.30	1200.4	334.9	407.7	3.6	2.94	0.34
P40142_TK	Tkt	Transketola	62	52.3	14.5	15.9	3.6	3.30	0.30	4353.2	1044.0	1270.7	4.2	3.43	0.29
Q9EPL8_IP	Ipo7	Importin-7	6	16.4	4.6	5.0	3.6	3.30	0.30	127.8	36.9	44.9	3.5	2.85	0.35
Q64514_TF	Tpp2	Tripeptidyl	12	15.5	4.3	4.7	3.6	3.30	0.30	314.0	60.1	73.1	5.2	4.30	0.23
P07901_HS	Hsp90aa1	Heat shock	85	94.0	26.2	28.5	3.6	3.29	0.30	18117.1	4830.8	5879.9	3.8	3.08	0.32
Q9ES74_NE	Nek7	Serine/thre	1	9.9	2.8	3.0	3.6	3.27	0.31	9.9	2.8	3.4	3.6	2.93	0.34
Q9CQY6_U	Uqcc2	Ubiquinol-	1	8.3	2.3	2.6	3.6	3.27	0.31	8.3	2.3	2.9	3.6	2.93	0.34
P15092_IFI	Ifi204	Interferon-	9	18.2	5.1	5.6	3.6	3.27	0.31	162.5	51.3	62.5	3.2	2.60	0.38
Q8BU30_SY	Iars	Isoleucine-	32	33.4	9.4	10.2	3.6	3.27	0.31	1190.5	433.6	527.8	2.7	2.26	0.44
Q8BMF4_O	Dlat	Dihydrolip	9	18.4	5.2	5.6	3.6	3.26	0.31	215.3	45.7	55.6	4.7	3.87	0.26
O88685_PI	Psmc3	26S protea	27	28.6	8.1	8.8	3.5	3.25	0.31	1379.4	296.2	360.5	4.7	3.83	0.26
O08539_BI	Bin1	Myc box-de	8	14.7	4.1	4.5	3.5	3.25	0.31	190.8	60.0	73.1	3.2	2.61	0.38
P63038_CH	Hspd1	60 kDa heat	27	30.9	8.7	9.5	3.5	3.25	0.31	1321.3	355.0	432.1	3.7	3.06	0.33
Q64362_AI	Aktip	AKT-interac	1	5.9	1.7	1.8	3.5	3.23	0.31	5.9	1.7	2.0	3.5	2.90	0.35
Q91VR8_BI	Brk1	Protein BRI	1	22.6	6.4	7.0	3.5	3.22	0.31	22.6	6.4	7.8	3.5	2.88	0.35
Q9CYG7_TC	Tomm34	Mitochond	2	12.2	3.5	3.8	3.5	3.20	0.31	24.4	7.0	8.5	3.5	2.87	0.35
P80317_TC	Cct6a	T-complex	34	60.0	17.2	18.8	3.5	3.20	0.31	5005.6	1771.8	2156.6	2.8	2.32	0.43
Q8QZT1_TH	Acat1	Acetyl-CoA	2	11.0	3.1	3.4	3.5	3.19	0.31	21.9	6.3	7.7	3.5	2.86	0.35
G3X9F7_G3	Ddx60	MCG11385	8	15.6	4.5	4.9	3.5	3.19	0.31	117.5	34.4	41.9	3.4	2.81	0.36
Q9D2R8_R	Mrps33	28S ribosor	1	17.2	5.0	5.4	3.5	3.18	0.31	17.2	5.0	6.0	3.5	2.85	0.35
Q8C1Z8_TN	Trmt10a	tRNA meth	2	17.4	5.0	5.5	3.5	3.16	0.32	34.8	10.1	12.3	3.5	2.83	0.35
Q8BUR4_D	Dock1	Dedicator c	4	20.9	6.1	6.6	3.4	3.16	0.32	81.3	24.9	30.3	3.3	2.68	0.37
Q8CCP0_NI	Nemf	Nuclear exp	1	9.2	2.7	2.9	3.4	3.14	0.32	9.2	2.7	3.3	3.4	2.82	0.35
P18760_CC	Cfl1	Cofilin-1 OS	5	47.6	13.9	15.1	3.4	3.14	0.32	262.9	92.6	112.7	2.8	2.33	0.43
Q8BKG3_P	Ptk7	Inactive tyr	2	20.6	6.0	6.6	3.4	3.14	0.32	41.2	12.0	14.6	3.4	2.81	0.36
Q99PL5_RF	Rrbp1	Ribosome-b	6	19.8	5.8	6.3	3.4	3.13	0.32	143.0	38.7	47.1	3.7	3.04	0.33
Q9JHI7_EX	Exosc9	Exosome cc	1	35.1	10.3	11.2	3.4	3.13	0.32	35.1	10.3	12.5	3.4	2.81	0.36
P61161_AF	Actr2	Actin-relate	8	19.3	5.7	6.2	3.4	3.12	0.32	162.7	42.8	52.1	3.8	3.12	0.32
P62196_PF	Psmc5	26S protea	20	33.9	9.9	10.8	3.4	3.12	0.32	1027.9	272.6	331.8	3.8	3.10	0.32
G3X920_G3	Armc8	Armadillo r	1	14.6	4.3	4.7	3.4	3.12	0.32	14.6	4.3	5.2	3.4	2.80	0.36
Q8BKC5_IP	Ipo5	Importin-5	26	25.2	7.4	8.1	3.4	3.12	0.32	976.2	235.5	286.6	4.1	3.41	0.29
Q8BP47_SY	Nars	Asparagine	4	18.4	5.4	5.9	3.4	3.11	0.32	97.7	21.3	26.0	4.6	3.76	0.27
Q8BMJ2_SY	Lars	Leucine--tR	40	32.9	9.7	10.6	3.4	3.11	0.32	1576.1	475.7	579.0	3.3	2.72	0.37
P57746_VA	Atp6v1d	V-type prot	5	17.7	5.2	5.7	3.4	3.10	0.32	95.6	29.8	36.3	3.2	2.64	0.38
P31230_AI	Aimp1	Aminoacyl	2	65.0	19.2	20.9	3.4	3.10	0.32	130.0	38.4	46.7	3.4	2.78	0.36
Q9CR26_VT	Vta1	Vacuolar pr	1	8.6	2.5	2.8	3.4	3.10	0.32	8.6	2.5	3.1	3.4	2.78	0.36
Q8BMS1_E	Hadha	Trifunction	9	33.3	9.9	10.8	3.4	3.10	0.32	301.8	84.2	102.5	3.6	2.94	0.34
Q9D1A2_CI	Cndp2	Cytosolic n	4	15.4	4.6	5.0	3.4	3.09	0.32	55.1	18.0	21.9	3.1	2.52	0.40
P08074_CE	Cbr2	Carbonyl re	4	35.2	10.5	11.4	3.4	3.09	0.32	131.7	70.3	85.6	1.9	1.54	0.65
Q9DBC7_K	Prkar1a	cAMP-depe	2	32.1	9.6	10.4	3.4	3.08	0.33	64.1	19.1	23.3	3.4	2.76	0.36
P62751_RL	Rpl23a	60S ribosor	19	162.5	48.5	52.9	3.4	3.07	0.33	6253.6	2149.6	2616.4	2.9	2.39	0.42
Q0VGY8_TA	Tanc1	Protein TAN	3	9.5	2.9	3.1	3.3	3.06	0.33	27.8	10.7	13.0	2.6	2.14	0.47
Q9JLI8_SAF	Sart3	Squamous	15	12.1	3.6	4.0	3.3	3.06	0.33	350.0	78.1	95.0	4.5	3.68	0.27
Q91VH2_SI	Snx9	Sorting nex	5	9.2	2.8	3.0	3.3	3.05	0.33	107.8	31.9	38.8	3.4	2.78	0.36
Q9DBC3_CI	Cmtr1	Cap-specifi	2	10.4	3.1	3.4	3.3	3.05	0.33	20.8	6.2	7.6	3.3	2.73	0.37
P19253_RL	Rpl13a	60S ribosor	15	75.7	22.8	24.9	3.3	3.05	0.33	1473.9	452.5	550.8	3.3	2.68	0.37
P70303_PY	Ctps2	CTP syntha	14	30.6	9.2	10.1	3.3	3.05	0.33	638.9	261.8	318.7	2.4	2.01	0.50

Q8R5H1_U	Usp15	Ubiquitin c	1	11.9	3.6	3.9	3.3	3.04	0.33	11.9	3.6	4.4	3.3	2.72	0.37
Q8C8R3_A	Ank2	Ankyrin-2	6	13.0	3.9	4.3	3.3	3.04	0.33	82.2	30.5	37.1	2.7	2.21	0.45
P50518_V	Atp6v1e1	V-type prot	4	24.7	7.5	8.2	3.3	3.03	0.33	96.5	36.9	44.9	2.6	2.15	0.47
Q80XI3_IF	Eif4g3	Eukaryotic	6	17.9	5.4	5.9	3.3	3.03	0.33	138.8	41.7	50.8	3.3	2.73	0.37
Q9D1R9_R	Rpl34	60S ribosor	9	25.4	7.7	8.4	3.3	3.02	0.33	2272.3	766.5	933.0	3.0	2.44	0.41
Q9CZ30_O	Ola1	Obg-like AT	3	8.9	2.7	2.9	3.3	3.02	0.33	37.8	8.3	10.1	4.6	3.74	0.27
Q9JLQ0_C	Cd2ap	CD2-associ	3	17.8	5.4	5.9	3.3	3.01	0.33	60.2	16.5	20.0	3.7	3.01	0.33
Q9JHQ5_L	Lztfl1	Leucine zip	1	21.7	6.6	7.2	3.3	3.01	0.33	21.7	6.6	8.0	3.3	2.70	0.37
Q9Z2X2_P	Psmd10	26S protea	3	9.7	3.0	3.2	3.3	3.01	0.33	25.7	9.6	11.7	2.7	2.20	0.45
Q9WVE8_P	Pacsin2	Protein kin	17	46.4	14.2	15.5	3.3	2.99	0.33	1104.0	351.8	428.2	3.1	2.58	0.39
Q99LX0_P	Park7	Protein deg	1	15.6	4.8	5.2	3.2	2.98	0.34	15.6	4.8	5.8	3.2	2.67	0.37
Q60597_O	Ogdh	2-oxogluta	3	6.4	2.0	2.2	3.2	2.98	0.34	27.2	6.5	8.0	4.2	3.42	0.29
Q9D051_O	Pdhb	Pyruvate de	6	21.9	6.7	7.4	3.2	2.98	0.34	164.5	42.7	52.0	3.9	3.17	0.32
G3XA21_G	Mroh1	MCG13444	1	13.1	4.0	4.4	3.2	2.97	0.34	13.1	4.0	4.9	3.2	2.66	0.38
Q8R1F6_H	Hid1	Protein HID	6	14.7	4.5	4.9	3.2	2.96	0.34	88.0	28.9	35.2	3.0	2.50	0.40
Q68FE6_FA	Fam65a	Protein FA	1	10.3	3.2	3.5	3.2	2.96	0.34	10.3	3.2	3.9	3.2	2.66	0.38
P14869_R	Rplp0	60S acidic	44	156.8	48.8	53.2	3.2	2.95	0.34	10025.1	3306.9	4025.1	3.0	2.49	0.40
Q9D7X3_D	Dusp3	Dual specifi	1	44.5	13.9	15.1	3.2	2.95	0.34	44.5	13.9	16.9	3.2	2.64	0.38
Q922Q2_R	Riok1	Serine/thre	1	25.1	7.8	8.5	3.2	2.94	0.34	25.1	7.8	9.5	3.2	2.64	0.38
Q9CWJ9_P	Atic	Bifunctiona	11	23.9	7.5	8.1	3.2	2.94	0.34	388.1	86.5	105.3	4.5	3.69	0.27
Q8CI94_PY	Pygb	Glycogen p	11	15.4	4.8	5.3	3.2	2.93	0.34	256.1	84.2	102.5	3.0	2.50	0.40
Q6P2K6_P	Smek1	Serine/thre	8	14.1	4.4	4.8	3.2	2.93	0.34	114.4	75.5	91.9	1.5	1.24	0.80
Q02053_U	Uba1	Ubiquitin-l	22	19.8	6.2	6.8	3.2	2.92	0.34	560.8	179.1	218.0	3.1	2.57	0.39
Q8CD92_T	Ttc27	Tetratricop	3	16.5	5.2	5.7	3.2	2.91	0.34	39.2	13.3	16.2	2.9	2.42	0.41
Q62384_Z	Zpr1	Zinc finger	1	12.2	3.9	4.2	3.2	2.91	0.34	12.2	3.9	4.7	3.2	2.61	0.38
O08529_C	Capn2	Calpain-2 c	11	15.1	4.8	5.2	3.2	2.91	0.34	171.6	55.5	67.6	3.1	2.54	0.39
G3X972_G	Sec24c	Protein Sec	8	19.0	6.0	6.6	3.2	2.90	0.34	193.3	67.6	82.3	2.9	2.35	0.43
Q9JHR7_ID	Ide	Insulin-deg	5	8.7	2.8	3.0	3.2	2.90	0.35	47.3	15.5	18.9	3.1	2.51	0.40
Q9CR00_P	Psmd9	26S protea	1	25.5	8.1	8.8	3.2	2.89	0.35	25.5	8.1	9.8	3.2	2.59	0.39
O35685_N	Nudc	Nuclear mi	10	14.8	4.7	5.1	3.2	2.89	0.35	214.2	61.0	74.2	3.5	2.89	0.35
Q9DCL9_P	Paics	Multifuncti	15	24.3	7.7	8.4	3.2	2.89	0.35	331.6	118.4	144.1	2.8	2.30	0.43
Q8BGA5_K	Krr1	KRR1 small	1	14.7	4.7	5.1	3.2	2.89	0.35	14.7	4.7	5.7	3.2	2.59	0.39
Q9QXG4_A	Acss2	Acetyl-coer	4	8.5	2.7	2.9	3.2	2.89	0.35	31.6	11.9	14.5	2.6	2.18	0.46
Q8BTY8_SC	Scfd2	Sec1 family	1	11.1	3.5	3.8	3.1	2.89	0.35	11.1	3.5	4.3	3.1	2.59	0.39
Q8VHN8_S	Nudt16l1	Protein syn	1	24.3	7.7	8.4	3.1	2.88	0.35	24.3	7.7	9.4	3.1	2.58	0.39
Q9CX56_P	Psmd8	26S protea	5	27.0	8.6	9.4	3.1	2.88	0.35	257.0	63.7	77.6	4.0	3.31	0.30
Q69ZS7_H	Hbs1l	HBS1-like p	3	11.3	3.6	3.9	3.1	2.87	0.35	33.2	11.0	13.4	3.0	2.47	0.40
P34152_F	Ptk2	Focal adhes	4	14.5	4.6	5.1	3.1	2.87	0.35	54.1	18.2	22.1	3.0	2.44	0.41
Q9D0K2_S	Oxct1	Succinyl-Co	3	10.4	3.3	3.6	3.1	2.86	0.35	34.3	11.5	13.9	3.0	2.46	0.41
Q91Z40_Q	Gbp7	Gbp6 prote	9	10.9	3.5	3.8	3.1	2.86	0.35	117.2	31.8	38.7	3.7	3.03	0.33
Q8BRN9_C	Cc2d1b	Coiled-coil	3	10.4	3.3	3.6	3.1	2.86	0.35	30.4	21.0	25.6	1.4	1.19	0.84
B2RXC1_T	Trappc11	Trafficking	3	15.9	5.1	5.6	3.1	2.86	0.35	40.8	14.3	17.4	2.9	2.35	0.43
Q922B2_S	Dars	Aspartate--	28	38.8	12.5	13.6	3.1	2.85	0.35	1388.6	411.6	501.0	3.4	2.77	0.36
O08528_H	Hk2	Hexokinase	3	12.8	4.1	4.5	3.1	2.85	0.35	38.2	12.1	14.7	3.2	2.59	0.39
Q3UZ39_L	Lrrfip1	Leucine-ric	5	11.8	3.8	4.1	3.1	2.85	0.35	58.4	33.8	41.1	1.7	1.42	0.70
Q3TCJ1_F1	Fam175b	BRISC com	2	9.8	3.2	3.4	3.1	2.84	0.35	19.6	6.3	7.7	3.1	2.55	0.39
Q9EQK5_M	Mvp	Major vault	10	16.4	5.3	5.8	3.1	2.84	0.35	154.6	68.2	83.1	2.3	1.86	0.54
Q8BYC6_T	Taok3	Serine/thre	1	13.7	4.4	4.8	3.1	2.84	0.35	13.7	4.4	5.4	3.1	2.54	0.39
Q6PAR5_G	Gapvd1	GTPase-acti	7	11.7	3.8	4.1	3.1	2.83	0.35	97.0	38.1	46.4	2.5	2.09	0.48
Q9ERF3_W	Wdr61	WD repeat-	7	25.7	8.3	9.1	3.1	2.83	0.35	196.6	65.2	79.4	3.0	2.48	0.40
P97461_R	Rps5	40S ribosor	9	16.9	5.5	6.0	3.1	2.82	0.35	450.1	264.4	321.8	1.7	1.40	0.71
Q9D071_M	Mms19	MMS19 nu	4	25.6	8.3	9.1	3.1	2.82	0.35	107.7	35.7	43.5	3.0	2.48	0.40
Q9D1H7_G	Get4	Golgi to ER	4	12.9	4.2	4.6	3.1	2.81	0.36	66.2	17.7	21.6	3.7	3.07	0.33
Q91XU3_P	Pip4k2c	Phosphatid	1	37.3	12.2	13.3	3.1	2.81	0.36	37.3	12.2	14.8	3.1	2.52	0.40
Q9R1P0_P	Psma4	Proteasom	2	16.3	5.3	5.8	3.1	2.80	0.36	32.7	10.7	13.0	3.1	2.51	0.40
Q91VA7_Q	Idh3b	Isocitrate d	4	26.4	8.6	9.4	3.1	2.80	0.36	96.9	30.9	37.6	3.1	2.58	0.39
A2AWP8_A	Arhgef10l	Rho guanin	1	9.7	3.2	3.5	3.0	2.79	0.36	9.7	3.2	3.9	3.0	2.50	0.40
Q99K70_R	Rragc	Ras-related	6	16.5	5.4	5.9	3.0	2.79	0.36	91.0	38.1	46.3	2.4	1.96	0.51
Q6P8X1_S	Snx6	Sorting nex	7	50.8	16.7	18.3	3.0	2.78	0.36	287.0	90.4	110.0	3.2	2.61	0.38
Q922H4_G	Gmppa	Mannose-1	1	4.0	1.3	1.4	3.0	2.78	0.36	4.0	1.3	1.6	3.0	2.49	0.40
P70349_H	Hint1	Histidine tr	1	258.1	85.2	93.0	3.0	2.78	0.36	258.1	85.2	103.7	3.0	2.49	0.40
O35350_C	Capn1	Calpain-1 c	11	22.4	7.4	8.1	3.0	2.77	0.36	264.5	82.6	100.5	3.2	2.63	0.38
Q9D5V5_C	Cul5	Cullin-5 OS	11	14.3	4.7	5.2	3.0	2.77	0.36	176.9	64.9	79.0	2.7	2.24	0.45
Q7TNP2_2	Ppp2r1b	Serine/thre	2	17.1	5.7	6.2	3.0	2.77	0.36	34.2	11.3	13.8	3.0	2.48	0.40
Q3THK7_G	Gmps	GMP synth	8	13.5	4.5	4.9	3.0	2.77	0.36	107.2	70.5	85.8	1.5	1.25	0.80
Q9D0I9_SY	Rars	Arginine--t	16	26.5	8.8	9.6	3.0	2.76	0.36	552.8	129.6	157.7	4.3	3.50	0.29
Q9CQI7_R	Snrpb2	U2 small nu	3	62.0	20.6	22.5	3.0	2.76	0.36	169.6	57.7	70.2	2.9	2.42	0.41
P50516_V	Atp6v1a	V-type prot	12	16.8	5.6	6.1	3.0	2.75	0.36	356.4	80.9	98.5	4.4	3.62	0.28
Q80X85_R	Mrps7	28S ribosor	1	8.1	2.7	2.9	3.0	2.75	0.36	8.1	2.7	3.3	3.0	2.47	0.41
Q9Z1D1_E	Eif3g	Eukaryotic	13	23.1	7.7	8.4	3.0	2.75	0.36	543.1	334.7	407.4	1.6	1.33	0.75
Q6P5H2_N	Nes	Nestin OS=	4	16.9	5.6	6.1	3.0	2.75	0.36	75.2	45.0	54.7	1.7	1.37	0.73
Q8BP67_R	Rpl24	60S ribosor	12	31.0	10.4	11.3	3.0	2.74	0.36	2600.0	1102.6	1342.1	2.4	1.94	0.52
P33175_K	Kif5a	Kinesin hea	9	21.4	7.2	7.8	3.0	2.74	0.36	364.3	100.8	122.7	3.6	2.97	0.34
P58252_E	Eef2	Elongation	62	56.7	19.0	20.7	3.0	2.74	0.36	5497.0	2177.2	2650.0	2.5	2.07	0.48
P42208_SE	2-Sep	Septin-2 O	7	46.9	15.7	17.1	3.0	2.74	0.37	306.7	97.7	118.9	3.1	2.58	0.39
F6ZAW1_F	Cald1	Protein Cal	1	9.7	3.3	3.6	3.0	2.74	0.37	9.7	3.3	4.0	3.0	2.45	0.41
Q61166_M	Mapre1	Microtubul	6	32.8	11.0	12.0	3.0	2.73	0.37	242.7	98.9	120.4	2.5	2.02	0.50
Q9Z2H5_E	Epb41l1	Band 4.1-li	1	7.9	2.6	2.9	3.0	2.72	0.37	7.9	2.6	3.2	3.0	2.44	0.41
Q9WVJ2_P	Psmd13	26S protea	24	21.5	7.2	7.9	3.0	2.72	0.37	909.8	218.2	265.5	4.2	3.43	0.29
Q6PER3_M	Mapre3	Microtubul	3	32.6	11.0	12.0	3.0	2.72	0.37	73.0	24.9	30.3	2.9	2.41	0.42
Q9CR29_C	Ccdc43	Coiled-coil	2	15.5	5.2	5.7	3.0	2.72	0.37	31.0	10.4	12.7	3.0	2.44	0.41
P16254_S	Srp14	Signal reco	2	31.8	10.7	11.7	3.0	2.72	0.37	63.5	21.4	26.1	3.0	2.43	0.41
P61759_P	Vbp1	Prefoldin s	7	16.2	5.5	6.0	3.0	2.71	0.37	107.0	46.6	56.7	2.3	1.89	0.53
Q05D44_IF	Eif5b	Eukaryotic	12	21.9	7.4	8.1	3.0	2.71	0.37	284.8	119.7	145.7	2.4	1.96	0.51
P51174_A	Acadl	Long-chain	1	9.7	3.3	3.6	3.0	2.71	0.37	9.7	3.3	4.0	3.0	2.43	0.41
Q9CQM9_	Glrx3	Glutaredox	6	27.2	9.2	10.1	2.9	2.70	0.37	154.4	61.7	75.2	2.5	2.05	0.49
Q9CWK8_S	Snx2	Sorting nex	7	17.4	5.9	6.5	2.9	2.69	0.37	136.2	61.0	74.2	2.2	1.84	0.54
Q9Z0N2_IF	Eif2s3y	Eukaryotic	1	16.0	5.5	6.0	2.9	2.68	0.37	16.0	5.5	6.7	2.9	2.40	0.42
Q9WVA3_E	Bub3	Mitotic che	2	9.4	3.2	3.5	2.9	2.67	0.37	18.7	6.4	7.8	2.9	2.40	0.42
Q9Z2I9_SU	Sucla2	Succinyl-Co	4	14.4	4.9	5.4	2.9	2.67	0.37	61.6	19.0	23.1	3.2	2.67	0.37
P32921_SY	Wars	Tryptophar	1	5.1	1.8	1.9	2.9	2.67	0.37	5.1	1.8	2.1	2.9	2.39	0.42
Q01853_T	Vcp	Transitiona	6	27.0	9.3	10.1	2.9	2.67	0.38	159.1	57.7	70.2	2.8	2.27	0.44
Q8BTS4_N	Nup54	Nuclear po	4	13.6	4.7	5.1	2.9	2.66	0.38	60.2	24.0	29.2	2.5	2.06	0.48
Q9CWM4_	Pfdn1	Prefoldin s	1	24.9	8.6	9.4	2.9	2.65	0.38	24.9	8.6	10.5	2.9	2.38	0.42
Q8K2Z2_P	Prpf39	Pre-mRNA-	1	10.2	3.5	3.9	2.9	2.64	0.38	10.2	3.5	4.3	2.9	2.37	0.42
P83882_R	Rpl36a	60S ribosor	4	200.2	69.7	76.0	2.9	2.63	0.38	863.0	282.6	344.0	3.1	2.51	0.40
Q80ZS3_RT	Mrps26	28S ribosor	2	13.6	4.7	5.2	2.9	2.63	0.38	27.3	9.5	11.6	2.9	2.36	0.42
P62827_R	Ran	GTP-bindin	5	44.9	15.7	17.1	2.9	2.62	0.38	283.6	98.1	119.4	2.9	2.38	0.42
Q9CXU9_E	Eif1b	Eukaryotic	2	27.6	9.7	10.6	2.9	2.62	0.38	55.2	19.3	23.5	2.9	2.34	0.43
Q9CZM2_R	Rpl15	60S ribosor	18	99.3	34.9	38.1	2.8	2.60	0.38	1750.1	862.7	1050.1	2.0	1.67	0.60
B2RR83_YT	Ythdc2	Probable A	1	10.1	3.6	3.9	2.8	2.59	0.39	10.1	3.6	4.4	2.8	2.33	0.43
O88738_B	Birc6	Baculoviral	2	14.9	5.3	5.7	2.8	2.59	0.39	29.8	10.5	12.8	2.8	2.32	0.43
Q8BVE3_V	Atp6v1h	V-type prot	12	20.2	7.1	7.8	2.8	2.59	0.39	264.2	88.9	108.3	3.0	2.44	0.41
Q9QUM9_	Psma6	Proteasom	1	27.6	9.9	10.7	2.8	2.57	0.39	27.6	9.9	12.0	2.8	2.31	0.43
Q8VCB2_M	Med25	Mediator o	2	9.0	3.2	3.5	2.8	2.57	0.39	18.0	6.4	7.8	2.8	2.30	0.43
P70398_U	Usp9x	Probable u	17	16.8	6.0	6.6	2.8	2.57	0.39	284.2	115.2	140.2	2.5	2.03	0.49
O88543_C	Cops3	COP9 signa	10	15.6	5.6	6.1	2.8	2.57	0.39	285.3	69.9	85.1	4.1	3.35	0.30
P62889_R	Rpl30	60S ribosor	10	162.5	58.1	63.4	2.8	2.57	0.39	3015.6	1309.8	1594.2	2.3	1.89	0.53
Q69ZF8_M	Msl2	E3 ubiquiti	1	9.6	3.4	3.7	2.8	2.56	0.39	9.6	3.4	4.2	2.8	2.30	0.44
Q6PIP5_N	Nudcd1	NudC doma	5	14.5	5.2	5.7	2.8	2.56	0.39	77.2	24.1	29.4	3.2	2.63	0.38
Q6NVF4_H	Helb	DNA helica	3	18.9	6.8	7.4	2.8	2.56	0.39	56.0	19.1	23.2	2.9	2.41	0.42
P17751_T	Tpi1	Triosephos	5	14.1	5.1	5.5	2.8	2.55	0.39	185.1	50.0	60.8	3.7	3.04	0.33
Q9Z2Q6_S	5-Sep	Septin-5 O	4	10.4	3.7	4.1	2.8	2.55	0.39	71.3	22.6	27.5	3.2	2.60	0.39

Q99LC5_ET	Etfa	Electron tra	1	5.6	2.0	2.2	2.8	2.55	0.39	5.6	2.0	2.5	2.8	2.28	0.44
Q9WV86_K	Katna1	Katanin p6	1	9.7	3.5	3.8	2.8	2.54	0.39	9.7	3.5	4.2	2.8	2.28	0.44
P12849_K	Prkar1b	cAMP-depe	1	5.0	1.8	2.0	2.8	2.53	0.39	5.0	1.8	2.2	2.8	2.27	0.44
G5E8T3_G	Srp19	Signal reco	6	7.0	2.5	2.8	2.8	2.53	0.40	138.9	54.1	65.9	2.6	2.11	0.47
Q8BV66_IF	Ifi44	Interferon-	7	18.2	6.6	7.2	2.8	2.53	0.40	170.6	73.9	89.9	2.3	1.90	0.53
P35283_R	Rab12	Ras-related	1	14.1	5.1	5.6	2.8	2.52	0.40	14.1	5.1	6.3	2.8	2.26	0.44
E9Q070_E	Gm8730	Uncharacte	4	154.2	56.2	61.3	2.7	2.52	0.40	655.7	295.3	359.4	2.2	1.82	0.55
Q9Z2U0_P	Psma7	Proteasom	6	14.6	5.3	5.8	2.7	2.52	0.40	102.8	38.7	47.2	2.7	2.18	0.46
Q91V12_B	Acot7	Cytosolic a	4	19.2	7.0	7.6	2.7	2.51	0.40	87.5	28.1	34.2	3.1	2.56	0.39
Q8BPA8_D	Dpcd	Protein DP	2	20.6	7.5	8.2	2.7	2.51	0.40	41.2	15.0	18.3	2.7	2.25	0.44
Q8BJU0_S	Sgta	Small gluta	5	24.3	8.9	9.7	2.7	2.51	0.40	222.3	41.8	50.8	5.3	4.37	0.23
P63323_R	Rps12	40S riboso	4	84.4	30.8	33.6	2.7	2.51	0.40	613.1	219.4	267.0	2.8	2.30	0.44
P62862_R	Fau	40S riboso	1	429.3	157.0	171.2	2.7	2.51	0.40	429.3	157.0	191.1	2.7	2.25	0.45
O08759_U	Ube3a	Ubiquitin-	3	13.6	5.0	5.5	2.7	2.50	0.40	36.4	13.2	16.0	2.8	2.28	0.44
P10922_H	H1f0	Histone H1	11	67.0	24.6	26.8	2.7	2.50	0.40	4475.7	2288.7	2785.7	2.0	1.61	0.62
O54916_R	Reps1	RalBP1-ass	1	7.5	2.8	3.0	2.7	2.49	0.40	7.5	2.8	3.4	2.7	2.24	0.45
F8VQC1_F	Srp72	Signal reco	31	30.5	11.2	12.2	2.7	2.49	0.40	1125.0	489.5	595.8	2.3	1.89	0.53
A2AWA9_R	Rabgap1	Rab GTPase	16	11.8	4.3	4.7	2.7	2.49	0.40	261.1	81.3	98.9	3.2	2.64	0.38
Q921L5_C	Cog2	Conserved	1	11.1	4.1	4.5	2.7	2.49	0.40	11.1	4.1	5.0	2.7	2.23	0.45
P80313_T	Cct7	T-complex	52	47.3	17.4	19.0	2.7	2.48	0.40	4879.1	1700.9	2070.3	2.9	2.36	0.42
P17426_A	Ap2a1	AP-2 compl	18	23.6	8.7	9.5	2.7	2.48	0.40	475.8	191.8	233.4	2.5	2.04	0.49
P48962_A	Slc25a4	ADP/ATP tr	3	28.0	10.4	11.3	2.7	2.48	0.40	70.4	27.6	33.6	2.5	2.09	0.48
Q9Z104_H	Hmg20b	SWI/SNF-re	1	4.6	1.7	1.8	2.7	2.47	0.40	4.6	1.7	2.1	2.7	2.22	0.45
Q9D0J4_A	Arl2	ADP-ribosy	4	20.0	7.4	8.1	2.7	2.47	0.40	75.2	29.7	36.2	2.5	2.08	0.48
P49117_N	Nr2c2	Nuclear rec	1	6.3	2.3	2.5	2.7	2.46	0.41	6.3	2.3	2.8	2.7	2.21	0.45
Q9Z1Q9_S	Vars	Valine--tRN	25	36.8	13.7	15.0	2.7	2.46	0.41	1478.4	372.8	453.8	4.0	3.26	0.31
P18653_K	Rps6ka1	Ribosomal	7	22.7	8.5	9.2	2.7	2.46	0.41	199.5	90.1	109.6	2.2	1.82	0.55
Q9D898_A	Arpc5l	Actin-relate	3	48.8	18.2	19.9	2.7	2.46	0.41	121.4	90.3	109.9	1.3	1.10	0.91
Q9DBB4_N	Naa16	N-alpha-ac	7	14.5	5.4	5.9	2.7	2.45	0.41	169.1	56.8	69.2	3.0	2.44	0.41
Q8BYY4_T	Ttc39b	Tetratricop	2	9.5	3.6	3.9	2.7	2.45	0.41	19.1	7.1	8.7	2.7	2.20	0.46
Q9QXB9_D	Drg2	Developme	9	31.9	11.9	13.0	2.7	2.45	0.41	325.1	126.9	154.4	2.6	2.11	0.47
Q9JHS4_C	Clpx	ATP-depen	3	7.5	2.8	3.1	2.7	2.45	0.41	22.9	8.0	9.7	2.9	2.36	0.42
Q9DBL7_C	Coasy	Bifunction	2	20.9	7.8	8.5	2.7	2.44	0.41	41.7	15.7	19.1	2.7	2.19	0.46
Q9CZT8_R	Rab3b	Ras-related	1	6.6	2.5	2.7	2.7	2.44	0.41	6.6	2.5	3.0	2.7	2.19	0.46
Q921J2_R	Rheb	GTP-bindin	3	92.1	34.6	37.8	2.7	2.44	0.41	254.0	91.2	111.0	2.8	2.29	0.44
Q9Z2V5_H	Hdac6	Histone de	2	31.1	11.7	12.8	2.7	2.44	0.41	62.2	23.4	28.5	2.7	2.18	0.46
Q8CHC4_S	Synj1	Synaptojan	3	7.0	2.6	2.9	2.7	2.44	0.41	21.3	8.2	9.9	2.6	2.14	0.47
P31324_K	Prkar2b	cAMP-depe	3	15.2	5.7	6.2	2.7	2.44	0.41	46.1	18.6	22.6	2.5	2.04	0.49
Q6NZR5_Q	Skiv2l	Protein Ski	11	15.6	5.9	6.4	2.7	2.43	0.41	178.0	75.4	91.8	2.4	1.94	0.52
P68181_K	Prkacb	cAMP-depe	3	10.4	3.9	4.3	2.6	2.43	0.41	41.9	15.0	18.3	2.8	2.30	0.44
Q61191_H	Hcfc1	Host cell fa	18	21.8	8.3	9.0	2.6	2.42	0.41	488.1	301.8	367.3	1.6	1.33	0.75
Q9Z2E1_M	Mbd2	Methyl-Cp	2	18.5	7.0	7.6	2.6	2.42	0.41	37.0	14.0	17.1	2.6	2.17	0.46
Q921Q7_R	Rin1	Ras and Ra	1	9.9	3.8	4.1	2.6	2.41	0.41	9.9	3.8	4.6	2.6	2.16	0.46
Q68FL6_SY	Mars	Methionin	21	18.4	7.0	7.7	2.6	2.41	0.42	612.2	185.9	226.3	3.3	2.71	0.37
Q3V1H1_C	Ckap2	Cytoskelet	5	14.3	5.5	6.0	2.6	2.40	0.42	66.1	31.1	37.8	2.1	1.75	0.57
Q6PDI5_EC	Ecm29	Proteasom	18	19.9	7.6	8.3	2.6	2.39	0.42	355.6	137.5	167.4	2.6	2.12	0.47
Q61753_S	Phgdh	D-3-phosp	24	66.4	25.4	27.8	2.6	2.39	0.42	2712.9	1310.3	1594.9	2.1	1.70	0.59
P70268_P	Pkn1	Serine/thre	2	8.8	3.4	3.7	2.6	2.39	0.42	17.6	6.7	8.2	2.6	2.14	0.47
P83741_W	Wnk1	Serine/thre	2	20.1	7.7	8.4	2.6	2.39	0.42	40.2	15.4	18.8	2.6	2.14	0.47
Q8K0Q5_R	Arhgap18	Rho GTPase	1	9.9	3.8	4.1	2.6	2.39	0.42	9.9	3.8	4.6	2.6	2.14	0.47
Q8VCC1_P	Hpgd	15-hydroxy	1	27.7	10.7	11.6	2.6	2.38	0.42	27.7	10.7	13.0	2.6	2.13	0.47
Q9QY24_Z	Zbp1	Z-DNA-bind	1	20.9	8.1	8.8	2.6	2.38	0.42	20.9	8.1	9.8	2.6	2.13	0.47
P27641_X	Xrcc5	X-ray repai	10	22.2	8.6	9.3	2.6	2.38	0.42	256.4	110.3	134.3	2.3	1.91	0.52
P54103_D	Dnajc2	DnaJ homo	2	11.4	4.4	4.8	2.6	2.38	0.42	22.7	8.8	10.7	2.6	2.13	0.47
Q9WTP7_K	Ak3	GTP:AMP p	1	5.8	2.2	2.4	2.6	2.37	0.42	5.8	2.2	2.7	2.6	2.13	0.47
P63158_H	Hmgb1	High mobil	1	4.6	1.8	2.0	2.6	2.37	0.42	4.6	1.8	2.2	2.6	2.13	0.47
P28867_K	Prkcd	Protein kin	5	11.3	4.4	4.8	2.6	2.37	0.42	60.7	28.1	34.2	2.2	1.78	0.56
Q61024_A	Asns	Asparagine	49	37.2	14.4	15.7	2.6	2.37	0.42	2779.9	847.3	1031.3	3.3	2.70	0.37
Q9DB05_S	Napa	Alpha-solu	10	14.0	5.4	5.9	2.6	2.36	0.42	221.7	70.2	85.5	3.2	2.59	0.39
S4R2A9_S4	Sec31a	Protein tra	1	8.6	3.4	3.7	2.6	2.36	0.42	8.6	3.4	4.1	2.6	2.12	0.47
Q9CZN7_Q	Shmt2	Protein Shr	19	36.4	14.1	15.4	2.6	2.36	0.42	822.5	454.3	552.9	1.8	1.49	0.67
E9PWG2_E	Trappc8	Protein Tra	1	5.1	2.0	2.2	2.6	2.36	0.42	5.1	2.0	2.4	2.6	2.11	0.47
Q8R4E9_C	Cdt1	DNA replica	3	12.0	4.7	5.1	2.6	2.35	0.43	29.4	13.4	16.3	2.2	1.80	0.55
O08599_S	Stxbp1	Syntaxin-bi	11	13.1	5.1	5.6	2.6	2.34	0.43	230.4	276.4	336.4	0.8	0.68	1.46
B2RUR8_O	Otud7b	OTU domai	7	12.3	4.8	5.3	2.5	2.33	0.43	103.0	37.3	45.3	2.8	2.27	0.44
Q80T06_Q	Eef1d	Elongation	16	27.5	10.8	11.8	2.5	2.32	0.43	1407.9	432.5	526.4	3.3	2.67	0.37
Q91W90_T	Txndc5	Thioredoxi	6	35.5	14.0	15.3	2.5	2.32	0.43	242.6	109.6	133.4	2.2	1.82	0.55
Q3UA06_P	Trip13	Pachytene	7	10.6	4.2	4.6	2.5	2.32	0.43	79.2	29.0	35.3	2.7	2.24	0.45
O88879_A	Apaf1	Apoptotic	1	13.2	5.2	5.7	2.5	2.32	0.43	13.2	5.2	6.3	2.5	2.08	0.48
Q9WU28_	Pfdn5	Prefoldin s	7	17.7	7.0	7.6	2.5	2.32	0.43	176.5	63.2	76.9	2.8	2.30	0.44
Q9JKF1_IQ	Iqgap1	Ras GTPase	141	43.3	17.1	18.7	2.5	2.32	0.43	10390.1	3711.8	4517.9	2.8	2.30	0.43
Q3TPX4_E	Exoc5	Exocyst cor	2	14.1	5.6	6.1	2.5	2.31	0.43	28.2	11.2	13.6	2.5	2.07	0.48
Q9ERH4_N	Nusap1	Nucleolar a	1	6.5	2.6	2.8	2.5	2.31	0.43	6.5	2.6	3.1	2.5	2.07	0.48
Q8BI72_CA	Cdkn2aip	CDKN2A-in	25	19.9	7.9	8.6	2.5	2.31	0.43	594.7	311.0	378.5	1.9	1.57	0.64
P63101_1	Ywhaz	14-3-3 prot	28	35.8	14.2	15.5	2.5	2.31	0.43	2545.8	900.8	1096.5	2.8	2.32	0.43
Q6ZWY3_R	Rps27l	40S riboso	9	26.8	10.7	11.7	2.5	2.30	0.43	633.1	266.1	323.9	2.4	1.95	0.51
P62849_R	Rps24	40S riboso	7	69.0	27.5	30.0	2.5	2.30	0.43	859.2	352.4	428.9	2.4	2.00	0.50
Q6NSQ7_L	Ltv1	Protein LT	6	16.7	6.7	7.3	2.5	2.30	0.43	103.1	42.6	51.9	2.4	1.99	0.50
Q91Z50_Q	Fen1	Flap endon	11	48.2	19.2	21.0	2.5	2.30	0.44	676.8	244.7	297.9	2.8	2.27	0.44
Q6P069_S	Sri	Sorcin OS=	1	19.5	7.8	8.5	2.5	2.30	0.44	19.5	7.8	9.5	2.5	2.06	0.49
Q6PHQ8_N	Naa35	N-alpha-ac	1	16.5	6.6	7.2	2.5	2.29	0.44	16.5	6.6	8.0	2.5	2.05	0.49
O70305_A	Atxn2	Ataxin-2 O	8	16.8	6.7	7.3	2.5	2.29	0.44	115.7	54.4	66.2	2.1	1.75	0.57
P26516_P	Psmd7	26S protea	6	37.7	15.1	16.5	2.5	2.29	0.44	327.0	105.7	128.7	3.1	2.54	0.39
Q6A099_Q	Gbf1	MKIAA024	15	13.9	5.6	6.1	2.5	2.28	0.44	286.4	124.7	151.8	2.3	1.89	0.53
P62331_A	Arf6	ADP-ribosy	14	15.3	6.2	6.7	2.5	2.27	0.44	542.0	273.9	333.3	2.0	1.63	0.62
Q99JY0_EC	Hadhb	Trifunction	3	19.2	7.8	8.5	2.5	2.27	0.44	63.9	31.4	38.2	2.0	1.67	0.60
Q9EQU5_S	Set	Protein SET	1	5.1	2.0	2.2	2.5	2.26	0.44	5.1	2.0	2.5	2.5	2.03	0.49
Q9DAT2_M	Mrgbp	MRG/MOR	1	6.9	2.8	3.0	2.5	2.26	0.44	6.9	2.8	3.4	2.5	2.03	0.49
P35235_P	Ptpn11	Tyrosine-pr	7	5.9	2.4	2.6	2.5	2.26	0.44	48.1	23.9	29.1	2.0	1.65	0.61
E9Q6J5_E9	Bod1l	Protein Bo	5	12.1	4.9	5.4	2.5	2.26	0.44	59.6	22.6	27.5	2.6	2.16	0.46
P12960_C	Cntn1	Contactin-	1	9.7	3.9	4.3	2.5	2.25	0.44	9.7	3.9	4.8	2.5	2.02	0.49
Q8BKT7_T	Thoc5	THO compl	4	12.3	5.0	5.5	2.5	2.25	0.44	49.0	22.4	27.3	2.2	1.79	0.56
Q8K0T4_K	Katnal1	Katanin p6	1	12.9	5.2	5.7	2.5	2.25	0.44	12.9	5.2	6.4	2.5	2.02	0.50
Q8VE18_S	Smg8	Protein SM	2	10.0	4.1	4.5	2.5	2.25	0.44	20.1	8.2	9.9	2.5	2.02	0.50
Q99KN2_C	Ciao1	Probable c	1	7.0	2.9	3.1	2.5	2.25	0.44	7.0	2.9	3.5	2.5	2.02	0.50
Q8BKT3_G	Gcfc2	GC-rich seq	3	7.9	3.2	3.5	2.5	2.25	0.45	24.2	11.1	13.5	2.2	1.79	0.56
P23475_X	Xrcc6	X-ray repai	7	31.1	12.8	13.9	2.4	2.24	0.45	314.7	100.3	122.1	3.1	2.58	0.39
Q91Z31_P	Ptbp2	Polypyrimi	14	39.7	16.3	17.8	2.4	2.23	0.45	677.8	340.1	414.0	2.0	1.64	0.61
A2AT37_A2	Upf2	Protein Up	4	18.2	7.5	8.2	2.4	2.23	0.45	83.1	32.2	39.2	2.6	2.12	0.47
Q8VE22_R	Mrps23	28S riboso	1	6.4	2.7	2.9	2.4	2.23	0.45	6.4	2.7	3.2	2.4	2.00	0.50
Q497V5_S	Srbd1	S1 RNA-bin	1	14.4	5.9	6.5	2.4	2.23	0.45	14.4	5.9	7.2	2.4	1.99	0.50
P18654_K	Rps6ka3	Ribosomal	6	15.6	6.4	7.0	2.4	2.23	0.45	107.4	50.5	61.5	2.1	1.75	0.57
Q8CBY1_S	Samd4a	Protein Sm	1	10.0	4.1	4.5	2.4	2.22	0.45	10.0	4.1	5.0	2.4	1.99	0.50
Q6Q899_D	Ddx58	Probable A	48	32.8	13.5	14.8	2.4	2.22	0.45	1797.6	807.9	983.4	2.2	1.83	0.55
Q9CVB6_A	Arpc2	Actin-relate	4	9.9	4.1	4.5	2.4	2.22	0.45	66.8	24.4	29.8	2.7	2.24	0.45
Q9D7S9_C	Chmp5	Charged m	1	16.2	6.7	7.3	2.4	2.22	0.45	16.2	6.7	8.1	2.4	1.99	0.50
Q9DBT5_A	Ampd2	AMP deami	9	14.9	6.1	6.7	2.4	2.22	0.45	142.5	73.6	89.5	1.9	1.59	0.63
Q8CGE8_IF	Ifi205a	Interferon-	3	30.6	12.6	13.8	2.4	2.21	0.45	90.1	30.2	36.8	3.0	2.45	0.41
Q62348_T	Tsn	Translin OS	1	10.3	4.3	4.7	2.4	2.21	0.45	10.3	4.3	5.2	2.4	1.98	0.50
P50544_A	Acadvl	Very long-c	1	4.8	2.0	2.2	2.4	2.21	0.45	4.8	2.0	2.4	2.4	1.98	0.50
P25444_R	Rps2	40S riboso	25	70.9	29.5	32.1	2.4	2.21	0.45	4281.0	1733.9	2110.4	2.5	2.03	0.49
Q8BHK9_E	Ercc6l	DNA excisi	2	10.0	4.2	4.5	2.4	2.20	0.45	20.0	8.3	10.1	2.4	1.98	0.51
G3X928_G	Sec23ip	SEC23-inte	9	21.6	9.0	9.8	2.4	2.20	0.45	219.2	95.8	116.6	2.3	1.88	0.53

