Protein	Descriptior	Gene	SaOS2_1	SaOS2_2	SaOS2_3	Osteoblast	Osteoblast	Osteoblast
A0A096LP	Protein LO	LOC10272	141499.3	184610.4	13242.11	0	0	0
A0A0C4DH	Protein IGH	IGKV3D-2(	656223.3	728444.8	857271.7	0	0	0
A4D1P6	WD repeat	WDR91	49644.28	24090.97	50446.61	0	0	0
A6NCE7	Microtubu	MAP1LC3E	33087.36	37795.51	30380.12	0	0	0
A8MUH7	Putative PI	PDZK1P1	12912.75	13263.25	9776.056	0	0	0
A8MWD9	Putative sn	SNRPGP15	58687.55	56687.87	66189.8	42343.49	523188.7	0
A8TX70	Collagen a	COL6A5	0	0	0	77088.55	58613.52	111480.6
B4DGG1	Uncharacterized prote		14005.25	14527.02	12710.08	0	0	0
B4E1Z4	Uncharacterized prote		688666.9	322695	407152	4228377	5263997	1517109
B5ME19	Eukaryotic	EIF3CL	195806.3	182204.9	129271.7	128058	63098.57	104513.3
B9A064	Immunogl	IGLL5	10129395	12438769	16442843	5589226	8012192	4820024
C9J1V9	HCG20432	EEF1E1-BL	18660.78	27038.32	32129.65	0	0	0
E7EVH7	Uncharacterized prote		19464.21	23470.3	25977.35	0	0	0
E9PSI1	Uncharacterized prote		18744.4	38557.19	71888.6	0	0	0
G3V3G9	Uncharacterized prote		9091.935	6935.12	3116.582	0	0	0
H3BMM5	Uncharacterized prote		5370.653	3559.923	6050.086	0	0	0
I3L0A0	HCG20447	TMEM189-	70481.13	65918.14	57565.6	50509.09	0	50917.48
O00139	Kinesin-lik	KIF2A	8474.253	6929.253	8572.156	0	0	0
O00151	PDZ and L	PDLIM1	14999.3	19948.86	26428.35	76848.63	0	47939.38
O00154	Cytosolic a	ACOT7	21264.24	129176.7	110010.1	0	0	0
O00159	Unconvent	MYO1C	39900.88	39972.77	35568.07	85332.45	0	133874.4
O00161	Synaptoso	SNAP23	35715.42	33009.78	30533.8	0	0	0
O00186	Syntaxin-b	STXBP3	25373.13	31545.86	23642.17	0	0	0
O00187	Mannan-b	MASP2	33129.7	35525	43714.66	111930.3	0	128323.7
O00193	Small acidi	SMAP	44162.9	65649.77	60520.91	0	0	0
O00203	AP-3 com	AP3B1	220408.4	184637.9	139501.5	129934.9	18222068	3270287
O00231	26S protea	PSMD11	62587.27	55786.2	68627.61	85492.82	0	73611.55
O00267	Transcripti	SUPT5H	11707.52	12259.52	17023.83	0	0	0
O00299	Chloride ir	CLIC1	141848	138296.2	138452	148484.3	148296	154672.1
O00303	Eukaryotic	EIF3F	106659.5	99040.09	127585.1	68613.09	0	77429.93
O00339	Matrilin-2	MATN2	57964.3	55033.91	59989.7	0	0	0
O00391	Sulfhydryl	QSOX1	127931.4	102492.4	159876.8	1010303	1379340	784346.1
O00401	Neural Wis	WASL	78995.66	90041.25	19113.47	0	0	0
O00410	Importin-5	IPO5	46588.96	33975.83	38039.55	68267	0	46220.8
O00468	Agrin	AGRN	443751.4	433029.4	426231.7	583264.7	734229.8	570367
O00469	Procollage	PLOD2	23142.45	20687.52	28107.99	195423.5	219409.1	167949.8
O00487	26S protea	PSMD14	69438.43	68440.6	82446.6	145536.8	0	164732.9
O00499	Myc box-c	BIN1	44225.93	40866.4	51361.67	0	0	0
O00505	Importin su	KPNA3	7862.523	7221.579	8497.945	0	0	0
O00507	Probable u	USP9Y	18380.16	15342.09	11781.53	0	0	0
O00560	Syntenin-1	SDCBP	310899.1	297567.8	233804.8	354369.2	0	338963.3
O00567	Nucleolar p	NOP56	12653.96	14112.15	22069.36	0	0	0
O00592	Podocalyxi	PODXL	61025.53	42096.55	43778.39	0	0	0
O00622	Protein CY	CYR61	54217.86	38638.99	38463.05	802018.5	495080.8	812536.9
O00754	Lysosomal	MAN2B1	108829.4	39959.31	42142.07	213196	275519.8	149103.6
O00764	Pyridoxal k	PDXK	4702.639	19454.74	2363.363	0	0	0
O14497	AT-rich int	ARID1A	1540.53	2154.799	4748.741	0	0	0
O14530	Thioredoxi	TXNDC9	21054.45	20144.54	16288.32	0	0	0
O14579	Coatomer	COPE	20546.4	15401.79	18944.64	0	0	0
O14657	Torsin-1B	TOR1B	6872.416	6350.871	11225.77	0	0	0
O14672	Disintegrin	ADAM10	394996	352000.7	291352.1	291035.2	0	319522.6
O14744	Protein arg	PRMT5	56303.07	48720.6	51507.09	0	0	0
O14745	Na(+)/H(+	SLC9A3R1	76609.27	77582	60351.39	0	0	0
O14786	Neuropilin	NRP1	25860.06	23479.54	21984.55	60399.73	88702.34	73123.23
O14787	Transportir	TNPO2	21191.19	11488.92	16619.69	0	0	0
O14817	Tetraspani	TSPAN4	460825.5	438188.4	330381.4	256016	0	479146.7
O14818	Proteasom	PSMA7	237447.5	230236.6	289526.2	86836.34	98504.18	79160.2

O14908	PDZ doma	GIPC1	37482.96	40029.09	51903.06	0	0	0
O14910	Protein lin	LIN7A	59755.05	67100.97	48191.22	0	0	0
O14929	Histone ac	HAT1	35149.08	35663.18	35229.2	0	0	0
O14936	Peripheral	CASK	29129.42	26528.72	20659.69	0	0	0
O14950	Myosin reg	MYL12B	137148.6	146589.8	192537.3	313671.6	241507	219710.3
O14964	Hepatocyt	HGS	30654.56	30393.87	25137.95	0	0	0
O14974	Protein ph	PPP1R12A	66087.78	53175.77	45851.25	0	0	0
O14976	Cyclin-G-a	GAK	6249.824	3817.157	6964.988	0	0	0
O14979	Heterogen	HNRNPDL	48424.54	72196.88	43218.22	0	0	0
O14980	Exportin-1	XPO1	21235.8	22609.02	24675.56	0	0	0
O15031	Plexin-B2	PLXNB2	28098.72	26532.78	19972.33	63621.37	83108.97	36291.48
O15042	U2 snRNP	U2SURP	9431.827	11609.72	11772.91	0	0	0
O15067	Phosphoril	PFAS	24412.12	20348	26294.41	0	0	0
O15118	Niemann-	NPC1	21294.96	24329.95	16474.8	0	0	0
O15144	Actin-relat	ARPC2	75503.6	86568.43	93427.43	0	392752.4	67848.52
O15145	Actin-relat	ARPC3	83148.11	102744.3	103726	41038.46	0	24972.87
O15162	Phospholip	PLSCR1	151555.6	163150	106336.4	0	0	0
O15212	Prefoldin s	PFDN6	27215.09	15832.9	16225.57	0	0	0
O15230	Laminin su	LAMA5	28238.91	24447.12	22173.59	36579.36	58980.03	29751.91
O15260	Surfeit loc	SURF4	22377.4	34837.45	0	143168.2	0	117005.4
O15305	Phosphom	PMM2	26150.37	20302.83	23033.31	0	0	0
O15347	High mobi	HMGB3	127026.3	110868.2	58628.38	0	0	0
O15355	Protein ph	PPM1G	132059.7	128754	79278.22	0	0	0
O15397	Importin-8	IPO8	10013.56	9499.487	12840.77	0	0	0
O15400	Syntaxin-7	STX7	83163.43	98403.66	80257.92	43829.52	82294.27	171820.5
O15427	Monocarb	SLC16A3	125132.7	106300	77092.64	169751.5	181709.3	233618.8
O15431	High affini	SLC31A1	17844.94	19590.13	12866.35	0	0	0
O15460	Prolyl 4-hy	P4HA2	5849.814	9942.443	9693.71	0	0	0
O15498	Synaptobr	YKT6	520485.7	353308	543818.4	0	0	0
O15511	Actin-relat	ARPC5	40817.92	44378.19	38737.5	0	0	0
O43150	Arf-GAP w	ASAP2	10210	9727.846	11152.53	0	0	0
O43169	Cytochrom	CYB5B	19282.42	10701.19	8468.618	0	0	0
O43172	U4/U6 sma	PRPF4	6850.562	4917.343	6782.071	0	0	0
O43175	D-3-phosp	PHGDH	196171.8	219714.8	201754.3	102313.8	88738.13	116331.9
O43237	Cytoplasm	DYNC1LI2	11044.23	19098.64	12744.37	0	0	0
O43242	26S protea	PSMD3	56978.7	58909.72	57192.66	132062.8	0	60403.45
O43252	Bifunctiona	PAPSS1	21942.83	10294.71	13562.62	0	0	0
O43264	Centromer	ZW10	9559.555	12187.39	6239.157	0	0	0
O43286	Beta-1,4-g	B4GALT5	78473.2	65443.34	77789.66	295101.6	376298.9	244293.5
O43294	Transformi	TGFB1I1	17621.09	17865.83	25918.78	158149.4	0	56003.31
O43390	Heterogen	HNRNPR	55777.64	65710.77	63801.98	40704.81	0	41427.71
O43399	Tumor pro	TPD52L2	30450.04	13275.01	21245.48	0	0	0
O43451	Maltase-gl	MGAM	65795.16	64550.81	71705.48	0	0	0
O43488	Aflatoxin B	AKR7A2	27302.59	24691.98	44761.04	0	0	0
O43491	Band 4.1-l	EPB41L2	109153.8	89511.09	59527.1	0	0	0
O43504	Ragulator	LAMTOR5	14039.87	12115.07	11018.28	0	0	0
O43505	Beta-1,4-g	B4GAT1	29334.64	25361.74	21604.42	163779.5	137959.4	101226.5
O43592	Exportin-T	XPOT	18236.65	11139.01	14845.52	0	0	0
O43617	Trafficking	TRAPPC3	28745.37	26932.52	27481.84	0	0	0
O43633	Charged m	CHMP2A	65247.84	67170.39	61491.55	0	0	0
O43657	Tetraspani	TSPAN6	33973.09	44773.97	35099.29	0	0	0
O43670	BUB3-inte	ZNF207	13523.37	24998.29	19573.31	0	0	0
O43681	ATPase AS	ASNA1	31161.07	26793.09	36324.37	0	0	0
O43684	Mitotic che	BUB3	54063.59	55308.32	58698.85	0	0	0
O43739	Cytohesin-	CYTH3	17327.97	13185.76	17056.87	0	0	0
O43747	AP-1 com	AP1G1	17394.21	18600.07	18016.53	0	2675926	2.56E+08
O43765	Small glut	SGTA	22575.02	14592.21	25563.88	0	0	0
O43795	Unconvent	MYO1B	33031	38887.7	30524.07	0	0	0

O43809	Cleavage a	NUDT21	44839.2	37576.32	47693.58	0	0	0
O43813	LanC-like p	LANCL1	40244.41	35069.76	48263.63	0	0	0
O43847	Nardilysin	NRD1	77834.38	74328.13	29329.99	0	0	0
O43852	Calumenin	CALU	14939.85	27927.01	26438.68	217148.3	230224.7	153953.6
O43854	EGF-like re	EDIL3	2134936	2313284	1849099	1517839	1147329	2769120
O43865	Adenosylh	AHCYL1	234959.3	227965.6	293691.1	199581.1	166282.1	224099
O60216	Double-str	RAD21	3951.496	3193.659	6122.842	0	0	0
O60231	Putative pr	DHX16	6954.763	5293.757	5811.263	0	0	0
O60264	SWI/SNF-r	SMARCA5	12874.43	19919.55	15052.13	0	0	0
O60271	C-Jun-ami	SPAG9	19422.79	70123.7	10146.6	0	0	0
O60291	E3 ubiquiti	MGRN1	9065.249	2585.408	1442.024	0	0	0
O60341	Lysine-spe	KDM1A	11099.18	10608.35	11586.68	0	0	0
O60361	Putative nu	NME2P1	89458.07	98934.98	63938.95	0	0	0
O60462	Neuropilin	NRP2	11816.4	11381.34	13903.14	95607.87	100312.9	46468.12
O60488	Long-chai	ACSL4	16217.34	19959.15	12412.56	0	0	0
O60493	Sorting ne	SNX3	48696.55	44300.34	42647.11	29374.17	0	24071.7
O60502	Protein O-	MGEA5	13711.99	17475.02	8012.048	0	0	0
O60506	Heterogen	SYNCRIP	39160.69	23992.06	72371.27	0	0	0
O60513	Beta-1,4-g	B4GALT4	11841.67	13195.18	16172.45	0	0	0
O60547	GDP-man	GMDS	29664.71	21206.11	33259.79	0	0	0
O60565	Gremlin-1	GREM1	0	15686.26	8710.181	194074	0	725320.3
O60568	Procollage	PLOD3	31836.68	25656.39	34588.95	27799.45	0	36297.83
O60610	Protein dia	DIAPH1	17478.88	15797.07	16292.37	0	0	0
O60669	Monocarb	SLC16A7	60437.17	68327.13	22969.07	0	0	0
O60684	Importin su	KPNA6	24170.79	21461.24	25541.04	0	0	0
O60687	Sushi repe	SRPX2	0	0	0	290020.5	141376.2	212756.8
O60716	Catenin de	CTNND1	24941.01	24732.76	20978.52	9478.817	0	32046.69
O60749	Sorting ne	SNX2	44622.94	54859.17	52614.49	0	0	0
O60763	General ve	USO1	146794.6	140339	300209.7	0	0	0
O60779	Thiamine t	SLC19A2	6143.897	5925.842	2353.223	0	0	0
O60784	Target of N	TOM1	10868.44	11370.73	10646.8	0	0	0
O60814	Histone H2	HIST1H2BK	31312240	31702434	24993308	1926069	11448047	5566483
O60832	H/ACA rib	DKC1	28755.02	31176.45	21534.57	34582.58	23718.96	0
O60841	Eukaryotic	EIF5B	51262.81	50926.56	27356.47	55386.78	0	34832.05
O60884	DnaJ hom	DNAJA2	23833.6	51498.72	60747.55	0	0	0
O60888	Protein Cu	CUTA	298176.3	257789.9	252053.5	2194230	2946819	1880132
O75044	SLIT-ROBO	SRGAP2	13605.73	16035.68	13807.75	0	0	0
O75054	Immunogl	IGSF3	1129045	1048.879	4195.75	0	0	0
O75083	WD repeat	WDR1	491880.2	565230	704536.9	84703.58	250799.3	241404.9
O75084	Frizzled-7	FZD7	24283.48	10132.69	18554.7	0	0	0
O75116	Rho-assoc	ROCK2	0	10034.95	15805.68	112059.3	0	34732.52
O75144	ICOS ligan	ICOSLG	32201.35	25875.46	21904.68	261061.1	344439.5	174962.5
O75153	Clustered r	CLUH	12907.87	11389.85	13582.83	0	0	0
O75165	DnaJ hom	DNAJC13	10735.96	7549.593	10389.17	19961.42	16769.07	23090.7
O75317	Ubiquitin c	USP12	8174.027	8274.313	5436.92	0	0	0
O75340	Programm	PDCD6	486803.4	451195.9	430892.3	145949.9	185389.6	256656.5
O75351	Vacuolar p	VPS4B	35124.89	27445.61	31158.83	0	0	0
O75367	Core histo	H2AFY	586215.8	626729.3	369002.3	165873.2	295734.2	158213.8
O75369	Filamin-B	FLNB	100576.7	108987	113109.7	63724.9	0	124895.7
O75382	Tripartite r	TRIM3	162998.1	355390	454901.8	0	0	0
O75390	Citrate syn	CS	15798.49	10381.33	31874.82	0	0	0
O75400	Pre-mRNA	PRPF40A	39195.66	33170.07	9818.353	0	0	0
O75436	Vacuolar p	VPS26A	32638.7	30082.15	25005.4	0	0	0
O75475	PC4 and SI	PSIP1	16671.66	34205.42	15250.24	0	0	0
O75487	Glypican-4	GPC4	43982.18	41845.14	31481.73	0	0	0
O75494	Serine/arg	SRSF10	27311.94	22568.44	13828.13	0	0	0
O75531	Barrier-to-	BANF1	458490.6	544134.9	499005	180065.9	400535.2	0
O75533	Splicing fa	SF3B1	30952.72	32010.8	29130.12	0	0	0

O75534	Cold shock	CSDE1	12526.96	15178.75	13532.73	0	0	0
O75643	U5 small n	SNRNP200	61136.34	56473.98	53832.71	0	0	0
O75674	TOM1-like	TOM1L1	14607.84	21663.88	12954.92	0	0	0
O75695	Protein XR	RP2	61448.32	58025.34	39314.43	0	0	0
O75718	Cartilage-a	CRTAP	22518.37	15713.76	135425.5	0	0	0
O75821	Eukaryotic	EIF3G	44755.61	28990.09	30075.97	0	0	0
O75822	Eukaryotic	EIF3J	65931.92	65479.95	120718.1	0	0	0
O75832	26S protea	PSMD10	15614.84	21532.83	21792.6	0	0	0
O75874	Isocitrate d	IDH1	136507.2	124622.5	154592.7	33301.76	45359.41	120190.2
O75891	Cytosolic 1	ALDH1L1	111590.9	90064.81	140615.8	84823.53	0	31407.48
O75915	PRA1 famil	ARL6IP5	14668.92	19182.84	21344.63	81814.47	0	64194.84
O75954	Tetraspani	TSPAN9	73467.23	66216.48	37364.92	40375.2	0	65267.51
O76003	Glutaredox	GLRX3	11865.25	18043.15	31871.33	0	0	0
O76021	Ribosomal	RSL1D1	16985.63	13072.92	10157.22	0	0	0
O76061	Stanniocalc	STC2	0	0	0	538649.4	736076.5	779267.9
O76094	Signal recc	SRP72	34246.25	38661.48	21227.98	0	0	0
O94760	N(G),N(G)-	DDAH1	73967.73	75278.88	47136.61	0	0	0
O94804	Serine/thre	STK10	19199.36	17673.49	23738.91	0	0	0
O94823	Probable p	ATP10B	0	0	0	592786.6	886658.8	752521.8
O94915	Protein fur	FRYL	22406.2	18662.73	17102.11	38147.28	0	30633.2
O94973	AP-2 comp	AP2A2	13071.74	13436.29	16826.58	0	0	0
O94985	Calsyntenin	CLSTN1	24302.73	20965.55	17878.12	69439.66	140893.7	0
O95084	Serine pro	PRSS23	55436.73	47856.45	52611.72	191351.6	205617.8	377140.4
O95104	Splicing fa	SCAF4	6743.67	6906.443	7406.815	0	0	0
O95155	Ubiquitin c	UBE4B	5843.782	6679.125	4971.745	0	0	0
O95163	Elongator	IKBKAP	9517.955	74860.1	12291.19	0	0	0
O95197	Reticulon-	RTN3	128840.1	153621.4	125313.5	104513.2	61486.48	103020
O95219	Sorting ne	SNX4	14202.81	9542.52	13300.14	0	0	0
O95249	Golgi SNA	GOSR1	9459.083	8760.057	7190.351	0	0	0
O95292	Vesicle-as	VAPB	48480.21	46724.24	49024.38	0	0	0
O95297	Myelin pro	MPZL1	34250.27	23901.13	7896.891	0	0	0
O95336	6-phosph	PGLS	33197.13	33037.99	37745.57	0	0	0
O95340	Bifunctiona	PAPSS2	7351.636	9975.137	11103.53	0	0	0
O95347	Structural	SMC2	8443.736	9242.499	9273.962	0	0	0
O95372	Acyl-prote	LYPLA2	24262.74	35822.87	36556.47	0	0	0
O95376	E3 ubiquiti	ARIH2	7369.685	2377.363	6659.694	0	0	0
O95394	Phosphoac	PGM3	22109.71	14675.37	10623.2	0	0	0
O95400	CD2 antige	CD2BP2	46428.08	45376.77	59536.73	0	0	0
O95433	Activator c	AHSA1	36908.42	15560.16	36641.13	0	0	0
O95445	Apolipopro	APOM	885318.5	949585.9	1018814	2831498	3249384	1914968
O95490	Adhesion	ADGRL2	30132.65	23647.2	24699.35	0	0	0
O95497	Pantethein	VNN1	209434	127434.6	168665.7	1422246	2069474	916991.6
O95498	Vascular n	VNN2	133097.2	116202.3	132934.5	1526596	2430510	953240.3
O95639	Cleavage a	CPSF4	10670.45	9832.484	12250.06	0	0	0
O95747	Serine/thre	OXSR1	46842.43	40915.29	47059.97	69762.28	40671.55	78193.48
O95807	Transmem	TMEM50A	35343.39	39234.22	25007.85	0	0	0
O95816	BAG family	BAG2	152718.6	135544.5	104489.4	0	0	0
O95819	Mitogen-a	MAP4K4	58200.7	52582.53	34801	147520	156364.6	143849.4
O95834	Echinoderm	EML2	198545.6	210953.6	295211.8	0	0	0
O95858	Tetraspani	TSPAN15	78085.5	79845.25	53929.04	0	0	0
O95865	N(G),N(G)-	DDAH2	101575.3	90698.16	75531.25	356854.1	272996.9	136166.9
O96014	Protein Wn	WNT11	28155.66	11338.75	32576.86	0	0	0
O96019	Actin-like	ACTL6A	60964.95	44826.36	61224.49	0	0	0
P00326	Alcohol de	ADH1C	32518.41	29531.43	49069.55	0	0	0
P00338	L-lactate d	LDHA	956233	1062564	1656782	1417967	1133633	1244605
P00352	Retinal deh	ALDH1A1	42812.81	38531.24	83077.2	45905.95	0	46841.77
P00374	Dihydrofol	DHFR	44414.39	45170.85	67604.57	0	0	0
P00387	NADH-cyt	CYB5R3	27889.34	25834.05	42335.89	80357.67	32311.95	62279.48

P00390	Glutathion	GSR	52846.21	37405.32	42111.75	110477.4	75510.74	66857.32
P00441	Superoxide	SOD1	184360.9	161980.3	120451	497276.2	522567.7	300515.3
P00450	Ceruloplas	CP	348696.3	316680.3	363856.1	90107.81	196353.4	135910.3
P00488	Coagulatic	F13A1	1366461	1183083	1967489	2800774	2963346	4349714
P00491	Purine nuc	PNP	11230.52	12968.63	12784.58	109750.7	125599.8	85691.2
P00492	Hypoxanth	HPRT1	48050.98	45616.55	37117.62	0	0	0
P00533	Epidermal	EGFR	13290.54	9513.288	8745.452	60279.79	90307.98	53028.61
P00558	Phosphogl	PGK1	468806.3	482940.7	559506.3	215485.5	104420.2	240834.3
P00568	Adenylate	AK1	33581.6	55875.82	72203.13	0	0	0
P00734	Prothromb	F2	14173715	14244998	20729996	7057864	3789778	6725526
P00736	Compleme	C1R	391925.2	459493.7	365101	865804.4	1312464	1004436
P00738	Haptoglob	HP	3131877	3893410	4584686	242131.8	0	561067.6
P00740	Coagulatic	F9	7790591	8506584	7005386	694409.9	1086583	573202.1
P00742	Coagulatic	F10	6981575	6428300	8054025	532302.2	825313.4	527205
P00747	Plasminog	PLG	284696.8	286622.1	433119	2657273	3331337	1611935
P00749	Urokinase-	PLAU	12077.33	11735.82	11065.26	0	0	0
P01008	Antithroml	SERPINC1	5267664	4654369	4623704	30211412	40719696	21346772
P01023	Alpha-2-m	A2M	1.54E+08	1.52E+08	1.7E+08	1.29E+08	1.28E+08	96147840
P01024	Compleme	C3	12567465	13738067	16523730	19360314	23938682	11885536
P01031	Compleme	C5	2978421	3133218	4084445	1889089	3999791	1238066
P01033	Metalloprc	TIMP1	107703.4	97982.53	95907.13	5632950	8258561	3181560
P01034	Cystatin-C	CST3	23853.01	21027.15	29235.92	478651.9	357385.6	371644
P01042	Kininogen-	KNG1	1890432	1794823	1705590	10547805	16567593	8058223
P01266	Thyroglob	TG	31138.81	39284.31	37654.79	0	0	0
P01344	Insulin-like	IGF2	405611.7	445961.1	662286.2	1340448	2355847	1486736
P01591	Immunogl	JCHAIN	8203974	8439080	18108578	1552234	1854049	1286563
P01620	Ig kappa chain V-III re		286202.6	260403.3	277409.3	425895.6	389333.9	185503.6
P01621	Ig kappa chain V-III re		610894.2	552671.1	591353.9	490984.3	452385.6	392804
P01833	Polymeric	PIGR	483145	501457.5	543649.6	0	0	0
P01871	Ig mu chai	IGHM	669459.8	544386.4	772827.5	0	0	0
P01891	HLA class I	HLA-A	386650	386665.6	275286.6	0	276833.3	308168.7
P01893	Putative H	HLA-H	613381.4	600485.3	444805.9	367584.1	0	567797.1
P02042	Hemoglob	HBD	57119048	76890608	85747320	1.64E+08	1.74E+08	1.67E+08
P02100	Hemoglob	HBE1	1525.919	21713.99	29138.93	47252.03	70522.69	49799.61
P02452	Collagen a	COL1A1	813268.6	798601.5	753355.9	43402192	60887532	57844964
P02458	Collagen a	COL2A1	186566.8	290246.2	411505.6	20690848	19684960	9763341
P02461	Collagen a	COL3A1	114011.8	96521.35	76736.88	2539115	3970310	2653301
P02462	Collagen a	COL4A1	0	0	0	237286	470051.9	201699.3
P02511	Alpha-crys	CRYAB	12222.24	10110.07	16179.96	0	0	0
P02533	Keratin, typ	KRT14	422883.2	602992.2	974671.7	1427313	3483941	2303723
P02538	Keratin, typ	KRT6A	77929.75	151146	198838.9	462970.6	1042913	1003104
P02647	Apolipopro	APOA1	35958608	28888082	11624467	47196760	59620932	18950614
P02649	Apolipopro	APOE	780747.9	761983.8	1101066	2960874	2121512	1423429
P02656	Apolipopro	APOC3	4517272	6564110	5899635	1624285	2062006	1517510
P02675	Fibrinogen	FGB	690656.8	545072.1	781828.6	204348.2	1194950	1453643
P02679	Fibrinogen	FGG	16638.92	8898.377	21345.36	652600.9	323055.3	578729.3
P02748	Compleme	C9	9729293	8321138	13339975	0	0	0
P02749	Beta-2-gly	APOH	850280.8	984588.9	795301.4	1993687	6668891	3616376
P02751	Fibronectir	FN1	3418344	3145330	3987303	1.76E+08	2.1E+08	2.49E+08
P02753	Retinol-bir	RBP4	605797.5	489203.9	539513.6	7708837	8963601	5013635
P02765	Alpha-2-H	AHSG	13646921	29884480	30641672	5.4E+08	4.82E+08	2.35E+08
P02768	Serum albu	ALB	5.23E+08	4.99E+08	4.49E+08	1.87E+10	1.72E+10	1.31E+10
P02771	Alpha-fetc	AFP	3593386	4434171	3642978	52023072	77304440	26327024
P02774	Vitamin D-	GC	4726051	5246422	4895485	30924030	44400800	23247808
P02787	Serotransfe	TF	38497.78	27758.16	34927.99	5493981	0	217694.3
P02788	Lactotrans	LTF	20629462	40448140	35610056	2.98E+08	4.57E+08	2.22E+08
P02790	Hemopexi	HPX	218497.6	189004.2	405777.3	588119.3	1366101	553144.3
P02792	Ferritin ligh	FTL	465729.3	416863.7	372041.8	500452.6	3513572	4951271

P02794	Ferritin hea	FTH1	315556.3	234673	246116.5	1591932	886506.6	462145.6
P03952	Plasma kal	KLKB1	79296.76	69330.6	73495.49	1166066	602828.3	283999.9
P03956	Interstitial	MMP1	0	0	0	245802.8	156423.7	120538.1
P04003	C4b-bindi	C4BPA	1963966	1731460	2170826	1036900	1155821	1730243
P04004	Vitronectir	VTN	17310884	15496377	20683634	19663492	6645257	37739532
P04040	Catalase	CAT	56123.2	62656.79	53884.05	292154.1	0	179690.2
P04062	Glucosylce	GBA	22850.59	15525.65	20152.43	0	0	0
P04066	Tissue alpl	FUCA1	50796.59	42719.27	70344.5	0	0	0
P04075	Fructose-b	ALDOA	502242.5	557468.8	416073.3	613206.5	790384.3	514858.7
P04080	Cystatin-B	CSTB	51375.89	49709.29	32151.46	0	0	0
P04083	Annexin A	ANXA1	734692.5	670252.9	695102.6	352890.1	339134	248198.2
P04114	Apolipopr	APOB	424098.6	493479.5	581863.8	3385774	3458774	2642429
P04180	Phosphatic	LCAT	86586.57	135186.1	168515.9	0	0	0
P04181	Ornithine a	OAT	5648.429	6610.43	6747.51	0	0	0
P04216	Thy-1 mer	THY1	93936.64	102093.4	64583.97	475917.8	514798.4	711335.2
P04259	Keratin, typ	KRT6B	121734.3	699643.6	383506.3	5356778	997069.3	1505684
P04264	Keratin, typ	KRT1	762160.8	1764779	1959761	10337758	19867054	10563592
P04275	von Willeb	VWF	15751.54	16830.79	16249.57	174714.3	137147.3	129039.4
P04278	Sex hormo	SHBG	177370.5	151687	163074.5	784091.8	1257457	741959.2
P04350	Tubulin be	TUBB4A	39665.99	45946.92	61301.18	0	0	0
P04406	Glyceralde	GAPDH	2052944	1941756	2657357	1739243	1198381	1925284
P04424	Argininosu	ASL	127541.8	116586.6	144804.2	0	0	0
P04745	Alpha-amy	AMY1A	155167.5	145714.2	139059.8	620849.6	870071.3	442593.3
P04792	Heat shock	HSPB1	123988.7	87926.35	195248.9	191661.7	181669.6	147272.5
P04899	Guanine n	GNAI2	455414.1	483430.5	322119.2	297261.3	258325.9	340356.3
P04920	Anion exch	SLC4A2	19204.37	19323.83	11225.57	0	0	0
P05023	Sodium/po	ATP1A1	469870.2	407601.1	290409.9	73673.88	208159.9	112211
P05026	Sodium/po	ATP1B1	43435.33	57728.18	39591.75	0	0	0
P05062	Fructose-b	ALDOB	24002.59	29359.61	49823.55	0	0	0
P05090	Apolipopr	APOD	195553	288144.4	349877.3	709488.9	1354631	1194718
P05106	Integrin be	ITGB3	102589.2	101861.3	128314.6	186609.5	202846	380741.4
P05107	Integrin be	ITGB2	31513.02	30625.44	25670.34	0	0	0
P05121	Plasminog	SERPINE1	5093.879	6210.39	0	3233969	3739385	2250639
P05155	Plasma pro	SERPING1	1123776	1021557	987487.4	4814396	6697312	3028103
P05156	Compleme	CFI	501203.3	479971.4	592205.1	2456741	3263148	1261623
P05160	Coagulatic	F13B	112480.5	93373.66	130912.4	112520.1	0	81283.26
P05161	Ubiquitin-l	ISG15	19164.39	28712.33	34344.59	0	0	0
P05186	Alkaline ph	ALPL	3417075	4594522	4581026	0	0	0
P05231	Interleukin	IL6	0	0	0	417961.8	593040.3	466689.3
P05386	60S acidic	RPLP1	346871.4	433389.2	0	949130.3	40380.62	721693.7
P05387	60S acidic	RPLP2	801520.4	734979	1039376	415662.4	0	328147.9
P05388	60S acidic	RPLP0	393481.5	350507.2	348348.1	152766.5	92050.16	77703.5
P05452	Tetranectir	CLEC3B	249626.1	427439.4	315799.5	2183074	2862270	2648154
P05455	Lupus La p	SSB	23858.69	15988.63	33789.04	0	0	0
P05543	Thyroxine-	SERPINA7	327520.9	293205.7	254682.1	1435918	1952742	1097828
P05546	Heparin co	SERPIND1	175471.8	140482.9	164677.2	428486.8	965370.8	444054.9
P05556	Integrin be	ITGB1	1373062	1280831	1175209	460622.6	438754.5	536648.9
P05771	Protein kin	PRKCB	25653.7	30005.92	12271.59	0	0	0
P05976	Myosin ligl	MYL1	62003.37	66854.13	68964.78	0	108986.6	136927.6
P05997	Collagen a	COL5A2	127419.7	161277.4	145208.3	451310	825428.4	403068.6
P06132	Uroporphy	UROD	61368.03	55912.15	79256	0	0	0
P06241	Tyrosine-p	FYN	29011.53	32385.32	16603.11	0	0	0
P06276	Cholineste	BCHE	79894.7	62203.85	69803.2	24746.38	34684.11	0
P06280	Alpha-gala	GLA	14714.76	10414.03	17387.91	0	0	0
P06396	Gelsolin	GSN	2219494	1989015	2164205	4862841	6779867	3406601
P06493	Cyclin-dep	CDK1	22068.2	22995.57	27310.7	0	0	0
P06727	Apolipopr	APOA4	1646564	1268682	2236332	617209.1	1151623	408372.7
P06730	Eukaryotic	EIF4E	44051.84	54267.04	33493.25	0	0	0

P06732	Creatine ki	CKM	22203.17	17939.79	23795.05	0	0	0
P06733	Alpha-enc	ENO1	1306483	1297698	1262257	689404.8	773133.4	696294.7
P06737	Glycogen p	PYGL	142341.2	140753.7	165026.5	363014.7	57072.76	248760.7
P06744	Glucose-6	GPI	123506.7	124396.6	94189.89	131988.2	0	116845.9
P06748	Nucleophc	NPM1	1468932	1499314	622165.1	358042.8	227261	254393.4
P06753	Tropomyo	TPM3	56168.04	55032.9	53595.86	56467.45	52839.91	0
P06756	Integrin alp	ITGAV	55607.38	49315.43	40678.95	101437.4	80761.59	92205.98
P06858	Lipoprotein	LPL	48727.18	40890.91	47572.89	0	0	0
P06865	Beta-hexo	HEXA	103492.8	97672.96	108218	92746.87	104162.4	0
P06888	Ig lambda chain V-I r		39775.19	8338.036	55451.2	0	0	0
P06899	Histone H2	HIST1H2BJ	3697460	4764003	3283117	100599.7	344947.4	268551.1
P07093	Glia-derive	SERPINE2	25497.15	25451.77	33608.23	457769.6	469718.5	506453.9
P07108	Acyl-CoA-	DBI	57114.36	49524.83	41667.02	0	0	0
P07148	Fatty acid-	FABP1	31746610	32515388	57592432	3125538	1.47E+09	7.85E+08
P07195	L-lactate d	LDHB	529917.2	536443.3	538254.3	292822.7	226628.2	222021.7
P07203	Glutathion	GPX1	70423.49	55615.93	107990.6	0	0	0
P07225	Vitamin K-	PROS1	2527758	2285477	3270995	2482576	2928418	1551278
P07237	Protein dis	P4HB	78242.94	73424.27	123465.8	64108.5	51358.36	45800.79
P07339	Cathepsin	CTSD	139286.3	168597.3	143696	95830.89	96158.34	153021.5
P07355	Annexin A2	ANXA2	1656750	2008596	1238861	943532.4	759536.7	1043306
P07437	Tubulin be	TUBB	1912717	1774259	2236325	2073206	605203.6	2824406
P07451	Carbonic a	CA3	28508.72	22100.24	29846.79	0	0	0
P07585	Decorin	DCN	0	0	0	2122213	2781883	2407803
P07602	Prosaposir	PSAP	48089.25	57646.1	51816.32	193225.8	300181.3	193927.3
P07686	Beta-hexo	HEXB	67423.7	56525.87	70425.74	92746.98	104162.2	0
P07737	Profilin-1	PFN1	416294.3	668366.3	549508.9	570275.9	414578.3	246133.2
P07738	Bisphosph	BPGM	59508.5	81727.3	135961.5	294303.5	293818.1	104174.7
P07814	Bifunctiona	EPRS	64866.37	78088.55	83663.41	66408.54	0	19529.06
P07858	Cathepsin	CTSB	0	21875.39	18390.2	141920.2	268427.5	225307
P07900	Heat shock	HSP90AA1	6475971	6181796	4890760	815443.8	680620.6	839277.8
P07910	Heterogen	HNRNPC	745194.1	848720.6	1222920	53965.45	64064.68	49368.46
P07942	Laminin su	LAMB1	119623.1	132715.6	128144.4	1245133	1898862	1111659
P07947	Tyrosine-p	YES1	169663.7	145067.6	113421.5	25294.37	0	33762.27
P07996	Thrombosp	THBS1	1843134	1662175	1566522	1.2E+08	1.42E+08	1.49E+08
P08069	Insulin-like	IGF1R	10685.06	14289.22	9376.871	0	0	0
P08123	Collagen a	COL1A2	143625.3	92299.9	119469	16283200	22820206	22035850
P08133	Annexin A6	ANXA6	1452599	1312335	1024093	329509.4	533282.4	456115.5
P08174	Compleme	CD55	44144.16	28661.36	50980.84	0	0	0
P08183	Multidrug	ABCB1	6134.854	265837.3	330966.9	0	0	0
P08195	4F2 cell-su	SLC3A2	420564	421544.2	314013.1	224560.8	200606.7	295840.9
P08237	ATP-depe	PFKM	18134.33	17968.95	18493.46	0	0	0
P08238	Heat shock	HSP90AB1	787041.8	871677.9	1062085	167274.3	171790.8	138891.1
P08243	Asparagine	ASNS	26934.94	33133.66	35776.97	0	0	0
P08253	72 kDa typ	MMP2	56470.52	38564.54	44776.05	4767561	7582943	4855409
P08294	Extracellula	SOD3	23265.73	21150.15	18751.69	86083.95	167536.3	0
P08473	Neprilysin	MME	103868.9	120557.4	103433.2	0	0	0
P08476	Inhibin bet	INHBA	0	0	0	277860.4	344188.5	247076.1
P08567	Pleckstrin	PLEK	495400.1	490365.6	485448.8	344736.1	182247.9	438759
P08572	Collagen a	COL4A2	0	0	0	241830.9	229149.3	99816.63
P08582	Melanotra	MFI2	75836.33	73645.6	58605.16	0	0	0
P08648	Integrin alp	ITGA5	39762.41	50151.55	40324.96	66235.57	110083.9	231015.3
P08670	Vimentin	VIM	166879.6	151313.9	159272	357802.6	337939.6	340517.4
P08697	Alpha-2-a	SERPINF2	6471511	6605011	5904361	17089592	52681304	25172122
P08708	40S riboso	RPS17	62200.93	86036.03	75178.7	0	0	0
P08727	Keratin, typ	KRT19	29269.63	28423.45	36009.53	38018.48	38059.3	158347.7
P08758	Annexin A5	ANXA5	1616279	1477506	1082476	1117415	1359860	1536302
P08779	Keratin, typ	KRT16	42068.65	31275.27	37263.38	53910.55	292206.1	43204.13
P08833	Insulin-like	IGFBP1	34217.27	35998.9	84146.01	0	0	0

P08865	40S riboso	RPSA	204263.4	204936.1	259636.5	396736.2	0	188253.2
P08962	CD63 antig	CD63	502617.9	573801.4	525924.9	963948.6	449293.1	1065170
P09110	3-ketoacyl	ACAA1	18599.79	13116.89	31224.32	0	0	0
P09211	Glutathion	GSTP1	130290.3	150370.4	156130.9	314307.7	226907.3	135854.6
P09234	U1 small n	SNRPC	14307.43	14566.25	17630.05	0	0	0
P09341	Growth-re	CXCL1	0	0	0	7859904	7623940	2650093
P09382	Galectin-1	LGALS1	167765.4	174848.8	163483	295349.5	571497.9	327089.2
P09429	High mobi	HMGB1	1679427	2203743	202364.1	466443.9	427932	389514.8
P09455	Retinol-bi	RBP1	19978.58	16395.62	29790.61	0	0	0
P09486	SPARC	SPARC	108548	92834.3	87123.9	4275316	7280123	3400598
P09493	Tropomyo	TPM1	56168.04	55670.32	53595.86	58146.41	51667.28	56522.45
P09496	Clathrin lig	CLTA	60011.2	92761.47	91076.89	0	0	0
P09525	Annexin A	ANXA4	48485.37	36413.05	42275.09	0	0	0
P09619	Platelet-de	PDGFRB	0	0	0	49292.74	95045.67	44908.23
P09651	Heterogen	HNRNPA1	237489.7	226087.1	209484.4	279193.2	0	259750.4
P09661	U2 small n	SNRPA1	10508.01	8711.71	15638.63	0	0	0
P09874	Poly [ADP-	PARP1	40375.67	45991.26	52099.46	0	0	0
P09960	Leukotrien	LTA4H	43765.72	56147.79	49451.91	0	0	0
P09972	Fructose-b	ALDOC	20671.75	21196.69	19600.27	116641	0	107956.1
P0C0L4	Compleme	C4A	1654021	1685727	2369401	3976250	4735114	3259220
P0C0S8	Histone H2	HIST1H2A(	59250600	70463440	77912424	1617089	4094493	3721678
P0C7U0	Protein ELF	ELFN1	6132602	6086253	6806122	1443784	1512039	1313869
P0DMV8	Heat shock	HSPA1A	608445.4	539432.9	729154.6	568768.5	437351.5	768514.4
P10114	Ras-relate	RAP2A	127719.3	131604.3	91544.06	0	0	0
P10124	Serglycin	SRGN	0	0	0	498227.2	710033.3	623048.3
P10145	Interleukin	CXCL8	0	0	0	1520724	1844316	669054.6
P10155	60 kDa SS-	TROVE2	13603.38	13147.09	13789.98	0	0	0
P10301	Ras-relate	RRAS	58676.8	61520.65	37475.37	100126.1	245577.8	34837.4
P10599	Thioredoxi	TXN	121560.6	103266.7	102057.7	225647.6	0	174902.8
P10619	Lysosomal	CTSA	43899.62	36764.67	48880.03	0	0	0
P10643	Compleme	C7	1604817	1308609	2193470	805346.6	1131515	930895.1
P10768	S-formylgl	ESD	87133.43	42667.21	126664	0	0	0
P10809	60 kDa hea	HSPD1	150644.1	160248.9	235657.5	0	0	0
P10915	Hyaluronal	HAPLN1	61887.12	50135.64	53850.88	0	269042.9	184374.5
P11021	78 kDa glu	HSPA5	85859.14	71668.91	94006.25	71909.9	175954.1	114792.6
P11047	Laminin su	LAMC1	97555.55	102967.4	96904.69	769181.1	1185000	722636.9
P11117	Lysosomal	ACP2	19409.1	22919.19	18110.38	0	0	0
P11142	Heat shock	HSPA8	737954.3	739128.8	812143.3	505054.3	444828.1	651406.8
P11166	Solute carr	SLC2A1	163444.1	166756.5	146602	389148.1	203733	585202.5
P11169	Solute carr	SLC2A3	146326.8	144526.2	152462.1	355022.8	277595.3	663835.8
P11171	Protein 4.1	EPB41	117151.4	116441.6	96110.34	0	0	0
P11172	Uridine 5-i	UMPS	19433.53	18879.25	28823.96	0	0	0
P11216	Glycogen p	PYGB	301697.3	285232.5	318823.2	613863.8	0	279215.6
P11217	Glycogen p	PYGM	30354.65	26834.59	32353.73	0	0	0
P11233	Ras-relate	RALA	26435.74	27032.88	8625.021	0	0	0
P11279	Lysosome-	LAMP1	118161.5	98758.09	111383.5	0	0	0
P11362	Fibroblast	FGFR1	146281.7	125334.1	105474.7	118196.1	179770.2	90240.34
P11387	DNA topoi	TOP1	185995.4	198341.5	102071.7	0	0	0
P11388	DNA topoi	TOP2A	13107.23	14934.81	9530.194	0	0	0
P11413	Glucose-6	G6PD	95555.25	89205.59	105960.9	134576.4	1334118	120024.2
P11717	Cation-ind	IGF2R	73201.55	61961.59	73307.3	424402.3	403580.5	348016.4
P11766	Alcohol de	ADH5	162452.1	162142.8	183939	81656.02	0	106451.5
P11802	Cyclin-dep	CDK4	13185.33	19777.07	10715.45	0	0	0
P11908	Ribose-ph	PRPS2	21362.93	20280.11	21178.11	0	0	0
P11940	Polyadeny	PABPC1	80857.2	71053.29	76951.81	41435.05	0	25945.5
P12004	Proliferatin	PCNA	28402.6	27364.62	22950.85	0	0	0
P12081	Histidine--	HARS	12253.78	9869.6	10502.04	0	0	0
P12107	Collagen a	COL11A1	42538.97	44012.18	29317.47	437364.8	787103.4	418072.1

P12109	Collagen a	COL6A1	1189964	1587157	2321552	26611642	37608784	19312486
P12110	Collagen a	COL6A2	82788.21	89228.97	95473.58	8113221	12491387	14542009
P12111	Collagen a	COL6A3	88701.85	65861.85	90017.36	8482742	12983499	16302902
P12259	Coagulatic	F5	1740140	1490065	2150609	1771764	1797123	1716002
P12268	Inosine-5-	IMPDH2	42143.42	38910.22	45186.32	22792.53	0	47820.7
P12270	Nucleopro	TPR	32033.17	23985.32	25227.02	0	0	0
P12277	Creatine ki	CKB	179642.9	155266.8	156170.2	0	0	0
P12429	Annexin A	ANXA3	53612.09	64231.03	67705.05	109345.4	0	220679.7
P12532	Creatine ki	CKMT1A	73849.92	51331.58	164702.2	0	0	0
P12814	Alpha-acti	ACTN1	161540.9	166599.1	217546.9	420413	416863.5	151910.5
P12955	Xaa-Pro di	PEPD	54578.39	40191.57	48359.02	46923.04	77766.69	78194.5
P12956	X-ray repa	XRCC6	236347.5	224859.4	233023.3	0	0	0
P13010	X-ray repa	XRCC5	123712.4	120032	136963.5	0	0	0
P13473	Lysosome-	LAMP2	114240.1	81692.53	105187.4	728902.3	929983.1	380651.4
P13489	Ribonuclea	RNH1	30930.77	43722.56	32998.15	0	967384.4	25124.95
P13497	Bone morp	BMP1	126327.1	134573.8	137365.2	103323.3	84347.03	164019.7
P13591	Neural cell	NCAM1	74150.53	88163.66	84894.39	405040.1	585858.6	315098.7
P13612	Integrin alp	ITGA4	1130147	1149601	946673.8	0	27137.66	22112.88
P13639	Elongation	EEF2	333523.3	340128.3	371968.5	212138.2	145287	229210.4
P13645	Keratin, typ	KRT10	1102471	1507826	2748892	6469691	15882172	7045640
P13647	Keratin, typ	KRT5	56585.93	81337.46	96688.63	166713	787060.1	319471.8
P13667	Protein dis	PDIA4	104340.1	107604.5	324578.5	0	0	0
P13671	Compleme	C6	1062772	1068041	1643792	0	0	0
P13674	Prolyl 4-hy	P4HA1	42327.25	39422.3	45583.51	0	0	0
P13693	Translatior	TPT1	55198.59	43762.71	35606.73	0	0	0
P13716	Delta-amir	ALAD	21421.57	12746.92	15608.19	0	0	0
P13796	Plastin-2	LCP1	90227.7	66803.59	72754.13	0	472448.1	298711
P13797	Plastin-3	PLS3	123870	133362.5	125198.9	165890.6	321151.1	164319.5
P13798	Acylamino	APEH	70869.64	62671.8	61488.81	203079	255145	130696.7
P13807	Glycogen [	GYS1	18478.82	17600.82	12532.83	0	0	0
P13861	cAMP-dep	PRKAR2A	83553.23	83079.51	107062.4	0	0	0
P13929	Beta-enola	ENO3	391620.9	531273	957385.3	656578.9	927322.9	666539
P13984	General tra	GTF2F2	38964.46	29636.22	24300.28	0	0	0
P14174	Macropha	MIF	410462	390880.1	360838.6	364194.1	633662.8	256857.4
P14324	Farnesyl py	FDPS	33002.28	28439.47	26313.88	0	0	0
P14543	Nidogen-1	NID1	118779	85851.2	130931.4	421199.3	854475.1	426171.2
P14550	Alcohol de	AKR1A1	142294.5	129107.4	102893.4	0	0	0
P14618	Pyruvate k	PKM	2132730	2219955	2807961	1522820	1172836	1636030
P14625	Endoplasm	HSP90B1	481699.3	466227.6	994270.3	142014.2	153715.8	134359.1
P14678	Small nucl	SNRPB	33025.38	29497.29	40655.99	0	0	0
P14866	Heterogen	HNRNPL	11231.95	17013.41	15937.95	0	0	0
P15104	Glutamine	GLUL	159213.6	174101.5	179977.7	0	0	0
P15121	Aldose red	AKR1B1	117689.1	113563.7	122325.6	52623.18	0	40846.57
P15151	Poliovirus	PVR	12154.99	6593.547	4496.318	0	0	0
P15169	Carboxype	CPN1	46482.28	66678.88	54944.85	94620.27	80507.63	69497.42
P15531	Nucleoside	NME1	91451.03	91324.38	74611.02	0	0	0
P15586	N-acetylgl	GNS	13351.4	12544.34	13222.23	0	0	0
P15880	40S riboso	RPS2	106056.5	77137.57	95866.86	167419.5	0	138721.3
P15927	Replicatior	RPA2	24840.48	37863.18	62798.56	0	0	0
P16035	Metalloprc	TIMP2	70159.12	53640.24	59949.79	674719.6	1076181	594139.3
P16070	CD44 antig	CD44	104224.5	72000.44	65786.1	706553.1	1354348	984418.4
P16112	Aggrecan	ACAN	44947.27	26397.58	20384.27	482052.2	648320.6	522338.6
P16278	Beta-galac	GLB1	45267.98	51500.66	67272.1	0	0	0
P16333	Cytoplasm	NCK1	16831.86	20235.08	45185.22	0	0	0
P16401	Histone H1	HIST1H1B	2151309	2426631	2440120	219667.9	484803.9	705374.2
P16402	Histone H1	HIST1H1D	1843018	2264410	2080636	217047.5	397714.7	475124.5
P16403	Histone H1	HIST1H1C	815237.5	1261318	1329781	175510.3	210927.8	203434.3
P16870	Carboxype	CPE	25701.29	22968.51	54229.46	0	0	0

P16885	1-phospha	PLCG2	26889.26	21542.47	33110.38	0	0	0
P16930	Fumarylac	FAH	36132.51	41086.45	31292.77	110371	138357.7	78087.6
P16949	Stathmin	STMN1	158817.8	39519.35	130157.9	0	0	0
P16989	Y-box-bin	YBX3	71762.99	81089.45	53938.5	0	0	0
P17066	Heat shock	HSPA6	544079.7	668749.6	1171797	618722.8	544536.9	756627.7
P17096	High mobi	HMGA1	34014.17	67432.05	58148.53	0	0	0
P17301	Integrin al	ITGA2	63232.96	17402.95	17945.22	50015.98	51923	45628.58
P17302	Gap junctio	GJA1	51261	48079.66	31358.19	0	0	0
P17480	Nucleolar t	UBTF	39280.84	59858.88	53267.96	0	0	0
P17516	Aldo-keto	AKR1C4	55950.19	63783.5	70506.08	0	0	0
P17655	Calpain-2	CAPN2	30630.72	34091.1	33519.94	10050.96	0	10921.24
P17812	CTP synth	CTPS1	21115.84	37614.98	17451.56	0	0	0
P17844	Probable A	DDX5	153426.6	162974.3	179207.9	68812.92	67227.61	67164.85
P17858	ATP-depe	PFKL	89725.2	78078.08	111217.3	99858.99	0	103868.5
P17936	Insulin-like	IGFBP3	31316.81	11951.65	15929.55	2017370	1273004	1964008
P17980	26S protea	PSMC3	103443.1	96338.68	109716.5	0	0	0
P17987	T-complex	TCP1	201128.4	203385.7	235180.9	130138.4	126603.8	117422.5
P18065	Insulin-like	IGFBP2	109870.2	91432.06	119532.5	1135821	1632740	798135
P18077	60S riboso	RPL35A	46069.51	31069.49	58018.93	0	0	0
P18085	ADP-ribos	ARF4	68027.17	62430.05	73535.67	62027.86	14358.39	78393.39
P18124	60S riboso	RPL7	129758.6	134859.2	72449.25	445772.2	0	41926.02
P18206	Vinculin	VCL	119106.5	111045.6	114148	291263.1	587345.9	255023.1
P18433	Receptor-t	PTPRA	17989.62	16302.21	10453.19	0	0	0
P18621	60S riboso	RPL17	83008.24	91502.78	53931.96	200641.6	20258.1	156001.8
P18669	Phosphogl	PGAM1	136898.2	133273.7	133521.3	0	0	0
P18754	Regulator	RCC1	34083.39	38689.96	44589.59	0	0	0
P19022	Cadherin-2	CDH2	6174.653	7886.018	32336.93	0	0	0
P19338	Nucleolin	NCL	1779301	1576615	997820.1	228344.8	130208.5	161819.3
P19367	Hexokinas	HK1	9727.605	10766.36	11612.55	0	0	0
P19388	DNA-direc	POLR2E	12097.49	8950.771	11208.33	0	0	0
P19525	Interferon-	EIF2AK2	48506.6	54229.96	30253.1	0	0	0
P19623	Spermidine	SRM	48887.33	39812.25	52215.4	0	0	0
P19784	Casein kin	CSNK2A2	13815.72	10868.18	11357.37	0	0	0
P19823	Inter-alpha	ITIH2	5379737	5910574	5774948	34503536	42908024	26339244
P19827	Inter-alpha	ITIH1	1174064	1095172	1174666	3924111	5111713	2982691
P19875	C-X-C mo	CXCL2	0	0	0	409247	392120.1	179692.2
P19876	C-X-C mo	CXCL3	0	0	0	298615.3	180220.1	61373.73
P20042	Eukaryotic	EIF2S2	38549.81	37135.23	44149.66	75326.13	2296786	23276.21
P20340	Ras-relate	RAB6A	146787.4	171617.1	66437	0	0	0
P20618	Proteasom	PSMB1	242367.6	239618.3	228910.9	158835	0	119417
P20700	Lamin-B1	LMNB1	20201.23	27629.24	24576.87	0	0	0
P20742	Pregnancy	PZP	3350150	2592085	4218732	2856046	3205320	2454337
P20774	Mimecan	OGN	64286.96	65609.48	89297.56	233844.1	343776.9	154995.6
P20809	Interleukin	IL11	8244.971	5799.101	9186.038	0	0	0
P20839	Inosine-5-	IMPDH1	28434.45	11616.16	12213.47	0	0	0
P20849	Collagen a	COL9A1	21063.87	17173.18	16120.08	141804.7	173300.7	92944.56
P20908	Collagen a	COL5A1	108893.3	104327.2	55109.14	727181.1	987781.4	637353.9
P20962	Parathymo	PTMS	562474.9	558268.2	1112674	0	0	0
P21266	Glutathion	GSTM3	20536.22	24249.74	21007.74	0	0	0
P21281	V-type pro	ATP6V1B2	26356.46	34796.66	43295.4	0	0	0
P21283	V-type pro	ATP6V1C1	5216.128	7068.552	9718.311	0	0	0
P21291	Cysteine a	CSRP1	76545.91	81908.09	81165.09	0	0	0
P21333	Filamin-A	FLNA	581512.4	577234.5	712668.6	690854.6	670321.5	765811.9
P21399	Cytoplasm	ACO1	120034.7	128484.1	177654.6	73739.38	0	88251.52
P21589	5-nucleoti	NT5E	459805.9	22296.39	17138.24	223716.3	251527.7	285565.7
P21810	Biglycan	BGN	2273531	0	1111034	3712922	6318149	5764266
P21926	CD9 antige	CD9	571201.3	273224.8	225608.8	202728.4	161303.1	221922
P21964	Catechol C	COMT	99910.95	90723.76	142283.7	0	0	0

P22059	Oxysterol-	OSBP	23967.59	32122.65	36158.64	0	0	0
P22102	Trifunction	GART	45732.05	38956.26	36302.03	0	0	0
P22105	Tenascin-X	TNXB	5748.149	5957.079	9428.358	133076.1	178456.4	164121.3
P22234	Multifuncti	PAICS	304425.4	315366.5	392010.2	0	0	0
P22314	Ubiquitin-l	UBA1	285016.7	272420.3	320315.3	58141.82	295258.8	75957.52
P22352	Glutathion	GPX3	425255.1	347478.8	490130.9	102954.1	321520.5	142458.1
P22392	Nucleoside	NME2	288076.6	335931.2	283734.5	0	99813.16	124463.2
P22413	Ectonuclec	ENPP1	13379.98	12325.41	10486.28	0	0	0
P22626	Heterogen	HNRNPA2	115876	120948.8	99617.23	286667.9	283283.8	208013.1
P22692	Insulin-like	IGFBP4	6878.482	31682.95	30931.81	527457.6	935729.9	311529.9
P22694	cAMP-dep	PRKACB	84482.21	79780.55	89412.09	0	0	0
P23142	Fibulin-1	FBLN1	369120.7	325806.3	403928	4094277	5281919	3169619
P23229	Integrin alp	ITGA6	53896.55	38537.28	64673.01	31793.19	50239.89	112400.1
P23246	Splicing fa	SFPQ	54850.76	40086.45	48208.7	80971.68	0	99451.78
P23258	Tubulin ga	TUBG1	9070.816	11510.21	7954.728	0	0	0
P23284	Peptidyl-p	PPIB	82174.38	75011.07	107621.6	66169.91	125086.5	121793.8
P23396	40S riboso	RPS3	222150.9	284406.9	287353	285864.1	121836.6	192196.1
P23458	Tyrosine-p	JAK1	23090.61	20849.8	14804.01	0	0	0
P23468	Receptor-t	PTPRD	3198.48	4072.884	3026.106	0	0	0
P23526	Adenosylh	AHCY	1063999	1204725	1360716	433160.9	399695.3	450404.5
P23528	Cofilin-1	CFL1	478543.7	512417.7	460710.2	353840.9	230560.1	369754.2
P23588	Eukaryotic	EIF4B	2925.571	4209.389	2840.817	0	0	0
P23919	Thymidylat	DTYMK	14590.89	14490.74	12528.21	0	0	0
P23921	Ribonuclec	RRM1	70782.22	81935.54	91336.98	32617.52	0	40310.43
P24043	Laminin su	LAMA2	0	0	0	61991.2	66399.36	19241.04
P24534	Elongation	EEF1B2	576811.8	389149.8	552814.8	0	0	0
P24666	Low molec	ACP1	84313.69	95075.8	104795.6	0	0	0
P24821	Tenascin	TNC	487322.4	523376.2	370434.4	1014257	1299209	1850307
P24844	Myosin reg	MYL9	17870.41	17310.47	25609.55	0	0	0
P24928	DNA-direc	POLR2A	11920.25	7455.715	11714.71	0	0	0
P24941	Cyclin-dep	CDK2	219208.4	118592.3	180197.8	0	0	0
P25098	Beta-adrer	ADRBK1	18763.15	11860.28	19671.07	0	0	0
P25205	DNA replic	MCM3	90711.72	86942.11	76741.9	0	0	0
P25325	3-mercapt	MPST	60459.57	50591	72981.33	0	0	0
P25391	Laminin su	LAMA1	0	0	0	72692.16	21761.62	15202.79
P25398	40S riboso	RPS12	34046.18	37248.63	27462.62	26241.1	0	29554.4
P25685	DnaJ homo	DNAJB1	16473.07	11486.68	12886.07	0	0	0
P25705	ATP synth	ATP5A1	22200.48	14611.96	31087.8	0	0	0
P25786	Proteasom	PSMA1	233251.7	246570.8	273191.5	155388.7	72433.41	176696.1
P25787	Proteasom	PSMA2	102317.4	51604.41	60531.47	60645.3	0	71392.14
P25788	Proteasom	PSMA3	186381.5	188940.9	214297.4	96510.58	48027.72	73604.73
P25789	Proteasom	PSMA4	445713.3	386584.5	389424	183114.4	0	181164.6
P25940	Collagen a	COL5A3	0	0	0	129074.5	213267.6	96113.13
P26006	Integrin alp	ITGA3	174660.1	128180	107024.2	65444	95352.14	98118.67
P26022	Pentraxin-	PTX3	0	0	0	5258973	5900698	4052882
P26038	Moesin	MSN	131884.1	138577.6	112245.4	175839.6	143079.8	142847.2
P26368	Splicing fa	U2AF2	66064.9	64322.71	51095.88	0	55446.54	27127.76
P26373	60S riboso	RPL13	67923.51	62054.81	35232	109179.1	0	92670.12
P26583	High mobi	HMGB2	439530.7	422200.9	160277	200395.9	0	265663.4
P26639	Threonine-	TARS	37815.06	36156.31	34757.71	0	0	0
P26640	Valine--tR	VARS	68121.7	58495.45	79243.3	34824.42	0	3077459
P26641	Elongation	EEF1G	414929.6	500936	530942.8	143115.5	0	121053.2
P26885	Peptidyl-p	FKBP2	15268.76	12225.91	12661.43	0	0	0
P26927	Hepatocyt	MST1	80747.79	70316.09	67348.72	496300.6	651340.6	337064.9
P27105	Erythrocyte	STOM	464154	437701.4	359974.1	90858.41	377093.6	537546.1
P27169	Serum par	PON1	374346.8	365786.8	445894.8	0	0	0
P27348	14-3-3 pro	YWHAQ	88349.98	105886.4	114268.9	0	81860.28	193102.2
P27361	Mitogen-a	MAPK3	16172.16	13694.01	18115.76	0	0	0

P27448	MAP/micr	MARK3	19386.84	40061.98	45521.68	0	0	0
P27635	60S riboso	RPL10	49591.62	140023.6	79563.59	370579.1	0	196406.8
P27694	Replicatior	RPA1	27206.8	26900.54	26514.49	0	0	0
P27695	DNA-(apu	APEX1	43686.14	29970.75	35718	0	0	0
P27701	CD82 antig	CD82	41354.58	35871.73	43274.29	336899.3	360719.3	285588.5
P27708	CAD prote	CAD	54837.93	39743.64	67165.18	98922.84	36475.49	102711
P27816	Microtubu	MAP4	25030.43	28049.96	36639.36	0	0	0
P27986	Phosphatic	PIK3R1	15022.52	13818.71	20351.87	0	0	0
P28062	Proteasom	PSMB8	20293.72	6969.765	16884.03	0	0	0
P28065	Proteasom	PSMB9	41575.64	48134.73	47159.17	48954.49	0	34380
P28066	Proteasom	PSMA5	132610.9	137171.8	166594.5	59979.58	0	88638.95
P28070	Proteasom	PSMB4	246705.6	233170.6	255621.1	0	0	0
P28072	Proteasom	PSMB6	173563.5	199769.3	175476.2	0	0	0
P28074	Proteasom	PSMB5	135962.4	151614	161483.1	88018.07	0	80479.29
P28300	Protein-lys	LOX	0	0	0	363726.5	517392.3	254507.6
P28340	DNA polyr	POLD1	189852.5	132716.2	386899.4	0	0	0
P28482	Mitogen-a	MAPK1	46535.07	13323.94	15482.33	0	0	0
P28838	Cytosol an	LAP3	74096.67	73620.34	72383.11	0	0	0
P29279	Connective	CTGF	20620.85	35882.24	46593.7	653843.9	183631.5	555122.1
P29317	Ephrin typ	EPHA2	138040	145347.8	98732.65	220922.2	122074	0
P29320	Ephrin typ	EPHA3	4484.18	8043.799	9980.746	0	0	0
P29323	Ephrin typ	EPHB2	83115.18	50089.21	43510.45	0	0	0
P29350	Tyrosine-p	PTPN6	14853.23	12256.8	33128.88	0	0	0
P29401	Transketol	TKT	85344.17	85381.7	94629.34	41212.16	105995.6	0
P29597	Non-recep	TYK2	0	0	0	624058.2	420228.9	221371.3
P29692	Elongation	EEF1D	661166.2	605299.6	1182976	0	0	0
P29966	Myristoylat	MARCKS	397019.8	456846.9	260907.2	145674.5	218640.9	173402
P30039	Phenazine	PBLD	39964.83	22965.02	49827.89	0	0	0
P30041	Peroxiredo	PRDX6	285976.4	278465	244141.4	259275.2	386791.8	203849.8
P30044	Peroxiredo	PRDX5	84015.89	72612.45	64011.63	18218.36	0	28496.21
P30046	D-dopach	DDT	44482.61	32280.64	58903.76	0	0	0
P30050	60S riboso	RPL12	105275.5	105470.8	132019.8	65994.09	38388.59	59679.95
P30085	UMP-CMP	CMPK1	92666.66	50642.41	43390.9	0	66511.83	18704.8
P30086	Phosphatic	PEBP1	110449.2	102772.3	106595.4	864857.3	749178.4	378717.7
P30101	Protein dis	PDIA3	36212.16	36726.36	30367.58	117309.3	106873.5	101523
P30419	Glycylpept	NMT1	12293.69	16835.65	19195.6	0	0	0
P30530	Tyrosine-p	AXL	165781.3	170322.3	371099.4	0	0	0
P30566	Adenylosu	ADSL	19201.99	18161.76	10553.79	0	0	0
P30613	Pyruvate k	PKLR	35110.94	32585.07	40821.05	0	0	0
P30622	CAP-Gly d	CLIP1	11580.77	12625.97	24881.77	0	0	0
P30626	Sorcin	SRI	301879.8	332103.8	278882.8	53859.1	0	121597.1
P30825	High affini	SLC7A1	101459.8	90856.12	71891.58	0	0	0
P30876	DNA-direc	POLR2B	11340.06	9582.868	15566.63	0	0	0
P31146	Coronin-1	CORO1A	111478	101793	170371.3	46749.95	0	73769.52
P31150	Rab GDP d	GDI1	77609.03	70970.45	30567.35	0	0	0
P31323	cAMP-dep	PRKAR2B	67863.91	47518.26	73831.23	0	0	0
P31327	Carbamoyl	CPS1	13742.95	19764.32	13547.57	0	0	0
P31350	Ribonuclec	RRM2	16451.16	35178.3	65293.35	0	0	0
P31431	Syndecan-	SDC4	187768.4	172156.6	220222.1	278091	341028.8	188536.7
P31641	Sodium- a	SLC6A6	50675.27	48697.55	38014.15	0	0	0
P31689	DnaJ homo	DNAJA1	16090.01	23328.18	18774.92	0	0	0
P31749	RAC-alpha	AKT1	3538.17	3812.836	3852.692	0	0	0
P31939	Bifunctiona	ATIC	150546.6	144006.9	184255.8	66230.28	0	78304.53
P31946	14-3-3 pro	YWHAB	415487.5	350298.7	430847	457719.9	665098	334443.9
P31948	Stress-indu	STIP1	44694.27	45904.95	49321.45	0	53418.32	39852.93
P31949	Protein S10	S100A11	46854.71	47228.26	42515.77	0	0	0
P32119	Peroxiredo	PRDX2	164155.9	108612.6	160750.8	874579.1	2926373	696385.6
P32754	4-hydroxy	HPD	8468.47	13527.14	8575.203	82480.48	0	29991.63

