

Protein	Description	Gene	MNNG_1	MNNG_2	MNNG_3	Osteoblast	Osteoblast	Osteoblast
A8TX70	Collagen a	COL6A5	0	0	0	77088.55	58613.52	111480.6
P07585	Decorin	DCN	0	0	0	2122213	2781883	2407803
P09341	Growth-re	CXCL1	0	0	0	7859904	7623940	2650093
P10124	Serglycin	SRGN	0	0	0	498227.2	710033.3	623048.3
P10145	Interleukin	CXCL8	0	0	0	1520724	1844316	669054.6
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
P52823	Stanniocal	STC1	0	0	0	108828.1	111768	47332.22
P80162	C-X-C mo	CXCL6	0	0	0	3016109	2149925	1037208
Q07092	Collagen a	COL16A1	0	0	0	240926.5	317998	344779.5
Q8WXE9	Stonin-2	STON2	0	0	0	549122.7	585295.3	794003.8
Q96JB6	Lysyl oxida	LOXL4	0	0	0	31368.49	19492.06	32217.52
Q9NZP8	Compleme	C1RL	0	0	0	56888.91	66546.84	50780.08
Q9UHI8	A disintegr	ADAMTS1	0	0	0	211929.6	79440.09	195730
A8MWD9	Putative sr	SNRPGP15	63594.16	95049.96	53115.07	42343.49	523188.7	0
A0A087W1	Uncharacterized prote		9714.664	14480.74	5925.99	0	0	0
A0A096LP	Protein LO	LOC10272	152189.5	154084.7	150459.3	0	0	0
B4E1Z4	Uncharacterized prote		122180.3	183847.4	223527.5	4228377	5263997	1517109
B5ME19	Eukaryotic	EIF3CL	164223.3	172962.4	90609.23	128058	63098.57	104513.3
A0A0A6YY	Protein TM	TMED7-TM	17229.21	18867.36	12040.91	0	0	0
A0A0B4J2	Peptidyl-p	PPIAL4C	23481.4	22666.08	41751.2	0	0	0
A0A0B4J2	Protein IGH	IGHV3OR1	37823.68	53582.5	13909.66	0	0	0
A3KN83	Protein str.	SBNO1	5233.223	12161.74	2815.211	0	0	0
A4D1P6	WD repeat	WDR91	8139.345	12592.53	8975.218	0	0	0
A5YKK6	CCR4-NO	CNOT1	6541.921	6222.137	6079.043	0	0	0
A6NCE7	Microtubu	MAP1LC3E	46981	42383.68	41339.83	0	0	0
A6NDG6	Phosphogl	PGP	10467.71	65009.96	95394.15	0	0	0
A6NHR9	Structural	SMCHD1	3359.228	5218.64	2018.592	0	0	0
A6NKD9	Coiled-coi	CCDC85C	1127.536	964.5623	860.812	0	0	0
A7E2V4	Zinc finger	ZSWIM8	5991.321	4794.427	2708.158	0	0	0
I3L0A0	HCG20447	TMEM189	125135.1	117916.1	193926.9	50509.09	0	50917.48
A7MBM2	Protein dis	DISP2	26876.95	2261.785	3508.535	0	0	0
B4DGG1	Uncharacterized prote		23604	24015.66	27385.82	0	0	0
C9J1V9	HCG20432	EEF1E1-BL	40491.64	29136.35	26898.63	0	0	0
C9JCJ5	Uncharacterized prote		8262.456	6991.103	13643.8	0	0	0
O00151	PDZ and L	PDLIM1	17320.04	19496.08	38135.75	76848.63	0	47939.38
E7EVH7	Uncharacterized prote		27565.83	26720.85	31656.91	0	0	0
O00159	Unconvent	MYO1C	252175.7	241570.9	342509.1	85332.45	0	133874.4
E9PSI1	Uncharacterized prote		23920.26	25103.4	22655.19	0	0	0
F2Z307	Protein AT	ATP6V1G2	10826.07	10472.56	13158.72	0	0	0
F6X3S4	Uncharacterized prote		5030.02	3922.003	6972.974	0	0	0
F8W031	Uncharacterized prote		5746.038	4762.398	7431.061	0	0	0
O00203	AP-3 com	AP3B1	133692.5	121127.8	167760.9	129934.9	18222068	3270287
G3V4G9	Uncharacterized prote		4719.036	5508.464	6807.835	0	0	0
H3BMM5	Uncharacterized prote		7071.395	4463.046	4640.757	0	0	0
O00231	26S protea	PSMD11	53729.27	56503.4	50450.32	85492.82	0	73611.55
H3BU86	Protein ST	STX16-NP	9003.442	8208.382	9885.055	0	0	0
M0QZK8	Uncharacterized prote		4848.69	5288.753	6601.1	0	0	0
M0R2C6	Uncharacterized prote		12346.98	8653.779	13557.85	0	0	0
O00299	Chloride ir	CLIC1	552548.4	475069.3	986037.8	148484.3	148296	154672.1
O00300	Tumor nec	TNFRSF111	18432.49	21400.26	15496.49	107663	0	143445.3
O00303	Eukaryotic	EIF3F	65265.67	73395.16	57540.51	68613.09	0	77429.93
O00115	Deoxyribo	DNASE2	4853.13	5349.089	9183.373	0	0	0
O00139	Kinesin-lik	KIF2A	7709.262	8263.728	7961.465	0	0	0
O00154	Cytosolic a	ACOT7	69158.48	68400.06	78899.82	0	0	0
O00161	Synaptoso	SNAP23	90840.74	78703.19	117998.1	0	0	0
O00410	Importin-ε	IPO5	38802.25	41660.65	67018.42	68267	0	46220.8

O00170	AH receptr AIP	19985.89	14545.18	37973.71	0	0	0
O00178	GTP-bindii GTPBP1	2928.422	3188.455	2051.141	0	0	0
O00186	Syntaxin-1c STXBP3	38590.55	39767.87	50074.15	0	0	0
O00214	Galectin-8 LGALS8	9791.705	11960.26	18787.66	0	0	0
O00468	Agrin AGRN	209416.5	224616.7	193461.5	583264.7	734229.8	570367
O00220	Tumor nec TNFRSF10b	39920.49	40442.76	50337.63	0	0	0
O00233	26S protea PSMD9	17657.07	17649.16	20882.52	0	0	0
O00487	26S protea PSMD14	60477.21	57638.53	57111.7	145536.8	0	164732.9
O00244	Copper tra ATOX1	10417.01	7607.144	12324.34	0	0	0
O00267	Transcripti SUPT5H	9604.226	6470.987	7052.246	0	0	0
O00308	NEDD4-lik WWP2	13136	12675.7	10852.45	0	0	0
O00329	Phosphatic PIK3CD	2971.18	2843.297	3155.511	0	0	0
O00401	Neural Wisc WASL	82202	10453.47	77704.58	0	0	0
O00442	RNA 3-terti RTCA	6505.251	7270.992	8044.883	0	0	0
O00560	Syntenin-1 SDCBP	1427549	1360671	1261309	354369.2	0	338963.3
O00443	Phosphatic PIK3C2A	3220.715	3639.743	6876.037	0	0	0
O00458	Interferon-1 IFRD1	1729.009	1920.504	727.3862	0	0	0
O00461	Golgi integ GOLIM4	6905.303	5613.868	6417.86	0	0	0
O00471	Exocyst co EXOC5	15407.95	15740.87	19255.98	0	0	0
O00499	Myc box-c BIN1	7337.121	6097.939	4919.383	0	0	0
O00505	Importin si KPNA3	10465.11	7726.271	14440.08	0	0	0
O00506	Serine/thre STK25	18166.43	18524.96	17570.84	0	0	0
O00507	Probable c USP9Y	6043.546	6277.849	3906.931	0	0	0
O00522	Krev intera KRIT1	5067.21	5031.125	7071.633	0	0	0
O00541	Pescadillo PES1	11314.47	7551.658	6363.34	0	0	0
O00567	Nucleolar j NOP56	36813.27	51347.98	20868.66	0	0	0
O00592	Podocalyxii PODXL	200909.4	216248.8	329704.2	0	0	0
O00629	Importin si KPNA4	13536.1	11439.37	15861.75	0	0	0
O14672	Disintegrin ADAM10	854852.9	821981.5	695727.5	291035.2	0	319522.6
O00762	Ubiquitin-1 UBE2C	14050.35	18940.35	15692.5	0	0	0
O00764	Pyridoxal k PDXK	20557.99	17701.83	23853.65	0	0	0
O14497	AT-rich int ARID1A	956.5964	951.3665	395.0994	0	0	0
O14530	Thioredoxi TXNDC9	12426.56	14253.25	15286.67	0	0	0
O14578	Citron Rho CIT	3758.719	3955.991	2893.972	0	0	0
O14579	Coatomer COPE	22512.98	19438.21	20271.33	0	0	0
O14595	Carboxy-tr CTDSP2	5376.086	3953.643	4147.205	0	0	0
O14657	Torsin-1B TOR1B	12675.73	11481.66	11435.96	0	0	0
O14786	Neuropilin NRP1	126290.1	112173.1	128614.1	60399.73	88702.34	73123.23
O14678	ATP-bindii ABCD4	6190.75	6112.544	4898.253	0	0	0
O14817	Tetraspani TSPAN4	744401.1	800118.4	825183.3	256016	0	479146.7
O14818	Proteasom PSMA7	92157.16	78363.68	103524.2	86836.34	98504.18	79160.2
O14737	Programm PDCD5	13504.67	12762.05	15512.43	0	0	0
O14744	Protein arg PRMT5	78372.83	76448.95	74802.19	0	0	0
O14745	Na(+)/H(+) SLC9A3R1	129184.4	113225.9	198750.5	0	0	0
O14763	Tumor nec TNFRSF10I	11324.06	12036.3	14312.32	0	0	0
O14773	Tripeptidyl TPP1	4845.25	5631.505	19192.66	0	0	0
O14776	Transcripti TCERG1	11278.89	12814.23	7250.168	0	0	0
O14950	Myosin re MYL12B	176839.4	191270.8	235043.7	313671.6	241507	219710.3
O14782	Kinesin-lik KIF3C	8761.979	9234.955	9686.021	0	0	0
O14787	Transporti TNPO2	7446.863	7073.521	17933.52	0	0	0
O14907	Tax1-bindi TAX1BP3	38534	33862.86	57083.14	0	0	0
O14908	PDZ doma GIPC1	106722.6	96166.16	139822.9	0	0	0
O14910	Protein lin LIN7A	75676.84	69106.99	118156.4	0	0	0
O14929	Histone ac HAT1	1801.485	8325.019	8492.766	0	0	0
O14936	Peripheral CASK	26958.93	24475.53	38662.57	0	0	0
O14939	Phospholi PLD2	5331.887	3616.48	2353.97	0	0	0
O15027	Protein tra SEC16A	9830.514	8723.038	8197.912	0	2417486	764338.8
O15031	Plexin-B2 PLXNB2	24154.6	21425.6	26960.93	63621.37	83108.97	36291.48