Q6PAV2_HI	Herc4	Probable E3	3	29.8	12.4	13.5	2.4	2.20	0.45	74.6	53.5	65.2	1.4	1.15	0.87
Q9JJK2_LAI	Lancl2	LanC-like pr	1	21.0	8.7	9.5	2.4	2.20	0.45	21.0	8.7	10.6	2.4	1.97	0.51
P22682_CE	Cbl	E3 ubiquiti	1	18.5	7.7	8.4	2.4	2.20	0.45	18.5	7.7	9.4	2.4	1.97	0.51
P51881_AI	Slc25a5	ADP/ATP tr	2	19.4	8.1	8.8	2.4	2.20	0.46	38.7	16.1	19.7	2.4	1.97	0.51
O88874_C	Ccnk	Cyclin-K OS	3	16.3	6.8	7.4	2.4	2.20	0.46	43.5	20.9	25.4	2.1	1.71	0.58
Q8BG40_K	Katnb1	Katanin p8	1	9.5	4.0	4.3	2.4	2.19	0.46	9.5	4.0	4.8	2.4	1.96	0.51
Q9EPC1_PA	Parva	Alpha-parvi	9	52.1	21.8	23.8	2.4	2.19	0.46	395.6	209.7	255.2	1.9	1.55	0.65
Q99PG2_O	Ogfr	Opioid grov	1	14.5	6.1	6.6	2.4	2.18	0.46	14.5	6.1	7.4	2.4	1.96	0.51
P14576_SR	Srp54	Signal reco	33	17.2	7.2	7.9	2.4	2.18	0.46	933.3	365.5	444.8	2.6	2.10	0.48
Q6P1F6_2A	Ppp2r2a	Serine/thre	8	11.8	5.0	5.4	2.4	2.17	0.46	149.1	385.1	468.8	0.4	0.32	3.14
Q8R050_EF	Gspt1	Eukaryotic	15	23.5	9.9	10.8	2.4	2.17	0.46	535.6	194.7	237.0	2.8	2.26	0.44
P46664_PU	Adss	Adenylosuc	2	5.6	2.4	2.6	2.4	2.17	0.46	11.2	4.7	5.7	2.4	1.94	0.51
P31938_M	Map2k1	Dual specifi	9	33.7	14.3	15.6	2.4	2.17	0.46	342.3	145.5	177.1	2.4	1.93	0.52
Q8BH04_P	Pck2	Phosphoen	15	12.3	5.2	5.7	2.4	2.16	0.46	240.7	88.7	108.0	2.7	2.23	0.45
P12970_RL	Rpl7a	60S riboso	32	64.8	27.5	30.0	2.4	2.16	0.46	5052.1	2499.5	3042.3	2.0	1.66	0.60
Q9D753_E	Exosc8	Exosome co	1	11.4	4.9	5.3	2.4	2.16	0.46	11.4	4.9	5.9	2.4	1.93	0.52
P61222_AE	Abce1	ATP-bindin	8	9.9	4.2	4.6	2.3	2.15	0.46	93.4	39.8	48.4	2.3	1.93	0.52
P11983_TC	Tcp1	T-complex	59	54.8	23.3	25.4	2.3	2.15	0.46	5349.1	2265.2	2757.1	2.4	1.94	0.52
P62911_RL	Rpl32	60S riboso	12	54.2	23.1	25.2	2.3	2.15	0.47	1069.1	415.5	505.7	2.6	2.11	0.47
P38647_GI	Hspa9	Stress-70 p	13	14.5	6.2	6.7	2.3	2.15	0.47	254.2	96.9	118.0	2.6	2.15	0.46
P80314_TC	Cct2	T-complex	63	48.3	20.7	22.5	2.3	2.15	0.47	7311.1	2712.8	3301.9	2.7	2.21	0.45
Q9CR55_CP087_MOUS	UPF0547 p		1	5.5	2.4	2.6	2.3	2.14	0.47	5.5	2.4	2.9	2.3	1.92	0.52
Q9D0R8_LS	Lsm12	Protein LSM	2	57.9	24.7	27.0	2.3	2.14	0.47	115.8	49.5	60.2	2.3	1.92	0.52
Q9Z2Y8_PF	Prosc	Proline syn	1	9.3	4.0	4.4	2.3	2.14	0.47	9.3	4.0	4.9	2.3	1.92	0.52
Q9CYX7_RF	Rrp15	RRP15-like	1	24.5	10.5	11.4	2.3	2.14	0.47	24.5	10.5	12.8	2.3	1.92	0.52
I7HJS4_I7H	Zfp683	Protein Zfp	1	6.4	2.8	3.0	2.3	2.13	0.47	6.4	2.8	3.4	2.3	1.91	0.52
O55236_M	Rngtt	mRNA-capp	2	13.3	5.7	6.2	2.3	2.13	0.47	26.6	11.4	13.9	2.3	1.91	0.52
Q9CR57_RI	Rpl14	60S riboso	10	104.4	45.0	49.1	2.3	2.13	0.47	3711.1	1424.5	1733.9	2.6	2.14	0.47
G3X8Y3_G	Naa15	N-alpha-ac	24	26.3	11.4	12.4	2.3	2.12	0.47	908.3	323.2	393.3	2.8	2.31	0.43
Q8R1Q8_D	Dync1li1	Cytoplasmi	28	17.1	7.4	8.1	2.3	2.12	0.47	970.7	520.4	633.4	1.9	1.53	0.65
Q9WV95_P	Phlda3	Pleckstrin h	1	45.4	19.7	21.5	2.3	2.12	0.47	45.4	19.7	24.0	2.3	1.90	0.53
O08915_AI	Aip	AH recepto	2	30.4	13.2	14.4	2.3	2.11	0.47	60.7	26.3	32.1	2.3	1.89	0.53
Q3V3R1_C	Mthfd1l	Monofunct	13	15.7	6.8	7.4	2.3	2.11	0.47	226.4	102.3	124.5	2.2	1.82	0.55
Q9Z1Q5_CI	Clic1	Chloride in	3	5.3	2.3	2.5	2.3	2.11	0.47	14.6	6.8	8.3	2.1	1.76	0.57
D3Z4S3_PT	Ptrhd1	Putative pe	3	21.8	9.5	10.3	2.3	2.11	0.47	61.5	27.4	33.3	2.2	1.85	0.54
Q6P5G6_U	Ubxn7	UBX domai	4	12.5	5.4	5.9	2.3	2.10	0.48	50.5	22.4	27.2	2.3	1.85	0.54
Q9WV80_S	Snx1	Sorting nex	26	18.5	8.1	8.8	2.3	2.10	0.48	672.4	288.3	350.9	2.3	1.92	0.52
Q9EQP2_EI	Ehd4	EH domain-	28	18.8	8.2	9.0	2.3	2.10	0.48	716.5	292.2	355.7	2.5	2.01	0.50
O89090_SF	Sp1	Transcripti	1	21.4	9.4	10.2	2.3	2.10	0.48	21.4	9.4	11.4	2.3	1.88	0.53
D3Z7P3_GI	Gls	Glutaminas	2	19.6	8.6	9.3	2.3	2.10	0.48	39.2	17.1	20.8	2.3	1.88	0.53
D3YZP9_CC	Ccdc6	Coiled-coil	3	7.5	3.3	3.6	2.3	2.10	0.48	22.2	8.8	10.7	2.5	2.07	0.48
Q7TT50_MI	Cdc42bpb	Serine/thre	8	21.4	9.4	10.2	2.3	2.09	0.48	1035.6	180.1	219.2	5.8	4.72	0.21
Q61820_RA	Rasl2-9	GTP-bindin	5	13.2	5.8	6.3	2.3	2.09	0.48	169.0	220.0	267.8	0.8	0.63	1.58
P80316_TC	Cct5	T-complex	43	49.8	21.9	23.9	2.3	2.09	0.48	4394.0	1670.4	2033.1	2.6	2.16	0.46
Q8BZX4_SF	Srek1	Splicing reg	1	8.4	3.7	4.0	2.3	2.08	0.48	8.4	3.7	4.5	2.3	1.86	0.54
Q8K2F0_BF	Brd3	Bromodom	2	49.4	21.8	23.8	2.3	2.08	0.48	98.8	43.6	53.0	2.3	1.86	0.54
P60670_NI	Nploc4	Nuclear pro	7	13.4	5.9	6.5	2.3	2.08	0.48	136.9	51.3	62.5	2.7	2.19	0.46
Q9CZ15_PS	Gins1	DNA replica	1	3.2	1.4	1.5	2.3	2.08	0.48	3.2	1.4	1.7	2.3	1.86	0.54
P17182_EN	Eno1	Alpha-enol	1	5.3	2.3	2.5	2.3	2.08	0.48	5.3	2.3	2.8	2.3	1.86	0.54
Q8VDP4_C	Ccar2	Cell cycle a	6	19.6	8.7	9.5	2.3	2.08	0.48	146.3	63.4	77.1	2.3	1.90	0.53
P08249_M	Mdh2	Malate deh	1	9.7	4.3	4.7	2.3	2.08	0.48	9.7	4.3	5.2	2.3	1.86	0.54
Q8R0J7_VF	Vps37b	Vacuolar pr	3	9.6	4.3	4.6	2.3	2.07	0.48	36.1	19.8	24.1	1.8	1.50	0.67
Q5RL79_KT	Krtcap2	Keratinocy	1	3.9	1.7	1.9	2.3	2.07	0.48	3.9	1.7	2.1	2.3	1.85	0.54
Q8CIG8_AN	Prmt5	Protein arg	6	18.6	8.3	9.0	2.3	2.07	0.48	110.3	46.9	57.1	2.4	1.93	0.52
Q91W36_U	Usp3	Ubiquitin c	1	7.5	3.3	3.6	2.2	2.05	0.49	7.5	3.3	4.1	2.2	1.84	0.54
P47738_AL	Aldh2	Aldehyde d	1	6.1	2.7	3.0	2.2	2.05	0.49	6.1	2.7	3.3	2.2	1.84	0.54
Q8BRT1_CL	Clasp2	CLIP-associ	8	17.9	8.0	8.7	2.2	2.05	0.49	168.4	90.0	109.6	1.9	1.54	0.65
P99029_PF	Prdx5	Peroxiredo	4	13.2	5.9	6.4	2.2	2.05	0.49	56.8	21.5	26.2	2.6	2.17	0.46
Q8BG94_C	Commd7	COMM dom	5	21.8	9.7	10.6	2.2	2.05	0.49	94.5	68.6	83.5	1.4	1.13	0.88
O88746_TO	Tom1	Target of M	1	11.2	5.0	5.5	2.2	2.05	0.49	11.2	5.0	6.1	2.2	1.83	0.54
O88844_ID	Idh1	Isocitrate d	3	11.4	5.1	5.6	2.2	2.05	0.49	38.9	19.6	23.8	2.0	1.63	0.61
Q8BG15_CT	Ctdspl2	CTD small p	1	18.3	8.2	8.9	2.2	2.05	0.49	18.3	8.2	10.0	2.2	1.83	0.55
Q9D9V3_E	Echdc1	Ethylmalon	1	13.0	5.8	6.3	2.2	2.04	0.49	13.0	5.8	7.1	2.2	1.83	0.55
Q9JKX6_NU	Nudt5	ADP-sugar p	1	12.4	5.6	6.1	2.2	2.04	0.49	12.4	5.6	6.8	2.2	1.83	0.55
P97770_TH	Thumpd3	THUMP dor	1	8.4	3.8	4.1	2.2	2.04	0.49	8.4	3.8	4.6	2.2	1.83	0.55
Q9CQQ4_G	Gemin2	Gem-associ	1	9.7	4.4	4.8	2.2	2.03	0.49	9.7	4.4	5.3	2.2	1.82	0.55
Q8VD65_PI	Pik3r4	Phosphoin	2	20.7	9.4	10.2	2.2	2.03	0.49	41.5	18.7	22.8	2.2	1.82	0.55
P62717_RL	Rpl18a	60S riboso	19	47.4	21.4	23.3	2.2	2.03	0.49	1583.4	778.9	948.0	2.0	1.67	0.60
Q3USH5_SF	Sfswap	Splicing fac	2	4.3	2.0	2.1	2.2	2.02	0.49	8.7	3.9	4.8	2.2	1.81	0.55
Q8R1J3_ZC	Zcchc9	Zinc finger	1	7.3	3.3	3.6	2.2	2.02	0.49	7.3	3.3	4.0	2.2	1.81	0.55
Q61576_FK	Fkbp10	Peptidyl-pr	3	20.5	9.3	10.1	2.2	2.02	0.49	68.8	36.2	44.0	1.9	1.56	0.64
E9Q3G8_E9	Nup153	Protein Nu	5	12.2	5.5	6.0	2.2	2.02	0.50	52.9	39.9	48.6	1.3	1.09	0.92
Q9DBG3_A	Ap2b1	AP-2 compl	13	18.8	8.6	9.3	2.2	2.02	0.50	381.3	140.1	170.6	2.7	2.24	0.45
P27659_RL	Rpl3	60S riboso	49	53.6	24.4	26.6	2.2	2.02	0.50	5123.8	2074.7	2525.3	2.5	2.03	0.49
P08113_EN	Hsp90b1	Endoplasm	76	57.3	26.1	28.4	2.2	2.01	0.50	10356.8	3943.0	4799.3	2.6	2.16	0.46
P37913_DI	Lig1	DNA ligase	17	15.3	7.0	7.6	2.2	2.01	0.50	351.9	135.3	164.7	2.6	2.14	0.47
Q9D1G5_LI	Lrrc57	Leucine-ric	5	15.3	7.0	7.6	2.2	2.01	0.50	100.0	41.7	50.7	2.4	1.97	0.51
P18155_M	Mthfd2	Bifunctiona	1	14.5	6.6	7.2	2.2	2.01	0.50	14.5	6.6	8.0	2.2	1.80	0.56
Q99L45_IF	Eif2s2	Eukaryotic	19	24.4	11.2	12.2	2.2	2.00	0.50	1036.8	503.6	612.9	2.1	1.69	0.59
Q8C2E7_ST	Kiaa0196	WASH com	4	15.4	7.1	7.7	2.2	2.00	0.50	62.9	33.5	40.8	1.9	1.54	0.65
Q8C142_AI	Ldlrap1	Low density	3	7.5	3.4	3.8	2.2	2.00	0.50	23.5	9.4	11.5	2.5	2.05	0.49
Q9Z160_CC	Cog1	Conserved	1	16.7	7.7	8.4	2.2	2.00	0.50	16.7	7.7	9.3	2.2	1.79	0.56
P70670_NA	Naca	Nascent po	7	25.3	11.6	12.6	2.2	2.00	0.50	279.3	118.3	144.0	2.4	1.94	0.52
Q9QYR6_M	Map1a	Microtubul	9	15.6	7.2	7.8	2.2	2.00	0.50	238.3	98.2	119.5	2.4	1.99	0.50
P12367_KA	Prkar2a	cAMP-depe	1	9.7	4.4	4.8	2.2	2.00	0.50	9.7	4.4	5.4	2.2	1.79	0.56
Q91WJ8_FI	Fubp1	Far upstrea	4	23.6	10.8	11.8	2.2	2.00	0.50	126.3	72.1	87.8	1.8	1.44	0.69
O35226_PS	Psmd4	26S protea	9	28.7	13.2	14.4	2.2	1.99	0.50	334.3	111.7	136.0	3.0	2.46	0.41
Q8CFE4_SC	Scyl2	SCY1-like p	5	17.0	7.8	8.5	2.2	1.99	0.50	84.6	52.9	64.4	1.6	1.31	0.76
P62257_UI	Ube2h	Ubiquitin-c	5	23.7	10.9	11.9	2.2	1.99	0.50	187.3	85.9	104.6	2.2	1.79	0.56
O35643_AI	Ap1b1	AP-1 compl	25	18.1	8.4	9.1	2.2	1.98	0.50	894.8	276.4	336.4	3.2	2.66	0.38
Q9ERK4_XF	Cse1l	Exportin-2	26	24.5	11.4	12.4	2.2	1.98	0.51	6362.8	8198.0	9978.3	0.8	0.64	1.57
Q3TML0_Q	Pdia6	Protein dis	19	39.9	18.5	20.1	2.2	1.98	0.51	1232.9	724.5	881.8	1.7	1.40	0.72
P26450_P8	Pik3r1	Phosphatid	2	13.5	6.3	6.8	2.2	1.98	0.51	27.0	12.5	15.3	2.2	1.77	0.56
Q9Z0N1_IF	Eif2s3x	Eukaryotic	13	35.1	16.3	17.8	2.2	1.98	0.51	622.1	276.3	336.3	2.3	1.85	0.54
O08663_M	Metap2	Methionine	2	11.1	5.2	5.6	2.2	1.97	0.51	22.2	10.3	12.5	2.2	1.77	0.57
P28741_KI	Kif3a	Kinesin-like	4	20.8	9.6	10.5	2.2	1.97	0.51	68.1	38.9	47.4	1.7	1.44	0.70
Q3TWF6_W	Wdr70	WD repeat-	1	20.7	9.6	10.5	2.2	1.97	0.51	20.7	9.6	11.7	2.2	1.77	0.57
Q9CX34_SU	Sugt1	Suppressor	2	20.3	9.4	10.3	2.2	1.97	0.51	40.6	18.9	22.9	2.2	1.77	0.57
P62082_RS	Rps7	40S riboso	12	83.7	38.9	42.5	2.2	1.97	0.51	2277.6	998.2	1215.0	2.3	1.87	0.53
P62814_VA	Atp6v1b2	V-type prot	8	21.0	9.8	10.7	2.1	1.97	0.51	299.0	90.2	109.8	3.3	2.72	0.37
P97789_XF	Xrn1	5'-3' exorib	8	22.0	10.3	11.2	2.1	1.97	0.51	176.8	93.0	113.2	1.9	1.56	0.64
Q9CQ71_RI	Rpa3	Replication	3	44.4	20.8	22.6	2.1	1.96	0.51	200.9	163.0	198.5	1.2	1.01	0.99
Q7TMY8_H	Huwe1	E3 ubiquiti	4	17.5	8.2	8.9	2.1	1.96	0.51	67.3	47.1	57.3	1.4	1.17	0.85
O54988_SL	Slk	STE20-like	15	12.1	5.6	6.2	2.1	1.96	0.51	347.2	143.8	175.0	2.4	1.98	0.50
Q8C547_HT	Heatr5b	HEAT repea	1	8.4	3.9	4.3	2.1	1.96	0.51	8.4	3.9	4.8	2.1	1.75	0.57
Q9CQ10_CI	Chmp3	Charged mu	1	11.7	5.5	6.0	2.1	1.96	0.51	11.7	5.5	6.7	2.1	1.75	0.57
O88477_IF	Igf2bp1	Insulin-like	13	18.9	8.8	9.7	2.1	1.96	0.51	440.9	223.0	271.4	2.0	1.62	0.62
Q3UPH1_P	Prrc1	Protein PRI	2	9.8	4.6	5.0	2.1	1.96	0.51	19.6	9.2	11.2	2.1	1.75	0.57
O35344_IN	Kpna3	Importin su	8	31.3	14.7	16.0	2.1	1.95	0.51	273.1	153.7	187.1	1.8	1.46	0.69
Q9WVA2_T	Timm8a1	Mitochond	1	6.9	3.2	3.5	2.1	1.95	0.51	6.9	3.2	3.9	2.1	1.75	0.57
Q9D8B3_CI	Chmp4b	Charged mu	2	23.3	10.9	11.9	2.1	1.95	0.51	46.5	21.8	26.6	2.1	1.75	0.57
Q9WVM3_	Anapc7	Anaphase-p	1	8.6	4.0	4.4	2.1	1.95	0.51	8.6	4.0	4.9	2.1	1.75	0.57
Q9DCC4_P	Pycrl	Pyrroline-5	3	64.7	30.4	33.2	2.1	1.95	0.51	305.2	151.9	184.9	2.0	1.65	0.61

O70591_PI	Pfdn2	Prefoldin su	2	21.6	10.2	11.1	2.1	1.95	0.51	43.2	20.3	24.7	2.1	1.75	0.57
P47713_PA	Pla2g4a	Cytosolic p	1	6.3	3.0	3.2	2.1	1.95	0.51	6.3	3.0	3.6	2.1	1.75	0.57
Q9ESN9_JII	Mapk8ip3	C-Jun-amin	3	9.0	4.2	4.6	2.1	1.95	0.51	27.2	12.4	15.1	2.2	1.80	0.56
Q9JM76_AI	Arpc3	Actin-relate	4	26.4	12.4	13.6	2.1	1.95	0.51	138.2	55.9	68.1	2.5	2.03	0.49
Q8C1D8_IV	Iws1	Protein IW:	1	9.0	4.3	4.7	2.1	1.94	0.52	9.0	4.3	5.2	2.1	1.74	0.57
P08032_SP	Spta1	Spectrin al	3	17.6	8.3	9.1	2.1	1.94	0.52	64.5	27.1	32.9	2.4	1.96	0.51
Q6NZL1_Q	Dhx37	DEAH (Asp-	2	18.1	8.5	9.3	2.1	1.94	0.52	36.1	17.1	20.8	2.1	1.74	0.58
Q3TLH4_PI	Prrc2c	Protein PRI	8	10.9	5.2	5.6	2.1	1.94	0.52	101.5	67.2	81.8	1.5	1.24	0.81
Q9Z2A0_PI	Pdpk1	3-phosphoi	2	12.1	5.7	6.2	2.1	1.94	0.52	24.2	11.4	13.9	2.1	1.73	0.58
P35585_AF	Ap1m1	AP-1 compl	7	12.6	6.0	6.5	2.1	1.93	0.52	94.1	40.6	49.4	2.3	1.90	0.53
Q61768_KI	Kif5b	Kinesin-1 h	17	28.3	13.4	14.7	2.1	1.93	0.52	638.5	253.7	308.8	2.5	2.07	0.48
Q9CWZ7_S	Napg	Gamma-sol	1	7.3	3.5	3.8	2.1	1.93	0.52	7.3	3.5	4.2	2.1	1.73	0.58
P10107_AN	Anxa1	Annexin A1	25	41.7	19.8	21.6	2.1	1.93	0.52	2030.5	620.5	755.2	3.3	2.69	0.37
P62748_HI	Hpcal1	Hippocalci	2	13.2	6.3	6.9	2.1	1.93	0.52	26.5	12.6	15.3	2.1	1.73	0.58
Q9R0X4_A	Acot9	Acyl-coenzy	3	7.0	3.3	3.6	2.1	1.93	0.52	23.8	11.5	14.0	2.1	1.70	0.59
Q922R5_P	Smek2	Serine/thre	2	9.5	4.5	4.9	2.1	1.92	0.52	18.9	9.0	11.0	2.1	1.72	0.58
Q80TR0_Q	Nfat5	MKIAA0827	1	6.5	3.1	3.4	2.1	1.92	0.52	6.5	3.1	3.8	2.1	1.72	0.58
Q6ZQ38_C	Cand1	Cullin-asso	20	22.5	10.8	11.7	2.1	1.92	0.52	650.3	227.1	276.4	2.9	2.35	0.43
Q5SSI6_UTI	Utp18	U3 small nu	1	3.9	1.9	2.0	2.1	1.92	0.52	3.9	1.9	2.3	2.1	1.72	0.58
Q3TDD9_PI	Ppp1r21	Protein pho	1	6.0	2.8	3.1	2.1	1.92	0.52	6.0	2.8	3.5	2.1	1.72	0.58
Q3ULL6_Q	Upf3b	Protein Up	3	11.1	5.3	5.8	2.1	1.92	0.52	31.3	17.8	21.7	1.8	1.45	0.69
P43275_H1	Hist1h1a	Histone H1	18	78.2	37.4	40.8	2.1	1.92	0.52	8543.8	4281.3	5211.1	2.0	1.64	0.61
A3KGB4_TE	Tbc1d8b	TBC1 doma	2	8.7	4.2	4.6	2.1	1.91	0.52	17.4	8.4	10.2	2.1	1.71	0.58
Q6NZN0_RI	Rbm26	RNA-bindir	6	12.7	6.1	6.7	2.1	1.91	0.52	89.1	55.4	67.4	1.6	1.32	0.76
Q9CXV9_D	Dcun1d5	DCN1-like p	2	13.8	6.6	7.2	2.1	1.91	0.52	27.5	13.2	16.1	2.1	1.71	0.58
Q08879_FE	Fbln1	Fibulin-1 O	1	41.8	20.1	21.9	2.1	1.91	0.52	41.8	20.1	24.5	2.1	1.71	0.59
A2A6Q5_CI	Cdc27	Cell divisio	2	4.8	2.3	2.5	2.1	1.91	0.52	9.6	4.6	5.6	2.1	1.71	0.59
P11499_HS	Hsp90ab1	Heat shock	62	79.5	38.2	41.7	2.1	1.91	0.52	11168.9	4691.8	5710.7	2.4	1.96	0.51
Q9WUA2_S	Farsb	Phenylalan	32	48.8	23.5	25.6	2.1	1.91	0.52	1528.4	776.3	944.9	2.0	1.62	0.62
P70336_RC	Rock2	Rho-associa	2	5.2	2.5	2.7	2.1	1.90	0.53	10.4	5.0	6.1	2.1	1.70	0.59
O88545_CS	Cops6	COP9 signa	8	21.7	10.5	11.4	2.1	1.90	0.53	255.8	92.6	112.7	2.8	2.27	0.44
Q922D4_PI	Ppp6r3	Serine/thre	1	6.5	3.1	3.4	2.1	1.90	0.53	6.5	3.1	3.8	2.1	1.70	0.59
P62702_RS	Rps4x	40S ribosor	47	62.3	30.1	32.9	2.1	1.90	0.53	4592.0	2678.6	3260.4	1.7	1.41	0.71
Q63918_SI	Sdpr	Serum depr	12	46.1	22.4	24.4	2.1	1.89	0.53	470.5	290.2	353.2	1.6	1.33	0.75
Q8C033_AI	Arhgef10	Rho guanin	2	7.4	3.6	3.9	2.1	1.89	0.53	14.7	7.1	8.7	2.1	1.69	0.59
P59997_KI	Kdm2a	Lysine-spec	2	15.2	7.4	8.0	2.1	1.89	0.53	30.3	14.7	17.9	2.1	1.69	0.59
P51410_RL	Rpl9	60S ribosor	19	33.0	16.0	17.5	2.1	1.89	0.53	2180.9	903.7	1100.0	2.4	1.98	0.50
Q8R5F7_IFI	Ifih1	Interferon-i	21	15.2	7.4	8.1	2.1	1.88	0.53	494.6	218.4	265.8	2.3	1.86	0.54
Q61595_KT	Ktn1	Kinectin OS	1	12.0	5.8	6.4	2.1	1.88	0.53	12.0	5.8	7.1	2.1	1.69	0.59
Q99JP6_HC	Homer3	Homer prot	1	7.5	3.7	4.0	2.1	1.88	0.53	7.5	3.7	4.5	2.1	1.69	0.59
P42932_TC	Cct8	T-complex	75	48.2	23.5	25.6	2.1	1.88	0.53	5936.6	2575.6	3134.9	2.3	1.89	0.53
Q8K012_FE	Fnbp1l	Formin-bin	3	22.3	10.9	11.9	2.1	1.88	0.53	66.8	38.4	46.7	1.7	1.43	0.70
P49615_CI	Cdk5	Cyclin-depe	4	14.4	7.0	7.7	2.0	1.88	0.53	50.6	26.2	31.9	1.9	1.59	0.63
Q91VL8_TE	Terf2ip	Telomeric r	2	8.8	4.3	4.7	2.0	1.88	0.53	17.6	8.6	10.5	2.0	1.68	0.59
P07742_RI	Rrm1	Ribonuclec	10	21.3	10.4	11.4	2.0	1.88	0.53	154.9	125.0	152.1	1.2	1.02	0.98
Q9WVF7_D	Pole	DNA polym	2	14.9	7.3	8.0	2.0	1.88	0.53	29.9	14.6	17.8	2.0	1.68	0.59
Q9JIF0_ANI	Prmt1	Protein arg	27	42.7	20.9	22.7	2.0	1.88	0.53	1692.4	604.9	736.3	2.8	2.30	0.44
P35979_RL	Rpl12	60S ribosor	11	113.8	55.6	60.7	2.0	1.87	0.53	3961.2	2036.3	2478.5	1.9	1.60	0.63
Q9D1J3_SA	Sarnp	SAP domair	1	6.9	3.4	3.7	2.0	1.87	0.53	6.9	3.4	4.1	2.0	1.68	0.60
Q9QYY8_SF	Spast	Spastin OS=	1	10.7	5.2	5.7	2.0	1.87	0.53	10.7	5.2	6.4	2.0	1.68	0.60
O35551_RA	Rabep1	Rab GTPase	1	8.8	4.3	4.7	2.0	1.87	0.54	8.8	4.3	5.3	2.0	1.68	0.60
P62274_RS	Rps29	40S ribosor	1	588.4	289.1	315.3	2.0	1.87	0.54	588.4	289.1	351.8	2.0	1.67	0.60
Q8C863_IT	Itch	E3 ubiquiti	2	13.8	6.8	7.4	2.0	1.87	0.54	27.6	13.5	16.5	2.0	1.67	0.60
A2AQ19_RT	Rtf1	RNA polym	7	9.8	4.8	5.3	2.0	1.87	0.54	150.5	56.1	68.3	2.7	2.20	0.45
Q9R0Y5_KA	Ak1	Adenylate k	1	16.4	8.0	8.8	2.0	1.87	0.54	16.4	8.0	9.8	2.0	1.67	0.60
Q6ZQK0_CI	Ncapd3	Condensin-	4	15.4	7.6	8.3	2.0	1.86	0.54	55.1	32.8	39.9	1.7	1.38	0.72
Q811D0_D	Dlg1	Disks large	4	11.6	5.7	6.2	2.0	1.86	0.54	45.2	22.6	27.5	2.0	1.65	0.61
Q8K009_AI	Aldh1l2	Mitochond	6	9.1	4.5	4.9	2.0	1.86	0.54	58.1	26.2	31.9	2.2	1.82	0.55
B1AY13_UE	Usp24	Ubiquitin c	9	12.2	6.0	6.5	2.0	1.86	0.54	126.9	48.1	58.6	2.6	2.17	0.46
P62259_14	Ywhae	14-3-3 prot	25	22.2	11.0	11.9	2.0	1.86	0.54	2062.8	624.3	759.9	3.3	2.71	0.37
Q8VBV3_E	Exosc2	Exosome cc	1	12.4	6.1	6.7	2.0	1.85	0.54	12.4	6.1	7.5	2.0	1.66	0.60
Q3UWL8_C	Pfdn4	Protein Pfd	2	15.0	7.4	8.1	2.0	1.85	0.54	30.1	14.9	18.1	2.0	1.66	0.60
Q8R3N6_TI	Thoc1	THO compl	9	10.4	5.1	5.6	2.0	1.85	0.54	98.4	60.4	73.5	1.6	1.34	0.75
Q8BFY9_TN	Tnpo1	Transportir	9	14.0	6.9	7.6	2.0	1.85	0.54	160.7	74.5	90.7	2.2	1.77	0.56
P61290_PS	Psme3	Proteasom	3	12.0	5.9	6.5	2.0	1.85	0.54	50.6	23.3	28.4	2.2	1.78	0.56
P41241_CS	Csk	Tyrosine-pr	2	10.2	5.0	5.5	2.0	1.85	0.54	20.3	10.1	12.2	2.0	1.66	0.60
O08808_DI	Diaph1	Protein dia	4	12.3	6.1	6.7	2.0	1.85	0.54	49.0	22.2	27.1	2.2	1.81	0.55
P28658_AT	Atxn10	Ataxin-10 C	18	23.5	11.7	12.7	2.0	1.85	0.54	484.1	233.0	283.7	2.1	1.71	0.59
Q8C1B7_SE	11-Sep	Septin-11 C	7	15.1	7.5	8.2	2.0	1.85	0.54	145.5	61.7	75.1	2.4	1.94	0.52
Q9CQS5_RI	Riok2	Serine/thre	4	14.7	7.3	8.0	2.0	1.85	0.54	51.7	29.0	35.3	1.8	1.46	0.68
Q9CXY6_ILI	Ilf2	Interleukin	36	41.4	20.5	22.4	2.0	1.85	0.54	1901.5	1125.7	1370.2	1.7	1.39	0.72
Q8C4B4_U	Unc119b	Protein unc	1	9.1	4.5	4.9	2.0	1.85	0.54	9.1	4.5	5.5	2.0	1.66	0.60
Q99LC8_EI	Eif2b1	Translation	15	13.9	6.9	7.5	2.0	1.85	0.54	288.6	117.3	142.8	2.5	2.02	0.49
Q9JLN9_M	Mtor	Serine/thre	1	9.8	4.9	5.3	2.0	1.84	0.54	9.8	4.9	5.9	2.0	1.65	0.60
Q99JX3_G	Gorasp2	Golgi reass	2	15.0	7.5	8.2	2.0	1.84	0.54	30.1	15.0	18.2	2.0	1.65	0.61
P33611_DI	Pola2	DNA polym	6	12.0	6.0	6.5	2.0	1.84	0.54	115.3	387.8	472.0	0.3	0.24	4.10
Q8CI43_M	Myl6b	Myosin ligh	5	49.2	24.5	26.7	2.0	1.84	0.54	2282.7	1424.4	1733.7	1.6	1.32	0.76
O88448_KI	Klc2	Kinesin ligh	6	29.3	14.6	15.9	2.0	1.84	0.54	171.4	83.0	101.0	2.1	1.70	0.59
Q9D1C9_RI	Rrp7a	Ribosomal	3	16.7	8.3	9.1	2.0	1.83	0.55	58.5	55.2	67.1	1.1	0.87	1.15
P68510_14	Ywhah	14-3-3 prot	13	14.2	7.1	7.7	2.0	1.83	0.55	462.3	178.0	216.6	2.6	2.13	0.47
Q9CXK8_NI	Nip7	60S ribosor	4	15.4	7.7	8.4	2.0	1.83	0.55	67.7	44.7	54.4	1.5	1.25	0.80
A2ASS6_TI	Ttn	Titin OS=M	1	34.0	17.0	18.6	2.0	1.83	0.55	34.0	17.0	20.7	2.0	1.64	0.61
Q8BGZ4_CI	Cdc23	Cell divisio	5	11.9	6.0	6.5	2.0	1.83	0.55	59.1	25.3	30.8	2.3	1.92	0.52
Q9EPQ8_TC	Tcf20	Transcripti	2	12.6	6.3	6.9	2.0	1.83	0.55	25.2	12.6	15.4	2.0	1.64	0.61
Q6P1G0_H	Heatr6	HEAT repea	4	11.1	5.6	6.1	2.0	1.83	0.55	39.5	25.1	30.6	1.6	1.29	0.77
Q61249_IG	Igbp1	Immunogl	4	12.1	6.1	6.6	2.0	1.83	0.55	42.5	24.7	30.1	1.7	1.41	0.71
Q8BY02_NI	Nkrf	NF-kappa-B	1	51.5	25.9	28.2	2.0	1.82	0.55	51.5	25.9	31.5	2.0	1.64	0.61
Q91WK2_E	Eif3h	Eukaryotic	23	28.2	14.2	15.5	2.0	1.82	0.55	1254.2	600.8	731.3	2.1	1.72	0.58
P10630_IF	Eif4a2	Eukaryotic	12	20.2	10.1	11.1	2.0	1.82	0.55	404.3	205.4	250.0	2.0	1.62	0.62
Q99KQ4_N	Nampt	Nicotinami	43	24.0	12.1	13.2	2.0	1.82	0.55	1603.1	1035.9	1260.8	1.5	1.27	0.79
Q9D6R2_ID	Idh3a	Isocitrate d	9	26.9	13.5	14.8	2.0	1.82	0.55	346.1	130.9	159.4	2.6	2.17	0.46
Q9WTP6_K	Ak2	Adenylate k	1	13.2	6.7	7.3	2.0	1.82	0.55	13.2	6.7	8.1	2.0	1.63	0.61
F2Z461_HE	Herc6	E3 ISG15--p	4	11.9	6.0	6.6	2.0	1.82	0.55	49.0	102.7	125.0	0.5	0.39	2.55
Q9JJC6_RIF	Rilpl1	RILP-like pr	4	17.9	9.1	9.9	2.0	1.82	0.55	123.8	31.3	38.1	4.0	3.25	0.31
Q9CPR4_RI	Rpl17	60S ribosor	18	141.9	71.7	78.2	2.0	1.81	0.55	4820.3	1842.2	2242.3	2.6	2.15	0.47
Q9CQ36_D	Pole4	DNA polym	1	40.7	20.6	22.4	2.0	1.81	0.55	40.7	20.6	25.0	2.0	1.63	0.61
Q8CEC0_NI	Nup88	Nuclear po	2	10.5	5.3	5.8	2.0	1.81	0.55	21.0	10.6	12.9	2.0	1.63	0.62
Q9D4H8_C	Cul2	Cullin-2 OS	6	15.2	7.7	8.4	2.0	1.81	0.55	96.1	56.3	68.5	1.7	1.40	0.71
Q8BWY3_E	Etf1	Eukaryotic	13	25.2	12.8	13.9	2.0	1.81	0.55	426.4	197.2	240.1	2.2	1.78	0.56
Q99KH8_S	Stk24	Serine/thre	8	10.4	5.3	5.8	2.0	1.81	0.55	122.8	44.4	54.1	2.8	2.27	0.44
Q62393_TI	Tpd52	Tumor prot	4	7.4	3.7	4.1	2.0	1.81	0.55	31.7	14.8	18.0	2.1	1.76	0.57
Q62077_PI	Plcg1	1-phosphat	1	4.0	2.0	2.2	2.0	1.81	0.55	4.0	2.0	2.4	2.0	1.62	0.62
Q8K4Z5_SF	Sf3a1	Splicing fac	26	23.9	12.1	13.2	2.0	1.81	0.55	866.2	486.8	592.5	1.8	1.46	0.68
E9PWE8_E	Dpysl3	Dihydropyı	22	16.7	8.5	9.2	2.0	1.81	0.55	382.2	193.2	235.2	2.0	1.62	0.62
A2ADY9_DI	Ddi2	Protein DD	1	7.2	3.7	4.0	2.0	1.81	0.55	7.2	3.7	4.4	2.0	1.62	0.62
Q6P549_SI	Inppl1	Phosphatid	9	12.3	6.2	6.8	2.0	1.81	0.55	107.3	53.9	65.6	2.0	1.64	0.61
Q99JX4_EII	Eif3m	Eukaryotic	20	23.5	11.9	13.0	2.0	1.81	0.55	613.2	387.3	471.5	1.6	1.30	0.77
Q9D902_T	Gtf2e2	General tra	4	10.0	5.1	5.5	2.0	1.80	0.55	40.4	33.6	40.9	1.2	0.99	1.01
Q3UVG3_F	Fam91a1	Protein FAI	9	21.3	10.9	11.8	2.0	1.80	0.55	200.5	126.7	154.2	1.6	1.30	0.77
Q9DBR1_XI	Xrn2	5'-3' exorib	12	12.8	6.5	7.1	2.0	1.80	0.56	170.6	87.9	107.0	1.9	1.59	0.63
Q9D9Z5_DI	Dda1	DET1- and I	1	12.1	6.1	6.7	2.0	1.80	0.56	12.1	6.1	7.5	2.0	1.61	0.62
P80315_TC	Cct4	T-complex	55	33.0	16.8	18.4	2.0	1.80	0.56	3564.6	1509.3	1837.1	2.4	1.94	0.52
Q6P5D8_SI	Smchd1	Structural	26	24.4	12.4	13.6	2.0	1.80	0.56	812.2	466.1	567.3	1.7	1.43	0.70

Q9JKC8_AF	Ap3m1	AP-3 compl	8	18.9	9.6	10.5	2.0	1.79	0.56	176.7	118.4	144.2	1.5	1.23	0.82
Q8CGC4_LS	Lsm14b	Protein LSN	1	19.7	10.1	11.0	2.0	1.79	0.56	19.7	10.1	12.3	2.0	1.61	0.62
P53026_RL	Rpl10a	60S ribosor	23	71.8	36.8	40.1	2.0	1.79	0.56	4118.7	1829.8	2227.2	2.3	1.85	0.54
Q8K2F8_LS	Lsm14a	Protein LSN	1	2.9	1.5	1.6	2.0	1.79	0.56	2.9	1.5	1.8	2.0	1.61	0.62
Q62448_IF	Eif4g2	Eukaryotic	27	20.3	10.4	11.3	2.0	1.79	0.56	554.8	275.9	335.8	2.0	1.65	0.61
Q8C0D4_RI	Arhgap12	Rho GTPase	1	7.8	4.0	4.3	2.0	1.79	0.56	7.8	4.0	4.8	2.0	1.60	0.62
Q9QXE7_TE	Tbl1x	F-box-like/	3	13.8	7.1	7.7	1.9	1.79	0.56	39.9	22.6	27.5	1.8	1.45	0.69
Q9R1P4_PS	Psma1	Proteasom	1	13.0	6.7	7.3	1.9	1.78	0.56	13.0	6.7	8.2	1.9	1.59	0.63
P14873_M	Map1b	Microtubul	47	18.2	9.4	10.3	1.9	1.77	0.56	1302.0	590.5	718.7	2.2	1.81	0.55
Q6P2B1_TN	Tnpo3	Transportir	3	18.4	9.5	10.4	1.9	1.77	0.57	50.2	26.6	32.4	1.9	1.55	0.65
Q6ZQ58_LA	Larp1	La-related p	19	16.3	8.4	9.2	1.9	1.77	0.57	382.2	242.1	294.7	1.6	1.30	0.77
P62843_RS	Rps15	40S ribosor	5	18.4	9.5	10.4	1.9	1.77	0.57	154.1	79.1	96.3	1.9	1.60	0.63
P84099_RL	Rpl19	60S ribosor	17	37.6	19.5	21.3	1.9	1.76	0.57	1197.0	939.3	1143.2	1.3	1.05	0.96
Q8CD76_Q	Klc1	Kinesin ligh	10	13.5	7.0	7.7	1.9	1.76	0.57	190.4	111.8	136.1	1.7	1.40	0.71
P35123_UI	Usp4	Ubiquitin c	6	12.7	6.6	7.2	1.9	1.76	0.57	74.8	41.8	50.8	1.8	1.47	0.68
O09130_NI	Nfatc2ip	NFATC2-int	3	8.2	4.3	4.6	1.9	1.76	0.57	25.2	12.5	15.2	2.0	1.65	0.60
Q64337_SC	Sqstm1	Sequestoso	3	20.2	10.5	11.4	1.9	1.76	0.57	60.6	29.7	36.2	2.0	1.68	0.60
Q9WTQ5_A	Akap12	A-kinase an	15	11.5	6.0	6.5	1.9	1.76	0.57	193.4	116.1	141.3	1.7	1.37	0.73
Q9D8U8_SI	Snx5	Sorting nex	10	17.8	9.3	10.1	1.9	1.76	0.57	221.9	121.9	148.4	1.8	1.50	0.67
Q6ZWU9_R	Rps27	40S ribosor	2	28.7	15.0	16.3	1.9	1.75	0.57	57.3	30.0	36.5	1.9	1.57	0.64
P62852_RS	Rps25	40S ribosor	9	82.0	42.9	46.8	1.9	1.75	0.57	1783.4	1456.9	1773.3	1.2	1.01	0.99
Q3UJD6_UI	Usp19	Ubiquitin c	1	9.2	4.8	5.2	1.9	1.75	0.57	9.2	4.8	5.8	1.9	1.57	0.64
Q3UKV0_Q	Eif2b3	Protein Eif2	11	14.2	7.5	8.2	1.9	1.75	0.57	203.8	151.9	184.9	1.3	1.10	0.91
Q9CPX6_AT	Atg3	Ubiquitin-l	1	6.7	3.5	3.9	1.9	1.75	0.57	6.7	3.5	4.3	1.9	1.56	0.64
F7AI87_F7A	Psmd4	26S protea:	2	10.5	5.5	6.0	1.9	1.74	0.57	21.0	11.0	13.4	1.9	1.56	0.64
A2AN08_UI	Ubr4	E3 ubiquiti	13	10.9	5.7	6.2	1.9	1.74	0.57	196.6	201.3	245.0	1.0	0.80	1.25
P15864_H1	Hist1h1c	Histone H1	20	84.7	44.6	48.6	1.9	1.74	0.57	10508.3	5441.4	6623.1	1.9	1.59	0.63
Q99LB4_QS	Capg	Capping pr	10	33.1	17.4	19.0	1.9	1.74	0.57	471.1	211.7	257.7	2.2	1.83	0.55
Q9WTJ8_FA	Fam50b	Protein FAN	1	31.1	16.4	17.9	1.9	1.74	0.58	31.1	16.4	20.0	1.9	1.56	0.64
Q5SWD9_T	Tsr1	Pre-rRNA-p	3	12.9	6.8	7.4	1.9	1.74	0.58	36.3	19.6	23.9	1.9	1.52	0.66
Q3UIX4_Q3	Srsf11	Protein Srs	10	25.6	13.5	14.7	1.9	1.74	0.58	314.9	154.6	188.1	2.0	1.67	0.60
B1AZI6_TH	Thoc2	THO compl	13	19.7	10.4	11.4	1.9	1.73	0.58	375.6	173.3	210.9	2.2	1.78	0.56
B2RXC6_B2	Polr3a	Polymerase	1	12.0	6.4	6.9	1.9	1.73	0.58	12.0	6.4	7.7	1.9	1.55	0.64
P61961_UI	Ufm1	Ubiquitin-f	1	15.2	8.1	8.8	1.9	1.73	0.58	15.2	8.1	9.8	1.9	1.55	0.64
Q61189_IC	Clns1a	Methylosor	2	11.7	6.2	6.8	1.9	1.73	0.58	23.4	12.4	15.1	1.9	1.55	0.65
Q8C9S4_CC	Ccdc186	Coiled-coil	2	7.9	4.2	4.6	1.9	1.73	0.58	15.9	8.4	10.2	1.9	1.55	0.65
Q6ZQH8_N	Nup188	Nucleopori	1	5.6	3.0	3.2	1.9	1.73	0.58	5.6	3.0	3.6	1.9	1.55	0.65
Q8K1R7_NI	Nek9	Serine/thre	3	12.9	6.8	7.5	1.9	1.72	0.58	30.9	19.2	23.4	1.6	1.32	0.76
Q9QZQ1_AI	Mllt4	Afadin OS=I	12	17.9	9.5	10.4	1.9	1.72	0.58	206.1	137.7	167.6	1.5	1.23	0.81
Q9D8E6_RI	Rpl4	60S ribosor	34	71.3	38.0	41.4	1.9	1.72	0.58	5443.8	2048.4	2493.2	2.7	2.18	0.46
Q8BSZ2_AP	Ap3s2	AP-3 compl	1	8.5	4.5	5.0	1.9	1.72	0.58	8.5	4.5	5.5	1.9	1.54	0.65
Q9JHU4_DY	Dync1h1	Cytoplasmi	47	18.7	10.0	10.9	1.9	1.72	0.58	1092.5	529.2	644.1	2.1	1.70	0.59
Q6URW6_M	Myh14	Myosin-14	5	34.1	18.2	19.9	1.9	1.72	0.58	1840.5	900.1	1095.5	2.0	1.68	0.60
A2ABV5_M	Med14	Mediator o	3	11.8	6.3	6.8	1.9	1.72	0.58	34.4	27.7	33.7	1.2	1.02	0.98
Q80ZM5_Q	H1fx	H1 histone	5	49.6	26.5	28.9	1.9	1.72	0.58	537.8	326.6	397.6	1.6	1.35	0.74
Q9Z0P5_TV	Twf2	Twinfilin-2	1	5.5	2.9	3.2	1.9	1.72	0.58	5.5	2.9	3.6	1.9	1.54	0.65
Q5F2E8_TA	Taok1	Serine/thre	3	22.1	11.8	12.9	1.9	1.71	0.58	77.0	38.8	47.3	2.0	1.63	0.61
Q5XFZ0_CR021_MOUS		UPF0711 p	1	11.1	6.0	6.5	1.9	1.71	0.58	11.1	6.0	7.2	1.9	1.53	0.65
Q80U72_SC	Scrib	Protein scri	2	5.7	3.1	3.4	1.9	1.71	0.59	11.5	6.1	7.5	1.9	1.53	0.65
E9Q4K7_E9	Kif13b	Kinesin-like	12	9.7	5.2	5.7	1.9	1.71	0.59	165.7	78.5	95.5	2.1	1.73	0.58
Q9JIH2_NU	Nup50	Nuclear po	8	15.3	8.2	9.0	1.9	1.71	0.59	173.6	79.9	97.2	2.2	1.79	0.56
Q9D832_D	Dnajb4	DnaJ homo	3	9.0	4.8	5.3	1.9	1.70	0.59	33.1	42.0	51.1	0.8	0.65	1.55
P12382_PF	Pfkl	ATP-depend	12	18.6	10.0	10.9	1.9	1.70	0.59	362.6	130.4	158.7	2.8	2.28	0.44
A2AIM4_A2	Tpm2	Tropomyos	6	11.5	6.2	6.7	1.9	1.70	0.59	96.8	78.1	95.0	1.2	1.02	0.98
Q8K368_FA	Fanci	Fanconi an	1	8.7	4.7	5.1	1.9	1.70	0.59	8.7	4.7	5.7	1.9	1.52	0.66
Q8C0D5_ET	Eftud1	Elongation	2	34.7	18.7	20.4	1.9	1.70	0.59	69.4	37.4	45.6	1.9	1.52	0.66
Q8R1X6_SF	Spg20	Spartin OS=	2	10.8	5.8	6.4	1.9	1.70	0.59	21.7	11.7	14.2	1.9	1.52	0.66
Q9JJ28_FLI	Flii	Protein flig	30	15.6	8.4	9.2	1.9	1.70	0.59	645.6	380.1	462.6	1.7	1.40	0.72
Q6PDL0_DY	Dync1li2	Cytoplasmi	6	11.8	6.4	7.0	1.8	1.70	0.59	82.2	55.0	67.0	1.5	1.23	0.81
Q61194_P3	Pik3c2a	Phosphatid	3	11.5	6.2	6.8	1.8	1.69	0.59	47.3	14.8	18.1	3.2	2.62	0.38
Q8K1H1_TI	Tdrd7	Tudor dom	9	11.5	6.2	6.8	1.8	1.69	0.59	103.9	57.9	70.4	1.8	1.47	0.68
Q8CFD4_SN	Snx8	Sorting nex	1	13.8	7.5	8.2	1.8	1.68	0.59	13.8	7.5	9.1	1.8	1.51	0.66
E9Q585_E9	Slc4a1ap	Protein Slc	1	5.3	2.9	3.2	1.8	1.68	0.59	5.3	2.9	3.5	1.8	1.51	0.66
P48722_HS	Hspa4l	Heat shock	1	3.6	1.9	2.1	1.8	1.68	0.60	3.6	1.9	2.4	1.8	1.50	0.66
Q9CSU0_RI	Rprd1b	Regulation	6	35.1	19.2	20.9	1.8	1.68	0.60	229.2	111.8	136.0	2.1	1.68	0.59
P97447_FH	Fhl1	Four and a	2	20.6	11.3	12.3	1.8	1.68	0.60	41.2	22.5	27.4	1.8	1.50	0.67
Q9ESX5_DK	Dkc1	H/ACA ribo	10	8.4	4.6	5.0	1.8	1.67	0.60	87.1	51.2	62.4	1.7	1.40	0.72
Q9R1T2_SA	Sae1	SUMO-activ	8	9.5	5.2	5.7	1.8	1.67	0.60	82.1	41.1	50.0	2.0	1.64	0.61
Q8CGC6_RI	Rbm28	RNA-bindir	14	27.9	15.3	16.7	1.8	1.67	0.60	410.0	220.8	268.7	1.9	1.53	0.66
P13439_UI	Umps	Uridine 5'-r	5	17.2	9.4	10.3	1.8	1.67	0.60	77.9	48.0	58.5	1.6	1.33	0.75
Q8VDS4_RI	Rprd1a	Regulation	7	33.3	18.3	20.0	1.8	1.67	0.60	263.2	126.8	154.4	2.1	1.70	0.59
Q8JZX4_SP	Rbm17	Splicing fac	10	21.9	12.1	13.2	1.8	1.66	0.60	320.6	227.7	277.1	1.4	1.16	0.86
P27546_M	Map4	Microtubul	69	32.3	17.8	19.4	1.8	1.66	0.60	2942.7	1779.3	2165.7	1.7	1.36	0.74
E9Q166_E9	Atad2b	Protein Ata	1	4.5	2.5	2.7	1.8	1.66	0.60	4.5	2.5	3.0	1.8	1.49	0.67
P97393_RH	Arhgap5	Rho GTPase	2	12.5	6.9	7.5	1.8	1.66	0.60	24.9	13.7	16.7	1.8	1.49	0.67
P68372_TE	Tubb4b	Tubulin bet	5	94.0	51.8	56.6	1.8	1.66	0.60	477.1	275.2	335.0	1.7	1.42	0.70
Q91YM2_R	Arhgap35	Rho GTPase	4	6.6	3.6	4.0	1.8	1.66	0.60	27.7	14.8	18.0	1.9	1.54	0.65
Q3UH28_Q	Zmynd8	Protein Zm	2	83.9	46.4	50.6	1.8	1.66	0.60	167.7	92.8	112.9	1.8	1.48	0.67
Q9WTK2_C	Cdyl	Chromodo	1	10.6	5.9	6.4	1.8	1.66	0.60	10.6	5.9	7.2	1.8	1.48	0.67
Q80X98_Q8	Dhx38	DEAH (Asp-	10	18.5	10.2	11.2	1.8	1.65	0.60	161.8	104.6	127.3	1.5	1.27	0.79
Q9D0D4_D	Dimt1	Probable di	4	18.8	10.4	11.4	1.8	1.65	0.60	60.8	47.4	57.7	1.3	1.05	0.95
Q9DAW9_C	Cnn3	Calponin-3	24	22.4	12.4	13.6	1.8	1.65	0.60	789.0	451.2	549.1	1.7	1.44	0.70
P14206_RS	Rpsa	40S ribosor	16	34.3	19.0	20.8	1.8	1.65	0.61	946.5	815.5	992.6	1.2	0.95	1.05
P61089_UI	Ube2n	Ubiquitin-c	5	87.8	48.8	53.3	1.8	1.65	0.61	429.2	300.4	365.6	1.4	1.17	0.85
Q8CCN5_BI	Bcas3	Breast carci	1	10.8	6.0	6.5	1.8	1.65	0.61	10.8	6.0	7.3	1.8	1.48	0.68
Q9CX86_RO	Hnrnpa0	Heterogene	10	31.4	17.5	19.1	1.8	1.65	0.61	679.9	545.8	664.3	1.2	1.02	0.98
Q9CQ19_M	Myl9	Myosin reg	19	43.3	24.1	26.3	1.8	1.64	0.61	2202.8	2543.7	3096.0	0.9	0.71	1.41
Q9DAW6_P	Prpf4	U4/U6 sma	12	31.4	17.5	19.1	1.8	1.64	0.61	488.5	280.5	341.4	1.7	1.43	0.70
Q7TQK5_CC	Ccdc93	Coiled-coil	3	10.3	5.7	6.2	1.8	1.64	0.61	33.8	18.7	22.7	1.8	1.49	0.67
Q91WN1_D	Dnajc9	DnaJ homo	7	33.6	18.8	20.5	1.8	1.64	0.61	224.9	223.1	271.6	1.0	0.83	1.21
Q60809_CI	Cnot7	CCR4-NOT t	3	18.6	10.4	11.3	1.8	1.64	0.61	65.1	38.2	46.5	1.7	1.40	0.71
Q922J3_CL	Clip1	CAP-Gly do	18	18.2	10.2	11.1	1.8	1.64	0.61	319.9	182.1	221.7	1.8	1.44	0.69
Q9Z2U1_PS	Psma5	Proteasom	4	26.5	14.8	16.1	1.8	1.64	0.61	130.5	67.5	82.1	1.9	1.59	0.63
Q9R0L7_AK	Akap8l	A-kinase an	1	28.6	16.0	17.5	1.8	1.64	0.61	28.6	16.0	19.5	1.8	1.47	0.68
O88811_ST	Stam2	Signal trans	6	12.2	6.8	7.4	1.8	1.64	0.61	94.5	83.5	101.6	1.1	0.93	1.07
Q9DBG5_P	Plin3	Perilipin-3	3	7.5	4.2	4.6	1.8	1.64	0.61	27.5	12.2	14.8	2.3	1.86	0.54
O70439_ST	Stx7	Syntaxin-7	1	4.4	2.5	2.7	1.8	1.63	0.61	4.4	2.5	3.0	1.8	1.47	0.68
Q91YE6_IP	Ipo9	Importin-9	2	7.7	4.3	4.7	1.8	1.63	0.61	15.4	8.7	10.5	1.8	1.46	0.68
Q9CPY7_AN	Lap3	Cytosol am	10	16.4	9.2	10.0	1.8	1.63	0.61	290.1	99.7	121.4	2.9	2.39	0.42
Q68FD5_CI	Cltc	Clathrin he	60	24.9	14.0	15.3	1.8	1.63	0.61	2924.9	1314.6	1600.1	2.2	1.83	0.55
Q69ZX6_M	Morc2a	MORC fami	1	23.7	13.4	14.6	1.8	1.63	0.61	23.7	13.4	16.3	1.8	1.46	0.69
Q60598_SF	Cttn	Src substra	25	32.7	18.4	20.1	1.8	1.63	0.62	1708.3	953.7	1160.8	1.8	1.47	0.68
P43274_H1	Hist1h1e	Histone H1	11	51.0	28.9	31.5	1.8	1.62	0.62	3918.3	1960.2	2385.9	2.0	1.64	0.61
Q91X20_AS	Ash2l	Set1/Ash2 I	1	8.1	4.6	5.0	1.8	1.62	0.62	8.1	4.6	5.6	1.8	1.45	0.69
Q91VY9_ZN	Znf622	Zinc finger	4	15.8	9.0	9.8	1.8	1.62	0.62	80.2	37.0	45.1	2.2	1.78	0.56
P97379_G3	G3bp2	Ras GTPase-	16	18.2	10.4	11.3	1.8	1.61	0.62	380.3	288.1	350.6	1.3	1.08	0.92
Q9D7M1_G	Gid8	Glucose-inc	3	11.3	6.4	7.0	1.8	1.61	0.62	37.4	20.8	25.3	1.8	1.48	0.68
Q8VEJ4_NL	Nle1	Notchless p	1	12.9	7.4	8.0	1.8	1.61	0.62	12.9	7.4	9.0	1.8	1.44	0.69
Q99MI1_RI	Erc1	ELKS/Rab6-	3	20.2	11.5	12.5	1.8	1.61	0.62	56.7	48.9	59.5	1.2	0.95	1.05
Q9QZ05_E2	Eif2ak4	Eukaryotic	3	9.2	5.3	5.7	1.8	1.61	0.62	28.8	32.7	39.8	0.9	0.72	1.38
Q8CGK3_LO	Lonp1	Lon protea:	16	11.7	6.6	7.3	1.8	1.61	0.62	243.4	143.9	175.1	1.7	1.39	0.72
P55937_GO	Golga3	Golgin subf	8	10.1	5.7	6.3	1.8	1.61	0.62	84.2	76.2	92.8	1.1	0.91	1.10
Q9ERR7_SE	15-Sep	15 kDa sele	2	30.2	17.2	18.8	1.8	1.61	0.62	60.4	34.4	41.9	1.8	1.44	0.69