P32856	Syntaxin-2	STX2	15608.09	16134.36	18839.5	0	0	0
P32929	Cystathion	CTH	28907.09	41243.05	29450.87	0	0	0
P32969	60S riboso	RPL9	27872.5	29621.61	30365.91	0	0	0
P32970	CD70 antig	CD70	54346.08	56919.22	36783.66	0	0	0
P33176	Kinesin-1 h	KIF5B	49265.25	49597.63	49652.58	20263.89	0	97795.73
P33527	Multidrug	ABCC1	15668.33	13833.22	7547.443	0	0	0
P33908	Mannosyl-	MAN1A1	54770.82	101723.7	65091.12	0	0	0
P33991	DNA replic	MCM4	22251.1	27875	29467.09	0	0	0
P33993	DNA replic	MCM7	28889.25	20490.44	24667	0	0	0
P34096	Ribonuclea	RNASE4	32676.08	18881.12	28434.48	394484.2	899940.6	176979
P34896	Serine hyd	SHMT1	8618.227	6260.318	12980.18	0	0	0
P34897	Serine hyd	SHMT2	23598.41	16485.12	21385.44	0	0	0
P34913	Bifunctiona	EPHX2	57125.16	54917.7	65207.22	0	0	0
P35052	Glypican-1	GPC1	614382.5	796508.3	746812	374183.1	449793.3	346271.7
P35080	Profilin-2	PFN2	211738.2	179955.1	171373.3	0	0	0
P35222	Catenin be	CTNNB1	29293.84	33156.42	26053.16	1837456	0	259060.6
P35237	Serpin B6	SERPINB6	9264.35	11498.37	10923.05	0	0	0
P35240	Merlin	NF2	7072.578	4849.767	3563.967	0	0	0
P35241	Radixin	RDX	704789.9	649860.1	570792.3	590720.6	0	491819.5
P35244	Replicatior	RPA3	1222820	1249290	1409038	0	0	0
P35268	60S riboso	RPL22	613199.4	741628.4	484094.1	0	0	0
P35269	General tra	GTF2F1	8048.758	9551.994	4785.076	0	0	0
P35442	Thrombosp	THBS2	180090.5	172860.3	134333.3	12761292	16182934	18263486
P35443	Thrombosp	THBS4	325752	291825.8	280280.8	4121698	5082330	3146594
P35527	Keratin, typ	KRT9	148544.5	179443.6	161202.7	1450968	1080219	952070.8
P35555	Fibrillin-1	FBN1	35617.91	83083.18	29521.66	736185.1	819462.9	334094.3
P35573	Glycogen d	AGL	47529.51	29865.36	33180.38	31137.61	0	22176.75
P35579	Myosin-9	MYH9	667659.4	627577.8	994871.4	1586663	1109664	2097555
P35580	Myosin-10	MYH10	32194.21	32790.91	28746.13	25781.76	0	41446.24
P35590	Tyrosine-p	TIE1	16120.08	15642.81	15409.33	75566.35	151418.4	75198.24
P35606	Coatomer	COPB2	50691.17	47536.23	57432.52	199634.6	0	51834.25
P35613	Basigin	BSG	422670.7	422055.3	299370.4	111841.6	370525.9	229997.5
P35637	RNA-bindi	FUS	17750.54	19829.03	18919.73	0	0	0
P35658	Nuclear po	NUP214	2302.381	3453.113	3565.557	0	0	0
P35659	Protein DE	DEK	129726.3	137297.8	21082.82	0	0	0
P35754	Glutaredox	GLRX	6943.45	11572.97	9915.056	27107.58	0	21645.74
P35813	Protein ph	PPM1A	25700.17	4414.968	16398.93	0	0	0
P35858	Insulin-like	IGFALS	61216.47	71474.52	78656.38	157362.4	0	137216
P35908	Keratin, typ	KRT2	270200.2	1008778	863845.8	3921650	4317927	3845191
P35998	26S protea	PSMC2	103083.8	109522.2	118717	130122.5	0	114981.1
P36222	Chitinase-3	CHI3L1	8082.493	0	5049.96	754833.6	900587.9	347659.8
P36404	ADP-ribos	ARL2	16991.81	16258.15	17728.17	0	0	0
P36507	Dual speci	MAP2K2	9080.926	15861.55	22561.29	0	0	0
P36543	V-type pro	ATP6V1E1	15178.47	14526.97	28344.23	0	0	0
P36578	60S riboso	RPL4	77879.3	71180.03	47406.86	439432.4	163174.8	164768.5
P36871	Phosphogl	PGM1	90325.07	62863.93	118690	70538.02	0	57453.18
P36915	Guanine nu	GNL1	24626.13	17376.03	9180.723	0	0	0
P36955	Pigment ep	SERPINF1	839415.6	569502.9	668234.7	6594453	9604032	5833403
P36969	Phospholip	GPX4	9258.574	16250.2	11769.9	0	0	0
P37108	Signal reco	SRP14	43545.65	51349.55	41983.61	0	0	0
P37198	Nuclear po	NUP62	45747.45	53294.63	61039.22	0	0	0
P37235	Hippocalci	HPCAL1	18799.28	17998.39	18864.69	0	0	0
P37802	Transgelin	TAGLN2	328933.3	286374.7	375242.2	535100.7	755208.1	510033.4
P37837	Transaldol	TALDO1	50351.46	49739.35	39819.48	36514.13	0	19887
P38571	Lysosomal	LIPA	19912.44	16344.34	27433.39	0	0	0
P38606	V-type pro	ATP6V1A	48940.38	44199.05	53919.29	0	0	0
P38646	Stress-70 p	HSPA9	22262.14	15218.52	25215.35	0	0	0
P38919	Eukaryotic	EIF4A3	86594.02	93981.12	97078.27	0	0	0

P39019	40S riboso	RPS19	19736.54	19842.55	42550.89	0	0	0
P39023	60S riboso	RPL3	38273.64	39182	5883.87	301901	0	143680.8
P39059	Collagen a	COL15A1	14541.08	16309.9	16518.73	299284.7	425056.8	527137.8
P39060	Collagen a	COL18A1	118806	168108.8	187130	152962.1	246012.4	199019.7
P40227	T-complex	CCT6A	142678.3	135973.5	182069.5	36129.03	0	26595.21
P40261	Nicotinami	NNMT	1282764	942868	0	128469.6	0	19585.66
P40306	Proteasom	PSMB10	17066.31	15321.54	18257.26	0	0	0
P40429	60S riboso	RPL13A	123177.6	137048.9	82806.3	374509.3	125134.8	187870.9
P40616	ADP-ribos	ARL1	14040.83	11158.45	15127.87	0	0	0
P40763	Signal tran	STAT3	17341.71	18326.75	16317.95	0	0	0
P40925	Malate deh	MDH1	74129.38	90999.45	71176.8	83937.3	76213.53	46654.41
P41091	Eukaryotic	EIF2S3	37931.29	35520.37	63317.66	0	0	0
P41227	N-alpha-a	NAA10	16975.91	13785.03	18305.02	0	0	0
P41240	Tyrosine-p	CSK	9406.902	6745.81	8641.141	0	0	0
P41250	Glycine--t	GARS	38310.95	39514.64	43832.33	86277.4	0	78438.21
P41252	Isoleucine-	IARS	81706.42	68584.87	81812.58	73344.55	0	47734.98
P41440	Folate tran	SLC19A1	37912.59	37153.65	24483.29	0	0	0
P42025	Beta-centr	ACTR1B	79471.84	89781.01	85237.64	0	0	0
P42229	Signal tran	STAT5A	16750.28	6197.475	13578.49	0	0	0
P42356	Phosphatic	PI4KA	16940.21	14046.82	10593.81	0	0	0
P42766	60S riboso	RPL35	43277.26	54021.02	21552.83	83681.4	0	68882.77
P42785	Lysosomal	PRCP	33795.95	32189.75	43788.98	0	0	0
P43007	Neutral an	SLC1A4	72022.8	72559.39	33836.39	84354.33	69500.54	160293.5
P43034	Platelet-ac	PAFAH1B1	41310.98	35453.46	45802.48	0	106988.5	140059.1
P43121	Cell surfac	MCAM	97642.95	39611.21	28953.99	0	0	0
P43243	Matrin-3	MATR3	24970.66	19391.43	24060.28	0	0	0
P43246	DNA mism	MSH2	14625.34	13903.53	16256.54	0	0	0
P43487	Ran-specif	RANBP1	27275.96	37739.22	34342.48	0	0	0
P43490	Nicotinami	NAMPT	18452.37	14414.38	8927.48	0	0	0
P43652	Afamin	AFM	555636.6	231295	190586.7	5852610	8279819	3657650
P45877	Peptidyl-p	PPIC	11227.6	9471.657	11059.4	22691.54	0	14425.15
P45973	Chromobc	CBX5	15392.67	93513.64	18202.35	0	0	0
P46019	Phosphory	PHKA2	6858.701	4625.603	8996.908	0	0	0
P46060	Ran GTPas	RANGAP1	86163.79	99932.84	74481.27	0	0	0
P46063	ATP-depe	RECQL	30725.17	16756.96	27755.96	0	0	0
P46087	Probable 2	NOP2	20393.09	26312.9	27328.54	0	0	0
P46109	Crk-like pr	CRKL	10381.57	8348.207	7278.943	0	0	0
P46776	60S riboso	RPL27A	130057.8	124076	60637.96	363245.3	0	244713.4
P46778	60S riboso	RPL21	16645.05	12254.72	15526.63	44947.46	0	25222.69
P46781	40S riboso	RPS9	374790	384924.1	295374.4	286528.7	0	212652.6
P46783	40S riboso	RPS10	52990.53	38530.86	60552.73	0	0	0
P46939	Utrophin	UTRN	14434.62	12519.82	9045.067	0	0	0
P46940	Ras GTPas	IQGAP1	440293.8	431765.4	431696.5	946158.3	3378706	751005.9
P46976	Glycogenir	GYG1	30380.06	37965.46	39977.43	0	0	0
P47755	F-actin-ca	CAPZA2	161269.4	145517.9	177772.6	257106.1	340079.7	255140.5
P47895	Aldehyde	ALDH1A3	14776.95	11429.68	16465.84	0	0	0
P47914	60S riboso	RPL29	107349.4	75737.77	45470.5	226760.7	0	122028.7
P47929	Galectin-7	LGALS7	7583.676	44176.23	21857.47	82412.69	0	124450
P48059	LIM and se	LIMS1	187765.7	211625.1	266051.6	267761.3	131554.8	389170.4
P48147	Prolyl endo	PREP	52083.03	55298.93	73436.13	0	0	0
P48163	NADP-dep	ME1	10776.74	95674.52	97023.55	0	0	0
P48449	Lanosterol	LSS	35546.91	29367.71	67631.88	0	0	0
P48506	Glutamate	GCLC	16151.95	15189.56	15916.99	0	54635.28	29257.06
P48507	Glutamate	GCLM	39427.75	54002.61	50308.85	93683.2	25525.57	118412.3
P48509	CD151 ant	CD151	328627.1	328434.7	223648.1	86873.29	0	162621.3
P48556	26S protea	PSMD8	25135.33	15441.4	24138.85	0	0	0
P48643	T-complex	CCT5	104705.8	101532.7	126333.3	68410.31	0	74324.78
P48723	Heat shock	HSPA13	41252.52	31925	45167.36	112141.1	196403.3	101769.1

P48730	Casein kin	CSNK1D	7446.854	7879.563	12663.36	0	0	0
P48735	Isocitrate c	IDH2	7256.993	7344.3	9385.871	0	0	0
P48736	Phosphatic	PIK3CG	26634.04	30964.31	34275.41	0	0	0
P48739	Phosphatic	PITPNB	13529.24	12815	16865.68	0	0	0
P48740	Mannan-b	MASP1	153546.7	144000.9	176904.5	544179.4	468809.7	546199.8
P49189	4-trimethy	ALDH9A1	105751.7	100757	147639.5	52866.31	0	39805
P49207	60S riboso	RPL34	53283.09	62510.73	14059.1	0	0	0
P49327	Fatty acid s	FASN	209991.4	240102.5	275241.9	341196.7	296635.1	22849.91
P49368	T-complex	CCT3	394440.3	350624.1	404847.4	251895.5	307944.7	226285.9
P49411	Elongation	TUFM	19037.47	10744.22	16113.03	0	0	0
P49458	Signal recc	SRP9	28172.12	31322.95	29999.03	0	0	0
P49585	Choline-pl	PCYT1A	7551.814	6768.244	9879.455	0	0	0
P49589	Cysteine---	CARS	19568.95	16991.93	16355.23	0	0	0
P49591	Serine--tR	SARS	115818	104296.2	134044.7	165330.3	0	69157.27
P49721	Proteasom	PSMB2	176935	182034.6	173772.4	107652.7	153592.3	124003.8
P49736	DNA replic	MCM2	33593.8	28703.87	30994.3	0	0	0
P49746	Thrombos	THBS3	198659.2	183244	168080.8	3353682	1933116	1242553
P49747	Cartilage c	COMP	96068.88	70543.24	70069.67	474714.5	842766	542616.3
P49756	RNA-bindi	RBM25	35067.46	29589.16	30961.38	0	0	0
P49773	Histidine tr	HINT1	69864.38	76598.16	62506.97	0	0	0
P49888	Estrogen s	SULT1E1	35848.73	49098.84	72429.11	0	0	0
P49902	Cytosolic p	NT5C2	28783.87	26086.69	30685.11	0	0	0
P49915	GMP synth	GMPS	74185.95	55979.45	80887.98	55682.5	28037.98	64366.95
P50148	Guanine n	GNAQ	59760.8	97100.49	39117.28	0	0	0
P50151	Guanine n	GNG10	100908.8	95660.51	103922.1	0	0	0
P50281	Matrix met	MMP14	58441.61	83455.52	64565.26	14407011	17113416	6649655
P50395	Rab GDP c	GDI2	117154.3	112762.1	112001.4	201159.8	289885.8	165554.2
P50443	Sulfate tra	SLC26A2	19484.75	10584.26	14805.71	0	0	0
P50454	Serpin H1	SERPINH1	132226.8	108527.8	169270.3	92115.6	0	58914.52
P50502	Hsc70-inte	ST13	866004.8	882052.1	820204.1	174720	113459.3	144820.3
P50570	Dynamin-2	DNM2	38394.77	36328.63	45233.65	42013.88	14185.54	80349.38
P50851	Lipopolysa	LRBA	17237.55	14605.54	16696.68	0	0	0
P50914	60S riboso	RPL14	159578.5	145793.5	99767.53	535075.2	0	202625.1
P50990	T-complex	CCT8	216785.2	247313.9	250833.7	67177.52	69977.49	176332.5
P50991	T-complex	CCT4	274828.1	251036	302247.3	129441.5	52399.73	139428.4
P50995	Annexin A	ANXA11	313368.9	333696.9	239435.6	111385.3	81562.49	167797.1
P51114	Fragile X m	FXR1	38178.46	19894.01	33947.29	0	0	0
P51148	Ras-relate	RAB5C	205019.5	220083.3	208406.7	0	0	0
P51149	Ras-relate	RAB7A	321381.4	291675.5	280910.1	167883.9	150092	231399.6
P51151	Ras-relate	RAB9A	17224.08	18940.72	22964.92	0	0	0
P51159	Ras-relate	RAB27A	14828.83	19694.02	22461.1	0	0	0
P51532	Transcripti	SMARCA4	73718.46	81628.46	41853.64	0	0	0
P51570	Galactokin	GALK1	237110	242460.3	315802.5	216940	0	310678.4
P51572	B-cell rece	BCAP31	27806.4	26337.57	43570.26	0	0	0
P51580	Thiopurine	TPMT	34746.58	34242.36	44740.43	0	0	0
P51610	Host cell fa	HCFC1	26817.96	41688.31	50297.96	0	0	0
P51659	Peroxisom	HSD17B4	9153.698	12158.51	7010.012	0	0	0
P51674	Neuronal r	GPM6A	245354.7	142804.5	205955.2	0	0	0
P51797	Chloride tr	CLCN6	3537.599	3288.095	2892.365	0	0	0
P51809	Vesicle-ass	VAMP7	16581.02	19378.41	12120.66	0	0	0
P51858	Hepatoma	HDGF	87786.61	71992.35	171471.3	0	0	0
P51884	Lumican	LUM	482596.4	448285.6	567798.1	5233277	7073753	2957281
P52209	6-phosph	PGD	121457.8	120351.7	103081.1	0	60463.39	59889.23
P52272	Heterogen	HNRNPM	23576.48	27871.64	33592.24	0	0	0
P52292	Importin s	KPNA2	37529.92	36005.7	36747.73	0	0	0
P52569	Cationic ar	SLC7A2	42107.63	30497.81	57546.32	0	0	0
P52597	Heterogen	HNRNPF	30818.81	56874.75	64132.42	0	0	0
P52655	Transcripti	GTF2A1	81657.59	74140.8	104257.9	0	0	0

P52657	Transcripti	GTF2A2	32249.65	40508.23	65602.2	0	0	0
P52701	DNA mism	MSH6	13745.83	16453.73	6149.989	0	0	0
P52823	Stanniocal	STC1	0	0	0	108828.1	111768	47332.22
P52888	Thimet oli	THOP1	12969.33	11376.35	12498.89	0	0	0
P52907	F-actin-ca	CAPZA1	149341.3	129258.5	157258.2	78834.39	117225.8	123305.7
P53004	Biliverdin r	BLVRA	46244.11	56021.96	50020.14	0	0	0
P53396	ATP-citrat	ACLY	134730.5	126902.6	166072.9	127618.5	70695.2	122859
P53621	Coatomer	COPA	40436.22	39818.22	49375.88	51662.27	0	17481.03
P53634	Dipeptidyl	CTSC	147937.8	68611.96	93799.59	291105.8	605369.6	322451.3
P53680	AP-2 com	AP2S1	88307.09	51568.83	51339.33	12192.28	0	14399.82
P53794	Sodium/m	SLC5A3	363541.3	388521.8	299671.5	0	0	0
P53801	Pituitary tu	PTTG1IP	1432780	1207313	878965.3	0	0	0
P53999	Activated	SUB1	335251.3	244127.3	377460.9	345443.1	0	240084.3
P54136	Arginine--	RARS	40592.72	35425.35	38261.52	0	0	0
P54289	Voltage-d	CACNA2D	31474.22	31313.18	22634.59	130190.4	168615.8	75846.95
P54577	Tyrosine--	YARS	53062.71	52059.23	56562.69	0	25972.88	2.32E+08
P54578	Ubiquitin c	USP14	36328.28	34251.16	36911.91	0	0	0
P54619	5-AMP-ac	PRKAG1	11131.12	12958.52	9282.23	0	0	0
P54652	Heat shock	HSPA2	1389067	1420702	1830620	1022708	834494.4	1333530
P54727	UV excisio	RAD23B	49844.4	42054.14	37261.27	0	0	0
P54760	Ephrin typ	EPHB4	165163.9	201905.8	135886.2	0	0	0
P54852	Epithelial r	EMP3	17350.43	20307.76	8371.177	0	0	0
P54886	Delta-1-p	ALDH18A1	840242.6	803135	1007150	0	0	0
P55001	Microfibrill	MFAP2	9421.579	12086.4	16495.51	57025.92	132073.6	59632.9
P55011	Solute carr	SLC12A2	46942.75	42599.17	18063.52	0	0	0
P55039	Developm	DRG2	3222.691	2295.709	4518.267	0	0	0
P55072	Transitiona	VCP	467807.2	465972.9	429047.7	601210.6	702868.1	434573.7
P55196	Afadin	MLLT4	24911.45	24758.43	14989.63	0	0	0
P55212	Caspase-6	CASP6	17924.1	18085.82	21224.19	0	0	0
P55263	Adenosine	ADK	183209.8	162624.8	241483.6	81258.3	74845.74	107763.4
P55265	Double-st	ADAR	6069.76	6856.715	5156.909	0	0	0
P55268	Laminin su	LAMB2	36345.05	34501.97	35529.5	240018.3	299273.3	269564.7
P55285	Cadherin-	CDH6	17597.43	11357.35	12418.93	263199.5	355019.1	180554.9
P55287	Cadherin-	CDH11	23550.57	29219.48	33604.36	51290.77	137032.8	63581.63
P55290	Cadherin-	CDH13	31893.23	27820.71	23921.04	313293	335220.8	271303.9
P55854	Small ubiq	SUMO3	258867	255533.7	202826.6	0	83022.21	36787.14
P55884	Eukaryotic	EIF3B	107772.6	105955.5	133261.8	49992.45	0	58704.16
P56192	Methionin	MARS	35795.14	47536.41	55317.01	0	0	0
P56537	Eukaryotic	EIF6	24169.62	31943.46	39802.88	0	0	0
P58546	Myotrophi	MTPN	49090.51	68205.77	55886.32	0	0	0
P59768	Guanine n	GNG2	115685.2	114727.1	81329.32	0	0	0
P59998	Actin-relat	ARPC4	200704.6	183650.3	205833.5	0	83282.08	79696.24
P60033	CD81 anti	CD81	3284281	3102439	2018679	1900062	1581627	3493846
P60174	Triosephos	TPI1	355550.3	318585.2	277085.8	612185.1	791724.8	478278.5
P60228	Eukaryotic	EIF3E	70418.11	58414.09	72892.71	0	34705.58	46802.96
P60520	Gamma-a	GABARAPL	23256.92	20288.32	20135.59	0	0	0
P60660	Myosin lig	MYL6	423192.8	437960.4	493658.3	710507.8	645990.9	834062.3
P60709	Actin, cyto	ACTB	5564763	5950465	6134320	6261976	7845540	5209281
P60763	Ras-relate	RAC3	720184.3	846042.8	837642.4	487732.5	501458.9	874617.4
P60842	Eukaryotic	EIF4A1	340220.1	308113.1	354919.2	274392.6	309223.2	259137.9
P60866	40S riboso	RPS20	62263.33	90231.87	53428.09	43334.54	0	43740.13
P60900	Proteasom	PSMA6	99097.66	130156.1	125590.5	89078.78	82337.61	75443.92
P60903	Protein S1	S100A10	256284.5	253626.4	179802.2	0	0	0
P60953	Cell divisio	CDC42	169799	166998	225238.6	141234.6	55109.74	193880.1
P60981	Destrin	DSTN	273391.7	342524.9	264736	240116	0	247415.7
P60983	Glia matur	GMFB	20812.43	39266.04	30790.73	0	0	0
P61011	Signal rec	SRP54	4939.184	13252.67	6979.289	145157.8	0	217647.1
P61019	Ras-relate	RAB2A	158628.7	158373.2	141555.8	87045.52	160335.3	91564.16

P61026	Ras-relate	RAB10	191252.4	133496.7	130919.6	103561.3	122831.8	244707.1
P61081	NEDD8-co	UBE2M	44043.53	77663.2	88465.66	0	0	0
P61086	Ubiquitin-	UBE2K	43268.25	46189.88	40701.89	0	0	0
P61088	Ubiquitin-	UBE2N	25880.01	50738.68	63390.57	0	0	0
P61106	Ras-relate	RAB14	67680.78	64597.68	54581.84	0	0	0
P61160	Actin-relat	ACTR2	92744.42	98432.35	109304.9	62835.01	0	45822.85
P61163	Alpha-cen	ACTR1A	163863.3	85114.27	197264.7	0	0	0
P61204	ADP-ribos	ARF3	501819.8	436581.8	534554.8	417896.3	304944.6	432398.3
P61221	ATP-bindi	ABCE1	24455.97	23661.07	32667.31	0	0	0
P61224	Ras-relate	RAP1B	1758139	1701734	1566477	951262.6	1428546	480165.9
P61247	40S riboso	RPS3A	128653.4	164638.3	103512.6	145218.5	46896.07	115120.1
P61289	Proteasom	PSME3	32448.28	25537.04	29832.59	0	0	0
P61313	60S riboso	RPL15	235530.2	68841.53	48245.68	206750.1	0	139648.8
P61353	60S riboso	RPL27	70014.19	75458.55	65438.18	160842	0	185503.7
P61586	Transformi	RHOA	78819.13	62945.84	71907.31	0	0	0
P61604	10 kDa hea	HSPE1	94993.73	49048.23	68693.08	0	0	0
P61758	Prefoldin s	VBP1	25826.17	23100.99	26205.08	0	0	0
P61764	Syntaxin-b	STXBP1	13358.16	11946.69	10492.41	0	0	0
P61769	Beta-2-mi	B2M	344726.5	227859.2	260142.9	876844.1	1359867	630079.4
P61966	AP-1 com	AP1S1	11714.13	11248.08	11305.65	0	0	0
P61970	Nuclear tra	NUTF2	93129.55	77307.84	117930.3	0	0	0
P61978	Heterogen	HNRNPK	128355	151000.5	152190.9	0	95889.98	23617.05
P61981	14-3-3 pro	YWHAG	180257.2	175921.2	193676.5	155837.7	175087.5	149514.7
P62140	Serine/thre	PPP1CB	78790.13	73804.94	87111.01	40180.05	0	35705.42
P62158	Calmodulin	CALM1	411982.8	400014.2	358586.8	782175.1	927278.9	665159.1
P62166	Neuronal c	NCS1	39961.32	30280.45	16383.3	0	0	0
P62191	26S protea	PSMC1	64656.25	58022.37	64933.38	45534.24	39560.24	69532.2
P62195	26S protea	PSMC5	42349.78	44201.44	51237.61	42887.3	0	39157.28
P62241	40S riboso	RPS8	256694.8	263118.7	75870.1	472493.3	241984.1	265366.6
P62249	40S riboso	RPS16	163581	151960.3	177116.4	234529.9	0	221601.8
P62256	Ubiquitin-	UBE2H	19216.91	14158.38	17309.44	0	0	0
P62258	14-3-3 pro	YWHAE	181789	203673.7	186209.2	211570.7	366755.4	138827.3
P62263	40S riboso	RPS14	94597.63	100726.6	77778.57	105136.9	93636.84	129242.1
P62266	40S riboso	RPS23	65823.3	56771.28	0	45551.25	0	49588.64
P62269	40S riboso	RPS18	168799.7	179419	176985	140462.4	90347.64	163563.9
P62277	40S riboso	RPS13	103982	106985.7	107022.6	87283.6	61189.55	75518.88
P62280	40S riboso	RPS11	74502.59	72979.09	70273.09	93967.92	0	81768.91
P62310	U6 snRNA-	LSM3	14892.2	16476.82	14400.07	0	0	0
P62314	Small nucl	SNRPD1	14890.81	15344.65	9867.654	0	0	0
P62318	Small nucl	SNRPD3	82518.2	74322.91	84643.73	53257.95	0	39733.36
P62330	ADP-ribos	ARF6	76545	71080.59	62870.73	68841.8	0	42646.13
P62333	26S protea	PSMC6	74717.64	70726.2	85199.57	172746	0	111203.6
P62424	60S riboso	RPL7A	92234.63	137428	94828.4	193385.7	110345.1	151183.5
P62633	Cellular nu	CNBP	82225.27	84455.45	22900.84	0	0	0
P62701	40S riboso	RPS4X	133658.9	144004.1	137342.4	172884.6	0	134552.5
P62736	Actin, aorti	ACTA2	457007.5	498850.1	531343.2	546390	757150.4	623295.3
P62750	60S riboso	RPL23A	13035.65	25976.37	14146.57	10187.77	0	14947.42
P62753	40S riboso	RPS6	191483	195177.7	74536.95	419110.5	0	225311.6
P62760	Visinin-like	VSNL1	62794.5	57764.54	49779.02	0	0	0
P62805	Histone H4	HIST1H4A	45412744	49646260	65450448	1319124	5238356	2664199
P62820	Ras-relate	RAB1A	589869	693849.6	605597.4	1081687	1032340	1383776
P62826	GTP-bindi	RAN	703378.5	675405.6	684438	471053.1	268026.7	583597.5
P62829	60S riboso	RPL23	65779.28	42985.37	34965.5	0	0	0
P62834	Ras-relate	RAP1A	141630.3	183622.9	194859.6	73275.25	0	85352.38
P62847	40S riboso	RPS24	31297	45967.29	36111.25	0	0	0
P62851	40S riboso	RPS25	87928.7	94253.62	28936.48	84136.37	26728.56	52238.82
P62854	40S riboso	RPS26	168928	204324	126072.8	192189.6	0	243160.2
P62857	40S riboso	RPS28	103038.5	101346.5	90826.77	83164.5	116205.3	56583.36

P62873	Guanine n	GNB1	171354.9	139850.1	140463	0	0	0
P62875	DNA-direc	POLR2L	12777.5	8623.563	16497.24	0	0	0
P62879	Guanine n	GNB2	446005	465087.8	426012.4	418117.8	285086.9	422605.3
P62899	60S riboso	RPL31	47251.68	34943.88	62733.37	0	0	0
P62906	60S riboso	RPL10A	215169.4	213361.8	243856.8	167471.6	0	140242.3
P62917	60S riboso	RPL8	101777.5	99416.82	58460.23	244910.3	147052.3	161696.1
P62937	Peptidyl-p	PPIA	769686.5	660855.4	696412.3	679068.9	738548	484851.5
P62942	Peptidyl-p	FKBP1A	81343.63	55616.59	77765.47	718601.1	951429	469706.2
P62979	Ubiquitin-	RPS27A	4036475	4226877	2912125	5457158	5896259	4741509
P62993	Growth fac	GRB2	13470.34	27838.29	20057.11	0	0	0
P62995	Transform	TRA2B	101159.2	75369.84	80343.02	530145.9	843934.4	670002.1
P63010	AP-2 com	AP2B1	64246.3	74915.03	70023.01	145662	0	64156.13
P63104	14-3-3 pr	YWHAZ	232862.3	204037.9	189256	217797.2	353191.5	247508.4
P63173	60S riboso	RPL38	22211.31	21478.7	14740.87	0	0	0
P63208	S-phase ki	SKP1	96362.03	74632.08	97337.48	0	0	0
P63218	Guanine n	GNG5	59106.38	28222.12	36247.52	0	0	0
P63244	Guanine n	GNB2L1	147116	116126.6	164318	67212.32	0	58400.58
P63261	Actin, cyto	ACTG1	185044.8	170929.5	338374.8	359404.6	364770.3	0
P63279	SUMO-co	UBE2I	37828.84	40072.05	39480.91	0	0	0
P67775	Serine/thre	PPP2CA	230716.2	206080.2	267448	162806.2	142829.9	141568.3
P67809	Nuclease-	YBX1	274258.5	302377.2	217592.3	0	0	0
P67870	Casein kin	CSNK2B	58943.88	73458.13	63669.95	134752.7	0	78242.53
P67936	Tropomyo	TPM4	173677.2	166943.8	216742.9	664716.5	824317.3	424795.4
P68036	Ubiquitin-	UBE2L3	31790.93	25713.42	24489.75	0	0	0
P68104	Elongation	EEF1A1	3962200	4057261	4043449	2665316	2023420	2707649
P68363	Tubulin al	TUBA1B	5102925	4610989	6212615	14435993	5758159	17968256
P68366	Tubulin al	TUBA4A	3374945	2889944	3737845	4405745	4899424	10116559
P68371	Tubulin be	TUBB4B	1611230	1599174	1713856	3311132	1586903	4510178
P68400	Casein kin	CSNK2A1	50104.26	42178.08	32887.39	55528.15	35800.42	76615.82
P68402	Platelet-ac	PAFAH1B2	12293.43	12511.84	14419.3	0	0	0
P68431	Histone H	HIST1H3A	19980.81	19317.62	19345.15	0	0	0
P69891	Hemoglob	HBG1	73415280	52586772	87295872	1.62E+08	1.78E+08	1.57E+08
P69905	Hemoglob	HBA1	33236204	33187128	46006168	44398616	40482928	43246024
P78310	Coxsackiev	CXADR	66783.45	68744.04	59377.53	0	0	0
P78344	Eukaryotic	EIF4G2	8215.866	7465.678	11633.98	0	0	0
P78347	General tra	GTF2I	12360.57	6404.353	15234.11	0	0	0
P78371	T-complex	CCT2	240989.2	196892.1	227986.1	177742.1	0	187005.8
P78527	DNA-depe	PRKDC	43241.3	44010.59	37956.18	1202790	2386365	812444.3
P78539	Sushi repe	SRPX	123520.1	120859.7	85224.05	389804.3	232763.3	283262.5
P80162	C-X-C mo	CXCL6	0	0	0	3016109	2149925	1037208
P80723	Brain acid	BASP1	334259	483781.8	379839.7	378723.9	700093.6	450837.5
P80748	Ig lambda chain V-III		150013.5	156279.5	163273.3	0	0	0
P83731	60S riboso	RPL24	28808.33	34716.73	14708.84	51250.79	0	32660.62
P83916	Chromobo	CBX1	49924.22	37995.59	59381.82	0	0	0
P84090	Enhancer	ERH	73108.08	73209.5	68187.99	0	0	0
P84095	Rho-relate	RHOG	41332.51	50475.22	44596.35	14677.78	0	33250.8
P84098	60S riboso	RPL19	123712.3	143914.1	51707.59	613335.1	0	167605.1
P84103	Serine/arg	SRSF3	446691.1	437924	132437.6	280170.1	250698.9	235834.3
P98088	Mucin-5A	MUC5AC	33675.5	42194.25	32996.29	0	0	0
P98095	Fibulin-2	FBLN2	8477.441	10050.14	15685.69	0	0	0
P98160	Basement	HSPG2	205528.6	191931.6	201243.5	403314.8	502427	701589.1
P98172	Ephrin-B1	EFNB1	26178.2	42324.65	23351.2	0	0	0
P98194	Calcium-tr	ATP2C1	23009.51	11439.84	23480.68	0	0	0
P98196	Probable	ATP11A	150453.9	183105.8	201999.7	8535011	11612708	4439523
P99999	Cytochrom	CYCS	15855.27	15172.78	12043.54	0	0	0
Q00013	55 kDa ery	MPP1	8637.649	9726.449	6703.822	0	0	0
Q00266	S-adenosy	MAT1A	98641.73	58549.1	82957.88	0	0	0
Q00341	Vigilin	HDLBP	19310.16	18551.78	18036.87	0	0	0

Q00577	Transcripti	PURA	33950.13	33145.2	37216.54	0	0	0
Q00610	Clathrin he	CLTC	478881.6	573875.6	577671.3	470776.2	624443.8	568830.6
Q00688	Peptidyl-p	FKBP3	6557.295	28290.59	4232.543	0	0	0
Q00796	Sorbitol de	SORD	59826.55	54648.29	78094.24	0	0	0
Q01082	Spectrin be	SPTBN1	9723.567	11274.36	9543.045	6173.706	0	32380.52
Q01105	Protein SE	SET	1731833	1672725	1105897	133960	0	74832.05
Q01130	Serine/arg	SRSF2	236129.5	237767.1	83185.67	246599.6	0	162563
Q01433	AMP dean	AMPD2	27736.06	35152.83	40811.56	47425.62	0	46546.25
Q01469	Fatty acid-	FABP5	99692.87	106270	74007.59	266190.1	151779.6	124789.8
Q01518	Adenylyl c	CAP1	121052.3	109945	137203.5	157799.9	137914.4	166223.9
Q01581	Hydroxym	HMGCS1	46920.77	49498.85	59680.86	0	0	0
Q01628	Interferon-	IFITM3	133776.6	161889	102644	27576.04	0	46307.61
Q01650	Large neut	SLC7A5	161949.7	164717.3	119627.3	0	0	0
Q01658	Protein Dr	DR1	65757.95	62623.65	98362.47	0	0	0
Q01813	ATP-depe	PFKP	37429.8	36932.15	41961.96	63212.09	0	74323.12
Q01970	1-phosph	PLCB3	14386.96	6924.42	47623.38	0	0	0
Q01974	Tyrosine-p	ROR2	21887.49	16152.01	9959.422	0	0	0
Q01995	Transgelin	TAGLN	13765.6	11065.92	0	0	90245.53	68393.84
Q02153	Guanylate	GUCY1B3	19305.89	11904.89	23321.86	0	0	0
Q02241	Kinesin-lik	KIF23	23031.48	29567.95	28233.91	0	0	0
Q02790	Peptidyl-p	FKBP4	21139.54	18764.15	34014.82	0	0	0
Q02809	Procollage	PLOD1	90076.16	88668.54	107827.3	138342.7	165899.1	140330.6
Q02818	Nucleobin	NUCB1	31105.26	24141.03	25240.88	134929.5	173293.9	115882
Q02878	60S riboso	RPL6	82552.75	94930.5	44057.17	123840.5	24586.78	26101.67
Q02880	DNA topoi	TOP2B	23059.59	24258.88	13378.6	0	0	0
Q03169	Tumor nec	TNFAIP2	15039.08	9558.908	8510.234	0	0	0
Q03181	Peroxisom	PPARD	1766035	1410524	1292452	95690448	1.2E+08	55573584
Q03405	Urokinase	PLAUR	13466.11	17445.48	35983.36	0	0	0
Q04206	Transcripti	RELA	4503.715	50803.96	46755.23	0	0	0
Q04446	1,4-alpha-	GBE1	14364.02	14834.7	15818.59	0	0	0
Q04637	Eukaryotic	EIF4G1	16030.5	14576.42	21414.24	0	0	0
Q04756	Hepatocyt	HGFAC	228458.1	182198.4	211394.9	572580.1	1077806	727438.1
Q04837	Single-stra	SSBP1	48046.17	66726.88	78565.27	0	0	0
Q04917	14-3-3 pro	YWHAH	57500.98	64823.29	60373.14	41405.19	0	52227.13
Q05193	Dynamin-	DNM1	18195.47	18912.98	16806.5	0	0	0
Q05397	Focal adhe	PTK2	28248.11	49131.19	53316.67	0	0	0
Q05519	Serine/arg	SRSF11	47043.46	44176.31	85377.81	133929	128881.6	91454.57
Q05682	Caldesmor	CALD1	11393.36	12033.42	13363.27	0	32964.65	26461.6
Q06033	Inter-alpha	ITIH3	550448.7	469569.1	528821	5470790	6167389	3656485
Q06124	Tyrosine-p	PTPN11	11622.82	8151.346	16134.24	0	0	0
Q06203	Amidopho	PPAT	106390.3	70866.59	80970.51	2732075	3298194	1831235
Q06210	Glutamine	GFPT1	44506.98	39314.11	43953.2	77428.16	286029.8	26590.38
Q06265	Exosome c	EXOSC9	8998.518	4233.493	9808.12	0	0	0
Q06323	Proteasom	PSME1	82485.34	77385.69	65245.28	15101.39	0	6016.05
Q06828	Fibromodu	FMOD	58348.44	52169.79	56266.26	472282	639771.8	355573.4
Q06830	Peroxiredo	PRDX1	489557.7	476384.9	420297.4	861762.8	1150091	615647
Q07020	60S riboso	RPL18	165285.5	186976.7	107693	295541.5	0	165165.9
Q07021	Compleme	C1QBP	33815.8	22344.21	47431.73	0	0	0
Q07092	Collagen a	COL16A1	0	0	0	240926.5	317998	344779.5
Q07157	Tight junct	TJP1	4825.894	9982.923	10480.33	0	0	0
Q07666	KH domair	KHDRBS1	15917.26	23711.01	24198.9	0	0	0
Q07954	Prolow-de	LRP1	63984.77	98467.05	105177.4	206711	227710.2	205834.2
Q07955	Serine/arg	SRSF1	1166930	1194879	460867.4	0	0	0
Q08209	Serine/thre	PPP3CA	86214.68	85660.75	97755.63	0	0	0
Q08257	Quinone o	CRYZ	36043.25	30029.86	41061.95	0	0	0
Q08380	Galectin-3	LGALS3BP	1781904	1550089	2034937	902531.9	560760.2	1261738
Q08431	Lactadheri	MFGE8	3443919	3178272	2633844	1901814	1495151	3789209
Q08629	Testican-1	SPOCK1	15692.02	15790.43	22611.01	370466.2	697844.5	330086.3

Q08722	Leukocyte	CD47	250293.1	237998.8	157576.6	0	0	0
Q08752	Peptidyl-p	PPID	12195.75	18999.23	20549.7	0	0	0
Q09666	Neuroblas	AHNAK	125881.1	123294.4	100791.7	0	165102.5	56424.61
Q0VGL1	Ragulator	LAMTOR4	16670.55	16393.15	15130.98	0	0	0
Q10469	Alpha-1,6-	MGAT2	13938.42	4878.456	25101.95	0	866996.6	322290.1
Q10471	Polypeptid	GALNT2	6171.406	9896.034	7637.675	54223.19	0	57685.2
Q10567	AP-1 com	AP1B1	27193.12	28872.72	35951.63	0	30350.18	56866.69
Q10570	Cleavage a	CPSF1	7610.597	7018.937	7137.819	0	0	0
Q12768	WASH con	KIAA0196	11619.68	12188.98	13139.22	0	0	0
Q12805	EGF-conta	EFEMP1	65165.54	43325.52	81778.47	555236.3	873508.7	402843.4
Q12841	Follistatin-	FSTL1	28672.36	19054.51	23428.08	864688.6	1442083	576107.3
Q12846	Syntaxin-4	STX4	12624.25	15443.61	9887.982	0	0	0
Q12860	Contactin-	CNTN1	19012.3	14206.33	14977.69	289396.3	354674.5	136727.6
Q12874	Splicing fa	SF3A3	24406.5	23976.15	15681.45	0	0	0
Q12884	Prolyl end	FAP	52544.31	54387.73	50831.2	232141.7	228566.4	229654.2
Q12904	Aminoacyl	AIMP1	22489.45	21802.48	30167.4	0	0	0
Q12905	Interleukin	ILF2	23553.71	25406.25	20457.5	0	0	0
Q12906	Interleukin	ILF3	20309.06	19415.6	22172.86	0	0	0
Q12907	Vesicular i	LMAN2	46115.1	50840.51	138981.3	175740	104373	145558.8
Q12931	Heat shock	TRAP1	10733367	10232100	9297304	1655165	1377226	1700805
Q12959	Disks large	DLG1	39553.15	31658.75	24703.19	0	0	0
Q12974	Protein tyr	PTP4A2	24662.51	32472.69	27462.7	0	0	0
Q13033	Striatin-3	STRN3	8910.953	5779.441	11071.34	0	0	0
Q13042	Cell divisio	CDC16	6436.604	5476.673	3370.446	0	0	0
Q13045	Protein flig	FLII	13814.41	14922.23	16847.75	0	0	0
Q13085	Acetyl-Co	ACACA	4410.638	6087.893	5536.934	0	0	0
Q13093	Platelet-ac	PLA2G7	20592.53	22725.75	26250.78	36724.54	58812.06	30298.66
Q13094	Lymphocy	LCP2	57970.05	44656.03	72589.76	0	0	0
Q13103	Secreted p	SPP2	736435.4	642104.8	535441.3	384678.6	352302.3	443168.6
Q13107	Ubiquitin c	USP4	23218.59	29428.53	41988.38	0	0	0
Q13131	5-AMP-ac	PRKAA1	12015.2	8452.006	12066.64	0	0	0
Q13148	TAR DNA-	TARDBP	13382.08	13759.72	14949	0	0	0
Q13155	Aminoacyl	AIMP2	6408.18	27319.52	30004.05	0	0	0
Q13162	Peroxiredo	PRDX4	58163.09	50874.79	54200.91	0	0	0
Q13163	Dual speci	MAP2K5	5052396	4445428	4091865	27340140	38997316	18936590
Q13200	26S protea	PSMD2	63773.46	52476.46	66001.48	94136.73	49600.45	109541.2
Q13228	Selenium-	SELENBP1	38444.38	20413.35	39010.23	0	0	0
Q13263	Transcripti	TRIM28	36204.4	35566.56	31042.63	0	0	0
Q13283	Ras GTPas	G3BP1	25275.16	26329.28	30272.57	0	0	0
Q13308	Inactive ty	PTK7	136296.1	107872.9	104739.7	213580	294510.3	145318.2
Q13330	Metastasis	MTA1	16010.5	10005.94	11393.93	0	0	0
Q13347	Eukaryotic	EIF3I	47251.84	43133.77	59829.05	33469.04	0	40554.53
Q13363	C-terminal	CTBP1	8340.75	6746.858	8430.361	0	0	0
Q13409	Cytoplasm	DYNC1I2	11494.72	43127.91	39527.61	0	0	0
Q13418	Integrin-lir	ILK	228877.3	251306.6	349387.5	268917.5	116830.2	371684.4
Q13428	Treacle pr	TCOF1	21565.87	17579.96	3158.736	0	0	0
Q13435	Splicing fa	SF3B2	42144.84	53493.4	23572.74	0	0	0
Q13442	28 kDa he	PDAP1	157219	90259.31	139826.7	0	0	0
Q13459	Unconvent	MYO9B	3358.011	6793.713	7710.44	0	0	0
Q13464	Rho-assoc	ROCK1	68925.7	110430.4	137386.2	0	0	0
Q13492	Phosphatic	PICALM	6930.742	6739.979	3752.849	0	0	0
Q13509	Tubulin be	TUBB3	52644.77	132622.3	63488.41	719906	0	1048418
Q13547	Histone de	HDAC1	59898.74	68694.62	207353.5	0	0	0
Q13555	Calcium/ca	CAMK2G	12717.28	8215.128	10219.81	0	0	0
Q13557	Calcium/ca	CAMK2D	44854.98	34067.16	38694.07	0	0	0
Q13561	Dynactin s	DCTN2	51324.3	46178.94	49156.44	0	0	0
Q13576	Ras GTPas	IQGAP2	18742.56	20629.66	22286.15	0	0	0
Q13595	Transform	TRA2A	46577.32	48323.38	21136.66	0	0	0

Q13596	Sorting ne	SNX1	8096.92	12294.74	17537.09	0	0	0
Q13616	Cullin-1	CUL1	10042.04	13400.56	12757.52	0	0	0
Q13617	Cullin-2	CUL2	17567.86	11230.7	3892.787	0	0	0
Q13618	Cullin-3	CUL3	35992.73	26630.46	7657.588	0	0	0
Q13620	Cullin-4B	CUL4B	11709.77	9979.91	10949.2	0	0	0
Q13630	GDP-L-fuc	TSTA3	15199.64	14604.88	11199.44	0	0	0
Q13637	Ras-relate	RAB32	57710.53	59005.7	51953.57	65917.03	0	64449.97
Q13641	Trophobla	TPBG	20332.89	19004.12	17185.82	0	0	0
Q13642	Four and a	FHL1	272812.2	287436.4	310998	545492.3	0	757147.1
Q13683	Integrin al	ITGA7	23438.79	22595.39	17957.47	0	0	0
Q13740	CD166 ant	ALCAM	10402.67	7687.235	7164.387	0	149907.5	66167.41
Q13748	Tubulin al	TUBA3C	730953.3	630486.2	783660.5	1258749	0	1384352
Q13822	Ectonuclec	ENPP2	20045.58	19425.86	23076.98	174375.2	226232	231670.7
Q13838	Spliceoson	DDX39B	27377.26	31950.15	32080.91	0	0	0
Q13867	Bleomycin	BLMH	56290.12	90045.63	49619.27	0	0	0
Q13868	Exosome c	EXOSC2	186161.3	208492.6	257964.5	0	0	0
Q13873	Bone mor	BMPR2	10386.81	7419.708	6545.542	0	0	0
Q13884	Beta-1-syr	SNTB1	23542.5	19259.13	21932	0	0	0
Q13895	Bystin	BYSL	6417.302	4948.587	5057.371	0	0	0
Q13907	Isopenteny	IDI1	32946.1	37181.5	43526.47	0	0	0
Q14008	Cytoskelet	CKAP5	9321.587	6663.742	9422.77	0	0	0
Q14019	Coactosin-	COTL1	70513.02	54869.69	98786.77	177453.7	0	203258.5
Q14103	Heterogen	HNRNPD	89207.92	85391.36	78013.41	43171.5	0	32162.7
Q14108	Lysosome	SCARB2	99141.08	91321.97	71295.09	0	0	0
Q14112	Nidogen-2	NID2	0	0	0	272059	382887.5	446308
Q14117	Dihydropy	DPYS	27383.79	24697.09	34447.11	0	0	0
Q14118	Dystroglyc	DAG1	23966.28	45014.05	11202.46	0	0	0
Q14141	Septin-6	6-Sep	13624.18	18394.52	23175.52	0	0	0
Q14151	Scaffold at	SAFB2	26096.83	22349.32	19313.12	0	0	0
Q14152	Eukaryotic	EIF3A	111971.6	119934.4	135736.3	3388728	0	1656833
Q14157	Ubiquitin-	UBAP2L	3715.755	4082.576	3620.42	0	0	0
Q14160	Protein scr	SCRIB	43432.66	42143.89	28705.34	0	0	0
Q14166	Tubulin--t	TTLL12	39747.81	24005.49	47060.7	0	0	0
Q14192	Four and a	FHL2	11488.68	8381.749	7330.956	0	0	0
Q14195	Dihydropy	DPYSL3	50109.7	47094.9	55423.18	0	0	0
Q14203	Dynactin s	DCTN1	23319.77	23141.09	20112.67	0	0	0
Q14204	Cytoplasm	DYNC1H1	139413	113832.7	157406.8	141071.6	87666.41	197685.1
Q14232	Translatior	EIF2B1	5230.043	9872.54	10029.31	0	0	0
Q14240	Eukaryotic	EIF4A2	32661.32	38488.04	38890.99	0	0	0
Q14254	Flotillin-2	FLOT2	45252.39	45992.73	48564.16	35988.51	0	63282.87
Q14258	E3 ubiquiti	TRIM25	13166.86	12167.86	14336.04	0	0	0
Q14289	Protein-ty	PTK2B	33900.46	33539.62	46673.49	61265.67	105555.6	0
Q14315	Filamin-C	FLNC	45249.61	45121.92	46100.23	0	0	0
Q14344	Guanine n	GNA13	320440.4	328842.5	217525.7	2337526	0	389962.7
Q14376	UDP-gluc	GALE	13594.22	7941.291	13226.22	0	0	0
Q14393	Growth arr	GAS6	63062.11	61843.34	56892.8	0	0	0
Q14444	Caprin-1	CAPRIN1	11506.17	9624.444	13462.72	0	0	0
Q14498	RNA-bindi	RBM39	63137.91	61138.8	5967.763	0	0	0
Q14515	SPARC-lik	SPARCL1	20153.53	4118.076	39962.94	0	102401	55028.52
Q14517	Protocadh	FAT1	19904.06	13707.19	18942.59	0	0	0
Q14520	Hyaluronai	HABP2	63847.25	71661.4	73334.14	56901.07	56525.19	55130.77
Q14566	DNA replic	MCM6	26076.7	26347.05	24707.46	0	0	0
Q14623	Indian hed	IHH	43959.48	40535.73	48873.57	0	0	0
Q14624	Inter-alpha	ITIH4	50068.2	53930.23	71529.54	210113.4	258568	202851.2
Q14644	Ras GTPas	RASA3	16720.2	19981.24	18448.42	439620.3	0	44306.38
Q14651	Plastin-1	PLS1	23070.17	15929.43	13096.02	0	0	0
Q14676	Mediator c	MDC1	266865.7	237684.2	356786.1	0	0	0
Q14677	Clathrin int	CLINT1	17179.13	3004.033	15877.83	0	0	0

Q14683	Structural	SMC1A	60385.91	11058.25	41598.79	0	0	0
Q14697	Neutral alp	GANAB	221443.4	199241	214996	112382.4	128031.8	87484.97
Q14699	Raftlin	RFTN1	10288.27	9634.925	2892.39	0	0	0
Q14703	Membrane	MBTPS1	10517.21	14325.89	17940.8	0	0	0
Q14764	Major vaul	MVP	63549.15	59321.39	48018.29	765741.1	804876	841241
Q14766	Latent-trar	LTBP1	0	0	0	380742.7	551262.3	152547.7
Q14839	Chromodc	CHD4	19152.58	29291.71	24079.1	0	0	0
Q14847	LIM and SH	LASP1	46148.71	41388.2	43334.17	0	0	0
Q14974	Importin su	KPNB1	120273.2	94289.96	121974.9	39158.12	57689.78	46835.98
Q14980	Nuclear mi	NUMA1	25304.07	37612.89	26413.02	0	0	0
Q14997	Proteasom	PSME4	6140.605	5417.959	5125.579	0	0	0
Q14C86	GTPase-ac	GAPVD1	19563.65	23334.56	10519.35	0	0	0
Q15008	26S protea	PSMD6	72472.98	55079.58	76585.72	61890.34	42058.74	51917.22
Q15012	Lysosomal	LAPTM4A	53018.74	42993.28	28058.18	0	0	0
Q15020	Squamous	SART3	15811.2	16120.18	8483.23	0	0	0
Q15021	Condensin	NCAPD2	5207.743	4712.166	9823.329	0	0	0
Q15029	116 kDa U	EFTUD2	40057.57	21124.47	41927.44	0	0	0
Q15063	Periostin	POSTN	147388.1	151838.5	164945	1602861	2226877	1816469
Q15084	Protein dis	PDIA6	36011.38	33761.95	32236.02	0	0	0
Q15102	Platelet-ac	PAFAH1B3	37486.62	37124.94	37294.18	0	38401.33	29813.59
Q15113	Procollage	PCOLCE	255275.4	258206.7	279626.2	4340181	5408422	4506807
Q15166	Serum par	PON3	295725.6	297007	345757.1	0	0	0
Q15181	Inorganic p	PPA1	45565.06	47980.01	45672.36	0	0	0
Q15185	Prostaglan	PTGES3	509169.3	518117	327304.7	0	0	0
Q15208	Serine/thre	STK38	17626.79	15920.34	15842.84	0	0	0
Q15233	Non-POU	NONO	56046.59	55042.13	111074.6	0	0	0
Q15257	Serine/thre	PPP2R4	6971.964	6878.412	5608.52	0	0	0
Q15262	Receptor-t	PTPRK	16289.72	19237.12	13037.17	0	0	0
Q15286	Ras-relate	RAB35	547844.8	642379.1	525859.8	1079379	660415.8	1388577
Q15334	Lethal(2) g	LLGL1	94329.69	4171.096	116984.5	0	0	0
Q15349	Ribosomal	RPS6KA2	10532.82	11778.35	17438.92	0	0	0
Q15365	Poly(rC)-b	PCBP1	248650.6	236784.4	227611	186053.2	118090.2	167179.7
Q15366	Poly(rC)-b	PCBP2	122635	140603	171560.3	345370.9	181962	339339.1
Q15369	Transcripti	TCEB1	31779.78	20842.93	38534.21	0	0	0
Q15382	GTP-bindi	RHEB	46805.18	54161.25	45425.63	0	0	0
Q15392	Delta(24)-s	DHCR24	40259.05	43389.69	28677.61	175281.1	0	129490.3
Q15393	Splicing fa	SF3B3	38296.47	24332.1	36584.75	0	0	0
Q15404	Ras suppre	RSU1	47990.5	45793.16	46567.84	101374.4	126301.4	109636.1
Q15417	Calponin-3	CNN3	62069.41	53295.91	56974.91	0	0	0
Q15435	Protein ph	PPP1R7	44268.76	30201.03	62938.93	0	0	0
Q15459	Splicing fa	SF3A1	9386.977	12669.16	22312.18	0	0	0
Q15493	Regucalcin	RGN	82682.27	66197.8	113182.7	175878.1	294994	258608.3
Q15555	Microtubu	MAPRE2	72525.87	78072.75	151994.1	78771.14	77669.15	111437.9
Q15582	Transformi	TGFBI	151284.5	148324.5	136648.7	3156945	4577377	4117508
Q15599	Na(+)/H(+	SLC9A3R2	25814.67	28551.87	20363.83	0	0	0
Q15631	Translin	TSN	16594.26	29009.75	21597.42	0	0	0
Q15691	Microtubu	MAPRE1	46530.89	50397.4	22871.67	0	0	0
Q15717	ELAV-like	ELAVL1	43625.73	41636.73	46509.08	0	0	0
Q15758	Neutral an	SLC1A5	405980.8	417745.5	319768	488744.4	489888.5	781771.8
Q15819	Ubiquitin-c	UBE2V2	31822.4	50130.31	33811.8	0	0	0
Q15907	Ras-relate	RAB11B	445299.9	515484.4	489943.9	73445.16	207065.8	366701.8
Q15942	Zyxin	ZYX	12395.89	7317.015	7636.639	0	0	0
Q16186	Proteasom	ADRM1	9171.905	16919.07	18914.13	0	0	0
Q16204	Coiled-coi	CCDC6	18608.24	21671	26169.98	0	0	0
Q16222	UDP-N-ac	UAP1	31389.38	28310.75	34286.63	0	0	0
Q16270	Insulin-like	IGFBP7	6405.242	7848.044	4625.715	1170431	1688007	859752.2
Q16363	Laminin su	LAMA4	39267.32	49247.2	39363.16	413254.1	400325.9	458215.7
Q16394	Exostosin-	EXT1	29310.16	26548.76	36173.36	64458.87	57028.74	56867.5

Q16401	26S protea	PSMD5	24961.02	29382.16	32909.76	80363.08	23702.31	33219.02
Q16513	Serine/thre	PKN2	16087.92	12074.76	18247.44	0	0	0
Q16539	Mitogen-a	MAPK14	84692.26	44322.49	124391.8	0	0	0
Q16543	Hsp90 co-	CDC37	150476.6	76025.5	96049.17	0	0	0
Q16555	Dihydropy	DPYSL2	108208.1	109166.3	143473.5	94712.34	68673.52	77048.34
Q16563	Synaptoph	SYPL1	66730.22	95100.84	24664.89	0	0	0
Q16576	Histone-bi	RBBP7	47143.55	52990.3	64377.57	0	0	0
Q16610	Extracellula	ECM1	0	0	0	209460.7	256405.7	324061.6
Q16625	Occludin	OCLN	14691.88	9764.231	9199.033	0	0	0
Q16630	Cleavage a	CPSF6	16749.11	107106.7	14682.2	0	0	0
Q16637	Survival m	SMN1	14635.19	20079.96	8747.484	0	0	0
Q16643	Drebrin	DBN1	24128.76	20209.7	19199.73	0	0	0
Q16658	Fascin	FSCN1	35356.37	41411.07	55433.93	79565.14	53311.13	56508.36
Q16674	Melanoma	MIA	11010.62	11125.72	0	89204.71	140415.5	80642.96
Q16719	Kynurenina	KYNU	15843.53	13161.28	16880.07	0	0	0
Q16739	Ceramide	UGCG	17364.15	19405.98	7672.003	0	0	0
Q16769	Glutaminyl	QPCT	68267.73	62104.71	91304.3	0	0	0
Q16851	UTP--gluc	UGP2	109297.8	98417.65	108547	0	0	0
Q16853	Membrane	AOC3	0	0	0	1155179	1155577	600363.4
Q16878	Cysteine d	CDO1	393585.1	301928.7	333529.5	0	0	0
Q29RF7	Sister chro	PDS5A	3368.198	2268.984	1900.922	0	0	0
Q2M2I8	AP2-assoc	AAK1	42159.77	41260.67	41010.76	0	0	0
Q2M389	WASH con	KIAA1033	5541.708	4259.333	5498.631	0	0	0
Q2TAY7	WD40 rep	SMU1	4689.566	5276.245	4925.664	0	0	0
Q31612	HLA class I	HLA-B	531601.2	546656.4	407419.4	638216.1	901350.4	427994.2
Q32P28	Prolyl 3-hy	P3H1	12004.4	5059.799	0	58860.05	0	42562.89
Q3SY69	Mitochonc	ALDH1L2	50170.14	0	27147.62	504748.3	1442816	1403507
Q3YEC7	Rab-like p	RABL6	10095.83	8437.834	6019.322	0	0	0
Q3ZCW2	Galectin-re	LGALSL	39218.03	49249.41	105015.6	0	0	0
Q4KMQ2	Anoctamir	ANO6	12686.55	16813.39	9771.506	0	0	0
Q4V9L6	Transmem	TMEM119	577448.3	574107.1	456327.7	0	0	0
Q502W6	von Willeb	VWA3B	116122.2	103847.4	112217.1	0	0	0
Q52LJ0	Protein FA	FAM98B	5657.071	3909.912	3674.849	0	0	0
Q53H76	Phospholip	PLA1A	49970.9	45914.52	49339.87	0	99442.86	74261.45
Q53H96	Pyrroline-5	PYCRL	11253.87	14493.65	15724.84	0	0	0
Q562R1	Beta-actin	ACTBL2	2729231	3188125	1552774	539130.9	3083245	1032835
Q58FF6	Putative he	HSP90AB4	514628.6	500122.9	379744	0	0	0
Q58FF8	Putative he	HSP90AB2	394145.3	395838.7	385362.6	83086.01	73887.04	78047.16
Q5BKZ1	DBIRD con	ZNF326	14271.05	12024.9	34143.63	0	0	0
Q5H9R7	Serine/thre	PPP6R3	68655.55	271773.5	300980.5	0	0	0
Q5JSH3	WD repeat	WDR44	20750.29	29017.45	12121.52	0	0	0
Q5JTH9	RRP12-like	RRP12	4864.862	4297.08	3110.464	0	0	0
Q5SSJ5	Heterochro	HP1BP3	30361.71	35315.55	8675.063	0	0	0
Q5T1M5	FK506-bin	FKBP15	2568.771	0	5221.436	260015.3	341091.1	0
Q5T447	E3 ubiquiti	HECTD3	27717.08	18808.13	22403.61	0	0	0
Q5T4S7	E3 ubiquiti	UBR4	27624.51	28987.74	22283.36	69927.66	15165.43	67587.99
Q5T9L3	Protein wn	WLS	5632.751	11412.64	10326.36	0	0	0
Q5TBA9	Protein fur	FRY	162992.3	380581.1	0	0	61508.5	418833.3
Q5TDH0	Protein DD	DDI2	13994.36	12208.03	16874.22	0	0	0
Q5TEC6	Histone H3	HIST2H3PS	46138948	43798472	55996348	2510084	2961339	3398035
Q5VU43	Myomegal	PDE4DIP	57893.06	42861.99	22876.02	1001814	1436005	595991.9
Q5VVQ6	Ubiquitin t	YOD1	11742.66	11392	15983.41	0	0	0
Q5W0Z9	Probable p	ZDHHC20	9329.87	7410.998	4460.522	0	0	0
Q5ZPR3	CD276 ant	CD276	24632.23	10919.37	7962.084	0	0	0
Q658P3	Metalloreo	STEAP3	156415.2	141672.8	89837.76	0	0	0
Q658Y4	Protein FA	FAM91A1	70194.81	33482.28	78855.3	0	0	0
Q66K14	TBC1 dom	TBC1D9B	17762.25	8166.455	9687.587	0	0	0
Q68CZ2	Tensin-3	TNS3	20389.53	117982.1	18871.84	0	0	0