O14960	Leukocyte LECT2	95342.47	96645.33	46062.03	0	0	0
O14964	Hepatocyte HGS	27308.48	23438.62	43629.61	0	0	0
O14974	Protein ph PPP1R12A	9872.902	15598.61	20008.65	0	0	0
O14976	Cyclin-G-α GAK	3427.099	3570.488	3216.339	0	0	0
O14979	Heterogen HNRNPDL	30310.67	32097.68	23676.99	0	0	0
O15144	Actin-relat ARPC2	102398.6	98962.77	183405.6	0	392752.4	67848.52
O15145	Actin-relat ARPC3	125456.1	102669	192562	41038.46	0	24972.87
O14980	Exportin-1 XPO1	14221.29	15845.43	16708.48	0	0	0
O15013	Rho guanin ARHGEF1C	18793.55	31976.13	22959.78	0	0	0
O15020	Spectrin β SPTBN2	5496.366	4310.359	8364.443	0	0	0
O15042	U2 snRNP-U2SURP	4337.548	6043.31	4729.971	0	0	0
O15056	Synaptojar SYNJ2	8344.859	5388.878	8743.329	0	0	0
O15230	Laminin su LAMA5	10857.12	8944.483	6679.583	36579.36	58980.03	29751.91
O15067	Phosphoril PFAS	34176.48	29266.4	38208.27	0	0	0
O15084	Serine/thr ANKRD28	5314.922	5824.885	2879.309	0	0	0
O15260	Surfeit loc SURF4	23360.42	50717.86	27077.71	143168.2	0	117005.4
O15118	Niemann-II NPC1	23714.63	18698.87	11629.16	0	0	0
O15160	DNA-direct POLR1C	14782.32	14969.26	13214.63	0	0	0
O15162	Phospholip PLSCR1	96912.42	52637.85	100797.1	0	0	0
O15194	CTD small CTDSPL	17592.22	17363.67	25440.59	0	0	0
O15197	Ephrin type EPHB6	2181.164	2673.779	5553.873	0	0	0
O15212	Prefoldin s PFDN6	24050.35	20830.57	29904.82	0	0	0
O15400	Syntaxin-7 STX7	90173.08	78609.19	67034.23	43829.52	82294.27	171820.5
O15240	Neurosecr VGF	166704.7	154963.9	246499.4	0	0	0
O15427	Monocarb SLC16A3	615011.1	608758.8	821714.4	169751.5	181709.3	233618.8
O15258	Protein RE RER1	13330.71	19569.66	17687.33	0	0	0
O15294	UDP-N-ac OGT	6642.263	8386.276	10541.41	0	0	0
O15305	Phosphom PMM2	19835.5	11026.12	20653.18	0	0	0
O15344	E3 ubiquiti MID1	2701.479	3520.133	2593.352	0	0	0
O15347	High mobi HMGB3	88955.7	82442.02	38128.46	0	0	0
O15355	Protein ph PPM1G	55718.28	58260.07	27177.97	0	0	0
O15397	Importin-ε IPO8	5318.68	5947.945	8058.086	0	0	0
O43175	D-3-phosph PHGDH	171736.7	207173.4	238294	102313.8	88738.13	116331.9
O15403	Monocarb SLC16A6	19228.39	17290.06	17608.46	0	0	0
O15431	High affini SLC31A1	24552.68	22326.04	29689.61	0	0	0
O43242	26S protea PSMD3	58665.23	62174.3	44308.48	132062.8	0	60403.45
O15498	Synaptojar YKT6	23638.22	24415.54	28996.41	0	0	0
O15511	Actin-relat ARPC5	73437.33	60839.19	121778.1	0	0	0
O15530	3-phosph PDPK1	12476.69	12633.75	10365.46	0	0	0
O43294	Transformi TGFB1I1	10544.77	8372.442	14647.66	158149.4	0	56003.31
O43390	Heterogen HNRNP R	26199.07	39512.67	30045.31	40704.81	0	41427.71
O43150	Arf-GAP w ASAP2	8895.131	8664.215	9516.291	0	0	0
O43169	Cytochrome CYB5B	28481.29	31948.06	29589.61	0	0	0
O43172	U4/U6 smα PRPF4	5374.791	3879.066	3822.706	0	0	0
O43194	G-protein GPR39	18548.63	22815.87	19581.98	0	0	0
O43237	Cytoplasm DYNC1LI2	22771.19	22932.21	17651.48	0	0	0
O43252	Bifunction PAPSS1	11913.03	9889.637	9453.79	0	0	0
O43264	Centromer ZW10	3598.544	6129.524	5907.408	0	0	0
O43396	Thioredoxi TXNL1	4399.815	2425.242	2089.03	0	0	0
O43399	Tumor pro TPD52L2	36539.2	34506.71	62280.84	0	0	0
O43427	Acidic fibr FIBP	5069.871	4736.122	10286.09	0	0	0
O43447	Peptidyl-p PPIH	3883.121	3426.136	4131.931	0	0	0
O43488	Aflatoxin BAKR7A2	18564.56	17923.4	20196.89	0	0	0
O43491	Band 4.1-I EPB41L2	117220.2	106816.8	129120.5	0	0	0
O43504	Ragulator LAMTOR5	13649.72	12526.17	15916.93	0	0	0
O43592	Exportin-T XPO1	19578.9	13022.73	15695.41	0	0	0
O43597	Protein spr SPRY2	24702.87	24503.53	25136.7	0	0	0
O43615	Mitochondr TIMM44	1364.369	2161.133	1978.403	0	0	0

O43617	Trafficking TRAPPC3	25405.53	23393.41	36480.84	0	0	0
O43633	Charged r CHMP2A	38638.69	34941.66	41892.39	0	0	0
O43657	Tetraspani TSPAN6	110992.6	109211.8	83746.31	0	0	0
O43747	AP-1 comp AP1G1	19941.06	18790.49	17032.53	0	2675926	2.56E+08
O43660	Pleiotropic PLRG1	3064.99	3281.869	1897.917	0	0	0
O43681	ATPase ASASNA1	37796.71	30942.58	45751.34	0	0	0
O43684	Mitotic chε BUB3	48765.99	49244.84	45491.19	0	0	0
O43688	Phospholig PLPP2	23722.12	19767.83	29858.24	0	0	0
O43739	Cytohesin- CYTH3	11068.6	15219.41	22088.31	0	0	0
O43741	5-AMP-ac PRKAB2	3474.627	4462.233	7208.125	0	0	0
O43752	Syntaxin-6 STX6	14144.77	16124.26	18527.27	0	0	0
O43854	EGF-like rε EDIL3	559448.1	524212	718662.6	1517839	1147329	2769120
O43865	Adenosylh AHCYL1	164616.8	158332.2	151078	199581.1	166282.1	224099
O43765	Small glutε SGTA	13374.82	16134.92	14804.33	0	0	0
O43795	Unconvent MYO1B	109772.7	120644.9	271156.4	0	0	0
O43809	Cleavage ε NUDT21	12652.73	10583.14	11712.66	0	0	0
O43813	LanC-like j LANCL1	26543.3	24348.56	20594.85	0	0	0
O43847	Nardilysin NRD1	15425.23	15191.42	16623.51	0	0	0
O43913	Origin recc ORC5	2938.377	3096.003	2394.553	0	0	0
O60216	Double-str RAD21	8456.998	9874.308	3592.068	0	0	0
O60231	Putative pr DHX16	4092.157	4665.945	4071.34	0	0	0
O60245	Protocadh PCDH7	10210.27	9373.186	9353.737	0	0	0
O60256	Phosphoril PRPSAP2	12669.73	16806.33	5868.087	0	0	0
O60264	SWI/SNF-r SMARCA5	15436.44	10723.13	13529.96	0	0	0
O60271	C-Jun-ami SPAG9	13029.14	12782.92	12983.24	0	0	0
O60291	E3 ubiquiti MGRN1	11368.92	9345.059	15076.41	0	0	0
O60341	Lysine-spe KDM1A	8655.527	4732.597	5821.596	0	0	0
O60343	TBC1 dom TBC1D4	7831.819	7869.825	3125.026	0	0	0
O60493	Sorting ne: SNX3	32147.15	33209.39	33346.6	29374.17	0	24071.7
O60353	Frizzled-6 FZD6	21208.21	22489.54	21190.57	0	0	0
O60361	Putative n NME2P1	64311.25	66138.25	67094.93	0	0	0
O60443	Non-syndi DFNA5	12925.85	5713.076	10024.73	0	0	0
O60488	Long-chain ACSL4	145813.5	140718.7	192223.6	0	0	0
O60499	Syntaxin-1 STX10	5756.519	6486.201	5960.083	0	0	0
O60502	Protein O- MGEA5	2763.688	6574.629	3479.288	0	0	0
O60568	Procollage PLOD3	16037.62	24280.66	21889.65	27799.45	0	36297.83
O60506	Heterogen SYNCRIP	25813.44	23616.69	17366.42	0	0	0
O60508	Pre-mRNA CDC40	4821.07	5112.182	2691.521	0	0	0
O60513	Beta-1,4-ç B4GALT4	3720.094	4839.098	5630.199	0	0	0
O60518	Ran-bindir RANBP6	40632.23	12277.21	31061.61	0	0	0
O60610	Protein diε DIAPH1	12319.26	13252.85	13985.14	0	0	0
O60635	Tetraspani TSPAN1	13526.18	10256.91	12139.16	0	0	0
O60645	Exocyst co EXOC3	12005.4	9998.491	17674.2	0	0	0
O60664	Perilipin-3 PLIN3	14982.25	13368.52	24725.67	0	0	0
O60669	Monocarb SLC16A7	27778.75	23634.93	14734.88	0	0	0
O60716	Catenin de CTNND1	63405.63	67213.55	107737.7	9478.817	0	32046.69
O60678	Protein arç PRMT3	4629.294	5221.577	7461.72	0	0	0
O60684	Importin sı KPNA6	15846.89	15890.85	16643.54	0	0	0
O60711	Leupaxin LPXN	7907.136	7622.924	2171.789	0	0	0
O60739	Eukaryotic EIF1B	25604.17	29545.13	32285.83	0	0	0
O60749	Sorting ne: SNX2	23018.19	24972.38	30514.99	0	0	0
O60814	Histone H2 HIST1H2B1	11074686	12037059	12324432	1926069	11448047	5566483
O60832	H/ACA ribı DKC1	36271.47	46941.2	12406.34	34582.58	23718.96	0
O60841	Eukaryotic EIF5B	20542.93	20998.46	10617.33	55386.78	0	34832.05
O60763	General ve USO1	37456.77	38749.72	32150.36	0	0	0
O60779	Thiamine t SLC19A2	19509.61	23202.52	14416.54	0	0	0
O60784	Target of M TOM1	32338.9	17213.19	42523	0	0	0
O60869	Endothelia EDF1	11049.35	15678.59	18762	0	0	0