P41105_RL	Rpl28	60S ribosor	13	89.0	50.8	55.4	1.8	1.61	0.62	3369.6	1085.0	1320.6	3.1	2.55	0.39
P19426_NI	Nelfe	Negative ele	4	12.8	7.3	8.0	1.8	1.60	0.62	52.5	30.7	37.3	1.7	1.41	0.71
O35492_CI	Clk3	Dual specifi	1	9.3	5.3	5.8	1.8	1.60	0.62	9.3	5.3	6.5	1.8	1.44	0.70
P59325_IF	Eif5	Eukaryotic	5	20.6	11.8	12.8	1.7	1.60	0.62	153.3	51.6	62.8	3.0	2.44	0.41
Q923D5_W	Wbp11	WW domai	1	29.0	16.6	18.1	1.7	1.60	0.62	29.0	16.6	20.2	1.7	1.44	0.70
P84084_AF	Arf5	ADP-ribosy	2	43.8	25.1	27.4	1.7	1.60	0.63	87.7	50.3	61.2	1.7	1.43	0.70
P33215_NI	Nedd1	Protein NEI	1	20.7	11.9	12.9	1.7	1.60	0.63	20.7	11.9	14.4	1.7	1.43	0.70
Q8K3W0_E	Bre	BRCA1-A cc	3	17.9	10.3	11.2	1.7	1.60	0.63	57.4	26.9	32.8	2.1	1.75	0.57
E9PZM4_CI	Chd2	Chromodor	1	7.3	4.2	4.6	1.7	1.60	0.63	7.3	4.2	5.1	1.7	1.43	0.70
Q8CG48_SI	Smc2	Structural r	57	31.8	18.2	19.9	1.7	1.60	0.63	2101.0	1264.1	1538.6	1.7	1.37	0.73
Q61655_DI	Ddx19a	ATP-depend	26	24.9	14.3	15.6	1.7	1.60	0.63	874.6	491.2	597.9	1.8	1.46	0.68
Q6P3Y5_Z2	Znf280c	Zinc finger	1	4.5	2.6	2.8	1.7	1.59	0.63	4.5	2.6	3.2	1.7	1.43	0.70
Q8R349_CI	Cdc16	Cell divisio	2	22.2	12.8	13.9	1.7	1.59	0.63	44.4	25.6	31.1	1.7	1.43	0.70
P14148_RL	Rpl7	60S ribosor	39	46.7	26.9	29.4	1.7	1.59	0.63	3737.2	2004.0	2439.2	1.9	1.53	0.65
Q9D1G1_R	Rab1b	Ras-related	4	9.7	5.6	6.1	1.7	1.59	0.63	48.0	34.7	42.2	1.4	1.14	0.88
Q9DCH4_EI	Eif3f	Eukaryotic	19	31.7	18.3	19.9	1.7	1.59	0.63	778.3	444.1	540.6	1.8	1.44	0.69
E9PYL2_E9	Prr12	Protein Prr	3	15.0	8.7	9.4	1.7	1.59	0.63	36.7	24.0	29.2	1.5	1.25	0.80
P10852_4F	Slc3a2	4F2 cell-sur	9	17.7	10.2	11.1	1.7	1.58	0.63	176.4	124.8	151.9	1.4	1.16	0.86
G5E8V9_G5	Arfip1	MCG18094	11	21.6	12.5	13.7	1.7	1.58	0.63	282.5	159.8	194.6	1.8	1.45	0.69
E9Q7C4_E9	Prr14l	Protein Prr	1	23.8	13.8	15.0	1.7	1.58	0.63	23.8	13.8	16.8	1.7	1.42	0.71
P48025_KS	Syk	Tyrosine-pr	1	4.0	2.3	2.5	1.7	1.58	0.63	4.0	2.3	2.8	1.7	1.42	0.71
P35288_RA	Rab23	Ras-related	1	5.5	3.2	3.5	1.7	1.58	0.63	5.5	3.2	3.9	1.7	1.42	0.71
Q3UFS4_GI	Gpatch11	G patch dor	1	12.7	7.4	8.0	1.7	1.58	0.63	12.7	7.4	9.0	1.7	1.41	0.71
P61957_SL	Sumo2	Small ubiqu	3	52.5	30.5	33.3	1.7	1.58	0.63	148.2	91.8	111.7	1.6	1.33	0.75
P97820_M	Map4k4	Mitogen-ac	1	8.1	4.7	5.1	1.7	1.57	0.64	8.1	4.7	5.7	1.7	1.41	0.71
Q9CXL3_CG050_MOUS		Uncharacte	5	111.8	65.2	71.1	1.7	1.57	0.64	487.5	230.0	279.9	2.1	1.74	0.57
Q3UM29_C	Cog7	Conserved	1	11.8	6.9	7.5	1.7	1.57	0.64	11.8	6.9	8.4	1.7	1.41	0.71
P62334_PF	Psmc6	26S protea	13	25.3	14.7	16.1	1.7	1.57	0.64	877.5	260.0	316.4	3.4	2.77	0.36
Q8K205_Q	Pop1	Blood vesse	1	7.2	4.2	4.6	1.7	1.57	0.64	7.2	4.2	5.1	1.7	1.41	0.71
Q99MP8_B	Brap	BRCA1-assc	3	6.3	3.7	4.0	1.7	1.57	0.64	18.9	14.5	17.7	1.3	1.07	0.93
Q6PHQ9_Q	Pabpc4	MCG5546,	7	56.1	32.8	35.8	1.7	1.57	0.64	328.9	208.1	253.3	1.6	1.30	0.77
Q61210_AI	Arhgef1	Rho guanin	11	14.2	8.3	9.1	1.7	1.57	0.64	146.7	103.0	125.4	1.4	1.17	0.85
P98083_SH	Shc1	SHC-transfo	5	10.2	6.0	6.5	1.7	1.57	0.64	109.7	38.5	46.8	2.9	2.34	0.43
Q62376_RI	Snrnp70	U1 small nu	5	33.3	19.5	21.2	1.7	1.57	0.64	178.6	138.2	168.3	1.3	1.06	0.94
Q8K2X3_S1	Obfc1	CST comple	3	4.3	2.5	2.7	1.7	1.57	0.64	19.5	8.9	10.9	2.2	1.79	0.56
Q8VCR7_AI	Abhd14b	Alpha/beta	1	3.2	1.9	2.1	1.7	1.57	0.64	3.2	1.9	2.3	1.7	1.40	0.71
Q8BKX1_BA	Baiap2	Brain-speci	5	18.7	11.0	12.0	1.7	1.57	0.64	77.9	45.7	55.6	1.7	1.40	0.71
Q6PE54_DI	Dhx40	Probable A	1	8.3	4.9	5.3	1.7	1.56	0.64	8.3	4.9	5.9	1.7	1.40	0.72
Q76MZ3_2	Ppp2r1a	Serine/thre	36	27.0	15.9	17.3	1.7	1.56	0.64	2021.8	772.5	940.2	2.6	2.15	0.47
Q7TPD0_IN	Ints3	Integrator	11	17.4	10.2	11.2	1.7	1.56	0.64	205.2	125.5	152.8	1.6	1.34	0.74
Q9CQV8_1	Ywhab	14-3-3 prot	28	29.0	17.1	18.7	1.7	1.55	0.64	2628.5	1028.3	1251.6	2.6	2.10	0.48
Q571G4_LI	Lin54	Protein lin-	2	8.8	5.2	5.7	1.7	1.55	0.64	17.7	10.4	12.7	1.7	1.39	0.72
Q8K4M5_C	Commd1	COMM dom	2	17.2	10.1	11.1	1.7	1.55	0.64	34.3	20.3	24.7	1.7	1.39	0.72
P62281_RS	Rps11	40S ribosor	10	204.1	120.6	131.6	1.7	1.55	0.64	3058.5	1665.1	2026.7	1.8	1.51	0.66
P28656_NI	Nap1l1	Nucleosom	7	18.5	11.0	12.0	1.7	1.55	0.65	289.8	82.5	100.5	3.5	2.88	0.35
Q9JIB4_TF2	Gtf2h2	General tra	1	10.1	6.0	6.5	1.7	1.55	0.65	10.1	6.0	7.3	1.7	1.39	0.72
O35984_PI	Pbx2	Pre-B-cell le	1	7.0	4.2	4.6	1.7	1.55	0.65	7.0	4.2	5.1	1.7	1.39	0.72
Q8VEK3_HI	Hnrnpu	Heterogene	54	38.2	22.6	24.7	1.7	1.55	0.65	5444.3	2751.1	3348.6	2.0	1.63	0.62
Q9CPR8_M	Ndnl2	Melanoma-	2	21.2	12.5	13.7	1.7	1.55	0.65	42.4	25.1	30.5	1.7	1.39	0.72
P60605_UI	Ube2g2	Ubiquitin-c	1	13.0	7.7	8.4	1.7	1.55	0.65	13.0	7.7	9.3	1.7	1.39	0.72
P60229_EI	Eif3e	Eukaryotic	40	28.4	16.8	18.4	1.7	1.55	0.65	1554.9	804.9	979.8	1.9	1.59	0.63
Q9CPT5_N	Nop16	Nucleolar p	3	6.8	4.1	4.4	1.7	1.54	0.65	39.6	23.1	28.1	1.7	1.41	0.71
O88544_CS	Cops4	COP9 signa	14	25.2	14.9	16.3	1.7	1.54	0.65	610.0	232.4	282.9	2.6	2.16	0.46
Q9D0M5_D	Dynll2	Dynein ligh	3	20.7	12.3	13.4	1.7	1.54	0.65	69.3	49.7	60.5	1.4	1.14	0.87
Q99ME2_W	Wdr6	WD repeat-	5	10.8	6.4	7.0	1.7	1.54	0.65	60.2	38.0	46.2	1.6	1.30	0.77
Q08509_EI	Eps8	Epidermal g	5	15.0	8.9	9.7	1.7	1.54	0.65	60.8	48.8	59.4	1.2	1.02	0.98
Q9CQU3_R	Rer1	Protein REF	2	15.7	9.4	10.2	1.7	1.54	0.65	31.5	18.8	22.9	1.7	1.38	0.73
Q91WG8_	Gne	Bifunctiona	1	8.8	5.3	5.8	1.7	1.54	0.65	8.8	5.3	6.4	1.7	1.38	0.73
P84091_AF	Ap2m1	AP-2 compl	9	16.5	9.9	10.7	1.7	1.54	0.65	362.5	168.7	205.3	2.1	1.77	0.57
Q99LG0_UI	Usp16	Ubiquitin c	1	9.5	5.7	6.2	1.7	1.54	0.65	9.5	5.7	6.9	1.7	1.38	0.73
P04627_AF	Araf	Serine/thre	1	14.5	8.7	9.5	1.7	1.53	0.65	14.5	8.7	10.6	1.7	1.37	0.73
P69566_RA	Ranbp9	Ran-bindin	3	17.5	10.5	11.4	1.7	1.53	0.65	40.2	31.7	38.6	1.3	1.04	0.96
P51660_DI	Hsd17b4	Peroxisoma	2	64.2	38.6	42.1	1.7	1.53	0.66	128.5	77.2	93.9	1.7	1.37	0.73
Q99ME9_N	Gtpbp4	Nucleolar G	5	14.7	8.8	9.6	1.7	1.53	0.66	86.8	42.5	51.7	2.0	1.68	0.60
Q5SYD0_M	Myo1d	Unconvent	3	10.8	6.5	7.1	1.7	1.53	0.66	27.3	17.7	21.5	1.5	1.27	0.79
Q61474_M	Msi1	RNA-bindir	3	7.2	4.4	4.7	1.7	1.52	0.66	24.5	15.2	18.5	1.6	1.32	0.76
Q8R570_SI	Snap47	Synaptosor	1	5.8	3.5	3.8	1.7	1.52	0.66	5.8	3.5	4.3	1.7	1.37	0.73
Q5XJE5_LE	Leo1	RNA polym	3	26.6	16.0	17.5	1.7	1.52	0.66	79.4	50.9	62.0	1.6	1.28	0.78
P54729_NI	Nub1	NEDD8 ulti	8	9.5	5.8	6.3	1.7	1.52	0.66	182.1	65.1	79.3	2.8	2.30	0.44
Q9DCA5_BI	Brix1	Ribosome b	3	12.5	7.5	8.2	1.7	1.52	0.66	60.1	28.6	34.8	2.1	1.73	0.58
Q8BMB3_II	Eif4e2	Eukaryotic	2	9.0	5.4	5.9	1.7	1.52	0.66	17.9	10.8	13.2	1.7	1.36	0.74
Q9EQS3_M	Mycbp	C-Myc-bind	5	59.2	35.8	39.0	1.7	1.52	0.66	214.2	153.0	186.2	1.4	1.15	0.87
P46735_M	Myo1b	Unconvent	6	15.8	9.5	10.4	1.7	1.52	0.66	110.6	67.6	82.3	1.6	1.34	0.74
P70677_CA	Casp3	Caspase-3 C	1	9.7	5.8	6.4	1.7	1.52	0.66	9.7	5.8	7.1	1.7	1.36	0.74
Q9D7Z3_N	Nol7	Nucleolar p	2	5.7	3.5	3.8	1.7	1.52	0.66	11.4	6.9	8.4	1.7	1.36	0.74
Q9WVK4_E	Ehd1	EH domain-	32	12.8	7.7	8.4	1.7	1.52	0.66	576.8	395.3	481.1	1.5	1.20	0.83
Q8C0E2_VF	Vps26b	Vacuolar pr	7	14.3	8.7	9.5	1.7	1.51	0.66	107.2	96.4	117.3	1.1	0.91	1.09
P56546_C1	Ctbp2	C-terminal-	3	39.4	23.8	26.0	1.7	1.51	0.66	95.3	67.2	81.8	1.4	1.17	0.86
Q8C7V8_C	Ccdc134	Coiled-coil	4	7.2	4.4	4.8	1.6	1.51	0.66	39.1	22.1	27.0	1.8	1.45	0.69
Q922L6_NI	Nelfcd	Negative el	8	15.4	9.3	10.2	1.6	1.51	0.66	151.9	238.8	290.7	0.6	0.52	1.91
Q91WC0_S	Setd3	Histone-lys	2	6.8	4.1	4.5	1.6	1.51	0.66	13.6	8.2	10.0	1.6	1.35	0.74
Q9CQ22_LT	Lamtor1	Ragulator c	1	12.9	7.8	8.6	1.6	1.51	0.66	12.9	7.8	9.5	1.6	1.35	0.74
Q8C9B9_DI	Dido1	Death-indu	3	3.9	2.4	2.6	1.6	1.51	0.66	12.0	12.6	15.3	1.0	0.78	1.28
Q9CPY6_GI	Gid4	Glucose-inc	1	10.9	6.6	7.2	1.6	1.51	0.66	10.9	6.6	8.1	1.6	1.35	0.74
Q8BR65_SI	Suds3	Sin3 histon	1	6.0	3.7	4.0	1.6	1.51	0.66	6.0	3.7	4.5	1.6	1.35	0.74
O35638_S1	Stag2	Cohesin sul	3	19.4	11.8	12.9	1.6	1.51	0.66	53.3	31.4	38.2	1.7	1.39	0.72
Q8BTM8_FI	Flna	Filamin-A C	85	101.9	62.1	67.7	1.6	1.51	0.66	15025.6	5893.0	7172.7	2.5	2.09	0.48
E9QQ10_E9	Akap9	A-kinase an	1	6.3	3.8	4.2	1.6	1.50	0.66	6.3	3.8	4.7	1.6	1.35	0.74
Q62433_NI	Ndrg1	Protein ND	1	13.4	8.2	8.9	1.6	1.50	0.67	13.4	8.2	10.0	1.6	1.35	0.74
Q60932_VI	Vdac1	Voltage-dep	3	14.1	8.6	9.4	1.6	1.50	0.67	46.6	33.3	40.5	1.4	1.15	0.87
Q9CQA1_TI	Trappc5	Trafficking	2	23.4	14.3	15.6	1.6	1.50	0.67	46.8	28.6	34.8	1.6	1.35	0.74
P47955_RL	Rplp1	60S acidic r	6	45.9	28.0	30.6	1.6	1.50	0.67	1870.5	1365.1	1661.5	1.4	1.13	0.89
Q925B0_PA	Pawr	PRKC apop	3	18.0	11.0	12.0	1.6	1.50	0.67	40.9	30.1	36.6	1.4	1.12	0.90
Q8C7R4_UI	Uba6	Ubiquitin-l	3	8.1	5.0	5.4	1.6	1.50	0.67	23.4	14.6	17.8	1.6	1.32	0.76
Q64152_BT	Btf3	Transcripti	8	16.3	10.0	10.9	1.6	1.49	0.67	173.6	84.1	102.3	2.1	1.70	0.59
P62245_RS	Rps15a	40S ribosor	27	43.3	26.6	29.0	1.6	1.49	0.67	2126.8	1312.6	1597.7	1.6	1.33	0.75
Q3UVL4_VI	Vps51	Vacuolar pr	1	11.9	7.3	8.0	1.6	1.49	0.67	11.9	7.3	8.9	1.6	1.33	0.75
P11352_GI	Gpx1	Glutathion	6	8.1	5.0	5.5	1.6	1.49	0.67	44.0	32.0	38.9	1.4	1.13	0.88
Q9D6V8_PA	Paip2	Polyadenyl	1	16.8	10.4	11.3	1.6	1.48	0.67	16.8	10.4	12.6	1.6	1.33	0.75
Q8JZK9_HN	Hmgcs1	Hydroxyme	1	8.0	5.0	5.4	1.6	1.48	0.67	8.0	5.0	6.0	1.6	1.33	0.75
O35250_EX	Exoc7	Exocyst cor	3	11.1	6.9	7.5	1.6	1.48	0.68	35.8	20.5	24.9	1.7	1.44	0.70
P80318_TC	Cct3	T-complex	51	36.0	22.3	24.3	1.6	1.48	0.68	3830.6	2015.3	2452.9	1.9	1.56	0.64
P68254_14	Ywhaq	14-3-3 prot	8	12.1	7.5	8.2	1.6	1.48	0.68	90.6	89.7	109.1	1.0	0.83	1.20
Q80ZX0_Q8	Sec24b	Protein Sec	8	8.3	5.1	5.6	1.6	1.48	0.68	90.8	50.8	61.9	1.8	1.47	0.68
P70168_IM	Kpnb1	Importin su	14	27.1	16.9	18.4	1.6	1.47	0.68	474.2	245.9	299.3	1.9	1.58	0.63
Q9D8M7_P	Phf10	PHD finger	1	10.2	6.3	6.9	1.6	1.47	0.68	10.2	6.3	7.7	1.6	1.32	0.76
Q9ESU6_BF	Brd4	Bromodom	12	10.2	6.4	6.9	1.6	1.47	0.68	166.5	109.9	133.7	1.5	1.25	0.80
Q91VR2_AT	Atp5c1	ATP syntha	2	13.9	8.7	9.5	1.6	1.47	0.68	27.8	17.4	21.1	1.6	1.32	0.76
Q8VCW8_A	Acsf2	Acyl-CoA sy	2	11.3	7.1	7.7	1.6	1.47	0.68	22.7	14.2	17.2	1.6	1.31	0.76
P67984_RL	Rpl22	60S ribosor	8	48.6	30.4	33.2	1.6	1.47	0.68	787.2	735.8	895.6	1.1	0.88	1.14
Q9CZU3_SK	Skiv2l2	Superkiller	33	18.5	11.6	12.7	1.6	1.47	0.68	882.0	558.6	679.9	1.6	1.30	0.77
P56183_RF	Rrp1	Ribosomal	3	17.3	10.9	11.8	1.6	1.46	0.68	45.5	29.0	35.3	1.6	1.29	0.78
P42232_ST	Stat5b	Signal trans	3	9.9	6.2	6.8	1.6	1.46	0.68	26.3	18.1	22.1	1.4	1.19	0.84

Q9CQU5_Z'	Zwint	ZW10 inter	1	8.0	5.0	5.5	1.6	1.46	0.68	8.0	5.0	6.1	1.6	1.31	0.76
Q61048_W	Wbp4	WW domai	3	12.3	7.7	8.4	1.6	1.46	0.68	34.5	27.2	33.1	1.3	1.04	0.96
A2AR02_PF	Ppig	Peptidyl-pr	2	15.1	9.5	10.3	1.6	1.46	0.68	30.2	18.9	23.0	1.6	1.31	0.76
Q8CIB5_FEI	Fermt2	Fermitin fa	34	20.5	12.9	14.0	1.6	1.46	0.69	1056.2	532.4	648.1	2.0	1.63	0.61
G3UVU2_G	Sf3a2	Splicing fac	9	17.4	10.9	11.9	1.6	1.46	0.69	183.9	126.6	154.0	1.5	1.19	0.84
Q3TJ22_Q3	Aamp	Angio-assoc	1	3.5	2.2	2.4	1.6	1.46	0.69	3.5	2.2	2.7	1.6	1.31	0.77
P29037_TE	Tbp	TATA-box-b	3	13.5	8.5	9.3	1.6	1.45	0.69	37.1	27.6	33.6	1.3	1.10	0.91
Q80YS6_AF	Afap1	Actin filam	1	9.7	6.1	6.7	1.6	1.45	0.69	9.7	6.1	7.5	1.6	1.30	0.77
Q8VEE1_LN	Lmcd1	LIM and cys	1	6.8	4.3	4.7	1.6	1.45	0.69	6.8	4.3	5.2	1.6	1.30	0.77
Q91W59_F	Rbms1	RNA-bindin	2	41.0	25.9	28.3	1.6	1.45	0.69	82.1	51.8	63.1	1.6	1.30	0.77
Q8BGQ7_S'	Aars	Alanine--tR	29	13.7	8.7	9.5	1.6	1.45	0.69	734.5	305.3	371.6	2.4	1.98	0.51
P49586_PC	Pcyt1a	Choline-ph	3	29.6	18.7	20.4	1.6	1.45	0.69	76.2	53.4	65.0	1.4	1.17	0.85
Q9D937_CK098_MOUS	Uncharacte		4	15.0	9.5	10.4	1.6	1.45	0.69	107.6	53.0	64.5	2.0	1.67	0.60
O35326_SF	Srsf5	Serine/argi	5	92.0	58.4	63.7	1.6	1.45	0.69	309.7	220.9	268.9	1.4	1.15	0.87
O35623_BI	Bet1	BET1 homo	1	5.3	3.4	3.7	1.6	1.44	0.69	5.3	3.4	4.1	1.6	1.29	0.77
Q9EQC8_Q	Prcc	Papillary re	2	8.8	5.6	6.1	1.6	1.44	0.69	17.6	11.2	13.6	1.6	1.29	0.77
Q91V41_R/	Rab14	Ras-related	5	26.4	16.8	18.3	1.6	1.44	0.69	128.9	101.9	124.1	1.3	1.04	0.96
Q99KC8_VI	Vwa5a	von Willeb	4	15.6	9.9	10.8	1.6	1.44	0.69	67.8	33.1	40.2	2.1	1.69	0.59
Q99JZ4_Q9	Sar1a	GTP-bindin	5	27.1	17.2	18.8	1.6	1.44	0.69	170.6	151.9	184.9	1.1	0.92	1.08
Q8K124_PI	Plekho2	Pleckstrin h	1	10.3	6.6	7.2	1.6	1.44	0.70	10.3	6.6	8.0	1.6	1.29	0.78
Q91YU8_SS	Ppan	Suppressor	3	9.9	6.3	6.9	1.6	1.44	0.70	30.3	19.2	23.4	1.6	1.29	0.77
Q3V4B5_C(	Commd6	COMM don	2	18.7	11.9	13.0	1.6	1.44	0.70	37.3	23.8	29.0	1.6	1.29	0.78
Q6A028_S\	Swap70	Switch-assc	9	9.9	6.3	6.9	1.6	1.43	0.70	102.2	96.2	117.1	1.1	0.87	1.15
Q9WV70_N	Noc2l	Nucleolar c	1	19.0	12.2	13.3	1.6	1.43	0.70	19.0	12.2	14.8	1.6	1.28	0.78
Q9D0P8_IF	Ift27	Intraflagell	2	14.4	9.2	10.1	1.6	1.43	0.70	28.8	18.4	22.4	1.6	1.28	0.78
Q8C3P7_M	Mettl3	N6-adenosi	3	10.8	6.9	7.5	1.6	1.43	0.70	32.7	25.9	31.5	1.3	1.04	0.96
Q3U1T3_BI	Brms1l	Breast canc	1	18.2	11.7	12.7	1.6	1.43	0.70	18.2	11.7	14.2	1.6	1.28	0.78
O55057_PI	Pde6d	Retinal rod	1	6.5	4.2	4.5	1.6	1.43	0.70	6.5	4.2	5.1	1.6	1.28	0.78
Q8BMA6_S	Srp68	Signal reco	19	12.2	7.8	8.5	1.6	1.43	0.70	265.1	174.1	211.9	1.5	1.25	0.80
Q8C052_M	Map1s	Microtubul	2	12.1	7.8	8.5	1.6	1.43	0.70	24.3	15.5	18.9	1.6	1.28	0.78
Q9CYZ2_TP	Tpd52l2	Tumor prot	4	25.5	16.3	17.8	1.6	1.43	0.70	118.2	59.3	72.2	2.0	1.64	0.61
Q6ZQK5_A(	Acap2	Arf-GAP wit	4	8.9	5.7	6.2	1.6	1.43	0.70	37.0	55.4	67.4	0.7	0.55	1.82
Q8K1M6_D	Dnm1l	Dynamin-1	39	15.9	10.2	11.1	1.6	1.43	0.70	762.2	504.7	614.2	1.5	1.24	0.81
Q6P542_AI	Abcf1	ATP-bindin	29	15.8	10.2	11.1	1.6	1.43	0.70	871.8	435.0	529.5	2.0	1.65	0.61
Q8R2Y8_P1	Ptrh2	Peptidyl-tR	1	15.5	10.0	10.9	1.6	1.42	0.70	15.5	10.0	12.2	1.6	1.28	0.78
P09103_PI	P4hb	Protein dis	21	55.8	35.9	39.2	1.6	1.42	0.70	1158.3	695.5	846.5	1.7	1.37	0.73
Q8K2T1_NI	Nmral1	NmrA-like f	1	10.9	7.0	7.7	1.6	1.42	0.70	10.9	7.0	8.6	1.6	1.28	0.78
Q9DB96_N	Ngdn	Neuroguidi	1	8.3	5.4	5.9	1.6	1.42	0.70	8.3	5.4	6.5	1.6	1.27	0.78
P16045_LE	Lgals1	Galectin-1	5	5.2	3.4	3.7	1.6	1.42	0.70	48.1	42.2	51.4	1.1	0.94	1.07
Q9D662_S(	Sec23b	Protein tra	12	12.8	8.3	9.0	1.5	1.42	0.70	175.8	137.6	167.5	1.3	1.05	0.95
Q8BWW9_	Pkn2	Serine/thre	3	6.5	4.2	4.6	1.5	1.42	0.71	22.1	12.3	15.0	1.8	1.47	0.68
Q8K194_SI	Snrnp27	U4/U6.U5 s	1	5.9	3.8	4.1	1.5	1.42	0.71	5.9	3.8	4.6	1.5	1.27	0.79
Q9JHH9_C(	Copz2	Coatomer s	1	43.0	27.9	30.4	1.5	1.42	0.71	43.0	27.9	33.9	1.5	1.27	0.79
P59708_SF	Sf3b6	Splicing fac	5	122.4	79.3	86.5	1.5	1.41	0.71	458.5	306.7	373.3	1.5	1.23	0.81
Q9Z110_P5	Aldh18a1	Delta-1-pyr	10	10.5	6.8	7.4	1.5	1.41	0.71	132.3	119.7	145.6	1.1	0.91	1.10
A2A4P0_DI	Dhx8	ATP-depen	8	13.9	9.1	9.9	1.5	1.41	0.71	108.3	76.6	93.2	1.4	1.16	0.86
Q8CB77_EL	Tceb3	Transcripti	2	14.3	9.3	10.2	1.5	1.41	0.71	28.7	18.6	22.7	1.5	1.26	0.79
F7CVJ5_F7	Ahnak2	Protein Ahr	1	32.1	20.9	22.9	1.5	1.41	0.71	32.1	20.9	25.5	1.5	1.26	0.79
G3X8R0_G	Reep5	Receptor ac	1	14.0	9.1	10.0	1.5	1.41	0.71	14.0	9.1	11.1	1.5	1.26	0.79
Q8CHS8_VI	Vps37a	Vacuolar pr	1	5.3	3.5	3.8	1.5	1.40	0.71	5.3	3.5	4.2	1.5	1.26	0.79
Q8VI94_OA	Oasl1	2'-5'-oligoa	19	15.8	10.3	11.2	1.5	1.40	0.71	351.9	229.0	278.7	1.5	1.26	0.79
Q5PRF0_H1	Heatr5a	HEAT repea	4	8.0	5.2	5.7	1.5	1.40	0.71	31.8	30.5	37.1	1.0	0.86	1.17
Q8C5L7_RI	Rbm34	RNA-bindin	3	16.0	10.5	11.4	1.5	1.40	0.71	51.2	37.8	46.0	1.4	1.11	0.90
Q3TIX9_SN	Usp39	U4/U6.U5 t	9	8.8	5.8	6.3	1.5	1.40	0.71	106.6	54.9	66.8	1.9	1.60	0.63
Q8VDP2_CX056_MOUS	UPF0428 p		1	13.2	8.7	9.5	1.5	1.40	0.71	13.2	8.7	10.6	1.5	1.25	0.80
Q99LB2_DI	Dhrs4	Dehydroge	3	8.9	5.8	6.3	1.5	1.40	0.71	25.9	16.6	20.2	1.6	1.28	0.78
P54276_M	Msh6	DNA misma	22	16.6	10.9	11.9	1.5	1.40	0.72	636.1	326.3	397.2	1.9	1.60	0.62
P43247_M	Msh2	DNA misma	43	17.4	11.4	12.4	1.5	1.40	0.72	1057.4	608.6	740.7	1.7	1.43	0.70
O35841_AI	Api5	Apoptosis i	25	18.9	12.4	13.6	1.5	1.40	0.72	606.1	382.2	465.2	1.6	1.30	0.77
Q80YV3_TF	Trrap	Transforma	1	6.5	4.2	4.6	1.5	1.39	0.72	6.5	4.2	5.2	1.5	1.25	0.80
Q3U1G5_I2	Isg20l2	Interferon-	2	17.1	11.2	12.2	1.5	1.39	0.72	34.1	22.5	27.3	1.5	1.25	0.80
P47963_RI	Rpl13	60S riboso	25	86.9	57.2	62.4	1.5	1.39	0.72	2371.0	2100.8	2557.1	1.1	0.93	1.08
P30412_PF	Ppic	Peptidyl-pr	1	3.0	2.0	2.2	1.5	1.39	0.72	3.0	2.0	2.4	1.5	1.25	0.80
P20108_PF	Prdx3	Thioredoxi	3	12.2	8.1	8.8	1.5	1.39	0.72	37.5	20.7	25.2	1.8	1.49	0.67
Q6P5B0_RI	Rrp12	RRP12-like	5	9.5	6.3	6.8	1.5	1.39	0.72	53.1	38.0	46.2	1.4	1.15	0.87
Q8C4Y3_NI	Nelfb	Negative el	11	17.4	11.5	12.5	1.5	1.39	0.72	250.5	133.1	162.0	1.9	1.55	0.65
Q8CDG3_V	Vcpip1	Deubiquiti	5	9.0	6.0	6.5	1.5	1.39	0.72	48.4	27.0	32.9	1.8	1.47	0.68
P70290_EI	Mpp1	55 kDa eryt	3	15.9	10.5	11.5	1.5	1.39	0.72	65.3	33.3	40.5	2.0	1.61	0.62
Q3THG9_A	Aarsd1	Alanyl-tRN	1	6.9	4.6	5.0	1.5	1.39	0.72	6.9	4.6	5.6	1.5	1.24	0.81
P61982_14	Ywhag	14-3-3 prot	13	33.9	22.5	24.5	1.5	1.38	0.72	736.5	393.8	479.4	1.9	1.54	0.65
Q91WM3_	Rrp9	U3 small nu	3	7.9	5.2	5.7	1.5	1.38	0.72	25.5	17.7	21.5	1.4	1.19	0.84
Q9ERA6_TF	Tfip11	Tuftelin-int	11	13.3	8.8	9.6	1.5	1.38	0.72	141.3	104.4	127.1	1.4	1.11	0.90
Q3TCH7_CI	Cul4a	Cullin-4A O	11	16.4	10.9	11.9	1.5	1.38	0.72	175.2	111.5	135.8	1.6	1.29	0.78
Q99JW4_LI	Lims1	LIM and ser	3	64.6	42.8	46.7	1.5	1.38	0.72	210.6	126.0	153.4	1.7	1.37	0.73
P67871_CS	Csnk2b	Casein kina	4	46.4	30.8	33.6	1.5	1.38	0.72	183.1	119.8	145.8	1.5	1.26	0.80
P59048_PI	Pdrg1	p53 and DN	1	13.5	8.9	9.7	1.5	1.38	0.72	13.5	8.9	10.9	1.5	1.24	0.81
Q9JM13_R	Rabgef1	Rab5 GDP/	2	7.5	5.0	5.4	1.5	1.38	0.72	14.9	9.9	12.1	1.5	1.24	0.81
Q9DBZ5_EI	Eif3k	Eukaryotic	9	30.3	20.1	22.0	1.5	1.38	0.72	371.1	300.1	365.3	1.2	1.02	0.98
Q8R4X3_RI	Rbm12	RNA-bindin	4	12.1	8.1	8.8	1.5	1.38	0.73	74.2	28.4	34.5	2.6	2.15	0.47
Q9R078_A/	Prkab1	5'-AMP-acti	3	17.1	11.3	12.4	1.5	1.38	0.73	48.4	31.8	38.6	1.5	1.25	0.80
Q8VEH3_AI	Arl8a	ADP-ribosy	2	9.8	6.5	7.1	1.5	1.38	0.73	19.6	13.0	15.9	1.5	1.24	0.81
Q9D554_SI	Sf3a3	Splicing fac	13	12.8	8.5	9.3	1.5	1.38	0.73	576.4	234.2	285.1	2.5	2.02	0.49
Q64339_IS	Isg15	Ubiquitin-l	22	50.6	33.7	36.7	1.5	1.38	0.73	2138.2	1592.5	1938.3	1.3	1.10	0.91
Q62193_RI	Rpa2	Replication	7	6.5	4.3	4.7	1.5	1.38	0.73	166.8	107.5	130.8	1.6	1.28	0.78
Q5SWU9_A	Acaca	Acetyl-CoA	36	17.8	11.9	13.0	1.5	1.38	0.73	713.4	543.2	661.1	1.3	1.08	0.93
P37040_N(	Por	NADPH--cy	2	8.2	5.5	6.0	1.5	1.38	0.73	16.4	11.0	13.3	1.5	1.23	0.81
Q9JKV1_AD	Adrm1	Proteasom	2	21.4	14.3	15.6	1.5	1.37	0.73	42.9	28.6	34.8	1.5	1.23	0.81
Q8BVY0_RI	Rsl1d1	Ribosomal	24	13.9	9.3	10.2	1.5	1.37	0.73	415.1	313.5	381.6	1.3	1.09	0.92
Q922U1_PI	Prpf3	U4/U6 sma	10	17.3	11.5	12.6	1.5	1.37	0.73	197.9	148.9	181.2	1.3	1.09	0.92
P39053_D'	Dnm1	Dynamin-1	28	16.4	10.9	11.9	1.5	1.37	0.73	761.3	617.0	750.9	1.2	1.01	0.99
Q8R3C0_M	Mcmbp	Mini-chron	1	13.9	9.3	10.1	1.5	1.37	0.73	13.9	9.3	11.3	1.5	1.23	0.81
P46062_SII	Sipa1	Signal-indu	1	7.8	5.2	5.7	1.5	1.37	0.73	7.8	5.2	6.3	1.5	1.23	0.81
E9Q447_E9	Sptan1	Spectrin al	1	18.0	12.0	13.1	1.5	1.37	0.73	18.0	12.0	14.6	1.5	1.23	0.81
P26187_M	Mgmt	Methylated	2	6.1	4.0	4.4	1.5	1.37	0.73	12.1	8.1	9.9	1.5	1.23	0.81
O09167_RI	Rpl21	60S riboso	14	71.2	47.6	51.9	1.5	1.37	0.73	4032.3	1568.8	1909.5	2.6	2.11	0.47
Q6WKZ8_U	Ubr2	E3 ubiquiti	2	5.0	3.3	3.6	1.5	1.37	0.73	9.9	6.7	8.1	1.5	1.23	0.81
Q8BQM4_H	Heatr3	HEAT repea	4	12.9	8.6	9.4	1.5	1.37	0.73	52.4	36.7	44.6	1.4	1.17	0.85
Q920D3_M	Med28	Mediator o	2	5.3	3.6	3.9	1.5	1.37	0.73	10.6	7.1	8.7	1.5	1.23	0.82
P59941_SII	Sirt6	NAD-depen	1	9.2	6.2	6.8	1.5	1.36	0.73	9.2	6.2	7.6	1.5	1.22	0.82
P14115_RI	Rpl27a	60S riboso	4	181.4	121.9	133.0	1.5	1.36	0.73	855.4	997.6	1214.3	0.9	0.70	1.42
P61021_R/	Rab5b	Ras-related	2	13.2	8.9	9.7	1.5	1.36	0.73	26.5	17.8	21.7	1.5	1.22	0.82
Q921Z5_TF	Tnfaip8	Tumor necr	1	3.4	2.3	2.5	1.5	1.36	0.73	3.4	2.3	2.8	1.5	1.22	0.82
Q9CPQ5_CI	Cenpq	Centromer	2	7.9	5.3	5.8	1.5	1.36	0.73	15.9	10.7	13.0	1.5	1.22	0.82
Q8CGB3_U	Uaca	Uveal auto	1	12.0	8.1	8.8	1.5	1.36	0.74	12.0	8.1	9.8	1.5	1.22	0.82
Q8CBE3_W	Wdr37	WD repeat-	1	18.5	12.5	13.7	1.5	1.36	0.74	18.5	12.5	15.3	1.5	1.22	0.82
E9QLA5_E9	Inf2	Inverted fo	11	14.3	9.7	10.5	1.5	1.36	0.74	174.4	121.6	148.1	1.4	1.18	0.85
P35980_RI	Rpl18	60S riboso	20	59.0	39.9	43.6	1.5	1.35	0.74	2835.0	1993.6	2426.6	1.4	1.17	0.86
P47911_RI	Rpl6	60S riboso	19	108.9	73.8	80.5	1.5	1.35	0.74	4977.6	2405.0	2927.3	2.1	1.70	0.59
Q9CR27_C(	Ccdc53	WASH com	2	10.4	7.0	7.7	1.5	1.35	0.74	20.8	14.1	17.1	1.5	1.21	0.82
O55102_BI	Bloc1s1	Biogenesis	2	32.5	22.0	24.0	1.5	1.35	0.74	64.9	44.1	53.7	1.5	1.21	0.83
P19096_FA	Fasn	Fatty acid s	63	49.0	33.3	36.3	1.5	1.35	0.74	5239.1	2655.2	3231.8	2.0	1.62	0.62
Q60855_RI	Ripk1	Receptor-ir	2	8.4	5.7	6.2	1.5	1.35	0.74	16.9	11.5	13.9	1.5	1.21	0.83
P11438_LA	Lamp1	Lysosome-a	1	23.0	15.7	17.1	1.5	1.35	0.74	23.0	15.7	19.1	1.5	1.21	0.83

Q6ZWY6_U	Ube2d2b	Ubiquitin-	1	27.0	18.4	20.0	1.5	1.35	0.74	27.0	18.4	22.3	1.5	1.21	0.83
Q91V89_Q	Ppp2r5d	Protein Pp	17	17.1	11.6	12.7	1.5	1.35	0.74	339.1	279.3	339.9	1.2	1.00	1.00
Q5NC05_T	Ttf2	Transcripti	2	9.3	6.3	6.9	1.5	1.35	0.74	18.5	12.6	15.4	1.5	1.21	0.83
Q8VCQ8_Q	Cald1	Caldesmon	24	20.4	13.9	15.2	1.5	1.34	0.74	740.4	457.1	556.4	1.6	1.33	0.75
P14211_C	Calr	Calreticulir	3	6.5	4.4	4.8	1.5	1.34	0.75	19.2	12.0	14.6	1.6	1.31	0.76
Q69ZA1_C	Cdk13	Cyclin-depe	3	11.3	7.7	8.4	1.5	1.34	0.75	42.7	22.1	26.9	1.9	1.59	0.63
Q8CFE3_R	Rcor1	REST corep	7	25.3	17.3	18.9	1.5	1.34	0.75	128.6	112.6	137.1	1.1	0.94	1.07
Q3TAQ9_Q	Wdr36	Protein Wd	2	9.6	6.6	7.2	1.5	1.34	0.75	19.2	13.2	16.0	1.5	1.20	0.84
Q9QZL0_R	Ripk3	Receptor-ir	1	19.0	13.0	14.2	1.5	1.34	0.75	19.0	13.0	15.8	1.5	1.20	0.84
Q9CXW4_	Rpl11	60S ribosor	14	44.1	30.3	33.0	1.5	1.34	0.75	5074.9	2043.6	2487.4	2.5	2.04	0.49
Q8CDJ8_ST	Ston1	Stonin-1 O	1	15.1	10.4	11.3	1.5	1.34	0.75	15.1	10.4	12.6	1.5	1.20	0.84
O54950_A	Prkag1	5'-AMP-acti	10	26.4	18.1	19.8	1.5	1.33	0.75	279.9	189.5	230.7	1.5	1.21	0.82
Q9JKY0_RC	Rqcd1	Cell differer	9	20.7	14.3	15.6	1.5	1.33	0.75	253.6	154.5	188.1	1.6	1.35	0.74
P35831_P	Ptpn12	Tyrosine-pr	1	4.9	3.4	3.7	1.5	1.33	0.75	4.9	3.4	4.1	1.5	1.20	0.84
Q9CWF2_T	Tubb2b	Tubulin bet	4	72.8	50.1	54.7	1.5	1.33	0.75	317.5	232.1	282.6	1.4	1.12	0.89
Q6ZWN5_	Rps9	40S ribosor	36	36.6	25.3	27.6	1.5	1.33	0.75	3951.4	2791.1	3397.3	1.4	1.16	0.86
E9Q634_M	Myo1e	Unconvent	7	13.1	9.0	9.9	1.4	1.33	0.75	109.8	69.9	85.1	1.6	1.29	0.77
P47962_R	Rpl5	60S ribosor	24	26.4	18.2	19.9	1.4	1.33	0.75	1876.8	739.9	900.6	2.5	2.08	0.48
E9Q450_E	Tpm1	Tropomyos	5	44.8	31.0	33.8	1.4	1.32	0.75	219.5	171.6	208.8	1.3	1.05	0.95
Q91WB4_	Plekhf2	Pleckstrin	1	5.3	3.6	4.0	1.4	1.32	0.76	5.3	3.6	4.4	1.4	1.18	0.84
Q99LI8_H	Hgs	Hepatocyte	5	15.1	10.5	11.5	1.4	1.32	0.76	61.9	53.0	64.6	1.2	0.96	1.04
P56959_F	Fus	RNA-bindir	6	16.8	11.7	12.7	1.4	1.32	0.76	198.1	87.7	106.7	2.3	1.86	0.54
Q5SRX1_T	Tom1l2	TOM1-like	2	7.1	4.9	5.4	1.4	1.32	0.76	14.2	9.9	12.0	1.4	1.18	0.85
Q922D8_C	Mthfd1	C-1-tetrahy	44	30.8	21.4	23.3	1.4	1.32	0.76	2050.6	1189.7	1448.0	1.7	1.42	0.71
Q8VDG3_P	Parn	Poly(A)-spe	2	5.5	3.8	4.2	1.4	1.32	0.76	11.0	7.7	9.3	1.4	1.18	0.85
P14131_R	Rps16	40S ribosor	17	71.6	49.8	54.3	1.4	1.32	0.76	2604.3	1882.5	2291.3	1.4	1.14	0.88
P97315_C	Csrp1	Cysteine an	5	29.0	20.2	22.1	1.4	1.31	0.76	628.3	608.8	741.0	1.0	0.85	1.18
Q9DBS9_O	Osbpl3	Oxysterol-b	3	12.8	8.9	9.7	1.4	1.31	0.76	95.7	41.9	51.0	2.3	1.88	0.53
P39054_D	Dnm2	Dynamin-2	40	18.5	13.0	14.1	1.4	1.31	0.76	1298.7	706.3	859.7	1.8	1.51	0.66
P00375_D	Dhfr	Dihydrofol	1	12.6	8.8	9.6	1.4	1.31	0.76	12.6	8.8	10.7	1.4	1.17	0.85
Q62418_D	Dbnl	Drebrin-lik	4	6.7	4.7	5.1	1.4	1.31	0.76	40.4	19.9	24.3	2.0	1.66	0.60
Q9R0Q3_T	Tmed2	Transmem	2	14.4	10.1	11.0	1.4	1.31	0.76	28.8	20.2	24.6	1.4	1.17	0.85
O55201_S	Supt5h	Transcripti	17	16.6	11.7	12.7	1.4	1.31	0.77	409.4	206.9	251.8	2.0	1.63	0.62
Q8BVL3_S	Snx17	Sorting nex	1	7.5	5.3	5.8	1.4	1.31	0.77	7.5	5.3	6.4	1.4	1.17	0.85
B2RX14_T	Zcchc11	Terminal u	2	17.6	12.3	13.4	1.4	1.31	0.77	35.1	24.7	30.0	1.4	1.17	0.85
O88665_B	Brd7	Bromodom	3	11.5	8.1	8.8	1.4	1.30	0.77	31.4	31.1	37.8	1.0	0.83	1.21
Q61771_K	Kif3b	Kinesin-like	3	8.3	5.8	6.3	1.4	1.30	0.77	29.3	18.4	22.4	1.6	1.31	0.76
Q9CXE7_T	Tmed5	Transmem	1	9.6	6.8	7.4	1.4	1.30	0.77	9.6	6.8	8.3	1.4	1.17	0.86
Q99MR6_S	Srrt	Serrate RN	27	26.1	18.4	20.1	1.4	1.30	0.77	1451.3	743.0	904.4	2.0	1.60	0.62
Q8BP22_F	Fam92a1	Protein FA	1	5.2	3.7	4.0	1.4	1.30	0.77	5.2	3.7	4.4	1.4	1.16	0.86
Q61635_Q	Ifi47	GTP-bindin	3	8.4	6.0	6.5	1.4	1.30	0.77	25.8	16.0	19.5	1.6	1.32	0.75
Q8CHP6_P	Phc3	Polyhomec	1	12.8	9.1	9.9	1.4	1.30	0.77	12.8	9.1	11.1	1.4	1.16	0.86
P14824_A	Anxa6	Annexin A6	9	5.7	4.1	4.4	1.4	1.29	0.77	60.8	52.2	63.5	1.2	0.96	1.05
P99024_T	Tubb5	Tubulin bet	21	129.9	92.2	100.6	1.4	1.29	0.77	4512.3	2936.1	3573.8	1.5	1.26	0.79
Q3UKR0_Q	Daxx	Death dom	2	10.8	7.7	8.4	1.4	1.29	0.77	21.7	15.4	18.7	1.4	1.16	0.86
P81269_A	Atf1	Cyclic AMP	1	6.6	4.7	5.1	1.4	1.29	0.77	6.6	4.7	5.7	1.4	1.16	0.86
Q6A026_P	Pds5a	Sister chro	21	13.3	9.4	10.3	1.4	1.29	0.77	479.3	387.6	471.8	1.2	1.02	0.98
Q6PGC1_D	Dhx29	ATP-depen	14	8.9	6.3	6.9	1.4	1.29	0.78	172.8	110.9	134.9	1.6	1.28	0.78
Q62018_C	Ctr9	RNA polym	3	14.1	10.0	11.0	1.4	1.29	0.78	45.2	26.9	32.7	1.7	1.38	0.72
Q03265_A	Atp5a1	ATP syntha	19	21.3	15.1	16.5	1.4	1.29	0.78	760.1	277.9	338.3	2.7	2.25	0.45
Q6PGF5_Q	Bms1	BMS1 hom	4	10.3	7.3	8.0	1.4	1.29	0.78	48.8	30.8	37.5	1.6	1.30	0.77
O88532_Z	Zfr	Zinc finger	13	23.0	16.4	17.9	1.4	1.29	0.78	286.1	208.0	253.2	1.4	1.13	0.89
Q61735_C	Cd47	Leukocyte	3	10.9	7.7	8.5	1.4	1.29	0.78	31.3	22.1	26.9	1.4	1.16	0.86
Q60715_P	P4ha1	Prolyl 4-hy	19	19.1	13.7	14.9	1.4	1.28	0.78	560.7	467.2	568.7	1.2	0.99	1.01
Q9Z0U1_Z	Tjp2	Tight juncti	12	21.1	15.1	16.4	1.4	1.28	0.78	207.9	163.6	199.1	1.3	1.04	0.96
Q8BGS0_M	Mak16	Protein MA	1	13.6	9.8	10.6	1.4	1.28	0.78	13.6	9.8	11.9	1.4	1.15	0.87
Q6IRU2_TP	Tpm4	Tropomyos	18	17.3	12.4	13.6	1.4	1.28	0.78	525.5	271.0	329.9	1.9	1.59	0.63
Q8K0V4_C	Cnot3	CCR4-NOT	2	7.5	5.4	5.8	1.4	1.28	0.78	14.9	10.7	13.1	1.4	1.14	0.87
P16460_A	Ass1	Argininosu	3	7.8	5.7	6.2	1.4	1.27	0.79	55.5	21.7	26.4	2.6	2.10	0.48
P52431_D	Pold1	DNA polym	6	8.3	6.0	6.5	1.4	1.27	0.79	54.0	42.1	51.3	1.3	1.05	0.95
Q9EQ28_D	Pold3	DNA polym	2	7.3	5.3	5.8	1.4	1.27	0.79	14.6	10.6	12.9	1.4	1.13	0.88
O08784_T	Tcof1	Treacle pro	3	5.4	3.9	4.3	1.4	1.27	0.79	17.0	25.0	30.5	0.7	0.56	1.80
Q9JJT9_PH	Phax	Phosphory	1	18.1	13.1	14.3	1.4	1.26	0.79	18.1	13.1	15.9	1.4	1.13	0.88
O54774_A	Ap3d1	AP-3 compl	19	17.7	12.8	14.0	1.4	1.26	0.79	436.9	410.3	499.4	1.1	0.87	1.14
P28063_P	Psmb8	Proteasom	1	4.2	3.1	3.3	1.4	1.26	0.79	4.2	3.1	3.7	1.4	1.13	0.88
A2RSY6_TR	Trmt1l	TRMT1-like	7	10.3	7.5	8.1	1.4	1.26	0.79	69.0	45.4	55.3	1.5	1.25	0.80
Q8JZQ9_E	Eif3b	Eukaryotic	37	28.6	20.8	22.7	1.4	1.26	0.79	1300.9	1144.9	1393.6	1.1	0.93	1.07
Q9Z1T1_A	Ap3b1	AP-3 compl	30	15.7	11.4	12.4	1.4	1.26	0.79	666.9	577.4	702.8	1.2	0.95	1.05
Q5EG47_A	Prkaa1	5'-AMP-acti	9	13.3	9.7	10.6	1.4	1.26	0.79	134.3	109.1	132.8	1.2	1.01	0.99
Q8BVF2_P	Pdcl3	Phosducin-	2	12.1	8.8	9.6	1.4	1.26	0.79	24.1	17.6	21.4	1.4	1.13	0.89
Q921C5_B	Bicd2	Protein bic	2	20.9	15.3	16.6	1.4	1.26	0.79	41.9	30.5	37.1	1.4	1.13	0.89
P09405_N	Ncl	Nucleolin	26	25.6	18.6	20.3	1.4	1.26	0.79	1510.0	847.3	1031.4	1.8	1.46	0.68
P84096_R	Rhog	Rho-relate	2	8.9	6.5	7.1	1.4	1.26	0.79	17.8	12.9	15.8	1.4	1.13	0.89
Q9CYC5_D	Dsn1	Kinetochor	1	9.8	7.2	7.8	1.4	1.26	0.80	9.8	7.2	8.7	1.4	1.13	0.89
F8WHY8_F	Mta1	Metastasis-	8	17.1	12.4	13.6	1.4	1.26	0.80	168.2	107.5	130.9	1.6	1.29	0.78
Q8QZY1_E	Eif3l	Eukaryotic	44	32.2	23.5	25.6	1.4	1.25	0.80	1914.1	1196.4	1456.2	1.6	1.31	0.76
Q9R1X4_T	Timeless	Protein tim	6	15.8	11.6	12.6	1.4	1.25	0.80	94.8	65.0	79.1	1.5	1.20	0.83
F7DBB3_F7	Ahnak2	Protein Ah	4	7.0	5.1	5.6	1.4	1.25	0.80	31.1	23.4	28.5	1.3	1.09	0.92
A2ASQ1_A	Agrn	Agrin OS=	1	2.4	1.7	1.9	1.4	1.25	0.80	2.4	1.7	2.1	1.4	1.12	0.89
Q9WUK4_	Rfc2	Replication	9	13.9	10.2	11.1	1.4	1.25	0.80	148.9	202.0	245.9	0.7	0.61	1.65
E9PWG6_E	Ncapg	Protein Nc	29	14.8	10.8	11.8	1.4	1.25	0.80	452.5	423.5	515.4	1.1	0.88	1.14
Q8VBV7_C	Cops8	COP9 signa	4	22.5	16.5	18.0	1.4	1.25	0.80	100.2	86.6	105.4	1.2	0.95	1.05
Q9D8S4_O	Rexo2	Oligoribon	1	10.0	7.4	8.0	1.4	1.25	0.80	10.0	7.4	8.9	1.4	1.12	0.89
Q9QXJ2_Q	Stat2	Signal trans	16	13.3	9.8	10.7	1.4	1.25	0.80	234.7	208.9	254.2	1.1	0.92	1.08
Q3TMP1_Q	Gtf3c3	General tra	5	9.2	6.7	7.4	1.4	1.24	0.80	45.2	33.8	41.1	1.3	1.10	0.91
Q9D0I8_M	Mrto4	mRNA turn	14	11.4	8.4	9.2	1.4	1.24	0.80	199.4	138.8	168.9	1.4	1.18	0.85
Q8BHL5_E	Elmo2	Engulfment	4	6.2	4.6	5.0	1.4	1.24	0.80	26.8	22.1	27.0	1.2	0.99	1.01
Q8CH25_S	Sltm	SAFB-like tr	4	11.6	8.6	9.4	1.4	1.24	0.81	58.2	43.6	53.1	1.3	1.10	0.91
P70399_T	Tp53bp1	Tumor sup	20	10.6	7.9	8.6	1.4	1.24	0.81	263.9	261.6	318.5	1.0	0.83	1.21
A6H5Z3_E	Exoc6b	Exocyst co	4	7.0	5.2	5.6	1.4	1.24	0.81	32.9	24.8	30.2	1.3	1.09	0.92
Q9D706_R	Rpap3	RNA polym	7	14.8	11.0	12.0	1.3	1.24	0.81	116.8	85.9	104.5	1.4	1.12	0.89
P61514_R	Rpl37a	60S ribosor	8	114.4	84.8	92.5	1.3	1.24	0.81	1580.4	738.3	898.6	2.1	1.76	0.57
O55142_R	Rpl35a	60S ribosor	9	75.7	56.2	61.3	1.3	1.24	0.81	895.7	909.2	1106.7	1.0	0.81	1.24
Q8BH15_C	Cnot10	CCR4-NOT	6	13.6	10.1	11.1	1.3	1.23	0.81	97.2	62.8	76.4	1.5	1.27	0.79
P97384_A	Anxa11	Annexin A1	1	8.4	6.2	6.8	1.3	1.23	0.81	8.4	6.2	7.6	1.3	1.11	0.90
Q8K297_G	Colgalt1	Procollage	6	9.8	7.3	8.0	1.3	1.23	0.81	66.2	47.8	58.1	1.4	1.14	0.88
Q3UHJ0_A	Aak1	AP2-associ	16	15.5	11.6	12.6	1.3	1.23	0.81	273.5	203.0	247.1	1.3	1.11	0.90
Q99LD9_E	Eif2b2	Translation	5	14.0	10.4	11.3	1.3	1.23	0.81	80.8	65.5	79.7	1.2	1.01	0.99
Q60710_S	Samhd1	Deoxynucl	41	28.4	21.2	23.1	1.3	1.23	0.81	1494.7	1211.3	1474.4	1.2	1.01	0.99
O35309_N	Nmi	N-myc-inte	1	9.1	6.8	7.4	1.3	1.23	0.81	9.1	6.8	8.2	1.3	1.10	0.91
P40201_C	Chd1	Chromodo	8	12.1	9.0	9.9	1.3	1.23	0.81	99.7	73.1	88.9	1.4	1.12	0.89
Q8VCD5_M	Med17	Mediator o	2	9.2	6.9	7.5	1.3	1.23	0.82	18.4	13.8	16.8	1.3	1.10	0.91
O54984_A	Asna1	ATPase Asn	4	19.5	14.5	15.9	1.3	1.23	0.82	83.3	63.4	77.2	1.3	1.08	0.93
P20664_P	Prim1	DNA prima	6	16.8	12.6	13.8	1.3	1.22	0.82	104.1	72.1	87.7	1.4	1.19	0.84
Q64124_S	Scx	Basic helix-	1	14.6	10.9	11.9	1.3	1.22	0.82	14.6	10.9	13.3	1.3	1.10	0.91
Q8QZY9_SF	Sf3b4	Splicing fac	3	60.7	45.5	49.6	1.3	1.22	0.82	164.3	124.7	151.8	1.3	1.08	0.92
P60122_R	Ruvbl1	RuvB-like 1	28	17.8	13.3	14.6	1.3	1.22	0.82	1318.2	1055.1	1284.3	1.2	1.03	0.97
A2A5V4_A	Sh3bp1	SH3 domai	16	16.2	12.2	13.3	1.3	1.22	0.82	366.7	212.0	258.1	1.7	1.42	0.70
Q9WU78_	Pdcd6ip	Programm	18	12.4	9.3	10.1	1.3	1.22	0.82	304.3	202.8	246.8	1.5	1.23	0.81
Q6PDG5_S	Smarcc2	SWI/SNF c	18	25.0	18.8	20.5	1.3	1.22	0.82	524.5	342.6	417.0	1.5	1.26	0.80
Q6TYB5_FE	Fez2	Fasciculati	1	10.2	7.6	8.3	1.3	1.22	0.82	10.2	7.6	9.3	1.3	1.09	0.92
Q3UKJ7_S	Smu1	WD40 repe	7	9.2	7.0	7.6	1.3	1.22	0.82	72.2	78.2	95.2	0.9	0.76	1.32
Q99LJ0_CT	Cttnbp2nl	CTTNBP2 N	3	10.7	8.1	8.8	1.3	1.22	0.82	30.5	23.2	28.3	1.3	1.08	0.93