Q68D91	Metallo-be	MBLAC2	5115.263	4129.619	3435.918	0	0	0
Q68EM7	Rho GTPas	ARHGAP17	27842.53	26076.09	27424.32	0	0	0
Q6B0K9	Hemoglob	HBM	27737.21	25217.56	35071.66	0	0	0
Q6DD88	Atlastin-3	ATL3	11601.07	12004.09	12260.95	56015	0	46711.82
Q6EMK4	Vasorin	VASN	44469.48	92577.54	76615.42	0	0	0
Q6GTS8	Probable c	PM20D1	33290.43	22762.76	38555.12	0	0	0
Q6IAA8	Ragulator	LAMTOR1	18616.33	14570.04	14390.28	0	0	0
Q6IBS0	Twinfilin-2	TWF2	23623	21980.02	24144.37	0	0	0
Q6IQ22	Ras-relate	RAB12	18749.48	12315.14	9022.387	0	0	0
Q6NYC1	Bifunctiona	JMJD6	11412.28	12479.59	4121.89	0	0	0
Q6P2Q9	Pre-mRNA	PRPF8	16303.5	16661.09	14585.47	0	0	0
Q6P988	Palmitoleo	NOTUM	528121.8	427346.2	522105.4	0	0	0
Q6P9B9	Integrator	INTS5	0	0	0	464583.6	674871.1	286240.6
Q6P9H4	Connector	CNKSR3	2710.137	2852.709	1514.042	0	0	0
Q6UWP2	Dehydroge	DHRS11	13799.22	13144.27	18982.93	0	0	0
Q6UX71	Plexin dom	PLXDC2	13105.13	6094.797	7633.669	0	0	0
Q6UY14	ADAMTS-l	ADAMTSL4	22004.92	145347.2	20239.81	0	0	0
Q6YHK3	CD109 ant	CD109	76646.91	35130.51	38996.32	443494.6	511132.1	318346.5
Q6ZNJ1	Neurobeac	NBEAL2	25937.61	18986.48	41347.77	0	0	0
Q70J99	Protein un	UNC13D	13714.35	9538.691	17532.47	0	0	0
Q71H61	Immunogl	ILDR2	29815.6	22737.29	38837.91	0	0	0
Q76LX8	A disintegr	ADAMTS13	106159.5	98403.42	112118.9	333701	390530.8	298895.4
Q76M96	Coiled-coi	CCDC80	9195.596	8759.98	6755.287	276036.1	556769.6	293690.9
Q7KYR7	Butyrophili	BTN2A1	21785.41	21101.63	22724.6	0	0	0
Q7KZ85	Transcripti	SUPT6H	573845.5	1146725	663199.2	1.03E+08	1.32E+08	80323176
Q7KZF4	Staphylocc	SND1	65635.26	74854.11	76147.82	0	0	0
Q7L014	Probable A	DDX46	21834.31	19240.8	15400.68	0	0	0
Q7L0J3	Synaptic ve	SV2A	13184.43	17743.91	11218.14	0	0	0
Q7L1Q6	Basic leuci	BZW1	103044.2	106676.7	72615.34	0	0	0
Q7L2E3	Putative A	DHX30	7188.385	7049.846	6856.984	0	0	0
Q7L2H7	Eukaryotic	EIF3M	78065.32	50173.52	94938.2	0	0	0
Q7L576	Cytoplasm	CYFIP1	33021.8	33226.01	32976.98	22524.39	21223.2	30570.35
Q7L5N1	COP9 sign	COPS6	35473.74	50262.85	66469.73	0	0	0
Q7L7X3	Serine/thre	TAOK1	11823.82	1560.685	19252.54	0	0	0
Q7LBR1	Charged m	CHMP1B	136610	134324.6	102966.4	0	0	0
Q7LDG7	RAS guany	RASGRP2	28874.96	27112.15	39520.31	54803.99	0	63936.05
Q7RTV0	PHD finger	PHF5A	6687.322	3273.442	10895.47	0	0	0
Q7Z2W4	Zinc finger	ZC3HAV1	10018.54	12131.8	5422.312	0	0	0
Q7Z304	MAM dom	MAMDC2	3335675	0	3220723	43753.21	0	349404.8
Q7Z3C6	Autophagy	ATG9A	32606.7	15717.69	15072.06	0	0	0
Q7Z3U7	Protein MC	MON2	43137.6	37816	48668.15	4238394	4733293	2830150
Q7Z406	Myosin-14	MYH14	471205.3	518398.3	722952.1	1153926	730364.6	1417264
Q7Z460	CLIP-asso	CLASP1	69623.2	24947.6	46459.55	0	0	0
Q7Z4F1	Low-densi	LRP10	27076.05	20224.04	16917.8	0	0	0
Q7Z4W1	L-xylulose	DCXR	144111.8	150150.4	145093.1	0	0	0
Q7Z6Z7	E3 ubiquiti	HUWE1	88884.54	78863.98	91705.41	15995571	20045522	4963382
Q7Z7A1	Centriolin	CNTRL	246758.3	714297.3	142905.5	0	0	0
Q7Z7G0	Target of N	ABI3BP	0	0	0	423851.2	473071.2	380172.4
Q86UD1	Out at first	OAF	40569.86	36500.46	43436.77	168282.2	209887.3	114285.3
Q86UP2	Kinectin	KTN1	57826.05	54990.71	69089.51	148453.7	0	87126.7
Q86UX7	Fermitin fa	FERMT3	355018.2	365910.7	458662.8	165117.6	152384.8	175049.1
Q86V81	THO comp	ALYREF	20081.77	34677.98	19352.59	0	0	0
Q86VE9	Serine inco	SERINC5	184459.4	196218.5	119405.6	0	0	0
Q86VI4	Lysosomal	LAPTM4B	217046.9	327586.3	113017.8	0	0	0
Q86VP6	Cullin-asso	CAND1	170956	165766.7	191714	66374.02	0	80426.06
Q86W92	Liprin-beta	PPFIBP1	9544.241	25788.99	12422.93	0	0	0
Q86X55	Histone-ar	CARM1	27340.07	34358.06	34887.5	0	0	0
Q86XF0	Dihydrofol	DHFRL1	23191.31	21681.97	21955.2	0	0	0

Q86XS8	E3 ubiquiti	RNF130	13261.31	9932.878	6246.138	0	0	0
Q86XX4	Extracellula	FRAS1	9623.444	6074.753	7131.569	0	0	0
Q86Y82	Syntaxin-1	STX12	53885.34	48403.73	66146.35	0	0	0
Q86YQ8	Copine-8	CPNE8	112307	104314.2	79349.48	66077.84	48093.49	86873.32
Q8IUL8	Cartilage in	CILP2	54643.96	21358.13	29437.15	212758	166226.9	168581.3
Q8IUR7	Armadillo	ARMC8	18511.08	16528.22	18820.04	0	0	0
Q8IUX7	Adipocyte	AEBP1	0	0	0	177514.9	237493.7	176406.4
Q8IV08	Phospholip	PLD3	42262.23	38044.58	33784.95	0	0	0
Q8IVB5	LIX1-like p	LIX1L	23713.07	25880.33	16806.68	0	0	0
Q8IWA0	WD repeat	WDR75	23172.6	5953.117	7463.631	0	0	0
Q8IWB7	WD repeat	WDFY1	12998.72	10447.97	15103.59	0	0	0
Q8IWT6	Volume-re	LRRC8A	47451.73	5546.188	3589.723	0	0	0
Q8IWX8	Calcium ho	CHERP	2886.865	1780.566	1387.939	0	0	0
Q8IWY4	Signal pep	SCUBE1	8526.536	6736.001	9994.779	0	0	0
Q8IX12	Cell divisio	CCAR1	21235.11	19913.77	10961.58	0	0	0
Q8IXI1	Mitochonc	RHOT2	185965	181306.5	131262.5	0	0	0
Q8IY81	pre-rRNA	FTSJ3	17520.48	16960.82	13703.64	0	0	0
Q8IY95	Transmem	TMEM192	57746.15	83501.91	59332.37	0	0	0
Q8IYB3	Serine/arg	SRRM1	22834.75	24838.54	9741.666	0	0	0
Q8IYS1	Peptidase	PM20D2	8606.948	8782.688	9234.586	0	0	0
Q8IYT4	Katanin p6	KATNAL2	88743.86	84276.98	89703.08	0	0	0
Q8IYU2	E3 ubiquiti	HACE1	4957.866	2865.334	4647.653	0	0	0
Q8IZ07	Ankyrin rep	ANKRD13A	3230.71	3478.205	3598.301	0	0	0
Q8IZ83	Aldehyde d	ALDH16A1	21096.34	14966.2	51514.38	41232.11	0	42253.07
Q8N163	Cell cycle a	CCAR2	51051.86	38052.56	52299.82	0	0	0
Q8N1G4	Leucine-ric	LRRC47	27170.99	23753.06	29146.71	0	0	0
Q8N1N4	Keratin, typ	KRT78	0	2388.625	13300.8	100808.7	71649.63	60882.41
Q8N392	Rho GTPas	ARHGAP18	304945.2	662174.9	93980.43	0	0	0
Q8N5I2	Arrestin do	ARRDC1	27324.77	30946.84	21610.78	0	0	0
Q8N7H5	RNA polyn	PAF1	12878.22	19122.9	12937.89	0	0	0
Q8N884	Cyclic GMP	MB21D1	88252.66	164978.7	108270.5	514410.3	727557.6	332782.3
Q8N8S7	Protein en	ENAH	24863.41	29857.07	27148.38	0	0	0
Q8N9N7	Leucine-ric	LRRC57	30089.45	29588.83	28392.21	0	0	0
Q8NAV1	Pre-mRNA	PRPF38A	21578.79	25511.15	11585.95	0	0	0
Q8NB90	Spermatog	SPATA5	88743.85	81354.8	87429.64	0	0	0
Q8NBF2	NHL repea	NHLRC2	18431.42	16661.52	28923.94	0	0	0
Q8NBJ4	Golgi mem	GOLM1	30827.44	28847.63	28117.15	317513.1	487378.2	232587.2
Q8NBJ5	Procollage	COLGALT1	13372.2	10398.02	12968.69	0	0	0
Q8NBM8	Prenylcyste	PCYOX1L	24447.2	17284.38	30534.93	0	0	0
Q8NBS9	Thioredoxi	TXNDC5	13241.39	16744.82	17630.41	59496.86	79353.56	49275.71
Q8NBZ7	UDP-gluc	UXS1	12231.38	10345.54	12710.93	0	0	0
Q8NC42	E3 ubiquiti	RNF149	12449.28	146346.9	126146.4	0	0	0
Q8NC51	Plasminog	SERBP1	25813.21	23379.21	36681.17	0	0	0
Q8NC54	Keratinocy	KCT2	14126	9094.699	6120.911	0	0	0
Q8NCH0	Carbohydr	CHST14	20973.11	17065.07	25764.95	0	0	0
Q8NDZ4	Deleted in	C3orf58	14089.42	17419.35	9654.741	0	0	0
Q8NE01	Metal tran	CNNM3	10753.1	8942.498	6479.776	0	0	0
Q8NE71	ATP-bindi	ABCF1	94216.11	134234.2	106702.7	0	0	0
Q8NFH8	RalBP1-ass	REPS2	9669.435	9709.561	12613.25	0	0	0
Q8NG11	Tetraspani	TSPAN14	62115.66	60142.71	64812.53	83921.62	0	106427.6
Q8NHP8	Putative ph	PLBD2	15081.99	13031.55	13366.56	46761.61	49197.2	33544.15
Q8NI35	InaD-like p	INADL	24516506	22018264	18046676	2.11E+08	3.29E+08	1.42E+08
Q8TAA9	Vang-like	VANGL1	5431.396	2833.003	89165.36	0	0	0
Q8TAT6	Nuclear pr	NPLOC4	21187.42	25233.33	30717.39	0	0	0
Q8TAV4	Stomatin-l	STOML3	813964.6	692726.2	615415.4	0	377093.6	1059369
Q8TB61	Adenosine	SLC35B2	10988.88	6349.682	0	44509.49	30410.88	32111.28
Q8TB73	Protein ND	NDNF	38234.76	47996.46	53906.52	96410.66	0	231979.5
Q8TBB5	Kelch dom	KLHDC4	6585.589	8941.035	2859.377	0	0	0

Q8TBC4	NEDD8-ac	UBA3	26701.1	24631.63	15152.36	0	0	0
Q8TBX8	Phosphatic	PIP4K2C	22003.59	11948.63	21884.92	0	0	0
Q8TCT8	Signal pep	SPPL2A	17060.61	21760.07	16777.54	0	0	0
Q8TCZ2	CD99 antig	CD99L2	7990.86	8436.614	7378.066	0	0	0
Q8TD19	Serine/thre	NEK9	493379.3	422443.5	540068.5	0	0	0
Q8TDB8	Solute carr	SLC2A14	29913.3	30150.52	36038.82	0	0	0
Q8TDZ2	Protein-m	MICAL1	7591.599	9793.289	9079.602	0	0	0
Q8TED0	U3 small n	UTP15	7961.152	7496.458	7787.739	0	0	0
Q8TEX9	Importin-4	IPO4	9421.168	8886.098	7130.212	0	0	0
Q8WTT2	Nucleolar	NOC3L	12434.9	14205.07	6536.394	0	0	0
Q8WTV0	Scavenger	SCARB1	35140.66	32000.99	23626.76	0	0	0
Q8WUJ3	Cell migrat	CEMIP	22959.54	17933.01	22132.45	146531.9	116685.5	141083.8
Q8WUM4	Programm	PDCD6IP	183112.4	193527.4	171298.9	88995.02	59865.63	160786.5
Q8WUM9	Sodium-de	SLC20A1	20638.7	19103.21	15627.59	0	0	0
Q8WUW1	Protein BR	BRK1	11567.66	13369.15	21339.51	0	0	0
Q8WV99	AN1-type	ZFAND2B	26219.07	21230.67	21172.56	0	0	0
Q8WVM8	Sec1 family	SCFD1	15584.17	14846.04	30596.65	0	0	0
Q8WWA0	Intelectin-	ITLN1	39375.2	37832.61	110422.4	287552.2	253904.9	260935.5
Q8WWI5	Choline tra	SLC44A1	83254.09	93211.17	75163.8	519212.8	0	161801.5
Q8WWU7	Intelectin-	ITLN2	130463.7	115302.5	183469.4	313265.5	289193	540924.7
Q8WWZ4	ATP-bindi	ABCA10	180477.4	134234.6	115519.4	1579875	2874770	1343837
Q8WWZ8	Oncoprote	OIT3	64825.69	80475.75	90064.46	197604.7	277849.5	190872.4
Q8WX93	Palladin	PALLD	32728.71	36750.25	33896.66	0	0	0
Q8WXE1	ATR-intera	ATRIP	23892.04	27032.73	25844.96	0	0	0
Q8WXE9	Stonin-2	STON2	0	0	0	549122.7	585295.3	794003.8
Q8WXI9	Transcripti	GATAD2B	31124.23	16005.74	20742.49	0	0	0
Q8WYA6	Beta-cater	CTNNBL1	4575.44	200565.9	17185.92	0	0	0
Q8WZA0	Protein LZI	LZIC	1219.495	14167.43	1591.11	0	0	0
Q92187	CMP-N-ac	ST8SIA4	102595.5	179661	104573.2	0	0	0
Q92499	ATP-depe	DDX1	30541.47	23935.94	30698.08	61581.58	0	46923.38
Q92520	Protein FA	FAM3C	26500.12	24589.18	26244.58	0	119390.1	58729.86
Q92522	Histone H1	H1FX	27025.2	34012.49	33035.54	0	0	0
Q92536	Y+L amino	SLC7A6	63148.52	61370.03	41704.43	0	0	0
Q92544	Transmem	TM9SF4	13674.55	13529.16	10770.18	23876.97	0	36278.88
Q92572	AP-3 com	AP3S1	18308.68	7971.684	14159.21	0	0	0
Q92597	Protein NI	NDRG1	49494.4	43519.82	48406.45	0	0	0
Q92598	Heat shock	HSPH1	34374.91	30158.14	28554.81	0	0	0
Q92600	Cell differe	RQCD1	8782.299	7443.275	6429.628	0	0	0
Q92614	Unconvent	MYO18A	29110.5	52211.92	51442.94	631656.5	889543.4	285507.7
Q92616	Translatior	GCN1L1	320257.3	313105.8	326598.2	13711688	21284766	3531866
Q92619	Minor histo	HMHA1	21647.84	19946.91	23793.08	0	0	0
Q92626	Peroxidasi	PXDN	2324.487	9515.65	4443.7	874253.5	959492.4	1894679
Q92688	Acidic leu	ANP32B	286313.5	344268.6	84988.09	0	0	0
Q92692	Nectin-2	PVRL2	12683.18	12447.25	9200.345	0	0	0
Q92743	Serine pro	HTRA1	34259.13	27247.38	39966.25	5173575	2761369	8269728
Q92747	Actin-relat	ARPC1A	27647.65	21066.77	27546.15	0	0	0
Q92769	Histone de	HDAC2	106527.8	107803.5	102573.3	0	0	0
Q92783	Signal tran	STAM	25837.98	21863.03	23955.91	0	0	0
Q92820	Gamma-gl	GGH	31805.72	34705.81	48273.19	19831.76	0	23583.55
Q92841	Probable A	DDX17	36799.95	32436.16	39600.64	0	0	0
Q92882	Osteoclast	OSTF1	66143.73	90562.15	106897.6	0	0	0
Q92888	Rho guani	ARHGEF1	26077.18	18076.33	26068.06	0	0	0
Q92896	Golgi appa	GLG1	17128.4	18767.73	19816.54	53510.26	0	34039.91
Q92905	COP9 sign	COPS5	9344.845	7242.421	15156.12	0	0	0
Q92922	SWI/SNF c	SMARCC1	23739.96	26566.4	34681.05	0	0	0
Q92930	Ras-relate	RAB8B	49911.94	67165.42	48256.68	42334.47	0	62894.6
Q92945	Far upstrea	KHSRP	60055.94	34121.27	35756.11	0	0	0
Q92954	Proteoglyc	PRG4	52428.74	68323.02	64170.7	142148.6	195878	91801.29

Q92974	Rho guani	ARHGEF2	7480.108	10895.31	13800.09	39711.62	0	79506.39
Q93008	Probable u	USP9X	41926.41	37011.71	27198.38	85802.86	33276.18	78836.37
Q93034	Cullin-5	CUL5	24178.56	26228.15	15812.13	0	0	0
Q93063	Exostosin-	EXT2	0	33639.18	23676.04	70040.61	0	37517.64
Q93088	Betaine--h	BHMT	48749.76	62972.19	67072.44	216999.3	266992.1	143047.1
Q93096	Protein tyr	PTP4A1	20854.47	12197.38	9517.491	0	0	0
Q969E2	Secretory c	SCAMP4	31554.38	48457.32	35178.51	0	0	0
Q969G3	SWI/SNF-r	SMARCE1	39562.21	39770.91	41006.15	0	0	0
Q969P0	Immunogl	IGSF8	419164.4	411984.5	434948.6	119654.4	85423.12	160093.8
Q96A65	Exocyst co	EXOC4	6996.314	5707.342	6532.365	0	0	0
Q96A72	Protein ma	MAGOHB	41602.92	37379.55	35479.18	0	0	0
Q96AC1	Fermitin fa	FERMT2	53339.9	39241.36	55136.43	0	0	0
Q96AE4	Far upstrea	FUBP1	12830	15734.07	17701.85	0	0	0
Q96B54	Zinc finger	ZNF428	22720.1	11980.95	20422.81	0	0	0
Q96BM9	ADP-ribos	ARL8A	68107.16	55111.69	51763.04	0	0	0
Q96CN7	Isochorism	ISOC1	24964.26	26806.04	31969.9	0	0	0
Q96CS7	Pleckstrin h	PLEKHB2	21637.11	20683.33	21773.48	0	0	0
Q96CW5	Gamma-tu	TUBGCP3	18452.98	16954.53	22555.25	0	0	0
Q96CX2	BTB/POZ c	KCTD12	23241.87	26904.79	24994.74	114435	111293.4	69247.63
Q96D15	Reticulocal	RCN3	55230.22	31914.85	43541.78	436612.4	604471.3	194022.6
Q96DI7	U5 small n	SNRNP40	18925.22	18031.55	30927.69	0	0	0
Q96EG1	Arylsulfata	ARSG	32288.32	31854.07	41019.49	47078.93	48014.05	25521.71
Q96EP5	DAZ-asso	DAZAP1	28216.26	21515.72	25649.68	0	0	0
Q96F85	CB1 canna	CNRIP1	17355.41	17124.27	17947.98	0	0	0
Q96FN4	Copine-2	CPNE2	12096.36	18597.13	14699.45	0	0	0
Q96FZ7	Charged m	CHMP6	18564.9	18847.16	11995.09	0	0	0
Q96G03	Phosphogl	PGM2	27084.48	14676.12	29984.81	0	0	0
Q96GQ7	Probable A	DDX27	15611.69	11802.06	6820.611	0	0	0
Q96HC4	PDZ and L	PDLIM5	20714.02	21030.85	20531.56	0	13015.1	19338.67
Q96I24	Far upstrea	FUBP3	3001.569	40706.8	2590.254	423461.2	0	619744.4
Q96IJ6	Mannose-	GMPPA	15179.77	14905.65	7595.913	0	0	0
Q96IY4	Carboxype	CPB2	281657.2	260377.5	288980.7	0	0	0
Q96J84	Kin of IRRE	KIRREL	25052.05	25522.98	17438.56	0	0	0
Q96JB6	Lysyl oxida	LOXL4	5890.837	11001.9	10489.66	31368.49	19492.06	32217.52
Q96JD6	1,5-anhydr	AKR1E2	101707.8	89868.04	108329.5	0	0	0
Q96K17	Transcripti	BTF3L4	96100.23	101582	161042.5	0	0	0
Q96KG7	Multiple ep	MEGF10	46181.52	61477.3	32704.2	0	0	0
Q96KP4	Cytosolic n	CNDP2	130073.6	124721.4	148275.9	0	0	0
Q96NY7	Chloride in	CLIC6	231707.3	215524.4	246365.9	0	0	0
Q96P48	Arf-GAP w	ARAP1	11889.15	10447.52	15088.45	0	0	0
Q96P70	Importin-9	IPO9	3686.25	6572.995	9410.343	0	0	0
Q96PD5	N-acetylm	PGLYRP2	86373.33	96010.08	102920.3	217558.9	382687	0
Q96PU5	E3 ubiquiti	NEDD4L	26297.7	20414.24	25642.31	0	0	0
Q96QD8	Sodium-co	SLC38A2	104784.9	114625.1	72061.76	0	0	0
Q96QR8	Transcripti	PURB	36555.27	25628.71	56179.55	0	0	0
Q96QZ0	Pannexin-3	PANX3	297498.4	327420.8	240778.2	0	0	0
Q96RD7	Pannexin-1	PANX1	9197.145	8866.015	9337.938	0	0	0
Q96RF0	Sorting ne	SNX18	8116.119	9656.274	8238.264	0	0	0
Q96RI0	Proteinase	F2RL3	36058.58	34065.67	42437.7	49568.36	0	105924.1
Q96RT1	Protein LA	ERBB2IP	23076.13	17677.23	20298.54	0	0	0
Q96RW7	Hemicentin	HMCN1	4992861	5515239	5621468	47601024	65044392	31404530
Q96S59	Ran-bindin	RANBP9	19570.26	14789.71	20445.15	0	0	0
Q96S86	Hyaluronan	HAPLN3	33984.2	24432.26	22454.03	142351.1	0	184007.1
Q96S97	Myeloid-a	MYADM	41844.48	43330.95	46306.13	0	0	0
Q96S99	Pleckstrin h	PLEKHF1	14835.73	17143.82	8410.818	0	0	0
Q96SI9	Spermatid	STRBP	25281.31	20647.09	27315.8	0	0	0
Q96SL1	Disrupted	DIRC2	4075.74	2911.556	2675.826	0	0	0
Q96ST3	Paired amp	SIN3A	36528.97	49527.71	4291.893	0	0	0

Q96T76	MMS19 nu	MMS19	6634.525	11605.88	7244.592	0	0	0
Q96TA1	Niban-like	FAM129B	49753.19	45780.28	42944.91	1247459	0	671176.1
Q99417	C-Myc-bir	MYCBP	7795.243	5358.316	8297.198	0	0	0
Q99426	Tubulin-fo	TBCB	28829.28	29086.64	25532.98	0	0	0
Q99436	Proteasom	PSMB7	252769	314945.4	291867.1	126185.6	98506.67	112890.4
Q99447	Ethanolam	PCYT2	32251.57	38989.96	39889.75	0	0	0
Q99459	Cell divisio	CDC5L	5435.303	4695.693	6185.081	0	0	0
Q99460	26S protea	PSMD1	38287.15	42598.61	40082.46	0	0	0
Q99497	Protein de	PARK7	146383	152684	116160.8	158832.8	163500.6	132105.1
Q99519	Sialidase-1	NEU1	20216	24147.75	23583.5	0	0	0
Q99536	Synaptic ve	VAT1	105779.2	113931.2	102982.9	73252.43	58272.39	64052.93
Q99569	Plakophilir	PKP4	4640.95	1458.447	2011.263	0	0	0
Q99584	Protein S1	S100A13	27553.62	4148.124	41804.3	0	0	0
Q99627	COP9 sign	COPS8	62971.47	60503.23	96160.61	0	0	0
Q99653	Calcineurir	CHP1	39140.98	32945.51	27627.23	0	0	0
Q99715	Collagen a	COL12A1	502278.3	513288.9	441786.7	9335523	8199789	12020047
Q99733	Nucleoson	NAP1L4	104627.9	108234.5	216473.7	0	0	0
Q99747	Gamma-s	NAPG	20738.41	24611.93	19523.61	0	0	0
Q99755	Phosphatic	PIP5K1A	29294.3	26106.52	16772.87	0	0	0
Q99805	Transmem	TM9SF2	61102.75	34165.84	36068.21	84320.18	32916.44	64334.05
Q99808	Equilibrati	SLC29A1	113963.8	76477.55	56456.77	47406.21	0	73315.46
Q99961	Endophilin	SH3GL1	22761.74	19556.73	30558.61	39432.07	0	30842.87
Q9BPX5	Actin-relat	ARPC5L	30031.43	38353	31656.5	0	0	0
Q9BQ04	RNA-bindi	RBM4B	8803.541	9041.789	7548.893	0	0	0
Q9BQ67	Glutamate	GRWD1	75748.84	67816.43	81459.94	0	0	0
Q9BQ69	O-acetyl-A	MACROD1	3086.928	2212.933	4267.688	0	0	0
Q9BQA1	Methyloso	WDR77	46617.79	56382.25	48814.41	0	0	0
Q9BQL6	Fermitin fa	FERMT1	70522.71	65720.07	60629.88	0	0	0
Q9BR76	Coronin-1	CORO1B	23217.15	19200.01	26895.09	0	0	0
Q9BRA2	Thioredoxi	TXNDC17	25442.29	19386.99	19063.95	25577.71	121196.9	42447.66
Q9BRF8	Serine/thre	CPPED1	18180.01	16460.45	19819.06	0	0	0
Q9BS26	Endoplasm	ERP44	33956.8	33034.59	35411.91	0	0	0
Q9BSJ8	Extended s	ESYT1	40492.5	44938.19	48217.16	39546.98	0	82468.09
Q9BSL1	Ubiquitin-a	UBAC1	6444.48	5079.911	9816.815	0	0	0
Q9BT67	NEDD4 far	NDFIP1	67610.97	41302.47	26668.38	0	0	0
Q9BT78	COP9 sign	COPS4	58652.11	51791.76	78504.2	0	0	0
Q9BTE3	Mini-chror	MCMBP	7013.478	7220.61	10029	0	0	0
Q9BTT0	Acidic leuc	ANP32E	701289.5	491494.9	95585.11	0	0	0
Q9BTT6	Leucine-ric	LRRC1	18409.89	5552.05	2998.248	0	0	0
Q9BTU6	Phosphatic	PI4K2A	10729.94	8612.029	5585.443	0	0	0
Q9BTW9	Tubulin-sp	TBCD	10474.12	12237.19	9426.516	0	0	0
Q9BTY2	Plasma alp	FUCA2	22384.68	300092.5	360999.1	0	0	0
Q9BUF5	Tubulin be	TUBB6	933451.9	1074654	1550402	6209379	2288837	5673297
Q9BUJ2	Heterogen	HNRNPUL	16072.52	14935.83	19715.04	0	0	0
Q9BUK6	Protein mi	MSTO1	6975.552	5096.681	7150.519	0	0	0
Q9BUL8	Programm	PDCD10	31003.13	36056.55	11666.46	0	0	0
Q9BUQ8	Probable A	DDX23	8695.975	9898.82	16594.57	0	0	0
Q9BV68	E3 ubiquiti	RNF126	11838.02	79487.35	14344.37	0	0	0
Q9BVA1	Tubulin be	TUBB2B	1050428	650279.2	669049.6	1458404	1150398	3119961
Q9BVC6	Transmem	TMEM109	45868.73	42969.63	37932.95	0	0	0
Q9BVJ7	Dual speci	DUSP23	6479.945	7552.057	8478.697	0	0	0
Q9BVK6	Transmem	TMED9	5148.307	4966.546	4508.469	0	0	0
Q9BVL2	Nucleopor	NUP58	29711.63	35815.4	43208.72	0	0	0
Q9BWU0	Kanadaptir	SLC4A1AP	9608.287	3823.021	10807.41	0	0	0
Q9BXB5	Oxysterol-	OSBPL10	13834.86	9880.867	14363.53	0	0	0
Q9BXD5	N-acetylne	NPL	11564.71	6578.91	13457.35	0	0	0
Q9BXF6	Rab11 fam	RAB11FIP5	13463.33	8384.521	6035.11	0	0	0
Q9BXI6	TBC1 dom	TBC1D10A	8338.125	9563.969	5346.156	0	0	0

Q9BXJ9	N-alpha-a	NAA15	23375.29	22017.31	19889.68	0	0	0
Q9BXP5	Serrate RN	SRRT	13514.08	16335.74	10681.43	0	0	0
Q9BXS4	Transmem	TMEM59	37243.09	30891.39	22218.46	0	0	0
Q9BY44	Eukaryotic	EIF2A	10191.52	11717.51	11396.84	0	0	0
Q9BY67	Cell adhesi	CADM1	66020.09	29125.69	15119.18	0	0	0
Q9BY76	Angiopoie	ANGPTL4	0	0	0	119535.9	91896.05	168165.9
Q9BYJ0	Fibroblast	FGFBP2	176319	153436.2	203435.3	0	0	0
Q9BZ29	Dedicator	DOCK9	11606.34	7071.942	12983.33	0	0	0
Q9BZE4	Nucleolar	GTPBP4	5548	8438.159	6508.488	0	0	0
Q9BZE9	Tether con	ASPSCR1	18967.48	22450.06	19754.41	0	0	0
Q9BZF1	Oxysterol-	OSBPL8	7907.301	7106.12	4178.018	0	0	0
Q9BZG1	Ras-relate	RAB34	22160.02	30297.55	34126.5	0	0	0
Q9BZK7	F-box-like	TBL1XR1	12471.4	5247.667	9973.001	0	0	0
Q9BZL6	Serine/thre	PRKD2	17850.66	18640.8	28426.73	17198.17	0	25297.49
Q9BZQ8	Protein Nil	FAM129A	14794.64	18419.54	18669.32	0	0	0
Q9BZX2	Uridine-cy	UCK2	6259.403	5783.995	4726.362	0	0	0
Q9GZX5	Zinc finger	ZNF350	497210.1	750187	663761.8	0	50420504	27278870
Q9H074	Polyadeny	PAIP1	7833.594	9529.987	7163.732	0	0	0
Q9H0N0	Ras-relate	RAB6C	13956.2	42881.96	30958.96	0	0	0
Q9H0U4	Ras-relate	RAB1B	21090.86	20998.71	20525.91	0	0	0
Q9H0W9	Ester hydr	C11orf54	16277.42	18832.56	6799.077	0	0	0
Q9H299	SH3 doma	SH3BGRL3	137290.2	126873.4	106816.4	470359	690882.8	355954
Q9H2G2	STE20-like	SLK	3921.093	63875.16	34930.58	0	0	0
Q9H2H9	Sodium-co	SLC38A1	33881	26869.04	15746.88	0	0	0
Q9H2K8	Serine/thre	TAOK3	30472.64	30972.75	40004.21	0	0	0
Q9H2U2	Inorganic p	PPA2	89165.82	95228.8	91929.24	0	0	0
Q9H3G5	Probable s	CPVL	138170	132121.3	205037.5	0	0	0
Q9H3K6	BolA-like p	BOLA2	7413.853	9259.148	8865.248	0	0	0
Q9H3S7	Tyrosine-p	PTPN23	19577.33	10816.52	12209.35	0	0	0
Q9H3U1	Protein un	UNC45A	37221.87	12699.67	19912.83	0	0	0
Q9H444	Charged m	CHMP4B	171003.2	131120.8	146230.1	0	0	0
Q9H4A4	Aminopep	RNPEP	85508.35	50768.27	56544.69	0	0	0
Q9H4B7	Tubulin be	TUBB1	1224558	1043437	1665712	3927363	1112367	5073463
Q9H583	HEAT repe	HEATR1	4390.542	53665.84	50483.21	460353.1	0	492470
Q9H6B4	CXADR-lik	CLMP	2895529	1958527	2630547	4471939	0	3086545
Q9H6X2	Anthrax to	ANTXR1	16443.95	27860.98	9531.994	0	0	0
Q9H7B2	Ribosome	RPF2	3768.719	3788.698	4713.287	0	0	0
Q9H7D7	WD repeat	WDR26	27182.3	24058.51	27231.06	0	0	0
Q9H7P6	Multivesic	MVB12B	41780.46	26596.75	26840.54	0	0	0
Q9H832	Ubiquitin-	UBE2Z	53451.9	32843.3	29550.35	0	0	0
Q9H853	Putative tu	TUBA4B	1865073	1748697	2301872	4566328	1709119	5628501
Q9H8W4	Pleckstrin	PLEKHF2	14835.73	17143.82	8410.818	0	0	0
Q9H9A6	Leucine-ri	LRRC40	11827.2	18862.13	14547.82	0	0	0
Q9H9H4	Vacuolar p	VPS37B	35838.31	31181.41	23221.92	0	0	0
Q9H9Q2	COP9 sign	COPS7B	12645.32	18183.93	23582.18	0	0	0
Q9H9T3	Elongator	ELP3	4660.234	4283.351	9785.958	0	0	0
Q9HAC8	Ubiquitin c	UBTD1	19590.64	18565.6	15963.08	0	0	0
Q9HAN9	Nicotinami	NMNAT1	16434.21	19836.18	21328.2	0	0	0
Q9HAV0	Guanine n	GNB4	26301.89	24984.24	30532.29	43964.9	0	72563.13
Q9HAV4	Exportin-5	XPO5	4281.771	3315.628	6559.085	0	0	0
Q9HB07	UPF0160 p	C12orf10	4509.724	5295.763	6750.101	0	0	0
Q9HB40	Retinoid-i	SCPEP1	21643.58	26131.95	26164.93	0	0	0
Q9HB71	Calcyclin-b	CACYBP	28465.05	40435.51	52067.83	0	0	0
Q9HBI1	Beta-parvi	PARVB	102580.5	109026.6	121320.1	0	84116.48	156210.9
Q9HC07	Transmem	TMEM165	21755.03	24314.63	16734.2	0	0	0
Q9HCE1	Putative he	MOV10	6272.73	8913.672	6249.299	0	0	0
Q9HD45	Transmem	TM9SF3	52717.57	55554.9	45629.59	0	0	0
Q9HD89	Resistin	RETN	28815.41	9762.866	47709.55	0	0	0

Q9HDC9	Adipocyte	APMAP	484776.2	330592.3	395224.1	5043623	4710812	3572824
Q9NP72	Ras-relate	RAB18	30436.59	29090.99	30306.02	0	0	0
Q9NP79	Vacuolar p	VTA1	10774.39	50577.18	34012.12	0	72524.54	61220.77
Q9NPD3	Exosome c	EXOSC4	25990.17	24990.02	35406.36	0	0	0
Q9NPG4	Protocadh	PCDH12	23943.15	146740.8	150248.2	0	215536.9	24885
Q9NPH2	Inositol-3-	ISYNA1	75633.45	73047.52	67139.38	0	0	0
Q9NPH3	Interleukin	IL1RAP	113159.1	101727.5	102769.5	534726.8	630523.4	404219
Q9NPQ8	Synembryr	RIC8A	13049.66	16211.07	3872.929	0	0	0
Q9NQC3	Reticulon-	RTN4	720517.4	786809.8	708951.6	990735.6	831440.5	818230.7
Q9NQH7	Probable X	XPNPEP3	4037457	4075236	2307890	277034.8	278955.9	274383.6
Q9NQW7	Xaa-Pro ar	XPNPEP1	41228.76	37837.81	49831.54	0	30603.16	24009.25
Q9NQX7	Integral m	ITM2C	100637.6	95648.8	95785.87	0	0	0
Q9NR12	PDZ and L	PDLIM7	36462.27	37332.43	36796.62	0	0	0
Q9NR19	Acetyl-coe	ACSS2	28517.71	19739.6	41960.1	0	0	0
Q9NR30	Nucleolar	DDX21	365492	24963.57	22579.46	59828184	63204688	35631700
Q9NR31	GTP-bindi	SAR1A	87743.66	124115.5	105681.4	94917.96	95572.46	164484.4
Q9NR50	Translatior	EIF2B3	17848.6	16622.52	12449.19	0	0	0
Q9NRA1	Platelet-de	PDGFC	38368.23	27870.36	46819.3	0	0	0
Q9NRA2	Sialin	SLC17A5	13338.89	12961.15	9429.67	0	0	0
Q9NRF9	DNA polyr	POLE3	63106.9	47786.38	88204.61	0	0	0
Q9NRG0	Chromatin	CHRAC1	95525.19	85302.58	133654.2	0	0	0
Q9NRN5	Olfactome	OLFML3	38871.85	36688.13	60010.43	246114.2	344209.4	317987
Q9NRN7	L-aminoac	AASDHPP1	8380.994	7056.291	6779.707	0	0	0
Q9NRR8	CDC42 sm	CDC42SE1	5440.984	5414.772	3965.822	0	0	0
Q9NRV9	Heme-bin	HEBP1	40234	42920.24	42265.41	0	0	0
Q9NRW1	Ras-relate	RAB6B	562997.6	509880.6	494363.2	0	0	0
Q9NRW7	Vacuolar p	VPS45	6264.358	15080.17	10394.36	0	0	0
Q9NRY6	Phospholip	PLSCR3	32690.84	32055.7	58700.91	1263432	0	474169.8
Q9NSD9	Phenylalan	FARSB	21695.94	21377.5	29003.78	0	0	0
Q9NT62	Ubiquitin-	ATG3	22819.31	12829.25	27246.32	0	0	0
Q9NTI5	Sister chro	PDS5B	13773.92	15709.72	13279.33	0	0	0
Q9NTJ3	Structural	SMC4	13019.76	15977.76	14799.26	0	0	0
Q9NTK5	Obg-like A	OLA1	57218.07	35584.44	60901.25	0	0	0
Q9NUM4	Transmem	TMEM106I	86303.37	59759.78	55634.58	0	0	0
Q9NUP9	Protein lin	LIN7C	60864.03	71350.48	54875.6	0	0	0
Q9NUQ9	Protein FA	FAM49B	58109.02	53680.8	44572.49	0	0	0
Q9NUU7	ATP-depe	DDX19A	25917.91	25426.77	31735.88	0	0	0
Q9NV96	Cell cycle c	TMEM30A	27648.04	27421.48	28103.38	0	0	0
Q9NVJ2	ADP-ribos	ARL8B	18854.73	18953.44	49209.09	0	0	0
Q9NY33	Dipeptidyl	DPP3	31348.02	33722.43	17803.71	0	0	0
Q9NY35	Claudin dc	CLDND1	38666.83	37347.08	28088.11	0	0	0
Q9NY97	N-acetylla	B3GNT2	4070.041	3950.878	6006.329	0	0	0
Q9NYB9	Abl interac	ABI2	14797.02	8018.041	23055.85	0	0	0
Q9NZB2	Constitutiv	FAM120A	3060.819	12912.69	1796.053	0	0	0
Q9NZD2	Glycolipid	GLTP	8747.665	5936.644	5020.73	0	0	0
Q9NZL4	Hsp70-bin	HSPBP1	15243.92	12685.24	13607.44	0	0	0
Q9NZL9	Methionin	MAT2B	25077.2	25691.54	28038.75	0	0	0
Q9NZN3	EH domair	EHD3	266798.1	261655	315225.3	157525	161339	250372.8
Q9NZP8	Compleme	C1RL	0	0	0	56888.91	66546.84	50780.08
Q9NZQ3	NCK-inter	NCKIPSD	8084.56	14772.29	7119.306	0	0	0
Q9NZR2	Low-densi	LRP1B	93076.25	72605.71	88516.09	0	0	0
Q9NZW5	MAGUK p5	MPP6	36399.8	40965.27	29627.5	0	0	0
Q9NZZ3	Charged m	CHMP5	361378.4	307630.4	148651.8	0	0	0
Q9P0M6	Core histo	H2AFY2	107714.2	104347.9	49688.86	0	0	0
Q9P0V3	SH3 doma	SH3BP4	41941.55	26476.44	37397.71	0	0	0
Q9P0V9	Septin-10	10-Sep	8628.681	9265.026	59636.67	0	0	0
Q9P1F3	Costars far	ABRACL	22174.07	18533.53	16547.56	0	0	0
Q9P258	Protein RC	RCC2	103011.1	102852.6	62192.63	0	0	0

Q9P265	Disco-inte	DIP2B	88822.07	38715.99	93339.91	0	109252.7	417751.8
Q9P273	Teneurin-3	TENM3	13187.99	13915.04	13530.17	0	0	0
Q9P287	BRCA2 and	BCCIP	22909.12	22825.72	33321.91	0	0	0
Q9P289	Serine/thre	STK26	67793.65	73954.7	36479.45	0	0	0
Q9P2B2	Prostaglan	PTGFRN	686270	625117.9	595948	429118	349189.3	619980.5
Q9P2D3	HEAT repe	HEATR5B	792510.6	756622.3	910830.4	1624527	2242156	2293727
Q9P2J5	Leucine--t	LARS	29335.52	23937.87	26187.05	0	0	0
Q9UBC2	Epidermal	EPS15L1	10841.03	14242.78	12496.5	0	0	0
Q9UBF2	Coatomer	COPG2	22428.72	15598.26	17517.78	40402.85	85860.48	28727.37
Q9UBG0	C-type ma	MRC2	38339.58	34401.91	29898.8	98426.73	154751.3	156549.5
Q9UBH6	Xenotropic	XPR1	33440.53	10775.99	14353.51	0	0	0
Q9UBQ0	Vacuolar p	VPS29	49826.15	49442.98	59047.95	0	0	0
Q9UBQ5	Eukaryotic	EIF3K	60137.81	64391.71	77436.23	0	0	0
Q9UBR2	Cathepsin	CTSZ	0	27012.45	41092.03	533875.4	626240.5	226822.2
Q9UBT2	SUMO-act	UBA2	38084.88	38617.39	34811.58	0	0	0
Q9UBV8	Peflin	PEF1	51200.88	33380.42	46867.77	21869.42	0	57074.88
Q9UBW8	COP9 sign	COPS7A	15498.07	17636.89	27276.81	0	0	0
Q9UDY2	Tight junct	TJP2	27982.29	29826.36	31045.35	32899.14	0	46084.13
Q9UDY4	DnaJ hom	DNAJB4	9561.356	12675.39	13122.68	0	0	0
Q9UGH3	Solute carr	SLC23A2	21736.17	25685.4	13297.23	0	0	0
Q9UGI8	Testin	TES	9454.752	7656.33	12450.62	0	0	0
Q9UGJ0	5-AMP-ac	PRKAG2	11536.66	12061.83	9604.96	0	0	0
Q9UGM3	Deleted in	DMBT1	242832	266193.3	358692.2	1620548	1058128	1228339
Q9UHA4	Ragulator	LAMTOR3	6580.117	25497.42	21201.44	0	0	0
Q9UHB9	Signal rec	SRP68	30531.81	34708.71	25652.8	0	0	0
Q9UHD1	Cysteine a	CHORDC1	9116.991	10092	7513.317	0	0	0
Q9UHD8	Septin-9	9-Sep	97985.07	100833.6	118307.1	69914.99	25911.91	65536.16
Q9UHG3	Prenylcyst	PCYOX1	20850.4	13802.2	19760.88	0	0	0
Q9UHI8	A disintegr	ADAMTS1	0	0	0	211929.6	79440.09	195730
Q9UHV9	Prefoldin s	PFDN2	18222.49	26043.94	13238.92	0	0	0
Q9UHY1	Nuclear re	NRBP1	17543.23	14011.73	15470.78	0	0	0
Q9UHY7	Enolase-pl	ENOPH1	6528.121	6808.953	3605.541	0	0	0
Q9UI12	V-type pro	ATP6V1H	6228.825	9231.917	21994.46	0	0	0
Q9UIA9	Exportin-7	XPO7	9659.821	6672.625	9955.162	0	0	0
Q9UID3	Vacuolar p	VPS51	6990.621	5824.829	6718.24	0	103561.2	74403.73
Q9UIK4	Death-ass	DAPK2	20031.38	23334.95	36342.08	0	0	0
Q9UIQ6	Leucyl-cys	LNPEP	19882.35	19047.55	8153.053	0	0	0
Q9UIW2	Plexin-A1	PLXNA1	11091.38	8985.498	7814.506	0	0	0
Q9UJU6	Drebrin-lik	DBNL	15779.32	15045.15	24806.47	0	0	0
Q9UK41	Vacuolar p	VPS28	67166.58	66087.68	53663.23	0	0	0
Q9UK55	Protein Z-	SERPINA10	178489.4	57520.68	157253.3	349665.4	471716.7	349283.9
Q9UKD2	mRNA turn	MRTO4	63837.15	72915.59	25577.58	0	0	0
Q9UKE5	TRAF2 and	TNIK	19132.91	24394.92	16525.75	0	0	0
Q9UKF6	Cleavage a	CPSF3	3843.606	3116.635	4058.461	0	0	0
Q9UKM9	RNA-bindi	RALY	30492.83	12053.69	10224.96	0	0	0
Q9UKN8	General tra	GTF3C4	584942.3	562643.6	349232.9	0	0	0
Q9UKS6	Protein kin	PACSIN3	23673.24	24716.13	14965.88	0	0	0
Q9UKV3	Apoptotic	ACIN1	21236.68	16994.12	3717.816	0	0	0
Q9UKZ9	Procollage	PCOLCE2	2310.149	4442.255	10382.41	0	0	0
Q9UL26	Ras-relate	RAB22A	15759.21	16521.86	12157.05	0	0	0
Q9UL46	Proteasom	PSME2	46830.05	42876.18	35987.9	0	0	0
Q9ULA0	Aspartyl ar	DNPEP	27445.75	30245.77	32475.42	0	0	0
Q9ULF5	Zinc transp	SLC39A10	18785.42	37891.93	17149.92	0	0	0
Q9ULV4	Coronin-1	CORO1C	23429.13	26718.26	28741.12	0	0	0
Q9UM47	Neurogeni	NOTCH3	22857.88	19846.8	22830.12	0	120623.2	54712.08
Q9UMS4	Pre-mRNA	PRPF19	56056.91	95934.89	67670.44	0	0	0
Q9UN37	Vacuolar p	VPS4A	77878.11	71936.73	67691.28	50112.12	35106.15	57587.57
Q9UN42	Protein AT	ATP1B4	63222.47	110597.4	85277.18	0	0	0

Q9UN70	Protocadh	PCDHGC3	11387.12	11695	10514.24	0	0	0
Q9UN86	Ras GTPas	G3BP2	30356.1	32348.29	54457.46	0	0	0
Q9UNF0	Protein kin	PACSIN2	35648.39	31884.04	27120.97	0	0	0
Q9UNH7	Sorting ne	SNX6	42651.24	27735.6	50663.5	0	0	0
Q9UNK4	Group IID	PLA2G2D	55866.6	88635.47	89049.34	0	0	0
Q9UNM6	26S protea	PSMD13	68060.84	67331.79	81492.82	56780.98	0	61337.15
Q9UNN5	FAS-assoc	FAF1	21887.25	21877.71	8121.015	0	0	0
Q9UNP9	Peptidyl-p	PPIE	235744.5	242995.1	303613.1	318547.6	381440.6	282898.7
Q9UNS2	COP9 sign	COPS3	36448.54	37617.13	22615.01	0	0	0
Q9UPN7	Serine/thre	PPP6R1	11126.77	11418.13	12587.47	0	0	0
Q9UPT5	Exocyst co	EXOC7	4439.416	11211.05	4452.255	0	0	0
Q9UPU5	Ubiquitin c	USP24	7747.759	5888.875	6247.616	0	0	0
Q9UPY3	Endoribon	DICER1	1627.267	2044.764	2532.464	0	0	0
Q9UPY5	Cystine/glu	SLC7A11	9500.317	5372.007	4496.247	0	0	0
Q9UQ16	Dynamin-3	DNM3	71319.62	66602.12	38599.18	97435.65	63464.75	119591.4
Q9UQ80	Proliferatic	PA2G4	66428.8	58409.76	92323.48	13828.51	0	30537.7
Q9UQB8	Brain-spec	BAIAP2	17138.28	16193.07	15435.23	0	0	0
Q9UQE7	Structural	SMC3	9488.166	1431752	1710087	0	0	0
Q9Y223	Bifunctiona	GNE	24067.93	18106.47	49840.45	0	0	0
Q9Y230	RuvB-like 2	RUVBL2	84520.06	94418.49	95244.67	15991016	32627920	83068.62
Q9Y240	C-type lec	CLEC11A	5841.518	7327.106	12486.78	101042.9	0	52002
Q9Y262	Eukaryotic	EIF3L	85524.73	82881.9	106572.2	21255.54	0	20137.19
Q9Y265	RuvB-like 1	RUVBL1	82612	72271.52	87167.19	91734.94	0	177367.7
Q9Y266	Nuclear mi	NUDC	47187.18	78040.1	91157.73	0	0	0
Q9Y281	Cofilin-2	CFL2	257973.8	260095.7	286833.8	682974.3	457304.1	446995.5
Q9Y287	Integral m	ITM2B	225969.2	209499.9	163697.1	0	0	0
Q9Y295	Developm	DRG1	10681.78	14985.96	8138.996	0	0	0
Q9Y2A7	Nck-assoc	NCKAP1	20839.93	18439.41	20179.45	18227.92	0	16128.25
Q9Y2J2	Band 4.1-l	EPB41L3	25747.86	47031.91	35859.38	0	1999146	902620.4
Q9Y2L1	Exosome c	DIS3	1581038	1012403	1497041	0	0	0
Q9Y2V2	Calcium-re	CARHSP1	34722.78	30155.79	32413.66	0	0	0
Q9Y2W1	Thyroid ho	THRAP3	29378.65	47645.38	20165.93	0	0	0
Q9Y2W2	WW doma	WBP11	5699.162	4064.354	4656.537	0	0	0
Q9Y2X7	ARF GTPas	GIT1	0	0	0	832881.3	749694.8	1166966
Q9Y2Z0	Protein SG	SUGT1	16000	11925.57	15006.19	0	0	0
Q9Y316	Protein ME	MEMO1	30670.01	29451.65	36360.7	0	0	0
Q9Y371	Endophilin	SH3GLB1	11540.39	11525.76	40400.96	0	0	0
Q9Y383	Putative RI	LUC7L2	28194.46	28084.47	14428.29	0	0	0
Q9Y3A3	MOB-like p	MOB4	13494.81	55609.16	49821.19	0	0	0
Q9Y3A5	Ribosome	SBDS	38043.47	34107.77	36848.19	0	0	0
Q9Y3A6	Transmem	TMED5	57752.02	53684.7	58360.82	0	0	0
Q9Y3D6	Mitochonc	FIS1	2931.268	20628.88	3317.344	0	0	0
Q9Y3E1	Hepatoma	HDGFRP3	26250.84	29099.95	10218.59	0	0	0
Q9Y3E7	Charged m	CHMP3	37195.05	34458.88	36860.11	0	0	0
Q9Y3F4	Serine-thr	STRAP	15787.64	26183.59	26125.86	0	0	0
Q9Y3I0	tRNA-splic	RTCB	37806.4	37111.32	46586.13	0	0	0
Q9Y3I1	F-box only	FBXO7	18438.79	18485.58	23468.11	0	0	0
Q9Y3U8	60S riboso	RPL36	68022.78	76169.39	26678.26	88326.1	0	59096.22
Q9Y450	HBS1-like	HBS1L	9968.987	49212.58	10845.24	0	0	0
Q9Y487	V-type prc	ATP6V0A2	3840.308	5887.121	5796.345	0	0	0
Q9Y490	Talin-1	TLN1	451503.4	486001.2	675320.1	683451.7	546153.9	838229.5
Q9Y4B6	Protein VP	VPRBP	3651.215	14211.77	3021.785	0	0	0
Q9Y4E8	Ubiquitin c	USP15	14358.05	13974.26	14312.97	0	0	0
Q9Y4K0	Lysyl oxida	LOXL2	70471.34	64553.14	61964.68	642683.1	872959.6	732888.2
Q9Y4L1	Hypoxia up	HYOU1	63096.88	60473.35	64754.23	0	0	0
Q9Y4X5	E3 ubiquiti	ARIH1	17346.91	10132.41	13615.69	0	0	0
Q9Y547	Intraflagell	HSPB11	25804.11	20791.77	19608.22	0	0	0
Q9Y570	Protein ph	PPME1	18997.23	18851.73	20132.18	0	0	0

Q9Y5K5	Ubiquitin c	UCHL5	25551.23	27034.94	7028.894	0	0	0
Q9Y5K6	CD2-assoc	CD2AP	7954	12901.26	14734.82	0	0	0
Q9Y5L0	Transportir	TNPO3	5588.255	7290.373	11156.73	0	0	0
Q9Y5S2	Serine/thre	CDC42BPB	9201.245	10764.94	9543.267	0	0	0
Q9Y5S9	RNA-bindi	RBM8A	23537.63	23201.31	33033.76	0	0	0
Q9Y5X1	Sorting ne	SNX9	14110.1	13727.7	12255.17	49476.39	0	45505.39
Q9Y5X3	Sorting ne	SNX5	36939.96	13082.38	55754.51	0	0	0
Q9Y5X9	Endothelia	LIPG	8146.457	4956.808	8339.469	0	0	0
Q9Y5Y0	Feline leuk	FLVCR1	21815.04	15239.83	10999.69	0	0	0
Q9Y613	FH1/FH2 d	FHOD1	16130.93	11208.68	9106.969	0	0	0
Q9Y617	Phosphose	PSAT1	92643.6	98747.38	108279.2	0	0	0
Q9Y625	Glypican-6	GPC6	28784.19	31556.45	27166.41	0	39932.67	69858.97
Q9Y639	Neuroplas	NPTN	55447.07	58211.63	42452.34	0	0	0
Q9Y678	Coatomer	COPG1	33639.73	26838.18	27905.62	0	0	0
Q9Y696	Chloride ir	CLIC4	35672.03	46258.71	42945.45	28295.85	0	84226.45
Q9Y6C2	EMILIN-1	EMILIN1	138208	28561.63	0	256856.4	238170.1	430163.6
Q9Y6D5	Brefeldin A	ARFGEF2	4056.799	1746.622	2585.3	0	0	0
Q9Y6E0	Serine/thre	STK24	27966.88	31846.62	24347.95	0	0	0
Q9Y6E2	Basic leuci	BZW2	21622.26	0	14896.17	1457851	3367015	0
Q9Y6G9	Cytoplasm	DYNC1LI1	40065.21	42716.57	47900.31	127102.4	0	36341.48
Q9Y6M4	Casein kin	CSNK1G3	26837.96	26641.95	17401.39	0	0	0
Q9Y6M5	Zinc transp	SLC30A1	16517.5	11612.06	10640.06	0	0	0
Q9Y6M7	Sodium bi	SLC4A7	30016.42	30517.58	25949.48	0	0	0
Q9Y6R7	IgGFc-bin	FCGBP	136969.7	127020.5	127508.2	0	0	0
Q9Y6U3	Adseverin	SCIN	24287.21	26020.5	25526.66	0	0	0
Q9Y6W5	Wiskott-Al	WASF2	26741.41	17386.43	15626.24	0	0	0

SaOS2.vs.C	SaOS2.vs.C	SaOS2.vs.C	SaOS2.vs.C	SaOS2.vs.C	GO_NUM	GO_Descri	KEGG_Des	KEGG_EC
Inf	0	Inf	Significant	up	--	--	WAS prote	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Molecular	--	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Molecular	--	--
0.214035	0.524987	-2.22408	Nonsignifi	None	--	--	small nucle	--
#NAME?	0	#NAME?	Significant	down	--	--	collagen, t	--
Inf	0	Inf	Significant	up	--	--	integrin al	--
0.128845	0.10208	-2.95629	Nonsignifi	None	2	Molecular	componen	3.4.21.47
1.715706	0.064113	0.778803	Nonsignifi	None	5	Molecular	translation	--
2.117696	0.029946	1.082495	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant	up	--	--	eukaryotic	--
Inf	0	Inf	Significant	up	1	Molecular	kinesin ligh	--
Inf	0	Inf	Significant	up	2	Biological	transmemb	--
Inf	0	Inf	Significant	up	2	Molecular	WD repeat	--
Inf	0	Inf	Significant	up	2	Biological	vacuolar p	--
1.274911	0.064874	0.350397	Nonsignifi	None	--	--	transmemb	--
Inf	0	Inf	Significant	up	4	Molecular	kinesin fam	--
0.327897	0.036292	-1.60868	Nonsignifi	None	2	Molecular	--	--
Inf	0	Inf	Significant	up	--	--	acyl-coenz	3.1.2.2
0.351089	0.208269	-1.51009	Nonsignifi	None	4	Molecular	myosin I	--
Inf	0	Inf	Significant	up	--	--	synaptosor	--
Inf	0	Inf	Significant	up	2	Biological	syntaxin-b	--
0.311807	0.001524	-1.68127	Nonsignifi	None	3	Molecular	mannan-b	3.4.21.104
Inf	0	Inf	Significant	up	--	--	--	--
0.025185	0.335128	-5.31132	Nonsignifi	None	3	Biological	AP-3 comp	--
0.783557	0.077651	-0.35189	Nonsignifi	None	1	Molecular	26S protea	--
Inf	0	Inf	Significant	up	--	--	transcriptic	--
0.927221	0.010222	-0.10901	Nonsignifi	None	1	Molecular	chloride in	--
1.521399	0.04533	0.605399	Nonsignifi	None	1	Molecular	translation	--
Inf	0	Inf	Significant	up	1	Molecular	--	--
0.122968	0.032199	-3.02364	Significant	down	3	Molecular	thiol oxida	1.8.3.2
Inf	0	Inf	Significant	up	1	Molecular	Wiskott-Al	--
0.690637	0.159638	-0.534	Nonsignifi	None	1	Molecular	importin-5	--
0.690206	0.064415	-0.5349	Nonsignifi	None	4	Molecular	agrin	--
0.123439	0.006606	-3.01813	Significant	down	2	Molecular	procollage	1.14.11.4
0.473407	0.003036	-1.07885	Nonsignifi	None	1	Molecular	26S protea	--
Inf	0	Inf	Significant	up	2	Molecular	amphiphys	--
Inf	0	Inf	Significant	up	5	Molecular	--	--
Inf	0	Inf	Significant	up	2	Biological	ubiquitin c	3.4.19.12
0.809878	0.125429	-0.30422	Nonsignifi	None	1	Molecular	syntenin-1	--
Inf	0	Inf	Significant	up	--	--	nucleolar p	--
Inf	0	Inf	Significant	up	--	--	podocalyxi	--
0.062248	0.023792	-4.00584	Significant	down	4	Biological	cysteine ric	--
0.299349	0.025579	-1.7401	Nonsignifi	None	5	Molecular	lysosomal	3.2.1.24
Inf	0	Inf	Significant	up	--	--	pyridoxine	2.7.1.35
Inf	0	Inf	Significant	up	1	Molecular	AT-rich int	--
Inf	0	Inf	Significant	up	1	Biological	--	--
Inf	0	Inf	Significant	up	--	--	coatomer s	--
Inf	0	Inf	Significant	up	1	Molecular	--	--
1.133771	0.384888	0.181129	Nonsignifi	None	--	--	disintegrin	3.4.24.81
Inf	0	Inf	Significant	up	2	Biological	type II prot	2.1.1.320
Inf	0	Inf	Significant	up	1	Molecular	Na(+)/H(+	--
0.320954	0.023699	-1.63956	Nonsignifi	None	1	Cellular Co	neuropilin	--
Inf	0	Inf	Significant	up	2	Biological	transportir	--
1.114851	0.695846	0.156851	Nonsignifi	None	1	Cellular Co	tetraspanir	--
2.862791	0.001089	1.517423	Nonsignifi	None	5	Molecular	20S protea	3.4.25.1

Inf	0	Inf	Significant	up	1	Molecular	PDZ doma	--
Inf	0	Inf	Significant	up	1	Molecular	protein lin	--
Inf	0	Inf	Significant	up	1	Biological	histone ac	2.3.1.48
Inf	0	Inf	Significant	up	4	Molecular	calcium/ca	2.7.11.1
0.614637	0.039836	-0.70219	Nonsignifi	None	1	Molecular	myosin reg	--
Inf	0	Inf	Significant	up	2	Biological	hepatocyte	--
Inf	0	Inf	Significant	up	1	Molecular	protein ph	--
Inf	0	Inf	Significant	up	3	Molecular	cyclin G-as	2.7.11.1
Inf	0	Inf	Significant	up	1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	2	Biological	exportin-1	--
0.407623	0.058925	-1.29469	Nonsignifi	None	2	Molecular	plexin B	--
Inf	0	Inf	Significant	up	3	Molecular	U2-associa	--
Inf	0	Inf	Significant	up	--	--	phosphoril	6.3.5.3
Inf	0	Inf	Significant	up	1	Cellular Co	Niemann-	--
0.369806	0.535721	-1.43516	Nonsignifi	None	4	Cellular Co	actin relate	--
2.924936	0.009107	1.548405	Nonsignifi	None	4	Cellular Co	actin relate	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	3	Biological	prefoldin b	--
0.597389	0.135155	-0.74326	Nonsignifi	None	5	Molecular	laminin, al	--
0.21991	0.019783	-2.18501	Significant	down	1	Cellular Co	ER-derivec	--
Inf	0	Inf	Significant	up	3	Molecular	phosphom	5.4.2.8
Inf	0	Inf	Significant	up	--	--	high mobil	--
Inf	0	Inf	Significant	up	1	Molecular	protein ph	3.1.3.16
Inf	0	Inf	Significant	up	2	Biological	importin-8	--
0.878772	0.782063	-0.18644	Nonsignifi	None	1	Molecular	syntaxin 7	--
0.527322	0.018631	-0.92324	Nonsignifi	None	2	Cellular Co	MFS transp	--
Inf	0	Inf	Significant	up	3	Molecular	solute carr	--
Inf	0	Inf	Significant	up	4	Molecular	prolyl 4-hy	1.14.11.2
Inf	0	Inf	Significant	up	2	Cellular Co	synaptobre	--
Inf	0	Inf	Significant	up	4	Cellular Co	actin relate	--
Inf	0	Inf	Significant	up	2	Molecular	Arf-GAP w	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Molecular	U4/U6 sma	--
2.009348	0.000635	1.006727	Nonsignifi	None	3	Biological	--	--
Inf	0	Inf	Significant	up	--	--	dynein ligh	--
0.59952	0.476779	-0.73812	Nonsignifi	None	4	Cellular Co	26S protea	--
Inf	0	Inf	Significant	up	1	Molecular	--	--
Inf	0	Inf	Significant	up	2	Cellular Co	protein tra	--
0.242118	0.025347	-2.04622	Significant	down	--	--	beta-1,4-g	2.4.1.-
0.191159	0.338554	-2.38716	Nonsignifi	None	1	Molecular	--	--
1.503995	0.013417	0.5888	Nonsignifi	None	1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Biological	--	--
Inf	0	Inf	Significant	up	--	--	aflatoxin B	--
Inf	0	Inf	Significant	up	5	Molecular	erythrocyte	--
Inf	0	Inf	Significant	up	5	Cellular Co	ragulator c	--
0.189348	0.025219	-2.40089	Significant	down	--	--	beta-1,4-g	2.4.1.-
Inf	0	Inf	Significant	up	2	Biological	exportin-T	--
Inf	0	Inf	Significant	up	--	--	trafficking	--
Inf	0	Inf	Significant	up	1	Biological	charged m	--
Inf	0	Inf	Significant	up	1	Cellular Co	tetraspanir	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Molecular	cell cycle a	--
Inf	0	Inf	Significant	up	2	Molecular	cytohesin	--
0.000139	0.493395	-12.8116	Nonsignifi	None	4	Biological	AP-1 com	--
Inf	0	Inf	Significant	up	1	Molecular	small gluta	--
Inf	0	Inf	Significant	up	4	Molecular	myosin I	--