O60884	DnaJ homcDNAJA2	181196.8	209547.8	140475.7	0	0	0
O60925	Prefoldin s PFDN1	15751.68	14895.18	20595.85	0	0	0
O75044	SLIT-ROBCSRGAP2	22530.57	22596.86	26473.5	0	0	0
O75083	WD repeatWDR1	466281.9	346072.4	455123.5	84703.58	250799.3	241404.9
O75051	Plexin-A2 PLXNA2	3139.327	3909.25	3802.322	0	0	0
O75054	ImmunoglgIGSF3	6670.226	4468.483	7748.208	0	0	0
O75116	Rho-assocROCK2	9635.088	12219.25	10856.25	112059.3	0	34732.52
O75084	Frizzled-7 FZD7	140582.3	127970.5	127724.7	0	0	0
O75110	Probable p ATP9A	6300.884	5320.237	5507.978	0	0	0
O75122	CLIP-assocCLASP2	715.933	1656.937	2481.256	0	0	0
O75146	Huntingtin HIP1R	3105.473	2612.941	3347.044	0	0	0
O75147	Obscurin-lOBSL1	10218.55	11575.11	14802.04	0	0	0
O75165	DnaJ homcDNAJC13	7271.77	8998.02	9597.621	19961.42	16769.07	23090.7
O75153	Clustered rCLUH	19562.49	18667.01	21123.51	0	0	0
O75197	Low-densi LRP5	3653.864	10434.69	2765.237	0	0	0
O75204	Transmem TMEM127	9809.47	7513.52	7204.813	0	0	0
O75317	Ubiquitin c USP12	20188.05	24507.47	19866.03	0	0	0
O75340	Programm PDCD6	305122.8	297807.3	325358.4	145949.9	185389.6	256656.5
O75326	SemaphoriSEMA7A	23058.77	26162.88	29198.78	0	0	0
O75347	Tubulin-sq TBCA	35969.48	36764.09	66973.47	0	0	0
O75351	Vacuolar p VPS4B	25130.69	25188.92	26553.79	0	0	0
O75367	Core histoiH2AFY	100891.7	109121.3	89624.02	165873.2	295734.2	158213.8
O75369	Filamin-B FLNB	75064.75	74700.32	101102.4	63724.9	0	124895.7
O75352	Mannose- MPDU1	7818.006	10402.05	7852.875	0	0	0
O75382	Tripartite r TRIM3	12420.73	10062.3	21221.64	0	0	0
O75387	Large neut SLC43A1	31845.58	14712.68	23986.45	0	0	0
O75390	Citrate syn CS	4760.755	5923.062	4828.793	0	0	0
O75396	Vesicle-traSEC22B	10195.33	9657.592	6318.584	0	0	0
O75400	Pre-mRNA PRPF40A	32270.91	19801.78	11196.72	0	0	0
O75436	Vacuolar p VPS26A	10784.5	18221.38	16190.42	0	0	0
O75475	PC4 and SIP SIP1	13745.63	13422.48	9056.984	0	0	0
O75494	Serine/arg SRSF10	19379.06	20526.05	10219.34	0	0	0
O75506	Heat shock HSBP1	6805.047	5287.289	10163.14	0	0	0
O75508	Claudin-1: CLDN11	38267.26	38168.76	25604.87	0	0	0
O75531	Barrier-to- BANF1	242967.7	325554.3	240583.5	180065.9	400535.2	0
O75509	Tumor nec TNFRSF21	18640.64	17337.61	18794.23	0	0	0
O75533	Splicing fa: SF3B1	53160.55	62202.07	34929.46	0	0	0
O75534	Cold shock CSDE1	13815.46	14104.98	14480.52	0	0	0
O75586	Mediator c MED6	2925.444	3170.267	2458.221	0	0	0
O75607	Nucleopla: NPM3	17005.7	16788.44	15370.42	0	0	0
O75608	Acyl-prote LYPLA1	31529.27	32396.55	18150.9	0	0	0
O75663	TIP41-like TIPRL	159180.3	135788.9	236696	2873284	3123115	5899021
O75643	U5 small n SNRNP20C	62929.13	73001.44	39380.61	0	0	0
O75674	TOM1-like TOM1L1	41584.37	39541.37	33259.69	0	0	0
O75694	Nuclear pc NUP155	4131.667	4409.521	3584.475	0	0	0
O75695	Protein XR RP2	38344.65	36895.84	50219.98	0	0	0
O75718	Cartilage-c: CRTAP	10353.21	11263.9	12085.19	0	0	0
O75762	Transient r TRPA1	12404.62	14480.94	17852.7	0	0	0
O75787	Renin rece ATP6AP2	8905.517	15126.71	6927.526	0	0	0
O75821	Eukaryotic EIF3G	38549.13	37759.25	35379.16	0	0	0
O75822	Eukaryotic EIF3J	28888.64	28308.26	23978.21	0	0	0
O75829	Leukocyte LECT1	5804.964	6713.703	8068.642	0	0	0
O75832	26S protea PSMD10	19215.39	17166.84	17937.1	0	0	0
O75874	Isocitrate c IDH1	31280.06	25150.32	37262.33	33301.76	45359.41	120190.2
O75891	Cytosolic 1ALDH1L1	88843.59	82750.43	92928.02	84823.53	0	31407.48
O75915	PRA1 fami ARL6IP5	10307.62	11993.13	11208.28	81814.47	0	64194.84
O75844	CAAX prer ZMPSTE24	7773.169	6871.872	4936.696	0	0	0
O75962	Triple func TRIO	1761.074	11325.98	5770.313	0	0	0

O75970	Multiple PIMPDZ	4496.937	5066.176	6873.104	0	0	0
O75976	Carboxype CPD	12044.52	10719.06	11201.97	0	0	0
O76003	Glutaredox GLRX3	34551.5	34633.41	47557.96	0	0	0
O76021	Ribosomal RSL1D1	21599.98	23818.42	13542.67	0	0	0
O76071	Probable c CIAO1	22092.24	7335.146	4946.132	0	0	0
O76081	Regulator RGS20	30821.95	29290.01	29970.06	0	0	0
O76094	Signal recc SRP72	13001.43	16797.3	9922.553	0	0	0
O94760	N(G),N(G)-DDAH1	25239.69	26476.37	42989.75	0	0	0
O94804	Serine/thrē STK10	68822.76	66102.2	97166.41	0	0	0
O94806	Serine/thrē PRKD3	11001.78	12823.7	11750.67	0	0	0
O94808	Glutamine GFPT2	16980.28	17314.28	17886.55	0	0	0
O94855	Protein tra SEC24D	10493.06	7424.935	8123.412	0	0	0
O94886	CSC1-like TMEM63A	9106.479	11573.46	8981.416	0	0	0
O94887	FERM, Rho FARP2	27979.18	27393.9	38857.37	0	0	0
O94973	AP-2 comē AP2A2	19427.12	19837.54	15217.25	0	0	0
O95071	E3 ubiquiti UBR5	2370.07	5307.956	3443.58	0	0	0
O94915	Protein fur FRYL	15291.81	16717.05	11450.64	38147.28	0	30633.2
O95104	Splicing fa SCAF4	10386.98	8822.06	9473.925	0	0	0
O94985	Calsyntenin CLSTN1	47813.27	42324.96	34166.79	69439.66	140893.7	0
O95154	Aflatoxin BAKR7A3	7979.134	13052.42	12101.29	0	0	0
O95084	Serine proē PRSS23	120215.4	119562.4	141096	191351.6	205617.8	377140.4
O95155	Ubiquitin c UBE4B	6013.146	6168.509	5774.751	0	0	0
O95163	Elongator IKBKAP	12311.37	9612.314	5804.875	0	0	0
O95164	Ubiquitin-UBL3	19142.15	13366.4	20250.98	0	0	0
O95183	Vesicle-asē VAMP5	50289.35	40081.11	75219.09	0	0	0
O95219	Sorting neē SNX4	6934.201	6553.077	11281.23	0	0	0
O95235	Kinesin-lik KIF20A	1544.929	4535.87	4310.571	0	0	0
O95248	Myotubulaē SBF1	5271.098	4970.402	9347.18	0	0	0
O95249	Golgi SNA GOSR1	16806.71	14549.31	13886.94	0	0	0
O95292	Vesicle-asē VAPB	22698.52	37576.39	31384.23	0	0	0
O95295	SNARE-asē SNAPIN	3965.779	3793.655	5464.64	0	0	0
O95297	Myelin proē MPZL1	87711.31	69133.22	71834.15	0	0	0
O95336	6-phosphoē PGLS	30982.48	34693.31	51079.31	0	0	0
O95340	Bifunctionē PAPSS2	8793.21	8771.822	10434.75	0	0	0
O95342	Bile salt ex ABCB11	33237.31	20929.03	33072.84	0	0	0
O95347	Structural I SMC2	10386.21	10620.44	10048.62	0	0	0
O95352	Ubiquitin- I ATG7	10943.07	11423.58	8212.559	0	0	0
O95372	Acyl-prote LYPLA2	5017.303	4831.922	4396.713	0	0	0
O95394	Phosphoacē PGM3	6357.634	8513.678	10037.83	0	0	0
O95415	Brain proteē BRI3	57961.84	48921.6	44941.4	0	0	0
O95433	Activator c AHSA1	46054.46	48582.41	58305.6	0	0	0
O95456	Proteasomē PSMG1	7229.596	10378.27	9345.041	0	0	0
O95466	Formin-likē FMNL1	19860.44	28148.51	25274.05	0	0	0
O95490	Adhesion (ADGRL2	4230.068	5826.26	9671.985	0	0	0
O95602	DNA-direct POLR1A	3460.085	4486.616	2431.639	0	0	0
O95630	STAM-binē STAMBP	8537.614	7098.293	9541.448	0	0	0
O95685	Protein ph PPP1R3D	4947.743	3628.936	3660.882	0	0	0
O95714	E3 ubiquiti HERC2	1821.174	2587.223	2252.566	0	0	0
O95497	Pantethein VNN1	131929	148657.3	178899.2	1422246	2069474	916991.6
O95498	Vascular nē VNN2	84767.4	77924.41	172021	1526596	2430510	953240.3
O95721	Synaptosoē SNAP29	16143.97	13923.99	28232.17	0	0	0
O95793	Double-strē STAU1	843.9343	1363.884	985.3718	0	0	0
O95807	Transmemē TMEM50A	26685.65	26319.46	38069.34	0	0	0
O95816	BAG family BAG2	38723.52	27929.93	27052.13	0	0	0
O95817	BAG family BAG3	3586.505	3806.371	3431.003	0	0	0
O95747	Serine/thrē OXSR1	63400.32	60024.89	79968.86	69762.28	40671.55	78193.48
O95834	Echinoderrē EML2	100509.3	97241.59	63201.06	0	0	0
O95835	Serine/thrē LATS1	3306.836	3448.257	7198.177	0	0	0

O95858	Tetraspani TSPAN15	76393.13	75681.09	87945.56	0	0	0
O95881	Thioredoxi TXNDC12	7527.94	5939.263	4290.47	0	0	0
O95819	Mitogen-a MAP4K4	84086.82	82987.44	84791.17	147520	156364.6	143849.4
O95967	EGF-conta EFEMP2	13965.23	15456.18	17873.56	0	0	0
O96013	Serine/thre PAK4	22916.34	26706.67	39075.21	0	0	0
O96019	Actin-like ACTL6A	36691.65	38431.38	41312.72	0	0	0
O95865	N(G),N(G)-DDAH2	47476.81	45391.6	69521.46	356854.1	272996.9	136166.9
P00326	Alcohol de ADH1C	14726.38	14322.28	15408.64	0	0	0
O95965	Integrin be ITGBL1	290.8407	514.5289	353.5128	20498.62	25871.37	0
P00367	Glutamate GLUD1	16857.28	14299.23	19278.68	0	0	0
P00374	Dihydrofol DHFR	16940.83	16672.42	23725.6	0	0	0
P00403	Cytochrome MT-CO2	10299.42	16541.53	6606.265	0	0	0
P00492	Hypoxanth HPRT1	47525.42	55887.29	74502.72	0	0	0
P00338	L-lactate d LDHA	1038312	1105905	1410588	1417967	1133633	1244605
P00352	Retinal de ALDH1A1	42387.75	39822.83	43137.13	45905.95	0	46841.77
P00505	Aspartate GOT2	7671.497	7108.434	11197.91	0	0	0
P00568	Adenylate AK1	7741.662	7507.194	10810.6	0	0	0
P00387	NADH-cyt CYB5R3	23738.14	27094.96	24231	80357.67	32311.95	62279.48
P00390	Glutathion GSR	20198.39	19773.94	29854.99	110477.4	75510.74	66857.32
P00749	Urokinase-PLAU	59801.43	68637.87	85627.86	0	0	0
P00750	Tissue-typ PLAT	5621.875	5270.362	5772.151	0	0	0
P00450	Ceruloplas CP	22793.57	16837.43	31018.95	90107.81	196353.4	135910.3
P01009	Alpha-1-a SERPINA1	41636.15	49913.2	13945.7	0	0	0
P00491	Purine nuc PNP	28991.06	24066.54	39896.23	109750.7	125599.8	85691.2
P01112	GTPase HF HRAS	57676.92	19281.46	44173.1	0	0	0
P01130	Low-densi LDLR	33765.61	32407.69	27168.42	0	0	0
P00533	Epidermal EGFR	112029.4	112613	140570.7	60279.79	90307.98	53028.61
P00558	Phosphogl PGK1	348808.3	366544.2	456857.4	215485.5	104420.2	240834.3
P01266	Thyroglob TG	14715.51	14106.69	31851.05	0	0	0
P00734	Prothromb F2	5114347	5383645	5239673	7057864	3789778	6725526
P00738	Haptoglob HP	67905.68	58402.08	25702	242131.8	0	561067.6
P00740	Coagulatic F9	455678	490727.6	483598.6	694409.9	1086583	573202.1
P00742	Coagulatic F10	977090	941241.8	966253.3	532302.2	825313.4	527205
P01859	Ig gamma-IGHG2	34857.79	57789.88	13207.87	0	0	0
P01871	Ig mu chain IGHM	8026.862	18436.28	5131.232	0	0	0
P02747	Compleme C1QC	623.343	2130.563	2302.567	0	0	0
P02748	Compleme C9	291082.6	257061	185990.1	0	0	0
P04049	RAF proto-RAF1	13084.3	11320.6	18538.99	0	0	0
P01023	Alpha-2-n A2M	38129136	37686836	49067864	1.29E+08	1.28E+08	96147840
P04062	Glucosylce GBA	5388.372	8582.935	3421.933	0	0	0
P01031	Compleme C5	126253.1	122667.1	114269.2	1889089	3999791	1238066
P01033	Metallopro TIMP1	105500	96807.67	230555.7	5632950	8258561	3181560
P04066	Tissue alph FUCA1	36333.91	35776.74	37752.38	0	0	0
P01042	Kininogen-KNG1	862552.8	865744.3	976370.8	10547805	16567593	8058223
P04080	Cystatin-B CSTB	105513.7	106576	130268.8	0	0	0
P04180	Phosphatic LCAT	50888.04	45220.72	52930.75	0	0	0
P04181	Ornithine OAT	4735.238	4822.464	4755.482	0	0	0
P04183	Thymidine TK1	8693.764	11355.38	14239.06	0	0	0
P04196	Histidine-r HRG	4380.845	6314.217	1026.66	0	0	0
P01620	Ig kappa chain V-III re	21487.88	27091.04	32643.32	425895.6	389333.9	185503.6
P04424	Argininosu ASL	54514.18	54996.44	52298.91	0	0	0
P04818	Thymidylat TYMS	26666.98	24320.54	24149.11	0	0	0
P04920	Anion excf SLC4A2	36852.95	36234.68	43214.77	0	0	0
P01891	HLA class I HLA-A	474251.1	471715.9	533965.3	0	276833.3	308168.7
P01893	Putative H HLA-H	258042.2	268184	273039	367584.1	0	567797.1
P05026	Sodium/pc ATP1B1	251746.4	108953	160967.8	0	0	0
P05062	Fructose-k ALDOB	18950.07	14864	16017.32	0	0	0
P05107	Integrin be ITGB2	138739.6	134042.8	154721.4	0	0	0