Q9WUU8_T	Tnip1	TNFAIP3-in	2	2.9	2.2	2.4	1.3	1.21	0.82	5.9	4.4	5.4	1.3	1.09	0.92
Q8CJ53_CI	Trip10	Cdc42-inte	4	18.3	13.8	15.1	1.3	1.21	0.82	77.2	47.5	57.8	1.6	1.33	0.75
Q62470_IT	Itga3	Integrin alp	1	12.0	9.0	9.8	1.3	1.21	0.82	12.0	9.0	11.0	1.3	1.09	0.92
O35609_SC	Scamp3	Secretory c	3	6.0	4.6	5.0	1.3	1.21	0.82	14.4	23.8	29.0	0.6	0.50	2.01
Q6NVF9_CI	Cpsf6	Cleavage ar	6	31.5	23.8	25.9	1.3	1.21	0.82	241.0	139.6	169.9	1.7	1.42	0.71
O70404_V/	Vamp8	Vesicle-assc	1	8.6	6.5	7.1	1.3	1.21	0.82	8.6	6.5	7.9	1.3	1.09	0.92
P62320_SN	Snrpd3	Small nucle	5	107.9	81.6	89.0	1.3	1.21	0.82	604.1	621.8	756.8	1.0	0.80	1.25
Q8BHA0_IN	Ino80c	INO80 com	4	5.7	4.3	4.7	1.3	1.21	0.82	24.2	18.3	22.3	1.3	1.09	0.92
Q6P5F9_XF	Xpo1	Exportin-1	23	18.8	14.2	15.5	1.3	1.21	0.83	739.7	392.5	477.8	1.9	1.55	0.65
Q9WV60_G	Gsk3b	Glycogen sy	2	19.3	14.6	15.9	1.3	1.21	0.83	38.7	29.2	35.6	1.3	1.09	0.92
Q80UZ2_SI	Sdad1	Protein SD/	1	11.4	8.7	9.5	1.3	1.21	0.83	11.4	8.7	10.5	1.3	1.09	0.92
Q9D1K2_V/	Atp6v1f	V-type prot	2	15.4	11.6	12.7	1.3	1.21	0.83	30.7	23.3	28.3	1.3	1.08	0.92
Q9ESE1_LR	Lrba	Lipopolysa	2	5.6	4.2	4.6	1.3	1.21	0.83	11.2	8.5	10.3	1.3	1.08	0.92
O35280_CI	Chek1	Serine/thre	1	1.8	1.3	1.5	1.3	1.21	0.83	1.8	1.3	1.6	1.3	1.08	0.92
Q60960_IN	Kpna1	Importin su	5	6.0	4.6	5.0	1.3	1.21	0.83	41.9	29.2	35.6	1.4	1.18	0.85
Q61234_SN	Snta1	Alpha-1-syr	2	4.9	3.7	4.1	1.3	1.21	0.83	9.9	7.5	9.1	1.3	1.08	0.92
Q9QWT9_K	Kifc1	Kinesin-like	9	8.6	6.5	7.1	1.3	1.21	0.83	142.7	69.7	84.9	2.0	1.68	0.59
Q8BKS9_KC	Kiaa0020	Pumilio do	1	10.4	7.9	8.6	1.3	1.21	0.83	10.4	7.9	9.6	1.3	1.08	0.92
Q9QYB5_AI	Add3	Gamma-add	4	9.1	6.9	7.5	1.3	1.21	0.83	39.0	26.8	32.7	1.5	1.19	0.84
Q9QUJ7_AC	Acsl4	Long-chain	1	6.5	5.0	5.4	1.3	1.20	0.83	6.5	5.0	6.1	1.3	1.08	0.93
Q9QXN3_TI	Trip4	Activating s	3	9.3	7.1	7.7	1.3	1.20	0.83	25.8	26.6	32.3	1.0	0.80	1.25
P97823_LY	Lypla1	Acyl-protei	1	10.4	7.9	8.7	1.3	1.20	0.83	10.4	7.9	9.7	1.3	1.08	0.93
Q8K224_N/	Nat10	N-acetyltra	6	10.1	7.7	8.4	1.3	1.20	0.83	82.1	50.9	61.9	1.6	1.33	0.75
Q9WTU0_P	Phf2	Lysine-spec	6	9.8	7.5	8.2	1.3	1.20	0.83	299.7	41.5	50.5	7.2	5.93	0.17
Q61187_TS	Tsg101	Tumor susc	5	28.1	21.5	23.5	1.3	1.20	0.83	120.7	109.3	133.1	1.1	0.91	1.10
Q6PB44_PT	Ptpn23	Tyrosine-pr	20	13.8	10.6	11.5	1.3	1.20	0.83	341.6	273.9	333.3	1.2	1.02	0.98
Q9WTI7_M	Myo1c	Unconvent	33	28.1	21.5	23.4	1.3	1.20	0.83	1827.2	893.9	1088.0	2.0	1.68	0.60
Q80UJ7_RE	Rab3gap1	Rab3 GTPas	4	9.1	7.0	7.6	1.3	1.20	0.83	36.7	30.5	37.1	1.2	0.99	1.01
Q80YV2_NI	Zc3hc1	Nuclear-int	4	8.8	6.7	7.3	1.3	1.20	0.84	34.9	26.8	32.6	1.3	1.07	0.93
Q99LI7_CS	Cstf3	Cleavage sti	14	13.0	9.9	10.8	1.3	1.20	0.84	228.9	177.3	215.8	1.3	1.06	0.94
Q9DC16_EI	Ergic1	Endoplasm	2	7.4	5.7	6.2	1.3	1.19	0.84	14.8	11.4	13.9	1.3	1.07	0.93
Q6PIJ4_NFI	Nfrkb	Nuclear fac	2	9.8	7.5	8.2	1.3	1.19	0.84	19.5	15.0	18.3	1.3	1.07	0.94
Q91YW3_D	Dnajc3	DnaJ homo	1	9.0	6.9	7.5	1.3	1.19	0.84	9.0	6.9	8.4	1.3	1.07	0.94
Q8VDW0_D	Ddx39a	ATP-depend	30	51.2	39.4	43.0	1.3	1.19	0.84	2118.9	2047.0	2491.5	1.0	0.85	1.18
Q9CQW9_I	Ifitm3	Interferon-i	1	12.9	10.0	10.9	1.3	1.19	0.84	12.9	10.0	12.1	1.3	1.07	0.94
Q99LE6_AE	Abcf2	ATP-bindin	19	15.5	11.9	13.0	1.3	1.19	0.84	415.5	315.3	383.8	1.3	1.08	0.92
Q8BQ30_PI	Ppp1r18	Phostensin	2	16.0	12.4	13.5	1.3	1.19	0.84	32.0	24.7	30.1	1.3	1.06	0.94
Q8K094_Q	Pvr	Nectin-2 OS	1	7.1	5.5	6.0	1.3	1.19	0.84	7.1	5.5	6.7	1.3	1.06	0.94
P58501_P/	Paxbp1	PAX3- and I	3	14.6	11.3	12.3	1.3	1.19	0.84	38.8	28.7	35.0	1.4	1.11	0.90
Q8CD94_LI	Lin52	Protein lin-	1	4.1	3.2	3.5	1.3	1.19	0.84	4.1	3.2	3.9	1.3	1.06	0.94
Q5SSL4_AB	Abr	Active brea	3	11.1	8.6	9.4	1.3	1.19	0.84	30.0	22.5	27.3	1.3	1.10	0.91
Q8K301_DI	Ddx52	Probable A	7	13.0	10.1	11.0	1.3	1.18	0.84	93.6	80.3	97.7	1.2	0.96	1.04
P62908_RS	Rps3	40S riboson	40	36.2	28.1	30.6	1.3	1.18	0.85	4418.0	2657.2	3234.2	1.7	1.37	0.73
Q99LB0_TD	Dnttip1	Deoxynucle	1	5.8	4.5	4.9	1.3	1.18	0.85	5.8	4.5	5.5	1.3	1.06	0.94
Q99M31_H	Hspa14	Heat shock	8	12.2	9.5	10.4	1.3	1.18	0.85	141.9	266.7	324.6	0.5	0.44	2.29
Q64701_RI	Rbl1	Retinoblast	2	12.6	9.8	10.7	1.3	1.18	0.85	25.1	19.5	23.8	1.3	1.06	0.95
Q8BH43_W	Wasf2	Wiskott-Alc	3	10.1	7.8	8.5	1.3	1.18	0.85	25.9	21.7	26.4	1.2	0.98	1.02
Q63932_M	Map2k2	Dual specifi	2	11.6	9.1	9.9	1.3	1.18	0.85	23.3	18.1	22.1	1.3	1.05	0.95
Q9JKP7_DF	Pole3	DNA polym	2	22.5	17.5	19.1	1.3	1.18	0.85	44.9	35.0	42.6	1.3	1.05	0.95
Q61584_F)	Fxr1	Fragile X m	26	19.9	15.6	17.0	1.3	1.17	0.85	789.2	817.3	994.7	1.0	0.79	1.26
Q3TLI0_TP(	Trappc10	Trafficking p	1	4.4	3.4	3.7	1.3	1.17	0.85	4.4	3.4	4.2	1.3	1.05	0.95
Q8VDJ3_VI	Hdlbp	Vigilin OS=I	76	25.5	20.0	21.8	1.3	1.17	0.85	3360.3	2270.9	2764.0	1.5	1.22	0.82
O54962_B/	Banf1	Barrier-to-a	3	88.1	68.9	75.2	1.3	1.17	0.85	229.4	186.5	227.0	1.2	1.01	0.99
P70388_R/	Rad50	DNA repair	15	22.9	18.0	19.6	1.3	1.17	0.85	366.0	239.8	291.8	1.5	1.25	0.80
Q91VR5_DI	Ddx1	ATP-depend	46	18.5	14.5	15.8	1.3	1.17	0.85	1848.1	1480.5	1802.0	1.2	1.03	0.98
P97479_M	Myo7a	Unconvent	1	4.7	3.7	4.0	1.3	1.17	0.86	4.7	3.7	4.5	1.3	1.05	0.95
O88952_LI	Lin7c	Protein lin-	1	12.0	9.4	10.3	1.3	1.17	0.86	12.0	9.4	11.5	1.3	1.05	0.95
P61255_RL	Rpl26	60S riboson	14	93.5	73.3	80.0	1.3	1.17	0.86	2991.4	2003.7	2438.8	1.5	1.23	0.82
Q8C3R1_BI	Brat1	BRCA1-assc	1	9.0	7.0	7.7	1.3	1.17	0.86	9.0	7.0	8.6	1.3	1.05	0.96
Q9WVA4_T	Tagln2	Transgelin-:	5	13.4	10.5	11.5	1.3	1.17	0.86	90.8	49.1	59.7	1.9	1.52	0.66
Q9CWN7_C	Cnot11	CCR4-NOT t	2	9.8	7.7	8.4	1.3	1.17	0.86	19.5	15.3	18.6	1.3	1.05	0.96
Q8BWY9_C	Kiaa1524	Protein CIP	2	9.8	7.7	8.4	1.3	1.17	0.86	19.7	15.5	18.8	1.3	1.04	0.96
P24788_CD	Cdk11b	Cyclin-depe	10	20.1	15.8	17.2	1.3	1.16	0.86	272.0	201.7	245.5	1.3	1.11	0.90
Q9EP71_R/	Rai14	Ankycorbin	4	8.9	7.0	7.6	1.3	1.16	0.86	41.2	30.4	36.9	1.4	1.11	0.90
Q8C570_R/	Rae1	mRNA expo	3	16.2	12.8	14.0	1.3	1.16	0.86	36.4	39.5	48.1	0.9	0.76	1.32
Q6NZJ6_IF4	Eif4g1	Eukaryotic	66	19.9	15.7	17.2	1.3	1.16	0.86	2182.5	1816.4	2210.9	1.2	0.99	1.01
P26039_TL	Tln1	Talin-1 OS=	153	54.4	43.0	46.9	1.3	1.16	0.86	21578.9	11748.9	14300.4	1.8	1.51	0.66
Q9DA08_SC	Ccdc101	SAGA-assoc	1	11.0	8.7	9.5	1.3	1.16	0.86	11.0	8.7	10.6	1.3	1.04	0.96
Q99JR8_SN	Smarcd2	SWI/SNF-re	3	16.6	13.1	14.3	1.3	1.16	0.86	66.0	46.5	56.6	1.4	1.17	0.86
Q9D0T2_DI	Dusp12	Dual specifi	1	3.3	2.6	2.8	1.3	1.16	0.86	3.3	2.6	3.1	1.3	1.04	0.96
P10404_ENV1_MOUSE	MLV-relate		3	14.1	11.2	12.2	1.3	1.16	0.86	31.9	35.9	43.7	0.9	0.73	1.37
Q8BFR5_EF	Tufm	Elongation	7	17.8	14.1	15.4	1.3	1.16	0.86	112.7	114.3	139.1	1.0	0.81	1.23
Q9ERU9_RI	Ranbp2	E3 SUMO-p	1	4.6	3.6	4.0	1.3	1.15	0.87	4.6	3.6	4.4	1.3	1.03	0.97
Q8BTU1_CI	Cfap20	Cilia- and fl	1	11.3	9.0	9.8	1.3	1.15	0.87	11.3	9.0	10.9	1.3	1.03	0.97
D3Z3H2_D.	Ino80e	Coiled-coil	1	5.8	4.6	5.0	1.3	1.15	0.87	5.8	4.6	5.6	1.3	1.03	0.97
Q9QYC0_AI	Add1	Alpha-addu	6	8.5	6.8	7.4	1.3	1.15	0.87	52.0	39.4	47.9	1.3	1.08	0.92
P61211_AF	Arl1	ADP-ribosy	2	9.6	7.7	8.4	1.3	1.15	0.87	19.2	15.3	18.7	1.3	1.03	0.97
Q6A0A2_L/	Larp4b	La-related p	3	16.8	13.4	14.6	1.3	1.15	0.87	49.3	42.8	52.0	1.2	0.95	1.06
Q9CXF4_TE	Tbc1d15	TBC1 doma	2	13.3	10.6	11.5	1.3	1.15	0.87	26.5	21.2	25.8	1.3	1.03	0.97
Q8BVE8_NS	Whsc1	Histone-lys	6	12.9	10.3	11.3	1.3	1.15	0.87	74.2	68.0	82.7	1.1	0.90	1.12
P23116_EII	Eif3a	Eukaryotic	60	28.6	22.8	24.9	1.3	1.15	0.87	2737.4	1767.0	2150.7	1.5	1.27	0.79
Q3UK78_P(	Pcgf5	Polycomb g	1	3.7	2.9	3.2	1.3	1.15	0.87	3.7	2.9	3.6	1.3	1.03	0.97
Q9CYA6_ZC	Zcchc8	Zinc finger	10	13.1	10.4	11.4	1.3	1.15	0.87	184.0	141.2	171.9	1.3	1.07	0.93
Q9QYJ0_DN	Dnaja2	DnaJ homo	12	30.7	24.6	26.8	1.2	1.15	0.87	559.2	460.0	560.0	1.2	1.00	1.00
P63168_DY	Dynll1	Dynein ligh	4	27.7	22.2	24.2	1.2	1.14	0.88	161.6	166.1	202.2	1.0	0.80	1.25
Q8R060_ZV	Zwilch	Protein zwi	3	7.9	6.4	6.9	1.2	1.14	0.88	22.7	19.4	23.6	1.2	0.96	1.04
Q5PSV9_M	Mdc1	Mediator o	2	7.1	5.7	6.2	1.2	1.14	0.88	14.2	11.4	13.9	1.2	1.02	0.98
Q3UMG5_L	Lrch2	Leucine-ric	2	11.0	8.9	9.7	1.2	1.14	0.88	22.1	17.7	21.6	1.2	1.02	0.98
Q60930_VI	Vdac2	Voltage-dep	1	9.8	7.9	8.6	1.2	1.14	0.88	9.8	7.9	9.6	1.2	1.02	0.98
Q08024_PI	Cbfb	Core-bindin	2	26.4	21.2	23.1	1.2	1.14	0.88	52.7	42.4	51.6	1.2	1.02	0.98
A2A432_CL	Cul4b	Cullin-4B O	19	16.5	13.3	14.5	1.2	1.14	0.88	372.7	370.6	451.1	1.0	0.83	1.21
Q64511_TC	Top2b	DNA topois	34	17.4	14.0	15.3	1.2	1.14	0.88	832.6	631.2	768.2	1.3	1.08	0.92
Q3UR91_Q	Pum2	Pumilio ho	6	24.6	19.9	21.7	1.2	1.14	0.88	342.0	132.3	161.1	2.6	2.12	0.47
Q8CIN4_PA	Pak2	Serine/thre	4	14.8	11.9	13.0	1.2	1.14	0.88	81.1	58.3	71.0	1.4	1.14	0.88
Q8R2K4_T/	Taf6l	TAF6-like R	2	7.8	6.3	6.8	1.2	1.13	0.88	15.5	12.6	15.3	1.2	1.02	0.98
Q8BX22_S/	Sall4	Sal-like pro	1	2.1	1.7	1.8	1.2	1.13	0.88	2.1	1.7	2.0	1.2	1.02	0.98
Q3TFK5_GF	Gpatch4	G patch dor	2	11.9	9.6	10.5	1.2	1.13	0.88	23.8	19.2	23.4	1.2	1.02	0.98
Q03145_EF	Epha2	Ephrin type	1	7.6	6.2	6.7	1.2	1.13	0.88	7.6	6.2	7.5	1.2	1.02	0.98
P57722_PC	Pcbp3	Poly(rC)-bir	2	3.8	3.1	3.4	1.2	1.13	0.88	7.6	6.1	7.5	1.2	1.02	0.98
P61750_AF	Arf4	ADP-ribosy	5	22.2	17.9	19.6	1.2	1.13	0.88	289.2	219.5	267.2	1.3	1.08	0.92
Q9JLV5_CL	Cul3	Cullin-3 OS	22	14.2	11.5	12.5	1.2	1.13	0.88	508.0	304.4	370.5	1.7	1.37	0.73
Q9WV30_N	Nfat5	Nuclear fac	3	7.4	6.0	6.5	1.2	1.13	0.88	21.0	16.6	20.2	1.3	1.04	0.96
Q8BGJ5_Q	Ptbp1	MCG13402	27	21.7	17.5	19.1	1.2	1.13	0.88	2664.4	1870.7	2277.0	1.4	1.17	0.85
Q6PR54_RI	Rif1	Telomere-a	17	13.2	10.7	11.7	1.2	1.13	0.88	246.5	212.1	258.1	1.2	0.95	1.05
Q99MU3_D	Adar	Double-stra	15	13.2	10.7	11.6	1.2	1.13	0.88	187.1	276.7	336.8	0.7	0.56	1.80
Q9Z1Z0_US	Uso1	General ves	33	18.5	15.0	16.4	1.2	1.13	0.88	1399.1	795.9	968.7	1.8	1.44	0.69
Q8VDP3_M	Mical1	Protein-me	6	7.7	6.3	6.9	1.2	1.13	0.89	49.7	37.6	45.7	1.3	1.09	0.92
Q9CZ04_CS	Cops7a	COP9 signa	5	16.8	13.6	14.8	1.2	1.13	0.89	154.8	57.2	69.7	2.7	2.22	0.45
P58404_ST	Strn4	Striatin-4 C	3	13.9	11.3	12.3	1.2	1.13	0.89	39.4	29.9	36.4	1.3	1.08	0.92
Q9D3E6_ST	Stag1	Cohesin sul	10	14.6	11.8	12.9	1.2	1.13	0.89	151.2	130.4	158.7	1.2	0.95	1.05
P70297_ST	Stam	Signal trans	5	9.1	7.4	8.1	1.2	1.13	0.89	388.0	157.9	192.2	2.5	2.02	0.50
Q08288_LY	Lyar	Cell growth	6	20.4	16.6	18.1	1.2	1.13	0.89	154.3	107.8	131.2	1.4	1.18	0.85
P70288_HI	Hdac2	Histone dea	1	6.6	5.3	5.8	1.2	1.12	0.89	6.6	5.3	6.5	1.2	1.01	0.99

P13020_GI	Gsn	Gelsolin OS	23	55.8	45.5	49.6	1.2	1.12	0.89	1736.9	1176.8	1432.4	1.5	1.21	0.82
Q9ERD7_TE	Tubb3	Tubulin bet	24	24.9	20.3	22.2	1.2	1.12	0.89	1814.1	1327.4	1615.6	1.4	1.12	0.89
Q922P9_GI	Glyr1	Putative ox	9	15.9	13.0	14.2	1.2	1.12	0.89	182.6	209.1	254.5	0.9	0.72	1.39
P62869_EL	Tceb2	Transcripti	7	37.7	30.9	33.7	1.2	1.12	0.89	279.4	201.3	245.0	1.4	1.14	0.88
Q99NF3_CI	Cep41	Centrosom	1	4.1	3.4	3.7	1.2	1.12	0.89	4.1	3.4	4.1	1.2	1.00	1.00
Q3TYA6_MI	Mphosph8	M-phase ph	1	6.6	5.4	5.9	1.2	1.12	0.89	6.6	5.4	6.6	1.2	1.00	1.00
P62317_SN	Snrpd2	Small nucle	17	25.3	20.7	22.6	1.2	1.12	0.90	968.8	849.0	1033.3	1.1	0.94	1.07
Q91Z67_SF	Srgap2	SLIT-ROBO	2	9.9	8.2	8.9	1.2	1.11	0.90	19.8	16.3	19.9	1.2	1.00	1.00
Q6P4T2_US	Snrnp200	U5 small nu	51	36.4	30.0	32.7	1.2	1.11	0.90	2824.5	2030.2	2471.1	1.4	1.14	0.87
Q9WTX5_S	Skp1	S-phase kin	7	23.3	19.2	20.9	1.2	1.11	0.90	185.1	223.9	272.5	0.8	0.68	1.47
Q8BKI2_TN	Tnrc6b	Trinucleoti	1	4.9	4.0	4.4	1.2	1.11	0.90	4.9	4.0	4.9	1.2	1.00	1.00
Q8VH51_RI	Rbm39	RNA-bindir	34	19.3	15.9	17.4	1.2	1.11	0.90	1221.1	1272.3	1548.6	1.0	0.79	1.27
Q1HFZ0_NS	Nsun2	tRNA (cytos	19	22.4	18.4	20.1	1.2	1.11	0.90	483.5	448.7	546.1	1.1	0.89	1.13
Q8K2K6_AC	Agfg1	Arf-GAP do	10	8.2	6.8	7.4	1.2	1.11	0.90	93.5	98.0	119.3	1.0	0.78	1.28
Q8CI33_C1	Cwf19l1	CWF19-like	3	12.7	10.5	11.5	1.2	1.11	0.90	42.4	31.3	38.1	1.4	1.11	0.90
P23249_M	Mov10	Putative he	31	18.4	15.2	16.6	1.2	1.11	0.90	662.6	508.4	618.9	1.3	1.07	0.93
Q80ZJ1_RA	Rap2a	Ras-related	1	24.0	19.8	21.6	1.2	1.11	0.90	24.0	19.8	24.1	1.2	0.99	1.01
P70318_TI	Tial1	Nucleolysir	4	22.7	18.8	20.5	1.2	1.11	0.90	159.5	94.4	114.9	1.7	1.39	0.72
Q8VI36_PA	Pxn	Paxillin OS	4	17.5	14.5	15.8	1.2	1.11	0.90	80.2	52.0	63.3	1.5	1.27	0.79
Q8BMQ2_T	Gtf3c4	General tra	5	8.8	7.3	7.9	1.2	1.11	0.90	50.1	35.7	43.4	1.4	1.16	0.87
P43406_IT	Itgav	Integrin alp	1	8.3	6.9	7.5	1.2	1.11	0.90	8.3	6.9	8.4	1.2	0.99	1.01
Q9D708_Q	S100a16	Protein S10	1	12.4	10.3	11.2	1.2	1.10	0.91	12.4	10.3	12.5	1.2	0.99	1.01
F8WI30_F8	Snx7	Sorting nex	7	17.5	14.5	15.8	1.2	1.10	0.91	135.8	101.1	123.1	1.3	1.10	0.91
P59017_B2	Bcl2l13	Bcl-2-like p	1	4.4	3.6	4.0	1.2	1.10	0.91	4.4	3.6	4.4	1.2	0.99	1.01
O88487_D	Dync1i2	Cytoplasmi	8	21.7	18.0	19.7	1.2	1.10	0.91	278.1	190.8	232.3	1.5	1.20	0.84
Q80SY5_PF	Prpf38b	Pre-mRNA-	6	14.2	11.8	12.9	1.2	1.10	0.91	91.2	70.3	85.6	1.3	1.06	0.94
Q91ZU6_D	Dst	Dystonin O	8	9.2	7.7	8.4	1.2	1.10	0.91	71.2	54.2	66.0	1.3	1.08	0.93
P28740_KI	Kif2a	Kinesin-like	7	9.6	8.0	8.8	1.2	1.10	0.91	111.5	80.0	97.3	1.4	1.15	0.87
Q8BL66_EE	Eea1	Early endos	47	15.2	12.7	13.8	1.2	1.10	0.91	851.7	626.4	762.4	1.4	1.12	0.90
E9Q616_E9	Ahnak	Protein Ahr	163	22.1	18.5	20.2	1.2	1.09	0.91	6414.9	4720.7	5745.8	1.4	1.12	0.90
Q8BJH1_ZC	Zc2hc1a	Zinc finger	1	29.3	24.6	26.8	1.2	1.09	0.91	29.3	24.6	29.9	1.2	0.98	1.02
P63330_PF	Ppp2ca	Serine/thre	4	9.3	7.8	8.5	1.2	1.09	0.92	52.6	35.1	42.8	1.5	1.23	0.81
Q6P6L6_Q	Gemin4	Gem (Nucle	2	9.1	7.7	8.4	1.2	1.09	0.92	18.2	15.3	18.6	1.2	0.98	1.02
Q8CI11_GN	Gnl3	Guanine nu	11	10.2	8.6	9.3	1.2	1.09	0.92	112.9	103.7	126.2	1.1	0.89	1.12
Q7TPV4_M	Mybbp1a	Myb-bindir	71	28.8	24.3	26.5	1.2	1.09	0.92	3888.0	3053.8	3716.9	1.3	1.05	0.96
F8VPK0_F8	Ttc37	Protein Ttc	10	11.1	9.4	10.2	1.2	1.09	0.92	169.5	96.4	117.3	1.8	1.44	0.69
Q921E6_EE	Eed	Polycomb	10	12.7	10.7	11.7	1.2	1.08	0.92	117.1	115.8	141.0	1.0	0.83	1.20
Q91YK2_RF	Rrp1b	Ribosomal	2	5.4	4.6	5.0	1.2	1.08	0.92	10.8	9.1	11.1	1.2	0.97	1.03
P40336_VF	Vps26a	Vacuolar pr	20	23.5	19.9	21.7	1.2	1.08	0.92	706.2	656.5	799.1	1.1	0.88	1.13
Q2EMV9_P	Parp14	Poly [ADP-r	23	20.3	17.2	18.8	1.2	1.08	0.92	527.1	440.8	536.5	1.2	0.98	1.02
Q01405_SC	Sec23a	Protein tra	12	12.0	10.2	11.1	1.2	1.08	0.92	223.6	126.1	153.5	1.8	1.46	0.69
Q61136_PI	Prpf4b	Serine/thre	8	9.9	8.4	9.2	1.2	1.08	0.92	76.2	62.7	76.3	1.2	1.00	1.00
Q60716_P4	P4ha2	Prolyl 4-hy	2	11.6	9.9	10.8	1.2	1.08	0.93	23.3	19.8	24.1	1.2	0.97	1.03
Q8R088_GI	Golph3l	Golgi phos	1	8.0	6.8	7.5	1.2	1.08	0.93	8.0	6.8	8.3	1.2	0.97	1.03
E0CX20_E0	Bud31	Protein BU	5	25.6	21.8	23.8	1.2	1.08	0.93	133.8	160.9	195.8	0.8	0.68	1.46
Q3V0C5_UI	Usp48	Ubiquitin c	6	9.1	7.7	8.4	1.2	1.08	0.93	56.8	45.1	54.9	1.3	1.03	0.97
Q8K1N4_SI	Spats2	Spermatog	4	15.6	13.3	14.5	1.2	1.08	0.93	66.0	46.9	57.1	1.4	1.16	0.86
P60762_M	Morf4l1	Mortality fa	1	2.4	2.1	2.3	1.2	1.08	0.93	2.4	2.1	2.5	1.2	0.96	1.04
P48193_41	Epb41	Protein 4.1	4	10.5	8.9	9.7	1.2	1.08	0.93	44.7	31.8	38.7	1.4	1.16	0.87
Q8BK64_AI	Ahsa1	Activator o	3	11.8	10.1	11.0	1.2	1.07	0.93	46.3	36.1	44.0	1.3	1.05	0.95
Q9D0A3_AI	Arpin	Arpin OS=M	3	7.9	6.8	7.4	1.2	1.07	0.93	25.2	39.7	48.3	0.6	0.52	1.92
Q9CQ39_M	Med21	Mediator o	1	9.6	8.2	8.9	1.2	1.07	0.93	9.6	8.2	9.9	1.2	0.96	1.04
Q8BWQ6_CP062_MOU		UPF0505 p	2	19.4	16.6	18.1	1.2	1.07	0.93	38.8	33.2	40.4	1.2	0.96	1.04
Q6DFW4_N	Nop58	Nucleolar p	19	8.5	7.2	7.9	1.2	1.07	0.93	189.8	180.3	219.5	1.1	0.86	1.16
P26231_C1	Ctnna1	Catenin alp	8	11.5	9.8	10.7	1.2	1.07	0.93	98.3	100.5	122.4	1.0	0.80	1.24
P97855_G3	G3bp1	Ras GTPase	18	18.3	15.6	17.1	1.2	1.07	0.93	570.8	441.0	536.7	1.3	1.06	0.94
P56873_SS	Sssca1	Sjoegren sy	1	35.9	30.8	33.6	1.2	1.07	0.93	35.9	30.8	37.4	1.2	0.96	1.04
P62900_RL	Rpl31	60S riboso	7	238.5	204.2	222.8	1.2	1.07	0.93	2469.5	2459.2	2993.2	1.0	0.83	1.21
O55022_P	Pgrmc1	Membrane	3	3.4	2.9	3.2	1.2	1.07	0.93	10.4	26.6	32.4	0.4	0.32	3.10
Q5XJY5_CC	Arcn1	Coatomer s	40	17.1	14.6	16.0	1.2	1.07	0.94	1082.9	947.4	1153.1	1.1	0.94	1.06
Q8R5C5_AC	Actr1b	Beta-centra	12	18.8	16.2	17.6	1.2	1.07	0.94	526.9	477.0	580.5	1.1	0.91	1.10
P42567_EP	Eps15	Epidermal	6	7.2	6.2	6.7	1.2	1.07	0.94	39.4	35.1	42.7	1.1	0.92	1.09
G3X8X0_G	Dhx16	DEAH (Asp-	1	6.7	5.8	6.3	1.2	1.06	0.94	6.7	5.8	7.0	1.2	0.95	1.05
P25976_UI	Ubtf	Nucleolar t	2	8.0	6.9	7.6	1.2	1.06	0.94	16.1	13.8	16.9	1.2	0.95	1.05
Q9Z0R4_IT	Itsn1	Intersectin-	6	5.6	4.9	5.3	1.2	1.06	0.94	50.5	27.1	33.0	1.9	1.53	0.65
F6ZDS4_TP	Tpr	Nucleoprot	22	15.5	13.4	14.6	1.2	1.06	0.94	465.3	319.2	388.5	1.5	1.20	0.83
Q61029_LA	Tmpo	Lamina-ass	1	10.1	8.7	9.5	1.2	1.06	0.94	10.1	8.7	10.6	1.2	0.95	1.05
P84078_AF	Arf1	ADP-ribosy	21	18.7	16.1	17.6	1.2	1.06	0.94	2357.2	1319.5	1606.0	1.8	1.47	0.68
E9QAE3_E9	Btaf1	Protein Bta	3	11.5	10.0	10.9	1.2	1.06	0.94	27.0	30.6	37.2	0.9	0.72	1.38
P48036_AN	Anxa5	Annexin A5	5	13.8	11.9	13.0	1.2	1.06	0.95	100.1	59.4	72.3	1.7	1.38	0.72
Q6P9R2_O	Oxsr1	Serine/thre	8	13.1	11.4	12.4	1.2	1.06	0.95	195.5	95.3	115.9	2.1	1.69	0.59
Q8K114_IN	Ints9	Integrator	5	8.4	7.3	8.0	1.2	1.06	0.95	54.6	42.5	51.7	1.3	1.06	0.95
A2BGI8_A2	Ppih	Peptidyl-pr	9	21.5	18.7	20.4	1.2	1.06	0.95	349.5	267.5	325.5	1.3	1.07	0.93
P97377_CI	Cdk2	Cyclin-depe	10	11.3	9.8	10.7	1.2	1.05	0.95	123.1	107.9	131.4	1.1	0.94	1.07
Q9CQH7_B	Btf3l4	Transcripti	4	11.7	10.2	11.1	1.1	1.05	0.95	59.9	62.1	75.6	1.0	0.79	1.26
B2RQC6_P	Cad	CAD protei	25	18.8	16.4	17.9	1.1	1.05	0.95	594.2	536.4	652.8	1.1	0.91	1.10
Q9QYJ3_DN	Dnajb1	DnaJ homo	1	14.3	12.4	13.6	1.1	1.05	0.95	14.3	12.4	15.1	1.1	0.94	1.06
Q6NS45_C	Ccdc66	Coiled-coil	1	4.8	4.2	4.5	1.1	1.05	0.95	4.8	4.2	5.1	1.1	0.94	1.06
Q8CHW4_E	Eif2b5	Translation	7	10.9	9.5	10.4	1.1	1.05	0.95	68.5	77.9	94.9	0.9	0.72	1.38
Q9WTX2_P	Prkra	Interferon-i	2	11.7	10.2	11.1	1.1	1.05	0.95	23.4	20.4	24.9	1.1	0.94	1.06
Q99PU8_D	Dhx30	Putative AT	8	12.5	10.9	11.9	1.1	1.05	0.95	100.3	88.2	107.3	1.1	0.93	1.07
E9PYB0_E9	Ahnak2	Protein Ahr	15	19.3	16.9	18.4	1.1	1.05	0.95	1102.9	655.1	797.4	1.7	1.38	0.72
Q8R1U1_C	Cog4	Conserved	1	8.5	7.4	8.1	1.1	1.05	0.95	8.5	7.4	9.0	1.1	0.94	1.06
Q8CG46_SI	Smc5	Structural	5	11.2	9.8	10.7	1.1	1.05	0.95	46.0	54.4	66.2	0.8	0.69	1.44
Q8CGY8_O	Ogt	UDP-N-acet	14	10.0	8.8	9.6	1.1	1.05	0.95	180.0	178.1	216.7	1.0	0.83	1.20
Q64727_VI	Vcl	Vinculin OS	40	22.2	19.4	21.2	1.1	1.05	0.95	1952.8	986.2	1200.4	2.0	1.63	0.61
P35700_PF	Prdx1	Peroxiredo	9	22.6	19.8	21.6	1.1	1.05	0.96	384.8	171.2	208.4	2.2	1.85	0.54
Q04692_SN	Smarcad1	SWI/SNF-re	2	5.9	5.2	5.7	1.1	1.05	0.96	11.8	10.4	12.6	1.1	0.94	1.07
Q5SNZ0_GI	Ccdc88a	Girdin OS=	1	14.0	12.3	13.4	1.1	1.05	0.96	14.0	12.3	15.0	1.1	0.94	1.07
Q8R3N1_N	Nop14	Nucleolar p	3	14.6	12.8	13.9	1.1	1.04	0.96	43.9	35.4	43.1	1.2	1.02	0.98
Q61214_D	Dyrk1a	Dual specifi	1	15.3	13.5	14.7	1.1	1.04	0.96	15.3	13.5	16.4	1.1	0.94	1.07
Q8R1F1_NI	Fam129b	Niban-like	23	14.5	12.8	13.9	1.1	1.04	0.96	766.8	336.3	409.3	2.3	1.87	0.53
P16546_SF	Sptan1	Spectrin al	109	27.1	23.8	26.0	1.1	1.04	0.96	4907.6	3498.5	4258.2	1.4	1.15	0.87
Q9D287_SI	Bcas2	Pre-mRNA-	9	13.6	12.0	13.1	1.1	1.04	0.96	283.1	205.1	249.6	1.4	1.13	0.88
Q3UYV9_N	Ncbp1	Nuclear ca	11	23.3	20.5	22.4	1.1	1.04	0.96	397.8	226.2	275.3	1.8	1.44	0.69
Q921F4_HI	Hnrnpll	Heterogene	17	18.3	16.1	17.6	1.1	1.04	0.96	332.1	312.5	380.4	1.1	0.87	1.15
Q8BU03_P	Pwp2	Periodic try	1	16.0	14.1	15.4	1.1	1.04	0.96	16.0	14.1	17.1	1.1	0.93	1.07
Q9JKB1_UC	Uchl3	Ubiquitin c	3	4.5	4.0	4.3	1.1	1.04	0.96	13.0	17.0	20.7	0.8	0.63	1.59
Q6P6L0_FI	Filip1l	Filamin A-ir	1	8.5	7.6	8.2	1.1	1.03	0.97	8.5	7.6	9.2	1.1	0.93	1.08
Q7TMK9_H	Syncrip	Heterogene	22	18.6	16.5	18.0	1.1	1.03	0.97	533.4	457.7	557.1	1.2	0.96	1.04
P12815_PI	Pdcd6	Programme	2	12.6	11.2	12.2	1.1	1.03	0.97	25.2	22.4	27.3	1.1	0.93	1.08
Q99PP9_TF	Trim16	Tripartite n	1	5.8	5.1	5.6	1.1	1.03	0.97	5.8	5.1	6.2	1.1	0.93	1.08
E9Q6R4_E9	Arid1b	Protein Ari	3	8.0	7.1	7.7	1.1	1.03	0.97	19.1	19.1	23.3	1.0	0.82	1.22
Q3UGC7_EI	Eif3j1	Eukaryotic	8	34.7	30.8	33.6	1.1	1.03	0.97	549.2	283.5	345.1	1.9	1.59	0.63
P42227_ST	Stat3	Signal trans	17	14.2	12.7	13.8	1.1	1.03	0.97	295.2	551.5	671.2	0.5	0.44	2.27
Q8CGZ0_CI	Cherp	Calcium ho	11	23.6	21.0	22.9	1.1	1.03	0.97	324.3	297.8	362.4	1.1	0.89	1.12
Q9CRA8_E	Exosc5	Exosome cc	2	12.3	11.0	11.9	1.1	1.03	0.97	24.6	21.9	26.7	1.1	0.92	1.08
Q61092_LA	Lamc2	Laminin sul	1	2.3	2.0	2.2	1.1	1.03	0.97	2.3	2.0	2.5	1.1	0.92	1.08
Q9JI10_STI	Stk3	Serine/thre	7	7.5	6.7	7.3	1.1	1.02	0.98	71.0	50.1	61.0	1.4	1.16	0.86
Q8R395_C	Commd5	COMM dor	3	8.5	7.6	8.3	1.1	1.02	0.98	22.2	23.4	28.5	0.9	0.78	1.29
Q6ZWX6_II	Eif2s1	Eukaryotic	21	19.1	17.1	18.6	1.1	1.02	0.98	624.8	478.1	581.9	1.3	1.07	0.93
Q9R0B7_ZI	Znf346	Zinc finger	2	11.4	10.2	11.1	1.1	1.02	0.98	22.7	20.3	24.8	1.1	0.92	1.09
D3Z2H9_D	Tpm3-rs7	Uncharacte	10	26.0	23.3	25.4	1.1	1.02	0.98	322.0	292.0	355.5	1.1	0.91	1.10