Inf	0	Inf	Significant	up	3	Molecular	cleavage a	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	--	--	nardilysin	3.4.24.61
0.115254	0.001762	-3.11711	Significant	down	1	Molecular	--	--
1.158812	0.602096	0.212647	Nonsignifi	None	1	Molecular	--	--
1.282482	0.106332	0.358939	Nonsignifi	None	3	Molecular	adenosylh	3.3.1.1
Inf	0	Inf	Significant	up	2	Cellular Co	cohesin co	--
Inf	0	Inf	Significant	up	3	Molecular	pre-mRNA	3.6.4.13
Inf	0	Inf	Significant	up	7	Molecular	SWI/SNF-r	3.6.4.-
Inf	0	Inf	Significant	up	--	--	c-Jun-ami	--
Inf	0	Inf	Significant	up	--	--	E3 ubiquiti	2.3.2.27
Inf	0	Inf	Significant	up	3	Molecular	lysine-spe	1.-.-.-
Inf	0	Inf	Significant	up	5	Molecular	nucleoside	2.7.4.6
0.153063	0.05759	-2.7078	Nonsignifi	None	1	Cellular Co	neuropilin	--
Inf	0	Inf	Significant	up	2	Molecular	long-chair	6.2.1.3
1.69198	0.00905	0.758712	Nonsignifi	None	1	Molecular	sorting ne	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	--	--	GDPmann	4.2.1.47
0.026535	0.340985	-5.23594	Nonsignifi	None	--	--	--	--
0.957732	0.78995	-0.06231	Nonsignifi	None	2	Molecular	--	--
Inf	0	Inf	Significant	up	4	Molecular	diaphanou	--
Inf	0	Inf	Significant	up	2	Cellular Co	MFS transp	--
Inf	0	Inf	Significant	up	5	Molecular	--	--
#NAME?	0	#NAME?	Significant	down	--	--	sushi repe	--
1.134279	0.845955	0.181776	Nonsignifi	None	1	Molecular	catenin (ca	--
Inf	0	Inf	Significant	up	2	Biological	sorting ne	--
Inf	0	Inf	Significant	up	6	Cellular Co	--	--
Inf	0	Inf	Significant	up	2	Biological	solute carr	--
Inf	0	Inf	Significant	up	2	Cellular Co	--	--
4.646526	0.002838	2.216152	Significant	up	1	Molecular	histone H2	--
0.931548	0.741288	-0.1023	Nonsignifi	None	2	Molecular	H/ACA rib	5.4.99.-
0.957271	0.889595	-0.063	Nonsignifi	None	1	Molecular	translation	--
Inf	0	Inf	Significant	up	2	Molecular	DnaJ hom	--
0.115083	0.022371	-3.11925	Significant	down	1	Biological	periplasmi	--
Inf	0	Inf	Significant	up	2	Molecular	SLIT-ROB	--
Inf	0	Inf	Significant	up	--	--	immunogl	--
3.053602	0.008698	1.610512	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant	up	3	Molecular	frizzled 1/7	--
0.176036	0.259161	-2.50606	Nonsignifi	None	4	Molecular	Rho-assoc	2.7.11.1
0.10248	0.040756	-3.28659	Significant	down	--	--	inducible T	--
Inf	0	Inf	Significant	up	--	--	protein TIF	--
0.479341	0.007606	-1.06088	Nonsignifi	None	--	--	DnaJ hom	--
Inf	0	Inf	Significant	up	2	Biological	ubiquitin c	3.4.19.12
2.328063	0.001999	1.21913	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant	up	1	Molecular	vacuolar p	--
2.552264	0.024883	1.351778	Nonsignifi	None	1	Molecular	histone H2	--
1.140467	0.739848	0.189625	Nonsignifi	None	1	Molecular	filamin	--
Inf	0	Inf	Significant	up	3	Molecular	tripartite m	--
Inf	0	Inf	Significant	up	--	--	citrate syn	2.3.3.1
Inf	0	Inf	Significant	up	1	Molecular	pre-mRNA	--
Inf	0	Inf	Significant	up	--	--	vacuolar p	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	3	Cellular Co	glypican 4	--
Inf	0	Inf	Significant	up	1	Molecular	FUS-intera	--
1.724225	0.097176	0.785948	Nonsignifi	None	1	Molecular	barrier-to-	--
Inf	0	Inf	Significant	up	--	--	splicing fa	--

Inf	0	Inf	Significant	up		1	Molecular	--	--
Inf	0	Inf	Significant	up		2	Molecular	pre-mRNA	3.6.4.13
Inf	0	Inf	Significant	up		2	Cellular Co	--	--
Inf	0	Inf	Significant	up	--		--	protein XR	--
Inf	0	Inf	Significant	up	--		--	cartilage-a	--
Inf	0	Inf	Significant	up		1	Molecular	translation	--
Inf	0	Inf	Significant	up		3	Molecular	translation	--
Inf	0	Inf	Significant	up		1	Molecular	26S protea	--
2.090618	0.06446	1.06393	Nonsignifi	None		1	Biological	isocitrate c	1.1.1.42
1.963168	0.134208	0.973183	Nonsignifi	None		4	Biological	formyltetra	1.5.1.6
0.252022	0.004458	-1.98838	Nonsignifi	None	--		--	PRA1 famil	--
1.117279	0.739594	0.15999	Nonsignifi	None		1	Cellular Co	tetraspanir	--
Inf	0	Inf	Significant	up		3	Molecular	--	--
Inf	0	Inf	Significant	up	--		--	ribosome I	--
#NAME?	0	#NAME?	Significant	down		2	Molecular	--	--
Inf	0	Inf	Significant	up		4	Molecular	signal reco	--
Inf	0	Inf	Significant	up	--		--	dimethylar	3.5.3.18
Inf	0	Inf	Significant	up		4	Molecular	serine/thre	2.7.11.1
#NAME?	0	#NAME?	Significant	down		2	Molecular	phospholip	3.6.3.1
0.563833	0.022638	-0.82666	Nonsignifi	None	--		--	--	--
Inf	0	Inf	Significant	up		4	Biological	AP-2 comp	--
0.200147	0.254928	-2.32087	Nonsignifi	None		3	Molecular	--	--
0.201399	0.074443	-2.31187	Nonsignifi	None		2	Molecular	serine prot	3.4.21.-
Inf	0	Inf	Significant	up		1	Molecular	splicing fac	--
Inf	0	Inf	Significant	up		5	Cellular Co	ubiquitin c	2.3.2.27
Inf	0	Inf	Significant	up		2	Biological	elongator	--
1.515782	0.05016	0.600062	Nonsignifi	None	--		--	reticulon-3	--
Inf	0	Inf	Significant	up		1	Molecular	sorting nex	--
Inf	0	Inf	Significant	up	--		--	golgi SNAI	--
Inf	0	Inf	Significant	up	--		--	vesicle-ass	--
Inf	0	Inf	Significant	up	--		--	myelin pro	--
Inf	0	Inf	Significant	up		1	Biological	6-phospho	3.1.1.31
Inf	0	Inf	Significant	up		1	Molecular	--	--
Inf	0	Inf	Significant	up		4	Molecular	structural r	--
Inf	0	Inf	Significant	up		1	Molecular	lysophospl	3.1.1.5
Inf	0	Inf	Significant	up	--		--	ariadne-2	2.3.2.27
Inf	0	Inf	Significant	up		2	Biological	phosphoac	5.4.2.3
Inf	0	Inf	Significant	up		1	Molecular	CD2 antige	--
Inf	0	Inf	Significant	up		3	Molecular	--	--
0.3569	0.047789	-1.48641	Nonsignifi	None	--		--	--	--
Inf	0	Inf	Significant	up		5	Molecular	latrophilin	--
0.114667	0.059188	-3.12448	Nonsignifi	None		1	Biological	pantethein	3.5.1.92
0.077843	0.072425	-3.6833	Nonsignifi	None		1	Biological	pantethein	3.5.1.92
Inf	0	Inf	Significant	up		3	Molecular	cleavage a	--
0.71473	0.195165	-0.48453	Nonsignifi	None		4	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up	--		--	BCL2-asso	--
0.325158	0.000226	-1.62079	Nonsignifi	None		3	Molecular	mitogen-a	2.7.11.1
Inf	0	Inf	Significant	up		1	Molecular	echinoderr	--
Inf	0	Inf	Significant	up		1	Cellular Co	tetraspanir	--
0.349606	0.121021	-1.5162	Nonsignifi	None	--		--	dimethylar	3.5.3.18
Inf	0	Inf	Significant	up		4	Molecular	wingless-t	--
Inf	0	Inf	Significant	up	--		--	actin-like p	--
Inf	0	Inf	Significant	up		1	Biological	alcohol de	1.1.1.1
0.968224	0.871446	-0.04659	Nonsignifi	None		2	Molecular	L-lactate c	1.1.1.27
1.181853	0.612621	0.241051	Nonsignifi	None		3	Biological	retinal deh	1.2.1.36
Inf	0	Inf	Significant	up		4	Molecular	dihydrofol	1.5.1.3
0.54907	0.153223	-0.86494	Nonsignifi	None		2	Molecular	cytochrom	1.6.2.2

0.523495	0.04643	-0.93375	Nonsignifi	None	3	Molecular	glutathion	1.8.1.7
0.353534	0.017291	-1.50008	Nonsignifi	None	3	Biological	superoxide	1.15.1.1
2.436794	0.003903	1.284985	Nonsignifi	None	3	Molecular	ceruloplas	1.16.3.1
0.446619	0.026793	-1.16288	Nonsignifi	None	2	Molecular	coagulatio	2.3.2.13
0.115199	0.014522	-3.1178	Significant	down	2	Molecular	purine-nu	2.4.2.1
Inf	0	Inf	Significant	up	1	Biological	hypoxanth	2.4.2.8
0.154945	0.03567	-2.69017	Significant	down	6	Molecular	epidermal	2.7.10.1
2.695105	0.003291	1.430342	Nonsignifi	None	2	Molecular	phosphogl	2.7.2.3
Inf	0	Inf	Significant	up	--	--	adenylate	2.7.4.3
2.796804	0.011976	1.483779	Nonsignifi	None	5	Molecular	coagulatio	3.4.21.5
0.382228	0.008299	-1.38749	Nonsignifi	None	2	Molecular	compleme	3.4.21.41
9.636439	0.008247	3.2685	Significant	up	2	Molecular	haptoglob	--
9.898316	0.00011	3.307183	Significant	up	5	Molecular	coagulatio	3.4.21.22
11.38777	0.00018	3.509413	Significant	up	5	Molecular	coagulatio	3.4.21.6
0.132153	0.046834	-2.91971	Significant	down	2	Molecular	plasminog	3.4.21.7
Inf	0	Inf	Significant	up	2	Molecular	urokinase	3.4.21.73
0.15763	0.043487	-2.66539	Significant	down	--	--	antithromb	--
1.345518	0.029105	0.428162	Nonsignifi	None	3	Molecular	alpha-2-m	--
0.77611	0.328458	-0.36567	Nonsignifi	None	3	Molecular	compleme	--
1.430638	0.320266	0.516659	Nonsignifi	None	3	Molecular	compleme	--
0.017665	0.062389	-5.82298	Nonsignifi	None	1	Molecular	metallopep	--
0.061371	0.00988	-4.02631	Significant	down	1	Molecular	cystatin-C	--
0.153264	0.058999	-2.70591	Nonsignifi	None	1	Molecular	kininogen	--
Inf	0	Inf	Significant	up	--	--	thyroglobu	--
0.29208	0.020072	-1.77557	Nonsignifi	None	2	Molecular	insulin-like	--
7.405236	0.091333	2.888546	Nonsignifi	None	--	--	--	--
0.823411	0.513878	-0.28031	Nonsignifi	None	--	--	--	--
1.313391	0.013773	0.393297	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant	up	--	--	polymeric	--
Inf	0	Inf	Significant	up	--	--	--	--
1.194984	0.33132	0.256991	Nonsignifi	None	2	Biological	major histo	--
1.182172	0.465896	0.24144	Nonsignifi	None	2	Biological	major histo	--
0.434724	0.00045	-1.20183	Nonsignifi	None	2	Molecular	hemoglob	--
0.312571	0.025556	-1.67775	Nonsignifi	None	2	Molecular	hemoglob	--
0.014588	0.0101	-6.09907	Significant	down	2	Molecular	collagen, t	--
0.017717	0.042231	-5.81872	Significant	down	2	Molecular	collagen, t	--
0.031352	0.023205	-4.9953	Significant	down	2	Molecular	collagen, t	--
#NAME?	0	#NAME?	Significant	down	2	Molecular	collagen, t	--
Inf	0	Inf	Significant	up	1	Molecular	crystallin, a	--
0.277277	0.048104	-1.8506	Nonsignifi	None	2	Molecular	type I kera	--
0.170553	0.021866	-2.55171	Significant	down	2	Molecular	type II kera	--
0.608032	0.306711	-0.71778	Nonsignifi	None	4	Cellular Co	apolipopro	--
0.406375	0.048238	-1.29912	Nonsignifi	None	4	Cellular Co	apolipopro	--
3.263195	0.003289	1.706285	Nonsignifi	None	4	Cellular Co	apolipopro	--
0.707185	0.511509	-0.49984	Nonsignifi	None	5	Molecular	fibrinogen	--
0.030162	0.037128	-5.05115	Significant	down	5	Molecular	fibrinogen	--
Inf	0	Inf	Significant	up	1	Molecular	compleme	--
0.214202	0.143267	-2.22296	Nonsignifi	None	--	--	beta-2-gly	--
0.016638	0.010204	-5.90939	Significant	down	2	Molecular	fibronectin	--
0.075372	0.028987	-3.72983	Significant	down	--	--	retinol-bin	--
0.058982	0.051317	-4.08359	Nonsignifi	None	1	Molecular	--	--
0.030043	0.011087	-5.05681	Significant	down	1	Cellular Co	serum albu	--
0.074977	0.082492	-3.73741	Nonsignifi	None	1	Cellular Co	alpha-feto	--
0.150832	0.045676	-2.72898	Significant	down	1	Cellular Co	vitamin D-	--
0.01181	0.478559	-6.40382	Nonsignifi	None	--	--	transferrin	--
0.099016	0.050501	-3.3362	Nonsignifi	None	--	--	lactotransf	3.4.21.-
0.324356	0.108239	-1.62435	Nonsignifi	None	--	--	hemopexir	--
0.139943	0.189021	-2.83708	Nonsignifi	None	2	Biological	ferritin ligh	--

0.270812	0.16155	-1.88464	Nonsignifi	None		2	Biological	ferritin hea	1.16.3.2
0.1082	0.141577	-3.20823	Nonsignifi	None		2	Molecular	plasma kal	3.4.21.34
#NAME?	0	#NAME?	Significant	down		4	Molecular	matrix met	3.4.24.7
1.495362	0.059861	0.580495	Nonsignifi	None	--	--		compleme	--
0.835165	0.719898	-0.25987	Nonsignifi	None		3	Molecular	vitronectin	--
0.243956	0.193748	-2.03531	Nonsignifi	None		3	Molecular	catalase	1.11.1.6
Inf	0	Inf	Significant	up	--	--		glucosylce	3.2.1.45
Inf	0	Inf	Significant	up		2	Molecular	alpha-L-fu	3.2.1.51
0.769259	0.178368	-0.37846	Nonsignifi	None		2	Molecular	fructose-b	4.1.2.13
Inf	0	Inf	Significant	up		1	Molecular	cystatin-A/	--
2.233565	0.000516	1.159348	Nonsignifi	None		2	Molecular	annexin A1	--
0.158053	0.00055	-2.66152	Significant	down		2	Molecular	apolipopro	--
Inf	0	Inf	Significant	up		2	Biological	lecithin-ch	2.3.1.43
Inf	0	Inf	Significant	up		2	Molecular	ornithine-·	2.6.1.13
0.153118	0.020154	-2.70729	Significant	down	--	--		Thy-1 cell	--
0.153302	0.247233	-2.70555	Nonsignifi	None		2	Molecular	type II kera	--
0.110053	0.059385	-3.18372	Nonsignifi	None		2	Molecular	type II kera	--
0.110755	0.011362	-3.17456	Significant	down		1	Molecular	von Willeb	--
0.176803	0.043512	-2.49979	Significant	down	--	--		--	--
Inf	0	Inf	Significant	up		1	Molecular	tubulin bet	--
1.367918	0.127968	0.451981	Nonsignifi	None		1	Biological	glyceraldel	1.2.1.12
Inf	0	Inf	Significant	up	--	--		argininosu	4.3.2.1
0.227535	0.05658	-2.13584	Nonsignifi	None		3	Molecular	alpha-amy	3.2.1.1
0.782099	0.331875	-0.35458	Nonsignifi	None	--	--		heat shock	--
1.407414	0.091864	0.493047	Nonsignifi	None		5	Molecular	guanine nu	--
Inf	0	Inf	Significant	up		3	Biological	solute carr	--
2.963829	0.017488	1.567462	Nonsignifi	None		2	Molecular	sodium/po	3.6.3.9
Inf	0	Inf	Significant	up		3	Cellular Co	sodium/po	--
Inf	0	Inf	Significant	up		2	Molecular	fructose-b	4.1.2.13
0.255789	0.01534	-1.96697	Nonsignifi	None	--	--		apolipopro	--
0.432052	0.141145	-1.21072	Nonsignifi	None	--	--		integrin be	--
Inf	0	Inf	Significant	up	--	--		integrin be	--
0.001838	0.019686	-9.08742	Significant	down	--	--		plasminog	--
0.215465	0.069398	-2.21447	Nonsignifi	None	--	--		C1 inhibitc	--
0.225364	0.089659	-2.14967	Nonsignifi	None		5	Molecular	compleme	3.4.21.45
1.158447	0.460847	0.212192	Nonsignifi	None	--	--		coagulatio	--
Inf	0	Inf	Significant	up		1	Molecular	ubiquitin c	--
Inf	0	Inf	Significant	up		2	Biological	alkaline ph	3.1.3.1
#NAME?	0	#NAME?	Significant	down		3	Molecular	interleukin	--
0.683957	0.645624	-0.54802	Nonsignifi	None	--	--		large subu	--
2.308721	0.029214	1.207094	Nonsignifi	None	--	--		large subu	--
3.38688	0.000714	1.759957	Nonsignifi	None		2	Cellular Co	large subu	--
0.129052	0.000419	-2.95397	Significant	down	--	--		C-type lec	--
Inf	0	Inf	Significant	up		2	Molecular	lupus La p	--
0.195121	0.039251	-2.35756	Significant	down	--	--		thyroxine-	--
0.26151	0.12384	-1.93506	Nonsignifi	None	--	--		heparin co	--
2.666457	0.000244	1.414924	Nonsignifi	None	--	--		integrin be	--
Inf	0	Inf	Significant	up		6	Molecular	classical pr	2.7.11.13
0.536291	0.013075	-0.89891	Nonsignifi	None		1	Molecular	myosin ligl	--
0.258307	0.088843	-1.95284	Nonsignifi	None		2	Molecular	collagen, t	--
Inf	0	Inf	Significant	up		2	Molecular	uroporphy	4.1.1.37
Inf	0	Inf	Significant	up		3	Molecular	tyrosine-p	2.7.10.2
2.377026	0.012464	1.249158	Nonsignifi	None	--	--		cholinester	3.1.1.8
Inf	0	Inf	Significant	up		1	Biological	alpha-gala	3.2.1.22
0.423456	0.096907	-1.23972	Nonsignifi	None	--	--		gelsolin	--
Inf	0	Inf	Significant	up		3	Molecular	--	--
2.366144	0.050411	1.242538	Nonsignifi	None		4	Cellular Co	apolipopro	--
Inf	0	Inf	Significant	up		4	Molecular	translation	--

Inf	0	Inf	Significant up		1	Molecular	creatine ki	2.7.3.2
1.790985	4.57E-05	0.840753	Nonsignifi	None	--	--	enolase	4.2.1.11
0.66999	0.496727	-0.57779	Nonsignifi	None	2	Biological	glycogen p	2.4.1.1
0.916523	0.511961	-0.12576	Nonsignifi	None	3	Molecular	glucose-6-	5.3.1.9
4.27584	0.083129	2.096208	Nonsignifi	None	1	Molecular	nucleopho	--
1.005097	0.877292	0.007335	Nonsignifi	None	--	--	tropomyos	--
0.530609	0.004349	-0.91428	Nonsignifi	None	--	--	integrin alp	--
Inf	0	Inf	Significant up		1	Molecular	lipoproteir	3.1.1.34
1.047466	0.479098	0.066904	Nonsignifi	None	1	Biological	hexosamin	3.2.1.52
Inf	0	Inf	Significant up	--	--	--	--	--
16.44673	0.00119	4.039729	Significant up		1	Molecular	histone H2	--
0.058968	7.17E-06	-4.08392	Significant down	--	--	--	glia-derive	--
Inf	0	Inf	Significant up		1	Molecular	diazepam-	--
0.053942	0.234814	-4.21245	Nonsignifi	None	--	--	fatty acid-	--
2.164092	0.00578	1.113762	Nonsignifi	None	2	Molecular	L-lactate d	1.1.1.27
Inf	0	Inf	Significant up		3	Molecular	glutathion	1.11.1.9
1.161148	0.498063	0.215552	Nonsignifi	None	3	Molecular	protein S	--
1.706065	0.087198	0.770672	Nonsignifi	None	1	Biological	protein dis	5.3.4.1
1.308885	0.167332	0.388339	Nonsignifi	None	2	Molecular	cathepsin I	3.4.23.5
1.785702	0.038833	0.836491	Nonsignifi	None	2	Molecular	annexin A2	--
1.076413	0.843577	0.106231	Nonsignifi	None	1	Molecular	tubulin bet	--
Inf	0	Inf	Significant up	--	--	--	carbonic a	4.2.1.1
#NAME?	0	#NAME?	Significant down		1	Molecular	decorin	--
0.229221	0.037473	-2.12519	Significant down		1	Biological	saposin	--
0.658088	0.016561	-0.60365	Nonsignifi	None	1	Biological	hexosamin	3.2.1.52
1.327527	0.320383	0.408742	Nonsignifi	None	--	--	profilin	--
0.400403	0.108742	-1.32048	Nonsignifi	None	--	--	--	--
1.758007	0.183216	0.813941	Nonsignifi	None	8	Molecular	--	--
0.095018	0.028032	-3.39566	Significant down		4	Molecular	cathepsin I	3.4.22.1
7.514327	0.008565	2.909644	Significant up		4	Molecular	molecular	--
16.82711	0.025859	4.072716	Significant up		1	Molecular	heterogen	--
0.089406	0.033647	-3.48348	Significant down	--	--	--	laminin, be	--
4.833245	0.012931	2.272992	Significant up		3	Molecular	tyrosine-p	2.7.10.2
0.012351	0.004072	-6.33926	Significant down		4	Molecular	thrombosp	--
Inf	0	Inf	Significant up		6	Molecular	insulin-like	2.7.10.1
0.005813	0.010184	-7.42653	Significant down		1	Molecular	collagen, t	--
2.872853	0.004114	1.522484	Nonsignifi	None	2	Molecular	annexin A6	--
Inf	0	Inf	Significant up	--	--	--	decay acce	--
Inf	0	Inf	Significant up		5	Molecular	ATP-bindi	3.6.3.44
1.603478	0.033804	0.681205	Nonsignifi	None	2	Molecular	solute carr	--
Inf	0	Inf	Significant up		2	Molecular	6-phosph	2.7.1.11
5.692582	0.010684	2.509083	Significant up		4	Molecular	molecular	--
Inf	0	Inf	Significant up		2	Molecular	asparagine	6.3.5.4
0.008126	0.025388	-6.94328	Significant down		4	Molecular	matrix met	3.4.24.24
0.166042	0.233718	-2.59038	Nonsignifi	None	3	Biological	superoxide	1.15.1.1
Inf	0	Inf	Significant up		2	Molecular	neprilysin	3.4.24.11
#NAME?	0	#NAME?	Significant down		2	Molecular	inhibin, be	--
1.523402	0.153277	0.607296	Nonsignifi	None	1	Biological	pleckstrin	--
#NAME?	0	#NAME?	Significant down		2	Molecular	collagen, t	--
Inf	0	Inf	Significant up	--	--	--	melanoma	--
0.319734	0.201193	-1.64505	Nonsignifi	None	--	--	integrin alp	--
0.460759	1.72E-05	-1.11792	Nonsignifi	None	2	Molecular	vimentin	--
0.199919	0.143084	-2.32251	Nonsignifi	None	--	--	alpha-2-a	--
Inf	0	Inf	Significant up		4	Molecular	small subu	--
0.399712	0.362608	-1.32297	Nonsignifi	None	2	Molecular	type I kera	--
1.040534	0.800455	0.057324	Nonsignifi	None	2	Molecular	annexin A5	--
0.284103	0.371368	-1.81551	Nonsignifi	None	2	Molecular	type I kera	--
Inf	0	Inf	Significant up		3	Biological	--	--

0.76222	0.454812	-0.39172	Nonsignifi	None		4	Molecular	small subu	--
0.646521	0.264516	-0.62923	Nonsignifi	None		1	Cellular Co	CD63 antig	--
Inf	0	Inf	Significant	up		1	Biological	acetyl-CoA	2.3.1.16
0.645121	0.258772	-0.63236	Nonsignifi	None		1	Molecular	glutathion	2.5.1.18
Inf	0	Inf	Significant	up		1	Molecular	U1 small n	--
#NAME?	0	#NAME?	Significant	down		3	Cellular Co	C-X-C mo	--
0.42389	0.119193	-1.23824	Nonsignifi	None		1	Molecular	galectin-1	--
3.182151	0.259317	1.670002	Nonsignifi	None	--		--	high mobil	--
Inf	0	Inf	Significant	up	--		--	--	--
0.01929	0.053174	-5.69598	Nonsignifi	None		4	Molecular	--	--
0.994578	0.893069	-0.00784	Nonsignifi	None	--		--	tropomyos	--
Inf	0	Inf	Significant	up		5	Molecular	clathrin lig	--
Inf	0	Inf	Significant	up		2	Molecular	annexin A4	--
#NAME?	0	#NAME?	Significant	down		2	Molecular	platelet-de	2.7.10.1
0.832569	0.038437	-0.26436	Nonsignifi	None		1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	--		--	U2 small n	--
Inf	0	Inf	Significant	up		4	Molecular	poly [ADP-	2.4.2.30
Inf	0	Inf	Significant	up		2	Molecular	leukotriene	3.3.2.6
0.182456	0.028309	-2.45438	Significant	down		2	Molecular	fructose-b	4.1.2.13
0.476932	0.012685	-1.06815	Nonsignifi	None		3	Molecular	compleme	--
22.01004	0.005868	4.46009	Significant	up		1	Molecular	histone H2	--
4.455819	3.34E-05	2.155691	Significant	up		1	Molecular	protein ph	--
1.057701	0.773996	0.080932	Nonsignifi	None	--		--	heat shock	--
Inf	0	Inf	Significant	up		2	Molecular	Ras-relate	--
#NAME?	0	#NAME?	Significant	down	--		--	proteoglyc	--
#NAME?	0	#NAME?	Significant	down		3	Cellular Co	interleukin	--
Inf	0	Inf	Significant	up		1	Molecular	60 kDa SS-	--
0.414338	0.355077	-1.27112	Nonsignifi	None		2	Molecular	Ras-relate	--
0.54406	0.021311	-0.87816	Nonsignifi	None		1	Biological	thioredoxi	--
Inf	0	Inf	Significant	up		2	Molecular	cathepsin A	3.4.16.5
1.780798	0.054321	0.832524	Nonsignifi	None		1	Molecular	compleme	--
Inf	0	Inf	Significant	up	--		--	S-formylgl	3.1.2.12
Inf	0	Inf	Significant	up		1	Molecular	chaperonir	--
0.243887	0.152078	-2.03572	Nonsignifi	None		2	Molecular	hyaluronar	--
0.693588	0.296611	-0.52785	Nonsignifi	None	--		--	heat shock	--
0.111112	0.032649	-3.16991	Significant	down	--		--	laminin, ga	--
Inf	0	Inf	Significant	up		1	Molecular	lysosomal	3.1.3.2
1.429615	0.025557	0.515626	Nonsignifi	None	--		--	heat shock	--
0.404727	0.167406	-1.30498	Nonsignifi	None		3	Cellular Co	MFS transp	--
0.341944	0.137432	-1.54817	Nonsignifi	None		3	Cellular Co	MFS transp	--
Inf	0	Inf	Significant	up		5	Molecular	erythrocyte	--
Inf	0	Inf	Significant	up		3	Molecular	--	--
0.676127	0.545999	-0.56463	Nonsignifi	None		2	Biological	glycogen p	2.4.1.1
Inf	0	Inf	Significant	up		2	Biological	glycogen p	2.4.1.1
Inf	0	Inf	Significant	up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		1	Cellular Co	lysosomal-	--
0.971366	0.904336	-0.04191	Nonsignifi	None		2	Molecular	fibroblast g	2.7.10.1
Inf	0	Inf	Significant	up		4	Molecular	DNA topoi	5.99.1.2
Inf	0	Inf	Significant	up		5	Molecular	DNA topoi	5.99.1.3
0.182991	0.39467	-2.45015	Nonsignifi	None		4	Molecular	--	--
0.177271	0.000153	-2.49597	Significant	down		4	Molecular	insulin-like	--
1.80228	0.010443	0.849824	Nonsignifi	None		1	Biological	--	--
Inf	0	Inf	Significant	up		3	Molecular	cyclin-dep	2.7.11.22
Inf	0	Inf	Significant	up		3	Molecular	ribose-pho	2.7.6.1
2.264375	0.008366	1.179113	Nonsignifi	None		2	Molecular	polyadeny	--
Inf	0	Inf	Significant	up		2	Molecular	proliferatir	--
Inf	0	Inf	Significant	up		3	Molecular	histidyl-tRI	6.1.1.21
0.070542	0.051099	-3.82537	Nonsignifi	None		1	Molecular	collagen, ty	--

0.061038	0.038505	-4.03415	Significant down	--	--	collagen, t	--
0.007611	0.025576	-7.03775	Significant down	--	--	collagen, t	--
0.006476	0.031288	-7.27075	Significant down	1	Molecular	collagen, t	--
1.018151	0.883852	0.025951	Nonsignifi	None	1	Molecular	coagulatio	--
1.191844	0.531962	0.253196	Nonsignifi	None	2	Molecular	IMP dehyd	1.1.1.205
Inf	0	Inf	Significant up		1	Biological	nucleopro	--
Inf	0	Inf	Significant up		1	Molecular	creatine ki	2.7.3.2
0.374816	0.313604	-1.41574	Nonsignifi	None	2	Molecular	annexin A	--
Inf	0	Inf	Significant up		1	Molecular	creatine ki	2.7.3.2
0.551652	0.178438	-0.85817	Nonsignifi	None	1	Molecular	actinin alp	--
0.705471	0.148846	-0.50334	Nonsignifi	None	2	Molecular	Xaa-Pro di	3.4.13.9
Inf	0	Inf	Significant up		3	Molecular	ATP-depe	--
Inf	0	Inf	Significant up		3	Molecular	ATP-depe	--
0.147641	0.068339	-2.75983	Nonsignifi	None	1	Cellular Co	lysosomal-	--
0.072309	0.507346	-3.78968	Nonsignifi	None	1	Molecular	ribonuclea	--
1.132435	0.58555	0.179428	Nonsignifi	None	3	Molecular	bone morp	3.4.24.19
0.189287	0.046945	-2.40135	Significant down		1	Molecular	neural cell	--
43.67359	0.00372	5.448689	Significant up	--	--		integrin alp	--
1.782401	0.005615	0.833822	Nonsignifi	None	1	Molecular	elongation	--
0.182301	0.060273	-2.45561	Nonsignifi	None	2	Molecular	type I kera	--
0.184263	0.204292	-2.44016	Nonsignifi	None	2	Molecular	type II kera	--
Inf	0	Inf	Significant up		1	Biological	protein dis	5.3.4.1
Inf	0	Inf	Significant up		1	Molecular	compleme	--
Inf	0	Inf	Significant up		4	Molecular	prolyl 4-hy	1.14.11.2
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	porphobili	4.2.1.24
0.198649	0.172459	-2.3317	Nonsignifi	None	2	Molecular	plastin-2	--
0.587126	0.226668	-0.76826	Nonsignifi	None	2	Molecular	plastin-3	--
0.331166	0.06699	-1.59438	Nonsignifi	None	2	Biological	acylamino	3.4.19.1
Inf	0	Inf	Significant up		2	Molecular	glycogen s	2.4.1.11
Inf	0	Inf	Significant up	--	--		cAMP-dep	--
0.835516	0.555162	-0.25926	Nonsignifi	None	--	--	enolase	4.2.1.11
Inf	0	Inf	Significant up		3	Cellular Co	transcriptio	3.6.4.12
0.926251	0.809765	-0.11052	Nonsignifi	None	--	--	phenylpyru	5.3.2.1
Inf	0	Inf	Significant up		1	Biological	--	--
0.197175	0.085424	-2.34245	Nonsignifi	None	2	Molecular	nidogen (e	--
Inf	0	Inf	Significant up	--	--		alcohol de	1.1.1.2
1.653085	0.020547	0.725161	Nonsignifi	None	4	Molecular	pyruvate k	2.7.1.40
4.515802	0.100715	2.174982	Nonsignifi	None	4	Molecular	heat shock	--
Inf	0	Inf	Significant up	--	--		small nucle	--
Inf	0	Inf	Significant up		1	Molecular	heterogen	--
Inf	0	Inf	Significant up		3	Molecular	glutamine	6.3.1.2
2.521874	0.000983	1.334496	Nonsignifi	None	--	--	aldehyde r	1.1.1.21
Inf	0	Inf	Significant up	--	--		poliovirus	--
0.687198	0.052325	-0.5412	Nonsignifi	None	3	Molecular	carboxype	3.4.17.3
Inf	0	Inf	Significant up		5	Molecular	nucleoside	2.7.4.6
Inf	0	Inf	Significant up		2	Biological	N-acetylgl	3.1.6.14
0.607696	0.029402	-0.71858	Nonsignifi	None	4	Molecular	small subu	--
Inf	0	Inf	Significant up	--	--		replication	--
0.078357	0.040125	-3.6738	Significant down		1	Molecular	Function:metalloendo	
0.07947	0.037561	-3.65345	Significant down		2	Molecular	CD44 antig	--
0.055502	0.008063	-4.17131	Significant down		2	Molecular	aggrecan	--
Inf	0	Inf	Significant up	--	--		beta-galac	3.2.1.23
Inf	0	Inf	Significant up		1	Molecular	NCK adapt	--
4.977891	0.00038	2.315535	Significant up		4	Cellular Co	histone H1	--
5.677712	0.000295	2.50531	Significant up		4	Cellular Co	histone H1	--
5.774701	0.027824	2.529746	Significant up		4	Cellular Co	histone H1	--
Inf	0	Inf	Significant up		3	Molecular	carboxype	3.4.17.10

Inf	0	Inf	Significant up		5	Molecular	phosphatic	3.1.4.11
0.332027	0.014554	-1.59063	Nonsignifi	None	4	Molecular	fumarylace	3.7.1.2
Inf	0	Inf	Significant up		1	Biological	stathmin	--
Inf	0	Inf	Significant up		1	Molecular	cold shock	--
1.242066	0.485252	0.312741	Nonsignifi	None	--	--	heat shock	--
Inf	0	Inf	Significant up	--	--	--	high mobil	--
0.668041	0.394854	-0.58199	Nonsignifi	None	--	--	integrin al	--
Inf	0	Inf	Significant up	--	--	--	gap junctic	--
Inf	0	Inf	Significant up	--	--	--	upstream-	--
Inf	0	Inf	Significant up	--	--	--	--	--
3.122919	0.000564	1.642895	Nonsignifi	None	4	Molecular	calpain-2	3.4.22.53
Inf	0	Inf	Significant up		2	Molecular	CTP synth	6.3.4.2
2.438955	0.00571	1.286263	Nonsignifi	None	2	Molecular	ATP-depe	3.6.4.13
0.913051	0.533323	-0.13123	Nonsignifi	None	2	Molecular	6-phosph	2.7.1.11
0.011266	0.018579	-6.47183	Significant down		3	Biological	insulin-like	--
Inf	0	Inf	Significant up		1	Molecular	26S protea	--
1.709661	0.001599	0.773711	Nonsignifi	None	1	Molecular	T-complex	--
0.089953	0.046553	-3.47469	Significant down		3	Biological	--	--
Inf	0	Inf	Significant up		4	Molecular	large subu	--
1.317957	0.446981	0.398303	Nonsignifi	None	1	Molecular	ADP-ribos	--
0.460759	0.63225	-1.11792	Nonsignifi	None	--	--	large subu	--
0.303714	0.129564	-1.71921	Nonsignifi	None	2	Biological	vinculin	--
Inf	0	Inf	Significant up		2	Molecular	receptor-t	3.1.3.48
0.606108	0.422367	-0.72235	Nonsignifi	None	3	Molecular	large subu	--
Inf	0	Inf	Significant up	--	--	--	2,3-bisphc	5.4.2.11
Inf	0	Inf	Significant up	--	--	--	regulator c	--
Inf	0	Inf	Significant up		3	Molecular	cadherin 2	--
8.366574	0.030371	3.064637	Significant up		1	Molecular	nucleolin	--
Inf	0	Inf	Significant up		2	Molecular	hexokinase	2.7.1.1
Inf	0	Inf	Significant up		3	Molecular	DNA-direc	--
Inf	0	Inf	Significant up		3	Molecular	eukaryotic	2.7.11.1
Inf	0	Inf	Significant up	--	--	--	spermidine	2.5.1.16
Inf	0	Inf	Significant up		3	Molecular	casein kina	2.7.11.1
0.164483	0.026214	-2.60399	Significant down		2	Molecular	inter-alpha	--
0.28655	0.043211	-1.80314	Nonsignifi	None	2	Molecular	inter-alpha	--
#NAME?	0	#NAME?	Significant down		3	Cellular Co	C-X-C mo	--
#NAME?	0	#NAME?	Significant down		3	Cellular Co	C-X-C mo	--
0.050027	0.41795	-4.32114	Nonsignifi	None	2	Molecular	translation	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
1.703245	0.008208	0.768286	Nonsignifi	None	3	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant up		2	Molecular	lamin B	--
1.193203	0.349093	0.25484	Nonsignifi	None	3	Molecular	--	--
0.299193	0.085815	-1.74085	Nonsignifi	None	1	Molecular	osteoglycir	--
Inf	0	Inf	Significant up	--	--	--	interleukin	--
Inf	0	Inf	Significant up		2	Molecular	IMP dehyd	1.1.1.205
0.133212	0.036659	-2.9082	Significant down	--	--	--	collagen, t	--
0.11407	0.002852	-3.132	Significant down		1	Molecular	collagen, t	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	glutathion	2.5.1.18
Inf	0	Inf	Significant up		3	Molecular	V-type H+	--
Inf	0	Inf	Significant up		2	Molecular	V-type H+	--
Inf	0	Inf	Significant up		1	Molecular	cysteine ar	--
0.879843	0.183797	-0.18468	Nonsignifi	None	1	Molecular	filamin	--
1.753899	0.08292	0.810565	Nonsignifi	None	1	Biological	aconitate h	4.2.1.3
0.656196	0.613477	-0.6078	Nonsignifi	None	2	Biological	5'-nucleot	3.1.3.5
0.321414	0.048731	-1.63749	Nonsignifi	None	1	Molecular	biglycan	--
1.826143	0.214957	0.8688	Nonsignifi	None	1	Cellular Co	CD9 antige	--
Inf	0	Inf	Significant up		1	Molecular	catechol O	2.1.1.6

Inf	0	Inf	Significant up	--	--	oxysterol-l	--
Inf	0	Inf	Significant up	3	Molecular	--	--
0.044431	0.007357	-4.4923	Significant down	1	Molecular	tenascin	--
Inf	0	Inf	Significant up	1	Biological	--	--
2.044336	0.126307	1.031632	Nonsignifi	None	1	Molecular	ubiquitin-a	6.2.1.45
2.227539	0.042355	1.155451	Nonsignifi	None	3	Molecular	glutathion	1.11.1.9
2.698285	0.003909	1.432043	Nonsignifi	None	5	Molecular	nucleoside	2.7.4.6
Inf	0	Inf	Significant up	7	Molecular	--	--
0.432464	0.005121	-1.20935	Nonsignifi	None	1	Molecular	heterogen	--
0.039157	0.089622	-4.67457	Nonsignifi	None	3	Biological	--	--
Inf	0	Inf	Significant up	3	Molecular	protein kin	2.7.11.11
0.087587	0.024591	-3.51313	Significant down	1	Molecular	fibulin 1/2	--
0.808025	0.651575	-0.30753	Nonsignifi	None	--	--	integrin alp	--
0.528926	0.017037	-0.91886	Nonsignifi	None	1	Molecular	splicing fac	--
Inf	0	Inf	Significant up	1	Molecular	tubulin gar	--
0.845893	0.496496	-0.24145	Nonsignifi	None	3	Biological	peptidyl-p	5.2.1.8
1.323412	0.281919	0.404263	Nonsignifi	None	1	Molecular	small subu	--
Inf	0	Inf	Significant up	2	Molecular	Janus kinas	2.7.10.2
Inf	0	Inf	Significant up	3	Molecular	receptor-t	3.1.3.48
2.828295	0.000847	1.499933	Nonsignifi	None	3	Molecular	adenosylh	3.3.1.1
1.521421	0.023494	0.605419	Nonsignifi	None	2	Molecular	cofilin	--
Inf	0	Inf	Significant up	1	Molecular	translation	--
Inf	0	Inf	Significant up	--	--	dTMP kina	2.7.4.9
2.231012	0.011937	1.157699	Nonsignifi	None	3	Molecular	ribonucleo	1.17.4.1
#NAME?	0	#NAME?	Significant down	5	Molecular	laminin, alp	--
Inf	0	Inf	Significant up	2	Molecular	elongation	--
Inf	0	Inf	Significant up	--	--	--	--
0.331702	0.020569	-1.59204	Nonsignifi	None	1	Molecular	tenascin	--
Inf	0	Inf	Significant up	1	Molecular	myosin reg	--
Inf	0	Inf	Significant up	3	Molecular	DNA-direc	2.7.7.6
Inf	0	Inf	Significant up	3	Molecular	cyclin-dep	2.7.11.22
Inf	0	Inf	Significant up	3	Molecular	beta-adren	2.7.11.15
Inf	0	Inf	Significant up	3	Molecular	DNA replic	3.6.4.12
Inf	0	Inf	Significant up	--	--	--	--
#NAME?	0	#NAME?	Significant down	5	Molecular	laminin, alp	--
1.179993	0.290104	0.238778	Nonsignifi	None	--	--	small subu	--
Inf	0	Inf	Significant up	--	--	DnaJ homo	--
Inf	0	Inf	Significant up	4	Molecular	F-type H+	--
1.861508	0.02662	0.896472	Nonsignifi	None	5	Molecular	20S protea	3.4.25.1
1.08279	0.807696	0.114754	Nonsignifi	None	5	Molecular	20S protea	3.4.25.1
2.702905	0.001725	1.434511	Nonsignifi	None	5	Molecular	20S protea	3.4.25.1
2.235872	0.002847	1.160838	Nonsignifi	None	5	Molecular	20S protea	3.4.25.1
#NAME?	0	#NAME?	Significant down	1	Molecular	collagen, t	--
1.583008	0.08947	0.662669	Nonsignifi	None	--	--	integrin alp	--
#NAME?	0	#NAME?	Significant down	--	--	--	--
0.828789	0.122878	-0.27092	Nonsignifi	None	3	Cellular Co	moesin	--
1.465214	0.213203	0.551111	Nonsignifi	None	1	Molecular	splicing fac	--
0.545656	0.049709	-0.87394	Nonsignifi	None	4	Molecular	large subu	--
1.461915	0.432841	0.547859	Nonsignifi	None	--	--	high mobil	--
Inf	0	Inf	Significant up	5	Molecular	threonyl-tl	6.1.1.3
0.044096	0.507149	-4.5032	Nonsignifi	None	4	Molecular	valyl-tRNA	6.1.1.9
3.651224	0.004596	1.86838	Nonsignifi	None	3	Molecular	elongation	--
Inf	0	Inf	Significant up	--	--	FK506-bin	5.2.1.8
0.147108	0.042978	-2.76505	Significant down	2	Molecular	--	--
1.25493	0.559301	0.327607	Nonsignifi	None	--	--	erythrocyte	--
Inf	0	Inf	Significant up	1	Molecular	--	--
0.747994	0.475728	-0.4189	Nonsignifi	None	--	--	14-3-3 pro	--
Inf	0	Inf	Significant up	3	Molecular	mitogen-a	2.7.11.24

Inf	0	Inf	Significant up		3	Molecular	MAP/micr	2.7.11.1
0.316503	0.07774	-1.65971	Nonsignifi	None	3	Molecular	large subu	--
Inf	0	Inf	Significant up		4	Molecular	replication	--
Inf	0	Inf	Significant up	--	--		AP endon	4.2.99.18
0.122559	0.005511	-3.02846	Significant down		1	Cellular Co	CD82 antig	--
0.679296	0.328496	-0.55789	Nonsignifi	None	5	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	microtubu	--
Inf	0	Inf	Significant up		1	Biological	phosphoin	--
Inf	0	Inf	Significant up		3	Molecular	20S protea	3.4.25.1
1.094941	0.559127	0.130853	Nonsignifi	None	3	Molecular	20S protea	3.4.25.1
1.957483	0.026474	0.969	Nonsignifi	None	5	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant up		3	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant up		3	Molecular	20S protea	3.4.25.1
1.776722	0.007245	0.829218	Nonsignifi	None	3	Molecular	20S protea	3.4.25.1
#NAME?	0	#NAME?	Significant down		2	Molecular	protein-lys	1.4.3.13
Inf	0	Inf	Significant up		3	Molecular	DNA polyr	2.7.7.7
Inf	0	Inf	Significant up		3	Molecular	mitogen-a	2.7.11.24
Inf	0	Inf	Significant up		3	Molecular	--	--
0.074032	0.094912	-3.75571	Nonsignifi	None	4	Biological	connective	--
0.742711	0.363749	-0.42913	Nonsignifi	None	3	Molecular	Eph recept	2.7.10.1
Inf	0	Inf	Significant up		3	Molecular	Eph recept	2.7.10.1
Inf	0	Inf	Significant up		3	Molecular	Eph recept	2.7.10.1
Inf	0	Inf	Significant up		2	Molecular	tyrosine-p	3.1.3.48
1.201727	0.726385	0.265109	Nonsignifi	None	--	--	transketola	2.2.1.1
#NAME?	0	#NAME?	Significant down		2	Molecular	non-recep	2.7.10.2
Inf	0	Inf	Significant up		2	Molecular	elongation	--
2.07316	0.0357	1.051831	Nonsignifi	None	1	Molecular	myristoylat	--
Inf	0	Inf	Significant up		2	Molecular	--	--
0.951367	0.816711	-0.07193	Nonsignifi	None	4	Molecular	--	--
3.148767	0.009393	1.654787	Nonsignifi	None	1	Molecular	peroxiredo	1.11.1.15
Inf	0	Inf	Significant up	--	--		D-dopach	4.1.1.84
2.08924	0.008125	1.062978	Nonsignifi	None	3	Molecular	large subu	--
1.460591	0.514962	0.546552	Nonsignifi	None	--	--	--	--
0.16049	0.062667	-2.63945	Nonsignifi	None	--	--	--	--
0.317176	0.000127	-1.65664	Nonsignifi	None	1	Biological	protein dis	5.3.4.1
Inf	0	Inf	Significant up		1	Molecular	glycylpepti	2.3.1.97
Inf	0	Inf	Significant up		3	Molecular	AXL recept	2.7.10.1
Inf	0	Inf	Significant up	--	--		adenylosu	4.3.2.2
Inf	0	Inf	Significant up		4	Molecular	pyruvate k	2.7.1.40
Inf	0	Inf	Significant up	--	--		CAP-Gly d	--
3.468543	0.006676	1.79433	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant up		3	Biological	solute carr	--
Inf	0	Inf	Significant up		2	Molecular	DNA-direc	2.7.7.6
2.122159	0.105284	1.085533	Nonsignifi	None	1	Molecular	coronin-1A	--
Inf	0	Inf	Significant up		2	Molecular	Rab GDP c	--
Inf	0	Inf	Significant up	--	--		cAMP-dep	--
Inf	0	Inf	Significant up		1	Molecular	carbamoyl	6.3.4.16
Inf	0	Inf	Significant up		1	Biological	ribonucleo	1.17.4.1
0.718309	0.177904	-0.47732	Nonsignifi	None	--	--	syndecan 4	--
Inf	0	Inf	Significant up		3	Molecular	solute carr	--
Inf	0	Inf	Significant up		2	Molecular	DnaJ homo	--
Inf	0	Inf	Significant up		4	Molecular	RAC serine	2.7.11.1
2.208508	0.013639	1.143072	Nonsignifi	None	3	Molecular	--	--
0.821152	0.432236	-0.28428	Nonsignifi	None	--	--	14-3-3 pro	--
1.000099	0.999369	0.000142	Nonsignifi	None	1	Molecular	stress-indu	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.096395	0.198765	-3.3749	Nonsignifi	None	4	Molecular	peroxiredo	1.11.1.15
0.181205	0.328851	-2.4643	Nonsignifi	None	--	--	4-hydroxy	1.13.11.27

Inf	0	Inf	Significant up		2	Molecular	syntaxin 1E	--
Inf	0	Inf	Significant up		1	Molecular	cystathioni	4.4.1.1
Inf	0	Inf	Significant up		4	Molecular	large subu	--
Inf	0	Inf	Significant up		3	Molecular	tumor nec	--
0.838647	0.846623	-0.25386	Nonsignifi	None	4	Molecular	kinesin fam	--
Inf	0	Inf	Significant up		5	Molecular	ATP-bindi	--
Inf	0	Inf	Significant up		3	Molecular	mannosyl-	3.2.1.113
Inf	0	Inf	Significant up		3	Molecular	DNA replic	3.6.4.12
Inf	0	Inf	Significant up		3	Molecular	DNA replic	3.6.4.12
0.054364	0.162648	-4.2012	Nonsignifi	None	--	--	ribonuclea	3.1.27.-
Inf	0	Inf	Significant up		1	Molecular	glycine hy	2.1.2.1
Inf	0	Inf	Significant up		1	Molecular	glycine hy	2.1.2.1
Inf	0	Inf	Significant up	--		--	--	--
1.8438	0.006239	0.882682	Nonsignifi	None	3	Cellular Co	glypican 1	--
Inf	0	Inf	Significant up	--		--	profilin	--
0.028143	0.419596	-5.15108	Nonsignifi	None	1	Molecular	catenin be	--
Inf	0	Inf	Significant up	--		--	serpin B	--
Inf	0	Inf	Significant up		3	Cellular Co	merlin	--
1.185756	0.204873	0.245807	Nonsignifi	None	3	Cellular Co	radixin	--
Inf	0	Inf	Significant up		5	Molecular	replication	--
Inf	0	Inf	Significant up		4	Molecular	large subu	--
Inf	0	Inf	Significant up		4	Molecular	transcriptio	--
0.010322	0.010438	-6.59812	Significant down		4	Molecular	thrombosp	--
0.072697	0.020709	-3.78195	Significant down		3	Molecular	thrombosp	--
0.140441	0.021415	-2.83197	Significant down		2	Molecular	type I kera	--
0.078435	0.058923	-3.67235	Nonsignifi	None	1	Molecular	fibrillin 1	--
1.382682	0.279816	0.46747	Nonsignifi	None	--	--	--	--
0.477715	0.053575	-1.06578	Nonsignifi	None	3	Molecular	myosin he	--
0.929486	0.721843	-0.10549	Nonsignifi	None	4	Molecular	myosin he	--
0.156105	0.078561	-2.67941	Nonsignifi	None	3	Molecular	tyrosine ki	2.7.10.1
0.412669	0.500062	-1.27694	Nonsignifi	None	5	Molecular	coatomer s	--
1.606053	0.166746	0.68352	Nonsignifi	None	--	--	basigin	--
Inf	0	Inf	Significant up		2	Molecular	RNA-bindi	--
Inf	0	Inf	Significant up	--		--	nuclear po	--
Inf	0	Inf	Significant up	--		--	protein DE	--
0.38878	0.011519	-1.36297	Nonsignifi	None	3	Molecular	glutaredox	--
Inf	0	Inf	Significant up		4	Molecular	protein ph	3.1.3.16
0.478305	0.004517	-1.064	Nonsignifi	None	1	Molecular	insulin-like	--
0.177316	0.00025	-2.4956	Significant down		2	Molecular	type II kera	--
0.901178	0.233196	-0.15012	Nonsignifi	None	1	Molecular	26S protea	--
0.009834	0.05729	-6.66798	Nonsignifi	None	1	Biological	chitinase-3	--
Inf	0	Inf	Significant up		1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant up		3	Molecular	mitogen-a	2.7.12.2
Inf	0	Inf	Significant up		1	Biological	V-type H+	--
0.256023	0.172769	-1.96565	Nonsignifi	None	3	Molecular	large subu	--
1.416134	0.301146	0.501958	Nonsignifi	None	2	Biological	phosphogl	5.4.2.2
Inf	0	Inf	Significant up		1	Molecular	--	--
0.094279	0.028189	-3.40691	Significant down	--		--	pigment ep	--
Inf	0	Inf	Significant up		3	Molecular	phospholip	1.11.1.12
Inf	0	Inf	Significant up		3	Biological	signal reco	--
Inf	0	Inf	Significant up	--		--	nuclear po	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.550201	0.030166	-0.86197	Nonsignifi	None	1	Molecular	transgelin	--
1.653753	0.093775	0.725744	Nonsignifi	None	1	Biological	transaldola	2.2.1.2
Inf	0	Inf	Significant up	--		--	lysosomal	3.1.1.13
Inf	0	Inf	Significant up		3	Molecular	V-type H+	3.6.3.14
Inf	0	Inf	Significant up	--		--	molecular	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13

Inf	0	Inf	Significant	up	3	Molecular	small subu	--
0.12469	0.04873	-3.00358	Significant	down	4	Molecular	large subu	--
0.037851	0.025901	-4.72353	Significant	down	3	Molecular	collagen, t	--
0.792725	0.287501	-0.33511	Nonsignifi	None	4	Molecular	collagen, t	--
4.896792	0.007505	2.291837	Significant	up	1	Molecular	T-complex	--
15.03244	0.028267	3.910007	Significant	up	1	Molecular	nicotinami	2.1.1.1
Inf	0	Inf	Significant	up	3	Molecular	20S protea	3.4.25.1
0.498946	0.208418	-1.00304	Nonsignifi	None	3	Molecular	large subu	--
Inf	0	Inf	Significant	up	1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant	up	2	Molecular	signal tran	--
1.142648	0.489331	0.192381	Nonsignifi	None	2	Molecular	malate deh	1.1.1.37
Inf	0	Inf	Significant	up	1	Molecular	translation	--
Inf	0	Inf	Significant	up	1	Molecular	N-alpha-a	2.3.1.255
Inf	0	Inf	Significant	up	3	Molecular	c-src tyros	2.7.10.2
0.492396	0.001412	-1.02211	Nonsignifi	None	4	Molecular	glycyl-tRN	6.1.1.14
1.277969	0.226801	0.353853	Nonsignifi	None	4	Molecular	isoleucyl-t	6.1.1.5
Inf	0	Inf	Significant	up	2	Biological	solute carr	--
Inf	0	Inf	Significant	up	--	--	centractin	--
Inf	0	Inf	Significant	up	2	Molecular	signal tran	--
Inf	0	Inf	Significant	up	1	Molecular	phosphatic	2.7.1.67
0.519349	0.072874	-0.94522	Nonsignifi	None	4	Molecular	large subu	--
Inf	0	Inf	Significant	up	2	Biological	lysosomal	3.4.16.2
0.567944	0.217017	-0.81618	Nonsignifi	None	2	Molecular	solute carr	--
0.330751	0.007728	-1.59618	Nonsignifi	None	1	Molecular	platelet-ac	--
Inf	0	Inf	Significant	up	--	--	melanoma	--
Inf	0	Inf	Significant	up	--	--	matrin 3	--
Inf	0	Inf	Significant	up	3	Molecular	DNA mism	--
Inf	0	Inf	Significant	up	1	Biological	Ran-bindir	--
Inf	0	Inf	Significant	up	--	--	nicotinami	2.4.2.12
0.054947	0.051345	-4.18581	Nonsignifi	None	1	Cellular Co	--	--
0.570429	0.086217	-0.80988	Nonsignifi	None	3	Biological	peptidyl-p	5.2.1.8
Inf	0	Inf	Significant	up	1	Cellular Co	chromobo	--
Inf	0	Inf	Significant	up	--	--	phosphory	--
Inf	0	Inf	Significant	up	3	Molecular	Ran GTPas	--
Inf	0	Inf	Significant	up	2	Molecular	ATP-depe	3.6.4.12
Inf	0	Inf	Significant	up	1	Molecular	25S rRNA	2.1.1.310
Inf	0	Inf	Significant	up	1	Molecular	proto-onc	--
0.345168	0.03245	-1.53463	Nonsignifi	None	--	--	large subu	--
0.422083	0.074583	-1.2444	Nonsignifi	None	4	Molecular	large subu	--
1.409092	0.11186	0.494766	Nonsignifi	None	3	Molecular	small subu	--
Inf	0	Inf	Significant	up	--	--	small subu	--
Inf	0	Inf	Significant	up	2	Molecular	--	--
0.256854	0.275249	-1.96098	Nonsignifi	None	2	Molecular	Ras GTPas	--
Inf	0	Inf	Significant	up	--	--	glycogenir	2.4.1.186
0.568514	0.014195	-0.81473	Nonsignifi	None	2	Cellular Co	capping pr	--
Inf	0	Inf	Significant	up	3	Biological	aldehyde c	1.2.1.5
0.436859	0.118874	-1.19476	Nonsignifi	None	4	Molecular	large subu	--
0.23725	0.032329	-2.07552	Significant	down	1	Molecular	galectin-7	--
0.843949	0.626514	-0.24477	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant	up	4	Molecular	prolyl oligo	3.4.21.26
Inf	0	Inf	Significant	up	3	Molecular	malate deh	1.1.1.40
Inf	0	Inf	Significant	up	--	--	lanosterol	5.4.99.7
0.375549	0.287055	-1.41293	Nonsignifi	None	2	Molecular	glutamate	6.3.2.2
0.604909	0.37685	-0.72521	Nonsignifi	None	--	--	glutamate	--
2.353317	0.050433	1.234696	Nonsignifi	None	1	Cellular Co	CD151 ant	--
Inf	0	Inf	Significant	up	--	--	26S protea	--
1.553329	0.031262	0.635363	Nonsignifi	None	1	Molecular	T-complex	--
0.288425	0.080737	-1.79373	Nonsignifi	None	--	--	stress 70 p	--

Inf	0	Inf	Significant	up	3	Molecular	casein kina	2.7.11.1
Inf	0	Inf	Significant	up	1	Biological	isocitrate c	1.1.1.42
Inf	0	Inf	Significant	up	1	Molecular	phosphatic	2.7.1.153
Inf	0	Inf	Significant	up	2	Cellular Co	--	--
0.304294	0.000187	-1.71646	Nonsignifi	None	2	Molecular	mannan-b	3.4.21.-
2.547701	0.036192	1.349196	Nonsignifi	None	3	Biological	--	--
Inf	0	Inf	Significant	up	4	Molecular	large subu	--
1.09786	0.841916	0.134694	Nonsignifi	None	2	Biological	fatty acid s	2.3.1.85
1.462758	0.014363	0.548691	Nonsignifi	None	1	Molecular	T-complex	--
Inf	0	Inf	Significant	up	1	Molecular	elongation	--
Inf	0	Inf	Significant	up	--	--	signal reco	--
Inf	0	Inf	Significant	up	2	Molecular	choline-ph	2.7.7.15
Inf	0	Inf	Significant	up	--	--	cysteinyl-t	6.1.1.16
1.006902	0.984158	0.009923	Nonsignifi	None	4	Molecular	seryl-tRNA	6.1.1.11
1.382852	0.022763	0.467647	Nonsignifi	None	3	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant	up	7	Molecular	DNA replic	3.6.4.12
0.084233	0.084977	-3.56948	Nonsignifi	None	3	Molecular	thrombosp	--
0.127242	0.040306	-2.97436	Significant	down	3	Molecular	thrombosp	--
Inf	0	Inf	Significant	up	2	Molecular	RNA-bindi	--
Inf	0	Inf	Significant	up	--	--	histidine tr	--
Inf	0	Inf	Significant	up	1	Molecular	estrone su	2.8.2.4
Inf	0	Inf	Significant	up	--	--	5'-nucleot	3.1.3.5
1.425194	0.188141	0.511159	Nonsignifi	None	4	Molecular	GMP synth	6.3.5.2
Inf	0	Inf	Significant	up	5	Molecular	guanine nu	--
Inf	0	Inf	Significant	up	3	Molecular	guanine nu	--
0.005409	0.056269	-7.53042	Nonsignifi	None	4	Molecular	matrix met	3.4.24.80
0.52074	0.104726	-0.94136	Nonsignifi	None	2	Molecular	Rab GDP c	--
Inf	0	Inf	Significant	up	3	Biological	solute carr	--
1.809903	0.099747	0.855913	Nonsignifi	None	--	--	serpin pep	--
5.931324	9.98E-06	2.568354	Significant	up	1	Molecular	suppressor	--
0.878492	0.801172	-0.1869	Nonsignifi	None	2	Molecular	dynamin G	3.6.5.5
Inf	0	Inf	Significant	up	--	--	--	--
0.366128	0.391316	-1.44958	Nonsignifi	None	4	Molecular	large subu	--
2.280578	0.023446	1.1894	Nonsignifi	None	1	Molecular	T-complex	--
2.577621	0.005652	1.36604	Nonsignifi	None	1	Molecular	T-complex	--
2.45742	0.010128	1.297144	Nonsignifi	None	2	Molecular	annexin A7	--
Inf	0	Inf	Significant	up	1	Molecular	fragile X m	--
Inf	0	Inf	Significant	up	2	Molecular	Ras-relate	--
1.627242	0.013928	0.702429	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up	4	Molecular	SWI/SNF-r	3.6.4.-
1.004985	0.979822	0.007174	Nonsignifi	None	1	Molecular	galactokin	2.7.1.6
Inf	0	Inf	Significant	up	3	Cellular Co	B-cell rece	--
Inf	0	Inf	Significant	up	1	Molecular	thiopurine	2.1.1.67
Inf	0	Inf	Significant	up	1	Molecular	host cell fa	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Cellular Co	--	--
Inf	0	Inf	Significant	up	4	Molecular	chloride ch	--
Inf	0	Inf	Significant	up	2	Cellular Co	vesicle-ass	--
Inf	0	Inf	Significant	up	--	--	hepatoma	--
0.098182	0.06108	-3.3484	Nonsignifi	None	1	Molecular	lumican	--
1.910445	0.005679	0.933909	Nonsignifi	None	3	Molecular	--	--
Inf	0	Inf	Significant	up	1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	5	Molecular	importin su	--
Inf	0	Inf	Significant	up	3	Biological	solute carr	--
Inf	0	Inf	Significant	up	1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	2	Cellular Co	transcriptic	--

Inf	0	Inf	Significant	up	2	Cellular Co	transcriptio	--
Inf	0	Inf	Significant	up	3	Molecular	DNA mism	--
#NAME?	0	#NAME?	Significant	down	2	Molecular	--	--
Inf	0	Inf	Significant	up	2	Molecular	thimet olig	3.4.24.15
1.36476	0.074903	0.448648	Nonsignifi	None	2	Cellular Co	capping pr	--
Inf	0	Inf	Significant	up	5	Molecular	biliverdin r	1.3.1.24
1.331701	0.178807	0.41327	Nonsignifi	None	3	Molecular	ATP citrate	2.3.3.8
1.249871	0.563623	0.321779	Nonsignifi	None	6	Molecular	coatomer s	--
0.254609	0.041946	-1.97365	Nonsignifi	None	2	Biological	cathepsin (	3.4.14.1
4.793786	0.050234	2.261165	Nonsignifi	None	--	--	AP-2 comp	--
Inf	0	Inf	Significant	up	4	Molecular	solute carr	--
Inf	0	Inf	Significant	up	--	--	--	--
1.089433	0.710757	0.123578	Nonsignifi	None	2	Molecular	--	--
Inf	0	Inf	Significant	up	5	Molecular	arginyl-tRN	6.1.1.19
0.228003	0.068213	-2.13288	Nonsignifi	None	--	--	voltage-de	--
0.000464	0.500077	-11.0721	Nonsignifi	None	5	Molecular	tyrosyl-tRN	6.1.1.1
Inf	0	Inf	Significant	up	2	Biological	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant	up	--	--	5'-AMP-ac	--
1.454333	0.076396	0.540358	Nonsignifi	None	--	--	heat shock	--
Inf	0	Inf	Significant	up	4	Molecular	UV excisio	--
Inf	0	Inf	Significant	up	3	Molecular	Eph recept	2.7.10.1
Inf	0	Inf	Significant	up	1	Cellular Co	--	--
Inf	0	Inf	Significant	up	3	Biological	--	--
0.152789	0.102817	-2.71039	Nonsignifi	None	1	Cellular Co	--	--
Inf	0	Inf	Significant	up	5	Molecular	solute carr	--
Inf	0	Inf	Significant	up	1	Molecular	uncharacte	--
0.783841	0.188938	-0.35137	Nonsignifi	None	1	Molecular	transitiona	--
Inf	0	Inf	Significant	up	2	Molecular	afadin	--
Inf	0	Inf	Significant	up	--	--	caspase 6	3.4.22.59
2.225808	0.013703	1.154329	Nonsignifi	None	--	--	adenosine	2.7.1.20
Inf	0	Inf	Significant	up	4	Molecular	double-str	3.5.4.37
0.131515	0.005259	-2.9267	Significant	down	--	--	laminin, be	--
0.051797	0.037427	-4.271	Significant	down	3	Molecular	cadherin 6	--
0.342885	0.174019	-1.54421	Nonsignifi	None	3	Molecular	cadherin 1	--
0.090926	0.004036	-3.45917	Significant	down	3	Molecular	cadherin 1	--
3.990937	0.008609	1.996727	Nonsignifi	None	--	--	small ubiq	--
2.128186	0.013957	1.089624	Nonsignifi	None	1	Molecular	translation	--
Inf	0	Inf	Significant	up	4	Molecular	methionyl-	6.1.1.10
Inf	0	Inf	Significant	up	2	Biological	translation	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	3	Molecular	guanine nu	--
2.41418	0.000948	1.271533	Nonsignifi	None	4	Cellular Co	actin relate	--
1.204983	0.539519	0.269013	Nonsignifi	None	1	Cellular Co	CD81 antig	--
0.50538	0.029494	-0.98456	Nonsignifi	None	2	Molecular	triosephos	5.3.1.1
1.649929	0.03634	0.722404	Nonsignifi	None	1	Molecular	translation	--
Inf	0	Inf	Significant	up	--	--	GABA(A) re	--
0.618477	0.009269	-0.69321	Nonsignifi	None	1	Molecular	myosin ligl	--
0.913689	0.517696	-0.13022	Nonsignifi	None	--	--	actin beta/	--
1.289762	0.247577	0.367105	Nonsignifi	None	2	Molecular	Ras-relate	--
1.190446	0.057581	0.251502	Nonsignifi	None	2	Molecular	translation	--
1.576603	0.151918	0.65682	Nonsignifi	None	--	--	small subu	--
1.437429	0.026199	0.523491	Nonsignifi	None	5	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant	up	--	--	calpactin-1	--
1.440288	0.269092	0.526357	Nonsignifi	None	2	Molecular	cell divisio	--
1.204233	0.216441	0.268115	Nonsignifi	None	2	Molecular	destrin (ac	--
Inf	0	Inf	Significant	up	2	Molecular	--	--
0.046253	0.130027	-4.43431	Nonsignifi	None	4	Molecular	signal recc	3.6.5.4
1.352897	0.177254	0.436052	Nonsignifi	None	2	Molecular	Ras-relate	--