P05161	Ubiquitin-l ISG15	18912.93	14981.06	19363.81	0	0	0
P05362	Intercellul ICAM1	92243.75	93404.09	127882	0	0	0
P02462	Collagen a COL4A1	23201.41	30719.4	13819.37	237286	470051.9	201699.3
P02533	Keratin, ty KRT14	199680.5	189530.1	249215.6	1427313	3483941	2303723
P02538	Keratin, ty KRT6A	61087.1	81660.94	79970.8	462970.6	1042913	1003104
P02647	Apolipoprotein APOA1	3566195	3211318	4207069	47196760	59620932	18950614
P05455	Lupus La p SSB	15005.09	16387.36	10818.8	0	0	0
P05771	Protein kinase PRKCB	7957.199	12195.61	14156.9	0	0	0
P02675	Fibrinogen FGB	40169.59	37442.22	38222.67	204348.2	1194950	1453643
P05783	Keratin, ty KRT18	47862.11	46341.58	34261.54	0	0	0
P05787	Keratin, ty KRT8	62895.14	66438.72	51442.44	0	0	0
P06132	Uroporphyrin UROD	34136.41	39413.57	42362.12	0	0	0
P02749	Beta-2-glycophosphohydroxy APOH	764665.2	687850.3	311122.6	1993687	6668891	3616376
P06213	Insulin receptor INSR	3771.061	3530.741	4670.533	0	0	0
P06241	Tyrosine-kinase FYN	6108.077	4328.935	12132.91	0	0	0
P06280	Alpha-galactosidase GLA	13836.96	14764.81	12962.98	0	0	0
P06493	Cyclin-dependent CDK1	32551.24	32638.16	38305.66	0	0	0
P02771	Alpha-fetoprotein AFP	3989637	3317228	6021138	52023072	77304440	26327024
P06730	Eukaryotic EIF4E	20143.56	32877.43	18613.91	0	0	0
P02787	Serotransferrin TF	26248.32	33175.98	14172.17	5493981	0	217694.3
P02788	Lactotransferrin LTF	31812180	28470140	46188920	2.98E+08	4.57E+08	2.22E+08
P02790	Hemopexin HPX	66061.12	58196.44	39061.2	588119.3	1366101	553144.3
P02792	Ferritin light chain FTL	116868.2	14613.7	23226.41	500452.6	3513572	4951271
P02794	Ferritin heavy chain FTH1	88327.31	76841.38	96281.02	1591932	886506.6	462145.6
P03952	Plasma kallikrein KLKB1	93928.84	90491.75	94944.51	1166066	602828.3	283999.9
P06732	Creatine kinase CKM	3448.854	2098.638	2665.878	0	0	0
P06858	Lipoprotein LPL	28676.19	28700.71	31456.48	0	0	0
P04004	Vitronectin VTN	2620111	4285880	2223351	19663492	6645257	37739532
P04040	Catalase CAT	13482.14	19106.28	12664.95	292154.1	0	179690.2
P07099	Epoxide hydrolase EPHX1	5144.57	4710.197	6738.792	0	0	0
P07108	Acyl-CoA dehydrogenase DBI	49397.74	39430.49	69706.17	0	0	0
P07203	Glutathione peroxidase GPX1	30987.56	23256.13	34364.98	0	0	0
P04075	Fructose-1,6-bisphosphate aldolase ALDOA	925505.6	760778.3	1013660	613206.5	790384.3	514858.7
P07305	Histone H1 H1FO	63000.95	77023.32	79524.94	0	0	0
P04083	Annexin A ANXA1	251130.8	330626.3	323213.2	352890.1	339134	248198.2
P07451	Carbonic anhydrase CA3	8450.354	8492.081	6524.04	0	0	0
P07948	Tyrosine-kinase LYN	101739.3	92154.27	108408.7	0	0	0
P07954	Fumarate hydratase FHH	16073.3	13120.11	23468.79	0	0	0
P08069	Insulin-like growth factor IGF1R	11273.27	10501.59	13199.98	0	0	0
P08174	Complement component CD55	121283.6	103616.1	117479	0	0	0
P08183	Multidrug resistance ABCB1	37561.44	36299.19	51257.31	0	0	0
P04259	Keratin, ty KRT6B	98793.64	185519.8	116900.5	5356778	997069.3	1505684
P04264	Keratin, ty KRT1	478837.4	659930.6	486762.9	10337758	19867054	10563592
P08237	ATP-dependent PFKM	14128.62	16507.12	12936.48	0	0	0
P08243	Asparaginase ASNS	49932.95	47405.25	54403.07	0	0	0
P04406	Glyceraldehyde GAPDH	2433859	2521315	3139118	1739243	1198381	1925284
P08473	Neprilysin MME	692.6804	7211.493	7695.079	0	0	0
P08581	Hepatocyte MET	4791.732	5626.188	4408.602	0	0	0
P04792	Heat shock protein HSPB1	48559.59	45902.87	51333.24	191661.7	181669.6	147272.5
P08582	Melanotransferrin MF12	17706.68	24083.08	19072.17	0	0	0
P04843	Dolichyl-diphosphate RPN1	16351	19855.4	23480.26	0	165713.3	110866.6
P04899	Guanine nucleotide GNAI2	910786	861150.8	1008147	297261.3	258325.9	340356.3
P09110	3-ketoacyl-CoA ACAA1	9560.212	4965.495	6533.26	0	0	0
P09132	Signal receptor SRP19	10658.6	11985.66	11905.24	0	0	0
P09234	U1 small nuclear SNRPC	11019.75	12788.01	7842.92	0	0	0
P09455	Retinol-binding RBP1	7978.721	8768.054	8028.932	0	0	0
P09496	Clathrin ligand CLTA	127947.7	108847.3	84292.3	0	0	0
P05106	Integrin beta ITGB3	10614.93	9568.82	9697.918	186609.5	202846	380741.4

P09497	Clathrin lig CLTB	55497.73	47762.19	42992.59	0	0	0
P09525	Annexin A-ANXA4	12417.85	12352.01	10085.96	0	0	0
P09874	Poly [ADP- PARP1	41419.47	45235.54	24617.12	0	0	0
P05156	Compleme CFI	149129.7	118610.5	175399.7	2456741	3263148	1261623
P05160	Coagulatc F13B	26652.7	24773.33	21627.8	112520.1	0	81283.26
P09960	Leukotrien LTA4H	15985.8	21428.18	27843.03	0	0	0
P0C0S5	Histone H2 H2AFZ	3849.286	3940.025	3577.001	0	0	0
P0C2W1	F-box/SPR FBXO45	2219.678	2369.097	2348.958	0	0	0
P05386	60S acidic RPLP1	70448.3	830439	195828.1	949130.3	40380.62	721693.7
P05387	60S acidic RPLP2	373761.2	358915.1	354522.9	415662.4	0	328147.9
P05388	60S acidic RPLP0	195657.6	202891.3	175257.4	152766.5	92050.16	77703.5
P10114	Ras-relate RAP2A	151503	142784.9	172708.2	0	0	0
P10155	60 kDa SS- TROVE2	18140.53	16838.74	13964.08	0	0	0
P10398	Serine/thre ARAF	8767.406	7732.216	1611.576	0	0	0
P05546	Heparin cc SERPIND1	83964.77	71745.66	104324.4	428486.8	965370.8	444054.9
P10515	Dihydrolip DLAT	13835.48	14314.02	15867.77	0	0	0
P10586	Receptor-1PTPRF	19504.26	18079.41	21031.97	0	0	0
P10619	Lysosomal CTSA	13146.4	8735.784	12780.54	0	0	0
P10768	S-formylgl ESD	61138.53	55163.58	65012.44	0	0	0
P05976	Myosin ligl MYL1	40987.26	98639.09	124450.2	0	108986.6	136927.6
P05997	Collagen a COL5A2	17440.98	19195.95	37631.48	451310	825428.4	403068.6
P10809	60 kDa he2 HSPD1	17079.11	22642.6	12393.07	0	0	0
P11117	Lysosomal ACP2	20693.02	17600.94	18018.21	0	0	0
P11171	Protein 4.1 EPB41	39084.23	48674.27	45209.2	0	0	0
P06276	Cholineste BCHE	4647.629	0	17798.31	24746.38	34684.11	0
P11172	Uridine 5-i UMPS	20353.48	21441.83	23497.86	0	0	0
P06396	Gelsolin GSN	1166686	1135214	1229693	4862841	6779867	3406601
P11233	Ras-relate RALA	101475.4	122071.6	78810.8	0	0	0
P06727	Apolipoppr APOA4	111924.4	50214.25	70075.11	617209.1	1151623	408372.7
P11279	Lysosome- LAMP1	102935.9	104048.4	89663.5	0	0	0
P11387	DNA topoi TOP1	229907.7	226396.2	149904.4	0	0	0
P06733	Alpha-enc ENO1	1245539	1345522	1978718	689404.8	773133.4	696294.7
P06737	Glycogen j PYGL	122409	121049.4	167119.1	363014.7	57072.76	248760.7
P06744	Glucose-6 GPI	48221.84	46286.14	67834.45	131988.2	0	116845.9
P06748	Nucleophc NPM1	696600.7	659720.3	463694.8	358042.8	227261	254393.4
P06753	Tropomyo TPM3	152176.1	175195.7	375084	56467.45	52839.91	0
P06756	Integrin al ITGAV	151717.2	145714.1	158102.1	101437.4	80761.59	92205.98
P11388	DNA topoi TOP2A	34838.95	40453.54	21249.37	0	0	0
P06865	Beta-hexo HEXA	25470.41	33876.23	26517.67	92746.87	104162.4	0
P11802	Cyclin-dec CDK4	2541.3	2504.462	4287.051	0	0	0
P11908	Ribose-ph PRPS2	14675.33	9476.764	8622.806	0	0	0
P12004	Proliferatir PCNA	14990.55	14162.23	15186.13	0	0	0
P12081	Histidine-- HARS	17499.47	18141.72	19666	0	0	0
P07148	Fatty acid- FABP1	18873052	15971322	55044576	3125538	1.47E+09	7.85E+08
P07195	L-lactate d LDHB	434666.4	419485.5	573096.8	292822.7	226628.2	222021.7
P12270	Nucleopro TPR	5257.117	4217.79	6446.768	0	0	0
P12277	Creatine ki CKB	71049.61	73818.14	95659.52	0	0	0
P07237	Protein dis P4HB	18336.94	18902.06	26950.16	64108.5	51358.36	45800.79
P12532	Creatine ki CKMT1A	16640.91	17471.53	22608.52	0	0	0
P07339	Cathepsin CTSD	43858.45	36603.43	47708.2	95830.89	96158.34	153021.5
P12931	Proto-onc SRC	26730.3	22842.86	27385.98	0	0	0
P07437	Tubulin be TUBB	1304867	1280879	1301473	2073206	605203.6	2824406
P12956	X-ray repa XRCC6	297949.1	296641.7	250138.4	0	0	0
P13010	X-ray repa XRCC5	233838.2	254406.8	220911.6	0	0	0
P07602	Prosaposir PSAP	56118.32	56670.49	77669.52	193225.8	300181.3	193927.3
P07686	Beta-hexo HEXB	29787.19	27512.04	39767.49	92746.98	104162.2	0
P13667	Protein dis PDIA4	12349.78	10801.92	8341.333	0	0	0
P07738	Bisphosph BPGM	92172.95	87674.13	112110.2	294303.5	293818.1	104174.7