Q9WVG6_	Carm1	Histone-arg	3	15.7	14.1	15.4	1.1	1.02	0.98	52.4	40.1	48.8	1.3	1.07	0.93
Q9D8S3_A	Arfgap3	ADP-ribosy	6	9.9	8.9	9.7	1.1	1.02	0.98	74.2	53.1	64.7	1.4	1.15	0.87
Q80U93_N	Nup214	Nuclear po	3	9.7	8.7	9.5	1.1	1.02	0.98	23.6	26.0	31.6	0.9	0.75	1.34
Q80X82_S	Sympk	Symplekin	15	10.2	9.2	10.0	1.1	1.02	0.98	208.0	153.1	186.4	1.4	1.12	0.90
Q9CXU1_M	Med31	Mediator o	1	10.5	9.5	10.3	1.1	1.02	0.98	10.5	9.5	11.5	1.1	0.91	1.10
Q6ZWV7_R	Rpl35	60S riboso	5	36.1	32.5	35.5	1.1	1.02	0.98	1643.7	450.7	548.6	3.6	3.00	0.33
Q09XV5_C	Chd8	Chromodo	3	10.2	9.2	10.0	1.1	1.02	0.98	31.8	28.3	34.4	1.1	0.92	1.08
Q9CY58_P	Serbp1	Plasminoge	4	16.1	14.6	15.9	1.1	1.02	0.98	71.7	58.2	70.9	1.2	1.01	0.99
O35134_R	Polr1a	DNA-direct	2	3.7	3.3	3.6	1.1	1.01	0.99	7.3	6.6	8.1	1.1	0.91	1.10
Q9Z0H3_S	Smarcb1	SWI/SNF-re	9	18.1	16.4	17.9	1.1	1.01	0.99	154.5	179.4	218.3	0.9	0.71	1.41
Q9D541_C	Ccdc7	Coiled-coil	1	1.2	1.1	1.2	1.1	1.01	0.99	1.2	1.1	1.3	1.1	0.91	1.10
Q9Z1Z2_ST	Strap	Serine-thre	10	14.3	12.9	14.1	1.1	1.01	0.99	163.5	126.5	154.0	1.3	1.06	0.94
Q99LF4_RT	Rtcb	tRNA-splici	22	39.4	35.7	39.0	1.1	1.01	0.99	1079.0	825.2	1004.4	1.3	1.07	0.93
Q8K0L9_Z	Zbtb20	Zinc finger	2	7.9	7.2	7.8	1.1	1.01	0.99	15.8	14.4	17.5	1.1	0.91	1.10
P62270_R	Rps18	40S riboso	13	200.7	182.3	198.9	1.1	1.01	0.99	3605.9	3428.4	4172.9	1.1	0.86	1.16
Q9Z1M8_R	Ik	Protein Re	15	15.7	14.2	15.5	1.1	1.01	0.99	346.4	268.4	326.7	1.3	1.06	0.94
Q9Z1K5_A	Arih1	E3 ubiquiti	3	15.1	13.8	15.0	1.1	1.01	0.99	37.0	46.2	56.2	0.8	0.66	1.52
Q3UMY5_E	Eml4	Echinoder	1	3.3	3.0	3.3	1.1	1.01	0.99	3.3	3.0	3.7	1.1	0.90	1.11
P47226_TE	Tes	Testin OS=	4	11.3	10.3	11.3	1.1	1.01	0.99	46.9	46.5	56.6	1.0	0.83	1.21
Q922H9_Z	Znf330	Zinc finger	2	17.3	15.8	17.2	1.1	1.00	1.00	34.6	31.6	38.5	1.1	0.90	1.11
Q9D1C8_V	Vps28	Vacuolar pr	5	17.1	15.6	17.1	1.1	1.00	1.00	115.0	66.2	80.6	1.7	1.43	0.70
Q9Z0G0_G	Gipc1	PDZ domai	2	9.5	8.7	9.5	1.1	1.00	1.00	19.0	17.4	21.1	1.1	0.90	1.11
Q9JJS0_SC	Scube2	Signal pept	1	16.4	15.0	16.4	1.1	1.00	1.00	16.4	15.0	18.3	1.1	0.90	1.11
Q9CU65_Z	Zmym2	Zinc finger	2	7.6	6.9	7.5	1.1	1.00	1.00	15.1	13.8	16.8	1.1	0.90	1.11
Q6PGF3_M	Med16	Mediator o	1	14.7	13.5	14.7	1.1	1.00	1.00	14.7	13.5	16.4	1.1	0.90	1.12
P97822_A	Anp32e	Acidic leuci	2	12.9	11.8	12.9	1.1	1.00	1.00	25.8	23.6	28.7	1.1	0.90	1.12
Q3TEA8_H	Hp1bp3	Heterochr	20	32.1	29.5	32.1	1.1	1.00	1.00	985.9	793.1	965.3	1.2	1.02	0.98
A2APB8_T	Tpx2	Targeting p	2	9.0	8.3	9.0	1.1	1.00	1.00	18.0	16.5	20.1	1.1	0.89	1.12
Q60949_T	Tbc1d1	TBC1 doma	9	9.0	8.2	9.0	1.1	1.00	1.00	108.1	174.0	211.8	0.6	0.51	1.96
O35144_T	Terf2	Telomeric	5	7.3	6.7	7.3	1.1	1.00	1.00	46.6	32.0	38.9	1.5	1.20	0.84
Q69ZR2_H	Hectd1	E3 ubiquiti	2	4.3	4.0	4.4	1.1	1.00	1.00	8.7	8.0	9.7	1.1	0.89	1.12
Q6PGB6_N	Naa50	N-alpha-ac	1	5.0	4.6	5.0	1.1	1.00	1.00	5.0	4.6	5.6	1.1	0.89	1.12
Q9DBS5_K	Klc4	Kinesin ligh	1	3.7	3.4	3.7	1.1	1.00	1.00	3.7	3.4	4.1	1.1	0.89	1.12
Q640M1_U	Utp14a	U3 small nu	2	11.8	10.9	11.9	1.1	1.00	1.00	23.7	21.8	26.5	1.1	0.89	1.12
Q8BGD9_I	Eif4b	Eukaryotic	2	8.9	8.2	8.9	1.1	0.99	1.01	17.7	16.3	19.9	1.1	0.89	1.12
Q8K212_P	Pacs1	Phosphofu	2	7.5	6.9	7.5	1.1	0.99	1.01	15.0	13.8	16.8	1.1	0.89	1.12
O54833_C	Csnk2a2	Casein kina	7	11.5	10.6	11.6	1.1	0.99	1.01	85.1	75.6	92.0	1.1	0.93	1.08
Q7TQH0_A	Atxn2l	Ataxin-2-li	10	11.2	10.4	11.3	1.1	0.99	1.01	153.8	114.9	139.9	1.3	1.10	0.91
Q9CQ92_F	Fis1	Mitochond	2	15.4	14.2	15.5	1.1	0.99	1.01	30.7	28.4	34.6	1.1	0.89	1.13
Q08093_C	Cnn2	Calponin-2	14	42.5	39.3	42.9	1.1	0.99	1.01	1027.1	782.4	952.3	1.3	1.08	0.93
Q8VHM5_	Hnrnpr	Heterogene	9	12.1	11.2	12.2	1.1	0.99	1.01	157.1	118.6	144.4	1.3	1.09	0.92
O09106_H	Hdac1	Histone de	25	18.7	17.3	18.9	1.1	0.99	1.01	488.2	602.0	732.7	0.8	0.67	1.50
Q8CBW3_	Abi1	Abl interac	5	6.3	5.9	6.4	1.1	0.99	1.01	77.2	34.4	41.9	2.2	1.84	0.54
Q8K2A7_I	Ints10	Integrator	5	13.3	12.3	13.5	1.1	0.99	1.01	57.9	66.3	80.7	0.9	0.72	1.39
Q6ZQL4_W	Wdr43	WD repeat-	3	7.1	6.6	7.2	1.1	0.99	1.01	19.2	29.2	35.6	0.7	0.54	1.85
Q9JIW9_R	Ralb	Ras-related	2	8.9	8.2	9.0	1.1	0.99	1.01	17.7	16.4	20.0	1.1	0.89	1.13
P70210_TE	Tead3	Transcripti	1	4.2	3.9	4.2	1.1	0.99	1.01	4.2	3.9	4.7	1.1	0.89	1.13
Q8BZR9_CQ085_MOUS		Uncharacte	8	18.0	16.7	18.2	1.1	0.99	1.01	169.8	119.3	145.2	1.4	1.17	0.86
Q4VA53_P	Pds5b	Sister chro	35	20.0	18.6	20.3	1.1	0.99	1.01	1179.7	959.6	1168.0	1.2	1.01	0.99
Q80WC7_	Agfg2	Arf-GAP do	2	9.6	9.0	9.8	1.1	0.99	1.01	19.3	17.9	21.8	1.1	0.88	1.13
Q8CG47_S	Smc4	Structural	66	20.0	18.6	20.3	1.1	0.99	1.01	2188.3	1630.4	1984.5	1.3	1.10	0.91
Q9JHS9_C	Cwc15	Spliceosom	1	4.7	4.4	4.8	1.1	0.99	1.02	4.7	4.4	5.3	1.1	0.88	1.13
Q9CXU0_M	Med10	Mediator o	4	9.6	9.0	9.8	1.1	0.98	1.02	48.9	41.5	50.6	1.2	0.97	1.03
Q2VPQ9_E	Meaf6	Chromatin	4	17.2	16.0	17.5	1.1	0.98	1.02	73.3	78.1	95.1	0.9	0.77	1.30
Q9WTX6_C	Cul1	Cullin-1 OS	45	12.3	11.5	12.6	1.1	0.98	1.02	763.1	584.4	711.3	1.3	1.07	0.93
Q6DID3_S	Scaf8	Protein SC	3	7.5	7.0	7.7	1.1	0.98	1.02	20.9	30.7	37.3	0.7	0.56	1.79
P20444_K	Prkca	Protein kin	2	15.7	14.7	16.1	1.1	0.98	1.02	31.5	29.4	35.8	1.1	0.88	1.14
Q99LE1_R	Rilpl2	RILP-like p	1	8.9	8.3	9.0	1.1	0.98	1.02	8.9	8.3	10.1	1.1	0.88	1.14
Q9D7W5_	Med8	Mediator o	1	6.1	5.7	6.2	1.1	0.98	1.02	6.1	5.7	6.9	1.1	0.88	1.14
P24369_P	Ppib	Peptidyl-pr	2	13.7	12.8	14.0	1.1	0.98	1.02	27.4	25.7	31.2	1.1	0.88	1.14
Q9EPJ9_AR	Arfgap1	ADP-ribosy	1	4.1	3.8	4.2	1.1	0.98	1.02	4.1	3.8	4.7	1.1	0.88	1.14
E9Q555_R	Rnf213	E3 ubiquiti	20	13.8	12.9	14.1	1.1	0.98	1.02	286.6	301.8	367.3	0.9	0.78	1.28
Q921N6_D	Ddx27	Probable A	5	7.2	6.8	7.4	1.1	0.98	1.02	35.6	34.2	41.6	1.0	0.86	1.17
Q9CXG3_P	Ppil4	Peptidyl-pr	3	7.6	7.1	7.8	1.1	0.97	1.03	19.3	22.3	27.2	0.9	0.71	1.41
Q6PEB6_P	Mob4	MOB-like p	2	29.6	27.8	30.4	1.1	0.97	1.03	59.1	55.6	67.7	1.1	0.87	1.15
Q3UIA2_R	Arhgap17	Rho GTPas	9	5.5	5.2	5.6	1.1	0.97	1.03	83.2	65.4	79.6	1.3	1.04	0.96
Q65Z40_W	Wapal	Wings apar	7	10.8	10.2	11.1	1.1	0.97	1.03	80.4	78.1	95.0	1.0	0.85	1.18
A2AJT4_PN	Pnisr	Arginine/se	1	22.7	21.4	23.4	1.1	0.97	1.03	22.7	21.4	26.1	1.1	0.87	1.15
Q5SUF2_L	Luc7l3	Luc7-like p	12	21.4	20.2	22.0	1.1	0.97	1.03	480.7	440.2	535.8	1.1	0.90	1.11
Q6ZQ08_C	Cnot1	CCR4-NOT	31	15.0	14.2	15.5	1.1	0.97	1.03	695.9	523.7	637.4	1.3	1.09	0.92
Q9CQU1_M	Mfap1	Microfibril	3	8.0	7.6	8.2	1.1	0.97	1.03	21.0	23.5	28.6	0.9	0.73	1.37
Q9R1P1_P	Psmb3	Proteasom	2	4.3	4.1	4.4	1.1	0.97	1.03	8.6	8.1	9.9	1.1	0.87	1.15
Q9JIF7_CO	Copb1	Coatomer	41	18.3	17.4	19.0	1.1	0.97	1.03	1266.2	1068.1	1300.0	1.2	0.97	1.03
Q9JHS3_LT	Lamtor2	Ragulator	2	7.8	7.4	8.1	1.1	0.97	1.03	15.6	14.8	18.0	1.1	0.87	1.15
Q8R3S6_E	Exoc1	Exocyst co	3	10.4	9.9	10.8	1.1	0.97	1.04	32.9	25.6	31.1	1.3	1.06	0.95
Q8JZM7_C	Cdc73	Parafibrom	11	25.1	23.8	26.0	1.1	0.96	1.04	251.7	277.2	337.4	0.9	0.75	1.34
Q61335_B	Bcap31	B-cell rece	1	13.7	13.1	14.3	1.1	0.96	1.04	13.7	13.1	15.9	1.1	0.86	1.16
P62918_R	Rpl8	60S riboso	10	116.0	110.4	120.4	1.1	0.96	1.04	1370.7	1392.1	1694.5	1.0	0.81	1.24
Q9Z1N5_D	Ddx39b	Spliceosom	32	15.0	14.3	15.6	1.0	0.96	1.04	1949.2	1106.0	1346.2	1.8	1.45	0.69
Q7TMI3_U	Uhrf2	E3 ubiquiti	2	6.5	6.2	6.8	1.0	0.96	1.04	13.0	12.4	15.1	1.0	0.86	1.16
O54790_M	Mafg	Transcripti	2	16.7	15.9	17.3	1.0	0.96	1.04	33.3	31.8	38.7	1.0	0.86	1.16
Q9ES28_A	Arhgef7	Rho guanin	8	10.0	9.5	10.4	1.0	0.96	1.04	91.5	106.1	129.2	0.9	0.71	1.41
P35279_R	Rab6a	Ras-related	6	14.0	13.4	14.6	1.0	0.96	1.04	122.2	86.8	105.6	1.4	1.16	0.86
P62627_D	Dynlrb1	Dynein ligh	3	15.9	15.2	16.6	1.0	0.96	1.04	58.5	50.4	61.3	1.2	0.95	1.05
Q64324_S	Stxbp2	Syntaxin-bi	2	8.2	7.8	8.5	1.0	0.96	1.04	16.4	15.7	19.0	1.0	0.86	1.16
Q9CR20_IR	Ier3ip1	Immediate	1	2.9	2.8	3.0	1.0	0.96	1.04	2.9	2.8	3.4	1.0	0.86	1.16
Q6A0A9_F1	FAM120A	Constitutiv	18	16.6	15.8	17.3	1.0	0.96	1.04	475.3	325.4	396.1	1.5	1.20	0.83
P07607_T	Tyms	Thymidylat	1	2.2	2.1	2.3	1.0	0.95	1.05	2.2	2.1	2.6	1.0	0.86	1.17
P33610_P	Prim2	DNA prima	11	11.9	11.4	12.4	1.0	0.95	1.05	188.8	171.5	208.7	1.1	0.90	1.11
Q9D4H1_E	Exoc2	Exocyst co	5	12.9	12.4	13.5	1.0	0.95	1.05	50.6	67.9	82.6	0.7	0.61	1.63
Q60902_E	Eps15l1	Epidermal	7	10.0	9.6	10.5	1.0	0.95	1.05	70.5	65.4	79.7	1.1	0.89	1.13
Q91Z69_S	Srgap1	SLIT-ROBO	1	3.8	3.7	4.0	1.0	0.95	1.05	3.8	3.7	4.4	1.0	0.85	1.17
Q9Z1X4_IL	Ilf3	Interleukin	38	14.4	13.8	15.1	1.0	0.95	1.05	955.5	700.7	852.9	1.4	1.12	0.89
P32233_D	Drg1	Developme	15	18.7	18.0	19.6	1.0	0.95	1.05	374.2	295.4	359.5	1.3	1.04	0.96
Q8BQZ5_C	Cpsf4	Cleavage a	4	11.1	10.7	11.7	1.0	0.95	1.05	59.3	59.7	72.7	1.0	0.82	1.23
P56960_E	Exosc10	Exosome c	15	7.9	7.6	8.3	1.0	0.95	1.05	178.4	113.8	138.5	1.6	1.29	0.78
Q8K1X1_W	Wdr11	WD repeat-	12	6.1	5.9	6.4	1.0	0.95	1.05	85.5	88.8	108.1	1.0	0.79	1.27
P58389_P	Ppp2r4	Serine/thre	5	11.3	10.9	11.8	1.0	0.95	1.05	85.8	50.3	61.2	1.7	1.40	0.71
P97351_R	Rps3a	40S riboso	25	41.7	40.2	43.9	1.0	0.95	1.05	2577.3	1811.2	2204.6	1.4	1.17	0.86
Q3UEB3_P	Puf60	Poly(U)-bin	26	18.1	17.5	19.1	1.0	0.95	1.05	1186.5	558.0	679.2	2.1	1.75	0.57
P21126_U	Ubl4a	Ubiquitin-	3	11.0	10.6	11.6	1.0	0.95	1.05	55.0	28.4	34.6	1.9	1.59	0.63
Q921K2_Q	Parp1	Poly (ADP-	36	26.7	25.9	28.2	1.0	0.95	1.05	1230.9	1302.8	1585.7	0.9	0.78	1.29
Q6ZWQ7_	Spcs3	Signal pept	1	7.9	7.7	8.4	1.0	0.95	1.06	7.9	7.7	9.4	1.0	0.85	1.18
Q921Y0_M	Mob1a	MOB kinas	9	16.6	16.1	17.6	1.0	0.95	1.06	467.2	367.7	447.6	1.3	1.04	0.96
Q9D903_E	Ebna1bp2	Probable r	7	11.3	10.9	11.9	1.0	0.95	1.06	86.8	80.7	98.2	1.1	0.88	1.13
Q69ZL1_F	Fgd6	FYVE, RhoG	1	13.2	12.8	14.0	1.0	0.94	1.06	13.2	12.8	15.6	1.0	0.85	1.18
Q921G8_G	Tubgcp2	Gamma-tu	10	7.8	7.6	8.3	1.0	0.94	1.06	88.5	79.8	97.2	1.1	0.91	1.10
P21956_M	Mfge8	Lactadheri	8	9.4	9.1	10.0	1.0	0.94	1.06	81.1	85.9	104.6	0.9	0.78	1.29
P22892_A	Ap1g1	AP-1 comp	7	12.6	12.2	13.3	1.0	0.94	1.06	141.7	72.3	88.0	2.0	1.61	0.62
Q5SWW4_	Med13	Mediator o	4	7.0	6.8	7.5	1.0	0.94	1.06	30.1	27.7	33.8	1.1	0.89	1.12
P53564_C	Cux1	Homeobox	7	10.0	9.7	10.6	1.0	0.94	1.06	60.6	65.5	79.7	0.9	0.76	1.31
Q9ESP1_SD	Sdf2l1	Stromal cel	4	8.9	8.7	9.4	1.0	0.94	1.06	63.3	36.3	44.2	1.7	1.43	0.70
O55222_IL	Ilk	Integrin-lin	18	10.8	10.6	11.5	1.0	0.94	1.06	203.7	226.0	275.0	0.9	0.74	1.35

Q91YJ2_SN	Snx4	Sorting nex	12	10.6	10.3	11.3	1.0	0.94	1.07	187.7	165.3	201.2	1.1	0.93	1.07
O35343_IN	Kpna4	Importin su	9	20.3	19.8	21.6	1.0	0.94	1.07	162.2	218.0	265.4	0.7	0.61	1.64
Q99K01_PI	Pdxdc1	Pyridoxal-d	7	7.0	6.8	7.5	1.0	0.94	1.07	54.9	49.1	59.8	1.1	0.92	1.09
Q60575_KI	Kif1b	Kinesin-like	1	2.5	2.4	2.7	1.0	0.93	1.07	2.5	2.4	3.0	1.0	0.84	1.19
Q9D1Q1_M	Mphosph6	M-phase ph	3	15.8	15.6	17.0	1.0	0.93	1.07	50.4	46.9	57.1	1.1	0.88	1.13
O70194_EI	Eif3d	Eukaryotic	28	17.4	17.1	18.7	1.0	0.93	1.07	731.1	541.7	659.4	1.3	1.11	0.90
B2RRE7_OT	Otud4	OTU domai	2	15.0	14.8	16.1	1.0	0.93	1.07	30.0	29.5	36.0	1.0	0.84	1.20
Q9D2R0_A	Aacs	Acetoacety	34	24.4	23.9	26.1	1.0	0.93	1.07	978.8	806.6	981.8	1.2	1.00	1.00
P70335_RO	Rock1	Rho-associa	4	7.6	7.4	8.1	1.0	0.93	1.07	33.0	29.5	35.9	1.1	0.92	1.09
Q9QWY8_A	Asap1	Arf-GAP wit	5	9.9	9.7	10.6	1.0	0.93	1.07	61.6	44.1	53.7	1.4	1.15	0.87
Q8R422_CI	Cd109	CD109 anti	2	9.2	9.0	9.9	1.0	0.93	1.07	18.4	18.1	22.0	1.0	0.83	1.20
P62754_RS	Rps6	40S riboson	10	27.0	26.6	29.0	1.0	0.93	1.07	680.2	381.6	464.5	1.8	1.46	0.68
Q4FK66_PF	Prpf38a	Pre-mRNA-	6	13.7	13.5	14.7	1.0	0.93	1.08	76.0	82.7	100.6	0.9	0.76	1.32
Q6Y7W8_P	Gigyf2	PERQ amin	5	4.2	4.2	4.5	1.0	0.93	1.08	32.6	32.9	40.1	1.0	0.81	1.23
Q9DBE7_Q	Stau1	Double-stra	8	13.9	13.7	14.9	1.0	0.93	1.08	124.5	148.1	180.2	0.8	0.69	1.45
Q5SVQ0_KA	Kat7	Histone ace	9	15.1	14.9	16.3	1.0	0.93	1.08	105.3	123.2	150.0	0.9	0.70	1.42
Q6P9Q4_FI	Fhod1	FH1/FH2 do	3	6.2	6.2	6.7	1.0	0.92	1.08	33.9	16.1	19.6	2.1	1.73	0.58
Q3UMB9_V	Kiaa1033	WASH com	6	7.0	7.0	7.6	1.0	0.92	1.08	52.7	41.6	50.6	1.3	1.04	0.96
Q9ESZ8_GT	Gtf2i	General tra	35	13.4	13.3	14.5	1.0	0.92	1.08	728.5	774.8	943.1	0.9	0.77	1.29
Q9EQH3_VI	Vps35	Vacuolar pr	50	26.9	26.8	29.2	1.0	0.92	1.08	2209.2	1846.9	2247.9	1.2	0.98	1.02
Q9CQI9_MI	Med30	Mediator o	1	22.0	21.9	23.9	1.0	0.92	1.08	22.0	21.9	26.6	1.0	0.83	1.21
Q9R1C7_PI	Prpf40a	Pre-mRNA-	34	20.5	20.4	22.3	1.0	0.92	1.08	1142.3	988.0	1202.5	1.2	0.95	1.05
Q6A065_CI	Cep170	Centrosom	5	12.1	12.0	13.1	1.0	0.92	1.08	61.1	59.6	72.5	1.0	0.84	1.19
Q91VJ4_ST	Stk38	Serine/thre	3	8.4	8.4	9.1	1.0	0.92	1.09	26.9	29.8	36.3	0.9	0.74	1.35
Q8BX17_GI	Gemin5	Gem-associ	5	11.0	11.0	12.0	1.0	0.92	1.09	57.1	54.0	65.7	1.1	0.87	1.15
O35382_EX	Exoc4	Exocyst cor	4	9.1	9.0	9.9	1.0	0.92	1.09	39.4	36.6	44.5	1.1	0.88	1.13
Q60749_KI	Khdrbs1	KH domain	16	49.8	49.6	54.1	1.0	0.92	1.09	1522.3	1371.2	1669.0	1.1	0.91	1.10
Q921E2_RA	Rab31	Ras-related	1	6.6	6.6	7.2	1.0	0.92	1.09	6.6	6.6	8.1	1.0	0.83	1.21
Q3U0V1_FI	Khsrp	Far upstrea	14	12.3	12.2	13.3	1.0	0.92	1.09	229.6	257.5	313.4	0.9	0.73	1.36
Q9QZB7_AI	Actr10	Actin-relate	4	6.7	6.7	7.3	1.0	0.92	1.09	36.9	40.7	49.5	0.9	0.75	1.34
Q9QZ88_VI	Vps29	Vacuolar pr	6	15.8	15.7	17.1	1.0	0.92	1.09	294.8	168.6	205.2	1.7	1.44	0.70
P48377_RF	Rfx1	MHC class I	3	11.3	11.3	12.3	1.0	0.92	1.09	30.4	28.2	34.3	1.1	0.88	1.13
Q9QZQ8_H	H2afy	Core histon	30	29.6	29.5	32.2	1.0	0.92	1.09	1224.6	1476.9	1797.6	0.8	0.68	1.47
Q8C079_ST	Strip1	Striatin-int	6	12.4	12.3	13.5	1.0	0.92	1.09	70.4	90.9	110.7	0.8	0.64	1.57
Q6P2L6_NS	Whsc1l1	Histone-lys	6	8.5	8.5	9.3	1.0	0.92	1.09	50.0	54.8	66.7	0.9	0.75	1.33
Q9QYB1_CI	Clic4	Chloride in	3	2.3	2.3	2.5	1.0	0.92	1.09	8.7	8.1	9.9	1.1	0.88	1.14
Q91YR7_PF	Prpf6	Pre-mRNA-	23	15.1	15.1	16.5	1.0	0.92	1.09	429.2	365.3	444.6	1.2	0.97	1.04
Q99PV0_PI	Prpf8	Pre-mRNA-	76	25.1	25.1	27.4	1.0	0.92	1.09	2497.7	2244.3	2731.7	1.1	0.91	1.09
Q3U898_M	Myeov2	Myeloma-o	1	22.4	22.4	24.4	1.0	0.92	1.09	22.4	22.4	27.2	1.0	0.82	1.22
Q3UA37_Q	Qrich1	Glutamine-	3	5.9	5.9	6.4	1.0	0.92	1.09	19.1	17.4	21.2	1.1	0.90	1.11
Q8CEJ2_Q8	Uxt	MCG11770	3	11.0	11.0	12.0	1.0	0.92	1.09	36.4	34.6	42.1	1.1	0.86	1.16
P61087_UI	Ube2k	Ubiquitin-c	3	30.6	30.6	33.4	1.0	0.92	1.09	98.5	75.0	91.3	1.3	1.08	0.93
Q8C8U0_LI	Ppfibp1	Liprin-beta	3	10.6	10.6	11.5	1.0	0.92	1.09	29.2	30.6	37.3	1.0	0.78	1.27
Q9JJA4_WI	Wdr12	Ribosome b	1	18.7	18.7	20.4	1.0	0.92	1.09	18.7	18.7	22.8	1.0	0.82	1.22
Q9WVC3_C	Cav2	Caveolin-2	1	6.0	6.0	6.5	1.0	0.92	1.09	6.0	6.0	7.3	1.0	0.82	1.22
Q8C050_KS	Rps6ka5	Ribosomal	1	4.5	4.5	4.9	1.0	0.92	1.09	4.5	4.5	5.5	1.0	0.82	1.22
P68373_TE	Tuba1c	Tubulin alp	7	15.7	15.7	17.1	1.0	0.92	1.09	176.1	417.1	507.7	0.4	0.35	2.88
Q9CWJ3_K	Katnbl1	KATNB1-lik	1	12.6	12.6	13.7	1.0	0.92	1.09	12.6	12.6	15.3	1.0	0.82	1.22
Q8R040_RI	Rpp21	Ribonuclea	1	8.4	8.4	9.2	1.0	0.92	1.09	8.4	8.4	10.2	1.0	0.82	1.22
Q9R1Q7_PI	Plp2	Proteolipid	1	183.1	183.1	199.7	1.0	0.92	1.09	183.1	183.1	222.8	1.0	0.82	1.22
Q9Z148_EH	Ehmt2	Histone-lys	3	14.1	14.1	15.4	1.0	0.92	1.09	42.5	47.4	57.7	0.9	0.74	1.36
Q9R0P5_DI	Dstn	Destrin OS=	1	17.5	17.5	19.1	1.0	0.92	1.09	17.5	17.5	21.3	1.0	0.82	1.22
D3YWS8_D	Leng8	Leukocyte r	2	10.5	10.5	11.5	1.0	0.92	1.09	21.1	21.1	25.6	1.0	0.82	1.22
Q9CQN3_TO	Tomm6	Mitochond	1	5.7	5.7	6.2	1.0	0.92	1.09	5.7	5.7	6.9	1.0	0.82	1.22
P62743_AF	Ap2s1	AP-2 compl	3	12.1	12.1	13.2	1.0	0.92	1.09	47.5	48.0	58.5	1.0	0.81	1.23
Q91W89_M	Man2c1	Alpha-man	1	9.0	9.0	9.8	1.0	0.92	1.09	9.0	9.0	10.9	1.0	0.82	1.22
Q9D1I6_RM	Mrpl14	39S riboson	1	8.2	8.2	9.0	1.0	0.92	1.09	8.2	8.2	10.0	1.0	0.82	1.22
Q9D7S7_RI	Rpl22l1	60S riboson	1	12.6	12.6	13.8	1.0	0.92	1.09	12.6	12.6	15.4	1.0	0.82	1.22
Q9CR41_HY	Hypk	Huntingtin	2	30.3	30.3	33.1	1.0	0.92	1.09	60.7	60.7	73.8	1.0	0.82	1.22
Q99L28_RL	Rsl24d1	Probable ri	3	8.8	8.8	9.6	1.0	0.92	1.09	36.9	30.9	37.6	1.2	0.98	1.02
Q63810_CA	Ppp3r1	Calcineurin	3	9.0	9.0	9.8	1.0	0.92	1.09	24.5	94.2	114.7	0.3	0.21	4.68
P62242_RS	Rps8	40S riboson	16	42.9	43.0	46.9	1.0	0.92	1.09	2711.5	1146.1	1395.0	2.4	1.94	0.51
Q9CWS4_II	Cpsf3l	Integrator c	4	11.0	11.0	12.0	1.0	0.91	1.09	38.4	60.0	73.0	0.6	0.53	1.90
E9Q2I4_E9	Elmsan1	Protein Elm	2	7.3	7.3	8.0	1.0	0.91	1.09	14.6	14.6	17.8	1.0	0.82	1.22
Q8BGW1_F	Fto	Alpha-keto	1	2.4	2.4	2.6	1.0	0.91	1.09	2.4	2.4	2.9	1.0	0.82	1.22
Q9ER80_RT	Rtp4	Receptor-tr	1	14.1	14.1	15.4	1.0	0.91	1.10	14.1	14.1	17.2	1.0	0.82	1.22
Q6ZPY7_KD	Kdm3b	Lysine-spec	7	7.4	7.5	8.1	1.0	0.91	1.10	44.1	53.9	65.6	0.8	0.67	1.49
P46061_RA	Rangap1	Ran GTPase	26	19.7	19.8	21.6	1.0	0.91	1.10	732.9	624.0	759.6	1.2	0.96	1.04
P53986_M	Slc16a1	Monocarbo	2	15.9	16.0	17.4	1.0	0.91	1.10	31.8	31.9	38.9	1.0	0.82	1.22
P53995_AF	Anapc1	Anaphase-p	5	11.2	11.3	12.3	1.0	0.91	1.10	59.9	53.3	64.9	1.1	0.92	1.08
Q99J87_DH	Dhx58	Probable AT	25	9.7	9.8	10.7	1.0	0.91	1.10	381.9	330.8	402.7	1.2	0.95	1.05
Q4QY64_AT	Atad5	ATPase fam	1	10.4	10.5	11.4	1.0	0.91	1.10	10.4	10.5	12.8	1.0	0.81	1.23
Q8C5Q4_G	Grsf1	G-rich sequ	1	7.1	7.1	7.8	1.0	0.91	1.10	7.1	7.1	8.7	1.0	0.81	1.23
P53569_CE	Cebpz	CCAAT/enh	5	7.9	7.9	8.7	1.0	0.91	1.10	46.1	45.0	54.8	1.0	0.84	1.19
Q9CZX8_RS	Rps19	40S riboson	10	78.6	79.3	86.5	1.0	0.91	1.10	2529.7	1648.1	2006.0	1.5	1.26	0.79
Q8BZ21_KA	Kat6a	Histone ace	1	6.2	6.3	6.8	1.0	0.91	1.10	6.2	6.3	7.6	1.0	0.81	1.23
Q62261_SF	Sptbn1	Spectrin be	81	21.9	22.2	24.2	1.0	0.91	1.10	3119.2	2204.4	2683.1	1.4	1.16	0.86
Q6A068_CI	Cdc5l	Cell divisio	32	11.8	12.0	13.1	1.0	0.90	1.11	528.0	499.4	607.9	1.1	0.87	1.15
Q8BL74_TF	Gtf3c2	General tra	2	8.0	8.2	8.9	1.0	0.90	1.11	16.1	16.3	19.9	1.0	0.81	1.23
Q6KCD5_N	Nipbl	Nipped-B-li	8	13.6	13.8	15.0	1.0	0.90	1.11	102.9	100.0	121.8	1.0	0.85	1.18
O55143_AT	Atp2a2	Sarcoplasm	1	7.0	7.2	7.8	1.0	0.90	1.11	7.0	7.2	8.7	1.0	0.81	1.24
P25206_M	Mcm3	DNA replica	80	21.5	21.9	23.8	1.0	0.90	1.11	2769.7	3473.7	4228.1	0.8	0.66	1.53
Q3U2P1_SO	Sec24a	Protein tra	4	7.4	7.6	8.3	1.0	0.90	1.11	36.9	37.2	45.2	1.0	0.81	1.23
Q8VD12_Z	Znf385a	Zinc finger	3	14.2	14.5	15.8	1.0	0.90	1.11	46.0	48.4	58.9	1.0	0.78	1.28
Q9DCN2_N	Cyb5r3	NADH-cyto	3	11.8	12.0	13.1	1.0	0.90	1.11	37.2	44.2	53.8	0.8	0.69	1.45
Q9D8C4_IN	Ifi35	Interferon-i	1	13.8	14.1	15.4	1.0	0.90	1.11	13.8	14.1	17.2	1.0	0.80	1.24
Q8K284_TF	Gtf3c1	General tra	2	12.8	13.1	14.3	1.0	0.90	1.11	25.6	26.1	31.8	1.0	0.80	1.24
P68369_TE	Tuba1a	Tubulin alp	77	80.3	82.1	89.6	1.0	0.90	1.11	12238.2	11127.4	13543.9	1.1	0.90	1.11
O88379_BA	Baz1a	Bromodom	6	9.7	10.0	10.9	1.0	0.90	1.12	61.9	63.8	77.6	1.0	0.80	1.25
Q9DB77_Q	Uqcrc2	Cytochrom	1	7.0	7.2	7.8	1.0	0.90	1.12	7.0	7.2	8.7	1.0	0.80	1.25
Q5SF07_IF	Igf2bp2	Insulin-like	22	19.1	19.6	21.4	1.0	0.89	1.12	452.9	532.0	647.6	0.9	0.70	1.43
Q3TZX8_NO	Nol9	Polynucleo	3	5.3	5.5	6.0	1.0	0.89	1.12	14.4	20.4	24.8	0.7	0.58	1.72
Q99L00_HA	Haus8	HAUS augm	1	18.5	18.9	20.7	1.0	0.89	1.12	18.5	18.9	23.0	1.0	0.80	1.25
Q3UJB0_Q3	Sf3b2	Protein Sf3	34	19.3	19.8	21.6	1.0	0.89	1.12	1373.4	1118.3	1361.1	1.2	1.01	0.99
P62876_RF	Polr2l	DNA-direct	1	35.3	36.3	39.6	1.0	0.89	1.12	35.3	36.3	44.1	1.0	0.80	1.25
Q9QZE5_CO	Copg1	Coatomer s	33	21.4	22.0	24.0	1.0	0.89	1.12	1458.4	1167.6	1421.2	1.2	1.03	0.97
E9PVA8_E9	Gcn1l1	Protein Gcn	36	15.5	16.0	17.5	1.0	0.89	1.12	931.3	760.6	925.8	1.2	1.01	0.99
A2AGT5_CK	Ckap5	Cytoskeleto	44	18.5	19.0	20.7	1.0	0.89	1.12	1303.8	915.3	1114.1	1.4	1.17	0.85
Q9CW46_R	Raver1	Ribonucleo	5	9.5	9.8	10.7	1.0	0.89	1.13	56.8	49.9	60.8	1.1	0.94	1.07
B9EJ54_B9	Nup205	MCG21756	5	6.6	6.8	7.4	1.0	0.89	1.13	40.5	47.9	58.3	0.8	0.69	1.44
Q7JJ13_BR	Brd2	Bromodom	6	12.2	12.6	13.7	1.0	0.89	1.13	109.3	91.3	111.1	1.2	0.98	1.02
Q9D7H3_R	RtcA	RNA 3'-term	6	7.3	7.6	8.3	1.0	0.89	1.13	74.2	65.5	79.7	1.1	0.93	1.07
Q5SUH6_Q	Clint1	Clathrin int	8	9.3	9.6	10.5	1.0	0.89	1.13	98.1	93.3	113.5	1.1	0.86	1.16
P81069_GA	Gabpb2	GA-binding	2	13.7	14.1	15.4	1.0	0.89	1.13	27.3	28.2	34.4	1.0	0.79	1.26
P51949_M	Mnat1	CDK-activat	1	3.2	3.3	3.6	1.0	0.89	1.13	3.2	3.3	4.0	1.0	0.79	1.26
Q9EPU0_RI	Upf1	Regulator c	45	19.6	20.3	22.2	1.0	0.88	1.13	1196.4	1311.4	1596.2	0.9	0.75	1.33
O35654_DI	Pold2	DNA polym	4	6.8	7.1	7.8	1.0	0.88	1.14	33.3	25.8	31.4	1.3	1.06	0.94
G3X963_G	Atad2	ATPase fam	17	12.9	13.5	14.7	1.0	0.88	1.14	299.3	310.1	377.5	1.0	0.79	1.26
P59999_AF	Arpc4	Actin-relate	3	45.2	47.4	51.7	1.0	0.88	1.14	319.7	154.3	187.8	2.1	1.70	0.59
Q9QXZ0_M	Macf1	Microtubul	29	9.6	10.1	11.0	1.0	0.87	1.15	412.1	370.7	451.2	1.1	0.91	1.09
Q8CIE6_CO	Copa	Coatomer s	43	27.5	28.9	31.5	1.0	0.87	1.15	2049.5	1974.5	2403.3	1.0	0.85	1.17
Q8BRF7_SC	Scfd1	Sec1 family	6	8.9	9.3	10.2	1.0	0.87	1.15	48.2	52.5	63.9	0.9	0.75	1.33
P55258_RA	Rab8a	Ras-related	2	8.6	9.1	9.9	1.0	0.87	1.15	17.3	18.2	22.1	1.0	0.78	1.28

Q6PCM2_I	Ints6	Integrator	3	8.0	8.4	9.2	0.9	0.87	1.15	22.0	22.4	27.2	1.0	0.81	1.24
P42128_FC	Foxk1	Forkhead b	2	9.0	9.5	10.4	0.9	0.87	1.15	18.0	19.0	23.1	0.9	0.78	1.28
P62874_GI	Gnb1	Guanine nu	7	29.8	31.5	34.4	0.9	0.87	1.15	294.0	251.1	305.6	1.2	0.96	1.04
Q8BHG9_C	Cggbp1	CGG triplet	1	30.5	32.3	35.2	0.9	0.87	1.15	30.5	32.3	39.3	0.9	0.78	1.29
O08810_U	Eftud2	116 kDa U5	47	32.9	34.9	38.0	0.9	0.87	1.16	2110.6	1955.8	2380.6	1.1	0.89	1.13
Q6A009_L1	Ltn1	E3 ubiquiti	2	9.3	9.9	10.8	0.9	0.87	1.16	18.7	19.8	24.1	0.9	0.78	1.29
Q00422_G	Gabpa	GA-binding	4	27.1	28.7	31.3	0.9	0.87	1.16	106.1	274.6	334.2	0.4	0.32	3.15
P35550_FE	Fbl	rRNA 2'-O-r	18	24.7	26.2	28.5	0.9	0.87	1.16	1067.5	1078.4	1312.6	1.0	0.81	1.23
Q8CCK0_H	H2afy2	Core histon	15	24.1	25.5	27.8	0.9	0.86	1.16	478.2	750.4	913.4	0.6	0.52	1.91
Q9D6N5_N	Drap1	Dr1-associa	5	11.3	12.1	13.2	0.9	0.86	1.16	69.9	54.5	66.3	1.3	1.05	0.95
Q9CQF3_CI	Nudt21	Cleavage an	11	15.1	16.0	17.5	0.9	0.86	1.16	614.2	461.4	561.6	1.3	1.09	0.91
Q7M6Y3_P	Picalm	Phosphatid	22	15.0	15.9	17.4	0.9	0.86	1.16	540.9	422.8	514.6	1.3	1.05	0.95
E9Q2H1_E	Ubr5	E3 ubiquiti	9	7.5	7.9	8.7	0.9	0.86	1.16	82.6	78.5	95.5	1.1	0.87	1.16
O09172_G	Gclm	Glutamate-	1	3.0	3.2	3.5	0.9	0.86	1.16	3.0	3.2	3.9	0.9	0.77	1.30
P54823_DI	Ddx6	Probable A	21	25.7	27.5	29.9	0.9	0.86	1.16	929.9	1074.7	1308.1	0.9	0.71	1.41
Q52KI8_SR	Srrm1	Serine/argi	14	25.1	26.9	29.3	0.9	0.86	1.17	536.8	425.5	517.8	1.3	1.04	0.96
Q9QZD9_EI	Eif3i	Eukaryotic	12	36.7	39.3	42.9	0.9	0.86	1.17	834.7	468.3	570.0	1.8	1.46	0.68
Q3UMC0_S	Spata5	Spermatog	6	8.6	9.2	10.0	0.9	0.86	1.17	48.3	55.9	68.0	0.9	0.71	1.41
E9PZJ8_AS	Ascc3	Activating	12	9.7	10.4	11.3	0.9	0.85	1.17	116.4	135.8	165.2	0.9	0.70	1.42
P10639_TH	Txn	Thioredoxi	2	10.6	11.4	12.4	0.9	0.85	1.17	21.2	22.8	27.7	0.9	0.77	1.31
Q80X73_PI	Pelo	Protein pel	2	13.7	14.7	16.0	0.9	0.85	1.17	27.3	29.3	35.7	0.9	0.77	1.31
Q99PG4_R	Rgs18	Regulator c	1	13.5	14.5	15.8	0.9	0.85	1.17	13.5	14.5	17.6	0.9	0.76	1.31
Q921H8_TI	Acaa1a	3-ketoacyl-	1	3.8	4.0	4.4	0.9	0.85	1.17	3.8	4.0	4.9	0.9	0.76	1.31
Q8C0C7_S	Farsa	Phenylalan	18	17.2	18.5	20.2	0.9	0.85	1.17	333.2	420.1	511.3	0.8	0.65	1.53
Q8CIE4_Q8	Parp10	Plec1 prote	1	1.7	1.9	2.0	0.9	0.85	1.17	1.7	1.9	2.3	0.9	0.76	1.31
A0A0A0MC	Swi5	DNA repair	2	12.8	13.8	15.1	0.9	0.85	1.17	25.7	27.7	33.7	0.9	0.76	1.31
Q8K2Z4_CI	Ncapd2	Condensin	34	15.1	16.2	17.7	0.9	0.85	1.18	813.8	700.1	852.2	1.2	0.96	1.05
Q9Z207_DI	Diaph3	Protein dia	1	6.3	6.8	7.5	0.9	0.85	1.18	6.3	6.8	8.3	0.9	0.76	1.31
Q6NV83_SI	U2surp	U2 snRNP-a	27	19.3	20.8	22.7	0.9	0.85	1.18	722.4	713.0	867.8	1.0	0.83	1.20
Q8VHX6_FI	Flnc	Filamin-C C	68	41.6	45.0	49.1	0.9	0.85	1.18	5531.0	3818.5	4647.7	1.4	1.19	0.84
Q8C3V4_Q	Stat1	Signal trans	70	22.2	24.0	26.2	0.9	0.85	1.18	3593.8	2426.5	2953.4	1.5	1.22	0.82
Q9D6L8_PI	Ppil3	Peptidyl-pr	4	17.4	18.8	20.5	0.9	0.85	1.18	68.7	70.5	85.8	1.0	0.80	1.25
Q810B6_AI	Ankfy1	Rabankyrin	7	9.1	9.8	10.7	0.9	0.85	1.18	73.1	74.5	90.7	1.0	0.81	1.24
Q8R326_PS	Pspc1	Paraspeckl	6	17.0	18.4	20.0	0.9	0.85	1.18	152.6	103.3	125.7	1.5	1.21	0.82
Q5DW34_E	Ehmt1	Histone-lys	5	9.8	10.6	11.6	0.9	0.85	1.18	42.7	55.7	67.8	0.8	0.63	1.59
Q8VDD9_P	Phip	PH-interact	6	12.2	13.2	14.4	0.9	0.85	1.18	62.7	79.7	97.0	0.8	0.65	1.55
Q80VD1_F	Fam98b	Protein FAI	7	24.3	26.3	28.7	0.9	0.84	1.18	314.9	221.7	269.8	1.4	1.17	0.86
O70551_SF	Srpk1	SRSF protei	4	8.3	9.0	9.9	0.9	0.84	1.18	35.5	38.7	47.1	0.9	0.75	1.33
Q9Z1R2_B	Bag6	Large prolir	16	6.9	7.5	8.2	0.9	0.84	1.19	122.1	165.6	201.6	0.7	0.61	1.65
Q8CF89_TA	Tab1	TGF-beta-a	1	7.1	7.7	8.4	0.9	0.84	1.19	7.1	7.7	9.4	0.9	0.75	1.33
Q60973_RI	Rbbp7	Histone-bir	4	7.6	8.3	9.0	0.9	0.84	1.19	40.0	49.3	60.0	0.8	0.67	1.50
O55131_SE	7-Sep	Septin-7 OS	4	9.2	10.0	10.9	0.9	0.84	1.19	37.1	38.8	47.2	1.0	0.79	1.27
Q91YD3_D	Dcp1a	mRNA-deca	1	3.5	3.8	4.1	0.9	0.84	1.19	3.5	3.8	4.6	0.9	0.75	1.33
E9Q614_E	Chd3	Protein Ch	3	6.0	6.5	7.1	0.9	0.84	1.19	19.0	21.0	25.6	0.9	0.74	1.35
P60843_IF	Eif4a1	Eukaryotic	97	42.6	46.6	50.8	0.9	0.84	1.19	9775.5	7762.8	9448.6	1.3	1.03	0.97
P63276_RS	Rps17	40S riboso	11	20.1	22.0	24.0	0.9	0.84	1.19	1544.7	662.4	806.3	2.3	1.92	0.52
Q924K8_M	Mta3	Metastasis-	7	6.5	7.1	7.7	0.9	0.84	1.19	41.3	57.9	70.5	0.7	0.59	1.71
Q924C1_XI	Xpo5	Exportin-5	8	11.4	12.4	13.6	0.9	0.84	1.20	135.6	102.8	125.1	1.3	1.08	0.92
Q80XR8_Q	Git2	ARF GTPase	2	6.6	7.3	7.9	0.9	0.83	1.20	13.2	14.6	17.7	0.9	0.75	1.34
P46467_VF	Vps4b	Vacuolar pr	4	10.9	12.0	13.1	0.9	0.83	1.20	80.7	55.3	67.3	1.5	1.20	0.83
Q3UI43_BA	Babam1	BRISC and E	2	15.1	16.6	18.1	0.9	0.83	1.20	30.2	33.2	40.4	0.9	0.75	1.34
Q5EE38_AC	Acd	Adrenocort	2	3.9	4.3	4.6	0.9	0.83	1.20	7.7	8.5	10.4	0.9	0.75	1.34
Q62419_SH	Sh3gl1	Endophilin	14	34.2	37.7	41.1	0.9	0.83	1.20	690.1	1268.1	1543.5	0.5	0.45	2.24
F8VPU2_FA	Farp1	FERM, Rho	8	10.9	12.0	13.1	0.9	0.83	1.20	104.9	125.7	153.0	0.8	0.69	1.46
P62737_AC	Acta2	Actin, aorti	63	217.2	239.5	261.3	0.9	0.83	1.20	20178.3	23874.6	29059.4	0.8	0.69	1.44
Q9QXT0_CI	Cnpy2	Protein can	3	11.3	12.5	13.7	0.9	0.83	1.20	30.7	32.3	39.3	0.9	0.78	1.28
P62984_RL	Uba52	Ubiquitin-6	21	119.9	132.3	144.4	0.9	0.83	1.20	5207.1	7601.7	9252.6	0.7	0.56	1.78
Q9CR60_G	Golt1b	Vesicle tran	1	4.8	5.3	5.8	0.9	0.83	1.21	4.8	5.3	6.5	0.9	0.74	1.34
Q920B9_SF	Supt16h	FACT comp	21	15.5	17.2	18.7	0.9	0.83	1.21	346.0	396.5	482.6	0.9	0.72	1.39
Q8R0L9_TA	Tada3	Transcripti	2	8.0	8.9	9.7	0.9	0.83	1.21	16.1	17.8	21.6	0.9	0.74	1.35
Q6NXI6_RF	Rprd2	Regulation	8	10.6	11.7	12.7	0.9	0.83	1.21	83.0	88.4	107.5	0.9	0.77	1.30
O70378_EI	Emc8	ER membra	3	6.2	6.9	7.5	0.9	0.83	1.21	17.3	18.5	22.5	0.9	0.77	1.31
P27773_PI	Pdia3	Protein dis	12	12.5	13.9	15.2	0.9	0.83	1.21	184.5	250.2	304.5	0.7	0.61	1.65
Q9CQ49_N	Ncbp2	Nuclear cap	4	20.4	22.6	24.7	0.9	0.83	1.21	72.1	107.0	130.2	0.7	0.55	1.81
Q9CY57_CI	Chtop	Chromatin	6	4.7	5.3	5.7	0.9	0.83	1.21	32.6	42.2	51.4	0.8	0.63	1.58
O55106_S1	Strn	Striatin OS=	3	5.6	6.2	6.8	0.9	0.83	1.21	17.9	23.0	28.0	0.8	0.64	1.56
O88845_AI	Akap10	A-kinase an	2	7.0	7.8	8.5	0.9	0.82	1.21	14.0	15.5	18.9	0.9	0.74	1.35
Q91YT7_YT	Ythdf2	YTH domai	3	26.1	29.0	31.6	0.9	0.82	1.21	62.1	69.9	85.1	0.9	0.73	1.37
Q3UPL0_S	Sec31a	Protein tra	45	17.6	19.6	21.4	0.9	0.82	1.21	1171.6	878.5	1069.3	1.3	1.10	0.91
O55029_C	Copb2	Coatomer s	36	24.1	26.8	29.3	0.9	0.82	1.22	1221.5	1313.4	1598.6	0.9	0.76	1.31
E9QKH0_E	Clasp1	CLIP-associ	14	7.8	8.7	9.5	0.9	0.82	1.22	167.3	128.0	155.8	1.3	1.07	0.93
Q9D1D4_TI	Tmed10	Transmemb	6	11.2	12.5	13.7	0.9	0.82	1.22	82.6	106.3	129.4	0.8	0.64	1.57
O88520_SH	Shoc2	Leucine-ric	5	5.7	6.3	6.9	0.9	0.82	1.22	37.6	34.8	42.3	1.1	0.89	1.12
Q9D4J7_PH	Phf6	PHD finger	2	20.5	23.0	25.0	0.9	0.82	1.22	41.1	45.9	55.9	0.9	0.73	1.36
O55128_SA	Sap18	Histone dea	12	27.8	31.1	33.9	0.9	0.82	1.22	382.7	568.1	691.5	0.7	0.55	1.81
Q91W40_K	Klc3	Kinesin ligh	8	7.4	8.4	9.1	0.9	0.82	1.23	79.1	80.8	98.3	1.0	0.80	1.24
Q9JM93_AI	Arl6ip4	ADP-ribosy	2	6.5	7.4	8.0	0.9	0.81	1.23	13.1	14.7	17.9	0.9	0.73	1.37
Q99KJ8_D	Dctn2	Dynactin su	20	16.4	18.5	20.2	0.9	0.81	1.23	425.1	556.0	676.8	0.8	0.63	1.59
Q03963_E	Eif2ak2	Interferon-i	32	23.3	26.3	28.7	0.9	0.81	1.23	1169.9	1060.4	1290.7	1.1	0.91	1.10
P16858_G	Gapdh	Glyceraldeh	17	12.3	13.9	15.2	0.9	0.81	1.23	499.6	656.3	798.8	0.8	0.63	1.60
Q99KP6_PI	Prpf19	Pre-mRNA-	15	35.3	39.9	43.6	0.9	0.81	1.23	912.4	796.7	969.8	1.1	0.94	1.06
P70698_P	Ctps1	CTP syntha	28	18.6	21.0	22.9	0.9	0.81	1.23	1256.4	814.9	991.9	1.5	1.27	0.79
G3X959_G	Pphln1	Periphilin 1	2	18.2	20.6	22.4	0.9	0.81	1.23	36.4	41.2	50.1	0.9	0.73	1.38
Q8BMG7_R	Rab3gap2	Rab3 GTPa	4	7.3	8.3	9.0	0.9	0.81	1.24	30.7	36.4	44.3	0.8	0.69	1.44
Q9QY06_M	Myo9b	Unconvent	4	7.7	8.7	9.5	0.9	0.81	1.24	31.7	36.1	43.9	0.9	0.72	1.38
Q8BJ05_ZC	Zc3h14	Zinc finger	7	15.8	17.9	19.5	0.9	0.81	1.24	126.8	158.3	192.7	0.8	0.66	1.52
P49817_CA	Cav1	Caveolin-1	1	20.3	23.0	25.1	0.9	0.81	1.24	20.3	23.0	28.0	0.9	0.72	1.38
Q501J6_DI	Ddx17	Probable A	47	30.4	34.5	37.7	0.9	0.81	1.24	3297.7	3610.0	4393.9	0.9	0.75	1.33
Q9CZY3_UE	Ube2v1	Ubiquitin-c	3	8.7	9.9	10.8	0.9	0.81	1.24	68.8	27.0	32.9	2.5	2.09	0.48
O54946_DI	Dnajb6	DnaJ homo	3	7.4	8.4	9.2	0.9	0.81	1.24	42.4	43.0	52.3	1.0	0.81	1.23
E9QML5_E	Zfml	Zinc finger	20	9.3	10.5	11.5	0.9	0.81	1.24	221.6	238.8	290.7	0.9	0.76	1.31
Q3UBZ5_M	Mif4gd	MIF4G dom	2	4.1	4.7	5.1	0.9	0.81	1.24	8.3	9.4	11.4	0.9	0.72	1.39
Q9D0F6_RI	Rfc5	Replication	22	10.0	11.4	12.4	0.9	0.80	1.24	267.9	366.4	445.9	0.7	0.60	1.66
Q8R5J9_PF	Arl6ip5	PRA1 famil	5	7.9	9.0	9.9	0.9	0.80	1.24	54.3	93.8	114.1	0.6	0.48	2.10
B2RQG2_B	Phf3	PHD finger	3	8.9	10.2	11.1	0.9	0.80	1.25	23.0	23.4	28.5	1.0	0.81	1.24
Q8C5N3_C	Cwc22	Pre-mRNA-	5	9.7	11.1	12.1	0.9	0.80	1.25	55.9	70.4	85.6	0.8	0.65	1.53
Q91W96_A	Anapc4	Anaphase-p	4	7.6	8.7	9.5	0.9	0.80	1.25	30.8	32.5	39.6	0.9	0.78	1.28
Q8JZY2_CO	Commd10	COMM dom	4	8.9	10.2	11.1	0.9	0.80	1.25	41.7	40.8	49.7	1.0	0.84	1.19
Q4VC33_M	Maea	Macrophag	2	11.1	12.7	13.8	0.9	0.80	1.25	22.2	25.4	30.9	0.9	0.72	1.39
Q8BYK6_YT	Ythdf3	YTH domai	13	14.0	16.1	17.5	0.9	0.80	1.25	205.1	203.2	247.3	1.0	0.83	1.21
Q9Z247_FK	Fkbp9	Peptidyl-pr	1	7.7	8.8	9.6	0.9	0.80	1.25	7.7	8.8	10.7	0.9	0.72	1.40
G5E8K5_AI	Ank3	Ankyrin-3 C	1	6.9	8.0	8.7	0.9	0.80	1.25	6.9	8.0	9.7	0.9	0.72	1.40
Q8K2D3_EI	Edc3	Enhancer o	3	6.8	7.8	8.5	0.9	0.80	1.26	16.8	24.2	29.5	0.7	0.57	1.75
O35127_C	Grcc10	Protein C1	1	2.6	2.9	3.2	0.9	0.80	1.26	2.6	2.9	3.6	0.9	0.71	1.40
Q8CI51_PD	Pdlim5	PDZ and LI	19	13.2	15.2	16.5	0.9	0.80	1.26	285.7	336.6	409.6	0.8	0.70	1.43
P62301_RS	Rps13	40S riboso	7	277.4	320.2	349.3	0.9	0.79	1.26	1957.2	2580.8	3141.2	0.8	0.62	1.60
Q5F2E7_NU	Nufip2	Nuclear fra	11	6.4	7.4	8.1	0.9	0.79	1.26	73.4	87.4	106.3	0.8	0.69	1.45
Q9CWZ3_R	Rbm8a	RNA-bindir	3	73.6	85.1	92.8	0.9	0.79	1.26	166.4	335.0	407.8	0.5	0.41	2.45
Q6PI63_Q6	Polr2j	DNA-direct	4	14.7	17.0	18.5	0.9	0.79	1.26	72.2	78.5	95.6	0.9	0.75	1.32
Q80X90_FL	Flnb	Filamin-B C	51	14.4	16.7	18.2	0.9	0.79	1.26	1286.8	1006.2	1224.7	1.3	1.05	0.95
P11862_G	Gas2	Growth arr	1	5.5	6.4	7.0	0.9	0.79	1.26	5.5	6.4	7.8	0.9	0.71	1.41
P97801_SI	Smn1	Survival mo	4	6.1	7.0	7.7	0.9	0.79	1.27	24.4	30.0	36.5	0.8	0.67	1.50
Q6P9Z1_SI	Smarcd3	SWI/SNF-re	4	7.0	8.2	8.9	0.9	0.79	1.27	32.7	31.4	38.3	1.0	0.85	1.17