0.967244	0.920444	-0.04805	Nonsignifi	None		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up	--		--	ubiquitin-	--
Inf	0	Inf	Significant	up	--		--	ubiquitin-	2.3.2.23
Inf	0	Inf	Significant	up	--		--	ubiquitin-	2.3.2.23
Inf	0	Inf	Significant	up		2	Molecular	Ras-relate	--
1.843595	0.014274	0.882522	Nonsignifi	None	--		--	actin-relat	--
Inf	0	Inf	Significant	up	--		--	centractin	--
1.275023	0.099236	0.350523	Nonsignifi	None		1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant	up		2	Molecular	ATP-bindi	--
1.75748	0.061164	0.813509	Nonsignifi	None		2	Molecular	Ras-relate	--
1.291535	0.430298	0.369087	Nonsignifi	None		3	Molecular	small subu	--
Inf	0	Inf	Significant	up		1	Cellular Co	proteasom	--
0.678635	0.539137	-0.55929	Nonsignifi	None		3	Molecular	large subu	--
0.405974	0.001915	-1.30054	Nonsignifi	None		4	Molecular	large subu	--
Inf	0	Inf	Significant	up		2	Molecular	Ras homol	--
Inf	0	Inf	Significant	up		2	Cellular Co	chaperonir	--
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up		2	Biological	syntaxin-b	--
0.290474	0.035438	-1.78352	Nonsignifi	None	--		--	beta-2-mi	--
Inf	0	Inf	Significant	up	--		--	AP-1 com	--
Inf	0	Inf	Significant	up		2	Cellular Co	--	--
2.40737	0.061169	1.267458	Nonsignifi	None		1	Molecular	heterogen	--
1.144482	0.068891	0.194695	Nonsignifi	None	--		--	14-3-3 pr	--
2.105858	0.004158	1.074408	Nonsignifi	None		1	Molecular	serine/thre	3.1.3.16
0.492958	0.006618	-1.02046	Nonsignifi	None		1	Molecular	calmodulir	--
Inf	0	Inf	Significant	up		1	Molecular	neuronal c	--
1.213322	0.308553	0.278963	Nonsignifi	None		1	Molecular	26S protea	--
1.119626	0.283071	0.163016	Nonsignifi	None		1	Molecular	26S protea	--
0.607937	0.251308	-0.71801	Nonsignifi	None	--		--	small subu	--
0.720052	0.009048	-0.47383	Nonsignifi	None		3	Molecular	small subu	--
Inf	0	Inf	Significant	up	--		--	ubiquitin-	2.3.2.23
0.79714	0.546082	-0.32709	Nonsignifi	None	--		--	14-3-3 pr	--
0.83259	0.217991	-0.26432	Nonsignifi	None		3	Molecular	small subu	--
1.288572	0.109364	0.365773	Nonsignifi	None		4	Molecular	small subu	--
1.331741	0.178614	0.413313	Nonsignifi	None		5	Molecular	small subu	--
1.41965	0.051101	0.505536	Nonsignifi	None		4	Molecular	small subu	--
0.826064	0.05041	-0.27567	Nonsignifi	None		4	Molecular	small subu	--
Inf	0	Inf	Significant	up	--		--	U6 snRNA	--
Inf	0	Inf	Significant	up	--		--	small nucl	--
1.731236	0.013443	0.791802	Nonsignifi	None	--		--	small nucl	--
1.258709	0.282173	0.331945	Nonsignifi	None		1	Molecular	ADP-ribos	--
0.541513	0.070276	-0.88493	Nonsignifi	None		1	Molecular	26S protea	--
0.713301	0.196682	-0.48742	Nonsignifi	None	--		--	large subu	--
Inf	0	Inf	Significant	up		2	Molecular	cellular nu	--
0.899925	0.375315	-0.15212	Nonsignifi	None		1	Molecular	small subu	--
0.771836	0.08797	-0.37363	Nonsignifi	None	--		--	actin, aorti	--
1.409938	0.427801	0.495632	Nonsignifi	None		3	Molecular	large subu	--
0.477118	0.153059	-1.06758	Nonsignifi	None		4	Molecular	small subu	--
Inf	0	Inf	Significant	up		1	Molecular	visinin-like	--
17.40567	0.001247	4.121485	Significant	up	--		--	histone H4	--
0.540144	0.009434	-0.88859	Nonsignifi	None		2	Molecular	Ras-relate	--
1.559883	0.114929	0.641438	Nonsignifi	None		2	Molecular	GTP-bindi	--
Inf	0	Inf	Significant	up		3	Molecular	large subu	--
2.185886	0.021802	1.128218	Nonsignifi	None		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		4	Molecular	small subu	--
1.294383	0.580021	0.372265	Nonsignifi	None	--		--	small subu	--
0.764634	0.237783	-0.38716	Nonsignifi	None		4	Molecular	small subu	--
1.153382	0.499899	0.205871	Nonsignifi	None		4	Molecular	small subu	--

Inf	0	Inf	Significant up		1	Molecular	guanine nu	--
Inf	0	Inf	Significant up		2	Molecular	DNA-direc	--
1.187683	0.204423	0.24815	Nonsignifi	None	1	Molecular	guanine nu	--
Inf	0	Inf	Significant up		3	Molecular	large subu	--
1.456738	0.022969	0.542742	Nonsignifi	None	--	--	large subu	--
0.468979	0.043241	-1.0924	Nonsignifi	None	4	Molecular	large subu	--
1.117997	0.418438	0.160916	Nonsignifi	None	3	Biological	peptidyl-p	5.2.1.8
0.100351	0.043497	-3.31687	Significant down		--	--	FK506-bin	5.2.1.8
0.694348	0.036554	-0.52627	Nonsignifi	None	4	Molecular	small subu	--
Inf	0	Inf	Significant up		1	Molecular	growth fac	--
0.125666	0.021753	-2.99233	Significant down		1	Molecular	transforme	--
0.664653	0.54621	-0.58933	Nonsignifi	None	4	Biological	AP-2 comp	--
0.765007	0.21051	-0.38645	Nonsignifi	None	--	--	14-3-3 pro	--
Inf	0	Inf	Significant up		4	Molecular	large subu	--
Inf	0	Inf	Significant up		1	Biological	S-phase ki	--
Inf	0	Inf	Significant up		3	Molecular	guanine nu	--
2.269197	0.023004	1.182182	Nonsignifi	None	1	Molecular	guanine nu	--
0.639209	0.155693	-0.64564	Nonsignifi	None	--	--	actin beta/	--
Inf	0	Inf	Significant up		--	--	ubiquitin-c	--
1.57477	0.010961	0.655142	Nonsignifi	None	1	Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significant up		1	Molecular	Y-box-bin	--
0.613697	0.155202	-0.7044	Nonsignifi	None	2	Cellular Co	casein kina	--
0.29123	0.057672	-1.77977	Nonsignifi	None	--	--	tropomyos	--
Inf	0	Inf	Significant up		--	--	ubiquitin-c	2.3.2.23
1.63092	0.018205	0.705686	Nonsignifi	None	1	Molecular	elongation	--
0.417336	0.175788	-1.26072	Nonsignifi	None	1	Molecular	tubulin alp	--
0.515028	0.22627	-0.95728	Nonsignifi	None	1	Molecular	tubulin alp	--
0.5234	0.219998	-0.93401	Nonsignifi	None	1	Molecular	tubulin bet	--
0.745305	0.327457	-0.4241	Nonsignifi	None	3	Molecular	casein kina	2.7.11.1
Inf	0	Inf	Significant up		--	--	platelet-ac	3.1.1.47
Inf	0	Inf	Significant up		1	Molecular	histone H3	--
0.429183	0.001405	-1.22033	Nonsignifi	None	2	Molecular	hemoglob	--
0.877481	0.302037	-0.18856	Nonsignifi	None	2	Molecular	hemoglob	--
Inf	0	Inf	Significant up		--	--	coxsackiev	--
Inf	0	Inf	Significant up		2	Molecular	translation	--
Inf	0	Inf	Significant up		--	--	transcriptic	--
1.217037	0.105355	0.283373	Nonsignifi	None	1	Molecular	T-complex	--
0.028446	0.094786	-5.13563	Nonsignifi	None	7	Molecular	DNA-depe	2.7.11.1
0.363869	0.016002	-1.45851	Nonsignifi	None	--	--	--	--
#NAME?	0	#NAME?	Significant down		3	Cellular Co	C-X-C mo	--
0.783105	0.359486	-0.35272	Nonsignifi	None	--	--	brain acid	--
Inf	0	Inf	Significant up		--	--	--	--
0.621559	0.221869	-0.68604	Nonsignifi	None	--	--	large subu	--
Inf	0	Inf	Significant up		1	Cellular Co	chromobo	--
Inf	0	Inf	Significant up		3	Biological	--	--
1.897324	0.068996	0.923966	Nonsignifi	None	2	Molecular	Ras homol	--
0.272606	0.421094	-1.87511	Nonsignifi	None	4	Molecular	large subu	--
1.326527	0.504763	0.407654	Nonsignifi	None	1	Molecular	splicing fac	--
Inf	0	Inf	Significant up		--	--	mucin-5A(	--
Inf	0	Inf	Significant up		2	Molecular	fibulin 1/2	--
0.372483	0.061517	-1.42475	Nonsignifi	None	1	Molecular	heparan su	--
Inf	0	Inf	Significant up		1	Cellular Co	ephrin-B	--
Inf	0	Inf	Significant up		2	Molecular	Ca2+-tran	3.6.3.8
0.021782	0.061063	-5.52072	Nonsignifi	None	2	Molecular	phospholip	3.6.3.1
Inf	0	Inf	Significant up		2	Molecular	cytochrom	--
Inf	0	Inf	Significant up		1	Molecular	55 kDa ery	--
Inf	0	Inf	Significant up		2	Molecular	S-adenosy	2.5.1.6
Inf	0	Inf	Significant up		1	Molecular	--	--

Inf	0	Inf	Significant up	--	--	transcriptic	--	
0.979795	0.849386	-0.02945	Nonsignifi	None	5	Molecular	clathrin he	--
Inf	0	Inf	Significant up	--	--	FK506-bin	5.2.1.8	
Inf	0	Inf	Significant up		1	Biological	L-iditol 2-	1.1.1.14
0.528104	0.613604	-0.92111	Nonsignifi	None	1	Molecular	spectrin be	--
14.40175	0.012373	3.848172	Significant up		2	Cellular Co	template-	--
0.907679	0.8131	-0.13975	Nonsignifi	None	1	Molecular	splicing fac	--
0.735684	0.085033	-0.44284	Nonsignifi	None	1	Molecular	AMP deam	3.5.4.6
0.515828	0.120045	-0.95504	Nonsignifi	None	--	--	fatty acid-	--
0.797078	0.053607	-0.32721	Nonsignifi	None	2	Molecular	adenylyl cy	--
Inf	0	Inf	Significant up		2	Molecular	hydroxyme	2.3.3.10
3.594025	0.025642	1.845601	Nonsignifi	None	2	Biological	interferon	--
Inf	0	Inf	Significant up		3	Biological	solute carr	--
Inf	0	Inf	Significant up	--	--	down-regu	--	
0.56385	0.007455	-0.82662	Nonsignifi	None	2	Molecular	6-phosphc	2.7.1.11
Inf	0	Inf	Significant up		7	Molecular	phosphatic	3.1.4.11
Inf	0	Inf	Significant up		3	Molecular	receptor ty	2.7.10.1
0.156528	0.026024	-2.67551	Significant down		1	Molecular	transgelin	--
Inf	0	Inf	Significant up		6	Molecular	guanylate	4.6.1.2
Inf	0	Inf	Significant up		4	Molecular	kinesin fam	--
Inf	0	Inf	Significant up		1	Molecular	FK506-bin	5.2.1.8
0.644601	0.008192	-0.63352	Nonsignifi	None	2	Molecular	procollage	1.14.11.4
0.189781	0.01966	-2.39759	Significant down		1	Molecular	nucleobinc	--
1.269362	0.687672	0.344104	Nonsignifi	None	4	Molecular	large subu	--
Inf	0	Inf	Significant up		5	Molecular	DNA topoi	5.99.1.3
Inf	0	Inf	Significant up		2	Cellular Co	tumor nec	--
0.016472	0.041865	-5.92385	Significant down		4	Cellular Co	peroxisom	--
Inf	0	Inf	Significant up	--	--	plasminog	--	
Inf	0	Inf	Significant up		1	Molecular	transcriptic	--
Inf	0	Inf	Significant up		3	Molecular	1,4-alpha-	2.4.1.18
Inf	0	Inf	Significant up		2	Molecular	translation	--
0.261605	0.058341	-1.93454	Nonsignifi	None	4	Molecular	hepatocyte	3.4.21.-
Inf	0	Inf	Significant up		1	Molecular	single-stra	--
1.300815	0.063268	0.379415	Nonsignifi	None	--	--	14-3-3 pro	--
Inf	0	Inf	Significant up		2	Molecular	dynamin G	3.6.5.5
Inf	0	Inf	Significant up		6	Molecular	focal adhe	2.7.10.2
0.49849	0.034869	-1.00436	Nonsignifi	None	1	Molecular	splicing fac	--
0.412725	0.006292	-1.27675	Nonsignifi	None	--	--	caldesmon	--
0.101267	0.025554	-3.30377	Significant down		2	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	tyrosine-p	3.1.3.48
0.032847	0.027186	-4.92809	Significant down		1	Biological	amidopho	2.4.2.14
0.327586	0.385549	-1.61006	Nonsignifi	None	2	Biological	glucosami	2.6.1.16
Inf	0	Inf	Significant up	--	--	exosome c	--	
7.106807	0.003205	2.829201	Significant up		1	Cellular Co	proteasom	--
0.113642	0.034272	-3.13743	Significant down		1	Molecular	fibromodu	--
0.527589	0.113038	-0.92251	Nonsignifi	None	4	Molecular	peroxiredc	1.11.1.15
0.665578	0.27203	-0.58732	Nonsignifi	None	--	--	large subu	--
Inf	0	Inf	Significant up		1	Cellular Co	compleme	--
#NAME?	0	#NAME?	Significant down	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	tight juncti	--
Inf	0	Inf	Significant up		1	Molecular	KH domair	--
0.418004	0.001055	-1.25841	Nonsignifi	None	2	Molecular	low-densit	--
Inf	0	Inf	Significant up		1	Molecular	splicing fac	--
Inf	0	Inf	Significant up		1	Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significant up		1	Biological	NADPH2:q	1.6.5.5
1.969494	0.023198	0.977825	Nonsignifi	None	2	Molecular	galectin-3	--
1.288034	0.407298	0.365171	Nonsignifi	None	1	Molecular	lactadherir	--
0.038682	0.06132	-4.69218	Nonsignifi	None	4	Molecular	sparc/oste	--

Inf	0	Inf	Significant up	--	--	CD47 antig	--
Inf	0	Inf	Significant up	4	Biological	peptidyl-p	5.2.1.8
1.053196	0.896803	0.074774	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up	--	--	ragulator c	--
0.024619	0.279358	-5.34408	Nonsignifi	None	4	Cellular Co	alpha-1,6-	2.4.1.143
0.141217	0.000136	-2.82401	Significant down	--	--	polypeptid	2.4.1.41
0.703361	0.304638	-0.50766	Nonsignifi	None	4	Biological	AP-1 comp	--
Inf	0	Inf	Significant up	2	Molecular	cleavage a	--
Inf	0	Inf	Significant up	1	Cellular Co	WASH con	--
0.103882	0.057762	-3.26698	Nonsignifi	None	1	Molecular	EGF-conta	--
0.024682	0.066487	-5.3404	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant up	2	Molecular	syntaxin 4	--
0.061727	0.063287	-4.01795	Nonsignifi	None	1	Molecular	contactin 1	--
Inf	0	Inf	Significant up	--	--	splicing fa	--
0.228522	2.85E-08	-2.12959	Significant down	2	Biological	fibroblast a	3.4.21.-
Inf	0	Inf	Significant up	1	Molecular	aminoacyl	--
Inf	0	Inf	Significant up	--	--	interleukin	--
Inf	0	Inf	Significant up	--	--	interleukin	--
0.554269	0.159077	-0.85134	Nonsignifi	None	1	Cellular Co	lectin, mar	--
6.393729	3.95E-05	2.676658	Significant up	4	Molecular	TNF recept	--
Inf	0	Inf	Significant up	1	Molecular	disks large	--
Inf	0	Inf	Significant up	2	Molecular	protein tyr	3.1.3.48
Inf	0	Inf	Significant up	1	Molecular	striatin 1/3	--
Inf	0	Inf	Significant up	--	--	anaphase-	--
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	3	Molecular	--	--
0.552858	0.099824	-0.85502	Nonsignifi	None	2	Molecular	platelet-ac	3.1.1.47
Inf	0	Inf	Significant up	1	Molecular	lymphocyt	--
1.621813	0.018609	0.697607	Nonsignifi	None	2	Cellular Co	--	--
Inf	0	Inf	Significant up	3	Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up	3	Molecular	5'-AMP-ac	2.7.11.11
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	aminoacyl	--
Inf	0	Inf	Significant up	4	Molecular	peroxiredo	1.11.1.15
0.159365	0.054145	-2.64959	Nonsignifi	None	4	Molecular	mitogen-a	2.7.12.2
0.71957	0.268776	-0.47479	Nonsignifi	None	--	--	26S protea	--
Inf	0	Inf	Significant up	1	Molecular	selenium-b	--
Inf	0	Inf	Significant up	3	Molecular	tripartite m	2.3.2.27
Inf	0	Inf	Significant up	3	Molecular	--	--
0.533982	0.083616	-0.90514	Nonsignifi	None	2	Molecular	PTK7 prote	2.7.10.1
Inf	0	Inf	Significant up	3	Molecular	metastasis	--
1.352854	0.158928	0.436007	Nonsignifi	None	1	Molecular	translation	--
Inf	0	Inf	Significant up	3	Biological	C-terminal	--
Inf	0	Inf	Significant up	3	Molecular	dynein inte	--
1.095242	0.785834	0.13125	Nonsignifi	None	2	Molecular	integrin-lir	2.7.11.1
Inf	0	Inf	Significant up	--	--	Treacher C	--
Inf	0	Inf	Significant up	1	Cellular Co	splicing fa	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	5	Molecular	myosin IX	--
Inf	0	Inf	Significant up	4	Molecular	Rho-assoc	2.7.11.1
Inf	0	Inf	Significant up	1	Molecular	phosphatic	--
0.093782	0.00798	-3.41454	Significant down	1	Molecular	tubulin bet	--
Inf	0	Inf	Significant up	--	--	histone de	3.5.1.98
Inf	0	Inf	Significant up	5	Molecular	calcium/ca	2.7.11.17
Inf	0	Inf	Significant up	5	Molecular	calcium/ca	2.7.11.17
Inf	0	Inf	Significant up	--	--	dynactin 2	--
Inf	0	Inf	Significant up	2	Molecular	Ras GTPas	--
Inf	0	Inf	Significant up	1	Molecular	transforme	--

Inf	0	Inf	Significant up		2	Biological	sorting ne	--
Inf	0	Inf	Significant up		2	Biological	cullin 1	--
Inf	0	Inf	Significant up		2	Biological	cullin 2	--
Inf	0	Inf	Significant up		2	Biological	cullin 3	--
Inf	0	Inf	Significant up		2	Biological	cullin 4	--
Inf	0	Inf	Significant up		2	Molecular	GDP-L-fuc	1.1.1.271
0.862538	0.051548	-0.21334	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.445888	0.178212	-1.16525	Nonsignifi	None	1	Molecular	four and a	--
Inf	0	Inf	Significant up	--	--		integrin al	--
0.077918	0.253136	-3.68189	Nonsignifi	None	--	--	activated l	--
0.541056	0.003881	-0.88615	Nonsignifi	None	1	Molecular	tubulin alp	--
0.098926	0.008918	-3.33751	Significant down		7	Molecular	ectonuclec	3.1.4.39
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		2	Molecular	bleomycin	3.4.22.40
Inf	0	Inf	Significant up		1	Molecular	exosome c	--
Inf	0	Inf	Significant up		5	Molecular	bone morp	2.7.11.30
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--		essential n	--
Inf	0	Inf	Significant up		1	Molecular	isopenteny	5.3.3.2
Inf	0	Inf	Significant up	--	--		cytoskelet	--
0.392544	0.009144	-1.34907	Nonsignifi	None	2	Molecular	--	--
2.235485	0.004249	1.160588	Nonsignifi	None	1	Molecular	heterogen	--
Inf	0	Inf	Significant up		1	Cellular Co	lysosome r	--
#NAME?	0	#NAME?	Significant down		2	Molecular	nidogen (e	--
Inf	0	Inf	Significant up		1	Molecular	dihydropy	3.5.2.2
Inf	0	Inf	Significant up		2	Biological	dystroglyc	--
Inf	0	Inf	Significant up		1	Molecular	septin 6/8/	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.048576	0.220406	-4.3636	Nonsignifi	None	1	Molecular	translation	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		1	Molecular	protein scr	--
Inf	0	Inf	Significant up		1	Biological	tubulin--ty	--
Inf	0	Inf	Significant up		1	Molecular	four and a	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--		dynactin 1	--
0.963017	0.88524	-0.05437	Nonsignifi	None	5	Molecular	dynein hea	--
Inf	0	Inf	Significant up		1	Biological	translation	--
Inf	0	Inf	Significant up		2	Molecular	translation	--
0.938903	0.860859	-0.09095	Nonsignifi	None	--	--	flotillin	--
Inf	0	Inf	Significant up		1	Molecular	tripartite m	2.3.2.27
0.456031	0.080078	-1.1328	Nonsignifi	None	6	Molecular	focal adhe	2.7.10.2
Inf	0	Inf	Significant up		1	Molecular	filamin	--
0.21187	0.468458	-2.23875	Nonsignifi	None	5	Molecular	guanine nu	--
Inf	0	Inf	Significant up	--	--		UDP-gluco	5.1.3.2
Inf	0	Inf	Significant up		2	Molecular	growth arr	--
Inf	0	Inf	Significant up	--	--		caprin-1	--
Inf	0	Inf	Significant up		1	Molecular	RNA-bindi	--
0.272014	0.081314	-1.87825	Nonsignifi	None	4	Molecular	--	--
Inf	0	Inf	Significant up		4	Molecular	protocadh	--
1.239004	0.010682	0.30918	Nonsignifi	None	3	Molecular	hyaluronar	3.4.21.-
Inf	0	Inf	Significant up		3	Molecular	DNA replic	3.6.4.12
Inf	0	Inf	Significant up		3	Biological	indian hed	--
0.261384	0.000902	-1.93576	Nonsignifi	None	2	Molecular	--	--
0.075976	0.460868	-3.71832	Nonsignifi	None	3	Molecular	Ras GTPas	--
Inf	0	Inf	Significant up		2	Molecular	plastin-1	--
Inf	0	Inf	Significant up		1	Molecular	mediator c	--
Inf	0	Inf	Significant up	--	--		--	--

Inf	0	Inf	Significant up		4	Molecular	structural r	--
1.938646	0.001619	0.955049	Nonsignifi	None	1	Biological	alpha 1,3-(	3.2.1.84
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		2	Molecular	membrane	3.4.21.112
0.070854	4.73E-06	-3.81902	Significant down	--		--	major vaul	--
#NAME?	0	#NAME?	Significant down		1	Molecular	latent tran	--
Inf	0	Inf	Significant up		5	Molecular	chromodo	3.6.4.12
Inf	0	Inf	Significant up		2	Molecular	--	--
2.342212	0.003539	1.227871	Nonsignifi	None	2	Biological	importin su	--
Inf	0	Inf	Significant up	--		--	nuclear mi	--
Inf	0	Inf	Significant up	--		--	proteasom	--
Inf	0	Inf	Significant up		1	Biological	--	--
1.309701	0.139098	0.389238	Nonsignifi	None	1	Molecular	26S protea	--
Inf	0	Inf	Significant up		1	Cellular Co	lysosomal-	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--		--	condensin	--
Inf	0	Inf	Significant up		1	Molecular	116 kDa U	--
0.082209	0.011	-3.60455	Significant down	--		--	--	--
Inf	0	Inf	Significant up		1	Biological	protein dis	5.3.4.1
1.093659	0.592775	0.129162	Nonsignifi	None	--	--	platelet-ac	3.1.1.47
0.055636	0.005403	-4.16785	Significant down	--		--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		4	Molecular	inorganic p	3.6.1.1
Inf	0	Inf	Significant up	--		--	cytosolic p	5.3.99.3
Inf	0	Inf	Significant up		4	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up		1	Molecular	non-POU	--
Inf	0	Inf	Significant up		1	Molecular	serine/thre	--
Inf	0	Inf	Significant up		4	Molecular	receptor-t	3.1.3.48
0.548555	0.092674	-0.86629	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Molecular	lethal(2) gi	--
Inf	0	Inf	Significant up		4	Molecular	ribosomal	2.7.11.1
1.51286	0.018949	0.597279	Nonsignifi	None	1	Molecular	poly(rC)-b	--
0.501687	0.060047	-0.99514	Nonsignifi	None	1	Molecular	poly(rC)-b	--
Inf	0	Inf	Significant up		1	Biological	transcriptic	--
Inf	0	Inf	Significant up		2	Molecular	Ras homol	--
0.245706	0.007796	-2.02499	Significant down		3	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	splicing fa	--
0.416088	0.011757	-1.26504	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--		--	protein ph	--
Inf	0	Inf	Significant up		3	Molecular	splicing fa	--
0.359246	0.014635	-1.47696	Nonsignifi	None	--	--	gluconolac	3.1.1.17
1.129591	0.69968	0.1758	Nonsignifi	None	2	Molecular	microtubu	--
0.036809	0.011871	-4.76379	Significant down	--		--	transformi	--
Inf	0	Inf	Significant up		1	Molecular	Na(+)/H(+	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	microtubu	--
Inf	0	Inf	Significant up		1	Molecular	ELAV-like	--
0.649563	0.114682	-0.62246	Nonsignifi	None	2	Molecular	solute carr	--
Inf	0	Inf	Significant up	--		--	ubiquitin-(	--
2.241501	0.037253	1.164465	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Molecular	zyxin	--
Inf	0	Inf	Significant up		2	Cellular Co	26S protea	--
Inf	0	Inf	Significant up	--		--	coiled-coil	--
Inf	0	Inf	Significant up		2	Biological	--	--
0.005077	0.0363	-7.62167	Significant down		4	Biological	--	--
0.100549	2.84E-05	-3.31403	Significant down		5	Molecular	laminin, al	--
0.516006	0.001634	-0.95454	Nonsignifi	None	3	Biological	--	--

0.635563	0.441985	-0.65389	Nonsignifi	None		1	Biological	26S protea	--
Inf	0	Inf	Significant	up		5	Molecular	protein kin	2.7.11.13
Inf	0	Inf	Significant	up		3	Molecular	p38 MAP k	2.7.11.24
Inf	0	Inf	Significant	up		1	Molecular	cell divisio	--
1.500818	0.044743	0.585749	Nonsignifi	None		1	Molecular	dihydropy	--
Inf	0	Inf	Significant	up		1	Cellular Co	--	--
Inf	0	Inf	Significant	up		1	Molecular	histone-bi	--
#NAME?	0	#NAME?	Significant	down		2	Cellular Co	--	--
Inf	0	Inf	Significant	up		1	Cellular Co	occludin	--
Inf	0	Inf	Significant	up		1	Molecular	cleavage a	--
Inf	0	Inf	Significant	up		4	Molecular	survival m	--
Inf	0	Inf	Significant	up		2	Molecular	--	--
0.698058	0.134623	-0.51858	Nonsignifi	None		1	Molecular	fascin 1/2	--
0.10702	0.038489	-3.22404	Significant	down	--		--	melanoma	--
Inf	0	Inf	Significant	up	--		--	kynurenina	3.7.1.3
Inf	0	Inf	Significant	up	--		--	ceramide g	2.4.1.80
Inf	0	Inf	Significant	up	--		--	glutaminyl	2.3.2.5
Inf	0	Inf	Significant	up		2	Biological	UTP--gluc	2.7.7.9
#NAME?	0	#NAME?	Significant	down		5	Molecular	primary-ar	1.4.3.21
Inf	0	Inf	Significant	up		2	Molecular	cysteine di	1.13.11.20
Inf	0	Inf	Significant	up	--		--	sister chro	--
Inf	0	Inf	Significant	up		3	Molecular	AP2-assoc	2.7.11.1
Inf	0	Inf	Significant	up	--		--	WASH con	--
Inf	0	Inf	Significant	up		1	Molecular	WD40 rep	--
0.755086	0.326732	-0.40529	Nonsignifi	None		2	Biological	major histo	--
0.168248	0.041381	-2.57134	Significant	down		2	Molecular	leucine pr	--
0.034609	0.071884	-4.85272	Nonsignifi	None		4	Biological	formyltetra	1.5.1.6
Inf	0	Inf	Significant	up		2	Molecular	--	--
Inf	0	Inf	Significant	up		1	Molecular	--	--
Inf	0	Inf	Significant	up		1	Molecular	anoctamin	--
Inf	0	Inf	Significant	up		1	Biological	--	--
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up	--		--	protein FA	--
0.557366	0.198464	-0.8433	Nonsignifi	None	--		--	phospholip	3.1.1.-
Inf	0	Inf	Significant	up	--		--	pyrroline-5	1.5.1.2
1.604681	0.364798	0.682287	Nonsignifi	None	--		--	--	--
Inf	0	Inf	Significant	up		4	Molecular	molecular	--
5.001045	1.93E-07	2.322229	Significant	up		4	Molecular	molecular	--
Inf	0	Inf	Significant	up		2	Molecular	zinc finger	--
Inf	0	Inf	Significant	up	--		--	serine/thre	--
Inf	0	Inf	Significant	up		1	Molecular	WD repeat	--
Inf	0	Inf	Significant	up	--		--	ribosomal	--
Inf	0	Inf	Significant	up		4	Cellular Co	--	--
0.01296	0.086169	-6.26981	Nonsignifi	None	--		--	FK506-bin	--
Inf	0	Inf	Significant	up		1	Molecular	E3 ubiquiti	2.3.2.26
0.516735	0.30212	-0.9525	Nonsignifi	None		1	Molecular	E3 ubiquiti	2.3.2.27
Inf	0	Inf	Significant	up	--		--	--	--
1.131639	0.893732	0.178413	Nonsignifi	None	--		--	--	--
Inf	0	Inf	Significant	up		3	Molecular	DNA dama	--
16.45352	0.006428	4.040324	Significant	up		1	Molecular	histone H3	--
0.040751	0.056962	-4.61702	Nonsignifi	None		1	Cellular Co	myomegal	--
Inf	0	Inf	Significant	up	--		--	ubiquitin t	3.1.2.-
Inf	0	Inf	Significant	up	--		--	palmitoyltr	2.3.1.225
Inf	0	Inf	Significant	up	--		--	immune co	--
Inf	0	Inf	Significant	up	--		--	metallored	1.16.1.-
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up	--		--	TBC1 dom	--
Inf	0	Inf	Significant	up		1	Molecular	tensin	--

Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	Rho GTPas	--
Inf	0	Inf	Significant up		2	Molecular	hemoglob	--
0.23276	0.074365	-2.10308	Nonsignifi	None	2	Molecular	atlastin	3.6.5.-
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Biological	carboxype	3.4.17.-
Inf	0	Inf	Significant up		10	Biological	ragulator c	--
Inf	0	Inf	Significant up		2	Molecular	twinfilin	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up	--	--	--	histone arg	1.14.11.-
Inf	0	Inf	Significant up		4	Molecular	pre-mRNA	--
Inf	0	Inf	Significant up		1	Molecular	O-palmito	3.1.1.98
#NAME?	0	#NAME?	Significant down	--	--	--	integrator	--
Inf	0	Inf	Significant up		4	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Cellular Co	--	--
Inf	0	Inf	Significant up		3	Molecular	--	--
0.118442	0.002976	-3.07774	Significant down		3	Molecular	CD109 ant	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	protein un	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.309523	0.011272	-1.69188	Nonsignifi	None	2	Molecular	a disintegr	3.4.24.87
0.021936	0.056003	-5.51055	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	butyrophili	--
0.007556	0.019817	-7.0481	Significant down		2	Molecular	transcriptio	--
Inf	0	Inf	Significant up	--	--	--	staphylocc	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		3	Cellular Co	MFS transp	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		1	Molecular	translation	--
1.335139	0.104728	0.41699	Nonsignifi	None	--	--	cytoplasmi	--
Inf	0	Inf	Significant up		1	Molecular	COP9 sign	--
Inf	0	Inf	Significant up		3	Molecular	thousand a	2.7.11.1
Inf	0	Inf	Significant up		1	Biological	charged m	--
0.536227	0.019889	-0.89908	Nonsignifi	None	4	Molecular	RAS guany	--
Inf	0	Inf	Significant up	--	--	--	PHD finge	--
Inf	0	Inf	Significant up		1	Molecular	poly [ADP-	2.4.2.30
16.67624	0.002796	4.059722	Significant up		1	Cellular Co	--	--
Inf	0	Inf	Significant up	--	--	--	autophagy	--
0.010983	0.020799	-6.50856	Significant down	--	--	--	--	--
0.518712	0.068981	-0.94699	Nonsignifi	None	3	Molecular	myosin he	--
Inf	0	Inf	Significant up	--	--	--	CLIP-asso	--
Inf	0	Inf	Significant up		1	Molecular	low-densit	--
Inf	0	Inf	Significant up	--	--	--	L-xylulose	1.1.1.10
0.006327	0.09472	-7.30416	Nonsignifi	None	1	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up	--	--	--	centriolin	--
#NAME?	0	#NAME?	Significant down		1	Molecular	--	--
0.244707	0.04572	-2.03087	Significant down	--	--	--	--	--
0.514775	0.093338	-0.95799	Nonsignifi	None	--	--	kinectin	--
2.394859	0.002404	1.259941	Nonsignifi	None	--	--	kindlin 3	--
Inf	0	Inf	Significant up		1	Molecular	THO comp	--
Inf	0	Inf	Significant up		1	Cellular Co	--	--
Inf	0	Inf	Significant up		1	Cellular Co	lysosomal-	--
2.399802	0.002955	1.262915	Nonsignifi	None	--	--	cullin-asso	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Biological	type I prot	2.1.1.319
Inf	0	Inf	Significant up		4	Molecular	dihydrofol	1.5.1.3

Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti	2.3.2.27
Inf	0	Inf	Significant up		3	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	syntaxin 1	--
1.472164	0.102042	0.557938	Nonsignifi	None	1	Molecular	--	--
0.19256	0.001252	-2.37662	Significant down	--		--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
#NAME?	0	#NAME?	Significant down		3	Molecular	adipocyte	--
Inf	0	Inf	Significant up		1	Molecular	phospholip	3.1.4.4
Inf	0	Inf	Significant up	--		--	LIX1-like p	--
Inf	0	Inf	Significant up		1	Molecular	NET1-assc	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	volume-re	--
Inf	0	Inf	Significant up		3	Molecular	calcium hc	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		2	Molecular	mitochonc	3.6.5.-
Inf	0	Inf	Significant up		4	Cellular Cc	AdoMet-d	2.1.1.-
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		1	Biological	serine/argi	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up		2	Molecular	katanin p6	3.6.4.3
Inf	0	Inf	Significant up		1	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up	--		--	ankyrin rep	--
0.699341	0.45304	-0.51593	Nonsignifi	None	3	Biological	--	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		3	Molecular	--	--
0.100857	0.021875	-3.30961	Significant down		2	Molecular	type II kera	--
Inf	0	Inf	Significant up		1	Biological	Rho GTPas	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		3	Biological	RNA polyn	--
0.229561	0.025464	-2.12305	Significant down	--		--	cyclic GMP	2.7.7.86
Inf	0	Inf	Significant up	--		--	enabled	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--		--	pre-mRNA	--
Inf	0	Inf	Significant up		1	Molecular	AAA family	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.084621	0.051667	-3.56284	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up	--		--	collagen b	2.4.1.50
Inf	0	Inf	Significant up		2	Biological	--	--
0.25311	0.031322	-1.98216	Nonsignifi	None	1	Biological	thioredoxi	--
Inf	0	Inf	Significant up		1	Molecular	UDP-gluc	4.1.1.35
Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti	2.3.2.27
Inf	0	Inf	Significant up	--		--	plasminog	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		2	Molecular	dermatan	2.8.2.35
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up	--		--	metal trans	--
Inf	0	Inf	Significant up		2	Molecular	ATP-bindi	--
Inf	0	Inf	Significant up		1	Molecular	RalBP1-ass	--
0.655185	0.205992	-0.61003	Nonsignifi	None	1	Cellular Cc	tetraspanir	--
0.320302	0.024763	-1.64249	Nonsignifi	None	--	--	--	--
0.094684	0.063337	-3.40073	Nonsignifi	None	1	Molecular	InaD-like p	--
Inf	0	Inf	Significant up		2	Biological	vang-like	--
Inf	0	Inf	Significant up	--		--	nuclear pr	--
0.984876	0.969878	-0.02199	Nonsignifi	None	--	--	erythrocyte	--
0.242992	0.020394	-2.04102	Significant down		1	Biological	solute carr	--
0.284494	0.332105	-1.81353	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--

Inf	0	Inf	Significant up		4	Molecular	ubiquitin-a	6.2.1.45
Inf	0	Inf	Significant up		2	Molecular	1-phospha	2.7.1.149
Inf	0	Inf	Significant up		2	Molecular	signal pep	3.4.23.-
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	NIMA (nev	2.7.11.1
Inf	0	Inf	Significant up		3	Cellular Co	--	--
Inf	0	Inf	Significant up		3	Molecular	F-actin mo	1.14.13.225
Inf	0	Inf	Significant up		3	Molecular	U3 small n	--
Inf	0	Inf	Significant up		3	Molecular	importin-4	--
Inf	0	Inf	Significant up	--	--	--	nucleolar c	--
Inf	0	Inf	Significant up		1	Cellular Co	scavenger	--
0.155886	0.000257	-2.68143	Significant down	--	--	--	cell migrat	3.2.1.35
1.769559	0.060684	0.82339	Nonsignifi	None	1	Molecular	programm	--
Inf	0	Inf	Significant up		3	Molecular	solute carr	--
Inf	0	Inf	Significant up	--	--	--	chromosor	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Biological	sec1 family	--
0.233838	0.00141	-2.09642	Significant down	--	--	--	intelectin	--
0.246328	0.387077	-2.02135	Nonsignifi	None	--	--	solute carr	--
0.375408	0.045271	-1.41347	Nonsignifi	None	--	--	intelectin	--
0.074197	0.063777	-3.75249	Nonsignifi	None	2	Molecular	ATP-bindi	--
0.353229	0.007638	-1.50132	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	palladin	--
Inf	0	Inf	Significant up	--	--	--	ATR intera	--
#NAME?	0	#NAME?	Significant down	--	--	--	stonin-1/2	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	beta-cater	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Biological	alpha-N-a	2.4.99.-
0.523328	0.024809	-0.93421	Nonsignifi	None	3	Molecular	ATP-depe	3.6.4.13
0.289445	0.284426	-1.78864	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		4	Cellular Co	histone H1	--
Inf	0	Inf	Significant up		3	Biological	solute carr	--
0.420839	0.035636	-1.24866	Nonsignifi	None	1	Cellular Co	transmemb	--
Inf	0	Inf	Significant up	--	--	--	AP-3 comp	--
Inf	0	Inf	Significant up	--	--	--	protein ND	--
Inf	0	Inf	Significant up	--	--	--	heat shock	--
Inf	0	Inf	Significant up	--	--	--	CCR4-NOT	--
0.073485	0.085599	-3.76641	Nonsignifi	None	4	Molecular	myosin XV	--
0.024916	0.13528	-5.3268	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		1	Biological	Rho GTPas	--
0.004367	0.063227	-7.83898	Nonsignifi	None	1	Molecular	peroxidase	1.11.1.7
Inf	0	Inf	Significant up	--	--	--	acidic leuc	--
Inf	0	Inf	Significant up	--	--	--	poliovirus	--
0.006262	0.078023	-7.31917	Nonsignifi	None	4	Biological	HtrA serine	3.4.21.-
Inf	0	Inf	Significant up		1	Molecular	actin relate	--
Inf	0	Inf	Significant up	--	--	--	histone de	3.5.1.98
Inf	0	Inf	Significant up		2	Molecular	signal tran	--
1.762584	0.089998	0.817692	Nonsignifi	None	2	Biological	gamma-gl	3.4.19.9
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	Rho guani	--
0.424234	0.232773	-1.23707	Nonsignifi	None	1	Cellular Co	golgi appa	--
Inf	0	Inf	Significant up		1	Molecular	COP9 sign	3.4.-.-
Inf	0	Inf	Significant up		1	Molecular	SWI/SNF r	--
1.047455	0.834107	0.066888	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Molecular	far upstrea	--
0.430224	0.109566	-1.21684	Nonsignifi	None	3	Molecular	--	--

0.179925	0.243684	-2.47453	Nonsignifi	None		2	Molecular	Rho guani	--
0.536272	0.146859	-0.89896	Nonsignifi	None		2	Biological	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant	up		2	Biological	cullin 5	--
0.532876	0.277686	-0.90813	Nonsignifi	None		3	Biological	--	--
0.285141	0.050449	-1.81025	Nonsignifi	None	--		--	betaine-h	2.1.1.5
Inf	0	Inf	Significant	up		2	Biological	protein tyr	3.1.3.48
Inf	0	Inf	Significant	up		2	Biological	secretory c	--
Inf	0	Inf	Significant	up	--		--	SWI/SNF-r	--
3.467133	0.000186	1.793743	Nonsignifi	None	--		--	immunogl	--
Inf	0	Inf	Significant	up		3	Cellular Co	exocyst co	--
Inf	0	Inf	Significant	up		1	Cellular Co	protein ma	--
Inf	0	Inf	Significant	up	--		--	kindlin 2	--
Inf	0	Inf	Significant	up		1	Molecular	far upstrea	--
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up		1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant	up		2	Molecular	--	--
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up		5	Biological	gamma-tu	--
0.254737	0.036709	-1.97292	Nonsignifi	None		1	Biological	BTB/POZ c	--
0.10581	0.090241	-3.24045	Nonsignifi	None		1	Molecular	--	--
Inf	0	Inf	Significant	up		1	Molecular	Prp8 bindi	--
0.871883	0.551396	-0.19779	Nonsignifi	None		2	Biological	arylsulfatas	3.1.6.-
Inf	0	Inf	Significant	up		1	Molecular	RNA-bindi	--
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up		1	Molecular	--	--
Inf	0	Inf	Significant	up		1	Biological	charged m	--
Inf	0	Inf	Significant	up		2	Biological	--	--
Inf	0	Inf	Significant	up		2	Molecular	ATP-depe	3.6.4.13
1.283239	0.384123	0.35979	Nonsignifi	None		2	Molecular	--	--
0.029587	0.11709	-5.07887	Nonsignifi	None		1	Molecular	far upstrea	--
Inf	0	Inf	Significant	up		2	Biological	mannose-	2.7.7.13
Inf	0	Inf	Significant	up		4	Molecular	carboxype	3.4.17.20
Inf	0	Inf	Significant	up	--		--	--	--
0.329598	0.013666	-1.60122	Nonsignifi	None		4	Molecular	lysyl oxida	1.4.3.-
Inf	0	Inf	Significant	up	--		--	1,5-anhyd	1.1.1.263
Inf	0	Inf	Significant	up	--		--	nascent po	--
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up		2	Biological	cytosolic n	3.4.13.18
Inf	0	Inf	Significant	up	--		--	chloride in	--
Inf	0	Inf	Significant	up		3	Molecular	Arf-GAP w	--
Inf	0	Inf	Significant	up		2	Biological	importin-9	--
0.316874	0.242747	-1.65802	Nonsignifi	None		2	Molecular	peptidogly	--
Inf	0	Inf	Significant	up		2	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant	up	--		--	solute carr	--
Inf	0	Inf	Significant	up	--		--	transcriptio	--
Inf	0	Inf	Significant	up		1	Cellular Co	pannexin 2	--
Inf	0	Inf	Significant	up		1	Cellular Co	pannexin 1	--
Inf	0	Inf	Significant	up		2	Molecular	sorting ne	--
0.482604	0.387518	-1.05109	Nonsignifi	None		3	Molecular	coagulatio	--
Inf	0	Inf	Significant	up		1	Molecular	erbb2-inte	--
0.111972	0.04812	-3.15879	Significant	down		1	Molecular	hemicentir	--
Inf	0	Inf	Significant	up		1	Molecular	--	--
0.165198	0.003522	-2.59773	Significant	down		2	Molecular	hyaluronar	--
Inf	0	Inf	Significant	up		1	Cellular Co	--	--
Inf	0	Inf	Significant	up		1	Molecular	--	--
Inf	0	Inf	Significant	up	--		--	spermatid	--
Inf	0	Inf	Significant	up	--		--	MFS transp	--
Inf	0	Inf	Significant	up	--		--	paired amp	--

Inf	0	Inf	Significant up	--	--	DNA repai	--
0.048117	0.194572	-4.37731	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	1	Molecular	tubulin-fol	--
2.546285	0.00093	1.348394	Nonsignifi	None	3	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant up	2	Molecular	ethanolam	2.7.7.14
Inf	0	Inf	Significant up	--	--	pre-mRNA	--
Inf	0	Inf	Significant up	--	--	26S protea	--
0.913716	0.430579	-0.13018	Nonsignifi	None	--	--	protein DJ	3.5.1.124
Inf	0	Inf	Significant up	--	--	sialidase-1	3.2.1.18
1.649949	0.001486	0.722421	Nonsignifi	None	1	Biological	--	--
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	COP9 sign	--
Inf	0	Inf	Significant up	1	Molecular	calcineurin	--
0.049309	0.014283	-4.342	Significant down	1	Molecular	collagen, t	--
Inf	0	Inf	Significant up	2	Cellular Co	nucleosom	--
Inf	0	Inf	Significant up	--	--	gamma-sc	--
Inf	0	Inf	Significant up	2	Molecular	1-phospha	2.7.1.68
0.723337	0.387809	-0.46726	Nonsignifi	None	1	Cellular Co	transmemb	--
1.363456	0.424707	0.447269	Nonsignifi	None	3	Molecular	solute carr	--
0.691352	0.132982	-0.53251	Nonsignifi	None	2	Molecular	endophilin	--
Inf	0	Inf	Significant up	4	Cellular Co	actin relate	--
Inf	0	Inf	Significant up	2	Molecular	RNA-bindi	--
Inf	0	Inf	Significant up	1	Molecular	ribosome a	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	1	Molecular	methyloso	--
Inf	0	Inf	Significant up	--	--	kindlin 1	--
Inf	0	Inf	Significant up	1	Molecular	coronin-1B	--
0.337662	0.291748	-1.56635	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up	1	Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significant up	1	Biological	endoplasm	--
0.730226	0.582944	-0.45359	Nonsignifi	None	2	Molecular	--	--
Inf	0	Inf	Significant up	--	--	Kip1 ubiqu	--
Inf	0	Inf	Significant up	2	Biological	--	--
Inf	0	Inf	Significant up	1	Molecular	COP9 sign	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	acidic leuc	--
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	1	Molecular	phosphatic	2.7.1.67
Inf	0	Inf	Significant up	--	--	tubulin-sp	--
Inf	0	Inf	Significant up	2	Molecular	alpha-L-fu	3.2.1.51
0.251103	0.099023	-1.99365	Nonsignifi	None	1	Molecular	tubulin bet	--
Inf	0	Inf	Significant up	1	Molecular	heterogen	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	programm	--
Inf	0	Inf	Significant up	2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up	2	Molecular	E3 ubiquiti	2.3.2.27
0.413659	0.147905	-1.27348	Nonsignifi	None	1	Molecular	tubulin bet	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	2	Biological	--	--
Inf	0	Inf	Significant up	2	Biological	p24 family	--
Inf	0	Inf	Significant up	--	--	nucleopori	--
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	oxysterol-I	--
Inf	0	Inf	Significant up	2	Biological	N-acetylne	4.1.3.3
Inf	0	Inf	Significant up	1	Molecular	Rab11 fam	--
Inf	0	Inf	Significant up	--	--	TBC1 dom	--

Inf	0	Inf	Significant up		1	Molecular	N-alpha-a	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	translation	--
Inf	0	Inf	Significant up	--	--	--	cell adhesi	--
#NAME?	0	#NAME?	Significant down	--	--	--	angiopoiet	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	dedicator (	--
Inf	0	Inf	Significant up		1	Molecular	nucleolar (	--
Inf	0	Inf	Significant up		1	Molecular	tether cont	--
Inf	0	Inf	Significant up	--	--	--	oxysterol-I	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Molecular	transducin	--
1.018429	0.946045	0.026345	Nonsignifi	None	4	Molecular	protein kin	2.7.11.13
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	uridine kin	2.7.1.48
0.016398	0.187169	-5.93035	Nonsignifi	None	3	Molecular	KRAB dom	--
Inf	0	Inf	Significant up		2	Molecular	polyadeny	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Cellular Co	--	--
0.244517	0.059137	-2.03199	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		4	Molecular	STE20-like	2.7.11.1
Inf	0	Inf	Significant up	--	--	--	solute carr	--
Inf	0	Inf	Significant up		3	Molecular	thousand a	2.7.11.1
Inf	0	Inf	Significant up		4	Molecular	inorganic p	3.6.1.1
Inf	0	Inf	Significant up		2	Molecular	vitellogeni	3.4.16.-
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	tyrosine-p	3.1.3.48
Inf	0	Inf	Significant up		1	Molecular	protein un	--
Inf	0	Inf	Significant up		1	Biological	charged m	--
Inf	0	Inf	Significant up		2	Molecular	aminopept	3.4.11.6
0.388968	0.220015	-1.36228	Nonsignifi	None	1	Molecular	tubulin bet	--
0.075942	0.000344	-3.71895	Significant down	--	--	--	U3 small n	--
0.66015	0.133978	-0.59913	Nonsignifi	None	1	Molecular	adipocyte-	--
Inf	0	Inf	Significant up		2	Molecular	anthrax to	--
Inf	0	Inf	Significant up	--	--	--	ribosome p	--
Inf	0	Inf	Significant up		1	Molecular	Function:protein bindi	
Inf	0	Inf	Significant up		1	Cellular Co	ESCRT-I co	--
Inf	0	Inf	Significant up	--	--	--	ubiquitin-(	2.3.2.23
0.496948	0.228462	-1.00883	Nonsignifi	None	1	Molecular	tubulin alp	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	ESCRT-I co	--
Inf	0	Inf	Significant up		1	Molecular	COP9 sign	--
Inf	0	Inf	Significant up		3	Molecular	elongator	2.3.1.48
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	--	--
0.46809	0.271551	-1.09514	Nonsignifi	None	1	Molecular	guanine nu	--
Inf	0	Inf	Significant up	--	--	--	exportin-5	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	serine carb	3.4.16.-
Inf	0	Inf	Significant up	--	--	--	calcyclin bi	--
0.923538	0.76267	-0.11476	Nonsignifi	None	1	Molecular	parvin	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	helicase M	3.6.4.13
Inf	0	Inf	Significant up		1	Cellular Co	transmemb	--
Inf	0	Inf	Significant up		2	Molecular	resistin	--

0.090836	0.011321	-3.46059	Significant down		2	Biological	adipocyte	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
0.47535	0.108379	-1.07294	Nonsignifi	None	--	--	vacuolar p	--
Inf	0	Inf	Significant up	--		--	exosome c	--
0.889914	0.891242	-0.16826	Nonsignifi	None		3	Molecular	protocadh --
Inf	0	Inf	Significant up		3	Molecular	myo-inosi	5.5.1.4
0.202397	0.023534	-2.30474	Significant down		2	Molecular	interleukin	--
Inf	0	Inf	Significant up	--		--	--	--
0.83937	0.079678	-0.25262	Nonsignifi	None	--	--	reticulon-4	--
12.54926	0.031679	3.64953	Significant up		2	Molecular	Xaa-Pro a	3.4.11.9
1.57349	0.057739	0.653968	Nonsignifi	None		1	Molecular	Xaa-Pro a	3.4.11.9
Inf	0	Inf	Significant up	--		--	integral m	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	acetyl-CoA	6.2.1.1
0.002603	0.026025	-8.5855	Significant down		5	Molecular	ATP-depe	3.6.4.13
0.894544	0.648431	-0.16078	Nonsignifi	None		1	Molecular	GTP-bindi	3.6.5.-
Inf	0	Inf	Significant up		2	Biological	translation	--
Inf	0	Inf	Significant up		2	Molecular	platelet de	--
Inf	0	Inf	Significant up		2	Cellular Co	MFS transp	--
Inf	0	Inf	Significant up	--		--	DNA polyr	2.7.7.7
Inf	0	Inf	Significant up	--		--	chromatin	--
0.149256	0.001044	-2.74414	Significant down	--		--	--	--
Inf	0	Inf	Significant up		2	Molecular	4'-phosph	2.7.8.-
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		2	Biological	vacuolar p	--
0.047363	0.283114	-4.40009	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		5	Molecular	phenylalar	6.1.1.20
Inf	0	Inf	Significant up	--		--	ubiquitin-l	--
Inf	0	Inf	Significant up	--		--	sister chro	--
Inf	0	Inf	Significant up		4	Molecular	structural r	--
Inf	0	Inf	Significant up		1	Molecular	obg-like A	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		1	Molecular	protein lin	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		1	Cellular Co	--	--
Inf	0	Inf	Significant up		1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant up	--		--	dipeptidyl	3.4.14.4
Inf	0	Inf	Significant up		1	Cellular Co	--	--
Inf	0	Inf	Significant up		3	Biological	N-acetylla	2.4.1.149
Inf	0	Inf	Significant up		2	Molecular	abl interac	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		4	Cellular Co	--	--
Inf	0	Inf	Significant up	--		--	hsp70-inte	--
Inf	0	Inf	Significant up	--		--	S-adenosy	2.5.1.6
1.482122	0.058281	0.567664	Nonsignifi	None		1	Molecular	EH domair	--
#NAME?	0	#NAME?	Significant down		2	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	low-densit	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Biological	charged m	--
Inf	0	Inf	Significant up		1	Molecular	histone H2	--
Inf	0	Inf	Significant up		1	Molecular	SH3 doma	--
Inf	0	Inf	Significant up		1	Molecular	septin 10	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up	--		--	--	--

0.279413	0.432406	-1.83953	Nonsignifi	None		2	Molecular	--	--
Inf	0	Inf	Significant	up		2	Biological	--	--
Inf	0	Inf	Significant	up	--		--	protein BC	--
Inf	0	Inf	Significant	up		3	Molecular	serine/thre	2.7.11.1
1.364051	0.115429	0.447898	Nonsignifi	None	--		--	prostaglan	--
0.399318	0.004969	-1.32439	Nonsignifi	None	--		--	--	--
Inf	0	Inf	Significant	up		4	Molecular	leucyl-tRN	6.1.1.4
Inf	0	Inf	Significant	up		1	Molecular	epidermal	--
0.358375	0.196067	-1.48046	Nonsignifi	None		5	Molecular	coatomer s	--
0.250509	0.031299	-1.99707	Nonsignifi	None	--		--	mannose r	--
Inf	0	Inf	Significant	up		1	Cellular Co	--	--
Inf	0	Inf	Significant	up	--		--	vacuolar p	--
Inf	0	Inf	Significant	up	--		--	translation	--
0.073656	0.070967	-3.76305	Nonsignifi	None		2	Biological	cathepsin X	3.4.18.1
Inf	0	Inf	Significant	up		1	Molecular	ubiquitin-l	6.2.1.45
1.110057	0.788759	0.150634	Nonsignifi	None		1	Molecular	--	--
Inf	0	Inf	Significant	up		1	Molecular	COP9 sign	--
0.749982	0.145338	-0.41507	Nonsignifi	None		1	Molecular	tight juncti	--
Inf	0	Inf	Significant	up	--		--	DnaJ homo	--
Inf	0	Inf	Significant	up		4	Molecular	solute carr	--
Inf	0	Inf	Significant	up		1	Molecular	--	--
Inf	0	Inf	Significant	up	--		--	5'-AMP-ac	--
0.222092	0.004001	-2.17077	Significant	down		2	Molecular	deleted in	--
Inf	0	Inf	Significant	up		1	Biological	ragulator c	--
Inf	0	Inf	Significant	up		4	Molecular	signal recc	--
Inf	0	Inf	Significant	up	--		--	cysteine ar	--
1.965293	0.027832	0.974745	Nonsignifi	None		1	Molecular	septin 3/9/	--
Inf	0	Inf	Significant	up		2	Biological	--	--
#NAME?	0	#NAME?	Significant	down		3	Molecular	a disintegr	3.4.24.-
Inf	0	Inf	Significant	up		3	Biological	prefoldin s	--
Inf	0	Inf	Significant	up		2	Molecular	nuclear rec	--
Inf	0	Inf	Significant	up	--		--	enolase-pl	3.1.3.77
Inf	0	Inf	Significant	up		1	Biological	V-type H+	--
Inf	0	Inf	Significant	up		2	Biological	exportin-7	--
0.073174	0.111216	-3.77252	Nonsignifi	None	--		--	vacuolar p	--
Inf	0	Inf	Significant	up		3	Molecular	death-assc	2.7.11.1
Inf	0	Inf	Significant	up		2	Molecular	cystinyl am	3.4.11.3
Inf	0	Inf	Significant	up		2	Molecular	plexin A	--
Inf	0	Inf	Significant	up		3	Molecular	drebrin-lik	--
Inf	0	Inf	Significant	up	--		--	ESCRT-I cc	--
0.335931	0.009368	-1.57376	Nonsignifi	None	--		--	serpin pep	--
Inf	0	Inf	Significant	up		2	Cellular Co	mRNA turr	--
Inf	0	Inf	Significant	up		3	Molecular	TRAF2 and	2.7.11.1
Inf	0	Inf	Significant	up	--		--	cleavage a	3.1.27.-
Inf	0	Inf	Significant	up		1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	--		--	general tra	2.3.1.48
Inf	0	Inf	Significant	up		1	Molecular	protein kin	--
Inf	0	Inf	Significant	up	--		--	apoptotic	--
Inf	0	Inf	Significant	up	--		--	--	--
Inf	0	Inf	Significant	up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		1	Cellular Co	proteasom	--
Inf	0	Inf	Significant	up		3	Molecular	aspartyl an	3.4.11.21
Inf	0	Inf	Significant	up		4	Cellular Co	solute carr	--
Inf	0	Inf	Significant	up		1	Molecular	coronin-1E	--
0.249179	0.295271	-2.00475	Nonsignifi	None		6	Molecular	Notch 3	--
Inf	0	Inf	Significant	up		3	Molecular	pre-mRNA	2.3.2.27
1.52309	0.026314	0.607001	Nonsignifi	None		1	Molecular	vacuolar p	--
Inf	0	Inf	Significant	up		3	Cellular Co	sodium/po	--

Inf	0	Inf	Significant	up	3	Molecular	protocadh	--
Inf	0	Inf	Significant	up	3	Molecular	--	--
Inf	0	Inf	Significant	up	1	Molecular	protein kin	--
Inf	0	Inf	Significant	up	1	Molecular	sorting ne	--
Inf	0	Inf	Significant	up	3	Molecular	secretory p	3.1.1.4
1.224116	0.121693	0.29174	Nonsignifi	None	1	Molecular	26S protea	--
Inf	0	Inf	Significant	up	1	Molecular	FAS-assoc	--
0.795974	0.136542	-0.32921	Nonsignifi	None	4	Biological	peptidyl-p	5.2.1.8
Inf	0	Inf	Significant	up	1	Molecular	COP9 sign	--
Inf	0	Inf	Significant	up	--	--	serine/thre	--
Inf	0	Inf	Significant	up	2	Cellular Co	exocyst co	--
Inf	0	Inf	Significant	up	2	Biological	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant	up	5	Molecular	endoribon	3.1.26.-
Inf	0	Inf	Significant	up	3	Biological	solute carr	--
0.629326	0.146223	-0.66812	Nonsignifi	None	2	Molecular	dynamin G	3.6.5.5
3.263175	0.041314	1.706276	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant	up	2	Molecular	BAI1-asso	--
Inf	0	Inf	Significant	up	4	Molecular	structural r	--
Inf	0	Inf	Significant	up	--	--	--	--
0.00563	0.227919	-7.4727	Nonsignifi	None	2	Molecular	RuvB-like p	3.6.4.12
0.111755	0.218403	-3.16158	Nonsignifi	None	--	--	C-type lec	--
4.428779	0.005252	2.146909	Significant	up	3	Molecular	translation	--
0.599649	0.425903	-0.73781	Nonsignifi	None	2	Molecular	RuvB-like p	--
Inf	0	Inf	Significant	up	--	--	--	--
0.507098	0.075172	-0.97966	Nonsignifi	None	2	Molecular	cofilin	--
Inf	0	Inf	Significant	up	--	--	integral me	--
Inf	0	Inf	Significant	up	1	Molecular	--	--
1.153772	0.117217	0.206358	Nonsignifi	None	--	--	NCK-asso	--
0.024959	0.235342	-5.32428	Nonsignifi	None	5	Molecular	erythrocyte	--
Inf	0	Inf	Significant	up	--	--	exosome c	3.1.13.-
Inf	0	Inf	Significant	up	1	Molecular	--	--
Inf	0	Inf	Significant	up	--	--	thyroid ho	--
Inf	0	Inf	Significant	up	1	Biological	WW doma	--
#NAME?	0	#NAME?	Significant	down	1	Molecular	G protein-	--
Inf	0	Inf	Significant	up	--	--	suppressor	--
Inf	0	Inf	Significant	up	--	--	MEMO1 fa	--
Inf	0	Inf	Significant	up	2	Molecular	endophilin	--
Inf	0	Inf	Significant	up	3	Molecular	RNA-bindi	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Biological	ribosome r	--
Inf	0	Inf	Significant	up	2	Biological	p24 family	--
Inf	0	Inf	Significant	up	--	--	mitochonc	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up	1	Biological	charged m	--
Inf	0	Inf	Significant	up	1	Molecular	serine-thre	--
Inf	0	Inf	Significant	up	2	Biological	tRNA-splic	6.5.1.3
Inf	0	Inf	Significant	up	1	Molecular	F-box prot	--
0.772703	0.511908	-0.37201	Nonsignifi	None	4	Molecular	large subu	--
Inf	0	Inf	Significant	up	1	Molecular	elongation	--
Inf	0	Inf	Significant	up	2	Molecular	V-type H+	--
0.779958	0.237728	-0.35853	Nonsignifi	None	5	Cellular Co	talin	--
Inf	0	Inf	Significant	up	--	--	HIV-1 Vpr	--
Inf	0	Inf	Significant	up	3	Molecular	ubiquitin c	3.4.19.12
0.087608	0.009385	-3.51279	Significant	down	4	Molecular	lysyl oxida	1.4.3.-
Inf	0	Inf	Significant	up	--	--	hypoxia up	--
Inf	0	Inf	Significant	up	--	--	ariadne-1	2.3.2.27
Inf	0	Inf	Significant	up	--	--	heat shock	--
Inf	0	Inf	Significant	up	--	--	protein ph	3.1.1.89

Inf	0	Inf	Significant up		3	Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up		1	Molecular	CD2-assoc	--
Inf	0	Inf	Significant up	--		--	transportir	--
Inf	0	Inf	Significant up		5	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up		1	Molecular	RNA-bindi	--
0.281408	0.000247	-1.82926	Nonsignifi	None	2	Molecular	sorting ne	--
Inf	0	Inf	Significant up		1	Molecular	sorting ne	--
Inf	0	Inf	Significant up		1	Molecular	endothelia	3.1.1.3
Inf	0	Inf	Significant up		2	Cellular Co	MFS transp	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up	--		--	phosphose	2.6.1.52
0.531352	0.333695	-0.91226	Nonsignifi	None	3	Cellular Co	glypican 6	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up		5	Molecular	coatomer s	--
0.73986	0.692964	-0.43468	Nonsignifi	None	--	--	chloride in	--
0.270382	0.085261	-1.88693	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	brefeldin A	--
Inf	0	Inf	Significant up		3	Molecular	serine/thre	2.7.11.1
0.007569	0.241526	-7.04572	Nonsignifi	None	1	Molecular	--	--
0.533036	0.554698	-0.9077	Nonsignifi	None	--	--	dynein ligh	--
Inf	0	Inf	Significant up		4	Molecular	casein kina	2.7.11.1
Inf	0	Inf	Significant up		4	Biological	solute carr	--
Inf	0	Inf	Significant up		3	Biological	solute carr	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up	--		--	gelsolin	--
Inf	0	Inf	Significant up		1	Molecular	WAS prote	--