P07814	Bifunctional EPRS	60988.82	58134.92	43366.07	66408.54	0	19529.06
P07858	Cathepsin B	55050.96	54162.07	65586.14	141920.2	268427.5	225307
P07900	Heat shock HSP90AA1	1928059	1861888	1452187	815443.8	680620.6	839277.8
P13674	Prolyl 4-hydroxylase	20042.46	22945.21	22113.2	0	0	0
P13693	Translation TPT1	58998.06	36754.55	101039.5	0	0	0
P13716	Delta-aminolevulinic acid dehydratase	4666.419	7703.957	12275.13	0	0	0
P13807	Glycogen phosphorylase	7351.718	8074.924	4950.488	0	0	0
P13861	cAMP-dependent protein kinase	27935.96	28442.06	33938.21	0	0	0
P13984	General transcription factor	15935.7	31961.78	14737.12	0	0	0
P14314	Glucosyltransferase	21339.18	21710.2	24609.13	0	0	0
P14324	Farnesyl pyrophosphatase	15144.14	9332.713	12694.47	0	0	0
P08133	Annexin A1	121468.2	123442.2	135587.5	329509.4	533282.4	456115.5
P14384	Carboxypeptidase	6025.773	3840.852	2075.499	0	0	0
P14550	Alcohol dehydrogenase	56387.24	50585.31	78445.86	0	0	0
P14678	Small nuclear ribonucleoprotein	31790.47	47351.36	27984.43	0	0	0
P14780	Matrix metalloproteinase	10628.71	13188.44	10096.4	0	0	0
P08238	Heat shock HSP90AB1	334909.5	344669.2	361799.9	167274.3	171790.8	138891.1
P14866	Heterogeneous nuclear ribonucleoprotein	13627.16	8838.115	7962.889	0	0	0
P14923	Junctional protein	37246.45	35297.31	47167.61	0	0	0
P15151	Poliovirus protein	43872.67	39793.6	113456.9	0	0	0
P15260	Interferon receptor	18606.91	13058.38	10886.19	0	0	0
P08567	Pleckstrin	89248.67	99393.5	84630.85	344736.1	182247.9	438759
P08572	Collagen alpha	114985.4	158425.3	100406.4	241830.9	229149.3	99816.63
P15374	Ubiquitin carboxyl-terminal hydrolase	19675.56	16189.67	24552.82	0	0	0
P15529	Membrane protein	44904.77	42337.14	32870.61	0	0	0
P08648	Integrin alpha	273242.5	301214.7	283916.4	66235.57	110083.9	231015.3
P08670	Vimentin	256760.6	255306.3	183404.1	357802.6	337939.6	340517.4
P08697	Alpha-2-macroglobulin	2437272	2250556	2900910	17089592	52681304	25172122
P08727	Keratin, type I	36822.04	58391.64	22831.16	38018.48	38059.3	158347.7
P08758	Annexin A1	944500.4	908257.1	1283685	1117415	1359860	1536302
P08779	Keratin, type I	14028.02	5877.961	0	53910.55	292206.1	43204.13
P08865	40S ribosomal protein	198294.8	203590.8	175546	396736.2	0	188253.2
P08962	CD63 antigen	1658945	869811.2	1327740	963948.6	449293.1	1065170
P15531	Nucleoside	88494.35	75304.55	153814.2	0	0	0
P15559	NAD(P)H dehydrogenase	49427.9	44952.7	48410.8	0	0	0
P09211	Glutathione	158315.5	142276.3	270304.4	314307.7	226907.3	135854.6
P15927	Replicator	12584.57	8522.134	6459.57	0	0	0
P16144	Integrin beta	9605.465	9644.426	13794.25	0	0	0
P09382	Galectin-1	414401.5	439649.1	613415.1	295349.5	571497.9	327089.2
P09429	High mobility group	305046.8	303180.1	115599.7	466443.9	427932	389514.8
P16278	Beta-galactosidase	13050.78	13046.36	12773.23	0	0	0
P09486	SPARC	67435.52	60164.76	137821.3	4275316	7280123	3400598
P09493	Tropomyosin	228460.1	106673.9	459597.8	58146.41	51667.28	56522.45
P16333	Cytoplasmic NCK1	10375.08	8129.122	19587.22	0	0	0
P16435	NADPH-dependent	4436.563	5719.792	8053.658	0	0	0
P16885	1-phosphatidylcholine	16438.52	14627.32	17757	0	0	0
P09619	Platelet-derived growth factor	9623.939	12211.33	15933.21	49292.74	95045.67	44908.23
P09651	Heterogeneous nuclear ribonucleoprotein	135511	137988.1	130886.8	279193.2	0	259750.4
P16949	Stathmin	50531.29	64060.07	82579.92	0	0	0
P16989	Y-box-binding protein	38745.35	35102.25	35574.76	0	0	0
P09972	Fructose-1,6-bisphosphate	91705.58	55548.84	100106.7	116641	0	107956.1
P17081	Rho-related	3164.247	1547.908	2731.854	0	0	0
P17096	High mobility group	694765.1	610616.2	675274.7	0	0	0
P17174	Aspartate aminotransferase	27377.22	23331.91	47311.23	0	0	0
P17252	Protein kinase	27123.24	22566.76	40730.75	0	0	0
P0DMV8	Heat shock HSPA1A	395081.9	393263.8	433320.8	568768.5	437351.5	768514.4
P17302	Gap junction	172181.4	164051.3	195959.2	0	0	0
P17480	Nucleolar protein	14864.66	16825.74	6869.563	0	0	0

P17516	Aldo-keto AKR1C4	31582.26	30912.36	17976.98	0	0	0
P17707	S-adenosy AMD1	11227.5	12270.33	19599.8	0	0	0
P10301	Ras-relate RRAS	132871.9	127812.5	160811.6	100126.1	245577.8	34837.4
P17812	CTP synth CTPS1	23241.02	23781.83	20131.16	0	0	0
P17980	26S protea PSMC3	96869.91	100093.2	108011.4	0	0	0
P18031	Tyrosine- γ PTPN1	6314.202	6191.712	5416.353	0	0	0
P10599	Thioredoxi TXN	42568.63	38197.79	70628.47	225647.6	0	174902.8
P18077	60S riboso RPL35A	73526.67	55964.53	72976.34	0	0	0
P18433	Receptor- β ITPRA	30137.42	29177.87	28883.37	0	0	0
P10646	Tissue fact TFPI	9930.383	10957.11	7963.848	26564.4	0	37333.99
P18669	Phosphogl PGAM1	92916.68	147603.2	138789.7	0	0	0
P18754	Regulator RCC1	18661.36	25640.63	12697.38	0	0	0
P10915	Hyaluronai HAPLN1	3101.464	4340.512	3168.849	0	269042.9	184374.5
P11021	78 kDa glu HSPA5	57530.84	60114.86	71469.1	71909.9	175954.1	114792.6
P18858	DNA ligase LIG1	2646.903	2724.193	6637.433	0	0	0
P18887	DNA repai XRCC1	9866.18	9894.3	1506.595	0	0	0
P19022	Cadherin- β CDH2	19120.52	16098.15	19171.93	0	0	0
P19367	Hexokinase HK1	5371.914	10711.53	3950.613	0	0	0
P11169	Solute carr SLC2A3	594337.3	560554.9	632729.1	355022.8	277595.3	663835.8
P19388	DNA-direc POLR2E	9955.114	15856.05	10433.08	0	0	0
P19438	Tumor nec TNFRSF1A	18606.84	11130.6	10773.21	0	0	0
P19525	Interferon- γ EIF2AK2	10716.45	10668.82	11576.07	0	0	0
P11216	Glycogen β PYGB	217079.7	219710.9	243820.2	613863.8	0	279215.6
P19623	Spermidine SRM	22164.73	21203.13	21654.78	0	0	0
P19634	Sodium/hy SLC9A1	7212.03	2902.614	4612.128	0	0	0
P19784	Casein kinase CSNK2A2	36802.74	36690.78	34147.75	0	0	0
P20338	Ras-relate RAB4A	9721.541	9459.133	10748.26	0	0	0
P20340	Ras-relate RAB6A	91599.44	74082.3	71865.57	0	0	0
P11413	Glucose-6 G6PD	147723.7	119507.9	175683.2	134576.4	1334118	120024.2
P20594	Atrial natri NPR2	7656.41	8551.671	11831.36	0	0	0
P11766	Alcohol de ADH5	99356.94	96002.73	101091.4	81656.02	0	106451.5
P20700	Lamin-B1 LMNB1	13003.01	11746.41	16914.62	0	0	0
P20809	Interleukin IL11	12296.69	11798.44	14022.56	0	0	0
P11940	Polyadeny PABPC1	80172.32	80975.27	84921.6	41435.05	0	25945.5
P20810	Calpastatin CAST	14568.1	7478.414	9979.36	0	0	0
P20839	Inosine-5- IMPDH1	9214.688	5939.464	49045.69	0	0	0
P20936	Ras GTPase RASA1	8365.184	7819.793	8638.061	0	0	0
P20962	Parathymic PTMS	18940.89	18500.38	22741.89	0	0	0
P21127	Cyclin-dep CDK11B	14305.44	15737.2	8083.735	0	0	0
P21266	Glutathion GSTM3	11409.74	9696.514	13221.66	0	0	0
P12259	Coagulatic F5	657252.1	650889.3	553385.6	1771764	1797123	1716002
P12268	Inosine-5- IMPDH2	35039.14	35754.82	42814.5	22792.53	0	47820.7
P21281	V-type prc ATP6V1B2	29456.55	28739.72	27595.12	0	0	0
P21283	V-type prc ATP6V1C1	9710.489	4237.625	8439.063	0	0	0
P12429	Annexin A ANXA3	10606.87	11070.98	11445.51	109345.4	0	220679.7
P21291	Cysteine ar CSRP1	55603.13	51854.77	84341.54	0	0	0
P12814	Alpha-acti ACTN1	1262216	932734.7	3355319	420413	416863.5	151910.5
P21359	Neurofibric NF1	19626.04	17635.84	23578.28	0	0	0
P12955	Xaa-Pro di PEPD	20508.11	23859.02	36813	46923.04	77766.69	78194.5
P21695	Glycerol-3 GPD1	9101.411	14225.56	2049.263	0	0	0
P21964	Catechol C COMT	28735.75	28395.68	24925.72	0	0	0
P13473	Lysosome- LAMP2	426126.1	403791.1	358709.4	728902.3	929983.1	380651.4
P13489	Ribonuclea RNH1	23214.5	21838.33	27179.7	0	967384.4	25124.95
P13497	Bone morph BMP1	33042.95	30022.37	26789.96	103323.3	84347.03	164019.7
P22059	Oxysterol- OSBP	133427.1	27385.07	7358.323	0	0	0
P22087	rRNA 2-O- FBL	56628.84	63363.98	44509.8	0	0	0
P22102	Trifunction GART	93224.44	87180.94	114661.9	0	0	0
P13639	Elongation EEF2	486905.7	471906.5	626652.6	212138.2	145287	229210.4