Q9CQE8_CN166_MOUS		UPF0568 p	14	54.7	63.7	69.5	0.9	0.79	1.27	937.2	980.8	1193.8	1.0	0.79	1.27
Q61624_ZN	Znf148	Zinc finger	7	10.0	11.7	12.7	0.9	0.79	1.27	73.0	102.2	124.4	0.7	0.59	1.70
P46460_NS	Nsf	Vesicle-fusi	14	13.7	16.0	17.4	0.9	0.79	1.27	293.2	322.3	392.3	0.9	0.75	1.34
Q9DCT6_BA	Bap18	Chromatin	4	14.7	17.2	18.8	0.9	0.78	1.28	71.2	71.3	86.8	1.0	0.82	1.22
P40240_CD	Cd9	CD9 antige	1	6.2	7.3	8.0	0.9	0.78	1.28	6.2	7.3	8.9	0.9	0.70	1.42
Q8BIH0_SP	Sap130	Histone dea	2	8.9	10.4	11.4	0.9	0.78	1.28	17.8	20.9	25.4	0.9	0.70	1.42
Q8CI71_CC	Ccdc132	Coiled-coil	2	6.2	7.3	7.9	0.9	0.78	1.28	12.4	14.5	17.7	0.9	0.70	1.43
P97868_RE	Rbbp6	E3 ubiquiti	4	9.7	11.4	12.4	0.9	0.78	1.28	40.0	43.8	53.3	0.9	0.75	1.33
Q8BMK4_C	Ckap4	Cytoskeleto	1	11.8	13.9	15.1	0.9	0.78	1.28	11.8	13.9	16.9	0.9	0.70	1.43
P61965_W	Wdr5	WD repeat-	5	8.2	9.6	10.5	0.9	0.78	1.28	168.5	106.3	129.3	1.6	1.30	0.77
Q7TT37_EL	Ikbkap	Elongator c	23	12.4	14.6	16.0	0.9	0.78	1.28	438.9	371.3	451.9	1.2	0.97	1.03
Q99LI5_ZN	Znf281	Zinc finger	2	6.0	7.0	7.7	0.9	0.78	1.28	11.9	14.0	17.1	0.9	0.70	1.43
Q9JI57_GT	Gtf2ird1	General tra	2	4.0	4.7	5.1	0.8	0.78	1.28	7.9	9.3	11.4	0.8	0.70	1.43
D3YW48_D	Capns1	Calpain sma	9	7.5	8.9	9.7	0.8	0.78	1.29	158.3	137.1	166.9	1.2	0.95	1.05
A6H5X4_PI	Phf11	PHD finger	6	61.3	72.3	78.9	0.8	0.78	1.29	447.0	481.1	585.6	0.9	0.76	1.31
E9Q6R7_E9	Utrn	Protein Utr	14	8.3	9.8	10.7	0.8	0.78	1.29	125.2	164.5	200.2	0.8	0.63	1.60
Q9QXK7_CI	Cpsf3	Cleavage ar	11	15.0	17.7	19.3	0.8	0.78	1.29	255.9	286.1	348.3	0.9	0.73	1.36
Q923D4_SF	Sf3b5	Splicing fac	3	22.3	26.3	28.7	0.8	0.78	1.29	63.9	85.1	103.6	0.8	0.62	1.62
Q80X32_CE024_MOUS		UPF0461 p	3	11.3	13.3	14.5	0.8	0.77	1.29	59.1	100.9	122.8	0.6	0.48	2.08
Q61510_TF	Trim25	E3 ubiquiti	2	11.0	13.1	14.3	0.8	0.77	1.29	22.1	26.2	31.8	0.8	0.69	1.44
Q8VDG6_M	Mlk4	Mitogen-ac	1	3.4	4.0	4.4	0.8	0.77	1.29	3.4	4.0	4.9	0.8	0.69	1.44
Q8BMB0_E	Emsy	Protein EM	3	5.3	6.3	6.9	0.8	0.77	1.29	17.4	20.5	25.0	0.8	0.70	1.44
Q3UA16_SI	Spc25	Kinetochor	2	9.1	10.7	11.7	0.8	0.77	1.29	18.1	21.5	26.2	0.8	0.69	1.44
Q8BX09_RI	Rbbp5	Retinoblast	7	11.8	14.0	15.2	0.8	0.77	1.29	91.4	99.0	120.5	0.9	0.76	1.32
Q9CQT1_M	Mri1	Methylthio	2	10.0	11.8	12.9	0.8	0.77	1.30	20.0	23.7	28.8	0.8	0.69	1.45
Q80X50_UI	Ubap2l	Ubiquitin-a	31	14.4	17.1	18.6	0.8	0.77	1.30	658.2	661.8	805.5	1.0	0.82	1.22
O54941_SN	Smarce1	SWI/SNF-re	9	9.4	11.2	12.2	0.8	0.77	1.30	115.1	113.8	138.5	1.0	0.83	1.20
P62821_RA	Rab1A	Ras-related	8	12.4	14.7	16.0	0.8	0.77	1.30	176.1	146.6	178.4	1.2	0.99	1.01
Q9CW03_S	Smc3	Structural r	76	18.2	21.7	23.7	0.8	0.77	1.30	1966.1	1990.0	2422.1	1.0	0.81	1.23
Q61550_RA	Rad21	Double-stra	17	7.7	9.1	9.9	0.8	0.77	1.30	214.8	313.9	382.0	0.7	0.56	1.78
O09044_SN	Snap23	Synaptosor	2	6.3	7.5	8.1	0.8	0.77	1.30	12.5	14.9	18.1	0.8	0.69	1.45
Q2KN98_C	Specc1l	Cytospin-A	1	4.3	5.2	5.6	0.8	0.77	1.30	4.3	5.2	6.3	0.8	0.69	1.45
P23949_TI	Zfp36l2	Zinc finger	1	5.6	6.7	7.3	0.8	0.77	1.30	5.6	6.7	8.2	0.8	0.69	1.45
Q80W00_F	Ppp1r10	Serine/thre	9	20.5	24.5	26.7	0.8	0.77	1.30	182.6	194.8	237.1	0.9	0.77	1.30
Q8C7V3_U	Utp15	U3 small nu	1	12.6	15.0	16.4	0.8	0.77	1.30	12.6	15.0	18.3	0.8	0.69	1.45
P36916_GI	Gnl1	Guanine nu	13	9.9	11.9	12.9	0.8	0.77	1.30	184.7	134.1	163.3	1.4	1.13	0.88
F8VQ29_F8	Iqgap3	Protein Iqg	1	6.2	7.4	8.0	0.8	0.77	1.30	6.2	7.4	9.0	0.8	0.69	1.45
Q9JIG7_CC	Ccdc22	Coiled-coil	6	6.6	7.9	8.6	0.8	0.77	1.30	38.0	53.7	65.3	0.7	0.58	1.72
Q9CZG9_PI	Pdzd11	PDZ domai	2	5.1	6.1	6.6	0.8	0.77	1.30	10.1	12.1	14.8	0.8	0.69	1.46
P33174_KI	Kif4	Chromosor	13	8.5	10.2	11.2	0.8	0.77	1.31	130.7	170.6	207.7	0.8	0.63	1.59
Q8BHD7_P	Ptbp3	Polypyrimi	11	16.0	19.1	20.9	0.8	0.76	1.31	1781.0	911.3	1109.3	2.0	1.61	0.62
Q8K363_DI	Ddx18	ATP-depen	4	16.6	19.9	21.7	0.8	0.76	1.31	75.1	78.4	95.4	1.0	0.79	1.27
Q921F2_TA	Tardbp	TAR DNA-bi	29	29.2	35.1	38.3	0.8	0.76	1.31	2538.4	4336.0	5277.6	0.6	0.48	2.08
Q9ERG2_ST	Strn3	Striatin-3 C	3	8.8	10.6	11.5	0.8	0.76	1.31	41.1	28.7	34.9	1.4	1.18	0.85
Q0P678_ZC	Zc3h18	Zinc finger	18	16.0	19.2	20.9	0.8	0.76	1.31	1162.5	478.5	582.4	2.4	2.00	0.50
Q9JHC9_EL	Elf2	ETS-related	2	7.8	9.4	10.2	0.8	0.76	1.31	15.6	18.7	22.8	0.8	0.68	1.46
Q9Z2Q2_KI	Knop1	Lysine-rich	2	7.3	8.8	9.6	0.8	0.76	1.31	14.6	17.6	21.4	0.8	0.68	1.46
Q9Z2F2_OA	Oasl2	2'-5'-oligoa	16	13.4	16.1	17.6	0.8	0.76	1.31	278.3	268.4	326.7	1.0	0.85	1.17
P70333_HI	Hnrnph2	Heterogene	4	20.2	24.3	26.6	0.8	0.76	1.32	83.0	101.8	124.0	0.8	0.67	1.49
P61963_DC	Dcaf7	DDB1- and	2	9.9	11.9	13.0	0.8	0.76	1.32	19.7	23.8	29.0	0.8	0.68	1.47
Q689Z5_SE	Sbno1	Protein stra	8	8.1	9.7	10.6	0.8	0.76	1.32	75.8	87.1	106.0	0.9	0.72	1.40
Q64282_IF	Ifit1	Interferon-i	51	28.0	33.8	36.9	0.8	0.76	1.32	2229.7	2135.9	2599.7	1.0	0.86	1.17
Q6ZWZ4_Q	Rpl36	60S ribosor	8	49.1	59.4	64.8	0.8	0.76	1.32	794.5	607.4	739.3	1.3	1.07	0.93
Q924W5_S	Smc6	Structural r	9	7.7	9.3	10.2	0.8	0.76	1.32	60.4	81.6	99.3	0.7	0.61	1.65
Q810A7_DI	Ddx42	ATP-depen	22	12.4	15.0	16.3	0.8	0.76	1.32	408.6	475.7	579.0	0.9	0.71	1.42
P62855_RS	Rps26	40S ribosor	5	41.3	50.1	54.7	0.8	0.76	1.32	1491.0	918.4	1117.9	1.6	1.33	0.75
Q9QZH3_PI	Ppie	Peptidyl-pr	5	11.0	13.4	14.6	0.8	0.76	1.32	63.3	77.0	93.7	0.8	0.68	1.48
P35293_RA	Rab18	Ras-related	5	8.5	10.3	11.2	0.8	0.76	1.32	115.8	73.6	89.6	1.6	1.29	0.77
Q9JLM8_DC	Dclk1	Serine/thre	3	10.0	12.2	13.3	0.8	0.75	1.32	25.3	33.9	41.2	0.7	0.61	1.63
Q9D7M8_F	Polr2d	DNA-direct	4	22.1	26.9	29.3	0.8	0.75	1.33	142.0	145.2	176.8	1.0	0.80	1.25
Q9Z2B9_KS	Rps6ka4	Ribosomal	1	6.2	7.6	8.3	0.8	0.75	1.33	6.2	7.6	9.2	0.8	0.68	1.48
Q99LS3_SE	Psph	Phosphose	1	11.4	13.9	15.1	0.8	0.75	1.33	11.4	13.9	16.9	0.8	0.68	1.48
O35345_IN	Kpna6	Importin su	3	4.6	5.6	6.2	0.8	0.75	1.33	13.0	20.4	24.8	0.6	0.52	1.91
P40630_TF	Tfam	Transcripti	1	4.5	5.5	6.0	0.8	0.75	1.33	4.5	5.5	6.6	0.8	0.67	1.48
Q9QWF0_C	Chaf1a	Chromatin	3	9.2	11.3	12.3	0.8	0.75	1.33	25.2	35.9	43.8	0.7	0.58	1.74
Q8C5D8_PI	Pias2	E3 SUMO-p	1	3.5	4.3	4.7	0.8	0.75	1.33	3.5	4.3	5.2	0.8	0.67	1.48
Q9CWK3_C	Cd2bp2	CD2 antige	3	7.1	8.6	9.4	0.8	0.75	1.33	24.8	25.2	30.6	1.0	0.81	1.23
Q91W92_E	Cdc42ep1	Cdc42 effec	3	4.1	5.0	5.5	0.8	0.75	1.33	13.1	14.4	17.5	0.9	0.75	1.34
Q6DFV1_CI	Ncapg2	Condensin-	8	11.4	13.9	15.2	0.8	0.75	1.33	98.9	110.5	134.6	0.9	0.73	1.36
Q9CU62_SI	Smc1a	Structural r	79	21.3	26.1	28.4	0.8	0.75	1.34	2537.1	2645.2	3219.6	1.0	0.79	1.27
Q91VX2_UI	Ubap2	Ubiquitin-a	16	9.7	11.9	12.9	0.8	0.75	1.34	197.1	322.1	392.1	0.6	0.50	1.99
P70353_NI	Nfyc	Nuclear tra	2	7.5	9.2	10.0	0.8	0.75	1.34	14.9	18.3	22.3	0.8	0.67	1.49
Q9QUR7_P	Pin1	Peptidyl-pr	5	18.8	23.0	25.1	0.8	0.75	1.34	171.6	197.3	240.1	0.9	0.71	1.40
P52479_UI	Usp10	Ubiquitin c	14	10.1	12.4	13.5	0.8	0.75	1.34	197.8	179.5	218.5	1.1	0.91	1.10
Q76KJ5_RF	Cd3eap	DNA-direct	2	4.2	5.2	5.7	0.8	0.75	1.34	8.4	10.4	12.6	0.8	0.67	1.50
Q9R190_M	Mta2	Metastasis-	17	13.8	17.0	18.5	0.8	0.75	1.34	274.0	345.5	420.6	0.8	0.65	1.54
Q9D1M0_S	Sec13	Protein SEC	4	11.8	14.5	15.8	0.8	0.74	1.34	92.3	97.8	119.0	0.9	0.78	1.29
A2A654_A2	Bptf	Protein Bpt	10	7.8	9.6	10.5	0.8	0.74	1.35	77.7	130.4	158.7	0.6	0.49	2.04
Q61466_SN	Smarcd1	SWI/SNF-re	2	11.2	13.8	15.1	0.8	0.74	1.35	22.4	27.6	33.6	0.8	0.67	1.50
Q9Z127_LA	Slc7a5	Large neutr	1	4.1	5.1	5.6	0.8	0.74	1.35	4.1	5.1	6.2	0.8	0.67	1.50
E9Q1A5_E9	Zfp384	Protein Zfp	1	10.5	13.0	14.2	0.8	0.74	1.35	10.5	13.0	15.8	0.8	0.67	1.50
Q8CHG7_R	Rapgef2	Rap guanin	2	11.6	14.3	15.6	0.8	0.74	1.35	23.2	28.7	34.9	0.8	0.67	1.50
Q6ZQ03_FN	Fnbp4	Formin-bin	3	7.4	9.2	10.0	0.8	0.74	1.35	34.8	22.5	27.4	1.5	1.27	0.79
Q8QZV7_AS	Asun	Protein asu	2	9.4	11.6	12.6	0.8	0.74	1.35	18.7	23.2	28.2	0.8	0.66	1.51
P49312_RO	Hnrnpa1	Heterogene	11	14.9	18.4	20.1	0.8	0.74	1.35	206.1	248.5	302.4	0.8	0.68	1.47
Q6ZQ88_KI	Kdm1a	Lysine-spec	14	11.5	14.2	15.5	0.8	0.74	1.35	181.4	199.4	242.7	0.9	0.75	1.34
P30415_NI	Nktr	NK-tumor r	2	7.0	8.7	9.5	0.8	0.74	1.35	14.0	17.4	21.2	0.8	0.66	1.51
P27661_H2	H2afx	Histone H2	4	64.8	80.7	88.1	0.8	0.74	1.36	254.3	340.4	414.3	0.7	0.61	1.63
Q9QWV9_C	Ccnt1	Cyclin-T1 O	4	5.4	6.7	7.3	0.8	0.73	1.36	28.2	29.1	35.4	1.0	0.80	1.26
Q60972_RI	Rbbp4	Histone-bir	14	41.4	51.8	56.5	0.8	0.73	1.36	1221.5	1025.8	1248.6	1.2	0.98	1.02
P29341_PA	Pabpc1	Polyadenyl	38	49.4	61.8	67.4	0.8	0.73	1.36	2947.7	2749.3	3346.3	1.1	0.88	1.14
Q9JM05_PI	Pias4	E3 SUMO-p	1	3.5	4.4	4.8	0.8	0.73	1.37	3.5	4.4	5.3	0.8	0.66	1.52
Q8BJ71_NU	Nup93	Nuclear poi	10	10.8	13.6	14.8	0.8	0.73	1.37	142.2	145.9	177.6	1.0	0.80	1.25
Q62241_RU	Snrpc	U1 small nu	2	9.6	12.1	13.2	0.8	0.73	1.37	19.2	24.1	29.4	0.8	0.65	1.53
P08046_EG	Egr1	Early growt	1	4.6	5.7	6.2	0.8	0.73	1.37	4.6	5.7	7.0	0.8	0.65	1.53
Q8BUK6_H	Hook3	Protein Ho	9	8.0	10.0	10.9	0.8	0.73	1.37	95.5	110.8	134.8	0.9	0.71	1.41
Q99K95_RT	Rtfdc1	Protein RTF	1	7.2	9.1	9.9	0.8	0.73	1.37	7.2	9.1	11.1	0.8	0.65	1.53
Q69ZQ2_IS	Isy1	Pre-mRNA-	3	5.6	7.0	7.6	0.8	0.73	1.37	19.3	37.9	46.1	0.5	0.42	2.39
Q8CG70_P3	Leprel2	Prolyl 3-hy	2	5.0	6.4	6.9	0.8	0.73	1.37	10.1	12.7	15.5	0.8	0.65	1.53
Q9ER00_ST	Stx12	Syntaxin-1	2	17.7	22.3	24.3	0.8	0.73	1.38	35.3	44.6	54.3	0.8	0.65	1.54
Q9Z2X1_HI	Hnrnpf	Heterogene	21	48.0	60.8	66.3	0.8	0.72	1.38	2622.9	2587.1	3149.0	1.0	0.83	1.20
Q9DCT5_SD	Sdf2	Stromal cel	2	5.2	6.6	7.2	0.8	0.72	1.38	10.4	13.1	16.0	0.8	0.65	1.54
Q9CQS9_HA	Haus2	HAUS augm	4	6.9	8.7	9.5	0.8	0.72	1.39	28.1	36.3	44.1	0.8	0.64	1.57
F8VPP8_F8	Zc3h7b	Protein Zc3	3	7.4	9.5	10.3	0.8	0.72	1.39	18.9	50.1	61.0	0.4	0.31	3.23
Q8BX10_PC	Pgam5	Serine/thre	2	8.9	11.3	12.3	0.8	0.72	1.39	17.7	22.6	27.5	0.8	0.64	1.56
Q8R4U7_LU	Luzp1	Leucine zip	8	8.7	11.2	12.2	0.8	0.72	1.39	81.0	97.3	118.5	0.8	0.68	1.46
O54825_BY	Bysl	Bystin OS=M	3	5.8	7.4	8.1	0.8	0.72	1.39	14.1	21.6	26.2	0.7	0.54	1.86
Q8C3W1_CA198_MOU		Uncharacte	2	2.0	2.5	2.7	0.8	0.72	1.40	3.9	5.0	6.1	0.8	0.64	1.56
Q3ULW8_C	Parp3	Protein Par	15	12.9	16.6	18.1	0.8	0.72	1.40	198.9	275.5	335.3	0.7	0.59	1.69
Q61235_SN	Sntb2	Beta-2-synt	3	2.4	3.1	3.3	0.8	0.72	1.40	8.9	11.3	13.7	0.8	0.65	1.54
P53762_AF	Arnt	Aryl hydroc	1	4.1	5.2	5.7	0.8	0.72	1.40	4.1	5.2	6.3	0.8	0.64	1.56
Q9QZ06_TC	Tollip	Toll-interac	2	6.5	8.4	9.1	0.8	0.71	1.40	13.1	16.8	20.4	0.8	0.64	1.56
P62830_RL	Rpl23	60S ribosor	15	20.1	25.8	28.2	0.8	0.71	1.40	3008.9	1233.9	1501.8	2.4	2.00	0.50

Q04750_T	Top1	DNA topois	14	13.1	16.8	18.3	0.8	0.71	1.40	229.4	306.2	372.7	0.7	0.62	1.63
Q9QXV1_C	Cbx8	Chromobo	4	6.3	8.0	8.8	0.8	0.71	1.40	25.6	59.6	72.6	0.4	0.35	2.84
Q60737_C	Csnk2a1	Casein kina	10	16.6	21.3	23.2	0.8	0.71	1.40	240.8	290.7	353.8	0.8	0.68	1.47
P83940_EL	Tceb1	Transcripti	3	14.4	18.5	20.2	0.8	0.71	1.40	65.3	61.7	75.1	1.1	0.87	1.15
A2A791_Z	Zmym4	Zinc finger	2	5.4	7.0	7.6	0.8	0.71	1.41	10.8	14.0	17.0	0.8	0.64	1.57
Q922S8_KI	Kif2c	Kinesin-like	1	6.8	8.7	9.5	0.8	0.71	1.41	6.8	8.7	10.6	0.8	0.64	1.57
P11928_O	Oas1a	2'-5'-oligoa	1	7.5	9.6	10.5	0.8	0.71	1.41	7.5	9.6	11.7	0.8	0.64	1.57
Q6NZF1_Z	Zc3h11a	Zinc finger	14	11.2	14.4	15.7	0.8	0.71	1.41	216.9	246.5	300.0	0.9	0.72	1.38
Q505F5_L	Lrrc47	Leucine-ric	16	13.1	17.0	18.6	0.8	0.71	1.41	285.3	323.2	393.3	0.9	0.73	1.38
Q9DBR7_M	Ppp1r12a	Protein pho	8	11.5	14.8	16.2	0.8	0.71	1.41	143.7	127.6	155.3	1.1	0.93	1.08
A0A0A6YW	Mbnl1	Muscleblin	2	8.1	10.5	11.4	0.8	0.71	1.41	16.2	21.0	25.5	0.8	0.63	1.58
Q80SU7_G	Gvin1	Interferon-	29	12.7	16.4	17.9	0.8	0.71	1.41	399.4	506.1	615.9	0.8	0.65	1.54
Q9CRC8_L	Lrrc40	Leucine-ric	11	8.1	10.5	11.4	0.8	0.71	1.41	107.3	128.5	156.4	0.8	0.69	1.46
O35075_D	Dscr3	Down synd	5	7.8	10.1	11.0	0.8	0.71	1.42	38.3	42.3	51.5	0.9	0.74	1.35
P61358_RL	Rpl27	60S riboso	4	278.2	361.1	393.9	0.8	0.71	1.42	2291.5	1545.4	1880.9	1.5	1.22	0.82
Q9R1R2_T	Trim3	Tripartite m	2	6.5	8.5	9.2	0.8	0.71	1.42	13.0	16.9	20.6	0.8	0.63	1.58
P63321_R	Rala	Ras-related	4	4.6	5.9	6.5	0.8	0.70	1.42	41.6	40.1	48.8	1.0	0.85	1.17
Q8VE10_N	Naa40	N-alpha-ace	5	3.6	4.7	5.2	0.8	0.70	1.42	28.5	45.1	54.9	0.6	0.52	1.93
Q8VE70_P	Pdcd10	Programme	4	4.6	6.0	6.5	0.8	0.70	1.42	38.5	25.6	31.2	1.5	1.24	0.81
Q8K1N2_P	Phldb2	Pleckstrin h	9	6.5	8.5	9.3	0.8	0.70	1.43	67.9	83.5	101.7	0.8	0.67	1.50
P60766_C	Cdc42	Cell divisio	3	16.4	21.4	23.3	0.8	0.70	1.43	50.8	67.7	82.4	0.8	0.62	1.62
Q5DTM8_B	Rnf20	E3 ubiquiti	9	12.1	15.8	17.3	0.8	0.70	1.43	109.2	144.3	175.7	0.8	0.62	1.61
G3X922_G	Dnajc13	MCG11560	10	7.1	9.3	10.1	0.8	0.70	1.43	75.7	106.5	129.7	0.7	0.58	1.71
Q9QWH1_	Phc2	Polyhomec	4	13.8	18.1	19.8	0.8	0.70	1.43	59.0	67.1	81.7	0.9	0.72	1.38
Q61188_E	Ezh2	Histone-lys	3	8.7	11.5	12.5	0.8	0.70	1.43	40.9	37.3	45.4	1.1	0.90	1.11
Q5RKN9_Q	Capza1	Capping pr	7	12.7	16.7	18.2	0.8	0.70	1.43	137.6	199.5	242.8	0.7	0.57	1.76
Q920Q6_M	Msi2	RNA-bindin	3	7.8	10.2	11.2	0.8	0.70	1.44	46.3	42.0	51.1	1.1	0.91	1.10
P56480_A	Atp5b	ATP syntha	6	8.4	11.1	12.1	0.8	0.70	1.44	71.2	62.4	76.0	1.1	0.94	1.07
Q9Z266_S	Snapin	SNARE-asso	4	10.8	14.3	15.5	0.8	0.70	1.44	54.7	57.6	70.1	0.9	0.78	1.28
Q6A4J8_U	Usp7	Ubiquitin c	7	7.2	9.6	10.4	0.8	0.69	1.44	80.2	54.8	66.7	1.5	1.20	0.83
Q8VEE4_R	Rpa1	Replication	27	9.0	11.9	12.9	0.8	0.69	1.44	476.0	352.9	429.5	1.3	1.11	0.90
P27048_R	Snrpb	Small nucle	11	21.0	27.7	30.3	0.8	0.69	1.44	725.5	681.4	829.4	1.1	0.87	1.14
O54956_D	Pole2	DNA polym	1	7.8	10.3	11.2	0.8	0.69	1.45	7.8	10.3	12.5	0.8	0.62	1.61
Q61216_M	Mre11a	Double-stra	10	9.8	13.0	14.2	0.8	0.69	1.45	146.3	143.4	174.6	1.0	0.84	1.19
Q62074_K	Prkci	Protein kin	7	9.2	12.3	13.4	0.8	0.69	1.45	90.5	91.3	111.1	1.0	0.82	1.23
Q9D967_M	Mdp1	Magnesium	2	11.3	15.0	16.4	0.8	0.69	1.45	22.6	30.1	36.6	0.8	0.62	1.62
P57780_A	Actn4	Alpha-actin	12	9.7	13.0	14.1	0.7	0.69	1.46	176.0	198.4	241.5	0.9	0.73	1.37
D3Z0M9_D	Ddx23	MCG18410	27	15.8	21.1	23.0	0.7	0.69	1.46	773.8	665.8	810.4	1.2	0.95	1.05
Q9QXK2_R	Rad18	E3 ubiquiti	1	3.6	4.8	5.2	0.7	0.69	1.46	3.6	4.8	5.8	0.7	0.61	1.63
O35730_R	Ring1	E3 ubiquiti	3	5.7	7.6	8.3	0.7	0.69	1.46	21.8	44.8	54.6	0.5	0.40	2.51
Q8VDD5_M	Myh9	Myosin-9 O	155	66.3	88.7	96.8	0.7	0.68	1.46	22450.4	18425.4	22426.8	1.2	1.00	1.00
Q8BHJ5_T	Tbl1xr1	F-box-like/	3	26.9	36.1	39.4	0.7	0.68	1.46	85.7	89.5	108.9	1.0	0.79	1.27
Q9DBR0_A	Akap8	A-kinase an	5	15.9	21.3	23.2	0.7	0.68	1.46	102.5	166.0	202.0	0.6	0.51	1.97
Q8VD75_H	Hip1	Huntingtin	2	5.9	7.9	8.6	0.7	0.68	1.47	11.7	15.7	19.1	0.7	0.61	1.64
P68040_G	Gnb2l1	Guanine nu	50	36.2	48.6	53.0	0.7	0.68	1.47	5110.5	3829.4	4661.1	1.3	1.10	0.91
Q8R151_Z	Znfx1	NFX1-type	3	8.7	11.7	12.7	0.7	0.68	1.47	26.3	31.6	38.5	0.8	0.68	1.46
P99027_RL	Rplp2	60S acidic	15	29.3	39.5	43.1	0.7	0.68	1.47	2585.8	2630.5	3201.8	1.0	0.81	1.24
Q9Z1B5_M	Mad2l1	Mitotic spi	1	8.1	10.9	11.9	0.7	0.68	1.47	8.1	10.9	13.3	0.7	0.61	1.64
Q6NS46_R	Pdcd11	Protein RR	22	12.6	17.0	18.5	0.7	0.68	1.47	336.7	394.9	480.6	0.9	0.70	1.43
P07356_A	Anxa2	Annexin A2	32	17.7	24.0	26.2	0.7	0.68	1.47	896.2	1199.0	1459.4	0.7	0.61	1.63
O35691_P	Pnn	Pinin OS=M	28	14.0	19.0	20.7	0.7	0.68	1.48	555.4	938.0	1141.7	0.6	0.49	2.06
Q99KY4_G	Gak	Cyclin-G-as	4	3.9	5.3	5.8	0.7	0.68	1.48	21.9	23.2	28.3	0.9	0.77	1.29
P83870_P	Phf5a	PHD finger-	2	52.3	71.0	77.4	0.7	0.68	1.48	104.6	141.9	172.8	0.7	0.61	1.65
Q7TQI3_OT	Otub1	Ubiquitin t	3	5.7	7.8	8.5	0.7	0.68	1.48	23.6	23.6	28.7	1.0	0.82	1.21
Q811S7_U	Ubp1	Upstream-	1	14.1	19.2	20.9	0.7	0.67	1.48	14.1	19.2	23.3	0.7	0.60	1.65
Q8VC70_R	Rbms2	RNA-bindin	4	21.2	28.8	31.5	0.7	0.67	1.48	95.4	120.6	146.8	0.8	0.65	1.54
Q80U70_S	Suz12	Polycomb	8	12.3	16.8	18.3	0.7	0.67	1.49	165.7	118.0	143.6	1.4	1.15	0.87
Q6ZWV3_R	Rpl10	60S riboso	15	35.4	48.3	52.7	0.7	0.67	1.49	963.9	1034.7	1259.4	0.9	0.77	1.31
P43276_H	Hist1h1b	Histone H1	16	45.8	62.5	68.2	0.7	0.67	1.49	5859.4	3276.2	3987.6	1.8	1.47	0.68
Q3U1J4_D	Ddb1	DNA damag	23	11.4	15.6	17.0	0.7	0.67	1.49	432.1	345.2	420.2	1.3	1.03	0.97
O08788_D	Dctn1	Dynactin su	43	14.0	19.2	21.0	0.7	0.67	1.49	953.8	873.3	1062.9	1.1	0.90	1.11
Q9CYR0_SS	Ssbp1	Single-stra	1	8.3	11.4	12.4	0.7	0.67	1.49	8.3	11.4	13.9	0.7	0.60	1.67
A2AGH6_M	Med12	Mediator o	3	8.6	11.8	12.8	0.7	0.67	1.49	24.2	32.2	39.2	0.7	0.62	1.62
Q6PDH0_P	Phldb1	Pleckstrin h	1	4.3	5.8	6.4	0.7	0.67	1.50	4.3	5.8	7.1	0.7	0.60	1.67
Q9QYS9_Q	Qki	Protein qua	5	9.6	13.2	14.4	0.7	0.67	1.50	61.0	76.3	92.9	0.8	0.66	1.52
Q3TIV5_ZC	Zc3h15	Zinc finger	8	12.9	17.7	19.3	0.7	0.67	1.50	180.4	181.2	220.6	1.0	0.82	1.22
E9QAP7_E	Taf4a	Protein Taf	3	8.6	11.9	12.9	0.7	0.67	1.50	29.1	44.7	54.5	0.7	0.54	1.87
Q924C6_L	Loxl4	Lysyl oxida	3	11.4	15.7	17.2	0.7	0.66	1.51	41.8	48.2	58.7	0.9	0.71	1.40
Q80XI4_PI	Pip4k2b	Phosphatid	1	2.8	3.8	4.2	0.7	0.66	1.51	2.8	3.8	4.7	0.7	0.59	1.68
Q80YQ2_M	Med23	Mediator o	6	10.0	13.9	15.1	0.7	0.66	1.51	57.4	78.1	95.0	0.7	0.60	1.66
Q9WV92_E	Epb41l3	Band 4.1-li	5	6.5	9.1	9.9	0.7	0.66	1.51	52.2	38.4	46.7	1.4	1.12	0.90
P14602_H	Hspb1	Heat shock	11	16.2	22.6	24.6	0.7	0.66	1.52	352.5	482.0	586.6	0.7	0.60	1.66
O09000_N	Ncoa3	Nuclear rec	1	2.2	3.0	3.3	0.7	0.66	1.52	2.2	3.0	3.7	0.7	0.59	1.69
A2RTL5_RS	Rsrc2	Arginine/se	7	13.9	19.4	21.2	0.7	0.66	1.52	211.0	182.3	221.8	1.2	0.95	1.05
Q8K327_C	Champ1	Chromoso	12	6.7	9.3	10.1	0.7	0.66	1.52	109.7	128.4	156.3	0.9	0.70	1.42
Q569Z5_D	Ddx46	Probable A	33	19.1	26.6	29.1	0.7	0.66	1.52	1104.9	1138.0	1385.1	1.0	0.80	1.25
Q8C156_C	Ncaph	Condensin	12	23.8	33.3	36.3	0.7	0.66	1.52	423.2	365.6	445.0	1.2	0.95	1.05
Q9Z2W0_D	Dnpep	Aspartyl am	16	13.7	19.2	20.9	0.7	0.66	1.52	350.5	353.0	429.7	1.0	0.82	1.23
Q99NB9_S	Sf3b1	Splicing fac	58	13.9	19.4	21.2	0.7	0.66	1.52	1952.0	1636.7	1992.1	1.2	0.98	1.02
Q9CSH3_R	Dis3	Exosome co	31	10.8	15.2	16.5	0.7	0.65	1.53	378.8	560.3	682.0	0.7	0.56	1.80
Q62167_D	Ddx3x	ATP-depen	57	31.7	44.4	48.5	0.7	0.65	1.53	4873.9	4248.9	5171.6	1.1	0.94	1.06
Q8BFQ4_W	Wdr82	WD repeat-	4	10.9	15.2	16.6	0.7	0.65	1.53	192.5	88.4	107.6	2.2	1.79	0.56
Q99K48_N	Nono	Non-POU d	17	22.1	31.1	33.9	0.7	0.65	1.53	560.1	733.5	892.8	0.8	0.63	1.59
Q91XU0_W	Wrnip1	ATPase WR	5	12.6	17.7	19.4	0.7	0.65	1.54	69.0	72.1	87.7	1.0	0.79	1.27
Q9ER69_FL	Wtap	Pre-mRNA-	4	7.5	10.6	11.6	0.7	0.65	1.54	31.1	43.9	53.4	0.7	0.58	1.72
Q8BIA4_FB	Fbxw8	F-box/WD	1	4.5	6.4	6.9	0.7	0.65	1.54	4.5	6.4	7.7	0.7	0.58	1.72
Q9D8Y0_E	Efhd2	EF-hand do	3	4.2	5.9	6.4	0.7	0.65	1.54	19.0	20.5	24.9	0.9	0.76	1.31
Q8CAS9_P	Parp9	Poly [ADP-	22	14.5	20.6	22.4	0.7	0.65	1.54	454.8	432.0	525.8	1.1	0.86	1.16
P19324_SE	Serpinh1	Serpin H1	68	42.9	60.7	66.2	0.7	0.65	1.54	7069.1	7325.5	8916.3	1.0	0.79	1.26
Q9EQC5_N	Scyl1	N-terminal	13	5.8	8.2	8.9	0.7	0.65	1.54	106.5	115.1	140.1	0.9	0.76	1.32
Q3UIR3_D	Dtx3l	E3 ubiquiti	12	15.9	22.5	24.6	0.7	0.65	1.55	230.1	256.1	311.7	0.9	0.74	1.35
O55101_S	Syngr2	Synaptogy	1	7.4	10.6	11.5	0.7	0.65	1.55	7.4	10.6	12.9	0.7	0.58	1.73
Q61937_N	Npm1	Nucleopho	22	14.6	20.7	22.6	0.7	0.65	1.55	882.4	769.3	936.3	1.1	0.94	1.06
P52432_R	Polr1c	DNA-direct	5	7.9	11.2	12.2	0.7	0.65	1.55	57.5	63.7	77.5	0.9	0.74	1.35
Q91YN9_B	Bag2	BAG family	4	18.5	26.4	28.8	0.7	0.64	1.55	92.9	114.6	139.5	0.8	0.67	1.50
B2RWS6_E	Ep300	Histone ace	1	15.2	21.7	23.6	0.7	0.64	1.55	15.2	21.7	26.4	0.7	0.58	1.73
Q03147_C	Cdk7	Cyclin-depe	3	7.0	10.0	10.9	0.7	0.64	1.55	15.8	32.9	40.1	0.5	0.39	2.54
P59328_W	Wdhd1	WD repeat	10	5.3	7.6	8.3	0.7	0.64	1.56	67.4	91.1	110.9	0.7	0.61	1.65
A2AJ72_A2	Fubp3	MCG13045	14	10.9	15.6	17.0	0.7	0.64	1.56	186.2	301.6	367.1	0.6	0.51	1.97
P50543_S1	S100a11	Protein S1	3	10.3	14.6	16.0	0.7	0.64	1.56	53.5	35.5	43.2	1.5	1.24	0.81
Q9CZ28_S	Snf8	Vacuolar-s	3	3.7	5.3	5.8	0.7	0.64	1.56	20.9	15.7	19.2	1.3	1.09	0.92
P70362_U	Ufd1l	Ubiquitin f	5	12.7	18.2	19.8	0.7	0.64	1.56	98.1	76.4	92.9	1.3	1.06	0.95
Q8BHN3_G	Ganab	Neutral alp	1	3.2	4.6	5.1	0.7	0.64	1.56	3.2	4.6	5.7	0.7	0.57	1.74
Q6PDM2_S	Srsf1	Serine/argi	13	50.5	72.4	79.0	0.7	0.64	1.57	660.6	1407.4	1713.1	0.5	0.39	2.59
Q91Z49_U	Fyttd1	UAP56-inte	4	10.5	15.1	16.4	0.7	0.64	1.57	46.7	60.3	73.4	0.8	0.64	1.57
Q8BXC6_C	Commd2	COMM dor	3	14.9	21.4	23.3	0.7	0.64	1.57	41.5	73.7	89.7	0.6	0.46	2.16
Q9CR11_Y	Yeats4	YEATS dom	6	6.1	8.8	9.6	0.7	0.64	1.57	60.3	52.7	64.1	1.1	0.94	1.06
P63087_P	Ppp1cc	Serine/thre	8	5.7	8.3	9.0	0.7	0.63	1.58	58.6	74.0	90.1	0.8	0.65	1.54
O35648_C	Cetn3	Centrin-3 C	3	5.7	8.2	8.9	0.7	0.63	1.58	24.7	22.1	26.9	1.1	0.92	1.09
P97310_M	Mcm2	DNA replica	92	17.1	24.7	26.9	0.7	0.63	1.58	3460.4	3608.4	4392.0	1.0	0.79	1.27
Q9D786_H	Haus5	HAUS augm	2	6.8	9.9	10.8	0.7	0.63	1.58	13.7	19.8	24.1	0.7	0.57	1.76
P97496_S	Smarcc1	SWI/SNF cc	23	12.2	17.6	19.2	0.7	0.63	1.58	372.0	674.7	821.2	0.6	0.45	2.21
O35737_H	Hnrnph1	Heterogene	20	27.8	40.3	44.0	0.7	0.63	1.58	1030.7	1853.5	2256.0	0.6	0.46	2.19

Q9ET54_PA	Palld	Palladin OS	6	6.9	10.0	10.9	0.7	0.63	1.59	54.4	60.2	73.3	0.9	0.74	1.35
O54724_PT	Ptrf	Polymerase	17	35.6	51.8	56.5	0.7	0.63	1.59	739.4	1034.2	1258.8	0.7	0.59	1.70
Q8VEM8_M	Slc25a3	Phosphate	2	8.0	11.6	12.7	0.7	0.63	1.59	16.0	23.2	28.3	0.7	0.56	1.77
E9QNF5_E9	Fmr1	Fragile X m	10	7.9	11.4	12.5	0.7	0.63	1.59	88.0	138.6	168.7	0.6	0.52	1.92
Q9JI18_LRI	Lrp1b	Low-densit	1	9.7	14.2	15.4	0.7	0.63	1.59	9.7	14.2	17.2	0.7	0.56	1.77
Q8BUH8_SI	Senp7	Sentrin-spe	1	5.0	7.3	8.0	0.7	0.63	1.59	5.0	7.3	8.9	0.7	0.56	1.77
Q9JIK5_DD	Ddx21	Nucleolar R	51	29.1	42.4	46.3	0.7	0.63	1.59	2823.6	3401.5	4140.2	0.8	0.68	1.47
Q9DC48_PI	Cdc40	Pre-mRNA-	8	9.5	13.9	15.2	0.7	0.63	1.59	73.1	107.1	130.4	0.7	0.56	1.78
Q61656_DI	Ddx5	Probable A	47	36.1	52.7	57.5	0.7	0.63	1.59	2612.8	3866.9	4706.6	0.7	0.56	1.80
Q60605_M	Myl6	Myosin ligh	14	57.1	83.6	91.2	0.7	0.63	1.60	3899.3	3654.6	4448.2	1.1	0.88	1.14
Q6PFA2_Q6	Clta	Clathrin lig	3	12.4	18.2	19.9	0.7	0.63	1.60	37.1	46.8	57.0	0.8	0.65	1.54
Q8BZH4_PC	Pogz	Pogo transp	15	12.4	18.1	19.8	0.7	0.62	1.60	173.6	276.8	336.9	0.6	0.52	1.94
O88569_RC	Hnrnpa2b1	Heterogene	26	31.2	45.8	50.0	0.7	0.62	1.60	1658.9	1762.8	2145.7	0.9	0.77	1.29
Q6PHZ2_KC	Camk2d	Calcium/ca	21	15.5	22.8	24.8	0.7	0.62	1.60	384.1	487.8	593.7	0.8	0.65	1.55
O35286_DI	Dhx15	Putative pr	34	15.8	23.3	25.4	0.7	0.62	1.61	1313.1	1100.8	1339.8	1.2	0.98	1.02
Q9D6F9_TE	Tubb4a	Tubulin bet	10	38.1	56.4	61.5	0.7	0.62	1.61	432.4	886.9	1079.5	0.5	0.40	2.50
S4R1W5_S4	Rbm6	Protein Rbr	4	7.0	10.4	11.3	0.7	0.62	1.62	27.4	42.6	51.9	0.6	0.53	1.89
Q9Z130_HI	Hnrnpdl	Heterogene	9	8.5	12.6	13.8	0.7	0.62	1.62	324.0	500.4	609.1	0.6	0.53	1.88
P24668_M	M6pr	Cation-dep	1	2.9	4.3	4.7	0.7	0.62	1.62	2.9	4.3	5.2	0.7	0.55	1.80
Q91VC3_IF	Eif4a3	Eukaryotic	31	29.0	43.1	47.1	0.7	0.62	1.62	1252.2	1997.9	2431.8	0.6	0.51	1.94
P97434_M	Mprip	Myosin pho	4	5.3	7.8	8.6	0.7	0.61	1.63	20.3	34.4	41.8	0.6	0.49	2.06
P46638_RE	Rab11b	Ras-related	10	19.7	29.7	32.3	0.7	0.61	1.64	347.3	476.2	579.6	0.7	0.60	1.67
Q8R2T8_TF	Gtf3c5	General tra	2	6.6	10.0	10.9	0.7	0.61	1.64	13.3	20.0	24.3	0.7	0.55	1.83
P33609_DI	Pola1	DNA polym	16	13.2	19.8	21.6	0.7	0.61	1.64	290.0	274.5	334.1	1.1	0.87	1.15
Q9D787_PI	Ppil2	Peptidyl-pr	7	6.8	10.2	11.2	0.7	0.61	1.64	55.9	87.4	106.4	0.6	0.53	1.90
Q60848_HI	Hells	Lymphocyt	10	13.9	21.0	22.9	0.7	0.61	1.65	160.0	215.9	262.8	0.7	0.61	1.64
Q8C854_M	Myef2	Myelin exp	33	14.4	21.7	23.6	0.7	0.61	1.65	859.9	1293.7	1574.7	0.7	0.55	1.83
Q9CQP2_TI	Trappc2	Trafficking	1	2.4	3.6	3.9	0.7	0.61	1.65	2.4	3.6	4.3	0.7	0.54	1.84
P17742_PF	Ppia	Peptidyl-pr	1	7.4	11.3	12.3	0.7	0.61	1.65	7.4	11.3	13.7	0.7	0.54	1.84
A2AMM0_I	Murc	Muscle-rela	5	7.8	11.9	12.9	0.7	0.61	1.65	44.2	72.2	87.9	0.6	0.50	1.99
Q8R2U4_N	Ntmt1	N-terminal	3	6.2	9.4	10.3	0.7	0.60	1.65	34.5	36.2	44.1	1.0	0.78	1.28
P47930_FC	Fosl2	Fos-related	2	9.7	14.7	16.0	0.7	0.60	1.66	19.3	29.4	35.8	0.7	0.54	1.85
P63017_HS	Hspa8	Heat shock	56	25.8	39.3	42.9	0.7	0.60	1.66	2679.4	3094.9	3767.0	0.9	0.71	1.41
P37889_FE	Fbln2	Fibulin-2 O	12	18.7	28.5	31.1	0.7	0.60	1.67	335.6	404.3	492.2	0.8	0.68	1.47
P62204_CA	Calm1	Calmodulin	9	8.6	13.1	14.3	0.7	0.60	1.67	213.1	272.5	331.7	0.8	0.64	1.56
Q8R015_BI	Bloc1s5	Biogenesis	3	5.2	7.9	8.6	0.7	0.60	1.67	25.6	30.8	37.4	0.8	0.68	1.46
Q9Z2N8_AC	Actl6a	Actin-like p	7	22.9	35.1	38.3	0.7	0.60	1.67	177.7	380.3	462.9	0.5	0.38	2.61
Q8R1A4_DC	Dock7	Dedicator c	15	12.1	18.6	20.3	0.7	0.60	1.68	261.7	277.2	337.3	0.9	0.78	1.29
Q91W50_C	Csde1	Cold shock	5	10.3	15.9	17.4	0.6	0.60	1.68	70.1	68.0	82.8	1.0	0.85	1.18
P97465_DC	Dok1	Docking pr	2	4.5	6.9	7.5	0.6	0.59	1.69	8.9	13.8	16.8	0.6	0.53	1.88
Q9D8X5_CI	Cnot8	CCR4-NOT t	1	5.7	8.8	9.6	0.6	0.59	1.69	5.7	8.8	10.7	0.6	0.53	1.88
O89079_CC	Cope	Coatomer s	6	10.9	16.8	18.3	0.6	0.59	1.69	55.6	112.6	137.0	0.5	0.41	2.46
Q00417_TC	Tcf7	Transcripti	1	1.4	2.2	2.4	0.6	0.59	1.69	1.4	2.2	2.7	0.6	0.53	1.89
Q99J95_CD	Cdk9	Cyclin-depe	6	5.8	9.0	9.9	0.6	0.59	1.69	49.8	50.6	61.6	1.0	0.81	1.24
P42669_PU	Pura	Transcripti	13	13.4	20.7	22.6	0.6	0.59	1.69	272.7	528.0	642.7	0.5	0.42	2.36
Q3URQ0_TI	Tex10	Testis-expre	7	6.5	10.1	11.0	0.6	0.59	1.69	50.1	73.2	89.1	0.7	0.56	1.78
P29391_FR	Ftl1	Ferritin ligh	1	2.2	3.4	3.7	0.6	0.59	1.70	2.2	3.4	4.2	0.6	0.53	1.89
Q6ZWQ9_C	Myl12a	MCG5400 (	12	34.9	54.3	59.3	0.6	0.59	1.70	1158.1	2475.9	3013.5	0.5	0.38	2.60
Q9WTK5_N	Nfkb2	Nuclear fac	6	6.4	10.0	10.9	0.6	0.59	1.70	36.0	65.1	79.3	0.6	0.45	2.20
Q6PDQ2_C	Chd4	Chromodo	82	14.0	21.8	23.8	0.6	0.59	1.70	2175.2	2699.5	3285.8	0.8	0.66	1.51
Q5FWK3_R	Arhgap1	Rho GTPase	6	7.6	11.8	12.8	0.6	0.59	1.70	68.7	87.0	105.9	0.8	0.65	1.54
Q8BH78_Q	Rtn4	RTN4 OS=M	7	11.9	18.6	20.3	0.6	0.59	1.70	177.1	195.2	237.6	0.9	0.75	1.34
Q9ESV0_DI	Ddx24	ATP-depend	2	5.5	8.6	9.4	0.6	0.59	1.70	11.0	17.3	21.0	0.6	0.53	1.90
Q9DB42_ZI	Znf593	Zinc finger	1	7.2	11.2	12.2	0.6	0.59	1.70	7.2	11.2	13.6	0.6	0.53	1.90
P58468_F2	Fam207a	Protein FAN	2	6.6	10.4	11.3	0.6	0.59	1.71	13.2	20.7	25.2	0.6	0.53	1.90
Q6P4S8_IN	Ints1	Integrator c	4	7.5	11.7	12.8	0.6	0.59	1.71	30.2	46.2	56.2	0.7	0.54	1.86
B2M1R6_B	Hnrnpk	Heterogene	57	33.9	53.1	57.9	0.6	0.59	1.71	8267.2	7792.8	9485.2	1.1	0.87	1.15
Q9JKP8_CH	Chrac1	Chromatin	2	15.4	24.2	26.4	0.6	0.58	1.71	30.8	48.4	58.9	0.6	0.52	1.91
G5E8R1_G5	Tpm1	Tropomyos	15	27.3	42.8	46.7	0.6	0.58	1.71	1041.3	767.9	934.7	1.4	1.11	0.90
P61164_AC	Actr1a	Alpha-centr	4	8.9	14.1	15.3	0.6	0.58	1.71	48.1	70.3	85.6	0.7	0.56	1.78
Q8K019_BC	Bclaf1	Bcl-2-assoc	22	12.0	18.8	20.5	0.6	0.58	1.72	462.5	740.4	901.2	0.6	0.51	1.95
Q8VE97_SR	Srsf4	Serine/argi	9	24.3	38.3	41.8	0.6	0.58	1.72	281.6	655.8	798.3	0.4	0.35	2.84
P52480_KF	Pkm	Pyruvate ki	5	9.0	14.2	15.5	0.6	0.58	1.72	57.6	55.1	67.0	1.0	0.86	1.16
Q00PI9_HN	Hnrnpul2	Heterogene	28	17.8	28.0	30.5	0.6	0.58	1.72	834.5	1140.9	1388.7	0.7	0.60	1.66
Q8R081_HI	Hnrnpl	Heterogene	27	15.3	24.2	26.5	0.6	0.58	1.72	754.8	797.2	970.3	0.9	0.78	1.29
Q9EQM6_D	Dgcr8	Microproce	1	10.2	16.0	17.5	0.6	0.58	1.72	10.2	16.0	19.5	0.6	0.52	1.92
P30051_TE	Tead1	Transcripti	1	12.7	20.0	21.9	0.6	0.58	1.73	12.7	20.0	24.4	0.6	0.52	1.93
Q62318_TI	Trim28	Transcripti	68	21.5	34.1	37.2	0.6	0.58	1.73	3454.4	4822.3	5869.5	0.7	0.59	1.70
Q8CH18_CC	Ccar1	Cell divisior	11	9.0	14.2	15.5	0.6	0.58	1.73	169.3	200.8	244.4	0.8	0.69	1.44
Q9JLB0_MI	Mpp6	MAGUK p5	7	5.7	9.0	9.8	0.6	0.58	1.73	74.6	60.9	74.1	1.2	1.01	0.99
Q8K298_AI	Anln	Actin-bindi	13	7.7	12.3	13.4	0.6	0.58	1.73	106.8	161.8	196.9	0.7	0.54	1.84
Q9ERG0_LI	Lima1	LIM domair	10	9.6	15.3	16.7	0.6	0.58	1.74	115.3	168.9	205.6	0.7	0.56	1.78
Q9Z2D6_M	Mecp2	Methyl-CpG	9	9.3	14.8	16.1	0.6	0.58	1.74	102.8	148.2	180.4	0.7	0.57	1.75
Q8C7I4_Q8	Apol9b	Protein Apo	4	15.1	24.0	26.2	0.6	0.58	1.74	65.0	121.3	147.6	0.5	0.44	2.27
Q810D6_G	Grwd1	Glutamate-	6	6.9	11.0	12.0	0.6	0.58	1.74	74.4	72.2	87.8	1.0	0.85	1.18
P56399_UI	Usp5	Ubiquitin c	7	8.2	13.1	14.3	0.6	0.58	1.74	65.2	86.0	104.6	0.8	0.62	1.60
Q9Z277_BA	Baz1b	Tyrosine-pr	63	12.9	20.7	22.5	0.6	0.57	1.74	1113.1	1479.8	1801.2	0.8	0.62	1.62
O08582_GT	Gtpbp1	GTP-bindin	7	9.0	14.4	15.7	0.6	0.57	1.74	149.5	87.5	106.5	1.7	1.40	0.71
B2RY56_RE	Rbm25	RNA-bindin	15	11.8	18.8	20.5	0.6	0.57	1.74	298.6	485.4	590.8	0.6	0.51	1.98
B1ARD6_B1	Slfn9	Protein Slfn	7	9.5	15.2	16.6	0.6	0.57	1.74	458.5	118.2	143.8	3.9	3.19	0.31
P15066_JU	Jund	Transcripti	2	6.3	10.1	11.1	0.6	0.57	1.75	12.7	20.3	24.7	0.6	0.51	1.95
Q9QXS1_PI	Plec	Plectin OS=	14	4.9	7.8	8.5	0.6	0.57	1.75	100.1	157.4	191.6	0.6	0.52	1.91
Q3UM18_L	Lsg1	Large subur	2	6.6	10.6	11.6	0.6	0.57	1.75	13.3	21.3	25.9	0.6	0.51	1.95
Q9D6T0_N	Nosip	Nitric oxide	2	10.4	16.7	18.3	0.6	0.57	1.75	20.9	33.5	40.8	0.6	0.51	1.95
Q5U4D9_TI	Thoc6	THO compl	5	9.3	15.0	16.4	0.6	0.57	1.75	87.5	62.7	76.3	1.4	1.15	0.87
Q64127_TI	Trim24	Transcripti	2	5.0	8.0	8.7	0.6	0.57	1.75	10.0	16.0	19.5	0.6	0.51	1.96
E9QNN1_E9	Dhx9	ATP-depend	88	35.7	57.4	62.6	0.6	0.57	1.75	4877.1	7894.6	9609.0	0.6	0.51	1.97
P32067_LA	Ssb	Lupus La pr	16	19.9	32.0	34.9	0.6	0.57	1.75	691.1	616.9	750.8	1.1	0.92	1.09
Q8C7B6_FX	Fbxl22	F-box and l	1	9.8	15.8	17.2	0.6	0.57	1.76	9.8	15.8	19.2	0.6	0.51	1.96
Q9JIG8_PR	Praf2	PRA1 family	2	4.7	7.6	8.3	0.6	0.57	1.76	9.5	15.3	18.6	0.6	0.51	1.96
P62267_RS	Rps23	40S riboson	8	26.3	42.5	46.4	0.6	0.57	1.76	2896.4	1272.4	1548.7	2.3	1.87	0.53
P52912_TI	Tia1	Nucleolysin	4	13.8	22.4	24.4	0.6	0.57	1.76	102.7	94.8	115.4	1.1	0.89	1.12
Q91VN6_D	Ddx41	Probable A	11	8.4	13.6	14.8	0.6	0.57	1.77	109.4	146.7	178.6	0.7	0.61	1.63
Q01320_TC	Top2a	DNA topois	50	14.8	24.0	26.2	0.6	0.56	1.77	1326.8	1756.6	2138.1	0.8	0.62	1.61
Q8R1B4_EI	Eif3c	Eukaryotic	27	15.4	25.1	27.4	0.6	0.56	1.77	803.6	623.6	759.0	1.3	1.06	0.94
Q9D824_FI	Fip1l1	Pre-mRNA 3	18	10.0	16.3	17.7	0.6	0.56	1.78	271.4	411.4	500.8	0.7	0.54	1.85
Q3TWW8_S	Srsf6	Serine/argi	8	22.2	36.2	39.5	0.6	0.56	1.78	253.0	446.5	543.5	0.6	0.47	2.15
Q6P5E4_UC	Uggt1	UDP-glucos	80	14.6	23.9	26.0	0.6	0.56	1.78	1997.1	2228.8	2712.8	0.9	0.74	1.36
Q9CQW1_Y	Ykt6	Synaptobre	3	4.9	8.1	8.8	0.6	0.56	1.78	15.5	33.4	40.6	0.5	0.38	2.62
Q8C5L3_CN	Cnot2	CCR4-NOT t	6	5.1	8.3	9.1	0.6	0.56	1.78	32.4	64.8	78.9	0.5	0.41	2.43
Q04690_NI	Nf1	Neurofibro	2	3.3	5.5	5.9	0.6	0.56	1.78	6.7	10.9	13.3	0.6	0.50	1.99
Q8CCF0_PF	Prpf31	U4/U6 sma	17	13.1	21.4	23.3	0.6	0.56	1.78	427.2	379.4	461.8	1.1	0.93	1.08
Q3UXZ9_KI	Kdm5a	Lysine-spec	3	6.8	11.2	12.2	0.6	0.56	1.78	27.5	43.2	52.6	0.6	0.52	1.92
Q60520_SI	Sin3a	Paired amp	9	5.6	9.1	9.9	0.6	0.56	1.79	77.9	74.8	91.0	1.0	0.86	1.17
P23927_CF	Cryab	Alpha-cryst	1	8.3	13.6	14.9	0.6	0.56	1.79	8.3	13.6	16.6	0.6	0.50	1.99
P35564_CA	Canx	Calnexin OS	5	10.8	17.6	19.3	0.6	0.56	1.79	72.9	84.3	102.6	0.9	0.71	1.41
Q9R0X0_M	Med20	Mediator o	2	10.4	17.0	18.6	0.6	0.56	1.79	20.7	34.0	41.4	0.6	0.50	2.00
P51655_GI	Gpc4	Glypican-4	4	4.7	7.8	8.5	0.6	0.56	1.79	21.1	41.9	51.0	0.5	0.41	2.41
Q6P9P6_KI	Kif11	Kinesin-like	13	6.9	11.4	12.5	0.6	0.56	1.80	102.9	189.6	230.8	0.5	0.45	2.24
Q99LC2_CS	Cstf1	Cleavage sti	4	5.0	8.2	8.9	0.6	0.56	1.80	34.8	34.2	41.6	1.0	0.84	1.20
P35601_RF	Rfc1	Replication	21	11.9	19.5	21.3	0.6	0.56	1.80	401.6	565.4	688.2	0.7	0.58	1.71
P61924_CC	Copz1	Coatomer s	4	46.5	77.0	84.1	0.6	0.55	1.81	280.0	386.2	470.1	0.7	0.60	1.68
Q91YE7_RE	Rbm5	RNA-bindin	5	7.8	12.9	14.1	0.6	0.55	1.81	223.2	109.9	133.8	2.0	1.67	0.60