KEGG_ko	COG_Func	COG_Func	COG_Class	IPR_Term	
ko04144	E	--	--	--	IPR021854	[WASH1, WAHD domain]
--	--	--	--	--	IPR013106	[Immunoglobulin V-set domain]
--	WD40 repe	R	General fu	IPR001680	[WD40 repeat]
--	--	--	--	IPR004241	[Autophagy protein Atg8 ubiquitin-like]
--	Periplasmi	O	Posttransla	IPR001478	[PDZ domain]
ko03040	S	Small nucl	K	Transcripti	IPR001163	[LSM domain, eukaryotic/archaea-type]
ko04151	P	Autotransp	UW	Intracellula	IPR002035	[von Willebrand factor, type A] ; IPR008160[
--	--	--	--	--	--
ko04610	C	Secreted tr	O	Posttransla	IPR000436	[Sushi/SCR/CCP domain] ; IPR001254[Serine
ko03013	R	--	--	--	IPR000717	[Proteasome component (PCI) domain] ; IPF
--	--	--	--	IPR003597	[Immunoglobulin C1-set]
--	--	--	--	--
ko05132	S	Tfp pilus a	NW	Cell motilit	IPR011990	[Tetratricopeptide-like helical domain] ; IPR
--	--	--	--	IPR004240	[Nonaspanin (TM9SF)] ; IPR005024[Snf7 fam
--	WD40 repe	R	General fu	IPR001680	[WD40 repeat] ; IPR006708[Pex19 protein]
	--	--	--	IPR001619	[Sec1-like protein]
--	Sterol desa	I	Lipid trans	IPR000608	[Ubiquitin-conjugating enzyme E2] ; IPR019
--	--	--	--	IPR001752	[Kinesin motor domain]
--	--	--	--	IPR001478	[PDZ domain] ; IPR001781[Zinc finger, LIM-
ko00062	F	Acyl-CoA	I	Lipid trans	IPR006683	[Thioesterase domain]
--	--	--	--	IPR000048	[IQ motif, EF-hand binding site] ; IPR001609
ko04130	S	--	--	--	IPR000928	[SNAP-25]
--	--	--	--	IPR001619	[Sec1-like protein]
ko04610	C	Secreted tr	O	Posttransla	IPR000436	[Sushi/SCR/CCP domain] ; IPR000859[CUB d
--	--	--	--	IPR028124	[Small acidic protein-like domain]
ko04142	L	--	--	--	IPR002553	[Clathrin/coatomer adaptor, adaptin-like, N
ko03050	P	--	--	--	IPR000717	[Proteasome component (PCI) domain]
--	Transcripti	K	Transcripti	IPR005100	[Transcription elongation factor Spt5, NGN
--	Glutathion	O	Posttransla	IPR004045	[Glutathione S-transferase, N-terminal]
ko03013	R	--	--	--	IPR000555	[JAB1/MPN/MOV34 metalloenzyme domain
--	Secreted p	R	General fu	IPR001881	[EGF-like calcium-binding domain] ; IPR002
--	--	--	--	IPR013766	[Thioredoxin domain] ; IPR017905[ERV/ALR
ko04062	C	Acyl transf	Q	Secondary	IPR000095	[CRIB domain] ; IPR000697[WH1/EVH1 dom
--	--	--	--	IPR000357	[HEAT repeat]
ko04512	E	--	--	--	IPR000082	[SEA domain] ; IPR000742[EGF-like domain]
ko00310	L	Glycosyltra	M	Cell wall/m	IPR005123	[Oxoglutarate/iron-dependent dioxygenase
ko03050	P	Proteasom	O	Posttransla	IPR000555	[JAB1/MPN/MOV34 metalloenzyme domain
ko04144	E	--	--	--	IPR001452	[SH3 domain] ; IPR004148[BAR domain]
--	--	--	--	IPR000225	[Armadillo] ; IPR002652[Importin-alpha, imp
--	--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
--	--	--	--	IPR001478	[PDZ domain]
ko03008	R	RNA proce	J	Translatior	IPR002687	[Nop domain] ; IPR012974[NOP5, N-termin
--	--	--	--	IPR013836	[CD34/Podocalyxin]
--	--	--	--	IPR000867	[Insulin-like growth factor-binding protein,
ko00511	C	Alpha-man	G	Carbohydr	IPR000602	[Glycoside hydrolase family 38, N-terminal d
ko00750	V	Pyridoxal/p	H	Coenzyme	IPR013749	[Pyridoxamine kinase/Phosphomethylpyrim
ko05225	H	--	--	--	IPR001606	[ARID DNA-binding domain] ; IPR033388[S
--	Negative r	O	Posttransla	IPR013766	[Thioredoxin domain]
--	--	--	--	--
--	ATP-depe	O	Posttransla	IPR010448	[Torsin]
ko05010	A	--	--	--	IPR001762	[Disintegrin domain] ; IPR002870[Peptidase
ko03013	R	Predicted I	R	General fu	IPR025799	[Protein arginine N-methyltransferase]
ko04530	T	Periplasmi	O	Posttransla	IPR001478	[PDZ domain] ; IPR015098[EBP50, C-termin
ko04360	A	Phage-rela	X	Mobilome:	IPR000421	[Coagulation factor 5/8 C-terminal domain]
--	--	--	--	IPR001494	[Importin-beta, N-terminal domain]
--	--	--	--	IPR018499	[Tetraspanin/Peripherin]
ko03050	P	20S protea	O	Posttransla	IPR000426	[Proteasome alpha-subunit, N-terminal dor

--	--	--	--	IPR001478	[PDZ domain]
--	--	--	--	IPR001478	[PDZ domain] ; IPR014775[L27 domain, C-te
ko05034 A	--	--	--	IPR019467	[Histone acetyl transferase HAT1 N-termina
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001478[PDZ do
ko04510 F	Ca2+-binc	T	Signal tran	IPR002048	[EF-hand domain] ; IPR015070[DJBP, EF-ha
ko04144 E	--	--	--	IPR000306	[FYVE zinc finger] ; IPR002014[VHS domain]
ko04022 c	Chromoso	D	Cell cycle c	IPR020683	[Ankyrin repeat-containing domain] ; IPR03
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR014020[Tensin
--	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
ko03008 R	--	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
ko04360 A	DNA-bind	R	General fu	IPR001627	[Sema domain] ; IPR002165[Plexin repeat] ;
ko03040 S	RNA recog	J	Translatior	IPR000061	[SWAP/Surp] ; IPR000504[RNA recognition
ko00230 P	Phosphorib	F	Nucleotide	IPR010918	[AIR synthase-related protein, C-terminal d
ko04142 L	Predicted e	R	General fu	IPR000731	[Sterol-sensing domain] ; IPR003392[Protein
ko04144 E	--	--	--	IPR007188	[Actin-related protein 2/3 complex subunit
ko04144 E	--	--	--	IPR007204	[Actin-related protein 2/3 complex subunit
--	Uncharacte	S	Function u	IPR005552	[Scramblase]
--	Prefoldin, c	O	Posttransla	IPR002777	[Prefoldin beta-like]
ko01100 M	Uncharacte	S	Function u	IPR000034	[Laminin IV] ; IPR001791[Laminin G domain]
--	Uncharacte	S	Function u	IPR002995	[Surfeit locus 4]
ko00051 F	Hydroxym	HR	Coenzyme	IPR005002	[Phosphomannomutase]
--	--	--	--	IPR009071	[High mobility group box domain]
--	Serine/thre	T	Signal tran	IPR001932	[PPM-type phosphatase domain]
--	--	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
ko04130 S	--	--	--	IPR000727	[Target SNARE coiled-coil homology doma
ko05230 C	Predicted a	G	Carbohydr	IPR011701	[Major facilitator superfamily]
ko01524 P	--	--	--	IPR007274	[Ctr copper transporter]
ko00330 A	Proline 4-h	JO	Translatior	IPR005123	[Oxoglutarate/iron-dependent dioxygenase
ko04130 S	--	--	--	IPR001388	[Synaptobrevin] ; IPR010908[Longin domair
ko04144 E	--	--	--	IPR006789	[Actin-related protein 2/3 complex subunit
ko04144 E	Ankyrin rep	T	Signal tran	IPR001164	[Arf GTPase activating protein] ; IPR001452[
--	Cytochrom	CI	Energy prc	IPR001199	[Cytochrome b5-like heme/steroid binding
ko03040 S	WD40 repe	R	General fu	IPR001680	[WD40 repeat] ; IPR014906[Pre-mRNA proc
ko00260 G	Phosphogl	HR	Coenzyme	IPR006139	[D-isomer specific 2-hydroxyacid dehydrog
ko04145 P	--	--	--	IPR022780	[Dynein family light intermediate chain]
ko03050 P	--	--	--	IPR000717	[Proteasome component (PCI) domain] ; IPF
ko00230 P	ATP sulfury	P	Inorganic i	IPR024951	[Sulphate adenylyltransferase catalytic dom
--	--	--	--	IPR009361	[RZZ complex, subunit Zw10]
ko00512 M	Glycosyltra	G	Carbohydr	IPR027791	[Galactosyltransferase, C-terminal] ; IPR027
--	--	--	--	IPR001781	[Zinc finger, LIM-type]
--	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
--	--	--	--	IPR007327	[Tumour protein D52]
ko00052 G	Alpha-glu	G	Carbohydr	IPR000322	[Glycoside hydrolase family 31] ; IPR000519
ko00980 M	Predicted e	R	General fu	IPR023210	[NADP-dependent oxidoreductase domain]
--	--	--	--	IPR007477	[SAB domain] ; IPR008379[Band 4.1, C-term
ko04150 m	--	--	--	IPR024135	[Ragulator complex protein LAMTOR5]
ko00515 M	--	--	--	--	--
ko03013 R	--	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
--	--	--	--	IPR007194	[Transport protein particle (TRAPP) compor
ko04144 E	--	--	--	IPR005024	[Snf7 family]
--	--	--	--	IPR018499	[Tetraspanin/Peripherin]
--	--	--	--	--	--
--	Anion-tran	P	Inorganic i	IPR025723	[Anion-transporting ATPase-like domain]
ko04110 C	Predicted	IT	Signal tran	IPR001680	[WD40 repeat]
ko04072 P	Guanine-n	R	General fu	IPR000904	[Sec7 domain] ; IPR001849[Pleckstrin homo
ko04142 L	--	--	--	IPR002553	[Clathrin/coatomer adaptor, adaptin-like, N
--	Tetratricop	R	General fu	IPR001440	[Tetratricopeptide repeat 1] ; IPR019734[Tet
--	--	--	--	IPR000048	[IQ motif, EF-hand binding site] ; IPR00160

ko03015 m	--	--	--	IPR016706	[Cleavage/polyadenylation specificity factor
--	Lantibiotic	V	Defense m	IPR007822	[Lanthionine synthetase C-like]
--	Secreted/p	O	Posttransla	IPR007863	[Peptidase M16, C-terminal] ; IPR011765[Pe
--	Ca2+-binc	T	Signal tran	IPR002048	[EF-hand domain]
--	--	--	--	IPR000421	[Coagulation factor 5/8 C-terminal domain]
ko00270 C	S-adenosy	H	Coenzyme	IPR000043	[Adenosylhomocysteinase] ; IPR015878[S-a
ko04110 C	--	--	--	IPR006909	[Rad21/Rec8-like protein, C-terminal, eukar
ko03040 S	HrpA-like	J	Translatior	IPR001650	[Helicase, C-terminal] ; IPR007502[Helicase-
--	Uncharacte	S	Function u	IPR000330	[SNF2-related, N-terminal domain] ; IPR001
--	--	--	--	IPR019143	[JNK/Rab-associated protein-1, N-terminal
ko04120 U	--	--	--	--	
--	Monoamir	E	Amino aci	IPR002937	[Amine oxidase] ; IPR007526[SWIRM domai
ko00230 P	Nucleoside	F	Nucleotide	IPR001564	[Nucleoside diphosphate kinase]
--	Regulatory	O	Posttransla	IPR000421	[Coagulation factor 5/8 C-terminal domain]
ko00061 F	Long-chai	I	Lipid trans	IPR000873	[AMP-dependent synthetase/ligase]
ko04144 E	--	--	--	IPR001683	[Phox homologous domain]
ko04931 Ir	N-acetyl-b	G	Carbohydr	IPR011496	[Beta-N-acetylglucosaminidase]
--	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
ko00533 G	Glycosyltra	G	Carbohydr	IPR027791	[Galactosyltransferase, C-terminal] ; IPR027
ko00051 F	GDP-D-m	M	Cell wall/m	IPR016040	[NAD(P)-binding domain]
--	--	--	--	IPR004133	[DAN]
ko00310 L	Glycosyltra	M	Cell wall/m	IPR005123	[Oxoglutarate/iron-dependent dioxygenase
ko04510 F	Transcripti	K	Transcripti	IPR009408	[Formin Homology 1] ; IPR010465[DRF auto
--	Predicted a	G	Carbohydr	IPR011701	[Major facilitator superfamily]
--	--	--	--	IPR000225	[Armadillo] ; IPR002652[Importin-alpha, imp
--	Outer men	M	Cell wall/m	IPR000436	[Sushi/SCR/CCP domain] ; IPR003410[HYR c
ko04015 R	--	--	--	IPR000225	[Armadillo]
ko04144 E	--	--	--	IPR001683	[Phox homologous domain] ; IPR005329[So
--	--	--	--	IPR006953	[Vesicle tethering protein Uso1/P115-like , I
ko04977 V	--	--	--	IPR002666	[Reduced folate carrier]
--	--	--	--	IPR002014	[VHS domain] ; IPR004152[GAT domain]
ko05034 A	--	--	--	IPR007125	[Histone H2A/H2B/H3]
ko03008 R	Glutamate	E	Amino aci	IPR002478	[PUA domain] ; IPR002501[Pseudouridine sy
ko03013 R	Translatior	J	Translatior	IPR004161	[Translation elongation factor EFTu-like, do
ko04141 P	DnaJ-class	O	Posttransla	IPR001305	[Heat shock protein DnaJ, cysteine-rich don
--	Uncharacte	P	Inorganic i	IPR004323	[Divalent ion tolerance protein, CutA]
ko04360 A	--	--	--	IPR000198	[Rho GTPase-activating protein domain] ; IP
--	--	--	--	IPR013106	[Immunoglobulin V-set domain]
--	Predicted	T	Signal tran	IPR001680	[WD40 repeat]
ko04150 m	--	--	--	IPR000539	[Frizzled protein] ; IPR020067[Frizzled doma
ko04022 c	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR015008[Rho bi
ko04514 C	--	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
--	Tetratricop	R	General fu	IPR025697	[CLU domain] ; IPR028275[Clustered mitoch
--	DnaJ-class	O	Posttransla	IPR001623	[DnaJ domain] ; IPR025640[Domain of unkn
--	--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
--	Ca2+-binc	T	Signal tran	IPR002048	[EF-hand domain]
ko04144 E	AAA+-typ	MDT	Cell wall/m	IPR003959	[ATPase, AAA-type, core] ; IPR007330[MIT]
ko04217 N	O-acetyl-A	J	Translatior	IPR002589	[Macro domain] ; IPR007125[Histone H2A/H
ko04010 M	Uncharacte	S	Function u	IPR001715	[Calponin homology domain] ; IPR017868[F
--	DNA-bind	R	General fu	IPR000315	[B-box-type zinc finger] ; IPR001258[NHL re
ko00020 C	Citrate syn	C	Energy prc	IPR002020	[Citrate synthase]
ko03040 S	--	--	--	IPR001202	[WW domain] ; IPR002713[FF domain]
ko04144 E	--	--	--	IPR028934	[Vacuolar protein sorting protein 26 related
--	--	--	--	IPR000313	[PWWP domain] ; IPR021567[Lens epitheliu
ko04310 W	--	--	--	IPR001863	[Glypican]
ko03040 S	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
--	--	--	--	IPR004122	[Barrier- to-autointegration factor, BAF]
ko03040 S	--	--	--	IPR015016	[Splicing factor 3B subunit 1]

--	--	--	--	IPR002059	[Cold-shock protein, DNA-binding] ; IPR02
ko03040	S	Replicative	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR004179[Sec63 do
--	--	--	--	IPR002014	[VHS domain] ; IPR004152[GAT domain]
--	--	--	--	IPR012945	[Tubulin binding cofactor C-like domain]
--	--	--	--	--	
ko03013	R	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR02467
ko03013	R	--	--	--	IPR013906 [Eukaryotic translation initiation factor 3 sub
--		Ankyrin rep	T	Signal tran	IPR002110 [Ankyrin repeat] ; IPR020683[Ankyrin repeat
ko00020	C	Isocitrate c	C	Energy prc	IPR024084 [Isopropylmalate dehydrogenase-like doma
ko00670	C	Acyl-CoA	C	Energy prc	IPR002376 [Formyl transferase, N-terminal] ; IPR00579
--	--	--	--	IPR004895	[Prenylated rab acceptor PRA1]
--	--	--	--	IPR018499	[Tetraspanin/Peripherin]
--		Glutaredox	O	Posttransla	IPR002109 [Glutaredoxin] ; IPR013766[Thioredoxin don
--	--	--	--	IPR028364	[Ribosomal protein L1/ribosomal biogenesis
--	--	--	--	IPR004978	[Stanniocalcin]
ko03060	P	Tetratricop	R	General fu	IPR013699 [Signal recognition particle, SRP72 subunit,
--		N-Dimethy	E	Amino acic	--
ko04914	P	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR022165[Polo ki
--		Magnesiur	P	Inorganic i	IPR008250 [P-type ATPase, A domain] ; IPR032630[P-
--	--	--	--	IPR025481	[Cell morphogenesis protein C-terminal] ; IP
ko04144	E	--	--	--	IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
--	--	--	--	IPR002126	[Cadherin]
--		V8-like Glu	E	Amino acic	IPR001254 [Serine proteases, trypsin domain]
--	--	--	--	IPR000504	[RNA recognition motif domain] ; IPR00690
ko04120	U	--	--	--	IPR003613 [U box domain] ; IPR019474[Ubiquitin conju
--	--	--	--	IPR006849	[Elongator complex subunit Iki3]
ko05010	A	--	--	--	IPR003388 [Reticulon]
ko04144	E	--	--	--	IPR001683 [Phox homologous domain]
ko04130	S	--	--	--	--
ko04979	C	--	--	--	IPR000535 [Major sperm protein (MSP) domain]
ko04514	C	--	--	--	IPR013106 [Immunoglobulin V-set domain]
ko00030	P	6-phospho	G	Carbohydr	IPR006148 [Glucosamine/galactosamine-6-phosphate
ko00230	P	ATP sulfury	P	Inorganic i	IPR024951 [Sulphate adenylyltransferase catalytic dom
		Chromoso	D	Cell cycle c	IPR003395 [RecF/RecN/SMC, N-terminal] ; IPR010935[
ko00564	G	Predicted e	R	General fu	IPR003140 [Phospholipase/carboxylesterase/thioestera
--	--	--	--	IPR002867	[IBR domain]
ko00520	A	Phosphom	G	Carbohydr	IPR005843 [Alpha-D-phosphohexomutase, C-terminal
--	--	--	--	IPR003169	[GYF domain]
--		Uncharacte	S	Function u	IPR013538 [Activator of Hsp90 ATPase homologue 1-li
--	--	--	--	IPR022734	[Apolipoprotein M]
--	--	--	--	IPR000203	[GPS motif] ; IPR000832[GPCR, family 2, sec
ko00770	P	Predicted a	R	General fu	IPR003010 [Carbon-nitrogen hydrolase]
ko00770	P	Predicted a	R	General fu	IPR003010 [Carbon-nitrogen hydrolase]
ko03015	m	--	--	--	IPR000571 [Zinc finger, CCCH-type] ; IPR001878[Zinc fi
--		Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR024678[Serine/
--	--	--	--	IPR007919	[Uncharacterised protein family UPF0220]
ko04141	P	--	--	--	--
ko04010	M	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR001180[Citron
--		WD40 repe	R	General fu	IPR001680 [WD40 repeat] ; IPR005108[HELP]
--	--	--	--	IPR018499	[Tetraspanin/Peripherin]
--		N-Dimethy	E	Amino acic	--
ko04150	m	--	--	--	IPR005817 [Wnt]
ko05225	H	Actin-relat	Z	Cytoskelet	IPR004000 [Actin family]
ko00010	G	Zn-depen	R	General fu	IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
ko00010	G	Malate/lac	C	Energy prc	IPR001236 [Lactate/malate dehydrogenase, N-termina
ko00830	R	Acyl-CoA	C	Energy prc	IPR015590 [Aldehyde dehydrogenase domain]
ko00670	C	Dihydrofol	H	Coenzyme	IPR001796 [Dihydrofolate reductase domain]
ko00520	A	Ferredoxin	C	Energy prc	IPR001433 [Oxidoreductase FAD/NAD(P)-binding] ; IPF

ko00480	G	Pyruvate/2	C	Energy prc	IPR004099 [Pyridine nucleotide-disulphide oxidoreduc
ko04146	P	Cu/Zn sup	P	Inorganic i	IPR001424 [Superoxide dismutase, copper/zinc binding
ko00860	P	Multicopp	DPM	Cell cycle c	IPR001117 [Multicopper oxidase, type 1] ; IPR011706[M
ko04610	C	--	--	--	IPR001102 [Transglutaminase, N-terminal] ; IPR002931
ko00230	P	Purine nuc	F	Nucleotide	IPR000845 [Nucleoside phosphorylase domain]
ko00230	P	Hypoxanth	F	Nucleotide	IPR000836 [Phosphoribosyltransferase domain]
ko01521	E	Serine/thre	T	Signal tran	IPR000494 [Receptor L-domain] ; IPR001245[Serine-th
ko00010	G	3-phosph	G	Carbohydr	IPR001576 [Phosphoglycerate kinase]
ko00230	P	Adenylate	F	Nucleotide	--
ko04080	N	Secreted tr	O	Posttransla	IPR000001 [Kringle] ; IPR000294[Gamma-carboxyglutai
ko04145	P	Secreted tr	O	Posttransla	IPR000436 [Sushi/SCR/CCP domain] ; IPR000859[CUB c
--		Secreted tr	O	Posttransla	IPR001254 [Serine proteases, trypsin domain]
ko04610	C	Secreted tr	O	Posttransla	IPR000294 [Gamma-carboxyglutamic acid-rich (GLA) c
ko04610	C	Secreted tr	O	Posttransla	IPR000294 [Gamma-carboxyglutamic acid-rich (GLA) c
ko04080	N	Secreted tr	O	Posttransla	IPR000001 [Kringle] ; IPR001254[Serine proteases, tryps
ko04064	N	Secreted tr	O	Posttransla	IPR000001 [Kringle] ; IPR001254[Serine proteases, tryps
ko04610	C	Serine pro	O	Posttransla	IPR023796 [Serpin domain]
ko04610	C	Uncharact	R	General fu	IPR001599 [Alpha-2-macroglobulin] ; IPR002890[Alpha
ko04145	P	Uncharact	R	General fu	IPR000020 [Anaphylatoxin/fibulin] ; IPR001599[Alpha-2
ko04610	C	Uncharact	R	General fu	IPR000020 [Anaphylatoxin/fibulin] ; IPR001599[Alpha-2
ko04066	H	--	--	--	IPR001820 [Protease inhibitor I35 (TIMP)]
ko04970	S	--	--	--	IPR000010 [Cystatin domain]
ko04610	C	ABC-type	P	Inorganic i	IPR000010 [Cystatin domain]
ko04918	T	Carboxyles	I	Lipid trans	IPR000716 [Thyroglobulin type-1] ; IPR002018[Carboxy
ko04010	M	--	--	--	IPR013576 [Insulin-like growth factor II E-peptide, C-te
--		--	--	--	IPR024110 [Immunoglobulin J chain]
--		--	--	--	IPR013106 [Immunoglobulin V-set domain]
--		--	--	--	IPR013106 [Immunoglobulin V-set domain]
ko04672	Ir	--	--	--	IPR013106 [Immunoglobulin V-set domain]
--		--	--	--	IPR003597 [Immunoglobulin C1-set]
ko04144	E	--	--	--	IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC
ko04144	E	--	--	--	IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC
--		--	--	--	IPR000971 [Globin]
--		--	--	--	IPR000971 [Globin]
ko04151	P	Autotransp	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[\
ko04151	P	Autotransp	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[\
ko04611	P	Autotransp	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[\
ko04151	P	Autotransp	UW	Intracellula	IPR001442 [Collagen IV, non-collagenous] ; IPR008160
ko04141	P	Molecular	O	Posttransla	IPR002068 [Alpha crystallin/Hsp20 domain] ; IPR00309
--		--	--	--	IPR001664 [Intermediate filament protein]
--		DNA repai	L	Replicatior	IPR001664 [Intermediate filament protein] ; IPR032444[
ko03320	P	--	--	--	IPR000074 [Apolipoprotein A/E]
ko04979	C	--	--	--	IPR000074 [Apolipoprotein A/E]
ko03320	P	--	--	--	IPR008403 [Apolipoprotein CIII]
ko04610	C	--	--	--	IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko04610	C	--	--	--	IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko04610	C	--	--	--	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IP
ko04979	C	--	--	--	IPR000436 [Sushi/SCR/CCP domain] ; IPR015104[Beta-
ko04151	P	Phage-rela	X	Mobilome:	IPR000083 [Fibronectin, type I] ; IPR000562[Fibronectin
--		--	--	--	IPR000566 [Lipocalin/cytosolic fatty-acid binding dom
--		--	--	--	IPR000010 [Cystatin domain]
ko04918	T	--	--	--	IPR014760 [Serum albumin, N-terminal]
ko04390	H	--	--	--	IPR014760 [Serum albumin, N-terminal]
--		--	--	--	IPR014760 [Serum albumin, N-terminal] ; IPR015247[Vi
ko04066	H	--	--	--	IPR001156 [Transferrin-like domain]
--		--	--	--	IPR001156 [Transferrin-like domain]
--		--	--	--	IPR018487 [Hemopexin-like repeats]
ko04216	F	Ferritin	P	Inorganic i	IPR008331 [Ferritin/DPS protein domain]

ko04216	F	Ferritin	P	Inorganic i	IPR008331 [Ferritin/DPS protein domain]
ko04610	C	Secreted tr	O	Posttransla	IPR001254 [Serine proteases, trypsin domain] ; IPR0036
ko03320	P	Predicted 2	O	Posttransla	IPR001818 [Peptidase M10, metallopeptidase] ; IPR002
ko04610	C	--	--	--	IPR000436 [Sushi/SCR/CCP domain]
ko04151	P	--	--	--	IPR001212 [Somatomedin B domain] ; IPR018487[Hem
ko00380	T	Catalase	P	Inorganic i	IPR010582 [Catalase immune-responsive domain] ; IPR
ko00511	C	O-Glycosy	M	Cell wall/m	IPR033452 [Glycosyl hydrolase family 30, beta sandwicl
ko00511	C	Alpha-L-fu	G	Carbohydr	IPR000933 [Glycoside hydrolase, family 29] ; IPR031919
ko00010	G	Fructose-b	G	Carbohydr	IPR000741 [Fructose-bisphosphate aldolase, class-I]
--		--	--	--	IPR000010 [Cystatin domain]
--		--	--	--	IPR018502 [Annexin repeat]
ko04975	F	PPE-repea	S	Function u	IPR001747 [Lipid transport protein, N-terminal] ; IPR00
ko00564	G	--	--	--	IPR003386 [Lecithin:cholesterol/phospholipid:diacylgly
ko00330	A	Acetylornit	E	Amino acid	IPR005814 [Aminotransferase class-III]
ko04670	L	--	--	--	IPR013151 [Immunoglobulin]
--		DNA repai	L	Replicatior	IPR001664 [Intermediate filament protein] ; IPR032444[
--		Uncharacte	S	Function u	IPR001664 [Intermediate filament protein] ; IPR032444[
ko04151	P	Secreted p	R	General fu	IPR001007 [VWFC domain] ; IPR001846[von Willebranc
--		--	--	--	IPR001791 [Laminin G domain]
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko00010	G	Glyceralde	G	Carbohydr	IPR020828 [Glyceraldehyde 3-phosphate dehydrogena
ko00220	A	Argininosu	E	Amino acid	IPR022761 [Fumarate lyase, N-terminal] ; IPR029419[A
ko00500	S	Glycosidas	G	Carbohydr	IPR006047 [Glycosyl hydrolase, family 13, catalytic dom
ko04010	M	Molecular	O	Posttransla	IPR002068 [Alpha crystallin/Hsp20 domain]
ko04015	R	--	--	--	IPR001019 [Guanine nucleotide binding protein (G-prc
ko04970	S	--	--	--	IPR011531 [Bicarbonate transporter, C-terminal] ; IPR0
ko04022	c	Magnesiur	P	Inorganic i	IPR004014 [Cation-transporting P-type ATPase, N-terr
ko04022	c	--	--	--	IPR000402 [Sodium/potassium-transporting ATPase su
ko00010	G	Fructose-b	G	Carbohydr	IPR000741 [Fructose-bisphosphate aldolase, class-I]
--		Bacterial lip	M	Cell wall/m	IPR000566 [Lipocalin/cytosolic fatty-acid binding dom
ko04015	R	Secreted p	R	General fu	IPR002369 [Integrin beta subunit, VWA domain] ; IPR0
ko04015	R	Secreted p	R	General fu	IPR002369 [Integrin beta subunit, VWA domain] ; IPR0
ko04066	H	Serine prot	O	Posttransla	IPR023796 [Serpin domain]
ko04610	C	Serine prot	O	Posttransla	IPR023796 [Serpin domain]
ko04610	C	Secreted tr	O	Posttransla	IPR001190 [SRCR domain] ; IPR001254[Serine protease
ko04610	C	--	--	--	IPR000436 [Sushi/SCR/CCP domain]
ko04622	R	--	--	--	IPR000626 [Ubiquitin domain]
ko00730	T	Alkaline ph	PR	Inorganic i	IPR001952 [Alkaline phosphatase]
ko01521	E	--	--	--	IPR003574 [Interleukin-6]
ko03010	R	--	--	--	--
ko03010	R	--	--	--	--
ko03010	R	Ribosomal	J	Translatior	IPR001790 [Ribosomal protein L10P]
--		Uncharacte	R	General fu	IPR001304 [C-type lectin-like]
ko05322	S	--	--	--	IPR000504 [RNA recognition motif domain] ; IPR00663
ko04918	T	Serine prot	O	Posttransla	IPR023796 [Serpin domain]
ko04610	C	Serine prot	O	Posttransla	IPR023796 [Serpin domain]
ko04015	R	Secreted p	R	General fu	IPR002369 [Integrin beta subunit, VWA domain] ; IPR0
ko01521	E	Serine/thre	T	Signal tran	IPR000008 [C2 domain] ; IPR000719[Protein kinase dor
--		Ca2+-binc	T	Signal tran	IPR002048 [EF-hand domain]
ko04974	P	Autotrans	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[
ko00860	P	Uroporphy	H	Coenzyme	IPR000257 [Uroporphyrinogen decarboxylase (URO-D)
ko04071	S	TolB amino	R	General fu	IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
--		Carboxyles	I	Lipid trans	IPR002018 [Carboxylesterase, type B] ; IPR014788[Acet
ko00052	G	Alpha-gala	G	Carbohydr	IPR002241 [Glycoside hydrolase, family 27]
ko04666	F	--	--	--	IPR007123 [Gelsolin-like domain]
ko04110	C	Predicted /	R	General fu	IPR000719 [Protein kinase domain]
ko04975	F	Chromoso	D	Cell cycle c	IPR000074 [Apolipoprotein A/E]
ko01521	E	--	--	--	IPR001040 [Translation Initiation factor eIF- 4e]

ko00330	A	Protein-ar	O	Posttransla	IPR022413 [ATP:guanido phosphotransferase, N-termi
ko00010	G	Enolase	G	Carbohydr	IPR020810 [Enolase, C-terminal TIM barrel domain] ; IP
ko00500	S	Glucan ph	G	Carbohydr	IPR000811 [Glycosyl transferase, family 35]
ko00010	G	Glucose-6	G	Carbohydr	IPR001672 [Phosphoglucose isomerase (PGI)]
--		--	--	--	IPR024057 [Nucleoplasmin core domain] ; IPR032569[N
ko04260	C	Uncharact	S	Function u	IPR000533 [Tropomyosin]
ko04145	P	Cytolysin,	U	Intracellula	IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
ko00561	G	Ca2+-binc	Q	Secondary	IPR001024 [PLAT/LH2 domain] ; IPR013818[Lipase/vitel
ko00511	C	N-acetyl-b	G	Carbohydr	IPR015883 [Glycoside hydrolase family 20, catalytic dor
--		--	--	--	IPR013106 [Immunoglobulin V-set domain]
ko05034	A	--	--	--	IPR007125 [Histone H2A/H2B/H3]
--		Serine pro	O	Posttransla	IPR023796 [Serpin domain]
ko03320	P	Acyl-CoA-	I	Lipid trans	IPR000582 [Acyl-CoA-binding protein, ACBP]
ko03320	P	--	--	--	--
ko00010	G	Malate/lac	C	Energy pro	IPR001236 [Lactate/malate dehydrogenase, N-termina
ko00480	G	Glutathion	VI	Defense m	IPR000889 [Glutathione peroxidase]
ko04610	C	--	--	--	IPR000294 [Gamma-carboxyglutamic acid-rich (GLA) c
ko04141	P	Negative r	O	Posttransla	IPR013766 [Thioredoxin domain]
ko04071	S	--	--	--	IPR012848 [Aspartic peptidase, N-terminal] ; IPR03312
--		--	--	--	IPR018502 [Annexin repeat]
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko00910	N	Carbonic a	P	Inorganic i	IPR001148 [Alpha carbonic anhydrase]
ko04350	T	Leucine-ri	K	Transcripti	IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04142	L	--	--	--	IPR003119 [Saposin A-type domain] ; IPR007856[Sapos
ko00511	C	N-acetyl-b	G	Carbohydr	IPR015883 [Glycoside hydrolase family 20, catalytic dor
ko04015	R	--	--	--	IPR005455 [Profilin]
ko00010	G	Phosphogl	G	Carbohydr	IPR013078 [Histidine phosphatase superfamily, clade-1
ko00860	P	Prolyl-tRN	J	Translatior	IPR000738 [WHEP-TRS domain] ; IPR002314[Aminoacy
ko04140	A	Cysteine p	O	Posttransla	IPR000668 [Peptidase C1A, papain C-terminal] ; IPR012
ko04141	P	Molecular	O	Posttransla	IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
ko03040	S	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
ko04151	P	Uncharact	S	Function u	IPR002049 [Laminin EGF domain] ; IPR008211[Laminin,
ko04520	A	Serine/thre	T	Signal tran	IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
ko04015	R	Alpha-tub	DZ	Cell cycle c	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IP
ko01521	E	Ankyrin re	T	Signal tran	IPR000494 [Receptor L-domain] ; IPR001245[Serine-th
ko04151	P	Autotransp	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160[(
--		--	--	--	IPR018502 [Annexin repeat]
ko04610	C	--	--	--	IPR000436 [Sushi/SCR/CCP domain]
ko02010	A	ABC-type	V	Defense m	IPR003439 [ABC transporter-like] ; IPR011527[ABC tran
ko04150	m	Glycosidas	G	Carbohydr	IPR006047 [Glycosyl hydrolase, family 13, catalytic dom
ko00010	G	6-phosph	G	Carbohydr	IPR000023 [Phosphofructokinase domain]
ko04141	P	Molecular	O	Posttransla	IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
ko00250	A	Asparagine	E	Amino aci	IPR001962 [Asparagine synthase] ; IPR017932[Glutamir
ko01522	E	Predicted	O	Posttransla	IPR000562 [Fibronectin, type II, collagen-binding] ; IPR
--		Cu/Zn sup	P	Inorganic i	IPR001424 [Superoxide dismutase, copper/zinc binding
ko04614	R	Predicted	O	Posttransla	IPR008753 [Peptidase M13, N-terminal domain] ; IPR01
ko04350	T	--	--	--	IPR001111 [Transforming growth factor-beta, N-termi
--		--	--	--	IPR000591 [DEP domain] ; IPR001849[Pleckstrin homol
ko04151	P	Autotransp	UW	Intracellula	IPR001442 [Collagen IV, non-collagenous] ; IPR008160
--		--	--	--	IPR001156 [Transferrin-like domain]
ko04145	P	Cytolysin,	U	Intracellula	IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
ko05169	E	--	--	--	IPR001664 [Intermediate filament protein] ; IPR006821[
ko04610	C	Serine pro	O	Posttransla	IPR023796 [Serpin domain]
ko03010	R	Ribosomal	J	Translatior	IPR001210 [Ribosomal protein S17e]
--		--	--	--	IPR001664 [Intermediate filament protein]
--		--	--	--	IPR018502 [Annexin repeat]
--		--	--	--	IPR001664 [Intermediate filament protein]
--		--	--	--	IPR000716 [Thyroglobulin type-1] ; IPR000867[Insulin-

ko03010	R	Ribosomal	J	Translatior	IPR001865 [Ribosomal protein S2] ; IPR032281[40S ribo
ko04142	L	--	--	--	IPR018499 [Tetraspanin/Peripherin]
ko00071	F	Acetyl-Co	I	Lipid trans	IPR020616 [Thiolase, N-terminal] ; IPR020617[Thiolase,
ko00480	G	Glutathion	O	Posttransla	IPR004045 [Glutathione S-transferase, N-terminal] ; IPR
ko03040	S	--	--	--	IPR013085 [Zinc finger, U1-C type]
ko04062	C	--	--	--	IPR001811 [Chemokine interleukin-8-like domain]
--	--	--	--	--	IPR001079 [Galectin, carbohydrate recognition domain
ko03410	B	--	--	--	IPR009071 [High mobility group box domain]
--	--	--	--	--	IPR000566 [Lipocalin/cytosolic fatty-acid binding doma
--	--	--	--	--	IPR002350 [Kazal domain] ; IPR015369[Follistatin/Osteo
ko04260	C	Cell divisio	D	Cell cycle c	IPR000533 [Tropomyosin]
ko04142	L	--	--	--	IPR000996 [Clathrin light chain]
--	--	Tfp pilus a	NW	Cell motilit	IPR018502 [Annexin repeat]
ko01521	E	Serine/thre	T	Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko03040	S	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR02166
ko03040	S	Leucine-ri	K	Transcripti	--
ko03410	B	WGR dom	K	Transcripti	IPR001357 [BRCT domain] ; IPR001510[Zinc finger, PAR
ko00590	A	Aminopep	E	Amino acid	IPR014782 [Peptidase M1, membrane alanine aminope
ko00010	G	Fructose-b	G	Carbohydr	IPR000741 [Fructose-bisphosphate aldolase, class-I]
ko04610	C	Uncharacte	R	General fu	IPR000020 [Anaphylatoxin/fibulin] ; IPR001599[Alpha-2
ko04217	N	--	--	--	IPR007125 [Histone H2A/H2B/H3] ; IPR032454[Histone
--	--	Leucine-ri	K	Transcripti	IPR001611 [Leucine-rich repeat]
ko03040	S	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
--	--	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
--	--	--	--	--	IPR007455 [Serglycin]
ko04060	C	--	--	--	IPR001811 [Chemokine interleukin-8-like domain]
ko05322	S	Secreted p	R	General fu	IPR008858 [TROVE domain]
ko04010	M	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko04621	N	Negative r	O	Posttransla	IPR013766 [Thioredoxin domain]
ko04142	L	Carboxype	E	Amino acid	IPR001563 [Peptidase S10, serine carboxypeptidase]
ko04610	C	--	--	--	IPR000436 [Sushi/SCR/CCP domain] ; IPR000884[Thron
ko01200	C	S-formylgl	V	Defense m	IPR000801 [Putative esterase]
ko03018	R	Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
--	--	--	--	--	IPR000538 [Link domain] ; IPR013106[Immunoglobulin
ko03060	P	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko04151	P	Methyl-ac	NT	Cell motilit	IPR000034 [Laminin IV] ; IPR002049[Laminin EGF doma
ko00740	R	--	--	--	IPR000560 [Histidine phosphatase superfamily, clade-2
ko03040	S	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko04066	H	Predicted a	G	Carbohydr	IPR005828 [Major facilitator, sugar transporter-like]
--	--	Predicted a	G	Carbohydr	IPR005828 [Major facilitator, sugar transporter-like]
--	--	--	--	--	IPR007477 [SAB domain] ; IPR008379[Band 4.1, C-term
ko00240	P	Orotate ph	F	Nucleotide	IPR000836 [Phosphoribosyltransferase domain] ; IPR00
ko00500	S	Glucan ph	G	Carbohydr	IPR000811 [Glycosyl transferase, family 35]
ko00500	S	Glucan ph	G	Carbohydr	IPR000811 [Glycosyl transferase, family 35]
ko04014	R	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko04140	A	--	--	--	IPR002000 [Lysosome-associated membrane glycopro
ko04010	M	PASTA dor	M	Cell wall/m	IPR001245 [Serine-threonine/tyrosine-protein kinase c
--	--	DNA topoi	L	Replicatior	IPR008336 [DNA topoisomerase I, DNA binding, eukar
ko01524	P	DNA gyras	L	Replicatior	IPR002205 [DNA topoisomerase, type IIA, subunit A/C-
ko00030	P	Glucose-6	G	Carbohydr	IPR022674 [Glucose-6-phosphate dehydrogenase, NA
ko04142	L	--	--	--	IPR000479 [Cation-independent mannose-6-phosphat
ko00010	G	Zn-depen	R	General fu	IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
ko01522	E	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
ko00030	P	Phosphorib	FE	Nucleotide	IPR005946 [Ribose-phosphate diphosphokinase] ; IPR0
ko03013	R	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR00200
ko03030	D	DNA polyr	L	Replicatior	IPR022648 [Proliferating cell nuclear antigen, PCNA, N-
ko00970	A	Histidyl-tR	J	Translatior	IPR000738 [WHEP-TRS domain] ; IPR004154[Anticodor
ko04974	P	Autotransp	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR001791[L

ko04151	P	Autotrans	UW	Intracellula	IPR002035	[von Willebrand factor, type A] ; IPR008160[
ko04151	P	Autotrans	UW	Intracellula	IPR002035	[von Willebrand factor, type A] ; IPR008160[
ko04151	P	Transcripti	K	Transcripti	IPR002035	[von Willebrand factor, type A] ; IPR002223[
ko04610	C	Multicopp	DPM	Cell cycle c	IPR000421	[Coagulation factor 5/8 C-terminal domain]
ko00230	P	CBS doma	T	Signal tran	IPR000644	[CBS domain] ; IPR001093[IMP dehydrogen
ko03013	R	--	--	--	IPR012929	[Nucleoprotein TPR/MLP1]
ko00330	A	Protein-ar	O	Posttransla	IPR022413	[ATP:guanido phosphotransferase, N-termi
--	--	--	--	--	IPR018502	[Annexin repeat]
ko00330	A	Protein-ar	O	Posttransla	IPR022413	[ATP:guanido phosphotransferase, N-termi
ko04510	F	--	--	--	IPR001715	[Calponin homology domain] ; IPR002017[S
--		Xaa-Pro a	E	Amino aci	IPR000994	[Peptidase M24] ; IPR007865[Aminopeptida
ko03450	N	--	--	--	IPR003034	[SAP domain] ; IPR005160[Ku70/Ku80 C-ter
ko03450	N	--	--	--	IPR005160	[Ku70/Ku80 C-terminal arm] ; IPR005161[Ku
ko04140	A	--	--	--	IPR002000	[Lysosome-associated membrane glycopro
--		Leucine-ri	K	Transcripti	IPR001611	[Leucine-rich repeat]
--		Tfp pilus a	NW	Cell motilit	IPR000859	[CUB domain] ; IPR001506[Peptidase M12A
ko04514	C	Uncharact	S	Function u	IPR003961	[Fibronectin type III] ; IPR013098[Immunogl
ko04151	P	Cytolysin,	U	Intracellula	IPR013517	[FG-GAP repeat] ; IPR013649[Integrin alpha
ko04152	A	Translatior	J	Translatior	IPR000640	[Translation elongation factor EFG, V domai
--	--	--	--	--	IPR001664	[Intermediate filament protein]
--	--	--	--	--	IPR001664	[Intermediate filament protein] ; IPR032444[
ko04141	P	Negative r	O	Posttransla	IPR013766	[Thioredoxin domain]
ko04610	C	--	--	--	IPR000436	[Sushi/SCR/CCP domain] ; IPR000884[Thron
ko00330	A	Proline 4-h	JO	Translatior	IPR005123	[Oxoglutarate/iron-dependent dioxygenase
--	--	--	--	--	IPR018105	[Translationally controlled tumour protein]
ko00860	P	Delta-amir	H	Coenzyme	IPR001731	[Delta-aminolevulinic acid dehydratase]
--	--	--	--	--	IPR001715	[Calponin homology domain] ; IPR002048[E
--	--	--	--	--	IPR001715	[Calponin homology domain] ; IPR002048[E
--		Dipeptidyl	E	Amino aci	IPR001375	[Peptidase S9, prolyl oligopeptidase, catalyt
ko00500	S	Glycosyltra	M	Cell wall/m	IPR008631	[Glycogen synthase]
ko04910	Ir	cAMP-bin	T	Signal tran	IPR000595	[Cyclic nucleotide-binding domain] ; IPR003
ko00010	G	Enolase	G	Carbohydr	IPR020810	[Enolase, C-terminal TIM barrel domain] ; IP
ko03022	B	--	--	--	IPR003196	[Transcription initiation factor IIF, beta subu
ko00350	T	Phenylpyr	Q	Secondary	IPR001398	[Macrophage migration inhibitory factor]
ko00900	T	Geranylge	H	Coenzyme	IPR000092	[Polyprenyl synthetase]
--		Glucose/ar	G	Carbohydr	IPR000033	[LDLR class B repeat] ; IPR000716[Thyroglob
ko00010	G	Aldo/keto	Q	Secondary	IPR023210	[NADP-dependent oxidoreductase domain]
ko00010	G	Phosphohi	T	Signal tran	IPR015793	[Pyruvate kinase, barrel] ; IPR015795[Pyruva
ko04141	P	Molecular	O	Posttransla	IPR001404	[Heat shock protein Hsp90 family] ; IPR0035
ko03040	S	--	--	--	IPR001163	[LSM domain, eukaryotic/archaea-type]
--	--	--	--	--	IPR000504	[RNA recognition motif domain]
ko00220	A	Glutamine	E	Amino aci	IPR008146	[Glutamine synthetase, catalytic domain] ; IP
ko00040	P	Aldo/keto	Q	Secondary	IPR023210	[NADP-dependent oxidoreductase domain]
ko04514	C	--	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
--		Bacillopep	O	Posttransla	IPR000834	[Peptidase M14, carboxypeptidase A]
ko00230	P	Nucleoside	F	Nucleotide	IPR001564	[Nucleoside diphosphate kinase]
ko00531	G	Arylsulfata	P	Inorganic i	IPR000917	[Sulfatase, N-terminal]
ko03010	R	Ribosomal	J	Translatior	IPR005324	[Ribosomal protein S5, C-terminal] ; IPR013
ko03030	D	--	--	--	IPR014892	[Replication protein A, C-terminal]
peptidase i		--	--	--	IPR001820	[Protease inhibitor I35 (TIMP)]
ko04512	E	--	--	--	IPR000538	[Link domain]
--		Spore coat	M	Cell wall/m	IPR000436	[Sushi/SCR/CCP domain] ; IPR000538[Link c
ko00052	G	Beta-galac	G	Carbohydr	IPR025300	[Beta-galactosidase jelly roll domain] ; IPR0
ko04012	E	--	--	--	IPR000980	[SH2 domain] ; IPR001452[SH3 domain]
--	--	--	--	--	IPR005818	[Linker histone H1/H5, domain H15]
--	--	--	--	--	IPR005818	[Linker histone H1/H5, domain H15]
--	--	--	--	--	IPR005818	[Linker histone H1/H5, domain H15]
ko04940	T	Bacillopep	O	Posttransla	IPR000834	[Peptidase M14, carboxypeptidase A]

ko00562	Ir	--	--	--	IPR000008 [C2 domain] ; IPR000909[Phosphatidylinosit
ko00350	T	2-keto-4-	Q	Secondary	IPR011234 [Fumarylacetoacetase, C-terminal-related] ;
ko04010	M	--	--	--	IPR000956 [Stathmin family]
ko04530	T	Cold shock	K	Transcripti	IPR002059 [Cold-shock protein, DNA-binding]
ko03040	S	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
--	--	--	--	--	--
ko04145	P	Ca2+-binc	Q	Secondary	IPR002035 [von Willebrand factor, type A] ; IPR013517[
ko04540	G	--	--	--	IPR013092 [Connexin, N-terminal] ; IPR013124[Gap jur
--	--	--	--	--	IPR009071 [High mobility group box domain] ; IPR029
ko00120	P	Aldo/keto	Q	Secondary	IPR023210 [NADP-dependent oxidoreductase domain]
ko04141	P	Serine pro	O	Posttransla	IPR001300 [Peptidase C2, calpain, catalytic domain] ; IP
ko00240	P	CTP synth	F	Nucleotide	IPR017456 [CTP synthase, N-terminal] ; IPR017926[Glu
ko03040	S	Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/D
ko00010	G	6-phosph	G	Carbohydr	IPR000023 [Phosphofructokinase domain]
ko04115	p	--	--	--	IPR000716 [Thyroglobulin type-1] ; IPR000867[Insulin-
ko03050	P	ATP-depe	O	Posttransla	IPR003959 [ATPase, AAA-type, core]
--		Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
--	--	--	--	--	IPR000716 [Thyroglobulin type-1] ; IPR000867[Insulin-
ko03010	R	Ribosomal	J	Translatior	IPR001780 [Ribosomal protein L35A]
--		GTPase SA	R	General fu	IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko03010	R	Ribosomal	J	Translatior	IPR012988 [Ribosomal protein L30, N-terminal] ; IPR01
ko04510	F	--	--	--	IPR006077 [Vinculin/alpha-catenin]
--		Protein tyr	T	Signal tran	IPR000242 [PTP type protein phosphatase]
ko03010	R	Ribosomal	J	Translatior	IPR001063 [Ribosomal protein L22/L17]
ko00010	G	Phosphogl	G	Carbohydr	IPR013078 [Histidine phosphatase superfamily, clade-1
--		Alpha-tub	DZ	Cell cycle c	IPR000408 [Regulator of chromosome condensation, R
ko04514	C	Large exop	U	Intracellula	IPR000233 [Cadherin, cytoplasmic domain] ; IPR00212
ko05130	P	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
ko00010	G	Hexokinas	G	Carbohydr	IPR022672 [Hexokinase, N-terminal] ; IPR022673[Hexo
ko00230	P	DNA-direc	K	Transcripti	IPR000783 [RNA polymerase, subunit H/Rpb5 C-termir
ko04141	P	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR014720[Double
ko00270	C	Spermidine	E	Amino acic	--
ko03008	R	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
--		Secreted p	R	General fu	IPR002035 [von Willebrand factor, type A] ; IPR010600[
--		Secreted p	R	General fu	IPR002035 [von Willebrand factor, type A] ; IPR010600[
ko04062	C	--	--	--	IPR001811 [Chemokine interleukin-8-like domain]
ko04062	C	--	--	--	IPR001811 [Chemokine interleukin-8-like domain]
ko03013	R	Translatior	J	Translatior	IPR002735 [Translation initiation factor IF2/IF5]
--		GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko03050	P	20S protea	O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta]
ko04210	A	--	--	--	IPR001322 [Lamin Tail Domain] ; IPR001664[Intermedia
--		Uncharact	R	General fu	IPR001599 [Alpha-2-macroglobulin] ; IPR002890[Alpha
--		Leucine-ri	K	Transcripti	IPR001611 [Leucine-rich repeat]
ko04060	C	--	--	--	IPR020438 [Interleukin-11]
ko00230	P	CBS doma	T	Signal tran	IPR000644 [CBS domain] ; IPR001093[IMP dehydrogen
ko04151	P	Autotransp	UW	Intracellula	IPR008160 [Collagen triple helix repeat]
ko04974	P	Autotransp	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160[
--	--	--	--	--	IPR004931 [Prothymosin/parathymosin]
ko00480	G	Glutathion	O	Posttransla	IPR004045 [Glutathione S-transferase, N-terminal] ; IP
ko00190	C	Archaeal/v	C	Energy prc	IPR000194 [ATPase, F1/V1/A1 complex, alpha/beta sub
ko00190	C	--	--	--	IPR004907 [ATPase, V1 complex, subunit C]
--	--	--	--	--	IPR001781 [Zinc finger, LIM-type]
ko04010	M	Autotransp	U	Intracellula	IPR001715 [Calponin homology domain] ; IPR017868[F
ko00020	C	Aconitase	C	Energy prc	IPR000573 [Aconitase A/isopropylmalate dehydratase s
ko00230	P	2',3'-cyclic	FV	Nucleotide	IPR004843 [Calcineurin-like phosphoesterase domain,
--		Leucine-ri	K	Transcripti	IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04640	H	--	--	--	IPR018499 [Tetraspanin/Peripherin]
ko00140	S	Predicted	R	General fu	IPR002935 [O-methyltransferase, family 3]

--	--	--	--	IPR000648	[Oxysterol-binding protein] ; IPR001849[Ple
ko00230	P	Phosphoril	F	Nucleotide	IPR002376 [Formyl transferase, N-terminal] ; IPR01091
ko04151	P	Phage-rela	X	Mobilome:	IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko00230	P	Phosphoril	F	Nucleotide	IPR000031 [PurE domain] ; IPR028923[SAICAR syntheta
ko04120	U	Ubiquitin	O	Posttransla	IPR000594 [THIF-type NAD/FAD binding fold] ; IPR018
ko00480	G	Glutathion	VI	Defense m	IPR000889 [Glutathione peroxidase]
ko00230	P	Nucleoside	F	Nucleotide	IPR001564 [Nucleoside diphosphate kinase]
ko00230	P	Predicted	R	General fu	IPR001212 [Somatomedin B domain] ; IPR001604[DNA
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
--	--	--	--	IPR000716	[Thyroglobulin type-1] ; IPR000867[Insulin-
ko01522	E	WD40 repe	R	General fu	IPR000719 [Protein kinase domain]
--	--	--	--	IPR001881	[EGF-like calcium-binding domain] ; IPR026
ko04151	P	Cytolysin, a	U	Intracellula	IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR01297
ko05165	H	Cell divisio	D	Cell cycle c	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
--		Peptidyl-p	O	Posttransla	IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans is
ko03010	R	Ribosomal	J	Translatior	IPR004044 [K Homology domain, type 2]
ko01521	E	PASTA dor	M	Cell wall/m	IPR001245 [Serine-threonine/tyrosine-protein kinase c
--		Protein tyr	T	Signal tran	IPR000242 [PTP type protein phosphatase] ; IPR003961
ko00270	C	S-adenosy	H	Coenzyme	IPR000043 [Adenosylhomocysteinase] ; IPR015878[S-a
ko04360	A	--	--	--	IPR002108 [Actin-depolymerising factor homology dor
ko03013	R	--	--	--	IPR000504 [RNA recognition motif domain]
ko00240	P	Thymidylat	F	Nucleotide	--
ko00230	P	Ribonuclec	F	Nucleotide	IPR000788 [Ribonucleotide reductase large subunit, C-
ko04151	P	DNA repai	L	Replicatior	IPR000034 [Laminin IV] ; IPR001791[Laminin G domain]
--	--	--	--	IPR014038	[Translation elongation factor EF1B, beta/de
ko00730	T	Protein-tyr	T	Signal tran	IPR023485 [Phosphotyrosine protein phosphatase I sup
ko04151	P	Phage-rela	X	Mobilome:	IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko04022	c	Ca2+-binc	T	Signal tran	IPR002048 [EF-hand domain]
ko00230	P	DNA-direc	K	Transcripti	IPR000684 [RNA polymerase II, heptapeptide repeat, e
ko04068	F	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
ko04062	C	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR001849[Pleckst
ko03030	D	DNA replic	L	Replicatior	IPR001208 [MCM domain] ; IPR027925[MCM N-termin
ko00270	C	3-mercapt	P	Inorganic i	IPR001763 [Rhodanese-like domain]
ko04151	P	Chromoso	D	Cell cycle c	IPR000034 [Laminin IV] ; IPR001791[Laminin G domain]
ko03010	R	Ribosomal	J	Translatior	IPR004038 [Ribosomal protein L7Ae/L30e/S12e/Gadd4
ko04141	P	DnaJ-class	O	Posttransla	IPR001623 [DnaJ domain] ; IPR002939[Chaperone Dna.
ko00190	C	FoF1-type	C	Energy prc	IPR000194 [ATPase, F1/V1/A1 complex, alpha/beta sub
ko03050	P	20S protea	O	Posttransla	IPR000426 [Proteasome alpha-subunit, N-terminal dor
ko03050	P	20S protea	O	Posttransla	IPR000426 [Proteasome alpha-subunit, N-terminal dor
ko03050	P	20S protea	O	Posttransla	IPR000426 [Proteasome alpha-subunit, N-terminal dor
ko03050	P	20S protea	O	Posttransla	IPR000426 [Proteasome alpha-subunit, N-terminal dor
ko04974	P	Autotransp	UW	Intracellula	IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160[C
ko04151	P	Cytolysin, a	U	Intracellula	IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
--		Autotransp	U	Intracellula	IPR001759 [Pentraxin-related]
ko04530	T	--	--	--	IPR011259 [Ezrin/radixin/moesin, C-terminal] ; IPR0189
ko03040	S	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
ko03010	R	Ribosomal	J	Translatior	IPR001380 [Ribosomal protein L13e]
--	--	--	--	IPR009071	[High mobility group box domain]
ko00970	A	Threonyl-t	J	Translatior	IPR002314 [Aminoacyl-tRNA synthetase, class II (G/ P/
ko00970	A	Tfp pilus a	NW	Cell motilit	IPR002300 [Aminoacyl-tRNA synthetase, class Ia] ; IPR0
ko05134	L	Glutathion	O	Posttransla	IPR001662 [Translation elongation factor EF1B, gamma
--		FKBP-type	O	Posttransla	IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
--		Secreted tr	O	Posttransla	IPR000001 [Kringle] ; IPR001254[Serine proteases, trys
--		Regulator	O	Posttransla	IPR001107 [Band 7 domain]
		Sugar lacto	G	Carbohydr	IPR002640 [Arylesterase]
ko04110	C	--	--	--	IPR023410 [14-3-3 domain]
ko01521	E	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]