P13645	Keratin, tyf KRT10	459066.4	722416.6	783018.3	6469691	15882172	7045640
P13647	Keratin, tyf KRT5	22177.18	29595.98	32355.87	166713	787060.1	319471.8
P22234	Multifuncti PAICS	97022.48	94979.05	121906.5	0	0	0
P22303	Acetylcholi ACHE	10570.71	8489.86	12988.13	0	0	0
P22413	Ectonuclec ENPP1	75215.02	67692.17	62413.17	0	0	0
P22681	E3 ubiquiti CBL	10152.89	10786.88	13242.69	0	0	0
P13796	Plastin-2 LCP1	34204.31	28443.73	48453.86	0	472448.1	298711
P13797	Plastin-3 PLS3	124580.6	118160.2	264599.6	165890.6	321151.1	164319.5
P22694	cAMP-dep PRKACB	34493.41	48845.73	39013	0	0	0
P23193	Transcripti TCEA1	6595.973	5000.095	4190.713	0	0	0
P23258	Tubulin ga TUBG1	23695.66	23183	25094.64	0	0	0
P13929	Beta-enola ENO3	315127.2	283497.6	532506.8	656578.9	927322.9	666539
P23297	Protein S1(S100A1	49638.37	60429.15	58444.11	0	0	0
P14174	Macrophag MIF	415447.1	389589.5	591258	364194.1	633662.8	256857.4
P23458	Tyrosine-p JAK1	32680.9	38501.95	36735.11	0	0	0
P23468	Receptor-iPTPRD	35166.16	31802.07	37551.32	0	0	0
P23469	Receptor-iPTPRE	17785.95	18294.19	24781.56	0	0	0
P14543	Nidogen-1 NID1	55282.1	59710.83	49302.47	421199.3	854475.1	426171.2
P23470	Receptor-iPTPRG	16761.96	16370.04	21254.85	0	0	0
P14618	Pyruvate k PKM	3099436	3125329	3635976	1522820	1172836	1636030
P14625	Endoplasm HSP90B1	92566.41	99789.14	100680.5	142014.2	153715.8	134359.1
P23588	Eukaryotic EIF4B	2406.792	2732.45	2425.612	0	0	0
P23677	Inositol-tri ITPKA	1672.253	1279.521	2700.441	0	0	0
P23919	Thymidylat DTYMK	57173.35	58443.31	75065.16	0	0	0
P24394	Interleukin IL4R	9235.203	7549.024	6571.08	0	0	0
P15121	Aldose red AKR1B1	109384.4	93177	148539.3	52623.18	0	40846.57
P15144	Aminopep ANPEP	196011	200049	247070.8	465741.3	521707.7	541507.1
P24534	Elongation EEF1B2	99687.82	116466.8	123797.4	0	0	0
P15169	Carboxype CPN1	26797.76	17493.04	27419.57	94620.27	80507.63	69497.42
P24666	Low molec ACP1	101211.4	94549.2	123357	0	0	0
P24928	DNA-direc POLR2A	8111.508	8836.933	2961.663	0	0	0
P24941	Cyclin-dep CDK2	116269.2	102008.5	107546	0	0	0
P25098	Beta-adrer ADRBK1	9530.075	15276.77	17431.15	0	0	0
P25116	Proteinase F2R	30561	31050.75	22490.27	0	0	0
P15880	40S riboso RPS2	193312.9	204388.4	107476.7	167419.5	0	138721.3
P25205	DNA replic MCM3	28227.07	28192.68	21344.93	0	0	0
P25325	3-mercapt MPST	33582.11	25845.43	23469.88	0	0	0
P16070	CD44 antiç CD44	736996.2	679014.9	691377.8	706553.1	1354348	984418.4
P25440	Bromodon BRD2	9446.306	10944.19	3093.128	0	0	0
P25685	DnaJ homc DNAJB1	16856.81	17207.24	15507.54	0	0	0
P25705	ATP synthc ATP5A1	42491.3	39517.13	28356.44	0	0	0
P26358	DNA (cyto) DNMT1	6195.049	7732.633	6172.214	0	0	0
P16401	Histone H1 HIST1H1B	1593504	1525119	952136.8	219667.9	484803.9	705374.2
P16402	Histone H1 HIST1H1D	1086562	994159.1	574944.5	217047.5	397714.7	475124.5
P16403	Histone H1 HIST1H1C	485607.8	419953.3	256089.1	175510.3	210927.8	203434.3
P26639	Threonine- TARS	55697.23	53795.52	62806.61	0	0	0
P26885	Peptidyl-p FKBP2	14743.77	13992.52	17489.52	0	0	0
P27361	Mitogen-a MAPK3	13789.18	10784.17	13668.69	0	0	0
P27448	MAP/micr MARK3	16765.87	15074.93	21181.33	0	0	0
P27694	Replicator RPA1	14970.99	14833.04	13709.24	0	0	0
P17066	Heat shock HSPA6	1556003	1277446	1462874	618722.8	544536.9	756627.7
P27695	DNA-(apu) APEX1	28696.77	27702.5	16580.17	0	0	0
P27816	Microtubu MAP4	17636.18	17102.9	7024.664	0	0	0
P27986	Phosphatic PIK3R1	8930.752	12648.53	13635.76	0	0	0
P28070	Proteasom PSMB4	77286.89	67371.33	34789.62	0	0	0
P28072	Proteasom PSMB6	82282.34	76746.45	74627.62	0	0	0
P28340	DNA polyr POLD1	183181	173371.3	110578.9	0	0	0
P28482	Mitogen-a MAPK1	7492.899	6657.74	8596.236	0	0	0

P28827	Receptor-1PTPRM	41198.73	20477.28	35799.1	0	0	0
P17655	Calpain-2 CAPN2	14517.59	17162.46	20845.02	10050.96	0	10921.24
P28838	Cytosol an LAP3	7987.523	7245.511	11198	0	0	0
P29218	Inositol mclMPA1	13834.76	14306.49	23228.87	0	0	0
P17844	Probable A DDX5	114237.4	117492.5	94579.6	68812.92	67227.61	67164.85
P17858	ATP-deperPFL	104981.5	92291.3	100704.1	99858.99	0	103868.5
P29323	Ephrin typeEPHB2	45012.48	29319.71	37010.28	0	0	0
P29350	Tyrosine- γ PTPN6	17980.91	7773.117	16827.63	0	0	0
P17987	T-complexTCP1	195204.9	205575.2	201871.5	130138.4	126603.8	117422.5
P29353	SHC-trans SHC1	6414.048	6003.935	6400.112	0	0	0
P18065	Insulin-likeIGFBP2	151380	142084.5	217400.5	1135821	1632740	798135
P29692	ElongationEEF1D	82269.87	81125.95	81622.02	0	0	0
P18085	ADP-ribosARF4	157544.4	155716.6	192821.9	62027.86	14358.39	78393.39
P18124	60S ribosoRPL7	184467.1	217539.5	72354.73	445772.2	0	41926.02
P18206	Vinculin VCL	118537.7	107852.8	174122.9	291263.1	587345.9	255023.1
P30039	Phenazine PBLD	23594.38	22098.85	25738.27	0	0	0
P18621	60S ribosoRPL17	97242.27	98449.33	62519.85	200641.6	20258.1	156001.8
P30046	D-dopachDDT	44246.42	42435.13	85219.42	0	0	0
P30260	Cell divisioCDC27	6891.573	8918.638	12827.61	0	0	0
P30419	GlycylpeptNMT1	16273.83	14926.55	14570.09	0	0	0
P30530	Tyrosine- γ AXL	55127	55695.98	66093.23	0	0	0
P30566	AdenylosuADSL	10156.51	11106.91	14195.79	0	0	0
P30613	Pyruvate k PKLR	24353.66	29210.43	29856.56	0	0	0
P30622	CAP-Gly d CLIP1	3167.257	4246.26	8003.413	0	0	0
P30825	High affiniSLC7A1	246973.3	240666.9	239251.3	0	0	0
P30876	DNA-directPOLR2B	5819.319	5881.792	5371.53	0	0	0
P31150	Rab GDP c GDI1	41581.97	44304.57	52227.71	0	0	0
P31323	cAMP-de γ PRKAR2B	19106.87	18451.5	19520.75	0	0	0
P31327	CarbamoylCPS1	17324.37	12972.05	6971.871	0	0	0
P31350	RibonuclecRRM2	13054.68	18760.88	21532.04	0	0	0
P31641	Sodium- a SLC6A6	216592.3	214590.8	195023.8	0	0	0
P31689	DnaJ homcDNAJA1	100706	90127.38	94920.65	0	0	0
P31749	RAC-alpha ϵ AKT1	7359.09	7020.173	9769.896	0	0	0
P31949	Protein S1(S100A11	99826.46	95983.29	150184.5	0	0	0
P20042	Eukaryotic EIF2S2	31896.56	30920.72	24210.65	75326.13	2296786	23276.21
P32121	Beta-arresARRB2	11189.97	8200.717	13454.53	0	0	0
P32856	Syntaxin-2STX2	19312.03	17139.54	21297	0	0	0
P32929	CystathionCTH	4921.546	2791.087	4221.825	0	0	0
P20618	ProteasomPSMB1	88496.27	76500.74	90753.15	158835	0	119417
P32969	60S ribosoRPL9	35485.27	46525.04	25244.35	0	0	0
P20742	PregnancyPZP	772607.7	650334.6	1199671	2856046	3205320	2454337
P20774	Mimecan OGN	41632.84	36182.14	42945.62	233844.1	343776.9	154995.6
P32970	CD70 anti γ CD70	17492.05	6921.311	5287.938	0	0	0
P33121	Long-chainACSL1	1977.265	2524.303	1778.806	0	0	0
P33151	Cadherin-1CDH5	21801.6	16816.25	22994.05	0	0	0
P33316	DeoxyuridiDUT	27107.27	25255.06	43638.39	0	0	0
P33527	Multidrug ABCC1	30484.73	29853.54	47311.4	0	0	0
P33764	Protein S1(S100A3	3938.167	3088.665	3595.72	0	0	0
P33908	Mannosyl- MAN1A1	13721.68	15073.85	6495.352	0	0	0
P33991	DNA replicMCM4	13053.68	11565.33	9251.054	0	0	0
P33993	DNA replicMCM7	12985.05	12757.79	11901.74	0	0	0
P34896	Serine hydSHMT1	10377.33	10697.94	10636.51	0	0	0
P34897	Serine hydSHMT2	19504.18	20609.59	21129.36	0	0	0
P34913	Bifunction ϵ EPHX2	47294.16	41341.43	42521.97	0	0	0
P21333	Filamin-A FLNA	437410.3	409915.4	654967.8	690854.6	670321.5	765811.9
P35080	Profilin-2 PFN2	80112.59	66979.52	103767.2	0	0	0
P21399	CytoplasmACO1	102683.3	105408.7	112605.2	73739.38	0	88251.52
P21589	5-nucleotiNT5E	783373.3	739843.4	1018308	223716.3	251527.7	285565.7