Q8VIJ6_SFF	Sfpq	Splicing fac	11	25.6	42.5	46.4	0.6	0.55	1.81	429.5	461.5	561.7	0.9	0.76	1.31
Q05CL8_LA	Larp7	La-related p	11	10.8	17.9	19.6	0.6	0.55	1.82	227.3	206.3	251.1	1.1	0.91	1.10
Q9CQZ1_HS	Hsbp1	Heat shock	1	2.6	4.3	4.7	0.6	0.55	1.82	2.6	4.3	5.2	0.6	0.49	2.03
Q8BTW3_E	Exosc6	Exosome cc	3	4.6	7.7	8.4	0.6	0.55	1.82	21.6	22.1	27.0	1.0	0.80	1.25
Q60953_PI	Pml	Protein PM	10	7.5	12.5	13.6	0.6	0.55	1.82	79.5	136.5	166.1	0.6	0.48	2.09
Q99PL6_UI	Ubxn6	UBX domai	3	7.5	12.5	13.7	0.6	0.55	1.83	36.2	27.8	33.8	1.3	1.07	0.93
E9PYH6_E9	Setd1a	Protein Set	7	6.5	11.0	12.0	0.6	0.55	1.83	66.1	94.4	114.9	0.7	0.58	1.74
Q60596_XI	Xrcc1	DNA repair	5	12.5	21.0	22.9	0.6	0.55	1.83	77.4	105.2	128.0	0.7	0.60	1.65
Q9DCD2_S	Xab2	Pre-mRNA-	14	7.9	13.2	14.4	0.6	0.55	1.83	126.1	174.2	212.1	0.7	0.59	1.68
Q921J4_UE	Ube2s	Ubiquitin-c	3	4.4	7.4	8.1	0.6	0.55	1.83	16.6	31.9	38.8	0.5	0.43	2.33
Q8BG81_PI	Poldip3	Polymerase	8	9.8	16.5	18.0	0.6	0.54	1.84	123.0	133.8	162.8	0.9	0.76	1.32
Q9CQD1_R	Rab5a	Ras-related	3	15.7	26.5	28.9	0.6	0.54	1.84	77.7	86.4	105.2	0.9	0.74	1.35
Q9CZH3_PS	Psmg3	Proteasom	1	1.7	2.9	3.2	0.6	0.54	1.84	1.7	2.9	3.5	0.6	0.49	2.05
Q7TQK1_IN	Ints7	Integrator c	3	5.7	9.6	10.5	0.6	0.54	1.84	23.6	25.4	30.9	0.9	0.76	1.31
Q62093_SF	Srsf2	Serine/argi	4	22.5	38.1	41.6	0.6	0.54	1.84	94.7	187.9	228.7	0.5	0.41	2.42
P60335_PC	Pcbp1	Poly(rC)-bir	28	19.8	33.8	36.9	0.6	0.54	1.86	1880.5	1973.7	2402.3	1.0	0.78	1.28
Q8BP48_M	Metap1	Methionine	2	7.0	11.9	13.0	0.6	0.54	1.86	14.0	23.8	29.0	0.6	0.48	2.07
Q3U319_BI	Rnf40	E3 ubiquiti	4	6.4	11.0	12.0	0.6	0.53	1.87	26.5	43.7	53.3	0.6	0.50	2.01
P26369_U2	U2af2	Splicing fac	8	13.6	23.4	25.5	0.6	0.53	1.88	244.6	221.2	269.2	1.1	0.91	1.10
Q99L20_Q9	Gstt3	Glutathion	1	2.1	3.6	3.9	0.6	0.53	1.88	2.1	3.6	4.4	0.6	0.48	2.09
A6H8H2_D	Dennd4c	DENN doma	2	12.5	21.6	23.5	0.6	0.53	1.88	25.1	43.2	52.5	0.6	0.48	2.09
P62915_TF	Gtf2b	Transcripti	9	5.4	9.4	10.2	0.6	0.53	1.88	82.5	82.3	100.1	1.0	0.82	1.21
Q8BNY6_N	Ncs1	Neuronal ca	1	6.2	10.8	11.7	0.6	0.53	1.88	6.2	10.8	13.1	0.6	0.48	2.10
Q8BMC4_N	Nop9	Nucleolar p	4	6.1	10.6	11.6	0.6	0.53	1.89	36.7	52.1	63.4	0.7	0.58	1.73
Q8BP92_RC	Rcn2	Reticulocal	4	4.5	7.8	8.5	0.6	0.53	1.89	38.7	40.1	48.7	1.0	0.79	1.26
Q61164_CT	Ctcf	Transcripti	4	15.2	26.3	28.7	0.6	0.53	1.89	75.9	97.7	118.9	0.8	0.64	1.57
Q6ZQ73_CA	Cand2	Cullin-asso	2	7.1	12.3	13.4	0.6	0.53	1.89	14.1	24.5	29.9	0.6	0.47	2.11
Q8R3B7_BI	Brd8	Bromodom	2	5.0	8.7	9.5	0.6	0.53	1.90	10.0	17.5	21.3	0.6	0.47	2.12
P97311_M	Mcm6	DNA replica	62	21.3	37.1	40.5	0.6	0.53	1.90	2424.2	3195.0	3888.9	0.8	0.62	1.60
Q9D6Z1_N	Nop56	Nucleolar p	23	9.2	16.2	17.7	0.6	0.52	1.91	355.9	414.4	504.4	0.9	0.71	1.42
Q9CQJ4_RI	Rnf2	E3 ubiquiti	3	10.5	18.3	20.0	0.6	0.52	1.91	42.5	47.1	57.3	0.9	0.74	1.35
P61967_AF	Ap1s1	AP-1 compl	2	7.7	13.5	14.7	0.6	0.52	1.92	15.3	27.0	32.8	0.6	0.47	2.14
P11440_CI	Cdk1	Cyclin-depe	28	12.6	22.2	24.2	0.6	0.52	1.92	563.0	979.5	1192.3	0.6	0.47	2.12
Q99JR5_TII	Tinagl1	Tubulointe	1	5.4	9.5	10.3	0.6	0.52	1.92	5.4	9.5	11.5	0.6	0.47	2.14
P49718_M	Mcm5	DNA replica	73	15.6	27.5	30.0	0.6	0.52	1.93	3145.7	3600.2	4382.0	0.9	0.72	1.39
Q8VD24_ZC	Zcchc18	Zinc finger	1	22.1	39.1	42.7	0.6	0.52	1.93	22.1	39.1	47.6	0.6	0.46	2.15
P63001_RA	Rac1	Ras-related	1	8.3	14.6	16.0	0.6	0.52	1.93	8.3	14.6	17.8	0.6	0.46	2.16
Q2YDW2_M	Msto1	Protein mis	6	6.0	10.6	11.5	0.6	0.52	1.94	38.0	64.0	77.9	0.6	0.49	2.05
Q61879_M	Myh10	Myosin-10	125	34.2	60.6	66.1	0.6	0.52	1.94	9296.0	10573.1	12869.2	0.9	0.72	1.38
Q69Z99_ZN	Znf512	Zinc finger	8	5.5	9.9	10.8	0.6	0.52	1.94	80.9	130.5	158.8	0.6	0.51	1.96
Q91ZW3_S	Smarca5	SWI/SNF-re	72	23.9	42.5	46.3	0.6	0.52	1.94	2650.1	3556.7	4329.0	0.7	0.61	1.63
G5E870_TR	Trip12	E3 ubiquiti	19	8.5	15.1	16.5	0.6	0.51	1.94	314.4	349.3	425.2	0.9	0.74	1.35
P49717_M	Mcm4	DNA replica	48	14.8	26.4	28.8	0.6	0.51	1.95	1616.3	2271.3	2764.5	0.7	0.58	1.71
Q9CYI4_LU	Luc7l	Putative RN	4	16.9	30.2	33.0	0.6	0.51	1.95	147.9	210.9	256.6	0.7	0.58	1.74
Q3TJD7_PD	Pdlim7	PDZ and LIN	13	7.4	13.3	14.5	0.6	0.51	1.95	148.5	216.4	263.4	0.7	0.56	1.77
P83887_TE	Tubg1	Tubulin gar	9	4.8	8.7	9.5	0.6	0.51	1.96	54.7	74.9	91.1	0.7	0.60	1.67
Q9Z0Y1_DC	Dctn3	Dynactin su	7	24.1	43.4	47.3	0.6	0.51	1.96	399.3	314.1	382.3	1.3	1.04	0.96
Q8CIM8_IN	Ints4	Integrator c	6	4.2	7.6	8.3	0.6	0.51	1.96	43.5	40.5	49.3	1.1	0.88	1.13
D3Z4Z0_D3	Tada2b	MCG49644	1	2.9	5.2	5.7	0.6	0.51	1.96	2.9	5.2	6.4	0.6	0.46	2.19
Q80WQ2_V	Vac14	Protein VAC	5	16.8	30.2	33.0	0.6	0.51	1.96	256.8	142.6	173.6	1.8	1.48	0.68
O70306_TE	Tbx15	T-box trans	1	3.5	6.2	6.8	0.6	0.51	1.97	3.5	6.2	7.6	0.6	0.46	2.19
E9PWW9_I	Rsf1	Protein Rsf	12	10.3	18.6	20.3	0.6	0.51	1.97	162.6	247.0	300.7	0.7	0.54	1.85
Q9CQB2_F	Fam195a	Protein FAM	1	3.4	6.1	6.7	0.6	0.51	1.97	3.4	6.1	7.5	0.6	0.46	2.20
O35218_CI	Cpsf2	Cleavage ar	11	6.3	11.4	12.5	0.6	0.51	1.97	93.3	122.7	149.3	0.8	0.62	1.60
Q7TPM1_P	Prrc2b	Protein PRI	1	5.3	9.6	10.4	0.6	0.51	1.98	5.3	9.6	11.6	0.6	0.45	2.21
Q6PGL7_FA	Fam21	WASH com	11	5.6	10.2	11.2	0.5	0.50	1.98	96.6	100.2	121.9	1.0	0.79	1.26
Q9CWG9_E	Bloc1s2	Biogenesis	1	6.1	11.0	12.0	0.5	0.50	1.98	6.1	11.0	13.4	0.5	0.45	2.21
Q61749_EI	Eif2b4	Translation	11	5.7	10.5	11.4	0.5	0.50	1.99	72.3	132.6	161.4	0.5	0.45	2.23
P46935_NI	Nedd4	E3 ubiquiti	17	7.0	12.7	13.9	0.5	0.50	2.00	184.2	219.3	266.9	0.8	0.69	1.45
Q8K2T8_PA	Paf1	RNA polym	5	11.3	20.7	22.6	0.5	0.50	2.00	88.0	100.5	122.3	0.9	0.72	1.39
Q02248_CT	Ctnnb1	Catenin bet	2	5.1	9.4	10.2	0.5	0.50	2.01	10.2	18.8	22.9	0.5	0.45	2.24
A2A6A1_GI	Gpatch8	G patch doi	3	9.7	17.9	19.5	0.5	0.50	2.01	29.6	56.9	69.3	0.5	0.43	2.34
P70255_NI	Nfic	Nuclear fac	4	3.1	5.7	6.2	0.5	0.50	2.01	16.9	20.1	24.5	0.8	0.69	1.45
Q9D0D5_T	Gtf2e1	General tra	3	4.7	8.6	9.4	0.5	0.50	2.01	13.6	31.6	38.5	0.4	0.35	2.82
Q61286_HT	Tcf12	Transcripti	2	4.3	7.9	8.6	0.5	0.50	2.01	8.5	15.8	19.2	0.5	0.44	2.25
A2BDX0_A	Adnp	Activity-de	21	7.9	14.6	16.0	0.5	0.50	2.02	208.0	390.1	474.9	0.5	0.44	2.28
Q60865_CA	Caprin1	Caprin-1 OS	23	20.1	37.4	40.8	0.5	0.49	2.03	1077.8	1297.9	1579.7	0.8	0.68	1.47
Q9D0B6_PI	Pbdc1	Protein PBI	5	10.1	18.8	20.5	0.5	0.49	2.03	105.8	80.5	98.0	1.3	1.08	0.93
Q99J62_RF	Rfc4	Replication	16	14.7	27.4	29.9	0.5	0.49	2.03	438.4	521.1	634.3	0.8	0.69	1.45
Q9CQE6_AS	Asf1a	Histone cha	2	3.2	6.0	6.5	0.5	0.49	2.03	6.4	12.0	14.6	0.5	0.44	2.26
Q99K30_ES	Eps8l2	Epidermal g	6	5.1	9.6	10.4	0.5	0.49	2.03	46.4	47.4	57.7	1.0	0.80	1.24
P70372_EL	Elavl1	ELAV-like pı	17	30.8	57.3	62.6	0.5	0.49	2.03	1507.8	1529.6	1861.7	1.0	0.81	1.23
Q9WVM1_I	Racgap1	Rac GTPase	2	4.1	7.7	8.4	0.5	0.49	2.03	8.2	15.4	18.7	0.5	0.44	2.27
Q6PE01_SN	Snrnp40	U5 small nu	10	13.9	25.9	28.2	0.5	0.49	2.03	213.7	288.1	350.7	0.7	0.61	1.64
Q9CYI0_NJMU_MOUSE		Protein Njn	1	1.8	3.3	3.6	0.5	0.49	2.04	1.8	3.3	4.1	0.5	0.44	2.27
Q64213_SF	Sf1	Splicing fac	8	5.7	10.8	11.7	0.5	0.49	2.05	52.2	95.4	116.1	0.5	0.45	2.22
Q61881_M	Mcm7	DNA replica	78	27.7	52.0	56.7	0.5	0.49	2.05	3280.5	5027.9	6119.7	0.7	0.54	1.87
Q07813_BA	Bax	Apoptosis r	4	9.5	17.8	19.4	0.5	0.49	2.05	38.6	76.0	92.5	0.5	0.42	2.40
Q69ZR9_F2	Fam208a	Protein FAM	3	7.1	13.4	14.6	0.5	0.49	2.06	27.0	40.6	49.4	0.7	0.55	1.83
P13864_DI	Dnmt1	DNA (cytosi	52	21.4	40.4	44.1	0.5	0.49	2.06	1661.3	3104.7	3778.9	0.5	0.44	2.27
Q9CY97_SS	Ssu72	RNA polym	2	3.5	6.5	7.1	0.5	0.49	2.06	6.9	13.1	15.9	0.5	0.44	2.30
Q8CFI7_RP	Polr2b	DNA-direct	29	11.7	22.1	24.1	0.5	0.49	2.06	448.3	679.5	827.0	0.7	0.54	1.84
Q8BFQ8_PI	Pddc1	Parkinson c	3	8.5	16.0	17.5	0.5	0.49	2.06	50.8	42.5	51.8	1.2	0.98	1.02
Q8VDN2_A	Atp1a1	Sodium/po	9	7.2	13.6	14.8	0.5	0.48	2.06	101.8	137.4	167.3	0.7	0.61	1.64
Q9CQJ2_PI	Pih1d1	PIH1 doma	3	10.3	19.6	21.4	0.5	0.48	2.06	47.2	65.1	79.2	0.7	0.60	1.68
P47757_CA	Capzb	F-actin-cap	11	9.6	18.2	19.8	0.5	0.48	2.07	343.9	272.2	331.4	1.3	1.04	0.96
D3Z5T8_D3	4930407I1	Protein 493	1	13.1	24.8	27.0	0.5	0.48	2.07	13.1	24.8	30.2	0.5	0.43	2.31
O70318_E4	Epb41l2	Band 4.1-lil	18	8.7	16.6	18.1	0.5	0.48	2.07	315.3	310.8	378.3	1.0	0.83	1.20
G3X9W0_G	Hnrnpd	Heterogene	1	8.4	16.0	17.5	0.5	0.48	2.07	8.4	16.0	19.5	0.5	0.43	2.31
P57784_RU	Snrpa1	U2 small nu	10	12.3	23.4	25.5	0.5	0.48	2.07	155.2	187.4	228.1	0.8	0.68	1.47
Q7TMM9_T	Tubb2a	Tubulin bet	97	34.5	65.6	71.6	0.5	0.48	2.07	6125.6	10294.4	12530.0	0.6	0.49	2.05
Q61990_PC	Pcbp2	Poly(rC)-bir	16	11.1	21.1	23.0	0.5	0.48	2.07	1378.5	1156.8	1408.0	1.2	0.98	1.02
Q925H1_TI	Trps1	Zinc finger	1	7.7	14.6	15.9	0.5	0.48	2.08	7.7	14.6	17.7	0.5	0.43	2.32
Q61142_SF	Spin1	Spindlin-1	4	5.7	10.9	11.8	0.5	0.48	2.08	124.0	45.2	55.0	2.7	2.25	0.44
P63325_RS	Rps10	40S riboson	9	51.7	98.5	107.5	0.5	0.48	2.08	2171.7	1534.7	1868.0	1.4	1.16	0.86
Q91VJ5_PC	Pqbp1	Polyglutam	1	1.5	2.9	3.2	0.5	0.48	2.08	1.5	2.9	3.5	0.5	0.43	2.32
Q9QXK3_CO	Copg2	Coatomer s	5	4.4	8.5	9.3	0.5	0.48	2.08	33.9	46.0	55.9	0.7	0.61	1.65
Q61545_EV	Ewsr1	RNA-bindin	5	10.3	19.6	21.4	0.5	0.48	2.09	105.9	170.0	206.9	0.6	0.51	1.95
Q8K221_AI	Arfip2	Arfaptin-2	1	6.3	12.1	13.2	0.5	0.48	2.09	6.3	12.1	14.7	0.5	0.43	2.33
Q9D0F4_NI	Nkap	NF-kappa-B	4	7.2	13.8	15.1	0.5	0.48	2.09	36.9	56.4	68.6	0.7	0.54	1.86
Q9D8N2_FA	Fam45a	Protein FAM	4	4.9	9.4	10.3	0.5	0.48	2.09	20.4	33.3	40.5	0.6	0.50	1.99
Q8R3C6_RI	Rbm19	Probable RI	7	7.6	14.5	15.8	0.5	0.48	2.09	58.7	90.6	110.3	0.6	0.53	1.88
Q3TJZ6_FA	Fam98a	Protein FAM	8	8.1	15.6	17.0	0.5	0.48	2.09	94.6	149.2	181.6	0.6	0.52	1.92
Q9JIX8_ACI	Acin1	Apoptotic c	28	18.0	34.5	37.6	0.5	0.48	2.09	634.4	1080.9	1315.6	0.6	0.48	2.07
A2RSX9_A2	Arfip1	Arfip1 prot	2	9.2	17.7	19.3	0.5	0.48	2.10	18.4	35.3	43.0	0.5	0.43	2.34
Q9R020_ZF	Zranb2	Zinc finger	14	7.6	14.7	16.0	0.5	0.48	2.10	208.0	566.9	690.0	0.4	0.30	3.32
Q9CY66_GA	Gar1	H/ACA ribo	1	4.5	8.6	9.4	0.5	0.48	2.10	4.5	8.6	10.5	0.5	0.43	2.34
P47856_GI	Gfpt1	Glutamine-	29	9.6	18.5	20.1	0.5	0.48	2.10	504.6	526.4	640.7	1.0	0.79	1.27
Q8BUI3_LR	LRWD1	Leucine-ric	1	3.9	7.6	8.3	0.5	0.48	2.10	3.9	7.6	9.2	0.5	0.43	2.35
Q3UFF7_LY	Lyplal1	Lysophospl	1	2.5	4.9	5.3	0.5	0.47	2.11	2.5	4.9	5.9	0.5	0.42	2.36
Q99K74_M	Med24	Mediator o	7	4.8	9.3	10.1	0.5	0.47	2.11	55.4	68.6	83.5	0.8	0.66	1.51
P09055_ITI	Itgb1	Integrin bet	10	8.9	17.4	18.9	0.5	0.47	2.12	158.4	198.5	241.6	0.8	0.66	1.53
P20029_GI	Hspa5	78 kDa gluc	30	20.8	40.5	44.2	0.5	0.47	2.12	823.0	1592.2	1937.9	0.5	0.42	2.35

Q922F4_TE	Tubb6	Tubulin bet	21	10.3	20.0	21.8	0.5	0.47	2.12	326.2	411.4	500.7	0.8	0.65	1.54
O88322_NI	Nid2	Nidogen-2 (	1	2.1	4.1	4.5	0.5	0.47	2.13	2.1	4.1	5.0	0.5	0.42	2.37
Q99M28_R	Rnps1	RNA-bindir	12	14.1	27.5	30.0	0.5	0.47	2.13	283.7	430.5	524.0	0.7	0.54	1.85
E9Q7G0_E9	Numa1	Protein Nu	128	14.2	27.8	30.4	0.5	0.47	2.14	3329.9	5545.7	6750.0	0.6	0.49	2.03
E9Q1P8_I2	Irf2bp2	Interferon r	3	9.6	18.8	20.5	0.5	0.47	2.14	25.2	50.0	60.8	0.5	0.41	2.41
Q64475_H1	Hist1h2bb	Histone H2	50	65.1	128.0	139.7	0.5	0.47	2.15	25628.9	46575.2	56689.8	0.6	0.45	2.21
Q0VBL3_Q(	Rbm15	Protein Rbr	8	5.5	10.9	11.9	0.5	0.47	2.15	53.3	97.0	118.1	0.5	0.45	2.22
Q8C1S0_M	Med19	Mediator o	2	7.0	13.7	15.0	0.5	0.47	2.15	14.0	27.5	33.5	0.5	0.42	2.40
Q9CQ80_VI	Vps25	Vacuolar pr	1	1.7	3.3	3.7	0.5	0.46	2.16	1.7	3.3	4.1	0.5	0.42	2.41
Q91WG4_E	Elp2	Elongator c	2	4.2	8.4	9.1	0.5	0.46	2.16	8.5	16.7	20.4	0.5	0.42	2.41
P83917_CE	Cbx1	Chromobo:	18	29.9	59.2	64.6	0.5	0.46	2.16	897.7	1966.4	2393.4	0.5	0.38	2.67
O54784_D/	Dapk3	Death-asso	1	4.9	9.7	10.5	0.5	0.46	2.16	4.9	9.7	11.8	0.5	0.41	2.41
P58871_TE	Tnks1bp1	182 kDa tar	33	7.1	14.1	15.4	0.5	0.46	2.16	505.2	583.3	710.0	0.9	0.71	1.41
Q7TMY4_TI	Thoc7	THO compl	4	6.3	12.5	13.6	0.5	0.46	2.17	54.1	43.1	52.5	1.3	1.03	0.97
A0A087WC	Srcap	Protein Src	4	7.4	14.9	16.2	0.5	0.46	2.18	36.1	66.3	80.7	0.5	0.45	2.24
Q9CQL1_M	Magohb	Protein ma	5	13.7	27.3	29.8	0.5	0.46	2.18	119.5	203.5	247.7	0.6	0.48	2.07
Q9D0R4_D	Ddx56	Probable A	4	4.1	8.1	8.9	0.5	0.46	2.18	17.6	42.3	51.4	0.4	0.34	2.93
Q3TKT4_SN	Smarca4	Transcripti	28	10.6	21.1	23.1	0.5	0.46	2.18	525.0	722.4	879.3	0.7	0.60	1.67
P60867_RS	Rps20	40S riboso	4	87.4	177.2	193.3	0.5	0.45	2.21	614.1	581.5	707.8	1.1	0.87	1.15
P49722_PS	Psma2	Proteasom	5	3.3	6.7	7.3	0.5	0.45	2.22	41.2	38.2	46.6	1.1	0.88	1.13
P61028_R/	Rab8b	Ras-related	1	4.1	8.3	9.0	0.5	0.45	2.22	4.1	8.3	10.1	0.5	0.40	2.47
Q8BTV2_CF	Cpsf7	Cleavage ar	4	11.3	22.9	25.0	0.5	0.45	2.22	62.4	83.8	102.1	0.7	0.61	1.64
P62309_RU	Snrpg	Small nucle	4	9.1	18.5	20.2	0.5	0.45	2.22	33.1	74.9	91.1	0.4	0.36	2.75
P63154_CF	Crnkl1	Crooked ne	13	7.8	16.0	17.4	0.5	0.45	2.22	121.3	265.9	323.6	0.5	0.37	2.67
Q9CQR2_R	Rps21	40S riboso	4	19.0	38.7	42.2	0.5	0.45	2.22	87.0	161.3	196.3	0.5	0.44	2.26
P68368_TE	Tuba4a	Tubulin alp	4	8.1	16.5	18.0	0.5	0.45	2.22	49.4	67.4	82.0	0.7	0.60	1.66
P97429_AI	Anxa4	Annexin A4	3	2.5	5.2	5.7	0.5	0.45	2.24	17.3	16.4	20.0	1.1	0.86	1.16
Q80UW8_F	Polr2e	DNA-direct	4	24.3	50.2	54.7	0.5	0.44	2.25	109.2	216.6	263.7	0.5	0.41	2.41
E9QN31_E9	Nop2	Probable 2	12	10.0	20.6	22.4	0.5	0.44	2.25	176.4	289.0	351.7	0.6	0.50	1.99
Q6RT24_CE	Cenpe	Centromer	1	2.9	6.0	6.5	0.5	0.44	2.25	2.9	6.0	7.3	0.5	0.40	2.51
Q08943_SS	Ssrp1	FACT comp	15	12.8	26.5	28.9	0.5	0.44	2.25	311.3	447.3	544.5	0.7	0.57	1.75
P62305_RU	Snrpe	Small nucle	12	9.2	19.1	20.9	0.5	0.44	2.26	320.6	589.2	717.2	0.5	0.45	2.24
F6ZBR8_F6	Wiz	Protein Wi	12	11.3	23.3	25.5	0.5	0.44	2.26	154.7	269.5	328.0	0.6	0.47	2.12
Q61686_CI	Cbx5	Chromobo:	9	13.2	27.4	29.9	0.5	0.44	2.27	339.3	652.8	794.6	0.5	0.43	2.34
Q9D187_M	Fam96b	Mitotic spi	2	6.5	13.6	14.8	0.5	0.44	2.27	13.1	27.2	33.1	0.5	0.39	2.53
Q8VE88_F1	Fam114a2	Protein FAI	1	2.3	4.7	5.1	0.5	0.44	2.27	2.3	4.7	5.7	0.5	0.39	2.54
O70400_PI	Pdlim1	PDZ and LI	7	11.1	23.1	25.2	0.5	0.44	2.28	116.6	162.1	197.3	0.7	0.59	1.69
Q9QXS6_DI	Dbn1	Drebrin OS	12	13.4	28.0	30.6	0.5	0.44	2.28	351.1	372.0	452.8	0.9	0.78	1.29
Q8BH64_EI	Ehd2	EH domain-	15	8.8	18.5	20.1	0.5	0.44	2.28	170.2	271.9	330.9	0.6	0.51	1.94
Q99K43_PI	Prc1	Protein reg	1	4.0	8.4	9.1	0.5	0.44	2.28	4.0	8.4	10.2	0.5	0.39	2.54
O35130_NI	Emg1	Ribosomal	3	5.6	11.8	12.9	0.5	0.44	2.28	16.8	30.1	36.6	0.6	0.46	2.17
Q99KV1_D.	Dnajb11	DnaJ homo	3	6.1	12.7	13.9	0.5	0.44	2.28	29.3	32.2	39.2	0.9	0.75	1.34
Q99MJ9_D	Ddx50	ATP-depen	7	14.7	30.9	33.7	0.5	0.44	2.28	109.9	210.8	256.6	0.5	0.43	2.33
Q5SVR0_TE	Tbc1d9b	TBC1 doma	1	5.4	11.3	12.4	0.5	0.44	2.28	5.4	11.3	13.8	0.5	0.39	2.55
P97863_NI	Nfib	Nuclear fac	2	5.2	10.8	11.8	0.5	0.44	2.28	10.3	21.7	26.4	0.5	0.39	2.55
Q9D6K8_FU	Fundc2	FUN14 don	1	3.0	6.3	6.9	0.5	0.44	2.29	3.0	6.3	7.7	0.5	0.39	2.56
Q62481_VI	Vps72	Vacuolar pr	3	4.9	10.3	11.3	0.5	0.44	2.29	15.6	30.1	36.6	0.5	0.43	2.35
P02340_P5	Tp53	Cellular tur	30	21.8	45.9	50.0	0.5	0.44	2.29	756.4	1929.2	2348.2	0.4	0.32	3.10
D3YWX2_D	Ylpm1	YLP motif-c	18	5.9	12.5	13.7	0.5	0.43	2.30	201.9	258.5	314.7	0.8	0.64	1.56
Q8CFQ3_A(	Aqr	Intron-binc	12	7.5	15.9	17.4	0.5	0.43	2.31	148.7	246.8	300.4	0.6	0.49	2.02
Q9D168_IN	Ints12	Integrator (	5	5.0	10.7	11.7	0.5	0.43	2.31	45.3	49.5	60.2	0.9	0.75	1.33
Q9D0F1_NI	Ndc80	Kinetochor	2	6.0	12.7	13.9	0.5	0.43	2.31	12.0	25.4	31.0	0.5	0.39	2.58
Q9DB40_M	Med27	Mediator o	1	1.7	3.5	3.9	0.5	0.43	2.31	1.7	3.5	4.3	0.5	0.39	2.58
O54931_AI	Akap2	A-kinase an	3	4.3	9.1	9.9	0.5	0.43	2.32	19.6	39.5	48.1	0.5	0.41	2.46
Q9CQ25_M	Mzt2	Mitotic-spi	1	2.0	4.3	4.7	0.5	0.43	2.33	2.0	4.3	5.2	0.5	0.39	2.59
O88712_CT	Ctbp1	C-terminal-	13	13.3	28.5	31.0	0.5	0.43	2.33	438.9	379.7	462.1	1.2	0.95	1.05
Q9QZ85_II(	Iigp1	Interferon-i	1	2.8	6.0	6.5	0.5	0.43	2.33	2.8	6.0	7.3	0.5	0.38	2.60
Q62422_O!	Ostf1	Osteoclast-	1	10.6	22.7	24.7	0.5	0.43	2.34	10.6	22.7	27.6	0.5	0.38	2.61
Q9JKB3_YB	Ybx3	Y-box-bindi	4	12.4	26.6	29.0	0.5	0.43	2.34	58.9	164.8	200.6	0.4	0.29	3.41
O35887_C/	Calu	Calumenin	11	15.1	32.6	35.5	0.5	0.43	2.35	278.7	543.8	661.9	0.5	0.42	2.38
P63328_PF	Ppp3ca	Serine/thre	1	5.0	10.7	11.7	0.5	0.43	2.35	5.0	10.7	13.0	0.5	0.38	2.62
Q6PIU9_YJ005_MOUSE		Uncharacte	6	7.0	15.2	16.6	0.5	0.43	2.35	58.9	85.3	103.9	0.7	0.57	1.76
Q6P9R4_AI	Arhgef18	Rho guanin	2	8.3	17.9	19.6	0.5	0.42	2.35	16.6	35.9	43.7	0.5	0.38	2.63
P62960_YE	Ybx1	Nuclease-se	17	34.1	73.6	80.3	0.5	0.42	2.35	2341.3	1816.2	2210.7	1.3	1.06	0.94
Q62101_KI	Prkd1	Serine/thre	1	4.1	8.9	9.7	0.5	0.42	2.36	4.1	8.9	10.8	0.5	0.38	2.64
O70126_AI	Aurkb	Aurora kina	2	4.0	8.7	9.5	0.5	0.42	2.36	8.0	17.4	21.1	0.5	0.38	2.64
Q8R5K4_N(	Nol6	Nucleolar p	4	4.7	10.2	11.2	0.5	0.42	2.37	30.2	41.2	50.1	0.7	0.60	1.66
P19157_GS	Gstp1	Glutathion	2	2.8	6.1	6.6	0.5	0.42	2.37	5.6	12.1	14.7	0.5	0.38	2.64
Q9CYD3_CI	Crtap	Cartilage-as	2	5.9	12.8	13.9	0.5	0.42	2.37	11.7	25.5	31.1	0.5	0.38	2.64
Q8CI08_SL/	Slain2	SLAIN moti	2	8.5	18.4	20.1	0.5	0.42	2.37	16.9	36.8	44.8	0.5	0.38	2.65
Q61823_PI	Pdcd4	Programme	2	8.9	19.3	21.1	0.5	0.42	2.37	17.8	38.7	47.1	0.5	0.38	2.65
P35278_R/	Rab5c	Ras-related	6	6.4	13.9	15.2	0.5	0.42	2.38	48.3	95.5	116.2	0.5	0.42	2.41
Q8VDM6_H	Hnrnpul1	Heterogene	5	8.9	19.5	21.3	0.5	0.42	2.38	62.5	125.0	152.2	0.5	0.41	2.44
P62488_RF	Polr2g	DNA-direct	6	8.3	18.3	19.9	0.5	0.42	2.39	141.9	169.8	206.6	0.8	0.69	1.46
Q9WTM5_I	Ruvbl2	RuvB-like 2	26	16.7	36.7	40.0	0.5	0.42	2.39	1076.7	1178.0	1433.8	0.9	0.75	1.33
Q6PAM1_T	Txlna	Alpha-taxili	1	2.7	5.8	6.4	0.5	0.42	2.40	2.7	5.8	7.1	0.5	0.37	2.67
Q3UX10_TI	Tubal3	Tubulin alp	2	3.7	8.2	8.9	0.5	0.42	2.40	7.4	16.4	20.0	0.5	0.37	2.68
Q9DBY8_N'	Nvl	Nuclear val	9	9.8	21.7	23.6	0.5	0.42	2.41	78.8	191.4	232.9	0.4	0.34	2.96
Q9CYL5_G/	Glipr2	Golgi-assoc	6	16.1	35.5	38.8	0.5	0.42	2.41	114.7	238.6	290.4	0.5	0.39	2.53
P51150_R/	Rab7a	Ras-related	11	9.6	21.3	23.2	0.5	0.42	2.41	223.2	291.1	354.4	0.8	0.63	1.59
Q9JK48_SH	Sh3glb1	Endophilin	3	8.2	18.1	19.8	0.5	0.41	2.42	40.0	52.4	63.7	0.8	0.63	1.59
Q8K310_M	Matr3	Matrin-3 O:	40	14.6	32.4	35.3	0.5	0.41	2.42	1308.2	2440.9	2970.9	0.5	0.44	2.27
Q8C788_Q	Snx18	Sorting nex	5	8.6	19.2	21.0	0.4	0.41	2.43	48.8	95.5	116.2	0.5	0.42	2.38
P54731_FA	Faf1	FAS-associa	6	12.1	27.1	29.6	0.4	0.41	2.43	116.0	151.7	184.7	0.8	0.63	1.59
Q9D920_L:	Loh12cr1	Loss of hete	1	2.3	5.2	5.7	0.4	0.41	2.43	2.3	5.2	6.4	0.4	0.37	2.72
O89112_L/	Lancl1	LanC-like pı	1	4.1	9.1	10.0	0.4	0.41	2.44	4.1	9.1	11.1	0.4	0.37	2.72
Q62523_Z	Zyx	Zyxin OS=M	7	19.5	43.7	47.6	0.4	0.41	2.44	212.3	240.0	292.1	0.9	0.73	1.38
Q8R0S1_A1	Atf7	Cyclic AMP	1	2.5	5.5	6.0	0.4	0.41	2.44	2.5	5.5	6.7	0.4	0.37	2.72
Q64012_R/	Raly	RNA-bindir	27	25.5	57.0	62.2	0.4	0.41	2.44	1558.5	2638.0	3210.9	0.6	0.49	2.06
O08750_NI	Nfil3	Nuclear fac	1	4.2	9.4	10.3	0.4	0.41	2.44	4.2	9.4	11.5	0.4	0.37	2.73
Q91WV0_N	Dr1	Protein Dr1	1	36.7	82.2	89.7	0.4	0.41	2.45	36.7	82.2	100.1	0.4	0.37	2.73
P08775_RF	Polr2a	DNA-direct	36	13.0	29.2	31.9	0.4	0.41	2.45	723.1	1020.9	1242.6	0.7	0.58	1.72
Q8BG30_N	Nelfa	Negative el	7	4.6	10.4	11.3	0.4	0.41	2.46	48.2	65.0	79.1	0.7	0.61	1.64
Q9CQ26_S1	Stambp	STAM-bindi	1	3.6	8.3	9.0	0.4	0.40	2.47	3.6	8.3	10.0	0.4	0.36	2.76
Q8BNV1_TI	Trmt2a	tRNA (uraci	4	3.7	8.4	9.1	0.4	0.40	2.47	21.8	33.5	40.7	0.7	0.53	1.87
Q4VBE8_W	Wdr18	WD repeat-	9	7.5	17.1	18.6	0.4	0.40	2.47	132.8	178.5	217.3	0.7	0.61	1.64
Q9CZX0_EL	Elp3	Elongator c	3	4.8	11.0	12.0	0.4	0.40	2.47	17.2	44.2	53.8	0.4	0.32	3.12
Q8VHK9_D	Dhx36	ATP-depen	6	6.7	15.3	16.6	0.4	0.40	2.48	45.5	89.3	108.7	0.5	0.42	2.39
P97360_ET	Etv6	Transcripti	2	7.3	16.6	18.1	0.4	0.40	2.48	14.6	33.1	40.3	0.4	0.36	2.76
Q8CCS6_P/	Pabpn1	Polyadenyl	4	21.5	48.9	53.3	0.4	0.40	2.48	113.5	220.6	268.5	0.5	0.42	2.37
P59326_YT	Ythdf1	YTH domaiı	8	5.8	13.2	14.4	0.4	0.40	2.48	114.6	140.8	171.4	0.8	0.67	1.50
Q569Z6_TF	Thrap3	Thyroid ho	35	17.7	40.3	44.0	0.4	0.40	2.49	979.1	2085.9	2538.9	0.5	0.39	2.59
P28659_CE	Celf1	CUGBP Elav	2	4.0	9.2	10.1	0.4	0.40	2.49	8.1	18.5	22.5	0.4	0.36	2.78
Q6ZQF0_TC	Topbp1	DNA topois	6	2.8	6.3	6.9	0.4	0.40	2.50	19.4	40.2	48.9	0.5	0.40	2.52
Q9Z204_HI	Hnrnpc	Heterogene	41	36.0	82.8	90.3	0.4	0.40	2.51	5510.9	5657.7	6886.3	1.0	0.80	1.25
Q63829_C(	Commd3	COMM don	2	11.3	26.0	28.4	0.4	0.40	2.51	22.6	52.0	63.3	0.4	0.36	2.80
O35295_PI	Purb	Transcripti	10	12.0	27.6	30.1	0.4	0.40	2.51	572.4	483.0	587.9	1.2	0.97	1.03
Q8BHJ9_SL	Slu7	Pre-mRNA-	1	2.6	5.9	6.4	0.4	0.40	2.51	2.6	5.9	7.2	0.4	0.36	2.80
Q571I9_A1	Aldh16a1	Aldehyde d	3	4.0	9.1	10.0	0.4	0.40	2.52	27.1	26.7	32.4	1.0	0.83	1.20
P39447_ZC	Tjp1	Tight juncti	19	8.7	20.1	22.0	0.4	0.39	2.54	188.2	404.4	492.3	0.5	0.38	2.62
Q6VN19_RI	Ranbp10	Ran-bindin	3	7.0	16.3	17.8	0.4	0.39	2.55	21.4	117.2	142.6	0.2	0.15	6.66
Q61127_N/	Nab2	NGFI-A-bin	5	8.7	20.4	22.2	0.4	0.39	2.56	77.3	97.7	119.0	0.8	0.65	1.54
Q9D0T1_NI	Nhp2l1	NHP2-like p	2	11.7	27.4	29.9	0.4	0.39	2.56	23.3	54.7	66.6	0.4	0.35	2.85