--	PASTA dor	M	Cell wall/m	IPR000719	[Protein kinase domain] ; IPR001772[Kinase
ko03010	R Ribosomal	J	Translatior	IPR016180	[Ribosomal protein L10e/L16]
ko03030	D ssDNA-bir	L	Replicatior	IPR004365	[OB-fold nucleic acid binding domain, AA-t
ko03410	B Exonuclea	L	Replicatior	IPR005135	[Endonuclease/exonuclease/phosphatase]
ko04115	p --	--	--	IPR018499	[Tetraspanin/Peripherin]
ko00240	P Carbamoyl	EF	Amino aci	IPR002474	[Carbamoyl-phosphate synthase, small sub
--	--	--	--	IPR001084	[Microtubule associated protein, tubulin-bi
ko01521	E --	--	--	IPR000198	[Rho GTPase-activating protein domain] ; IF
ko03050	P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]
ko03050	P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]
ko03050	P 20S protea	O	Posttransla	IPR000426	[Proteasome alpha-subunit, N-terminal dor
ko03050	P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]
ko03050	P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]
ko03050	P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]
--	--	--	--	IPR001695	[Lysyl oxidase]
ko00230	P DNA polyr	L	Replicatior	IPR006133	[DNA-directed DNA polymerase, family B, e
ko01521	E Outer men	M	Cell wall/m	IPR000719	[Protein kinase domain]
ko00330	A Leucyl ami	E	Amino aci	IPR000819	[Peptidase M17, leucyl aminopeptidase, C-t
ko04371	A --	--	--	IPR000867	[Insulin-like growth factor-binding protein,
ko04010	M Ankyrin re	T	Signal tran	IPR001090	[Ephrin receptor ligand binding domain] ; IF
ko04360	A Ankyrin re	T	Signal tran	IPR001090	[Ephrin receptor ligand binding domain] ; IF
ko04360	A Ankyrin re	T	Signal tran	IPR001090	[Ephrin receptor ligand binding domain] ; IF
ko04520	A Protein tyr	T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR00098C
ko00030	P Transketol	G	Carbohydr	IPR005474	[Transketolase, N-terminal] ; IPR005475[Tra
ko04217	N Serine/thre	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
ko05168	H --	--	--	IPR014038	[Translation elongation factor EF1B, beta/de
ko04666	F --	--	--	IPR002101	[Myristoylated alanine-rich C-kinase substra
--	Predicted e	R	General fu	IPR003719	[Phenazine biosynthesis PhzF protein]
ko01100	M Alkyl hydro	V	Defense m	IPR000866	[Alkyl hydroperoxide reductase subunit C/ T
ko04146	P Peroxiredo	O	Posttransla	IPR013740	[Redoxin]
--	Phenylpyru	Q	Secondary	IPR001398	[Macrophage migration inhibitory factor]
ko03010	R Ribosomal	J	Translatior	IPR020783	[Ribosomal protein L11, C-terminal] ; IPR02
ko00240	P Adenylate	F	Nucleotide	--	
--	Uncharacte	R	General fu	IPR008914	[Phosphatidylethanolamine-binding protein
ko04141	P Negative r	O	Posttransla	IPR013766	[Thioredoxin domain]
--	--	--	--	IPR022676	[Myristoyl-CoA:protein N-myristoyltransfera
ko01521	E Ankyrin re	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
ko00230	P Adenylosu	F	Nucleotide	IPR019468	[Adenylosuccinate lyase C-terminal] ; IPR02
ko00010	G Phosphohi	T	Signal tran	IPR015793	[Pyruvate kinase, barrel] ; IPR015795[Pyruva
ko04150	m --	--	--	IPR000938	[CAP Gly-rich domain] ; IPR032108[CLIP1, z
--	--	--	--	IPR002048	[EF-hand domain]
ko05206	M Amino aci	E	Amino aci	IPR002293	[Amino acid/polyamine transporter I] ; IPR0
ko00230	P DNA-direc	K	Transcripti	IPR007120	[DNA-directed RNA polymerase, subunit 2,
ko04145	P Membrane	M	Cell wall/m	IPR001680	[WD40 repeat] ; IPR015048[Domain of unkn
--	--	--	--	IPR018203	[GDP dissociation inhibitor]
ko04910	Ir cAMP-bin	T	Signal tran	IPR000595	[Cyclic nucleotide-binding domain] ; IPR003
ko00220	A Carbamoyl	EF	Amino aci	IPR002474	[Carbamoyl-phosphate synthase, small sub
ko00230	P Ribonuclec	F	Nucleotide	IPR000358	[Ribonucleotide reductase small subunit fan
ko04512	E --	--	--	IPR027789	[Syndecan/Neurexin domain]
--	Na+-depe	R	General fu	IPR000175	[Sodium:neurotransmitter symporter]
ko04141	P DnaJ-class	O	Posttransla	IPR001305	[Heat shock protein DnaJ, cysteine-rich don
ko01521	E Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001849[Pleckst
ko00230	P AICAR tran	F	Nucleotide	IPR002695	[AICARFT/IMPCHase bienzyme] ; IPR011607
ko04110	C --	--	--	IPR023410	[14-3-3 domain]
ko05020	P Uncharacte	S	Function u	IPR011990	[Tetratricopeptide-like helical domain] ; IPR
--	--	--	--	IPR002048	[EF-hand domain] ; IPR013787[S100/CaBP-
	Alkyl hydro	V	Defense m	IPR000866	[Alkyl hydroperoxide reductase subunit C/ T
ko00130	U 4-hydroxy	ER	Amino aci	IPR004360	[Glyoxalase/fosfomycin resistance/dioxygen

ko04130	S	--	--	--	IPR000727	[Target SNARE coiled-coil homology doma
ko00260	G	Cystathion	E	Amino aci	IPR000277	[Cys/Met metabolism, pyridoxal phosphate-
ko03010	R	Ribosomal	J	Translatior	IPR020040	[Ribosomal protein L6, alpha-beta domain]
ko04060	C	--	--	--	IPR006052	[Tumour necrosis factor domain]
ko04144	E	--	--	--	IPR001752	[Kinesin motor domain]
ko01523	A	ABC-type	V	Defense m	IPR003439	[ABC transporter-like] ; IPR011527[ABC tran
ko00510	N	--	--	--	IPR001382	[Glycoside hydrolase family 47]
ko03030	D	DNA replic	L	Replicatior	IPR001208	[MCM domain] ; IPR027925[MCM N-termin
ko03030	D	DNA replic	L	Replicatior	IPR001208	[MCM domain] ; IPR027925[MCM N-termin
--	--	--	--	--	IPR023412	[Ribonuclease A-domain]
ko00260	G	Glycine/se	E	Amino aci	IPR001085	[Serine hydroxymethyltransferase]
ko00260	G	Glycine/se	E	Amino aci	IPR001085	[Serine hydroxymethyltransferase]
ko00590	A	Lysophosp	I	Lipid trans	IPR000073	[Alpha/beta hydrolase fold-1] ; IPR023214[
ko05205	P	--	--	--	IPR001863	[Glypican]
ko04015	R	--	--	--	IPR005455	[Profilin]
ko04015	R	--	--	--	IPR000225	[Armadillo]
ko05146	A	Serine pro	O	Posttransla	IPR023796	[Serpin domain]
ko04390	H	--	--	--	IPR011259	[Ezrin/radixin/moesin, C-terminal] ; IPR0189
ko04530	T	--	--	--	IPR011259	[Ezrin/radixin/moesin, C-terminal] ; IPR0189
ko03030	D	--	--	--	IPR013970	[Replication factor A protein 3]
ko03010	R	--	--	--	IPR002671	[Ribosomal protein L22e]
ko03022	B	--	--	--	IPR008851	[Transcription initiation factor IIF, alpha sub
ko04145	P	Alpha-tub	DZ	Cell cycle c	IPR000884	[Thrombospondin type-1 (TSP1) repeat] ; IP
ko04145	P	Alpha-tub	DZ	Cell cycle c	IPR001881	[EGF-like calcium-binding domain] ; IPR003
--	--	--	--	--	IPR001664	[Intermediate filament protein]
--	--	--	--	--	IPR001881	[EGF-like calcium-binding domain] ; IPR017
ko00500	S	Glycogen c	G	Carbohydr	IPR029436	[Eukaryotic glycogen debranching enzyme,
ko04530	T	Chromoso	D	Cell cycle c	IPR001609	[Myosin head, motor domain] ; IPR002928[
ko04530	T	Chromoso	D	Cell cycle c	IPR000048	[IQ motif, EF-hand binding site] ; IPR001609
--		Serine/thre	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
--		WD40 repe	R	General fu	IPR001680	[WD40 repeat] ; IPR006692[Coatomer, WD a
--		--	--	--	--	
ko05202	T	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain] ; IPR00187
ko03013	R	--	--	--	--	
--		--	--	--	IPR014876	[DEK, C-terminal]
--		Glutaredox	O	Posttransla	IPR002109	[Glutaredoxin]
ko04010	M	Serine/thre	T	Signal tran	IPR001932	[PPM-type phosphatase domain] ; IPR0129
--		Leucine-ric	K	Transcripti	IPR000372	[Leucine-rich repeat N-terminal domain] ; I
--		Uncharacte	S	Function u	IPR001664	[Intermediate filament protein] ; IPR032444[
ko03050	P	ATP-depe	O	Posttransla	IPR003959	[ATPase, AAA-type, core]
--		Chitinase,	G	Carbohydr	IPR001223	[Glycoside hydrolase family 18, catalytic dor
--		GTPase SA	R	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
ko01521	E	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
ko00190	C	Archaeal/v	C	Energy pro	IPR002842	[ATPase, V1/A1 complex, subunit E]
ko03010	R	Ribosomal	J	Translatior	IPR002136	[Ribosomal protein L4/L1e] ; IPR025755[60S
ko00010	G	Phosphogl	G	Carbohydr	IPR005843	[Alpha-D-phosphohexomutase, C-terminal
--		Ribosome	J	Translatior	IPR006073	[GTP binding domain]
ko04310	W	Serine pro	O	Posttransla	IPR023796	[Serpin domain]
ko00480	G	Glutathion	VI	Defense m	IPR000889	[Glutathione peroxidase]
ko03060	P	--	--	--	IPR003210	[Signal recognition particle, SRP14 subunit]
ko03013	R	--	--	--	IPR007758	[Nucleoporin, NSP1-like, C-terminal]
--		Ca2+-binc	T	Signal tran	IPR002048	[EF-hand domain]
--		--	--	--	IPR000557	[Calponin repeat] ; IPR001715[Calponin hor
ko00030	P	Transaldol	G	Carbohydr	IPR001585	[Transaldolase/Fructose-6-phosphate aldol
ko00100	S	Lysophosp	I	Lipid trans	IPR000073	[Alpha/beta hydrolase fold-1]
ko00190	C	Archaeal/v	C	Energy pro	IPR000194	[ATPase, F1/V1/A1 complex, alpha/beta sub
ko03018	R	Molecular	O	Posttransla	IPR013126	[Heat shock protein 70 family]
ko03013	R	Superfamil	L	Replicatior	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DE

ko03010	R	Ribosomal	J	Translatior	IPR001266	[Ribosomal protein S19e]
ko03010	R	Ribosomal	J	Translatior	IPR000597	[Ribosomal protein L3]
ko04974	P	Autotransp	UW	Intracellula	IPR008160	[Collagen triple helix repeat] ; IPR010515[Co
ko04974	P	Autotransp	UW	Intracellula	IPR008160	[Collagen triple helix repeat] ; IPR010363[Do
--		Chaperoni	O	Posttransla	IPR002423	[Chaperonin Cpn60/TCP-1 family]
ko00760	N	--	--	--	IPR000940	[Methyltransferase, NNMT/PNMT/TEMT]
ko03050	P	20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta] ; IPR0246
ko03010	R	Ribosomal	J	Translatior	IPR005822	[Ribosomal protein L13]
--		GTPase SA	R	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
ko01521	E	--	--	--	IPR000980	[SH2 domain] ; IPR013799[STAT transcriptio
ko00020	C	Malate/lac	C	Energy prc	IPR001236	[Lactate/malate dehydrogenase, N-termina
ko03013	R	Translatior	J	Translatior	IPR004161	[Translation elongation factor EFTu-like, do
--		Ribosomal	J	Translatior	IPR000182	[GNAT domain]
ko05120	E	PASTA dor	M	Cell wall/m	IPR000980	[SH2 domain] ; IPR001245[Serine-threonine
ko00970	A	Glycyl-tRN	J	Translatior	IPR000738	[WHEP-TRS domain] ; IPR002314[Aminoacy
ko00970	A	Isoleucyl-t	J	Translatior	IPR002300	[Aminoacyl-tRNA synthetase, class Ia] ; IPR0
ko01523	A	--	--	--	IPR002666	[Reduced folate carrier]
--		Actin-relat	Z	Cytoskelet	IPR004000	[Actin family]
ko04012	E	--	--	--	IPR000980	[SH2 domain] ; IPR013799[STAT transcriptio
ko00562	Ir	--	--	--	IPR000403	[Phosphatidylinositol 3-/4-kinase, catalytic
ko03010	R	Ribosomal	J	Translatior	IPR001854	[Ribosomal protein L29]
ko04614	R	--	--	--	IPR008758	[Peptidase S28]
--		Na+/H+-c	C	Energy prc	IPR001991	[Sodium:dicarboxylate symporter]
ko00565	E	WD40 repe	R	General fu	IPR001680	[WD40 repeat] ; IPR006594[LIS1 homology
--		--	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01315
--		--	--	--	--	
ko01524	P	DNA mism	L	Replicatior	IPR000432	[DNA mismatch repair protein MutS, C-tern
ko05166	H	--	--	--	IPR000156	[Ran binding domain]
ko00760	N	Nicotinic a	H	Coenzyme	IPR007229	[Nicotinate phosphoribosyltransferase famil
--		--	--	--	IPR014760	[Serum albumin, N-terminal]
--		Peptidyl-p	O	Posttransla	IPR002130	[Cyclophilin-type peptidyl-prolyl cis-trans is
--		--	--	--	IPR008251	[Chromo shadow domain] ; IPR023780[Chro
ko04020	C	Glucoamyl	G	Carbohydr	IPR011613	[Glycoside hydrolase family 15/Phosphoryla
ko03013	R	Leucine-ri	K	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR009109[Ran-GTPa
--		Superfamil	L	Replicatior	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DE
--		16S rRNA	J	Translatior	IPR001678	[SAM-dependent methyltransferase RsmB/N
ko04010	M	--	--	--	IPR000980	[SH2 domain] ; IPR001452[SH3 domain] ; IP
ko03010	R	Ribosomal	J	Translatior	IPR021131	[Ribosomal protein L18e/L15P]
ko03010	R	Ribosomal	J	Translatior	IPR001147	[Ribosomal protein L21e]
ko03010	R	Ribosomal	J	Translatior	IPR001912	[Ribosomal protein S4/S9, N-terminal] ; IPR
ko03010	R	--	--	--	IPR005326	[Plectin/S10, N-terminal]
--		--	--	--	IPR000433	[Zinc finger, ZZ-type] ; IPR001715[Calponin
ko04520	A	--	--	--	IPR000048	[IQ motif, EF-hand binding site] ; IPR00059
ko00500	S	Alpha-N-a	M	Cell wall/m	IPR002495	[Glycosyl transferase, family 8]
ko04144	E	--	--	--	IPR002189	[F-actin-capping protein subunit alpha]
ko00010	G	Acyl-CoA	C	Energy prc	IPR015590	[Aldehyde dehydrogenase domain]
ko03010	R	--	--	--	IPR002673	[Ribosomal protein L29e]
--		WGR dom	K	Transcripti	IPR001079	[Galectin, carbohydrate recognition domain
--		--	--	--	IPR001781	[Zinc finger, LIM-type]
ko04614	R	Prolyl oligo	E	Amino acid	IPR001375	[Peptidase S9, prolyl oligopeptidase, catalyt
ko00620	P	Malic enzy	C	Energy prc	IPR012301	[Malic enzyme, N-terminal domain] ; IPR01
ko00100	S	Squalene c	I	Lipid trans	IPR032696	[Squalene cyclase, C-terminal] ; IPR032697[
ko00270	C	--	--	--	IPR004308	[Glutamate-cysteine ligase catalytic subunit
ko00270	C	Aldo/keto	Q	Secondary	IPR023210	[NADP-dependent oxidoreductase domain
--		--	--	--	IPR018499	[Tetraspanin/Peripherin]
ko03050	P	--	--	--	IPR033464	[CSN8/PSMD8/EIF3K]
--		Chaperoni	O	Posttransla	IPR002423	[Chaperonin Cpn60/TCP-1 family]
--		Molecular	O	Posttransla	IPR013126	[Heat shock protein 70 family]

ko04340	H	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
ko00020	C	Isocitrate c	C	Energy pro	IPR024084 [Isopropylmalate dehydrogenase-like doma
ko00562	Ir	--	--	--	IPR000341 [Phosphatidylinositol 3-kinase Ras-binding
--		--	--	--	IPR001666 [Phosphatidylinositol transfer protein]
ko04610	C	Secreted tr	O	Posttransla	IPR000436 [Sushi/SCR/CCP domain] ; IPR000859[CUB c
ko00010	G	Acyl-CoA r	C	Energy pro	IPR015590 [Aldehyde dehydrogenase domain]
ko03010	R	Ribosomal	J	Translatior	IPR008195 [Ribosomal protein L34Ae]
ko00061	F	NADP-dep	C	Energy pro	IPR001031 [Thioesterase] ; IPR009081[Phosphopanteth
--		Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
--		Translatior	J	Translatior	IPR004160 [Translation elongation factor EFTu/EF1A, C
ko03060	P	--	--	--	--
ko00440	P	Glycerol-3	M	Cell wall/m	IPR004821 [Cytidyltransferase-like domain]
ko00970	A	Cysteinyl-t	J	Translatior	IPR032678 [tRNA synthetases class I, catalytic domain]
ko00970	A	Seryl-tRNA	J	Translatior	IPR002314 [Aminoacyl-tRNA synthetase, class II (G/ P/
ko03050	P	20S protea	O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta]
ko03030	D	DNA replic	L	Replicatior	IPR001208 [MCM domain] ; IPR008045[DNA replicatior
ko04145	P	DNA-bind	R	General fu	IPR001881 [EGF-like calcium-binding domain] ; IPR003
ko04145	P	Alpha-tub	DZ	Cell cycle c	IPR001881 [EGF-like calcium-binding domain] ; IPR003
ko03040	S	ABC-type	P	Inorganic i	IPR000504 [RNA recognition motif domain] ; IPR00248
--		Diadenosir	FGR	Nucleotide	IPR001310 [Histidine triad (HIT) protein]
ko00140	S	--	--	--	IPR000863 [Sulfotransferase domain]
ko00230	P	Chromoso	D	Cell cycle c	IPR008380 [HAD-superfamily hydrolase, subfamily IG,
ko00230	P	GMP synth	F	Nucleotide	IPR001674 [GMP synthase, C-terminal] ; IPR017926[Glu
ko04015	R	--	--	--	IPR001019 [Guanine nucleotide binding protein (G-pro
ko04014	R	--	--	--	IPR015898 [G-protein gamma-like domain]
ko04668	T	Predicted Z	O	Posttransla	IPR001818 [Peptidase M10, metallopeptidase] ; IPR002
--		--	--	--	IPR018203 [GDP dissociation inhibitor]
--		Sulfate per	P	Inorganic i	IPR002645 [STAS domain] ; IPR011547[SLC26A/SulP tra
--		Serine prot	O	Posttransla	IPR023796 [Serpin domain]
--		Tetratricop	R	General fu	IPR019734 [Tetratricopeptide repeat]
ko04072	P	--	--	--	IPR000375 [Dynamin central domain] ; IPR001849[Plecl
--		ATP-, malt	K	Transcripti	IPR000409 [BEACH domain] ; IPR010508[Domain of un
ko03010	R	Ribosomal	J	Translatior	IPR002784 [Ribosomal protein L14e domain]
--		Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
--		Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
--		Tfp pilus a	NW	Cell motilit	IPR018502 [Annexin repeat]
ko03013	R	--	--	--	IPR004088 [K Homology domain, type 1] ; IPR008395[A
ko04014	R	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko04137	M	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko05162	M	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
--		GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko05225	H	Uncharacte	S	Function u	IPR000330 [SNF2-related, N-terminal domain] ; IPR001
ko00052	G	Galactokin	G	Carbohydr	IPR006204 [GHMP kinase N-terminal domain] ; IPR013
ko04141	P	--	--	--	IPR008417 [B-cell receptor-associated protein 29/31]
ko00983	D	SAM-depe	QR	Secondary	IPR008854 [TPMT family]
ko05168	H	N-acetylne	M	Cell wall/m	IPR006652 [Kelch repeat type 1]
ko00120	P	NAD(P)-de	IQR	Lipid trans	IPR002347 [Short-chain dehydrogenase/reductase SDF
--		--	--	--	IPR001614 [Myelin proteolipid protein PLP]
--		Nucleotide	T	Signal tran	IPR000644 [CBS domain] ; IPR001807[Chloride channel
ko04130	S	--	--	--	IPR001388 [Synaptobrevin] ; IPR010908[Longin domair
--		--	--	--	IPR000313 [PWWP domain]
ko05205	P	Leucine-ric	K	Transcripti	IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko00030	P	6-phospho	G	Carbohydr	IPR006114 [6-phosphogluconate dehydrogenase, C-te
ko03040	S	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR02466
ko05164	Ir	--	--	--	IPR000225 [Armadillo] ; IPR002652[Importin-alpha, imp
--		Amino acic	E	Amino acic	IPR002293 [Amino acid/polyamine transporter I] ; IPR0
--		--	--	--	IPR000504 [RNA recognition motif domain] ; IPR01299
ko03022	B	--	--	--	IPR004855 [Transcription factor IIA, alpha/beta subunit

ko03022	B	--	--	--	IPR015871 [Transcription initiation factor IIA, gamma su
ko01524	P	DNA mism	L	Replicatior	IPR000313 [PWWP domain] ; IPR000432[DNA mismatc
--		--	--	--	IPR004978 [Stanniocalcin]
ko04614	R	Zn-depen	E	Amino aci	IPR001567 [Peptidase M3A/M3B catalytic domain]
ko04144	E	--	--	--	IPR002189 [F-actin-capping protein subunit alpha]
ko00860	P	Predicted	R	General fu	IPR000683 [Oxidoreductase, N-terminal] ; IPR015249[B
ko00020	C	Citrate syn	C	Energy prc	IPR002020 [Citrate synthase] ; IPR003781[CoA-binding
--		Predicted	T	Signal tran	IPR001680 [WD40 repeat] ; IPR006692[Coatomer, WD a
ko04142	L	Cysteine p	O	Posttransla	IPR000668 [Peptidase C1A, papain C-terminal] ; IPR014
ko04144	E	--	--	--	IPR022775 [AP complex, mu/sigma subunit]
--		Uncharacte	R	General fu	IPR001734 [Sodium/solute symporter]
--		--	--	--	--
--		--	--	--	IPR003173 [Transcriptional coactivator p15 (PC4)]
ko00970	A	Arginyl-tR	J	Translatior	IPR001278 [Arginine-tRNA ligase] ; IPR005148[Arginyl
ko04010	M	Secreted p	R	General fu	IPR002035 [von Willebrand factor, type A] ; IPR013608[
ko00970	A	Tryptopha	J	Translatior	IPR002305 [Aminoacyl-tRNA synthetase, class Ic] ; IPR0
--		--	--	--	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04068	F	CBS doma	T	Signal tran	IPR000644 [CBS domain]
ko03040	S	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko03420	N	Ubiquitin	O	Posttransla	IPR000626 [Ubiquitin domain] ; IPR015360[XPC-bindin
ko04360	A	Ankyrin re	T	Signal tran	IPR001090 [Ephrin receptor ligand binding domain] ; IP
--		--	--	--	IPR004031 [PMP-22/EMP/MP20/Claudin superfamily]
ko00330	A	Gamma-gl	E	Amino aci	IPR001048 [Aspartate/glutamate/uridylate kinase] ; IPR
--		--	--	--	IPR003582 [ShKT domain] ; IPR008673[Microfibril-asso
ko04970	S	Amino aci	E	Amino aci	IPR004841 [Amino acid permease/ SLC12A domain] ; IP
--		Ribosome-	J	Translatior	IPR004095 [TGS] ; IPR006073[GTP binding domain] ; IP
ko04141	P	ATP-depe	O	Posttransla	IPR003338 [CDC48, N-terminal subdomain] ; IPR00395
ko04014	R	--	--	--	IPR000159 [Ras-associating (RA) domain] ; IPR000253[
ko04210	A	--	--	--	--
ko00230	P	Sugar or n	G	Carbohydr	IPR011611 [Carbohydrate kinase PfkB]
ko04623	C	--	--	--	IPR000607 [Double-stranded RNA-specific adenosine
ko04151	P	Methyl-ac	NT	Cell motilit	IPR002049 [Laminin EGF domain] ; IPR008211[Laminin,
--		Large exo	U	Intracellula	IPR000233 [Cadherin, cytoplasmic domain] ; IPR00212
--		Large exo	U	Intracellula	IPR000233 [Cadherin, cytoplasmic domain] ; IPR00212
--		Large exo	U	Intracellula	IPR002126 [Cadherin] ; IPR014868[Cadherin prodomai
ko03013	R	--	--	--	IPR022617 [Rad60/SUMO-like domain]
ko03013	R	--	--	--	IPR000504 [RNA recognition motif domain] ; IPR01397
ko00450	S	Methionyl-	J	Translatior	IPR000738 [WHEP-TRS domain] ; IPR004046[Glutathior
ko03008	R	Translatior	J	Translatior	IPR002769 [Translation initiation factor IF6]
--		Predicted	T	Signal tran	IPR020683 [Ankyrin repeat-containing domain]
ko04014	R	--	--	--	IPR015898 [G-protein gamma-like domain]
ko04144	E	--	--	--	IPR008384 [Actin-related protein 2/3 complex subunit
ko04662	B	--	--	--	IPR018499 [Tetraspanin/Peripherin]
ko00010	G	Triosephos	G	Carbohydr	IPR000652 [Triosephosphate isomerase]
ko03013	R	--	--	--	IPR000717 [Proteasome component (PCI) domain] ; IPF
ko04068	F	--	--	--	IPR004241 [Autophagy protein Atg8 ubiquitin-like]
ko04270	V	Ca2+-binc	T	Signal tran	IPR002048 [EF-hand domain]
ko04015	R	Actin-relat	Z	Cytoskelet	IPR004000 [Actin family]
ko04010	M	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko03013	R	Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DE
ko03010	R	Ribosomal	J	Translatior	IPR027486 [Ribosomal protein S10 domain]
ko03050	P	20S protea	O	Posttransla	IPR000426 [Proteasome alpha-subunit, N-terminal dor
--		--	--	--	IPR013787 [S100/CaBP-9k-type, calcium binding, subd
ko04010	M	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
--		--	--	--	IPR002108 [Actin-depolymerising factor homology dor
--		--	--	--	IPR002108 [Actin-depolymerising factor homology dor
ko03060	P	Signal recc	U	Intracellula	IPR000897 [Signal recognition particle, SRP54 subunit,
ko04152	A	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]

ko04144	E	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608	[Ubiquitin-conjugating enzyme E2]
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608	[Ubiquitin-conjugating enzyme E2] ; IPR015
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608	[Ubiquitin-conjugating enzyme E2]
ko04152	A	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko04530	T	Actin-relat	Z	Cytoskelet	IPR004000	[Actin family]
--		Actin-relat	Z	Cytoskelet	IPR004000	[Actin family]
ko04144	E	GTPase SA	R	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
--		Translatior	J	Translatior	IPR003439	[ABC transporter-like] ; IPR007209[RNase L
ko04010	M	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko03010	R	Ribosomal	J	Translatior	IPR001593	[Ribosomal protein S3Ae]
ko03050	P	--	--	--	IPR003185	[Proteasome activator pa28, N-terminal dor
ko03010	R	Ribosomal	J	Translatior	IPR000439	[Ribosomal protein L15e]
ko03010	R	--	--	--	IPR001141	[Ribosomal protein L27e] ; IPR005824[KOW
ko04014	R	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
--		Co-chaper	O	Posttransla	IPR020818	[GroES chaperonin family]
--		--	--	--	IPR004127	[Prefoldin alpha-like]
ko04721	S	--	--	--	IPR001619	[Sec1-like protein]
ko04612	A	--	--	--	IPR003597	[Immunoglobulin C1-set]
ko04142	L	--	--	--	IPR022775	[AP complex, mu/sigma subunit]
--		--	--	--	IPR002075	[Nuclear transport factor 2]
ko03040	S	--	--	--	IPR004088	[K Homology domain, type 1] ; IPR012987[R
ko04110	C	--	--	--	IPR023410	[14-3-3 domain]
ko03015	m	Diadenosir	T	Signal tran	IPR004843	[Calcineurin-like phosphoesterase domain,
ko04014	R	Ca2+-binc	T	Signal tran	IPR002048	[EF-hand domain]
--		Ca2+-binc	T	Signal tran	IPR002048	[EF-hand domain]
ko03050	P	ATP-depei	O	Posttransla	IPR003959	[ATPase, AAA-type, core]
ko03050	P	ATP-depei	O	Posttransla	IPR003959	[ATPase, AAA-type, core]
ko03010	R	Ribosomal	J	Translatior	IPR022309	[Ribosomal protein S8e/ribosomal biogenes
ko03010	R	Ribosomal	J	Translatior	IPR000754	[Ribosomal protein S9]
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608	[Ubiquitin-conjugating enzyme E2]
ko04110	C	--	--	--	IPR023410	[14-3-3 domain]
ko03010	R	Ribosomal	J	Translatior	IPR001971	[Ribosomal protein S11]
ko03010	R	Ribosomal	J	Translatior	IPR006032	[Ribosomal protein S12/S23]
ko03010	R	Ribosomal	J	Translatior	IPR001892	[Ribosomal protein S13]
ko03010	R	Ribosomal	J	Translatior	IPR000589	[Ribosomal protein S15] ; IPR012606[Ribosc
ko03010	R	Ribosomal	J	Translatior	IPR000266	[Ribosomal protein S17/S11] ; IPR032440[4(
ko03018	R	Small nucl	K	Transcripti	IPR001163	[LSM domain, eukaryotic/archaea-type]
ko03040	S	--	--	--	IPR001163	[LSM domain, eukaryotic/archaea-type]
ko03040	S	--	--	--	IPR001163	[LSM domain, eukaryotic/archaea-type]
ko04014	R	GTPase SA	R	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
ko03050	P	ATP-depei	O	Posttransla	IPR003959	[ATPase, AAA-type, core]
ko03010	R	Ribosomal	J	Translatior	IPR004038	[Ribosomal protein L7Ae/L30e/S12e/Gadd4
--		--	--	--	IPR001878	[Zinc finger, CCHC-type]
ko03010	R	Ribosomal	J	Translatior	IPR002942	[RNA-binding S4 domain] ; IPR005824[KOW
ko04270	V	Actin-relat	Z	Cytoskelet	IPR004000	[Actin family]
ko03010	R	Ribosomal	J	Translatior	IPR005633	[Ribosomal protein L23/L25, N-terminal] ; IF
ko01521	E	Ribosomal	J	Translatior	IPR001377	[Ribosomal protein S6e]
--		Ca2+-binc	T	Signal tran	IPR002048	[EF-hand domain]
ko05034	A	--	--	--	--	
ko05134	L	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko03008	R	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko03010	R	Ribosomal	J	Translatior	IPR000218	[Ribosomal protein L14P]
ko04010	M	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko03010	R	Ribosomal	J	Translatior	IPR001976	[Ribosomal protein S24e]
ko03010	R	--	--	--	IPR004977	[Ribosomal protein S25]
ko03010	R	Ribosomal	J	Translatior	IPR000892	[Ribosomal protein S26e]
ko03010	R	Ribosomal	J	Translatior	IPR000289	[Ribosomal protein S28e]

ko04014	R	WD40 repe	R	General fu	IPR001680 [WD40 repeat]
ko00230	P	DNA-direc	K	Transcripti	IPR000268 [DNA-directed RNA polymerase, subunit N/
ko04014	R	WD40 repe	R	General fu	IPR001680 [WD40 repeat]
ko03010	R	Ribosomal	J	Translatior	IPR000054 [Ribosomal protein L31e]
ko03010	R	Ribosomal	J	Translatior	IPR028364 [Ribosomal protein L1/ribosomal biogenesis
ko03010	R	Ribosomal	J	Translatior	IPR022666 [Ribosomal Proteins L2, RNA binding doma
ko04217	N	Peptidyl-p	O	Posttransla	IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans is
--		FKBP-type	O	Posttransla	IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
ko03010	R	Ubiquitin	O	Posttransla	IPR000626 [Ubiquitin domain] ; IPR002906[Ribosomal p
ko01521	E	--	--	--	IPR000980 [SH2 domain] ; IPR001452[SH3 domain]
ko03040	S	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
ko04144	E	Predicted	T	Signal tran	IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
ko04110	C	--	--	--	IPR023410 [14-3-3 domain]
ko03010	R	--	--	--	IPR002675 [Ribosomal protein L38e]
ko04110	C	--	--	--	IPR016072 [SKP1 component, dimerisation] ; IPR01607
ko04014	R	--	--	--	IPR015898 [G-protein gamma-like domain]
ko05162	M	Uncharacte	R	General fu	IPR001680 [WD40 repeat]
ko04015	R	Actin-relat	Z	Cytoskelet	IPR004000 [Actin family]
ko03013	R	Ubiquitin-	O	Posttransla	IPR000608 [Ubiquitin-conjugating enzyme E2]
ko03015	m	Diadenosir	T	Signal tran	IPR004843 [Calcineurin-like phosphoesterase domain,
--		Cold shock	K	Transcripti	IPR002059 [Cold-shock protein, DNA-binding]
ko03008	R	--	--	--	IPR000704 [Casein kinase II, regulatory subunit]
ko04260	C	Chromoso	D	Cell cycle c	IPR000533 [Tropomyosin]
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608 [Ubiquitin-conjugating enzyme E2]
ko03013	R	Translatior	J	Translatior	IPR004160 [Translation elongation factor EFTu/EF1A, C
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko03008	R	PASTA dor	M	Cell wall/m	IPR000719 [Protein kinase domain]
ko00565	E	Lysophosp	E	Amino acic	IPR013830 [SGNH hydrolase-type esterase domain]
ko05034	A	--	--	--	IPR007125 [Histone H2A/H2B/H3]
--		--	--	--	IPR000971 [Globin]
ko05143	A	Hemoglob	C	Energy prc	IPR000971 [Globin]
ko05416	V	--	--	--	IPR013106 [Immunoglobulin V-set domain] ; IPR01315
ko03013	R	--	--	--	IPR003307 [W2 domain] ; IPR003890[MIF4G-like, type 3
ko03022	B	--	--	--	IPR004212 [GTF2I-like repeat]
--		Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
ko03450	N	--	--	--	IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic c
--		--	--	--	IPR000436 [Sushi/SCR/CCP domain] ; IPR003410[HYR c
ko04062	C	--	--	--	IPR001811 [Chemokine interleukin-8-like domain]
--		--	--	--	IPR008408 [Brain acid soluble protein 1]
--		--	--	--	IPR013106 [Immunoglobulin V-set domain]
ko03010	R	Ribosomal	J	Translatior	IPR000988 [Ribosomal protein L24e-related]
--		--	--	--	IPR008251 [Chromo shadow domain] ; IPR023780[Chro
--		--	--	--	IPR000781 [Enhancer of rudimentary]
ko05100	B	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko03010	R	Ribosomal	J	Translatior	IPR000196 [Ribosomal protein L19/L19e]
ko03040	S	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
ko04657	IL	Leucine-ric	K	Transcripti	IPR001846 [von Willebrand factor, type D domain] ; IPF
--		--	--	--	IPR000020 [Anaphylatoxin/fibulin] ; IPR001881[EGF-like
ko04512	E	Outer men	M	Cell wall/m	IPR000034 [Laminin IV] ; IPR000742[EGF-like domain] ;
ko04360	A	--	--	--	IPR001799 [Ephrin receptor-binding domain]
--		Magnesiur	P	Inorganic i	IPR004014 [Cation-transporting P-type ATPase, N-terr
--		Magnesiur	P	Inorganic i	IPR008250 [P-type ATPase, A domain] ; IPR032630[P-t
ko00920	S	Cytochrom	C	Energy prc	IPR009056 [Cytochrome c-like domain]
--		Guanylate	F	Nucleotide	IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
ko00270	C	S-adenosy	H	Coenzyme	IPR022628 [S-adenosylmethionine synthetase, N-termi
--		--	--	--	IPR004088 [K Homology domain, type 1]

--	--	--	--	IPR006628	[Purine-rich element binding protein family
ko04142 L	--	--	--	IPR000547	[Clathrin, heavy chain/VPS, 7-fold repeat] ; I
--	FKBP-type	O	Posttransla	IPR001179	[FKBP-type peptidyl-prolyl cis-trans isomer
ko00040 P	Threonine	ER	Amino aci	IPR013149	[Alcohol dehydrogenase, C-terminal] ; IPR0
--	--	--	--	IPR001715	[Calponin homology domain] ; IPR002017[S
--	--	--	--	IPR002164	[Nucleosome assembly protein (NAP)]
ko03040 S	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
ko00230 P	Adenosine	F	Nucleotide	IPR001365	[Adenosine/AMP deaminase domain]
ko03320 P	--	--	--	IPR000566	[Lipocalin/cytosolic fatty-acid binding doma
--	--	--	--	IPR013912	[Adenylate cyclase-associated CAP, C-term
ko00072 S	3-hydroxy	I	Lipid trans	IPR013528	[Hydroxymethylglutaryl-coenzyme A syntha
--	--	--	--	IPR007593	[CD225/Dispanin family]
ko04150 m	Amino aci	E	Amino aci	IPR002293	[Amino acid/polyamine transporter I]
--	--	--	--	IPR003958	[Transcription factor CBF/NF-Y/archaeal his
ko00010 G	6-phosph	G	Carbohydr	IPR000023	[Phosphofructokinase domain]
ko00562 Ir	--	--	--	IPR000008	[C2 domain] ; IPR000909[Phosphatidylinosit
--	Ankyrin re	T	Signal tran	IPR000001	[Kringle] ; IPR001245[Serine-threonine/tyro
--	--	--	--	IPR000557	[Calponin repeat] ; IPR001715[Calponin hor
ko00230 P	GAF doma	T	Signal tran	IPR001054	[Adenylyl cyclase class-3/4/guanylyl cyclase
ko05206 M	--	--	--	IPR001752	[Kinesin motor domain] ; IPR032384[Kinesin
ko04915 E	FKBP-type	O	Posttransla	IPR001179	[FKBP-type peptidyl-prolyl cis-trans isomer
ko00310 L	Glycosyltra	M	Cell wall/m	IPR005123	[Oxoglutarate/iron-dependent dioxygenase
--	--	--	--	IPR002048	[EF-hand domain]
ko03010 R	--	--	--	IPR000915	[60S ribosomal protein L6E] ; IPR005568[Rib
ko01524 P	DNA gyras	L	Replicatior	IPR002205	[DNA topoisomerase, type IIA, subunit A/C-
--	--	--	--	IPR010326	[Exocyst complex component EXOC3/Sec6]
ko03320 P	--	--	--	IPR000536	[Nuclear hormone receptor, ligand-binding
ko04610 C	--	--	--	IPR016054	[Ly-6 antigen/uPA receptor-like]
ko01523 A	--	--	--	IPR011539	[Rel homology domain (RHD), DNA-binding
ko00500 S	1,4-alpha-	G	Carbohydr	IPR004193	[Glycoside hydrolase, family 13, N-terminal]
ko03013 R	--	--	--	IPR003307	[W2 domain] ; IPR003890[MIF4G-like, type 3
--	Secreted tr	O	Posttransla	IPR000001	[Kringle] ; IPR000083[Fibronectin, type I] ; IP
ko03030 D	Single-stra	L	Replicatior	IPR000424	[Primosome PriB/single-strand DNA-bindin
ko04110 C	--	--	--	IPR023410	[14-3-3 domain]
ko04072 P	--	--	--	IPR000375	[Dynamin central domain] ; IPR001849[Pleck
ko01522 E	Ankyrin re	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
--	--	--	--	IPR000504	[RNA recognition motif domain]
ko04270 V	Cell divisio	D	Cell cycle c	IPR006018	[Caldesmon/lymphocyte specific protein]
--	Secreted p	R	General fu	IPR002035	[von Willebrand factor, type A] ; IPR010600[
ko04014 R	Protein tyr	T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR00098C
ko00230 P	Glutamine	F	Nucleotide	IPR000836	[Phosphoribosyltransferase domain]
ko00250 A	Glucosami	M	Cell wall/m	IPR001347	[Sugar isomerase (SIS)]
ko03018 R	Exosome c	J	Translatior	IPR001247	[Exoribonuclease, phosphorolytic domain 1]
ko03050 P	--	--	--	IPR003185	[Proteasome activator pa28, N-terminal dor
--	Leucine-ric	K	Transcripti	IPR000372	[Leucine-rich repeat N-terminal domain] ; I
ko04146 P	Alkyl hydro	V	Defense m	IPR000866	[Alkyl hydroperoxide reductase subunit C/ T
ko03010 R	--	--	--	IPR021131	[Ribosomal protein L18e/L15P]
ko05168 H	--	--	--	IPR003428	[Mitochondrial glycoprotein]
--	Autotransp	UW	Intracellula	IPR008160	[Collagen triple helix repeat]
ko04520 A	--	--	--	IPR000906	[ZU5 domain] ; IPR001478[PDZ domain] ; IP
--	--	--	--	IPR004088	[K Homology domain, type 1] ; IPR032335[S
ko04979 C	Glucose/ar	G	Carbohydr	IPR000033	[LDLR class B repeat] ; IPR001881[EGF-like c
ko03040 S	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
ko04010 M	Diadenosir	T	Signal tran	IPR004843	[Calcineurin-like phosphoesterase domain,
--	NADPH:qu	CR	Energy pro	IPR013149	[Alcohol dehydrogenase, C-terminal] ; IPR0
--	--	--	--	IPR001190	[SRCR domain] ; IPR011705[BTB/Kelch-asso
--	--	--	--	IPR000421	[Coagulation factor 5/8 C-terminal domain]
--	--	--	--	IPR000716	[Thyroglobulin type-1] ; IPR002350[Kazal do

ko04512	E	--	--	--	IPR013147 [CD47 transmembrane] ; IPR013270[CD47 i
ko04217	N	Peptidyl-p	O	Posttransla	IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans i
--		Ca2+-binc	Q	Secondary	--
ko04150	m	--	--	--	--
ko00510	N	--	--	--	IPR007754 [N-acetylglucosaminyltransferase II]
ko00512	M	Glycosyltra	G	Carbohydr	IPR000772 [Ricin B, lectin domain] ; IPR001173[Glycosy
ko04142	L	Predicted	IT	Signal tran	IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
ko03015	m	--	--	--	IPR004871 [Cleavage/polyadenylation specificity factor
ko04144	E	--	--	--	IPR019393 [WASH complex, subunit strumpellin]
--		--	--	--	IPR001881 [EGF-like calcium-binding domain] ; IPR026
--		--	--	--	IPR002350 [Kazal domain] ; IPR015369[Follistatin/Ostec
ko04130	S	--	--	--	IPR000727 [Target SNARE coiled-coil homology doma
ko04514	C	Sugar lactc	G	Carbohydr	IPR003961 [Fibronectin type III] ; IPR013098[Immunogl
ko03040	S	--	--	--	IPR021966 [Splicing factor SF3a60 binding domain] ; IP
--		Dipeptidyl	E	Amino acic	IPR001375 [Peptidase S9, prolyl oligopeptidase, catalyt
--		tRNA-binc	J	Translatior	IPR002547 [tRNA-binding domain]
--		--	--	--	IPR006561 [DZF domain]
--		--	--	--	IPR006561 [DZF domain] ; IPR014720[Double-strandec
ko04141	P	--	--	--	IPR005052 [Legume-like lectin]
--		Molecular	O	Posttransla	IPR001404 [Heat shock protein Hsp90 family]
ko04390	H	Guanylate	F	Nucleotide	IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
--		Protein-tyı	T	Signal tran	IPR000242 [PTP type protein phosphatase]
		Predicted	IT	Signal tran	IPR001680 [WD40 repeat] ; IPR013258[Striatin, N-termi
ko04110	C	Tetratricop	R	General fu	--
--		Leucine-ric	K	Transcripti	IPR001611 [Leucine-rich repeat] ; IPR007123[Gelsolin-l
ko00061	F	Biotin carb	I	Lipid trans	IPR000022 [Carboxyl transferase] ; IPR000089[Biotin/lip
ko00565	E	Predicted	R	General fu	IPR005065 [Platelet-activating factor acetylhydrolase-li
ko04015	R	--	--	--	IPR000980 [SH2 domain] ; IPR001660[Sterile alpha mot
--		--	--	--	IPR010892 [Secreted phosphoprotein 24]
--		Ubiquitin (	O	Posttransla	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04068	F	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR032270[AMPK,
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
--		--	--	--	IPR004046 [Glutathione S-transferase, C-terminal] ; IPR
		Alkyl hydrc	V	Defense m	IPR000866 [Alkyl hydroperoxide reductase subunit C/ T
ko04010	M	Serine/thre	T	Signal tran	IPR000270 [PB1 domain] ; IPR000719[Protein kinase dc
ko03050	P	--	--	--	IPR002015 [Proteasome/cyclosome repeat]
--		DNA-bind	R	General fu	IPR008826 [Selenium-binding protein]
--		--	--	--	IPR000315 [B-box-type zinc finger] ; IPR001841[Zinc fi
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR00207
--		PASTA dor	M	Cell wall/m	IPR001245 [Serine-threonine/tyrosine-protein kinase c
--		--	--	--	IPR000679 [Zinc finger, GATA-type] ; IPR000949[ELM2
ko03013	R	WD40 repe	R	General fu	IPR001680 [WD40 repeat]
ko04310	W	Lactate del	CHR	Energy prc	IPR006139 [D-isomer specific 2-hydroxyacid dehydrog
ko04145	P	Predicted	IT	Signal tran	IPR001680 [WD40 repeat] ; IPR025956[Cytoplasmic dyr
ko03320	P	Ankyrin rep	T	Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko03008	R	--	--	--	IPR003993 [Treacher Collins syndrome, treacle]
ko03040	S	--	--	--	IPR003034 [SAP domain] ; IPR006568[PSP, proline-rich
--		--	--	--	IPR019380 [Casein kinase substrate, phosphoprotein PI
--		--	--	--	IPR000048 [IQ motif, EF-hand binding site] ; IPR00015
ko04022	c	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR015008[Rho bi
--		--	--	--	IPR011417 [AP180 N-terminal homology (ANTH) doma
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko04110	C	Acetoin uti	BQ	Chromatin	IPR023801 [Histone deacetylase domain]
ko04012	E	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR013543[Calciur
ko04012	E	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR013543[Calciur
ko04962	V	--	--	--	--
ko04810	R	--	--	--	IPR000048 [IQ motif, EF-hand binding site] ; IPR00059
ko03040	S	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]

ko04144	E	--	--	--	IPR001683 [Phox homologous domain] ; IPR005329[So
ko04110	C	--	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko04066	H	--	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko04120	U	--	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko03420	N	--	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko00051	F	Nucleoside	M	Cell wall/m	IPR001509 [NAD-dependent epimerase/dehydratase]
--		GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
--		Leucine-ri	K	Transcripti	IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04630	Ja	--	--	--	IPR001781 [Zinc finger, LIM-type]
ko04151	P	Cytolysin, a	U	Intracellula	IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
ko04514	C	--	--	--	IPR013162 [CD80-like, immunoglobulin C2-set]
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko00565	E	Predicted p	R	General fu	IPR001212 [Somatomedin B domain] ; IPR001604[DNA
ko03013	R	Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DE
--		Aminopep	E	Amino acic	IPR004134 [Peptidase C1B, bleomycin hydrolase]
ko03018	R	Exosome c	J	Translatior	IPR004088 [K Homology domain, type 1] ; IPR025721[E
ko04060	C	Serine/thre	T	Signal tran	IPR000472 [Activin types I and II receptor domain] ; IPR
--		--	--	--	IPR001478 [PDZ domain] ; IPR001849[Pleckstrin homol
--		--	--	--	IPR007955 [Bystin]
ko00900	T	Isopenteny	I	Lipid trans	IPR000086 [NUDIX hydrolase domain]
--		--	--	--	IPR024395 [CLASP N-terminal domain]
--		--	--	--	IPR002108 [Actin-depolymerising factor homology dor
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR01295
ko04142	Ly	--	--	--	IPR002159 [CD36 family]
--		Glucose/ar	G	Carbohydr	IPR000033 [LDLR class B repeat] ; IPR000716[Thyroglob
ko00240	P	Dihydroor	F	Nucleotide	IPR006680 [Amidohydrolase-related]
ko04512	E	--	--	--	IPR008465 [Dystroglycan]
ko05100	B	--	--	--	IPR030379 [Septin-type guanine nucleotide-binding (G
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR00303
ko03013	R	16S rRNA	J	Translatior	IPR000717 [Proteasome component (PCI) domain]
--		--	--	--	IPR022166 [Protein of unknown function DUF3697, ubi
ko04390	H	Leucine-ri	K	Transcripti	IPR001478 [PDZ domain] ; IPR001611[Leucine-rich rep
--		--	--	--	IPR004344 [Tubulin-tyrosine ligase/Tubulin polyglutam
ko04380	C	--	--	--	IPR001781 [Zinc finger, LIM-type]
--		Dihydroor	F	Nucleotide	IPR006680 [Amidohydrolase-related]
ko04962	V	Uncharacte	S	Function u	IPR000938 [CAP Gly-rich domain] ; IPR022157[Dynein a
ko04145	P	--	--	--	IPR004273 [Dynein heavy chain domain] ; IPR011704[A
ko03013	R	Translatior	J	Translatior	IPR000649 [Initiation factor 2B-related]
ko03013	R	Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DE
ko04910	Ir	Uncharacte	S	Function u	IPR001107 [Band 7 domain] ; IPR031905[Flotillin, C-ter
ko04064	N	--	--	--	IPR003877 [SPRY domain] ; IPR006574[SPRY-associate
ko04020	C	Serine/thre	T	Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko04010	M	Uncharacte	S	Function u	IPR001715 [Calponin homology domain] ; IPR017868[F
ko04022	cI	--	--	--	IPR001019 [Guanine nucleotide binding protein (G-pro
ko00052	G	UDP-gluco	M	Cell wall/m	IPR016040 [NAD(P)-binding domain]
ko01521	E	--	--	--	IPR000294 [Gamma-carboxyglutamic acid-rich (GLA) c
--		--	--	--	IPR022070 [Cytoplasmic activation/proliferation-associ
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR02912
--		--	--	--	IPR002350 [Kazal domain] ; IPR015369[Follistatin/Osteo
--		Large exop	U	Intracellula	IPR000742 [EGF-like domain] ; IPR001791[Laminin G do
--		Secreted tr	O	Posttransla	IPR000001 [Kringle] ; IPR000742[EGF-like domain] ; IPR
ko03030	D	DNA replic	L	Replicatior	IPR001208 [MCM domain] ; IPR027925[MCM N-termin
ko04340	H	--	--	--	IPR000320 [Hedgehog, N-terminal signalling domain]
--		Secreted p	R	General fu	IPR002035 [von Willebrand factor, type A] ; IPR010600[
ko04014	R	--	--	--	IPR000008 [C2 domain] ; IPR001562[Zinc finger, Btk mo
--		--	--	--	IPR001715 [Calponin homology domain] ; IPR002048[E
--		--	--	--	IPR000253 [Forkhead-associated (FHA) domain] ; IPR0
--		--	--	--	IPR013809 [ENTH domain]

ko04110	C	Chromoso	D	Cell cycle c	IPR003395 [RecF/RecN/SMC, N-terminal] ; IPR010935[S
ko00510	N	Alpha-glu	G	Carbohydr	IPR000322 [Glycoside hydrolase family 31] ; IPR025887
--		--	--	--	IPR028169 [Raftlin family]
ko04141	P	Serine pro	O	Posttransla	IPR000209 [Peptidase S8/S53 domain]
--		Uncharacte	S	Function u	IPR002499 [Major vault protein, N-terminal] ; IPR02187
ko04350	T	--	--	--	IPR001881 [EGF-like calcium-binding domain] ; IPR017
ko05165	H	Uncharacte	S	Function u	IPR000330 [SNF2-related, N-terminal domain] ; IPR001
--		--	--	--	IPR000900 [Nebulin repeat] ; IPR001452[SH3 domain] ;
ko03013	R	--	--	--	IPR001494 [Importin-beta, N-terminal domain]
--		--	--	--	--
ko03050	P	--	--	--	IPR021843 [Protein of unknown function DUF3437] ; IP
--		--	--	--	IPR001936 [Ras GTPase-activating protein] ; IPR003123
ko03050	P	--	--	--	IPR000717 [Proteasome component (PCI) domain] ; IPR
ko04142	L	--	--	--	IPR004687 [Lysosomal-associated transmembrane pro
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR00866
		--	--	--	IPR024324 [Condensin complex subunit 1, N-terminal]
ko03040	S	Translatior	J	Translatior	IPR000640 [Translation elongation factor EFG, V domai
--		Uncaracter	R	General fu	IPR000782 [FAS1 domain]
ko04141	P	Negative r	O	Posttransla	IPR013766 [Thioredoxin domain]
ko00565	E	Lysophosp	E	Amino aci	IPR013830 [SGNH hydrolase-type esterase domain]
--		--	--	--	IPR000859 [CUB domain] ; IPR018933[Netrin module, r
		Sugar lacto	G	Carbohydr	IPR002640 [Arylesterase]
ko00190	C	Inorganic p	CP	Energy prc	IPR008162 [Inorganic pyrophosphatase]
ko00590	A	--	--	--	IPR007052 [CS domain]
--		Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR017892[Protein
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR01297
ko04931	Ir	--	--	--	IPR004327 [Phosphotyrosyl phosphatase activator, PTP
--		Protein tyr	T	Signal tran	IPR000242 [PTP type protein phosphatase] ; IPR000998
ko04144	E	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko04390	H	--	--	--	IPR001680 [WD40 repeat] ; IPR013577[Lethal giant larv
ko04010	M	Cell divisio	D	Cell cycle c	IPR000719 [Protein kinase domain] ; IPR017892[Protein
ko03040	S	--	--	--	IPR004088 [K Homology domain, type 1]
ko04216	F	--	--	--	IPR004088 [K Homology domain, type 1]
ko04066	H	--	--	--	IPR016073 [SKP1 component, POZ domain]
ko04072	P	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko00100	S	FAD/FMN-	C	Energy prc	IPR006094 [FAD linked oxidase, N-terminal]
ko03040	S	--	--	--	IPR004871 [Cleavage/polyadenylation specificity factor
--		Leucine-ri	K	Transcripti	IPR001611 [Leucine-rich repeat]
--		--	--	--	IPR000557 [Calponin repeat] ; IPR001715[Calponin hor
--		Leucine-ri	K	Transcripti	--
ko03040	S	--	--	--	IPR000061 [SWAP/Surp] ; IPR000626[Ubiquitin domain
ko00030	P	Sugar lacto	G	Carbohydr	IPR013658 [SMP-30/Gluconolactonase/LRE-like region
--		--	--	--	IPR001715 [Calponin homology domain] ; IPR004953[E
--		Uncaracter	R	General fu	IPR000782 [FAS1 domain]
ko04960	A	Periplasmi	O	Posttransla	IPR001478 [PDZ domain] ; IPR015098[EBP50, C-termin
--		--	--	--	IPR002848 [Translin family]
--		--	--	--	IPR001715 [Calponin homology domain] ; IPR004953[E
ko04152	A	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
ko04974	P	Na+/H+-c	C	Energy prc	IPR001991 [Sodium:dicarboxylate symporter]
		--	--	--	IPR000608 [Ubiquitin-conjugating enzyme E2]
ko04144	E	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
ko04510	F	--	--	--	IPR001781 [Zinc finger, LIM-type]
ko03050	P	--	--	--	IPR006773 [26S proteasome complex ubiquitin recepto
ko05200	P	--	--	--	IPR019152 [Protein of unknown function DUF2046]
ko00520	A	UDP-N-ac	G	Carbohydr	IPR002618 [UDPGP family]
--		--	--	--	IPR000867 [Insulin-like growth factor-binding protein,
ko04151	P	Methyl-ac	NT	Cell motilit	IPR001791 [Laminin G domain] ; IPR002049[Laminin EG
ko00534	G	--	--	--	IPR004263 [Exostosin-like] ; IPR015338[Exostosin , C-te

--	--	--	--	IPR019538	[26S proteasome non-ATPase regulatory su
ko04151	P	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR011072[HR1 rh
ko01522	E	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
ko04151	P	--	--	--	IPR013855 [Cdc37, N-terminal domain] ; IPR013873[Cc
ko04360	A	Dihydroor	F	Nucleotide	IPR006680 [Amidohydrolase-related]
--	--	--	--	--	IPR008253 [Marvel domain]
--	--	WD40 rep	R	General fu	IPR001680 [WD40 repeat] ; IPR022052[Histone-binding
--	--	--	--	--	IPR008605 [Extracellular matrix protein 1]
ko04514	C	--	--	--	IPR008253 [Marvel domain] ; IPR010844[Occludin hom
ko03015	m	Uncharact	S	Function u	IPR000504 [RNA recognition motif domain]
ko03013	R	--	--	--	IPR010304 [Survival motor neuron]
--	--	--	--	--	IPR002108 [Actin-depolymerising factor homology dor
--	--	--	--	--	IPR022768 [Fascin domain]
--	--	--	--	--	IPR011511 [Variant SH3 domain]
ko00380	T	Kynurenin	E	Amino aci	IPR000192 [Aminotransferase class V domain]
ko00600	S	Glycosyltra	N	Cell motilit	IPR025993 [Ceramide glucosyltransferase]
--	--	Zn-depen	O	Posttransla	IPR007484 [Peptidase M28]
ko00040	P	UDP-N-ac	G	Carbohydr	IPR002618 [UDPGP family]
ko00260	G	Cu2+-con	Q	Secondary	IPR015798 [Copper amine oxidase, C-terminal] ; IPR01
ko00270	C	Predicted	R	General fu	IPR010300 [Cysteine dioxygenase type I]
--	--	--	--	--	--
--	--	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
ko04144	E	--	--	--	IPR028191 [WASH complex subunit 7, N-terminal] ; IPF
--	--	Predicted	T	Signal tran	IPR001680 [WD40 repeat]
ko04144	E	--	--	--	IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC
--	--	--	--	--	IPR005123 [Oxoglutarate/iron-dependent dioxygenase
ko00670	C	Acyl-CoA	C	Energy pro	IPR002376 [Formyl transferase, N-terminal] ; IPR00579
--	--	--	--	--	IPR001806 [Small GTPase superfamily]
--	--	--	--	--	IPR001079 [Galectin, carbohydrate recognition domain
--	--	--	--	--	IPR007632 [Anoctamin] ; IPR032394[Anoctamin, dimeri
--	--	--	--	--	IPR031453 [Transmembrane protein 119]
--	--	Secreted p	R	General fu	IPR002035 [von Willebrand factor, type A] ; IPR032770[
--	--	--	--	--	IPR018797 [Uncharacterised protein family FAM98]
ko04014	R	Ca2+-binc	Q	Secondary	IPR013818 [Lipase/vitellogenin]
ko00330	A	Pyrroline-5	E	Amino aci	IPR028939 [Pyrroline-5-carboxylate reductase, catalytic
--	--	Actin-relat	Z	Cytoskelet	IPR004000 [Actin family]
ko04141	P	Molecular	O	Posttransla	IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
ko04141	P	Molecular	O	Posttransla	IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
--	--	--	--	--	IPR007071 [A-kinase anchoring protein 95 (AKAP95)]
--	--	--	--	--	IPR007587 [SIT4 phosphatase-associated protein famil
--	--	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
--	--	--	--	--	IPR012978 [Uncharacterised domain NUC173]
--	--	--	--	--	IPR005818 [Linker histone H1/H5, domain H15]
--	--	FKBP-type	O	Posttransla	IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
--	--	--	--	--	IPR000569 [HECT domain] ; IPR004939[APC10/DOC dc
ko05165	H	--	--	--	IPR003126 [Zinc finger, UBR-type] ; IPR025704[E3 ubiq
--	--	--	--	--	--
--	--	--	--	--	IPR025481 [Cell morphogenesis protein C-terminal] ; IF
--	--	--	--	--	IPR000626 [Ubiquitin domain] ; IPR019103[Aspartic pep
ko05034	A	--	--	--	IPR007125 [Histone H2A/H2B/H3]
--	--	--	--	--	IPR010630 [Neuroblastoma breakpoint family (NBPF) d
ko04141	P	--	--	--	IPR003323 [OTU domain]
--	--	--	--	--	IPR001594 [Palmitoyltransferase, DHHC domain]
ko04514	C	--	--	--	IPR013106 [Immunoglobulin V-set domain]
ko04115	p	Predicted	R	General fu	IPR013130 [Ferric reductase transmembrane compone
--	--	--	--	--	IPR028091 [FAM91, N-terminal domain] ; IPR028097[F/
--	--	--	--	--	IPR000195 [Rab-GTPase-TBC domain] ; IPR004182[GR/
--	--	--	--	--	IPR000980 [SH2 domain] ; IPR013625[Tensin/EPS8 pho

--	Glyoxylase	R	General fu	IPR001279	[Metallo-beta-lactamase]
ko04530 T	--	--	--	IPR000198	[Rho GTPase-activating protein domain] ; IF
--	Hemoglob	C	Energy pro	IPR000971	[Globin]
--	--	--	--	IPR003191	[Guanylate-binding protein, C-terminal] ; IP
--	Leucine-ri	K	Transcripti	IPR000742	[EGF-like domain] ; IPR001611[Leucine-rich
--	Acetylornit	E	Amino aci	IPR002933	[Peptidase M20] ; IPR011650[Peptidase M2(
ko04150 m	--	--	--	IPR028209	[LAMTOR1/MEH1]
--	--	--	--	IPR002108	[Actin-depolymerising factor homology dor
--	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
--	Ribosomal	J	Translatior	IPR003347	[JmjC domain]
ko03040 S	--	--	--	IPR000555	[JAB1/MPN/MOV34 metalloenzyme domair
ko04310 W	--	--	--	IPR004963	[Pectinacetylesterase/NOTUM]
--	--	--	--	IPR029444	[Integrator complex subunit 5, C-terminal] ;
--	--	--	--	IPR001478	[PDZ domain] ; IPR001660[Sterile alpha mot
--	NADP-dep	C	Energy pro	IPR002347	[Short-chain dehydrogenase/reductase SDF
--	Serine prot	O	Posttransla	IPR002165	[Plexin repeat]
--	--	--	--	IPR000884	[Thrombospondin type-1 (TSP1) repeat] ; IP
--	Uncharacte	R	General fu	IPR001599	[Alpha-2-macroglobulin] ; IPR002890[Alpha
--	WD40 repe	R	General fu	IPR000409	[BEACH domain] ; IPR001680[WD40 repeat]
--	--	--	--	IPR000008	[C2 domain] ; IPR019558[Mammalian uncoc
--	--	--	--	IPR008664	[LISCH7]
--	--	--	--	IPR000884	[Thrombospondin type-1 (TSP1) repeat] ; IP
--	--	--	--	IPR025232	[Domain of unknown function DUF4174]
--	--	--	--	IPR003877	[SPRY domain] ; IPR006574[SPRY-associate
--	Transcripti	K	Transcripti	IPR000980	[SH2 domain] ; IPR003029[S1 domain] ; IPR(
ko05169 E	Endonucle	L	Replicatior	IPR002999	[Tudor domain] ; IPR016071[Staphylococcal
ko03040 S	Superfamil	L	Replicatior	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DE
ko04512 E	Predicted a	G	Carbohydr	IPR001646	[Pentapeptide repeat] ; IPR005828[Major fa
--	--	--	--	IPR003307	[W2 domain]
--	HrpA-like	J	Translatior	IPR001650	[Helicase, C-terminal] ; IPR007502[Helicase-
--	--	--	--	IPR000717	[Proteasome component (PCI) domain]
ko03013 R	--	--	--	IPR008081	[Cytoplasmic FMR1-interacting] ; IPR00982
--	--	--	--	IPR000555	[JAB1/MPN/MOV34 metalloenzyme domair
ko04010 M	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
ko04144 E	--	--	--	IPR005024	[Snf7 family]
ko04010 M	--	--	--	IPR000651	[Ras-like guanine nucleotide exchange fact
ko03040 S	--	--	--	IPR005345	[PHF5-like]
--	--	--	--	IPR004170	[WWE domain] ; IPR012317[Poly(ADP-ribos
--	Phage-rela	X	Mobilome:	IPR000998	[MAM domain]
ko04136 A	--	--	--	IPR007241	[Autophagy-related protein 9]
--	--	--	--	IPR015403	[Sec7, C-terminal] ; IPR032629[Mon2, dimer
ko04530 T	--	--	--	IPR001609	[Myosin head, motor domain] ; IPR002928[M
--	--	--	--	IPR024395	[CLASP N-terminal domain]
--	--	--	--	IPR000859	[CUB domain] ; IPR002172[Low-density lipo
ko00040 P	NAD(P)-de	IQR	Lipid trans	--	
ko04120 U	--	--	--	IPR000569	[HECT domain] ; IPR004170[WWE domain] ;
--	Leucine-ri	K	Transcripti	--	
--	--	--	--	IPR003961	[Fibronectin type III]
--	--	--	--	IPR026315	[Out at first protein]
--	--	--	--	--	
ko04611 P	--	--	--	IPR001849	[Pleckstrin homology domain] ; IPR019748[F
ko03013 R	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain] ; IPR02571
--	--	--	--	IPR005016	[Serine incorporator/TMS membrane protei
ko04142 Ly	--	--	--	IPR004687	[Lysosomal-associated transmembrane prot
--	--	--	--	IPR013932	[TATA-binding protein interacting (TIP20)]
--	--	--	--	IPR001660	[Sterile alpha motif domain]
ko01522 E	Predicted I	R	General fu	IPR020989	[Histone-arginine methyltransferase CARM1
ko00670 C	Dihydrofol	H	Coenzyme	IPR001796	[Dihydrofolate reductase domain]