P35232	Prohibitin PHB	2886.695	5125.908	5821.724	0	0	0
P35237	Serpin B6 SERPINB6	8808.258	9515.639	9871.672	0	0	0
P21926	CD9 antigen CD9	718234.3	652926.2	456902.1	202728.4	161303.1	221922
P35240	Merlin NF2	26075.44	27144.38	40840.92	0	0	0
P21980	Protein-glucosyltransferase 2	16821.71	17980.83	19928.7	73070.27	0	106890.9
P35244	Replication factor A3	33729.11	15954.05	14144.2	0	0	0
P35249	Replication factor C4	11488.21	8619.161	6660.342	0	0	0
P35250	Replication factor C2	13065.78	11050.78	5016.322	0	0	0
P35268	60S ribosomal RPL22	236111.8	261111.6	148032.5	0	0	0
P35269	General transcription factor GTF2F1	7056.173	7640.515	1848.895	0	0	0
P35354	Prostaglandin synthase 2	6558.06	7693.055	8526.099	0	0	0
P22314	Ubiquitin-like UBA1	127806.8	108332.5	134989.2	58141.82	295258.8	75957.52
P22352	Glutathione peroxidase 3	131898.4	136731.9	163313.6	102954.1	321520.5	142458.1
P22392	Nucleoside diphosphate NME2	355494.3	338784.8	581146.1	0	99813.16	124463.2
P35367	Histamine receptor HRH1	12022.04	16919.21	13725.27	0	0	0
P35520	Cystathionine CBS	27564.65	26884.89	30941.89	0	0	0
P35609	Alpha-actinin ACTN2	22421.93	20471.07	44183.7	0	0	0
P22692	Insulin-like growth factor binding protein 4	29563.62	26317.71	44641.88	527457.6	935729.9	311529.9
P35611	Alpha-adducin ADD1	10741.25	9989.042	14698.54	0	0	0
P35637	RNA-binding protein FUS	19292	24988.25	19649.38	0	0	0
P35658	Nuclear pore complex NUP214	964.4434	1457.868	1353.282	0	0	0
P23229	Integrin alpha 1 ITGA6	167377.6	178332.2	175004.8	31793.19	50239.89	112400.1
P23246	Splicing factor SFPO	34932.01	40752.93	44826.71	80971.68	0	99451.78
P35659	Protein DEK	119075.1	134272.4	42952.19	0	0	0
P23284	Peptidyl-prolyl isomerase PPIB	89327.59	98706.02	48691.02	66169.91	125086.5	121793.8
P35813	Protein phosphatase PPM1A	8622.58	9606.839	20036.44	0	0	0
P23396	40S ribosomal RPS3	256059.1	299012.5	212715.7	285864.1	121836.6	192196.1
P36269	Gamma-glutamyl transferase 5	13013.02	24153.54	30110.04	0	0	0
P36383	Gap junction protein GJC1	128046.9	77833.18	107782.1	0	0	0
P36404	ADP-ribosylation ARL2	16199.74	14869.77	15361.65	0	0	0
P36507	Dual specific GTPase MAP2K2	14863.04	13571.1	15011.65	0	0	0
P23471	Receptor-interacting protein PRZ1	2822.011	0	2957.248	15068.59	22215.65	0
P23526	Adenosylhomocysteinase AHCY	745874.1	688900.1	705447.1	433160.9	399695.3	450404.5
P36543	V-type proton-ATPase ATP6V1E1	30882.48	10232.98	23468.35	0	0	0
P36551	Oxygen-dependent CPOX	6193.224	6815.133	5975.004	0	0	0
P36639	7,8-dihydroxy NUDT1	3179.866	2925.28	3457.738	0	0	0
P36894	Bone morphogenetic protein BMPR1A	12609.21	11757.71	12380.08	0	0	0
P23921	Ribonucleoprotein RRM1	42990.75	37418.51	34266.7	32617.52	0	40310.43
P24043	Laminin subunit LAMA2	8974.317	7443.303	5518.571	61991.2	66399.36	19241.04
P36896	Activin receptor ACVR1B	10133.77	11621.09	29951.14	0	0	0
P36897	TGF-beta type 1 TGFBR1	26381.23	26044.59	26015.45	0	0	0
P36915	Guanine nucleotide-binding protein GNL1	10292.88	11303.46	8574.918	0	0	0
P36941	Tumor necrosis factor receptor LTBR	20968.71	18677.68	10706.77	0	0	0
P36959	GMP reductase GMPR	9849.145	3252.265	4834.638	0	0	0
P36969	Phospholipase GPX4	11533.08	11498.85	15236.4	0	0	0
P37108	Signal receptor SRP14	86547.21	120143.7	33203.75	0	0	0
P37173	TGF-beta type 2 TGFBR2	33377.68	35200.91	33017.77	0	0	0
P37235	Hippocalcin HPCAL1	41750.04	40827.84	51818.88	0	0	0
P38117	Electron transfer ETFB	10405.04	13729.18	12310.86	0	0	0
P25391	Laminin subunit LAMA1	14186.43	12767.95	6352.202	72692.16	21761.62	15202.79
P25398	40S ribosomal RPS12	39422.31	38069.2	32940.75	26241.1	0	29554.4
P38159	RNA-binding protein RBMX	13235.5	6644.252	1865.198	0	0	0
P38571	Lysosomal lipase LIPA	6765.333	6789.467	6871.945	0	0	0
P38606	V-type proton-ATPase ATP6V1A	31615.94	27944.68	33922.17	0	0	0
P25786	Proteasome PSMA1	108202.3	91972.45	123313.1	155388.7	72433.41	176696.1
P25787	Proteasome PSMA2	21258.87	29191.49	38576.7	60645.3	0	71392.14
P25788	Proteasome PSMA3	40023.33	54196.21	46838.64	96510.58	48027.72	73604.73
P25789	Proteasome PSMA4	179328.4	159924.2	197636.3	183114.4	0	181164.6

P25940	Collagen a COL5A3	10596.12	11531.22	7936.853	129074.5	213267.6	96113.13
P38646	Stress-70 γ HSPA9	47222.86	48588.89	47108.47	0	0	0
P38919	Eukaryotic EIF4A3	49351.53	46574.24	38379.57	0	0	0
P26038	Moesin MSN	254326.1	256822.2	492531.3	175839.6	143079.8	142847.2
P39019	40S riboso RPS19	57228.01	89572.45	63246.11	0	0	0
P26368	Splicing fa U2AF2	43281.77	48151.11	38362.63	0	55446.54	27127.76
P26373	60S riboso RPL13	102692.4	117380.8	126005.3	109179.1	0	92670.12
P26583	High mobi HMGB2	90788.68	88021.07	33877.8	200395.9	0	265663.4
P39656	Dolichyl-d DDOST	16649.81	19255.85	17402.66	0	0	0
P26640	Valine--tR VARS	66822.09	70364.8	56925.75	34824.42	0	3077459
P26641	Elongation EEF1G	216517.9	179491.8	184130	143115.5	0	121053.2
P39748	Flap endor FEN1	27953.95	20555.34	17214.97	0	0	0
P40189	Interleukin IL6ST	18923.34	24006.84	19502.88	0	0	0
P27105	Erythrocyte STOM	269583.8	235786.3	164352.3	90858.41	377093.6	537546.1
P27348	14-3-3 protein YWHAQ	149061.7	86467.25	187980.8	0	81860.28	193102.2
P40616	ADP-ribos ARL1	18749.66	19743.87	18326.34	0	0	0
P40763	Signal tran STAT3	6916.801	7937.895	6843.205	0	0	0
P40818	Ubiquitin c USP8	22921.98	24483.25	23824.39	0	0	0
P40938	Replicator RFC3	6900.486	7617.923	4836.217	0	0	0
P41091	Eukaryotic EIF2S3	45393.48	48972.49	42229.56	0	0	0
P27701	CD82 antiç CD82	523348.5	467632.8	439667.3	336899.3	360719.3	285588.5
P27708	CAD prote CAD	107825.1	54682.5	91780.85	98922.84	36475.49	102711
P41227	N-alpha-a NAA10	7160.972	7909.905	7879.768	0	0	0
P41240	Tyrosine-p CSK	14600.11	10557.69	16529.11	0	0	0
P41440	Folate tran SLC19A1	102293.6	83642.31	96832.57	0	0	0
P28066	Proteasom PSMA5	83833.33	70561.16	77377.77	59979.58	0	88638.95
P41743	Protein kin PRKCI	10517.8	10864.86	21007.95	0	0	0
P42025	Beta-centr ACTR1B	41447.53	40823.5	33350	0	0	0
P28074	Proteasom PSMB5	68379.91	62504.56	78576.91	88018.07	0	80479.29
P42166	Lamina-as TMPO	8602.988	12327.75	10012.87	0	0	0
P42229	Signal tran STAT5A	7465.691	7070.489	3894.25	0	0	0
P42285	Superkiller SKIV2L2	5301.561	5376.515	811.5549	0	0	0
P42336	Phosphatic PIK3CA	2813.146	2726.57	3716.157	0	0	0
P42338	Phosphatic PIK3CB	680.3585	823.9152	985.1498	0	0	0
P42345	Serine/thre MTOR	14292.03	14909.59	13045.13	0	0	0
P29279	Connective CTGF	140418.4	150863.3	91465.05	653843.9	183631.5	555122.1
P29317	Ephrin type EPHA2	176886	157751.8	181480.1	220922.2	122074	0
P42356	Phosphatic PI4KA	18931.88	15933.14	21479.38	0	0	0
P42357	Histidine a HAL	6218.617	5680.365	6121.737	0	0	0
P42704	Leucine-ric LRPPRC	11604.98	10998.19	6799.508	0	0	0
P29401	Transketol. TKT	59903.84	48137.9	90812.98	41212.16	105995.6	0
P29597	Non-receç TYK2	13974.01	13162.69	13776.13	624058.2	420228.9	221371.3
P42858	Huntingtin HTT	5134.502	6516.057	2517.558	0	0	0
P29966	Myristoylat MARCKS	421927.3	392549.7	558231.1	145674.5	218640.9	173402
P42892	Endothelin ECE1	18905.95	18232.92	16469.19	0	0	0
P30041	Peroxiredc PRDX6	228949.5	248215.7	336565.1	259275.2	386791.8	203849.8
P30044	Peroxiredc PRDX5	39048.96	30359.79	42550.73	18218.36	0	28496.21
P43121	Cell surfac MCAM	15694.35	17218.85	20017.13	0	0	0
P30050	60S riboso RPL12	95969.59	119888.6	97896.27	65994.09	38388.59	59679.95
P30085	UMP-CMP CMPK1	26652.87	26300.17	45513.7	0	66511.83	18704.8
P43243	Matrin-3 MATR3	10502.43	11256.45	9218.329	0	0	0
P30101	Protein dis PDIA3	42477.07	41376.61	52616.04	117309.3	106873.5	101523
P43246	DNA mism MSH2	7591.462	8849.781	7102.081	0	0	0
P43250	G protein- GRK6	17685.54	17827.36	18468.77	0	0	0
P43487	Ran-specif RANBP1	23691.81	36058.16	42680.43	0	0	0
P43490	Nicotinami NAMPT	37000.21	36515.98	47472.59	0	0	0
P45880	Voltage-d VDAC2	5874.949	7306.691	8196.414	0	0	0
P45984	Mitogen-a MAPK9	14038.59	16767.15	19992.09	0	0	0