Q99NH0_A	Ankrd17	Ankyrin rep	11	6.7	15.9	17.3	0.4	0.39	2.56	125.0	162.6	197.9	0.8	0.63	1.58
Q8VDF2_U	Uhrf1	E3 ubiquiti	21	7.5	17.8	19.4	0.4	0.39	2.57	210.9	643.7	783.5	0.3	0.27	3.72
P97386_D	Lig3	DNA ligase	9	5.4	12.8	14.0	0.4	0.39	2.60	76.9	125.0	152.2	0.6	0.51	1.98
Q9DCR2_A	Ap3s1	AP-3 compl	7	4.9	11.7	12.7	0.4	0.39	2.60	90.0	94.3	114.8	1.0	0.78	1.28
Q99LX5_M	Mmtag2	Multiple m	1	3.1	7.4	8.0	0.4	0.38	2.61	3.1	7.4	9.0	0.4	0.34	2.91
P47811_M	Mapk14	Mitogen-ac	1	1.7	4.1	4.5	0.4	0.38	2.61	1.7	4.1	5.0	0.4	0.34	2.91
G3XA30_G	Nsmce4a	MCG1618,	3	5.3	12.7	13.8	0.4	0.38	2.61	23.3	43.0	52.4	0.5	0.44	2.25
Q61687_A	Atrx	Transcripti	13	5.1	12.2	13.4	0.4	0.38	2.62	94.4	171.0	208.1	0.6	0.45	2.21
Q8BWW4_	Larp4	La-related	11	8.9	21.4	23.3	0.4	0.38	2.62	145.0	232.7	283.3	0.6	0.51	1.95
Q8BFW7_L	Lpp	Lipoma-pre	4	4.0	9.6	10.5	0.4	0.38	2.63	19.7	41.9	51.0	0.5	0.39	2.59
P62835_R	Rap1a	Ras-related	6	8.8	21.2	23.1	0.4	0.38	2.64	120.3	194.5	236.7	0.6	0.51	1.97
Q921M3_S	Sf3b3	Splicing fac	39	10.8	26.2	28.6	0.4	0.38	2.65	564.6	1322.2	1609.3	0.4	0.35	2.85
P48678_L	Lmna	Prelamin-A	30	7.0	17.1	18.6	0.4	0.38	2.65	463.1	651.3	792.8	0.7	0.58	1.71
Q9D3D9_A	Atp5d	ATP syntha	1	2.6	6.2	6.8	0.4	0.38	2.65	2.6	6.2	7.6	0.4	0.34	2.96
B2RVL6_ZC	Zcchc24	Zinc finger	1	5.3	12.8	14.0	0.4	0.38	2.65	5.3	12.8	15.6	0.4	0.34	2.96
E9Q5F9_SE	Setd2	Histone-lys	6	4.9	12.1	13.1	0.4	0.38	2.66	28.2	70.1	85.3	0.4	0.33	3.02
Q8C6B9_A	Rps19bp1	Active regu	3	13.5	32.9	35.8	0.4	0.38	2.66	40.0	82.7	100.6	0.5	0.40	2.51
Q9DCG9_T	Trmt112	Multifuncti	3	29.8	72.9	79.5	0.4	0.38	2.67	1113.6	6062.4	7378.9	0.2	0.15	6.63
Q7TNC4_L	Luc7l2	Putative R	19	24.1	59.0	64.4	0.4	0.37	2.67	1335.7	1585.6	1930.0	0.8	0.69	1.44
Q9WU62_I	Incenp	Inner centr	4	4.2	10.2	11.1	0.4	0.37	2.67	16.2	47.7	58.1	0.3	0.28	3.58
Q8R080_G	Gtse1	G2 and S p	2	12.2	29.9	32.6	0.4	0.37	2.67	24.4	59.7	72.7	0.4	0.34	2.98
E9Q6H8_E	Plekha5	Protein Ple	1	5.4	13.2	14.4	0.4	0.37	2.68	5.4	13.2	16.1	0.4	0.33	2.99
Q6PAL7_A	Ahdc1	AT-hook D	3	3.4	8.4	9.1	0.4	0.37	2.68	13.7	21.9	26.6	0.6	0.51	1.95
Q8VHZ7_I	Imp4	U3 small nu	1	1.7	4.2	4.6	0.4	0.37	2.68	1.7	4.2	5.1	0.4	0.33	2.99
P25799_N	Nfkb1	Nuclear fac	8	4.4	10.8	11.8	0.4	0.37	2.69	34.5	82.6	100.5	0.4	0.34	2.91
Q922V4_P	Plrg1	Pleiotropic	4	6.6	16.3	17.8	0.4	0.37	2.69	45.8	68.5	83.4	0.7	0.55	1.82
Q9Z199_S	Supt4h1b	Transcripti	1	16.4	40.6	44.2	0.4	0.37	2.70	16.4	40.6	49.4	0.4	0.33	3.01
Q8K2Q0_C	Commd9	COMM don	2	3.2	8.0	8.7	0.4	0.37	2.70	6.5	16.0	19.4	0.4	0.33	3.01
P62700_Y	Ypel5	Protein yip	3	6.4	15.8	17.2	0.4	0.37	2.70	54.2	70.2	85.5	0.8	0.63	1.58
P63037_D	Dnaja1	DnaJ homo	12	7.5	18.7	20.4	0.4	0.37	2.71	323.5	327.8	399.0	1.0	0.81	1.23
Q9JI44_D	Dmap1	DNA methy	7	7.0	17.4	19.0	0.4	0.37	2.72	84.5	117.9	143.5	0.7	0.59	1.70
P52293_I	Kpna2	Importin su	18	6.8	17.1	18.6	0.4	0.37	2.73	192.0	362.0	440.7	0.5	0.44	2.29
P61216_T	Taf13	Transcripti	1	5.3	13.2	14.4	0.4	0.37	2.73	5.3	13.2	16.1	0.4	0.33	3.05
Q3UJB9_E	Edc4	Enhancer o	25	5.8	14.4	15.8	0.4	0.37	2.73	235.8	377.3	459.3	0.6	0.51	1.95
Q9WVR4_F	Fxr2	Fragile X m	3	7.9	19.8	21.6	0.4	0.37	2.73	19.2	48.0	58.5	0.4	0.33	3.05
Q9R059_F	Fhl3	Four and a	6	8.5	21.2	23.2	0.4	0.37	2.73	59.5	161.3	196.3	0.4	0.30	3.30
Q9D1C1_U	Ube2c	Ubiquitin-	3	5.2	13.2	14.4	0.4	0.36	2.75	14.0	32.4	39.5	0.4	0.35	2.82
O70433_F	Fhl2	Four and a	1	2.0	5.0	5.4	0.4	0.36	2.76	2.0	5.0	6.0	0.4	0.33	3.08
A2BH40_A	Arid1a	AT-rich inte	8	4.1	10.3	11.3	0.4	0.36	2.77	53.4	81.9	99.7	0.7	0.54	1.87
Q8C2Q3_R	Rbm14	RNA-bindin	14	21.7	55.2	60.2	0.4	0.36	2.77	315.0	638.9	777.6	0.5	0.41	2.47
Q9JKX4_A	Aatf	Protein AA	4	4.1	10.5	11.4	0.4	0.36	2.78	18.6	42.3	51.5	0.4	0.36	2.77
Q80V86_I	Ints8	Integrator	1	2.4	6.2	6.8	0.4	0.36	2.78	2.4	6.2	7.6	0.4	0.32	3.11
Q9JMH9_	Myo18a	Unconvent	14	5.8	14.8	16.2	0.4	0.36	2.79	107.9	222.8	271.2	0.5	0.40	2.51
Q3UQA7_S	Selh	Selenoprot	3	10.0	25.6	27.9	0.4	0.36	2.80	34.4	81.0	98.5	0.4	0.35	2.87
Q68FF6_G	Git1	ARF GTPase	1	3.6	9.2	10.1	0.4	0.36	2.80	3.6	9.2	11.3	0.4	0.32	3.12
Q6XLQ8_Q	Calu	Calumenin	3	7.1	18.3	20.0	0.4	0.36	2.80	28.6	45.5	55.4	0.6	0.52	1.94
Q9DCT8_C	Crip2	Cysteine-ri	1	4.3	11.0	12.0	0.4	0.36	2.81	4.3	11.0	13.4	0.4	0.32	3.13
Q8R0K4_C	Ccdc137	Coiled-coil	1	4.2	10.9	11.9	0.4	0.36	2.81	4.2	10.9	13.3	0.4	0.32	3.14
Q8K4L0_D	Ddx54	ATP-depen	1	3.5	9.0	9.8	0.4	0.36	2.81	3.5	9.0	10.9	0.4	0.32	3.14
Q921Y2_I	Imp3	U3 small nu	4	1.9	4.9	5.3	0.4	0.35	2.82	7.5	20.6	25.1	0.4	0.30	3.34
P23198_C	Cbx3	Chromobo	11	50.9	131.7	143.7	0.4	0.35	2.82	708.7	1730.4	2106.2	0.4	0.34	2.97
Q9CQS2_N	Nop10	H/ACA ribo	2	2.8	7.2	7.9	0.4	0.35	2.83	5.6	14.4	17.5	0.4	0.32	3.15
Q8BSP2_C	Ncaph2	Condensin-	4	6.1	15.9	17.3	0.4	0.35	2.83	21.9	58.7	71.4	0.4	0.31	3.26
P52927_H	Hmga2	High mobil	1	6.9	17.8	19.5	0.4	0.35	2.83	6.9	17.8	21.7	0.4	0.32	3.16
Q8R3W5_S	Tsen15	tRNA-splici	1	2.1	5.5	6.0	0.4	0.35	2.84	2.1	5.5	6.7	0.4	0.32	3.16
Q9Z315_S	Sart1	U4/U6.U5	22	8.5	22.2	24.3	0.4	0.35	2.84	337.6	551.2	670.9	0.6	0.50	1.99
Q8BFZ3_AC	Actbl2	Beta-actin-	12	74.6	194.1	211.7	0.4	0.35	2.84	2890.7	3746.8	4560.5	0.8	0.63	1.58
Q8K3X4_I2	Irf2bpl	Interferon	6	4.5	11.8	12.9	0.4	0.35	2.84	35.3	122.5	149.1	0.3	0.24	4.23
Q00899_T	Yy1	Transcripti	3	5.0	13.2	14.4	0.4	0.35	2.86	28.4	33.6	40.9	0.8	0.69	1.44
P26040_EZ	Ezr	Ezrin OS=M	3	5.6	14.7	16.1	0.4	0.35	2.87	23.8	40.9	49.8	0.6	0.48	2.09
E9Q5G3_K	Kif23	Kinesin-like	3	2.2	5.7	6.2	0.4	0.35	2.88	6.8	17.7	21.6	0.4	0.31	3.19
Q9CQE0_R	Rnf138	E3 ubiquiti	2	10.6	28.1	30.7	0.4	0.35	2.90	21.2	56.3	68.5	0.4	0.31	3.23
Q9DBD5_P	Pelp1	Proline-, gl	8	9.4	24.9	27.1	0.4	0.35	2.90	107.9	192.4	234.2	0.6	0.46	2.17
Q6P9Q6_F	Fkbp15	FK506-bin	3	2.6	6.8	7.4	0.4	0.34	2.91	15.7	21.5	26.1	0.7	0.60	1.67
Q9DAM7_T	Tmem263	Transmem	3	6.3	16.8	18.4	0.4	0.34	2.91	16.9	51.9	63.2	0.3	0.27	3.73
Q9EPU4_C	Cpsf1	Cleavage a	17	6.1	16.4	17.9	0.4	0.34	2.91	113.0	259.7	316.1	0.4	0.36	2.80
Q62186_S	Ssr4	Translocon	1	1.6	4.3	4.7	0.4	0.34	2.91	1.6	4.3	5.3	0.4	0.31	3.25
O54734_O	Ddost	Dolichyl-di	1	2.3	6.2	6.7	0.4	0.34	2.92	2.3	6.2	7.5	0.4	0.31	3.26
Q61103_R	Dpf2	Zinc finger	6	6.6	17.6	19.2	0.4	0.34	2.93	69.9	109.5	133.3	0.6	0.52	1.91
Q9CPR1_R	Rwdd4	RWD doma	3	10.2	27.4	29.9	0.4	0.34	2.93	77.4	60.1	73.2	1.3	1.06	0.95
Q9WTM3_	Sema6c	Semaphori	1	2.7	7.2	7.8	0.4	0.34	2.95	2.7	7.2	8.8	0.4	0.30	3.30
P62858_R	Rps28	40S riboso	4	31.4	85.0	92.7	0.4	0.34	2.96	216.8	491.7	598.5	0.4	0.36	2.76
P70271_P	Pdlim4	PDZ and LI	7	6.5	17.8	19.4	0.4	0.34	2.97	48.8	183.5	223.4	0.3	0.22	4.57
Q9CWW7_	Cxxc1	CXXC-type	3	3.1	8.4	9.1	0.4	0.33	2.99	10.2	21.2	25.8	0.5	0.40	2.52
Q62276_M	Med22	Mediator o	3	2.7	7.3	7.9	0.4	0.33	2.99	29.0	29.2	35.5	1.0	0.82	1.22
Q3UGS4_F	Fam195b	Protein FA	1	3.5	9.7	10.6	0.4	0.33	2.99	3.5	9.7	11.8	0.4	0.30	3.34
Q62219_T	Tgfb1i1	Transformi	1	2.7	7.6	8.2	0.4	0.33	3.02	2.7	7.6	9.2	0.4	0.30	3.37
F8VQL9_F8	Ncor2	Nuclear rec	20	5.6	15.4	16.8	0.4	0.33	3.02	204.7	398.5	485.0	0.5	0.42	2.37
Q99M46_C	Polr2c	DNA-direct	6	9.5	26.3	28.7	0.4	0.33	3.03	135.0	191.6	233.2	0.7	0.58	1.73
Q3U7R1_E	Esyt1	Extended s	4	5.6	15.5	16.9	0.4	0.33	3.03	26.7	60.5	73.7	0.4	0.36	2.76
Q99104_M	Myo5a	Unconvent	3	2.6	7.3	7.9	0.4	0.33	3.03	7.1	23.3	28.3	0.3	0.25	3.96
Q3UPH7_A	Arhgef40	Rho guanin	5	4.5	12.4	13.5	0.4	0.33	3.04	22.2	60.1	73.2	0.4	0.30	3.30
Q8BH97_R	Rcn3	Reticulocal	3	2.6	7.2	7.9	0.4	0.33	3.04	7.4	22.0	26.7	0.3	0.28	3.61
Q6ZPZ3_ZC	Zc3h4	Zinc finger	9	4.1	11.4	12.4	0.4	0.33	3.04	47.9	106.1	129.1	0.5	0.37	2.70
Q9JL16_IS	Isg20	Interferon-	3	7.3	20.4	22.2	0.4	0.33	3.04	43.4	62.2	75.8	0.7	0.57	1.74
Q78YZ6_SC	Scoc	Short coile	1	8.0	22.3	24.3	0.4	0.33	3.04	8.0	22.3	27.1	0.4	0.29	3.39
Q9ES56_TP	Trappc4	Trafficking	2	2.5	6.8	7.5	0.4	0.33	3.05	4.9	13.7	16.7	0.4	0.29	3.40
Q9CQA5_	Med4	Mediator o	1	4.6	12.7	13.9	0.4	0.33	3.05	4.6	12.7	15.5	0.4	0.29	3.40
P58462_F	Foxp1	Forkhead b	6	5.8	16.2	17.7	0.4	0.33	3.05	40.7	90.3	110.0	0.5	0.37	2.70
O70493_S	Snx12	Sorting nex	7	6.5	18.1	19.8	0.4	0.33	3.06	82.4	159.3	193.9	0.5	0.43	2.35
Q9WTV6_	Usp18	Ubl carbox	1	4.0	11.1	12.1	0.4	0.33	3.06	4.0	11.1	13.5	0.4	0.29	3.41
Q9CPV5_P	Pmf1	Polyamine-	2	3.9	11.0	12.0	0.4	0.33	3.07	7.8	22.0	26.8	0.4	0.29	3.42
Q8CGP6_H	Hist1h2ah	Histone H2	26	126.4	356.6	389.0	0.4	0.32	3.08	10364.3	30520.1	37148.0	0.3	0.28	3.58
Q9CWX9_	Ddx47	Probable A	3	5.9	16.7	18.2	0.4	0.32	3.08	39.0	42.1	51.3	0.9	0.76	1.32
Q60632_C	Nr2f1	COUP trans	3	7.3	20.6	22.4	0.4	0.32	3.08	42.5	63.3	77.1	0.7	0.55	1.81
Q8BSQ9_P	Pbrm1	Protein pol	21	7.4	20.8	22.7	0.4	0.32	3.09	300.2	401.8	489.1	0.7	0.61	1.63
Q3UMU9_	Hdgfrp2	Hepatoma-	3	3.7	10.4	11.3	0.4	0.32	3.10	11.9	31.6	38.5	0.4	0.31	3.25
Q9CQU0_T	Txndc12	Thioredoxi	4	6.4	18.3	19.9	0.4	0.32	3.10	35.5	277.6	337.9	0.1	0.10	9.53
Q61033_L	Tmpo	Lamina-ass	25	5.0	14.2	15.5	0.3	0.32	3.12	209.7	441.0	536.8	0.5	0.39	2.56
E9PVX6_E9	Mki67	Protein Mk	17	4.0	11.5	12.5	0.3	0.32	3.12	147.7	261.5	318.3	0.6	0.46	2.16
Q8VHR5_P	Gatad2b	Transcripti	12	7.1	20.5	22.3	0.3	0.32	3.13	112.9	254.0	309.1	0.4	0.37	2.74
Q8VEH5_E	Epm2aip1	EPM2A-inte	4	4.7	13.4	14.6	0.3	0.32	3.14	17.4	55.2	67.1	0.3	0.26	3.86
Q80WE4_K	Kif20b	Kinesin-like	1	2.6	7.6	8.3	0.3	0.32	3.15	2.6	7.6	9.2	0.3	0.28	3.51
Q9CQ82_C	Itgb3bp	Centromer	1	3.6	10.3	11.2	0.3	0.32	3.15	3.6	10.3	12.5	0.3	0.28	3.51
Q9JK91_M	Mlh1	DNA misma	2	5.1	14.6	15.9	0.3	0.32	3.15	10.1	29.2	35.6	0.3	0.28	3.51
P08752_G	Gnai2	Guanine nu	7	4.1	11.7	12.8	0.3	0.32	3.15	30.7	87.6	106.6	0.4	0.29	3.47
Q8K268_A	Abcf3	ATP-bindin	3	2.5	7.3	8.0	0.3	0.32	3.17	9.1	21.4	26.1	0.4	0.35	2.87
Q7TSZ8_N	Nacc1	Nucleus ac	1	1.9	5.6	6.1	0.3	0.32	3.17	1.9	5.6	6.8	0.3	0.28	3.54
Q80UU9_P	Pgrmc2	Membrane-	2	3.9	11.4	12.4	0.3	0.31	3.18	7.8	22.7	27.7	0.3	0.28	3.54
O88291_Z	Znf326	DBIRD com	8	8.3	24.2	26.4	0.3	0.31	3.19	106.6	207.2	252.2	0.5	0.42	2.37
O55098_S	Stk10	Serine/thre	1	2.6	7.5	8.2	0.3	0.31	3.19	2.6	7.5	9.2	0.3	0.28	3.56
Q5SFM8_R	Rbm27	RNA-bindin	3	3.5	10.3	11.2	0.3	0.31	3.20	10.1	28.9	35.2	0.3	0.29	3.48
Q9QUI0_R	Rhoa	Transformi	1	3.1	9.3	10.2	0.3	0.31	3.23	3.1	9.3	11.4	0.3	0.28	3.61

Q9D720_N	Nsmce1	Non-structu	2	4.0	11.8	12.9	0.3	0.31	3.24	8.0	23.6	28.8	0.3	0.28	3.61
Q8BY71_H	Hat1	Histone ace	5	4.5	13.5	14.8	0.3	0.31	3.24	39.9	66.2	80.5	0.6	0.49	2.02
P27600_GI	Gna12	Guanine nu	1	101.0	300.9	328.3	0.3	0.31	3.25	101.0	300.9	366.3	0.3	0.28	3.63
Q4FZF3_DD	Ddx49	Probable A	1	2.9	8.7	9.4	0.3	0.31	3.25	2.9	8.7	10.5	0.3	0.28	3.63
P62996_TR	Tra2b	Transforme	6	36.8	110.0	120.0	0.3	0.31	3.26	655.5	788.1	959.2	0.8	0.68	1.46
P45481_CE	Crebbp	CREB-bindi	5	5.0	15.0	16.3	0.3	0.31	3.26	21.3	60.3	73.4	0.4	0.29	3.45
Q8R2Q8_B	Bst2	Bone marro	9	9.2	27.5	30.0	0.3	0.31	3.26	132.0	282.5	343.8	0.5	0.38	2.60
P62315_SN	Snrpd1	Small nucle	9	9.9	29.7	32.4	0.3	0.31	3.26	275.1	386.4	470.3	0.7	0.58	1.71
P40338_VI	Vhl	Von Hippel	1	2.3	7.0	7.6	0.3	0.31	3.27	2.3	7.0	8.5	0.3	0.27	3.64
Q8BTI8_SRI	Srrm2	Serine/argi	37	7.2	21.6	23.6	0.3	0.31	3.27	520.2	1029.3	1252.8	0.5	0.42	2.41
Q60668_HI	Hnrnpd	Heterogene	13	9.7	29.3	31.9	0.3	0.30	3.29	286.5	630.8	767.8	0.5	0.37	2.68
Q9JJI8_RL3	Rpl38	60S riboso	3	15.6	47.1	51.3	0.3	0.30	3.30	104.8	288.6	351.3	0.4	0.30	3.35
Q99KG3_RI	Rbm10	RNA-bindir	10	6.6	19.9	21.7	0.3	0.30	3.30	97.5	236.3	287.6	0.4	0.34	2.95
O55013_TF	Trappc3	Trafficking	3	8.1	24.5	26.7	0.3	0.30	3.31	23.5	70.5	85.8	0.3	0.27	3.65
Q8CBY8_D	Dctn4	Dynactin su	8	6.3	19.2	20.9	0.3	0.30	3.33	188.7	204.9	249.4	0.9	0.76	1.32
Q8BIZ6_SN	Snip1	Smad nucle	2	4.5	13.8	15.0	0.3	0.30	3.33	9.0	27.5	33.5	0.3	0.27	3.71
P28033_CE	Cebpb	CCAAT/enh	1	2.6	7.9	8.6	0.3	0.30	3.34	2.6	7.9	9.6	0.3	0.27	3.73
E9PX91_E9	Pisd	Phosphatid	1	1.6	5.1	5.5	0.3	0.30	3.34	1.6	5.1	6.1	0.3	0.27	3.73
P53994_R	Rab2a	Ras-related	6	6.5	20.1	22.0	0.3	0.30	3.35	79.6	120.6	146.8	0.7	0.54	1.84
P28574_M	Max	Protein ma	2	4.3	13.4	14.6	0.3	0.30	3.36	8.7	26.8	32.6	0.3	0.27	3.75
Q9CQT2_RI	Rbm7	RNA-bindir	6	8.7	26.7	29.1	0.3	0.30	3.36	124.5	136.0	165.5	0.9	0.75	1.33
Q6PGF7_E	Exoc8	Exocyst cor	2	2.2	6.9	7.5	0.3	0.30	3.38	4.4	13.8	16.8	0.3	0.27	3.77
O08573_LE	Lgals9	Galectin-9	1	3.0	9.2	10.1	0.3	0.29	3.39	3.0	9.2	11.2	0.3	0.26	3.79
P68433_H	Hist1h3a	Histone H3	21	77.8	242.6	264.6	0.3	0.29	3.40	11776.4	20792.3	25307.7	0.6	0.47	2.15
P54116_ST	Stom	Erythrocyte	1	2.7	8.4	9.2	0.3	0.29	3.41	2.7	8.4	10.3	0.3	0.26	3.81
P62307_RU	Snrpf	Small nucle	3	5.0	15.8	17.2	0.3	0.29	3.43	23.7	60.7	73.9	0.4	0.32	3.12
P61027_R	Rab10	Ras-related	5	4.7	15.0	16.4	0.3	0.29	3.45	45.4	70.1	85.4	0.6	0.53	1.88
A2AJI0_MA	Map7d1	MAP7 dom	1	4.6	14.5	15.8	0.3	0.29	3.46	4.6	14.5	17.7	0.3	0.26	3.86
Q99020_R	Hnrnpab	Heterogene	8	17.8	56.7	61.8	0.3	0.29	3.47	275.3	647.2	787.7	0.4	0.35	2.86
Q6PFD9_N	Nup98	Nuclear po	2	3.2	10.3	11.2	0.3	0.29	3.47	6.5	20.6	25.0	0.3	0.26	3.88
Q3V1T4_P	Lepre1	Prolyl 3-hy	3	4.9	15.6	17.1	0.3	0.29	3.48	33.9	54.1	65.9	0.6	0.52	1.94
Q62383_SF	Supt6h	Transcripti	32	5.8	18.5	20.2	0.3	0.29	3.50	374.9	711.3	865.8	0.5	0.43	2.31
Q8BIW9_C	Chtf18	Chromosor	2	2.5	8.0	8.7	0.3	0.28	3.52	5.0	16.0	19.5	0.3	0.25	3.92
Q02566_M	Myh6	Myosin-6 O	1	5.5	17.7	19.3	0.3	0.28	3.52	5.5	17.7	21.5	0.3	0.25	3.93
Q99JH1_RF	Rpp25l	Ribonuclea	1	6.4	20.6	22.5	0.3	0.28	3.52	6.4	20.6	25.1	0.3	0.25	3.93
P47754_C	Capza2	F-actin-cap	6	10.4	33.7	36.7	0.3	0.28	3.53	96.5	199.8	243.2	0.5	0.40	2.52
Q9D8C6_N	Med11	Mediator o	1	4.4	14.2	15.4	0.3	0.28	3.53	4.4	14.2	17.2	0.3	0.25	3.94
Q8BG05_R	Hnrnpa3	Heterogene	5	7.2	23.3	25.4	0.3	0.28	3.54	44.6	156.6	190.6	0.3	0.23	4.27
Q8BHS3_RI	Rbm22	Pre-mRNA-	7	7.1	23.2	25.4	0.3	0.28	3.55	97.7	235.1	286.2	0.4	0.34	2.93
Q8VHN7_G	Gpr98	G-protein c	1	8.9	29.3	31.9	0.3	0.28	3.57	8.9	29.3	35.6	0.3	0.25	3.98
Q9R061_N	Nubp2	Cytosolic F	1	2.6	8.5	9.2	0.3	0.28	3.58	2.6	8.5	10.3	0.3	0.25	3.99
O08547_S	Sec22b	Vesicle-traf	2	1.9	6.2	6.8	0.3	0.28	3.59	3.8	12.4	15.1	0.3	0.25	4.01
P11276_FI	Fn1	Fibronectir	57	14.7	48.5	52.9	0.3	0.28	3.60	2307.0	3718.4	4525.9	0.6	0.51	1.96
Q9CSN1_SI	Snw1	SNW doma	19	6.8	22.6	24.7	0.3	0.28	3.60	253.0	658.0	800.9	0.4	0.32	3.17
Q9R1P3_P	Psmb2	Proteasom	1	2.8	9.2	10.0	0.3	0.27	3.64	2.8	9.2	11.2	0.3	0.25	4.06
Q9WU00_N	Nrf1	Nuclear res	3	3.8	12.7	13.9	0.3	0.27	3.65	11.3	36.8	44.8	0.3	0.25	3.95
P60710_A	Actb	Actin, cyto	32	61.0	204.9	223.5	0.3	0.27	3.66	6346.8	11871.9	14450.1	0.5	0.44	2.28
Q9D4H9_P	Phf14	PHD finger	6	3.5	11.7	12.8	0.3	0.27	3.68	27.1	73.1	89.0	0.4	0.30	3.28
O55135_IF	Eif6	Eukaryotic	2	5.5	18.4	20.1	0.3	0.27	3.68	10.9	36.8	44.8	0.3	0.24	4.11
Q921W4_C	Cryzl1	Quinone ox	1	1.9	6.3	6.9	0.3	0.27	3.69	1.9	6.3	7.7	0.3	0.24	4.12
Q8R0F5_RE	Rbmx2	RNA-bindir	1	8.2	27.7	30.2	0.3	0.27	3.70	8.2	27.7	33.7	0.3	0.24	4.13
Q61696_H	Hspa1a	Heat shock	5	16.9	57.5	62.8	0.3	0.27	3.72	112.6	369.9	450.2	0.3	0.25	4.00
Q8BGF0_Q	AW551984	Protein AW	1	1.4	4.6	5.1	0.3	0.27	3.72	1.4	4.6	5.6	0.3	0.24	4.15
P17809_G	Slc2a1	Solute carri	1	4.1	14.1	15.3	0.3	0.27	3.77	4.1	14.1	17.1	0.3	0.24	4.20
O54864_SU	Suv39h1	Histone-lys	1	5.5	19.1	20.8	0.3	0.27	3.77	5.5	19.1	23.2	0.3	0.24	4.21
Q8C4J7_TB	Tbl3	Transducin	3	3.0	10.3	11.2	0.3	0.26	3.78	25.2	32.3	39.3	0.8	0.64	1.56
O70157_T	Top3a	DNA topois	1	2.3	7.9	8.6	0.3	0.26	3.78	2.3	7.9	9.6	0.3	0.24	4.22
Q6GSS7_H	Hist2h2aa1	Histone H2	8	22.9	79.9	87.2	0.3	0.26	3.80	1306.0	1846.1	2247.0	0.7	0.58	1.72
Q9CQ79_T	Txndc9	Thioredoxi	2	4.7	16.4	17.9	0.3	0.26	3.82	9.4	32.8	39.9	0.3	0.23	4.26
Q8CHI8_EP	Ep400	E1A-bindin	5	3.2	11.1	12.1	0.3	0.26	3.82	21.9	51.1	62.2	0.4	0.35	2.84
P30999_C	Ctnnd1	Catenin del	5	4.2	14.8	16.1	0.3	0.26	3.83	86.0	60.2	73.3	1.4	1.17	0.85
Q9CY50_SS	Ssr1	Translocon	1	3.2	11.4	12.4	0.3	0.26	3.84	3.2	11.4	13.8	0.3	0.23	4.29
Q9DCF9_S	Ssr3	Translocon	1	2.4	8.4	9.1	0.3	0.26	3.84	2.4	8.4	10.2	0.3	0.23	4.29
Q9JJG0_TA	Tacc2	Transformi	1	1.7	6.2	6.7	0.3	0.26	3.86	1.7	6.2	7.5	0.3	0.23	4.31
Q80TM9_N	Nisch	Nischarin C	3	4.1	14.7	16.0	0.3	0.26	3.87	10.6	41.3	50.3	0.3	0.21	4.75
Q8R323_RI	Rfc3	Replication	8	4.8	16.9	18.5	0.3	0.26	3.89	45.4	144.1	175.4	0.3	0.26	3.87
Q920Q4_VI	Vps16	Vacuolar pr	3	2.0	7.3	7.9	0.3	0.26	3.92	12.1	27.4	33.4	0.4	0.36	2.76
Q8C6G8_W	Wdr26	WD repeat-	3	2.5	9.0	9.8	0.3	0.26	3.92	9.7	28.4	34.5	0.3	0.28	3.55
Q8BZ20_P	Parp12	Poly [ADP-r	1	4.0	14.4	15.8	0.3	0.25	3.94	4.0	14.4	17.6	0.3	0.23	4.40
P62806_H	Hist1h4a	Histone H4	29	26.6	96.4	105.1	0.3	0.25	3.95	13669.1	25951.4	31587.2	0.5	0.43	2.31
Q99LT0_DF	Dpy30	Protein dpy	1	7.4	26.9	29.4	0.3	0.25	3.95	7.4	26.9	32.8	0.3	0.23	4.40
P70257_NI	Nfix	Nuclear fac	11	3.3	12.3	13.4	0.3	0.25	4.00	81.8	138.7	168.9	0.6	0.48	2.06
A2BE28_LA	Las1l	Ribosomal	4	4.3	15.8	17.2	0.3	0.25	4.02	27.8	63.1	76.8	0.4	0.36	2.76
Q925J9_MI	Med1	Mediator o	1	2.9	10.7	11.7	0.3	0.25	4.02	2.9	10.7	13.1	0.3	0.22	4.48
Q3UPF5_Z	Zc3hav1	Zinc finger	7	2.9	10.5	11.5	0.3	0.25	4.02	26.1	65.6	79.8	0.4	0.33	3.05
Q63871_RI	Polr2k	DNA-direct	1	12.3	45.5	49.6	0.3	0.25	4.03	12.3	45.5	55.3	0.3	0.22	4.49
Q80YR9_R1	Rbm12b1	RNA-bindir	1	2.4	8.7	9.5	0.3	0.25	4.03	2.4	8.7	10.6	0.3	0.22	4.50
Q99K28_AI	Arfgap2	ADP-ribosy	8	4.4	16.2	17.7	0.3	0.25	4.04	43.7	132.3	161.0	0.3	0.27	3.68
Q9D0W5_I	Ppil1	Peptidyl-pr	2	5.0	18.5	20.1	0.3	0.25	4.04	10.0	36.9	44.9	0.3	0.22	4.51
Q3THS6_M	Mat2a	S-adenosyl	2	1.7	6.4	7.0	0.3	0.25	4.05	3.5	12.8	15.6	0.3	0.22	4.51
Q8BU11_T	Tox4	TOX high m	5	4.2	15.6	17.0	0.3	0.25	4.06	58.7	102.1	124.3	0.6	0.47	2.12
Q64310_SU	Surf4	Surfeit locu	1	9.5	35.6	38.9	0.3	0.25	4.07	9.5	35.6	43.4	0.3	0.22	4.54
A6PWY4_W	Wdr76	WD repeat-	7	2.3	8.4	9.2	0.3	0.24	4.08	18.7	62.4	75.9	0.3	0.25	4.06
Q8BL97_SF	Srsf7	Serine/argi	5	15.4	58.0	63.2	0.3	0.24	4.11	263.7	357.8	435.5	0.7	0.61	1.65
Q9D0E1_HI	Hnrnpm	Heterogene	139	13.0	49.1	53.6	0.3	0.24	4.13	5701.0	13172.3	16032.9	0.4	0.36	2.81
Q9ER81_IF	Tor1aip2	Torsin-1A-i	1	5.5	21.0	22.9	0.3	0.24	4.13	5.5	21.0	25.5	0.3	0.22	4.61
Q60974_N	Ncor1	Nuclear rec	3	2.9	11.1	12.1	0.3	0.24	4.14	16.2	33.2	40.5	0.5	0.40	2.50
Q9Z2D8_M	Mbd3	Methyl-Cp	8	4.6	17.3	18.9	0.3	0.24	4.14	43.5	157.1	191.2	0.3	0.23	4.39
P61022_CI	Chp1	Calcineurir	4	3.3	12.4	13.5	0.3	0.24	4.15	14.5	47.6	57.9	0.3	0.25	4.00
Q3U5F4_YI	Yrdc	YrdC domai	1	1.4	5.3	5.7	0.3	0.24	4.15	1.4	5.3	6.4	0.3	0.22	4.63
Q91VM5_R	Rbmxl1	RNA bindin	12	25.5	97.1	105.9	0.3	0.24	4.15	697.2	1304.7	1588.0	0.5	0.44	2.28
Q9D8Y8_IN	Ing5	Inhibitor o	2	4.0	15.2	16.6	0.3	0.24	4.17	7.9	30.4	37.0	0.3	0.21	4.66
Q8VI33_TA	Taf9	Transcripti	1	2.7	10.6	11.5	0.3	0.24	4.22	2.7	10.6	12.9	0.3	0.21	4.71
Q60875_AI	Arhgef2	Rho guanin	14	6.2	24.0	26.2	0.3	0.24	4.22	215.4	405.4	493.5	0.5	0.44	2.29
Q91WQ5_1	Taf5l	TAF5-like R	1	2.3	9.1	9.9	0.3	0.24	4.24	2.3	9.1	11.1	0.3	0.21	4.73
B2RRF6_Z5	Znf518a	Zinc finger	1	5.2	20.3	22.1	0.3	0.24	4.25	5.2	20.3	24.7	0.3	0.21	4.74
Q8CHY6_P	Gatad2a	Transcripti	11	5.1	19.8	21.6	0.3	0.23	4.26	152.7	234.8	285.7	0.7	0.53	1.87
Q9D0N7_C	Chaf1b	Chromatin	3	1.9	7.5	8.2	0.3	0.23	4.27	9.6	21.8	26.5	0.4	0.36	2.78
Q6PHZ5_RI	Rbm15b	Putative RN	3	2.6	10.3	11.2	0.3	0.23	4.27	19.2	29.0	35.4	0.7	0.54	1.84
Q05186_R	Rcn1	Reticulocal	4	3.5	13.9	15.2	0.3	0.23	4.30	14.6	67.6	82.3	0.2	0.18	5.62
D3YXK2_SA	Safb	Scaffold att	11	4.2	16.6	18.1	0.3	0.23	4.33	143.8	259.4	315.8	0.6	0.46	2.20
O35682_M	Myadm	Myeloid-as	2	8.9	35.3	38.5	0.3	0.23	4.35	17.7	70.6	85.9	0.3	0.21	4.85
A5D6P6_A	Twist2	Twist homo	2	1.4	5.7	6.2	0.3	0.23	4.36	2.8	11.4	13.9	0.3	0.21	4.87
Q9QX47_S	Son	Protein SO	20	5.5	22.3	24.3	0.2	0.23	4.42	330.9	601.2	731.8	0.6	0.45	2.21
P84104_SF	Srsf3	Serine/argi	9	15.9	64.4	70.2	0.2	0.23	4.43	439.3	2181.8	2655.6	0.2	0.17	6.04
Q9DC51_G	Gnai3	Guanine nu	1	2.4	9.8	10.7	0.2	0.23	4.43	2.4	9.8	12.0	0.2	0.20	4.95
Q8BSN5_PI	Phf23	PHD finger	2	3.0	12.0	13.1	0.2	0.22	4.45	5.9	24.0	29.3	0.2	0.20	4.96
Q8K0H5_T	Taf10	Transcripti	1	1.6	6.4	7.0	0.2	0.22	4.46	1.6	6.4	7.8	0.2	0.20	4.97
P62264_RS	Rps14	40S riboso	10	16.1	66.0	72.0	0.2	0.22	4.47	652.2	1333.9	1623.6	0.5	0.40	2.49
Q3TUF7_YE	Yeats2	YEATS dom	2	2.6	10.6	11.5	0.2	0.22	4.47	5.2	21.1	25.7	0.2	0.20	4.98
Q9CQN1_TI	Trap1	Heat shock	2	9.6	39.8	43.5	0.2	0.22	4.51	19.3	79.7	97.0	0.2	0.20	5.04
Q66T02_PI	Plekhg5	Pleckstrin	2	3.4	14.1	15.4	0.2	0.22	4.52	6.8	28.2	34.4	0.2	0.20	5.04
Q8CJF7_EL	Ahctf1	Protein ELY	1	3.3	13.5	14.7	0.2	0.22	4.52	3.3	13.5	16.4	0.2	0.20	5.04

Q9R233_TI	Tapbp	Tapasin OS=	1	3.2	13.2	14.3	0.2	0.22	4.52	3.2	13.2	16.0	0.2	0.20	5.05
Q9DAS9_GI	Gng12	Guanine nu	1	8.2	34.6	37.7	0.2	0.22	4.61	8.2	34.6	42.1	0.2	0.19	5.14
Q9CQ65_N	Mtap	S-methyl-5'	1	1.8	7.5	8.1	0.2	0.22	4.61	1.8	7.5	9.1	0.2	0.19	5.14
Q99L48_NI	Nmd3	60S ribosor	2	2.7	11.3	12.3	0.2	0.22	4.62	5.3	22.6	27.5	0.2	0.19	5.15
Q9D2D7_Zl	Znf687	Zinc finger	4	4.7	19.9	21.7	0.2	0.22	4.65	28.7	74.5	90.6	0.4	0.32	3.15
P63044_VA	Vamp2	Vesicle-assc	1	10.2	43.7	47.7	0.2	0.21	4.66	10.2	43.7	53.2	0.2	0.19	5.20
Q8BP71_RI	Rbfox2	RNA bindin	6	6.9	29.5	32.2	0.2	0.21	4.68	39.3	199.8	243.2	0.2	0.16	6.18
Q923D1_Q	Zfp61	Protein Zfp	1	3.7	16.0	17.4	0.2	0.21	4.71	3.7	16.0	19.4	0.2	0.19	5.25
Q91ZX7_LF	Lrp1	Prolow-der	1	1.6	7.0	7.6	0.2	0.21	4.72	1.6	7.0	8.5	0.2	0.19	5.26
Q8BMZ5_SI	Tsen34	tRNA-splici	1	2.1	9.1	9.9	0.2	0.21	4.74	2.1	9.1	11.1	0.2	0.19	5.28
P14404_EV	Mecom	MDS1 and I	4	3.3	14.3	15.6	0.2	0.21	4.74	27.6	59.6	72.5	0.5	0.38	2.63
Q8BPM2_N	Map4k5	Mitogen-ac	2	9.0	39.1	42.6	0.2	0.21	4.75	18.0	78.1	95.1	0.2	0.19	5.30
D3YWT1_D	Hnrnph3	MCG11326	5	4.9	21.6	23.6	0.2	0.21	4.79	81.8	126.0	153.4	0.6	0.53	1.88
O88522_NI	Ikbkg	NF-kappa-B	1	2.1	9.2	10.0	0.2	0.21	4.79	2.1	9.2	11.2	0.2	0.19	5.35
Q61329_ZF	Zfhx3	Zinc finger I	1	2.0	8.9	9.8	0.2	0.21	4.80	2.0	8.9	10.9	0.2	0.19	5.35
E9Q7N9_E9	Dnah11	Protein Dna	2	14.9	65.4	71.4	0.2	0.21	4.80	29.7	130.9	159.3	0.2	0.19	5.36
Q9D2L9_F1	Fam111a	Protein FAI	1	3.3	14.5	15.9	0.2	0.21	4.81	3.3	14.5	17.7	0.2	0.19	5.37
Q8R149_BI	Bud13	BUD13 hon	3	4.4	19.4	21.1	0.2	0.21	4.82	15.5	54.4	66.2	0.3	0.23	4.26
Q91YE5_BA	Baz2a	Bromodom	2	2.1	9.3	10.2	0.2	0.21	4.82	4.2	18.6	22.7	0.2	0.19	5.38
P01899_HA	H2-D1	H-2 class I h	23	4.8	21.3	23.3	0.2	0.21	4.85	219.1	497.2	605.1	0.4	0.36	2.76
P84089_EF	Erh	Enhancer o	2	17.2	76.4	83.3	0.2	0.21	4.86	34.3	152.8	186.0	0.2	0.18	5.42
Q8VDP6_CI	Cdipt	CDP-diacyl	1	1.4	6.2	6.8	0.2	0.20	4.89	1.4	6.2	7.6	0.2	0.18	5.46
P28653_PC	Bgn	Biglycan OS	1	2.7	12.0	13.0	0.2	0.20	4.90	2.7	12.0	14.5	0.2	0.18	5.46
Q9CZX5_PI	Pinx1	PIN2/TERF1	1	2.4	10.7	11.7	0.2	0.20	4.92	2.4	10.7	13.0	0.2	0.18	5.49
Q6DID5_M	Mum1	PWWP don	1	2.1	9.4	10.3	0.2	0.20	4.95	2.1	9.4	11.5	0.2	0.18	5.52
Q8K2B0_SC	Leprel4	Synaptoner	1	1.5	7.0	7.6	0.2	0.20	4.97	1.5	7.0	8.5	0.2	0.18	5.55
G5E8P1_G5	Brd1	MCG7283 (	4	4.9	22.6	24.6	0.2	0.20	4.99	35.5	112.2	136.5	0.3	0.26	3.84
Q923G2_RI	Polr2h	DNA-direct	5	6.1	27.8	30.4	0.2	0.20	4.99	34.7	156.6	190.6	0.2	0.18	5.49
E9Q4F8_E9	Ankrd11	Protein Ank	1	1.9	8.7	9.5	0.2	0.20	5.01	1.9	8.7	10.6	0.2	0.18	5.59
Q9D883_U	U2af1	Splicing fac	5	11.7	54.4	59.4	0.2	0.20	5.07	118.3	485.7	591.2	0.2	0.20	5.00
Q9D083_SI	Spc24	Kinetochor	2	1.8	8.3	9.0	0.2	0.20	5.10	3.5	16.5	20.1	0.2	0.18	5.69
P01887_B2	B2m	Beta-2-micr	2	12.9	60.4	65.9	0.2	0.20	5.12	25.7	120.8	147.0	0.2	0.17	5.72
P20152_VI	Vim	Vimentin O	7	4.8	22.7	24.8	0.2	0.19	5.16	53.3	154.1	187.5	0.3	0.28	3.52
P05627_JU	Jun	Transcripti	1	1.8	8.7	9.5	0.2	0.19	5.17	1.8	8.7	10.6	0.2	0.17	5.76
F6ZQA3_F6	Numa1	Protein Nu	2	6.5	30.6	33.4	0.2	0.19	5.17	12.9	61.2	74.5	0.2	0.17	5.77
Q80XP8_FA	Fam76b	Protein FAI	3	3.9	18.6	20.3	0.2	0.19	5.19	25.9	45.9	55.8	0.6	0.46	2.15
Q80YR5_SA	Safb2	Scaffold att	5	3.5	16.4	17.9	0.2	0.19	5.19	19.2	79.9	97.2	0.2	0.20	5.07
Q99PP7_TF	Trim33	E3 ubiquiti	2	3.1	14.8	16.1	0.2	0.19	5.19	6.2	29.5	35.9	0.2	0.17	5.79
Q64522_H	Hist2h2ab	Histone H2	3	32.1	153.4	167.4	0.2	0.19	5.22	481.0	727.5	885.5	0.7	0.54	1.84
Q61602_GI	Gli3	Transcripti	1	1.4	6.8	7.5	0.2	0.19	5.30	1.4	6.8	8.3	0.2	0.17	5.92
Q78ZM0_Q	Snx3	Sorting nex	7	11.6	56.7	61.9	0.2	0.19	5.34	169.2	335.0	407.7	0.5	0.42	2.41
Q8C7Q4_RI	Rbm4	RNA-bindir	4	2.5	12.1	13.2	0.2	0.19	5.35	23.7	49.9	60.8	0.5	0.39	2.56
Q91YH5_AT	Atl3	Atlastin-3 C	2	2.4	12.0	13.1	0.2	0.19	5.37	4.9	24.0	29.2	0.2	0.17	5.99
P97314_CS	Csrp2	Cysteine an	7	12.3	60.6	66.1	0.2	0.19	5.37	580.3	858.0	1044.4	0.7	0.56	1.80
Q61792_LA	Lasp1	LIM and SH	9	8.6	43.0	46.9	0.2	0.18	5.43	197.1	317.8	386.9	0.6	0.51	1.96
P97376_FF	Frg1	Protein FRC	1	1.8	8.8	9.6	0.2	0.18	5.51	1.8	8.8	10.8	0.2	0.16	6.14
Q91V81_RI	Rbm42	RNA-bindir	4	2.9	14.6	15.9	0.2	0.18	5.57	25.2	52.9	64.4	0.5	0.39	2.56
Q6PFQ7_RA	Rasa4	Ras GTPase-	1	1.5	8.0	8.7	0.2	0.18	5.66	1.5	8.0	9.7	0.2	0.16	6.32
O35216_CI	Cenpa	Histone H3	1	2.2	11.7	12.8	0.2	0.18	5.68	2.2	11.7	14.2	0.2	0.16	6.33
J3QNW0_J3	Dnmt1	DNA (cytosi	2	3.6	19.0	20.8	0.2	0.18	5.71	7.3	38.1	46.3	0.2	0.16	6.37
P51480_CI	Cdkn2a	Cyclin-depe	1	2.9	15.3	16.7	0.2	0.17	5.74	2.9	15.3	18.6	0.2	0.16	6.41
Q6ZWY9_H	Hist1h2bc	Histone H2	1	179.0	944.5	1030.3	0.2	0.17	5.76	179.0	944.5	1149.6	0.2	0.16	6.42
Q5SU73_C(	Coil	Coilin OS=N	1	2.6	13.8	15.1	0.2	0.17	5.76	2.6	13.8	16.8	0.2	0.16	6.43
Q9CQL7_M	Mrfap1	MORF4 fam	2	3.7	19.4	21.2	0.2	0.17	5.79	7.3	38.8	47.3	0.2	0.15	6.46
P15379_CI	Cd44	CD44 antig	1	6.4	33.7	36.8	0.2	0.17	5.79	6.4	33.7	41.1	0.2	0.15	6.46
Q8K1E0_ST	Stx5	Syntaxin-5	1	0.9	4.8	5.3	0.2	0.17	5.84	0.9	4.8	5.9	0.2	0.15	6.51
Q9QYH6_N	Maged1	Melanoma-	1	2.2	11.9	12.9	0.2	0.17	5.87	2.2	11.9	14.4	0.2	0.15	6.55
P0C0A3_CI	Chmp6	Charged mu	1	1.8	10.0	10.9	0.2	0.17	5.94	1.8	10.0	12.2	0.2	0.15	6.63
Q00288_PA	Pax8	Paired box	2	2.8	15.3	16.6	0.2	0.17	5.99	5.6	30.5	37.1	0.2	0.15	6.68
Q9JIY2_HAI	Cbll1	E3 ubiquiti	1	2.3	13.0	14.2	0.2	0.16	6.08	2.3	13.0	15.9	0.2	0.15	6.79
P60898_RF	Polr2i	DNA-direct	2	7.6	43.8	47.8	0.2	0.16	6.25	15.3	87.6	106.6	0.2	0.14	6.97
Q9JHJ0_TN	Tmod3	Tropomodu	19	7.6	43.9	47.9	0.2	0.16	6.31	439.9	1439.2	1751.8	0.3	0.25	3.98
Q148V8_FA	Fam83h	Protein FAI	1	1.2	6.7	7.3	0.2	0.16	6.33	1.2	6.7	8.1	0.2	0.14	7.07
Q922G2_FA	Fam76a	Protein FAI	1	2.3	13.6	14.8	0.2	0.16	6.35	2.3	13.6	16.5	0.2	0.14	7.08
Q3THW5_H	H2afv	Histone H2	3	86.6	505.5	551.4	0.2	0.16	6.36	1203.0	2191.6	2667.5	0.5	0.45	2.22
Q8R344_C(	Ccdc12	Coiled-coil	2	4.2	24.6	26.9	0.2	0.16	6.42	8.4	49.3	60.0	0.2	0.14	7.17
Q9D0B0_SI	Srsf9	Serine/argi	13	4.8	28.6	31.2	0.2	0.15	6.50	209.9	685.9	834.9	0.3	0.25	3.98
G3X9B1_G3	Heatr1	HEAT repea	1	2.1	13.0	14.2	0.2	0.15	6.68	2.1	13.0	15.8	0.2	0.13	7.45
Q8BVG8_N	Nat14	N-acetyltra	1	1.8	10.9	11.8	0.2	0.15	6.70	1.8	10.9	13.2	0.2	0.13	7.47
Q9WTX8_N	Mad1l1	Mitotic spi	5	2.9	18.0	19.7	0.2	0.15	6.73	18.8	82.0	99.8	0.2	0.19	5.32
Q91VT1_NS	Nsmce2	E3 SUMO-p	1	2.3	14.8	16.1	0.2	0.14	7.00	2.3	14.8	18.0	0.2	0.13	7.81
A2A9Z5_A2	Gm53	Protein Gm	1	1.7	11.3	12.4	0.2	0.14	7.21	1.7	11.3	13.8	0.2	0.12	8.04
Q9R0U0_SI	Srsf10	Serine/argi	8	13.1	86.6	94.5	0.2	0.14	7.22	108.4	659.8	803.1	0.2	0.13	7.41
P07214_SF	Sparc	SPARC OS=I	1	3.0	20.0	21.8	0.2	0.14	7.23	3.0	20.0	24.4	0.2	0.12	8.06
P62892_RL	Rpl39	60S ribosor	1	2.8	18.9	20.6	0.1	0.14	7.31	2.8	18.9	23.0	0.1	0.12	8.15
Q9EP97_SE	Senp3	Sentrin-spe	1	1.9	13.0	14.2	0.1	0.13	7.43	1.9	13.0	15.8	0.1	0.12	8.29
Q91W39_N	Ncoa5	Nuclear rec	3	3.0	20.5	22.4	0.1	0.13	7.56	10.0	57.3	69.7	0.2	0.14	6.94
Q921M4_G	Golga2	Golgin subf	1	1.3	9.3	10.1	0.1	0.13	7.67	1.3	9.3	11.3	0.1	0.12	8.56
E9PYI4_E9I	Mroh8	Protein Mr	1	1.8	12.9	14.1	0.1	0.13	7.71	1.8	12.9	15.8	0.1	0.12	8.60
Q9CPW7_Z	Zmat2	Zinc finger	1	1.9	13.4	14.7	0.1	0.13	7.72	1.9	13.4	16.4	0.1	0.12	8.61
Q810F8_TE	Tbx10	T-box trans	1	2.4	17.5	19.1	0.1	0.13	7.81	2.4	17.5	21.3	0.1	0.11	8.72
Q6PDN3_N	Mylk	Myosin ligh	1	4.2	30.7	33.5	0.1	0.13	7.97	4.2	30.7	37.4	0.1	0.11	8.89
P62071_RF	Rras2	Ras-related	3	1.4	10.7	11.6	0.1	0.12	8.08	39.7	31.4	38.3	1.3	1.04	0.96
Q5DTT3_F2	Fam208b	Protein FAI	1	2.0	16.0	17.5	0.1	0.12	8.59	2.0	16.0	19.5	0.1	0.10	9.59
Q9JJD0_TH	Thap11	THAP doma	1	1.4	10.9	11.9	0.1	0.12	8.69	1.4	10.9	13.3	0.1	0.10	9.69
P17918_PC	Pcna	Proliferatin	9	3.4	28.3	30.9	0.1	0.11	9.12	73.9	251.6	306.2	0.3	0.24	4.14
A0A0A6YW	Ighg1	Ig gamma-1	1	24.2	227.1	247.8	0.1	0.10	10.26	24.2	227.1	276.5	0.1	0.09	11.44
Q6PFR5_TF	Tra2a	Transforme	5	2.5	26.8	29.3	0.1	0.09	11.62	50.3	256.7	312.4	0.2	0.16	6.21
P09450_JU	Junb	Transcripti	1	1.4	15.8	17.3	0.1	0.08	12.59	1.4	15.8	19.3	0.1	0.07	14.05
Q9ER88_R1	Dap3	28S ribosor	1	1.8	22.4	24.4	0.1	0.07	13.38	1.8	22.4	27.2	0.1	0.07	14.93
Q8BHX3_B(	Cdca8	Borealin OS	2	1.7	22.4	24.5	0.1	0.07	14.58	3.4	44.9	54.6	0.1	0.06	16.26
P31001_DI	Des	Desmin OS=	2	5.3	79.5	86.7	0.1	0.06	16.23	10.7	159.0	193.5	0.1	0.06	18.11
Q99N96_RI	Mrpl1	39S ribosor	1	3.1	50.9	55.5	0.1	0.06	18.15	3.1	50.9	61.9	0.1	0.05	20.25
Q8R3Y5_CS047_MOUS		Uncharacte	1	14.9	280.7	306.2	0.1	0.05	20.57	14.9	280.7	341.7	0.1	0.04	22.95
H3BL88_H3	9930021J0	Protein 993	1	1.4	28.9	31.6	0.0	0.04	23.05	1.4	28.9	35.2	0.0	0.04	25.71
F7ARK3_F7	Sall2	Sal-like pro	1	1.4	44.5	48.6	0.0	0.03	35.70	1.4	44.5	54.2	0.0	0.03	39.83
Q9JMB0_G	Gkap1	G kinase-an	2	2.1	73.5	80.2	0.0	0.03	38.28	4.2	147.0	179.0	0.0	0.02	42.71
Q3UBX0_TI	Tmem109	Transmemb	1	1.6	69.8	76.1	0.0	0.02	46.15	1.6	69.8	84.9	0.0	0.02	51.49