--	--	--	--	IPR001841	[Zinc finger, RING-type] ; IPR003137[PA do
--	Uncharacte	S	Function u	IPR001007	[VWFC domain] ; IPR003644[Na-Ca exchan
ko04145 P	--	--	--	IPR000727	[Target SNARE coiled-coil homology doma
--	--	--	--	IPR000008	[C2 domain] ; IPR010734[Copine]
--	Uncharacte	R	General fu	IPR000884	[Thrombospondin type-1 (TSP1) repeat] ; IP
--	--	--	--	IPR000225	[Armadillo]
--	Bacillopep	O	Posttransla	IPR000421	[Coagulation factor 5/8 C-terminal domain]
ko00564 G	Phosphatic	I	Lipid trans	IPR001736	[Phospholipase D/Transphosphatidylase] ; II
	--	--	--	IPR029270	[Limb expression 1]
ko03008 R	WD40 repe	R	General fu	IPR001680	[WD40 repeat]
--	Uncharacte	R	General fu	IPR000306	[FYVE zinc finger] ; IPR001680[WD40 repeat
--	Leucine-ric	K	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR021040[LRRC8, pa
ko03040 S	--	--	--	IPR000061	[SWAP/Surp] ; IPR000467[G-patch domain]
--	--	--	--	IPR000859	[CUB domain] ; IPR001881[EGF-like calcium
--	--	--	--	IPR003034	[SAP domain] ; IPR025223[S1-like RNA binc
ko04137 M	--	--	--	IPR001806	[Small GTPase superfamily] ; IPR013566[EF h
--	23S rRNA I	J	Translatior	IPR002877	[Ribosomal RNA methyltransferase FtsJ dom
--	--	--	--	IPR029399	[TMEM192 family]
ko03013 R	--	--	--	IPR002483	[PWI domain]
--	Metal-dep	R	General fu	IPR002933	[Peptidase M20] ; IPR011650[Peptidase M20
--	AAA+-typ	MDT	Cell wall/m	IPR003959	[ATPase, AAA-type, core] ; IPR006594[LIS1 I
--	Ankyrin rep	T	Signal tran	IPR000569	[HECT domain] ; IPR020683[Ankyrin repeat-
--	Ankyrin rep	T	Signal tran	IPR021832	[Ankyrin repeat domain-containing protein
--	Acyl-CoA	C	Energy pro	IPR015590	[Aldehyde dehydrogenase domain]
--	--	--	--	IPR025223	[S1-like RNA binding domain] ; IPR025954[I
--	Phenylalan	J	Translatior	IPR001611	[Leucine-rich repeat] ; IPR005146[B3/B4 tRN
--	--	--	--	IPR001664	[Intermediate filament protein] ; IPR032444[
--	--	--	--	IPR000198	[Rho GTPase-activating protein domain]
--	--	--	--	IPR011021	[Arrestin-like, N-terminal] ; IPR011022[Arres
	--	--	--	IPR007133	[RNA polymerase II associated factor Paf1]
ko04623 C	--	--	--	IPR024810	[Mab-21 domain]
ko04360 A	Membrane	M	Cell wall/m	IPR000697	[WH1/EVH1 domain] ; IPR014885[VASP tetr
--	Leucine-ric	K	Transcripti	IPR001611	[Leucine-rich repeat]
ko03040 S	--	--	--	IPR005037	[Pre-mRNA-splicing factor 38] ; IPR024767[
ko03008 R	ATP-depe	O	Posttransla	IPR003959	[ATPase, AAA-type, core]
--	DNA-bind	R	General fu	IPR001258	[NHL repeat] ; IPR012336[Thioredoxin-like f
--	--	--	--	--	
ko00310 L	Glycosyltra	M	Cell wall/m	IPR002654	[Glycosyl transferase, family 25]
--	--	--	--	IPR010795	[Prenylcysteine lyase]
ko04141 P	Negative r	O	Posttransla	IPR013766	[Thioredoxin domain]
ko00520 A	Nucleoside	M	Cell wall/m	IPR016040	[NAD(P)-binding domain] ; IPR021761[UDP
--	--	--	--	IPR001841	[Zinc finger, RING-type] ; IPR003137[PA do
--	--	--	--	IPR006861	[Hyaluronan/mRNA-binding protein] ; IPR0
--	--	--	--	--	
ko00532 G	Putative Zr	R	General fu	IPR005331	[Sulfotransferase]
--	--	--	--	IPR022049	[FAM69, protein-kinase domain]
--	Hemolysin	R	General fu	IPR000644	[CBS domain]
--	ATPase co	R	General fu	IPR003439	[ABC transporter-like] ; IPR032781[ABC-tra
--	--	--	--	IPR000261	[EH domain]
--	--	--	--	IPR018499	[Tetraspanin/Peripherin]
--	--	--	--	IPR007000	[Phospholipase B-like]
ko04390 H	--	--	--	IPR001478	[PDZ domain] ; IPR015132[L27-2]
ko04310 W	--	--	--	IPR009539	[Vang-like protein]
ko04141 P	--	--	--	IPR007716	[NPL4, zinc-binding putative] ; IPR007717[N
--	Regulator	O	Posttransla	IPR001107	[Band 7 domain]
--	--	--	--	IPR013657	[UAA transporter]
--	--	--	--	IPR019326	[Protein of unknown function DUF2369]
--	N-acetylne	M	Cell wall/m	IPR011498	[Kelch repeat type 2]

ko04120	U	Ubiquitin	O	Posttransla	IPR000594 [THIF-type NAD/FAD binding fold] ; IPR014
ko00562	Ir	--	--	--	IPR002498 [Phosphatidylinositol-4-phosphate 5-kinase
--		--	--	--	IPR003137 [PA domain] ; IPR007369[Peptidase A22B, si
--		--	--	--	IPR022078 [CD99 antigen-like protein 2]
--		Alpha-tub	DZ	Cell cycle c	IPR000408 [Regulator of chromosome condensation, R
--		Predicted a	G	Carbohydr	IPR005828 [Major facilitator, sugar transporter-like]
--		--	--	--	IPR001715 [Calponin homology domain] ; IPR001781[Z
ko03008	R	WD40 repe	R	General fu	IPR001680 [WD40 repeat] ; IPR018983[U3 small nucleo
--		--	--	--	IPR000357 [HEAT repeat] ; IPR001494[Importin-beta, N
--		--	--	--	IPR005612 [CCAAT-binding factor] ; IPR011501[Nuclec
ko04145	P	--	--	--	IPR002159 [CD36 family]
--		Plastocyan	C	Energy prc	IPR019316 [G8 domain] ; IPR025155[WxxW domain]
ko04144	E	--	--	--	IPR004328 [BRO1 domain] ; IPR025304[ALIX V-shaped
--		Phosphate	P	Inorganic i	IPR001204 [Phosphate transporter]
ko04810	R	--	--	--	--
--		--	--	--	IPR000058 [Zinc finger, AN1-type]
--		--	--	--	IPR001619 [Sec1-like protein]
--		--	--	--	--
ko05231	C	--	--	--	IPR007603 [Choline transporter-like]
--		--	--	--	--
ko02010	A	ABC-type	V	Defense m	IPR003439 [ABC transporter-like]
--		--	--	--	IPR001507 [Zona pellucida domain]
--		--	--	--	IPR013098 [Immunoglobulin I-set]
ko03460	F	--	--	--	--
--		--	--	--	IPR022699 [Stonin-2, N-terminal] ; IPR028565[Mu hom
--		--	--	--	IPR000679 [Zinc finger, GATA-type] ; IPR032346[Transc
ko03040	S	--	--	--	IPR013180 [Beta-catenin-like protein 1, N-terminal]
--		--	--	--	IPR009428 [Beta-catenin-interacting ICAT]
--		--	--	--	IPR001675 [Glycosyl transferase family 29]
--		Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR003877[SPRY dor
--		--	--	--	--
--		--	--	--	IPR005818 [Linker histone H1/H5, domain H15]
--		Amino acic	E	Amino acic	IPR002293 [Amino acid/polyamine transporter I]
--		--	--	--	IPR004240 [Nonaspanin (TM9SF)]
ko04142	L	--	--	--	IPR022775 [AP complex, mu/sigma subunit]
--		Pimeloyl-A	HR	Coenzyme	IPR004142 [NDRG]
ko04141	P	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko03018	R	--	--	--	--
--		--	--	--	IPR001478 [PDZ domain] ; IPR001609[Myosin head, mo
--		Predicted	T	Signal tran	--
--		--	--	--	IPR000198 [Rho GTPase-activating protein domain]
--		Ca2+-binc	Q	Secondary	IPR001007 [VWFC domain] ; IPR001611[Leucine-rich re
--		Leucine-ric	K	Transcripti	--
ko04514	C	--	--	--	IPR013106 [Immunoglobulin V-set domain] ; IPR01316
--		Periplasmic	O	Posttransla	IPR000867 [Insulin-like growth factor-binding protein,
ko04144	E	WD40 repe	R	General fu	IPR001680 [WD40 repeat]
ko04110	C	Acetoin uti	BQ	Chromatin	IPR023801 [Histone deacetylase domain]
ko04144	E	--	--	--	IPR001452 [SH3 domain] ; IPR002014[VHS domain] ; IP
ko00790	F	Gamma-gl	E	Amino acic	IPR011697 [Peptidase C26]
--		Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DE
--		Ankyrin rep	T	Signal tran	IPR001452 [SH3 domain] ; IPR020683[Ankyrin repeat-c
ko04270	V	--	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR015212[R
ko04514	C	--	--	--	IPR001893 [Cysteine-rich Golgi apparatus protein 1 rep
--		Proteasom	O	Posttransla	IPR000555 [JAB1/MPN/MOV34 metalloenzyme domain
ko05225	H	--	--	--	IPR001005 [SANT/Myb domain] ; IPR007526[SWIRM do
ko04530	T	GTPase SA	R	General fu	IPR001806 [Small GTPase superfamily]
--		--	--	--	IPR004088 [K Homology domain, type 1] ; IPR015096[D
--		Leucine-ric	K	Transcripti	IPR001212 [Somatomedin B domain] ; IPR018487[Hem

ko04530	T	--	--	--	IPR000219 [Dbl homology (DH) domain]
--	--	--	--	--	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04120	U	--	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko00534	G	--	--	--	IPR004263 [Exostosin-like] ; IPR015338[Exostosin , C-te
ko00260	G	Methionine	E	Amino acid	IPR003726 [Homocysteine-binding domain]
--	--	Protein-ty	T	Signal tran	IPR000340 [Dual specificity phosphatase, catalytic dom
--	--	--	--	--	IPR007273 [SCAMP]
ko05225	H	--	--	--	IPR009071 [High mobility group box domain]
--	--	--	--	--	IPR013106 [Immunoglobulin V-set domain]
--	--	--	--	--	IPR007191 [Sec8 exocyst complex component specific
ko03013	R	--	--	--	IPR004023 [Mago nashi protein]
--	--	--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR019748[F
--	--	Uncharacte	S	Function u	IPR004088 [K Homology domain, type 1] ; IPR015096[D
--	--	--	--	--	--
--	--	GTPase SA	R	General fu	IPR006689 [Small GTPase superfamily, ARF/SAR type]
--	--	Nicotinami	HR	Coenzyme	IPR000868 [Isochorismatase-like]
--	--	--	--	--	IPR001849 [Pleckstrin homology domain]
--	--	--	--	--	IPR007259 [Gamma-tubulin complex component prote
--	--	--	--	--	IPR003131 [Potassium channel tetramerisation-type BT
--	--	--	--	--	IPR002048 [EF-hand domain]
ko03040	S	WD40 repe	R	General fu	IPR001680 [WD40 repeat]
ko04142	L	Arylsulfata	P	Inorganic i	IPR000917 [Sulfatase, N-terminal]
ko03015	m	RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain]
--	--	--	--	--	IPR029204 [CB1 cannabinoid receptor-interacting prot
--	--	Ca2+-dep	R	General fu	IPR000008 [C2 domain] ; IPR010734[Copine]
ko04144	E	--	--	--	IPR005024 [Snf7 family]
ko00010	G	Phosphom	G	Carbohydr	IPR005843 [Alpha-D-phosphohexomutase, C-terminal
--	--	Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DE
--	--	--	--	--	IPR001478 [PDZ domain] ; IPR001781[Zinc finger, LIM-
--	--	--	--	--	IPR004088 [K Homology domain, type 1]
ko00051	F	NDP-suga	JM	Translatior	IPR001451 [Hexapeptide repeat] ; IPR005835[Nucleotic
ko04610	C	Murein trip	M	Cell wall/m	IPR000834 [Peptidase M14, carboxypeptidase A] ; IPR0
--	--	Outer men	M	Cell wall/m	IPR013098 [Immunoglobulin I-set] ; IPR013162[CD80-I
--	--	--	--	--	IPR001190 [SRCR domain] ; IPR001695[Lysyl oxidase]
--	--	Aldo/keto	Q	Secondary	IPR023210 [NADP-dependent oxidoreductase domain]
		--	--	--	IPR002715 [Nascent polypeptide-associated complex N
--	--	--	--	--	IPR002049 [Laminin EGF domain] ; IPR013032[EGF-like
ko00330	A	Acetylornit	E	Amino acid	IPR002933 [Peptidase M20] ; IPR011650[Peptidase M20
--	--	Glutathion	O	Posttransla	--
ko04144	E	--	--	--	IPR000159 [Ras-associating (RA) domain] ; IPR000198[I
--	--	--	--	--	IPR001494 [Importin-beta, N-terminal domain]
--	--	N-acetylm	M	Cell wall/m	IPR002502 [N-acetylmuramoyl-L-alanine amidase dom
ko04120	U	--	--	--	IPR000008 [C2 domain] ; IPR000569[HECT domain] ; IP
ko04724	G	--	--	--	IPR013057 [Amino acid transporter, transmembrane do
--	--	--	--	--	IPR006628 [Purine-rich element binding protein family
--	--	--	--	--	IPR000990 [Innexin]
ko04621	N	--	--	--	IPR000990 [Innexin]
--	--	--	--	--	IPR001452 [SH3 domain] ; IPR001683[Phox homologou
ko04015	R	--	--	--	IPR000276 [G protein-coupled receptor, rhodopsin-like
ko04621	N	Leucine-ric	K	Transcripti	IPR001478 [PDZ domain] ; IPR001611[Leucine-rich rep
--	--	Outer men	M	Cell wall/m	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IP
--	--	--	--	--	IPR003877 [SPRY domain] ; IPR006594[LIS1 homology
--	--	--	--	--	IPR000538 [Link domain] ; IPR013106[Immunoglobulin
--	--	--	--	--	IPR008253 [Marvel domain]
--	--	--	--	--	IPR000306 [FYVE zinc finger] ; IPR001849[Pleckstrin hor
--	--	--	--	--	IPR006561 [DZF domain] ; IPR014720[Double-strandec
--	--	Predicted a	G	Carbohydr	--
ko04919	T	--	--	--	IPR003822 [Paired amphipathic helix] ; IPR013194[Histo

--	--	--	--	IPR024687	[MMS19, C-terminal]
--	--	--	--	--	
--	--	--	--	--	
--	--	--	--	IPR000626	[Ubiquitin domain] ; IPR000938[CAP Gly-ric
ko03050	P	20S protea	O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta] ; IPR0246
ko00440	P	Glycerol-3	M	Cell wall/m	IPR004821 [Cytidyltransferase-like domain]
ko03040	S	--	--	--	IPR021786 [Pre-mRNA splicing factor component Cdc5
ko03050	P	Predicted I	T	Signal tran	IPR002015 [Proteasome/cyclosome repeat]
ko05012	P	Putative in	R	General fu	IPR002818 [DJ-1/PfpI]
ko00511	C	Neuramini	GM	Carbohydr	IPR011040 [Sialidases]
--		NADPH:qu	CR	Energy pro	IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
--	--	--	--	--	IPR000225 [Armadillo]
--	--	--	--	--	IPR013787 [S100/CaBP-9k-type, calcium binding, subc
--	--	--	--	--	IPR033464 [CSN8/PSMD8/EIF3K]
--	--	--	--	--	IPR002048 [EF-hand domain]
ko04974	P	Cell divisio	D	Cell cycle c	IPR002035 [von Willebrand factor, type A] ; IPR003961[
--	--	--	--	--	IPR002164 [Nucleosome assembly protein (NAP)]
--	--	--	--	--	
ko00562	Ir	--	--	--	IPR002498 [Phosphatidylinositol-4-phosphate 5-kinase
--	--	--	--	--	IPR004240 [Nonaspanin (TM9SF)]
--	--	--	--	--	IPR002259 [Equilibrative nucleoside transporter]
ko04144	E	--	--	--	IPR001452 [SH3 domain] ; IPR004148[BAR domain]
ko04144	E	--	--	--	IPR006789 [Actin-related protein 2/3 complex subunit
--		RNA recog	J	Translatior	IPR000504 [RNA recognition motif domain] ; IPR00187
--		Predicted /	R	General fu	IPR001680 [WD40 repeat] ; IPR022052[Histone-binding
--		O-acetyl-A	J	Translatior	IPR002589 [Macro domain]
--		Predicted /	R	General fu	IPR001680 [WD40 repeat]
--	--	--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR019748[I
--		Membrane	M	Cell wall/m	IPR001680 [WD40 repeat] ; IPR015048[Domain of unkn
--	--	--	--	--	IPR010357 [Protein of unknown function DUF953, thior
--		3',5'-cyclic	T	Signal tran	IPR004843 [Calcineurin-like phosphoesterase domain,
--		Negative r	O	Posttransla	IPR013766 [Thioredoxin domain]
--	--	--	--	--	IPR000008 [C2 domain] ; IPR031468[Synaptotagmin-lik
--	--	--	--	--	IPR015940 [Ubiquitin-associated domain]
--	--	--	--	--	IPR019325 [NEDD4/Bsd2]
--	--	--	--	--	IPR000717 [Proteasome component (PCI) domain]
--	--	--	--	--	IPR019140 [Mini-chromosome maintenance complex-
--	--	--	--	--	
--		Leucine-ri	K	Transcripti	IPR001611 [Leucine-rich repeat]
ko00562	Ir	--	--	--	IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic
--	--	--	--	--	IPR022577 [Tubulin-specific chaperone D, C-terminal]
ko00511	C	Alpha-L-fu	G	Carbohydr	IPR000933 [Glycoside hydrolase, family 29] ; IPR031919
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko05164	Ir	--	--	--	IPR003034 [SAP domain] ; IPR003877[SPRY domain]
--	--	--	--	--	IPR019605 [Misato Segment II tubulin-like domain] ; IP
--	--	--	--	--	
ko03040	S	Superfamil	L	Replicatior	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DE
--	--	--	--	--	IPR001841 [Zinc finger, RING-type]
ko04145	P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
--	--	--	--	--	
--		Protein-ty	T	Signal tran	IPR000340 [Dual specificity phosphatase, catalytic dom
--	--	--	--	--	IPR009038 [GOLD domain]
ko03013	R	--	--	--	--
--		Forkhead a	T	Signal tran	IPR000253 [Forkhead-associated (FHA) domain] ; IPR0
--	--	--	--	--	IPR000648 [Oxysterol-binding protein]
ko00520	A	Dihydrodip	EM	Amino acid	IPR002220 [DapA-like]
ko04144	E	--	--	--	IPR000008 [C2 domain] ; IPR019018[Rab-binding dom
--	--	--	--	--	IPR000195 [Rab-GTPase-TBC domain]

--	Tetratricop	R	General fu	IPR019734	[Tetratricopeptide repeat] ; IPR021183[N-te
--	--	--	--	IPR007042	[Arsenite-resistance protein 2] ; IPR021933[
--	--	--	--	IPR022065	[Uncharacterised protein family, TMEM59]
--	--	--	--	IPR013979	[Translation initiation factor, beta propellor-
ko04514 C	--	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
ko03320 P	--	--	--	IPR002181	[Fibrinogen, alpha/beta/gamma chain, C-te
--	--	--	--	IPR010510	[FGF binding 1]
--	--	--	--	IPR001849	[Pleckstrin homology domain] ; IPR010703[I
ko03008 R	GTP-bindi	R	General fu	IPR010674	[Nucleolar GTP-binding protein 1, Rossman
ko05202 T	--	--	--	IPR001012	[UBX domain] ; IPR021569[TUG ubiquitin-lik
--	--	--	--	IPR000648	[Oxysterol-binding protein] ; IPR001849[Ple
--	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko04310 W	Predicted I	T	Signal tran	IPR001680	[WD40 repeat] ; IPR006594[LIS1 homology
ko04015 R	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR002219[Protein
--	--	--	--	--	
ko00240 P	Uridine kin	F	Nucleotide	IPR006083	[Phosphoribulokinase/uridine kinase]
--	FOG: Zn-fi	R	General fu	IPR001909	[Krueppel-associated box] ; IPR007087[Zinc
ko03013 R	--	--	--	IPR003890	[MIF4G-like, type 3] ; IPR009818[Ataxin-2, C
--	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko05134 L	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
--	--	--	--	IPR015021	[Domain of unknown function DUF1907]
--	--	--	--	IPR006993	[SH3-binding, glutamic acid-rich protein]
ko04114 C	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR022165[Polo ki
ko04724 G	--	--	--	IPR013057	[Amino acid transporter, transmembrane do
ko04010 M	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
ko00190 C	Inorganic p	CP	Energy pro	IPR008162	[Inorganic pyrophosphatase]
--	Carboxype	E	Amino acid	IPR001563	[Peptidase S10, serine carboxypeptidase]
--	Acid stress	T	Signal tran	IPR002634	[BolA protein]
--	Protein tyr	T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR004328
--	Tetratricop	R	General fu	IPR019734	[Tetratricopeptide repeat] ; IPR024660[UNC
ko04144 E	--	--	--	IPR005024	[Snf7 family]
--	Aminopep	E	Amino acid	IPR014782	[Peptidase M1, membrane alanine aminope
ko04145 P	--	--	--	IPR003008	[Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko03008 R	--	--	--	IPR012954	[BP28, C-terminal domain] ; IPR022125[U3 s
--	--	--	--	IPR007110	[Immunoglobulin-like domain] ; IPR013106[
ko04621 N	--	--	--	IPR002035	[von Willebrand factor, type A] ; IPR008399[
--	--	--	--	IPR007109	[Brix domain]
ng (GO:00	WD40 repe	R	General fu	IPR001680	[WD40 repeat]
ko04144 E	--	--	--	IPR018798	[Multivesicular body subunit 12]
ko04120 U	--	--	--	IPR000608	[Ubiquitin-conjugating enzyme E2]
ko04145 P	--	--	--	IPR003008	[Tubulin/FtsZ, GTPase domain]
--	--	--	--	IPR000306	[FYVE zinc finger] ; IPR001849[Pleckstrin hom
--	Leucine-ric	K	Transcripti	IPR001611	[Leucine-rich repeat]
ko04144 E	--	--	--	IPR009851	[Modifier of rudimentary, Modr]
--	--	--	--	IPR000717	[Proteasome component (PCI) domain]
--	Histone ac	KB	Transcripti	IPR000182	[GNAT domain] ; IPR007197[Radical SAM] ;
--	Ubiquitin	O	Posttransla	IPR000626	[Ubiquitin domain] ; IPR032752[Ubiquitin-b
ko00760 N	Nicotinic a	H	Coenzyme	IPR004821	[Cytidyltransferase-like domain]
ko04014 R	WD40 repe	R	General fu	IPR001680	[WD40 repeat]
ko03013 R	--	--	--	IPR013598	[Exportin-1/Importin-beta-like]
--	Uncharacte	S	Function u	IPR003226	[Metal-dependent protein hydrolase]
--	Carboxype	E	Amino acid	IPR001563	[Peptidase S10, serine carboxypeptidase]
ko04310 W	--	--	--	IPR007052	[CS domain] ; IPR007699[SGS domain] ; IPR
ko04510 F	--	--	--	IPR001715	[Calponin homology domain]
--	Putative C	R	General fu	IPR001727	[Gdt1 family]
--	Superfamil	L	Replicatior	--	
--	--	--	--	IPR004240	[Nonaspanin (TM9SF)]
--	--	--	--	IPR009714	[Resistin]

--	Sugar lactc	G	Carbohydr	IPR018119	[Strictosidine synthase, conserved region]
--	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko04144 E	--	--	--	--	
ko03018 R	Ribonuclea	J	Translatior	IPR001247	[Exoribonuclease, phosphorolytic domain 1]
--	Large exop	U	Intracellula	IPR002126	[Cadherin] ; IPR013164[Cadherin, N-termina
ko00562 Ir	Myo-inosit	I	Lipid trans	IPR002587	[Myo-inositol-1-phosphate synthase] ; IPR(
ko04010 M	--	--	--	IPR000157	[Toll/interleukin-1 receptor homology (TIR)
--	--	--	--	IPR019318	[Guanine nucleotide exchange factor, Ric8]
ko05010 A	--	--	--	IPR003388	[Reticulon]
--	Xaa-Pro ar	E	Amino acic	IPR000994	[Peptidase M24] ; IPR007865[Aminopeptida
--	Xaa-Pro ar	E	Amino acic	IPR000587	[Creatinase, N-terminal] ; IPR000994[Peptid
--	--	--	--	IPR007084	[BRICHOS domain]
--	--	--	--	IPR001478	[PDZ domain] ; IPR001781[Zinc finger, LIM-
ko00010 G	Acyl-coen	I	Lipid trans	IPR000873	[AMP-dependent synthetase/ligase] ; IPR02
	Superfamil	L	Replicatior	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DE
ko04141 P	GTPase SA	R	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
ko03013 R	NDP-suga	JM	Translatior	IPR005835	[Nucleotidyl transferase domain]
ko01521 E	--	--	--	IPR000072	[PDGF/VEGF domain] ; IPR000859[CUB dom
ko04142 L	Sugar pho	G	Carbohydr	IPR011701	[Major facilitator superfamily]
ko00230 P	--	--	--	IPR003958	[Transcription factor CBF/NF-Y/archaeal his
--	--	--	--	IPR003958	[Transcription factor CBF/NF-Y/archaeal his
--	--	--	--	IPR003112	[Olfactomedin-like domain]
ko00770 P	Phosphop	H	Coenzyme	IPR008278	[4'-phosphopantetheinyl transferase superf
--	--	--	--	--	
--	DNA gyras	L	Replicatior	IPR006917	[SOUL haem-binding protein]
--	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko04144 E	--	--	--	IPR001619	[Sec1-like protein]
--	Uncharacte	S	Function u	IPR005552	[Scramblase]
ko00970 A	Phenylalan	J	Translatior	IPR005146	[B3/B4 tRNA-binding domain] ; IPR005147[
ko04136 A	--	--	--	IPR007134	[Autophagy-related protein 3, N-terminal] ;
--	--	--	--	--	
	Chromoso	D	Cell cycle c	IPR003395	[RecF/RecN/SMC, N-terminal] ; IPR010935[
--	Ribosome-	J	Translatior	IPR006073	[GTP binding domain] ; IPR013029[Domain
--	--	--	--	IPR009790	[Protein of unknown function DUF1356, TM
--	--	--	--	IPR001478	[PDZ domain] ; IPR014775[L27 domain, C-te
--	--	--	--	IPR009828	[Protein of unknown function DUF1394]
--	Superfamil	L	Replicatior	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DE
--	--	--	--	IPR005045	[CDC50/LEM3 family]
--	GTPase SA	R	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
--	--	--	--	--	
--	--	--	--	IPR004031	[PMP-22/EMP/MP20/Claudin superfamily]
ko00533 G	--	--	--	IPR002659	[Glycosyl transferase, family 31]
ko04810 R	--	--	--	IPR001452	[SH3 domain] ; IPR012849[Abl-interactor, h
--	--	--	--	--	
--	--	--	--	IPR014830	[Glycolipid transfer protein domain]
ko04141 P	--	--	--	IPR013918	[Nucleotide exchange factor Fes1]
ko00270 C	dTDP-4-d	M	Cell wall/m	IPR029903	[RmlD-like substrate binding domain]
ko04144 E	Replicatior	L	Replicatior	IPR000261	[EH domain] ; IPR022812[Dynamin superfan
--	Secreted tr	O	Posttransla	IPR000859	[CUB domain] ; IPR001254[Serine proteases
--	--	--	--	IPR001452	[SH3 domain] ; IPR018556[Domain of unkno
--	Glucose/ar	G	Carbohydr	IPR000033	[LDLR class B repeat] ; IPR000742[EGF-like c
--	Guanylate	F	Nucleotide	IPR001478	[PDZ domain] ; IPR008145[Guanylate kinase
ko04144 E	--	--	--	IPR005024	[Snf7 family]
ko04217 N	O-acetyl-A	J	Translatior	IPR002589	[Macro domain] ; IPR007125[Histone H2A/H
--	--	--	--	IPR000906	[ZU5 domain] ; IPR001452[SH3 domain] ; IP
--	--	--	--	IPR030379	[Septin-type guanine nucleotide-binding (G
--	--	--	--	IPR027817	[Costars domain]
--	Alpha-tub	DZ	Cell cycle c	IPR000408	[Regulator of chromosome condensation, R

--	Thioestera	Q	Secondary	IPR000873	[AMP-dependent synthetase/ligase] ; IPR01
--	DNA-bind	R	General fu	IPR009471	[Teneurin intracellular, N-terminal] ; IPR028
--	--	--	--	IPR025602	[BCP1 family]
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
--	--	--	--	IPR013106	[Immunoglobulin V-set domain]
--	--	--	--	--	
ko00970 A	Leucyl-tRN	J	Translatior	IPR002300	[Aminoacyl-tRNA synthetase, class Ia] ; IPR0
ko04144 E	Uncharacte	S	Function u	IPR000261	[EH domain]
--	--	--	--	IPR002553	[Clathrin/coatomer adaptor, adaptin-like, N
ko04145 P	Ca2+-binc	Q	Secondary	IPR000562	[Fibronectin, type II, collagen-binding] ; IPR
--	--	--	--	IPR004331	[SPX domain] ; IPR004342[EXS, C-terminal]
ko04144 E	Predicted	R	General fu	IPR024654	[Calcineurin-like phosphoesterase domain,
--	--	--	--	IPR033464	[CSN8/PSMD8/EIF3K]
ko04142 L	Cysteine p	O	Posttransla	IPR000668	[Peptidase C1A, papain C-terminal]
ko04120 U	Molybdop	H	Coenzyme	IPR000594	[THIF-type NAD/FAD binding fold] ; IPR028
--	--	--	--	IPR002048	[EF-hand domain]
--	--	--	--	IPR000717	[Proteasome component (PCI) domain]
ko04530 T	--	--	--	IPR001478	[PDZ domain] ; IPR008145[Guanylate kinase
--	DnaJ-class	O	Posttransla	IPR001623	[DnaJ domain] ; IPR002939[Chaperone Dna
--	Xanthine/u	F	Nucleotide	IPR006043	[Xanthine/uracil/vitamin C permease]
--	--	--	--	IPR001781	[Zinc finger, LIM-type] ; IPR010442[PET don
ko04068 F	CBS doma	T	Signal tran	IPR000644	[CBS domain]
ko04970 S	--	--	--	IPR000859	[CUB domain] ; IPR001190[SRCR domain] ; I
ko04010 M	--	--	--	IPR015019	[Ragulator complex protein LAMTOR3]
ko03060 P	--	--	--	IPR026258	[Signal recognition particle subunit SRP68]
--	--	--	--	IPR007051	[CHORD domain] ; IPR007052[CS domain]
ko05100 B	Predicted	R	General fu	IPR030379	[Septin-type guanine nucleotide-binding (G
ko00900 T	Protoporp	H	Coenzyme	IPR010795	[Prenylcysteine lyase]
--	--	--	--	IPR000884	[Thrombospondin type-1 (TSP1) repeat] ; IP
--	Prefoldin,	O	Posttransla	IPR002777	[Prefoldin beta-like]
--	Serine/thre	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
ko00270 C	Enolase-pl	E	Amino acic	--	
ko00190 C	--	--	--	IPR011987	[ATPase, V1 complex, subunit H, C-terminal
--	--	--	--	IPR001494	[Importin-beta, N-terminal domain]
--	--	--	--	--	
ko04140 A	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
ko04614 R	Aminopep	E	Amino acic	IPR014782	[Peptidase M1, membrane alanine aminope
ko04360 A	DNA-bind	R	General fu	IPR001627	[Sema domain] ; IPR002165[Plexin repeat] ;
--	--	--	--	IPR001452	[SH3 domain] ; IPR002108[Actin-depolymer
ko04144 E	--	--	--	IPR007143	[Vacuolar protein sorting-associated, VPS28
--	Serine pro	O	Posttransla	IPR023796	[Serpin domain]
--	Ribosomal	J	Translatior	IPR001790	[Ribosomal protein L10P]
	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001180[Citron
ko03015 m	RNA proce	J	Translatior	IPR001279	[Metallo-beta-lactamase] ; IPR011108[Zn-d
--	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
--	--	--	--	IPR024761	[Transcription factor IIIC, 90kDa subunit, N-
--	--	--	--	IPR001060	[FCH domain] ; IPR001452[SH3 domain]
ko03013 R	--	--	--	IPR003034	[SAP domain] ; IPR032552[Acin1, RNSP1-SA
--	--	--	--	IPR000859	[CUB domain] ; IPR018933[Netrin module, r
ko04144 E	GTPase SA	R	General fu	IPR001806	[Small GTPase superfamily]
ko03050 P	--	--	--	IPR003185	[Proteasome activator pa28, N-terminal dor
--	Aspartyl ar	E	Amino acic	IPR001948	[Peptidase M18]
--	Zinc transp	P	Inorganic i	IPR003689	[Zinc/iron permease]
--	Membrane	M	Cell wall/m	IPR001680	[WD40 repeat] ; IPR015048[Domain of unkn
ko01522 E	Ankyrin rep	T	Signal tran	IPR000742	[EGF-like domain] ; IPR000800[Notch doma
ko03040 S	Predicted	R	General fu	IPR001680	[WD40 repeat] ; IPR003613[U box domain] ;
ko04144 E	AAA+-typ	MDT	Cell wall/m	IPR003959	[ATPase, AAA-type, core] ; IPR007330[MIT]
ko04022 c	--	--	--	IPR000402	[Sodium/potassium-transporting ATPase su

--	Large exop	U	Intracellula	IPR002126	[Cadherin] ; IPR013164[Cadherin, N-termina
--	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain] ; IPR00207
--	--	--	--	IPR001060	[FCH domain] ; IPR001452[SH3 domain]
ko04144	E --	--	--	IPR001683	[Phox homologous domain] ; IPR015404[So
ko00564	G --	--	--	IPR016090	[Phospholipase A2 domain]
ko03050	P --	--	--	IPR000717	[Proteasome component (PCI) domain]
ko04217	N --	--	--	IPR001012	[UBX domain]
ko03040	S Peptidyl-p	O	Posttransla	IPR000504	[RNA recognition motif domain] ; IPR00213
--	--	--	--	IPR000717	[Proteasome component (PCI) domain]
--	--	--	--	IPR007587	[SIT4 phosphatase-associated protein famil
ko04910	Ir --	--	--	IPR004140	[Exocyst complex component Exo70]
--	--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko05206	M dsRNA-sp	K	Transcripti	IPR000999	[Ribonuclease III domain] ; IPR001650[Helic
ko04216	F Amino acic	E	Amino acic	IPR002293	[Amino acid/polyamine transporter I]
ko04072	P --	--	--	IPR000375	[Dynamin central domain] ; IPR001849[Plecl
--	Methionin	J	Translatior	IPR000994	[Peptidase M24]
ko04520	A --	--	--	IPR001452	[SH3 domain] ; IPR013606[IMD/I-BAR doma
ko04110	C Chromoso	D	Cell cycle c	IPR003395	[RecF/RecN/SMC, N-terminal] ; IPR010935[
ko00520	A UDP-N-ac	M	Cell wall/m	IPR000600	[ROK family] ; IPR003331[UDP-N-acetylgluc
--	DNA helic	K	Transcripti	IPR010339	[TIP49, C-terminal]
--	Spore coat	M	Cell wall/m	IPR001304	[C-type lectin-like]
--	--	--	--	IPR019382	[Translation initiation factor 3 complex subu
ko04310	W DNA helic	K	Transcripti	IPR010339	[TIP49, C-terminal]
--	--	--	--	IPR007052	[CS domain] ; IPR025934[NudC N-terminal
ko04360	A --	--	--	IPR002108	[Actin-depolymerising factor homology dor
--	--	--	--	IPR007084	[BRICHOS domain]
--	Ribosome-	J	Translatior	IPR004095	[TGS] ; IPR006073[GTP binding domain] ; IP
ko04810	R --	--	--	IPR019137	[Nck-associated protein 1]
--	--	--	--	IPR007477	[SAB domain] ; IPR008379[Band 4.1, C-term
ko03018	R Exoribonu	K	Transcripti	IPR002716	[PIN domain] ; IPR033770[Exosome comple
--	Cold shock	K	Transcripti	IPR002059	[Cold-shock protein, DNA-binding]
--	--	--	--	IPR029199	[THRAP3/BCLAF1 family]
ko03040	S --	--	--	IPR019007	[WW domain binding protein 11]
ko04144	E Ankyrin re	T	Signal tran	IPR001164	[Arf GTPase activating protein] ; IPR013724[
ko04621	N Serine/thre	T	Signal tran	IPR007052	[CS domain] ; IPR007699[SGS domain]
--	Predicted	R	General fu	IPR002737	[MEMO1 family]
ko04140	A --	--	--	IPR001452	[SH3 domain] ; IPR004148[BAR domain]
--	--	--	--	IPR004882	[Luc7-related]
--	--	--	--	IPR005301	[MOB kinase activator family]
ko03008	R Ribosome	J	Translatior	IPR018978	[Ribosome maturation protein SBDS, C-terr
--	--	--	--	IPR009038	[GOLD domain]
ko04137	M --	--	--	IPR028058	[Fis1, N-terminal tetratricopeptide repeat] ;
--	--	--	--	IPR000313	[PWWP domain]
ko04144	E --	--	--	IPR005024	[Snf7 family]
ko03013	R Predicted	T	Signal tran	IPR001680	[WD40 repeat]
--	RNA-splici	J	Translatior	IPR001233	[tRNA-splicing ligase, RtcB]
--	--	--	--	IPR001810	[F-box domain] ; IPR021625[PI31 proteason
ko03010	R --	--	--	IPR000509	[Ribosomal protein L36e]
ko03015	m Translatior	J	Translatior	IPR004160	[Translation elongation factor EFTu/EF1A, C
ko00190	C Archaeal/v	C	Energy prc	IPR002490	[V-type ATPase, V0 complex, 116kDa subu
ko04015	R --	--	--	IPR002558	[I/LWEQ domain] ; IPR015009[Vinculin-binc
--	WD40 rep	R	General fu	--	
ko04137	M Ubiquitin	O	Posttransla	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
--	--	--	--	IPR001190	[SRCR domain] ; IPR001695[Lysyl oxidase]
ko04141	P Molecular	O	Posttransla	IPR013126	[Heat shock protein 70 family]
--	--	--	--	IPR002867	[IBR domain]
--	--	--	--	IPR000421	[Coagulation factor 5/8 C-terminal domain]
--	Lysophosp	I	Lipid trans	IPR000073	[Alpha/beta hydrolase fold-1]

--	--	--	--	IPR001578	[Peptidase C12, ubiquitin carboxyl-terminal
ko05100 B	--	--	--	IPR001452	[SH3 domain]
--	--	--	--	IPR013598	[Exportin-1/Importin-beta-like]
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001180[Citron
ko03013 R	RNA recog	J	Translatior	IPR000504	[RNA recognition motif domain]
--	--	--	--	IPR001452	[SH3 domain] ; IPR001683[Phox homologou
ko04144 E	--	--	--	IPR001683	[Phox homologous domain] ; IPR015404[So
ko00561 G	Ca2+-binc	Q	Secondary	IPR001024	[PLAT/LH2 domain] ; IPR013818[Lipase/vitel
--	Sugar pho	G	Carbohydr	IPR011701	[Major facilitator superfamily]
--	--	--	--	IPR015425	[Formin, FH2 domain]
ko00260 G	Phosphose	HE	Coenzyme	IPR000192	[Aminotransferase class V domain]
--	--	--	--	IPR001863	[Glypican]
--	--	--	--	--	
--	--	--	--	IPR002553	[Clathrin/coatomer adaptor, adaptin-like, N
--	Glutathion	O	Posttransla	--	
--	Chromoso	D	Cell cycle c	IPR001073	[C1q domain] ; IPR008160[Collagen triple he
ko04144 E	Guanine-n	R	General fu	IPR000904	[Sec7 domain] ; IPR015403[Sec7, C-termina
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
--	--	--	--	IPR003307	[W2 domain]
ko04145 P	--	--	--	IPR022780	[Dynein family light intermediate chain]
ko04340 H	Periplasmic	U	Intracellula	IPR000719	[Protein kinase domain] ; IPR022247[Casein
ko04978 M	Co/Zn/Cd	P	Inorganic i	IPR002524	[Cation efflux protein]
--	--	--	--	IPR011531	[Bicarbonate transporter, C-terminal] ; IPR0
--	Large exop	U	Intracellula	IPR001846	[von Willebrand factor, type D domain] ; IPR
ko04666 F	--	--	--	IPR007123	[Gelsolin-like domain]
ko04520 A	--	--	--	IPR003124	[WH2 domain]

domain] ; IPR001254[Serine proteases, trypsin domain] ; IPR001881[EGF-like calcium-binding doma

-terminal] ; IPR029390[AP-3 complex subunit beta, C-terminal domain] ; IPR029394[AP-3 complex

domain] ; IPR005824[KOW] ; IPR022581[Spt5 transcription elongation factor, N-terminal]

2035[von Willebrand factor, type A] ; IPR019466[Matrilin, coiled-coil trimerisation domain] ; IPR0268

] ; IPR001791[Laminin G domain] ; IPR002049[Laminin EGF domain] ; IPR002350[Kazal domain] ; IPR

IGFBP] ; IPR001007[VWFC domain] ; IPR006208[Glycoprotein hormone subunit beta, cystine knot]
domain] ; IPR011682[Glycosyl hydrolase family 38, C-terminal] ; IPR015341[Glycoside hydrolase fam

| ; IPR000859[CUB domain] ; IPR000998[MAM domain] ; IPR022579[Neuropilin, C-terminal]

omain] ; IPR008145[Guanylate kinase/L-type calcium channel beta subunit] ; IPR011511[Variant SH3

] ; IPR024641[Hepatocyte growth factor-regulated tyrosine kinase substrate, helical domain]

] ; IPR002049[Laminin EGF domain] ; IPR008211[Laminin, N-terminal] ; IPR009254[Laminin alpha, do

SH3 domain] ; IPR001849[Pleckstrin homology domain] ; IPR020683[Ankyrin repeat-containing dor

enase, catalytic domain] ; IPR006140[D-isomer specific 2-hydroxyacid dehydrogenase, NAD-bindir

inal] ; IPR014847[FERM adjacent (FA)] ; IPR018979[FERM, N-terminal] ; IPR018980[FERM, C-termina

-terminal] ; IPR008152[Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdoma

-associated domain] ; IPR011545[DEAD/DEAH box helicase domain] ; IPR011709[Domain of unknov
650[Helicase, C-terminal] ; IPR015194[ISWI, HAND domain] ; IPR015195[SLIDE domain] ; IPR02083

| ; IPR000859[CUB domain] ; IPR000998[MAM domain] ; IPR022579[Neuropilin, C-terminal]

regulatory] ; IPR010472[Formin, FH3 domain] ; IPR010473[Formin, GTPase-binding domain] ; IPR01

nthase II, N-terminal] ; IPR012960[Dyskerin-like] ; IPR032819[tRNA pseudouridylate synthase B, C-

epeat] ; IPR017868[Filamin/ABP280 repeat-like] ; IPR027370[RING-type zinc-finger, LisH dimerisatic

3[Formyl transferase, C-terminal] ; IPR009081[Phosphopantetheine binding ACP domain] ; IPR0155

RNA-binding] ; IPR019734[Tetratricopeptide repeat] ; IPR031545[Putative TPR-like repeat]

PR025614[Cell morphogenesis protein N-terminal] ; IPR029473[Cell morphogenesis central region]
-terminal] ; IPR003164[Clathrin adaptor, alpha-adaptin, appendage, C-terminal subdomain] ; IPR0

retin-like] ; IPR000922[D-galactoside/L-rhamnose binding SUEL lectin domain] ; IPR001879[GPCR,

reonine/tyrosine-protein kinase catalytic domain] ; IPR006211[Furin-like cysteine-rich domain] ; IPR

mic acid-rich (GLA) domain] ; IPR001254[Serine proteases, trypsin domain] ; IPR018992[Thrombin li

a-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding] ; IPR011625[A
2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobu
2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobu

rminal globular domain] ; IPR012290[Fibrinogen, alpha/beta/gamma chain, coiled coil domain]
rminal globular domain] ; IPR012290[Fibrinogen, alpha/beta/gamma chain, coiled coil domain]
PR002172[Low-density lipoprotein (LDL) receptor class A repeat] ; IPR020864[Membrane attack com

9454[Lipid transport, open beta-sheet] ; IPR015255[Vitellinogen, open beta-sheet] ; IPR022176[Apo

d factor, type D domain] ; IPR002035[von Willebrand factor, type A] ; IPR002919[Trypsin Inhibitor-lik

ase, NAD(P) binding domain] ; IPR020829[Glyceraldehyde 3-phosphate dehydrogenase, catalytic do

minal] ; IPR006068[Cation-transporting P-type ATPase, C-terminal] ; IPR008250[P-type ATPase, A d

12896[Integrin beta subunit, tail] ; IPR013111[EGF-like domain, extracellular] ; IPR014836[Integrin be
12896[Integrin beta subunit, tail] ; IPR014836[Integrin beta subunit, cytoplasmic domain] ; IPR03376

12896[Integrin beta subunit, tail] ; IPR013111[EGF-like domain, extracellular] ; IPR014836[Integrin be
main] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding domain] ; IPR017892[I

domain] ; IPR000742[EGF-like domain] ; IPR001791[Laminin G domain] ; IPR001881[EGF-like calcium

l-tRNA synthetase, class II (G/ P/ S/T)] ; IPR004046[Glutathione S-transferase, C-terminal] ; IPR0041

R001007[VWFC domain] ; IPR003367[Thrombospondin, type 3-like repeat] ; IPR008859[Thrombosp
reonine/tyrosine-protein kinase catalytic domain] ; IPR006211[Furin-like cysteine-rich domain]

001818[Peptidase M10, metallopeptidase] ; IPR002477[Peptidoglycan binding-like] ; IPR018487[He

RP-type] ; IPR004102[Poly(ADP-ribose) polymerase, regulatory domain] ; IPR008893[WGR domain] ;
ptidase, N-terminal] ; IPR015211[Peptidase M1, leukotriene A4 hydrolase/aminopeptidase C-termi

2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobu

nbospondin type-1 (TSP1) repeat] ; IPR002172[Low-density lipoprotein (LDL) receptor class A repea

inal] ; IPR014847[FERM adjacent (FA)] ; IPR018979[FERM, N-terminal] ; IPR018980[FERM, C-termina

yotic-type] ; IPR013500[DNA topoisomerase I, catalytic core, eukaryotic-type] ; IPR025834[Topoisor
-terminal] ; IPR003594[Histidine kinase-like ATPase, C-terminal domain] ; IPR006171[TOPRIM domi

minal arm] ; IPR005161[Ku70/Ku80, N-terminal alpha/beta] ; IPR006164[Ku70/Ku80 beta-barrel do
70/Ku80, N-terminal alpha/beta] ; IPR006164[Ku70/Ku80 beta-barrel domain] ; IPR014893[Ku, C-te

n] ; IPR004161[Translation elongation factor EFTu-like, domain 2] ; IPR005517[Translation elongatic

nbospondin type-1 (TSP1) repeat] ; IPR002172[Low-density lipoprotein (LDL) receptor class A repea

3117[cAMP-dependent protein kinase regulatory subunit, dimerization-anchoring domain]

ulin type-1] ; IPR001881[EGF-like calcium-binding domain] ; IPR003886[NIDO domain] ; IPR00660

:ol-specific phospholipase C, X domain] ; IPR000980[SH2 domain] ; IPR001452[SH3 domain] ; IPR00

PR002048[EF-hand domain] ; IPR022682[Peptidase C2, calpain, large subunit, domain III]

a-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding] ; IPR011625[A

unit, nucleotide-binding domain] ; IPR004100[ATPase, F1/V1/A1 complex, alpha/beta subunit, N-t

small subunit, swivel domain] ; IPR001030[Aconitase/3-isopropylmalate dehydratase large subunit,

3[AIR synthase-related protein, C-terminal domain] ; IPR016188[PurM-like, N-terminal domain] ; IP
rminal globular domain] ; IPR003961[Fibronectin type III] ; IPR013111[EGF-like domain, extracellula

965[Ubiquitin-activating enzyme E1, C-terminal] ; IPR019572[Ubiquitin-activating enzyme, catalytic

/RNA non-specific endonuclease] ; IPR002591[Type I phosphodiesterase/nucleotide pyrophosphata

terminal] ; IPR005144[ATP-cone domain] ; IPR013509[Ribonucleotide reductase large subunit, N-te
] ; IPR002049[Laminin EGF domain] ; IPR008211[Laminin, N-terminal] ; IPR009254[Laminin alpha, dc
elta subunit, guanine nucleotide exchange domain] ; IPR018940[Elongation factor 1 beta central aci

rminal globular domain] ; IPR003961[Fibronectin type III] ; IPR013111[EGF-like domain, extracellula

ukaryotic] ; IPR000722[RNA polymerase, alpha subunit] ; IPR007066[RNA polymerase Rpb1, domain

] ; IPR002049[Laminin EGF domain] ; IPR008211[Laminin, N-terminal] ; IPR009254[Laminin alpha, dc

unit, nucleotide-binding domain] ; IPR000793[ATP synthase, alpha subunit, C-terminal] ; IPR00410

79[FERM, N-terminal] ; IPR018980[FERM, C-terminal PH-like domain] ; IPR019748[FERM central dc

S/T)] ; IPR004095[TGS] ; IPR004154[Anticodon-binding] ; IPR012947[Threonyl/alanyl tRNA syntheta
04046[Glutathione S-transferase, C-terminal] ; IPR013155[Methionyl/Valyl/Leucyl/Isoleucyl-tRNA s
chain, conserved] ; IPR004045[Glutathione S-transferase, N-terminal] ; IPR004046[Glutathione S-tr

tRNA synthetase-type] ; IPR007199[Replication factor-A protein 1, N-terminal] ; IPR013955[Replicat

unit N-terminal domain] ; IPR005479[Carbamoyl-phosphate synthetase large subunit-like, ATP-bin

exonuclease domain] ; IPR006134[DNA-directed DNA polymerase, family B, multifunctional domain]

IGFBP] ; IPR000884[Thrombospondin type-1 (TSP1) repeat] ; IPR001007[VWFC domain] ; IPR00620
PR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha mot
PR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha mot
PR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha mot

nsketolase-like, pyrimidine-binding domain] ; IPR033248[Transketolase, C-terminal domain]

elta subunit, guanine nucleotide exchange domain] ; IPR018940[Elongation factor 1 beta central aci

domain 6] ; IPR007641[RNA polymerase Rpb2, domain 7] ; IPR007642[RNA polymerase Rpb2, dom

3117[cAMP-dependent protein kinase regulatory subunit, dimerization-anchoring domain]
unit N-terminal domain] ; IPR005479[Carbamoyl-phosphate synthetase large subunit-like, ATP-bin

)79[FERM, N-terminal] ; IPR018980[FERM, C-terminal PH-like domain] ; IPR019748[FERM central do
)79[FERM, N-terminal] ; IPR018980[FERM, C-terminal PH-like domain] ; IPR019748[FERM central do

'R001007[VWFC domain] ; IPR001881[EGF-like calcium-binding domain] ; IPR003367[Thrombospor
3367[Thrombospondin, type 3-like repeat] ; IPR008859[Thrombospondin, C-terminal] ; IPR024665[T

N-terminal domain] ; IPR032788[Glycogen debranching enzyme, central domain] ; IPR032790[Glyc

)[Myosin head, motor domain] ; IPR002928[Myosin tail] ; IPR004009[Myosin, N-terminal, SH3-like]

] ; IPR005844[Alpha-D-phosphohexomutase, alpha/beta/alpha domain I] ; IPR005845[Alpha-D-ph

unit, nucleotide-binding domain] ; IPR004100[ATPase, F1/V1/A1 complex, alpha/beta subunit, N-t

omain of unknown function DUF959, collagen XVIII, N-terminal] ; IPR010515[Collagenase NC10/enc

n factor, protein interaction] ; IPR013800[STAT transcription factor, all-alpha domain] ; IPR013801[S

n factor, protein interaction] ; IPR013800[STAT transcription factor, all-alpha domain] ; IPR013801[S

ninal] ; IPR007695[DNA mismatch repair protein MutS-like, N-terminal] ; IPR007696[DNA mismatch

EAH box helicase domain] ; IPR032284[ATP-dependent DNA helicase RecQ, zinc-binding domain]
NOP2-type] ; IPR012586[P120R repeat] ; IPR031341[Ribosomal RNA small subunit methyltransferase

homology domain] ; IPR002017[Spectrin repeat] ; IPR015153[EF-hand domain, type 1] ; IPR015154
3[RasGAP protein, C-terminal] ; IPR001715[Calponin homology domain] ; IPR001936[Ras GTPase-ac

(PI3K RBD) domain] ; IPR000403[Phosphatidylinositol 3-/4-kinase, catalytic domain] ; IPR001263[Ph

eine binding ACP domain] ; IPR013149[Alcohol dehydrogenase, C-terminal] ; IPR013217[Methyltra

licensing factor Mcm2] ; IPR027925[MCM N-terminal domain] ; IPR033762[MCM OB domain]
367[Thrombospondin, type 3-like repeat] ; IPR008859[Thrombospondin, C-terminal] ; IPR024665[T
367[Thrombospondin, type 3-like repeat] ; IPR008859[Thrombospondin, C-terminal] ; IPR024665[T

477[Peptidoglycan binding-like] ; IPR018487[Hemopexin-like repeats] ; IPR021805[Peptidase M10A

kstrin homology domain] ; IPR003130[Dynamin GTPase effector] ; IPR022812[Dynamin superfamily]
known function DUF1088] ; IPR023362[PH-BEACH domain] ; IPR031570[Domain of unknown functi

genet-like domain] ; IPR022034[Fragile X-related 1 protein, C-terminal core] ; IPR032172[Fragile X

487[Bromodomain] ; IPR001650[Helicase, C-terminal] ; IPR006576[BRK domain] ; IPR014012[Helica
750[GHMP kinase, C-terminal domain] ; IPR019539[Galactokinase galactose-binding domain]

ubunit, C-terminal] ; IPR015872[Transcription initiation factor IIA, gamma subunit, N-terminal]
h repair protein MutS, C-terminal] ; IPR007695[DNA mismatch repair protein MutS-like, N-terminal

] ; IPR005811[ATP-citrate lyase/succinyl-CoA ligase] ; IPR032263[ATP-citrate synthase, citrate-bindi
associated region] ; IPR010714[Coatomer, alpha subunit, C-terminal] ; IPR024977[Anaphase-promo

VWA N-terminal] ; IPR013680[Voltage-dependent calcium channel, alpha-2/delta subunit, conserv

PR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha mot

PR013612[Amino acid permease, N-terminal] ; IPR018491[SLC12A transporter, C-terminal]

9[ATPase, AAA-type, core] ; IPR004201[CDC48, domain 2] ; IPR015415[Vps4 oligomerisation, C-ter
Forkhead-associated (FHA) domain] ; IPR001478[PDZ domain] ; IPR002710[Dilute domain]

deaminase (DRADA)] ; IPR002466[Adenosine deaminase/editase] ; IPR014720[Double-stranded RN

GTPase domain] ; IPR004125[Signal recognition particle, SRP54 subunit, M-domain] ; IPR013822[Si

inhibitor RLI, possible metal-binding domain] ; IPR017896[4Fe-4S ferredoxin-type, iron-sulphur bir

V] ; IPR013843[Ribosomal protein S4e, N-terminal] ; IPR013845[Ribosomal protein S4e, central regic

-terminal] ; IPR008152[Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdoma

domain] ; IPR003151[PIK-related kinase, FAT] ; IPR003152[FATC domain] ; IPR012582[NUC194]

R002919[Trypsin Inhibitor-like, cysteine rich domain] ; IPR014853[Uncharacterised domain, cysteine-

IPR001791[Laminin G domain] ; IPR002049[Laminin EGF domain] ; IPR002172[Low-density lipoprot

minal] ; IPR006068[Cation-transporting P-type ATPase, C-terminal] ; IPR008250[P-type ATPase, A

inal] ; IPR022629[S-adenosylmethionine synthetase, central domain] ; IPR022630[S-adenosylmethio

IPR015348[Clathrin, heavy chain, linker, core motif] ; IPR022365[Clathrin, heavy chain, propeller repe

ase, N-terminal] ; IPR013746[Hydroxymethylglutaryl-coenzyme A synthase C-terminal domain]

ol-specific phospholipase C, X domain] ; IPR001711[Phospholipase C, phosphatidylinositol-specific
sine-protein kinase catalytic domain] ; IPR013098[Immunoglobulin I-set] ; IPR020067[Frizzled doma

ase domain] ; IPR001440[Tetratricopeptide repeat 1] ; IPR013105[Tetratricopeptide repeat 2]

-terminal] ; IPR003594[Histidine kinase-like ATPase, C-terminal domain] ; IPR006171[TOPRIM dom

| ; IPR006047[Glycosyl hydrolase, family 13, catalytic domain] ; IPR006048[Alpha-amylase/branching

R000562[Fibronectin, type II, collagen-binding] ; IPR000742[EGF-like domain] ; IPR001254[Serine p

kstrin homology domain] ; IPR003130[Dynamin GTPase effector] ; IPR022812[Dynamin superfamily]
atalytic domain] ; IPR005189[Focal adhesion kinase, targeting (FAT) domain] ; IPR019748[FERM cen

R008145[Guanylate kinase/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain]

calcium-binding domain] ; IPR002172[Low-density lipoprotein (LDL) receptor class A repeat] ; IPR02

-terminal] ; IPR008152[Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdoma

/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain] ; IPR015143[L27-1] ; IPR01

oyl attachment] ; IPR005479[Carbamoyl-phosphate synthetase large subunit-like, ATP-binding dor

hydrolase] ; IPR006615[Peptidase C19, ubiquitin-specific peptidase, DUSP domain] ; IPR028135[Ub

domain] ; IPR001005[SANT/Myb domain] ; IPR001025[Bromo adjacent homology (BAH) domain]

enase, catalytic domain] ; IPR006140[D-isomer specific 2-hydroxyacid dehydrogenase, NAD-bindir

[Ras-associating (RA) domain] ; IPR000198[Rho GTPase-activating protein domain] ; IPR001609[My

[RasGAP protein, C-terminal] ; IPR001715[Calponin homology domain] ; IPR001936[Ras GTPase-ac

/RNA non-specific endonuclease] ; IPR002591[Type I phosphodiesterase/nucleotide pyrophosphata

ɔulin type-1] ; IPR001881[EGF-like calcium-binding domain] ; IPR003886[NIDO domain] ; IPR00660

.TPase, dynein-related, AAA domain] ; IPR013594[Dynein heavy chain, domain-1] ; IPR013602[Dyne

atalytic domain] ; IPR005189[Focal adhesion kinase, targeting (FAT) domain] ; IPR019748[FERM cen

domain] ; IPR001791[Laminin G domain] ; IPR001881[EGF-like calcium-binding domain] ; IPR013032

ɔtif] ; IPR001849[Pleckstrin homology domain] ; IPR001936[Ras GTPase-activating protein]

.650[Helicase, C-terminal] ; IPR009462[Domain of unknown function DUF1086] ; IPR009463[Domair

R019585[26S proteasome regulatory subunit Rpn7/COP9 signalosome complex subunit 1]

n] ; IPR004161[Translation elongation factor EFTu-like, domain 2] ; IPR005517[Translation elongatic

5800[Copper amine oxidase, N2-terminal] ; IPR015802[Copper amine oxidase, N3-terminal]

R028282[WASH complex subunit 7, central domain] ; IPR028283[WASH complex subunit 7, C-termi

3[Formyl transferase, C-terminal] ; IPR009081[Phosphopantetheine binding ACP domain] ; IPR0155

PR025614[Cell morphogenesis protein N-terminal] ; IPR029473[Cell morphogenesis central region]

n] ; IPR012591[PRO8NT domain] ; IPR012592[PROCN domain] ; IPR012984[PROCT domain] ; IPR019

tif domain] ; IPR010599[Connector enhancer of kinase suppressor of ras 2] ; IPR017874[CRIC domai

a-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding] ; IPR011625[A

027999[Death-like domain of Spt6] ; IPR028083[Spt6 acidic, N-terminal domain] ; IPR028088[Helix-

-associated domain] ; IPR011545[DEAD/DEAH box helicase domain] ; IPR011709[Domain of unknov

or, N-terminal] ; IPR001895[Ras guanine-nucleotide exchange factors catalytic domain] ; IPR002048

risation and cyclophilin-binding domain] ; IPR032691[Guanine nucleotide exchange factor, N-termi

; IPR010309[E3 ubiquitin ligase, domain of unknown function DUF908] ; IPR010314[E3 ubiquitin liga

-binding domain] ; IPR011641[Tyrosine-protein kinase ephrin type A/B receptor-like] ; IPR024731[E

nain] ; IPR012920[Ribosomal RNA methyltransferase, Spb1, C-terminal] ; IPR024576[Ribosomal RNA

Nuclear pore localisation protein NPL4, C-terminal] ; IPR024682[Nuclear pore localisation protein Np

:inc finger, LIM-type] ; IPR002938[FAD-binding domain] ; IPR022735[Domain of unknown function

omain] ; IPR032448[SMARCC, SWIRM-associated domain] ; IPR032450[SMARCC, N-terminal] ; IPR0:

] ; IPR005844[Alpha-D-phosphohexomutase, alpha/beta/alpha domain I] ; IPR005845[Alpha-D-ph

Rho GTPase-activating protein domain] ; IPR001164[Arf GTPase activating protein] ; IPR001660[Ste

PR001881[EGF-like calcium-binding domain] ; IPR006605[G2 nidogen/fibulin G2F] ; IPR013098[Imm

Dedicator of cytokinesis, C-terminal] ; IPR021816[Dedicator of cytokinesis C/D, N-terminal] ; IPR027

ptidase, N-terminal] ; IPR015211[Peptidase M1, leukotriene A4 hydrolase/aminopeptidase C-termi

5110[AMP-binding enzyme C-terminal domain] ; IPR032387[Acetyl-coenzyme A synthetase, N-ter

; IPR007135[Autophagy-related protein 3] ; IPR019461[Autophagy-related protein 3, C-terminal]

domain] ; IPR001881[EGF-like calcium-binding domain] ; IPR002172[Low-density lipoprotein (LDL) r
e/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain] ; IPR014775[L27 domain, C

-terminal] ; IPR013040[Coatomer, gamma subunit, appendage, Ig-like subdomain] ; IPR032154[Co

077[Ubiquitin/SUMO-activating enzyme ubiquitin-like domain] ; IPR032426[SUMO-activating enzy

R001590[Peptidase M12B, ADAM/reprolysin] ; IPR002870[Peptidase M12B, propeptide] ; IPR01029

dependent metallo-hydrolase, RNA specificity domain] ; IPR021718[Pre-mRNA 3'-end-processing e

in] ; IPR001881[EGF-like calcium-binding domain] ; IPR010660[Notch, NOD domain] ; IPR011656[N

al] ; IPR031904[Cadherin, C-terminal catenin-binding domain] ; IPR032455[Cadherin, cytoplasmic C

ase, C-terminal] ; IPR003100[PAZ domain] ; IPR005034[Dicer dimerisation domain] ; IPR011545[DEA

kstrin homology domain] ; IPR003130[Dynamin GTPase effector] ; IPR022812[Dynamin superfamily]

inal] ; IPR014847[FERM adjacent (FA)] ; IPR018979[FERM, N-terminal] ; IPR018980[FERM, C-termina

GIT, Spa2 homology (SHD) domain] ; IPR020683[Ankyrin repeat-containing domain] ; IPR022018[A

-terminal] ; IPR004161[Translation elongation factor EFTu-like, domain 2] ; IPR015033[HBS1-like pr

ding site-containing domain] ; IPR015224[Talin, central] ; IPR018979[FERM, N-terminal] ; IPR019748

hydrolase] ; IPR006615[Peptidase C19, ubiquitin-specific peptidase, DUSP domain] ; IPR028135[Ub

homology (CNH) domain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding d

-terminal] ; IPR013040[Coatomer, gamma subunit, appendage, Ig-like subdomain] ; IPR032154[Coa

l] ; IPR032629[Mon2, dimerisation and cyclophilin-binding domain] ; IPR032691[Guanine nucleotide

R002919[Trypsin Inhibitor-like, cysteine rich domain] ; IPR014853[Uncharacterised domain, cysteine-

family 2, extracellular hormone receptor domain] ; IPR003112[Olfactomedin-like domain] ; IPR0033

Alpha-2-macroglobulin, N-terminal 2] ; IPR011626[Alpha-macroglobulin complement component]
lin, receptor-binding] ; IPR011625[Alpha-2-macroglobulin, N-terminal 2] ; IPR011626[Alpha-macro
lin, receptor-binding] ; IPR011625[Alpha-2-macroglobulin, N-terminal 2] ; IPR011626[Alpha-macro

ke, cysteine rich domain] ; IPR014853[Uncharacterised domain, cysteine-rich] ; IPR032361[von Willel

.54[Anticodon-binding] ; IPR016061[Proline-tRNA ligase, class II, C-terminal] ; IPR020058[Glutamyl/

; IPR012317[Poly(ADP-ribose) polymerase, catalytic domain] ; IPR012982[PADR1 domain]

lin, receptor-binding] ; IPR011625[Alpha-2-macroglobulin, N-terminal 2] ; IPR011626[Alpha-macro

ain] ; IPR012542[DTHCT] ; IPR013506[DNA topoisomerase, type IIA, subunit B, domain 2] ; IPR03166

at] ; IPR002350[Kazal domain] ; IPR020864[Membrane attack complex component/perforin (MACPF

5[G2 nidogen/fibulin G2F] ; IPR024731[EGF domain] ; IPR026823[Complement Clr-like EGF domain]

Alpha-2-macroglobulin, N-terminal 2] ; IPR011626[Alpha-macroglobulin complement component]

R020560[Phosphoribosylglycinamide synthetase, C-domain] ; IPR020561[Phosphoribosylglycinamic

cysteine domain] ; IPR032418[Ubiquitin-activating enzyme E1, FCCH domain] ; IPR032420[Ubiquiti

3] ; IPR007073[RNA polymerase Rpb1, domain 7] ; IPR007075[RNA polymerase Rpb1, domain 6] ;

ding domain] ; IPR005480[Carbamoyl-phosphate synthetase, large subunit oligomerisation domain

if domain] ; IPR003961[Fibronectin type III] ; IPR027936[Ephrin receptor, transmembrane domain]
if domain] ; IPR003961[Fibronectin type III] ; IPR011641[Tyrosine-protein kinase ephrin type A/B rec
if domain] ; IPR003961[Fibronectin type III] ; IPR011641[Tyrosine-protein kinase ephrin type A/B rec

ain 2] ; IPR007644[RNA polymerase, beta subunit, protrusion] ; IPR007645[RNA polymerase Rpb2, c

ding domain] ; IPR005480[Carbamoyl-phosphate synthetase, large subunit oligomerisation domain

ndin, type 3-like repeat] ; IPR008859[Thrombospondin, C-terminal] ; IPR024731[EGF domain]

ogen debranching enzyme, C-terminal] ; IPR032792[Glycogen debranching enzyme, glucanotransfe

osphohexomutase, alpha/beta/alpha domain II] ; IPR005846[Alpha-D-phosphohexomutase, alpha/

repair protein MutS, core] ; IPR007860[DNA mismatch repair protein MutS, connector domain] ; IP

osphoinositide 3-kinase, accessory (PIK) domain] ; IPR002420[Phosphatidylinositol 3-kinase, C2 do

nsferase type 12] ; IPR013968[Polyketide synthase, ketoreductase domain] ; IPR014030[Beta-ketoac

-related 1 protein, C-terminal region 1] ; IPR032177[Fragile X-related 1 protein, C-terminal region

se/SANT-associated domain] ; IPR014978[Glutamine-Leucine-Glutamine, QLQ] ; IPR029295[Snf2, A

l] ; IPR007696[DNA mismatch repair protein MutS, core] ; IPR007860[DNA mismatch repair protein l

if domain] ; IPR003961[Fibronectin type III] ; IPR011641[Tyrosine-protein kinase ephrin type A/B rec

:ein (LDL) receptor class A repeat] ; IPR007110[Immunoglobulin-like domain] ; IPR013098[Immunog

:, Y domain] ; IPR014815[Phospholipase C-beta, C-terminal domain] ; IPR015359[Phosphoinositide-

ain] ; IPR012542[DTHCT] ; IPR013506[DNA topoisomerase, type IIA, subunit B, domain 2] ; IPR03166

26823[Complement Clr-like EGF domain] ; IPR032485[Domain of unknown function DUF5050]

.9583[PDZ-associated domain of NMDA receptors] ; IPR019590[Disks large homologue 1, N-termir

main] ; IPR005481[Biotin carboxylase-like, N-terminal domain] ; IPR005482[Biotin carboxylase, C-te

5[G2 nidogen/fibulin G2F] ; IPR024731[EGF domain] ; IPR026823[Complement Clr-like EGF domain]

ein heavy chain, domain-2] ; IPR024317[Dynein heavy chain, P-loop containing D4 domain] ; IPR024

n of unknown function DUF1087] ; IPR012957[CHD, C-terminal 2] ; IPR012958[CHD, N-terminal] ; IP

on factor EFG/EF2, domain IV] ; IPR009022[Elongation factor G, III-V domain] ; IPR031950[116 kDa U

)580[Pre-mRNA-processing-splicing factor 8, U6-snRNA-binding] ; IPR019581[Pre-mRNA-process

Alpha-2-macroglobulin, N-terminal 2] ; IPR011626[Alpha-macroglobulin complement component]

turn-helix DNA-binding domain of Spt6] ; IPR028231[Transcription elongation factor Spt6, YqgF d

3[EF-hand domain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding domain]

se, domain of unknown function DUF913] ; IPR015940[Ubiquitin-associated domain] ; IPR025527[D

osphohexomutase, alpha/beta/alpha domain II] ; IPR005846[Alpha-D-phosphohexomutase, alpha/

receptor class A repeat] ; IPR026823[Complement Clr-like EGF domain] ; IPR032485[Domain of unk

lotch, NODP domain] ; IPR013032[EGF-like, conserved site] ; IPR020683[Ankyrin repeat-containing

RF GTPase-activating protein GIT1, C-terminal] ; IPR032352[Arf GTPase-activating protein GIT1/2, c

iquitin-like domain, USP-type] ; IPR029346[Ubiquitin carboxyl-terminal hydrolase, C-terminal]

domain] ; IPR014930[Myotonic dystrophy protein kinase, coiled coil] ; IPR031597[KELK-motif contai

ɔglobulin complement component] ; IPR018933[Netrin module, non-TIMP type] ; IPR019565[Alpha

/glutaminyl-tRNA synthetase, class Ib, catalytic domain] ; IPR020059[Glutamyl/glutaminyl-tRNA syn

ɔglobulin complement component] ; IPR018933[Netrin module, non-TIMP type] ; IPR019565[Alpha

de synthetase, ATP-grasp (A) domain] ; IPR020562[Phosphoribosylglycinamide synthetase, N-termi

IPR007080[RNA polymerase Rpb1, domain 1] ; IPR007081[RNA polymerase Rpb1, domain 5] ; IPR0

ı] ; IPR006131[Aspartate/ornithine carbamoyltransferase, Asp/Orn-binding domain] ; IPR006132[Asp

domain 3] ; IPR007646[RNA polymerase Rpb2, domain 4] ; IPR007647[RNA polymerase Rpb2, doma

ı] ; IPR011607[Methylglyoxal synthase-like domain] ; IPR017926[Glutamine amidotransferase]

yl synthase, N-terminal] ; IPR014031[Beta-ketoacyl synthase, C-terminal] ; IPR014043[Acyl transfera

ing-splicing factor 8, U5-snRNA-binding] ; IPR019582[RNA recognition motif, spliceosomal PrP8] ;

partate/ornithine carbamoyltransferase, carbamoyl-P binding] ; IPR006680[Amidohydrolase-relatec

ıse] ; IPR020807[Polyketide synthase, dehydratase domain] ; IPR032821[Ketoacyl-synthetase, C-tern

d] ; IPR011607[Methylglyoxal synthase-like domain] ; IPR017926[Glutamine amidotransferase]