P30626	Sorcin	SRI	44208.93	46071.52	53334.46	53859.1	0	121597.1
P46013	Antigen KI	MKI67	3072.207	2964.772	939.5162	0	0	0
P46019	Phosphoryl	PHKA2	3349.768	2601.018	2776.464	0	0	0
P31146	Coronin-1	CORO1A	101136	98691.66	93705.97	46749.95	0	73769.52
P46060	Ran GTPas	RANGAP1	26626.15	29234.86	29163.38	0	0	0
P31151	Protein S1	S100A7	45079	45280.29	3761.288	69399.45	0	377961.9
P46063	ATP-depei	RECQL	31585.74	33800.11	21341.4	0	0	0
P46087	Probable 2	NOP2	34271.87	34868.05	20234.6	0	0	0
P46108	Adapter m	CRK	17214.71	15009.74	17620.34	0	0	0
P31431	Syndecan-	SDC4	753140.3	848567.4	738181.8	278091	341028.8	188536.7
P46109	Crk-like pr	CRKL	22936.29	22751.1	35028.62	0	0	0
P46379	Large proli	BAG6	22415.69	23032.68	22424.22	0	0	0
P46531	Neurogeni	NOTCH1	16955.89	27588.26	29731.89	0	0	0
P31939	Bifunction;	ATIC	98358.36	97387.98	117389	66230.28	0	78304.53
P31946	14-3-3 pr	YWHAB	917682.9	656130.5	1267186	457719.9	665098	334443.9
P31948	Stress-ind	STIP1	26841.81	26505.06	33504.53	0	53418.32	39852.93
P46734	Dual speci	MAP2K3	13293.03	12459.04	12602.88	0	0	0
P32119	Peroxired	PRDX2	123095.4	68571.63	106601.6	874579.1	2926373	696385.6
P46783	40S riboso	RPS10	30459.32	46334.92	32564.05	0	0	0
P32754	4-hydroxy	HPD	10089.49	11184.93	13777.71	82480.48	0	29991.63
P46821	Microtubu	MAP1B	25773.43	28673.76	19679.41	0	0	0
P46926	Glucosami	GNPDA1	3625.633	4449.779	29109.27	0	0	0
P46939	Utrophin	UTRN	14846.53	15819.15	27847.37	0	0	0
P46977	Dolichyl-d	STT3A	8517.228	11342.29	6643.588	0	0	0
P47895	Aldehyde	ALDH1A3	15607.66	7971.764	14094.99	0	0	0
P48029	Sodium- a	SLC6A8	17581.65	15994.75	17965.61	0	0	0
P33176	Kinesin-1	KIF5B	42729.84	44399.88	48807.75	20263.89	0	97795.73
P48060	Glioma pai	GLIPR1	9499.113	11133.89	9944.029	0	0	0
P48067	Sodium- a	SLC6A9	5652.875	5000.419	4348.914	0	0	0
P48147	Prolyl end	PREP	39244.99	32289.44	29923.54	0	0	0
P48163	NADP-de	ME1	19486.72	18322.06	24583.77	0	0	0
P48449	Lanosterol	LSS	13414.38	11354.46	5127.253	0	0	0
P48556	26S protea	PSMD8	21407.71	28886.92	31992.06	0	0	0
P34096	Ribonucle	RNASE4	82090.18	80774.61	38634.3	394484.2	899940.6	176979
P48729	Casein kin	CSNK1A1	17262.44	21352.84	19912.07	0	0	0
P48730	Casein kin	CSNK1D	8412.51	12133.42	8313.053	0	0	0
P48735	Isocitrate	IDH2	3390.727	3163.903	2704.303	0	0	0
P35052	Glypican-1	GPC1	191736.3	204671.3	178509.9	374183.1	449793.3	346271.7
P48736	Phosphatic	PIK3CG	20771.04	20528.28	14665.44	0	0	0
P35222	Catenin be	CTNNB1	61304.24	58968.08	80288.88	1837456	0	259060.6
P48739	Phosphatic	PITPNB	8348.716	13718.34	19977.95	0	0	0
P48960	CD97 anti	CD97	70076.71	67890.73	80080.42	0	0	0
P49023	Paxillin	PXN	7141.334	6524.711	10887.6	0	0	0
P49207	60S riboso	RPL34	57408.89	55380.42	34893.34	0	0	0
P49257	Protein ER	LMAN1	18685.56	18600.92	20399.24	0	0	0
P49411	Elongation	TUFM	30034.6	30828.87	17679.29	0	0	0
P49419	Alpha-ami	ALDH7A1	16270.5	15140.52	16282.7	0	0	0
P49447	Cytochrome	CYB561	13391.72	11659.58	13786.17	0	0	0
P49458	Signal recc	SRP9	32313.18	41136.12	28892.41	0	0	0
P49589	Cysteine--	CARS	9283.98	9920.099	9485.4	0	0	0
P49736	DNA replic	MCM2	12820.68	11070.1	8357.704	0	0	0
P49748	Very long-	ACADVL	7965.069	7861.862	9652.026	0	0	0
P49756	RNA-bindi	RBM25	14571.71	14909.19	10205.65	0	0	0
P49757	Protein nu	NUMB	47048.76	42811.87	51685.15	0	0	0
P49770	Translatio	EIF2B2	683.6071	5537.881	15359.81	0	0	0
P35555	Fibrillin-1	FBN1	47309.51	48076.39	30203.04	736185.1	819462.9	334094.3
P35573	Glycogen	AGL	12894.43	13441.87	15775.92	31137.61	0	22176.75
P35579	Myosin-9	MYH9	470436.1	480709.5	356054.5	1586663	1109664	2097555

P35580	Myosin-1C MYH10	64108.35	60821.52	75964.15	25781.76	0	41446.24
P35590	Tyrosine- α TIE1	13501.38	12630.42	20341.81	75566.35	151418.4	75198.24
P35606	Coatomer COPB2	42706.72	45844.41	42908.01	199634.6	0	51834.25
P49773	Histidine tr HINT1	35424.2	33424.39	47712.75	0	0	0
P49795	Regulator RGS19	10778.69	10389.43	14592.99	0	0	0
P49840	Glycogen α GSK3A	3375.468	4880	3985.006	0	0	0
P49888	Estrogen s SULT1E1	36887.92	31844.78	33328.92	0	0	0
P49902	Cytosolic α NT5C2	22306.34	22590.49	20825.07	0	0	0
P50148	Guanine n GNAQ	115727.9	116393.9	174143.6	0	0	0
P35754	Glutaredox GLRX	40127.46	37349.79	62349.31	27107.58	0	21645.74
P50151	Guanine n GNG10	31075.97	41220.29	43891.38	0	0	0
P35858	Insulin-like IGFALS	26564.95	23874.54	27456.04	157362.4	0	137216
P50443	Sulfate tra SLC26A2	31774.56	31746.82	44370.5	0	0	0
P35998	26S protea PSMC2	110993	110298.6	94850.27	130122.5	0	114981.1
P36222	Chitinase- β CHI3L1	6953.175	4252.586	0	754833.6	900587.9	347659.8
P50479	PDZ and L PDLIM4	32737.97	30298.92	60552.13	0	0	0
P50748	Kinetochor KNTC1	4561.056	7002.858	8866.626	0	0	0
P50750	Cyclin-dep CDK9	2671.155	2616.078	2946.918	0	0	0
P50851	Lipopolysa LRBA	4529.664	9498.809	10825.12	0	0	0
P50897	Palmitoyl- PPT1	13581.03	13567.53	19554.92	0	0	0
P51114	Fragile X n FXR1	15660.11	13629.69	10384.29	0	0	0
P36578	60S riboso RPL4	173308	194089.5	82523.64	439432.4	163174.8	164768.5
P51148	Ras-relate RAB5C	245891.1	240517.3	267695.4	0	0	0
P36871	Phosphogl PGM1	33408.46	34754.8	32376.15	70538.02	0	57453.18
P51151	Ras-relate RAB9A	12283.29	12621.09	12256.56	0	0	0
P51159	Ras-relate RAB27A	19043	19512.23	17761.73	0	0	0
P51178	1-phospho PLCD1	4651.876	5393.086	15950.16	0	0	0
P51452	Dual speci DUSP3	7369.307	7111.66	11674.4	0	0	0
P51532	Transcripti SMARCA4	19671.71	20832.22	10689.99	0	0	0
P51572	B-cell rece BCAP31	23044.18	13982.08	15999.28	0	0	0
P51580	Thiopurine TPMT	18756.72	17927.5	21068.73	0	0	0
P51610	Host cell fa HCFC1	4493.265	4562.6	5840.893	0	0	0
P51636	Caveolin-2 CAV2	21773.01	7245.498	7625.608	0	0	0
P51674	Neuronal r GPM6A	26911.71	22870.98	9710.324	0	0	0
P51797	Chloride tr CLCN6	6280.584	5596.687	4858.071	0	0	0
P37802	Transgelin TAGLN2	297932.1	282958.8	502218.7	535100.7	755208.1	510033.4
P37837	Transaldol TALDO1	17129.11	13593.3	16013.91	36514.13	0	19887
P51798	H(+)/Cl(-) CLCN7	7847.145	14022.89	8577.588	0	0	0
P51809	Vesicle-as VAMP7	17163.83	17346.61	15945.57	0	0	0
P51812	Ribosomal RPS6KA3	18354.11	17270.47	16947.38	0	0	0
P51858	Hepatoma HDGF	22027.56	33783.16	28695.33	0	0	0
P52272	Heterogen HNRNPM	19726.71	22244.19	17278.25	0	0	0
P52292	Importin si KPNA2	48157.3	54451.33	65319.85	0	0	0
P52294	Importin si KPNA1	12558.93	12848.06	8546.392	0	0	0
P39023	60S riboso RPL3	60258.24	66561.45	30646.7	301901	0	143680.8
P52306	Rap1 GTP α RAP1GDS1	5450.765	5789.446	7231.336	0	0	0
P52569	Cationic ar SLC7A2	66198.71	57589.34	46533.64	0	0	0
P52594	Arf-GAP d AGFG1	17092.98	18277.44	20602.17	0	0	0
P52597	Heterogen HNRNPF	19165.09	17018.85	10522.13	0	0	0
P52655	Transcripti GTF2A1	46526.58	45682.93	47335.24	0	0	0
P40227	T-complex CCT6A	121364.6	106855.4	125607.9	36129.03	0	26595.21
P40261	Nicotinami NNMT	239112	112835.8	0	128469.6	0	19585.66
P40429	60S riboso RPL13A	130316.6	144134.3	116604.5	374509.3	125134.8	187870.9
P52701	DNA mism MSH6	6107.78	10023.59	5293.487	0	0	0
P52789	Hexokinasi HK2	3337.502	4373.523	3242.911	0	0	0
P52799	Ephrin-B2 EFNB2	9368.004	6559.927	11905.27	0	0	0
P40925	Malate deH MDH1	29442.4	26367.95	47837.05	83937.3	76213.53	46654.41
P52888	Thimet oli THOP1	8539.733	7777.709	12008.03	0	0	0

P52926	High mobi HMGA2	8470.669	7802.011	6799.641	0	0	0
P41221	Protein Wr WNT5A	37783.46	39966.83	45992.85	200939.4	197744.2	462463.6
P53004	Biliverdin r BLVRA	40365.8	37372.24	51905.5	0	0	0
P53041	Serine/thr PPP5C	9006.059	14940.55	17720.09	0	0	0
P41250	Glycine--t GARS	34161.42	35595.27	43946.58	86277.4	0	78438.21
P41252	Isoleucine- IARS	54017.95	58589.42	42497.66	73344.55	0	47734.98
P53384	Cytosolic FNUBP1	10895.41	9317.939	13874.51	0	0	0
P53582	Methionin METAP1	7058.33	10268.23	9315.187	0	0	0
P53675	Clathrin he CLTCL1	15170.03	16530.57	24744.83	0	0	0
P53794	Sodium/m SLC5A3	304536.5	285821.5	301101.5	0	0	0
P53801	Pituitary tu PTTG1P	1658634	1618432	1287901	0	0	0
P54105	Methyloso CLNS1A	8416.308	10898.18	13300.11	0	0	0
P54136	Arginine-- RARS	43521.72	40144.11	44543.83	0	0	0
P54252	Ataxin-3 ATXN3	15709.49	6836.897	9324.684	0	0	0
P54578	Ubiquitin c USP14	33515.46	34659.92	47323.62	0	0	0
P54619	5-AMP-ac PRKAG1	4726.517	5202.966	7183.008	0	0	0
P54687	Branched- BCAT1	37938.09	34240.41	51882.81	0	0	0
P54727	UV excision RAD23B	15104.53	15367.77	40633.24	0	0	0
P42766	60S riboso RPL35	40375.41	52069.66	29400.79	83681.4	0	68882.77
P54760	Ephrin typ EPHB4	189883.1	189097.9	198305.6	0	0	0
P54764	Ephrin typ EPHA4	3643.74	2161.399	6369.492	0	0	0
P43007	Neutral an SLC1A4	236452.7	256757.2	255742.5	84354.33	69500.54	160293.5
P43034	Platelet-ac PAFAH1B1	50150.27	33425.61	37588.9	0	106988.5	140059.1
P54852	Epithelial r EMP3	105105.3	85815.63	94096.59	0	0	0
P55011	Solute carr SLC12A2	51709.36	49378.19	61839.07	0	0	0
P55036	26S protea PSMD4	23642.43	20429.15	21815.84	0	0	0
P55039	Developm DRG2	13765.56	14133.03	15453	0	0	0
P55082	Microfibril MFAP3	17470.15	14934.8	20837.91	0	0	0
P55085	Proteinase F2RL1	73427.7	120679.9	112771.4	0	0	0
P43652	Afamin AFM	551426.5	477733.4	965276.7	5852610	8279819	3657650
P45877	Peptidyl-p PPIC	5812.783	6029.38	7495.885	22691.54	0	14425.15
P55196	Afadin MLLT4	119688.1	114578.7	189049.2	0	0	0
P55212	Caspase-6 CASP6	8684.266	10430.12	10422.64	0	0	0
P55769	NHP2-like SNU13	14381.5	10904.92	14757.38	0	0	0
P55795	Heterogen HNRNPH2	7475.54	8267.629	6717.408	0	0	0
P56182	Ribosomal RRP1	14645.79	14936.76	3771.328	0	0	0
P56192	Methionin MARS	99965.66	103355.8	88071.84	0	0	0
P56537	Eukaryotic EIF6	45075.93	43457.3	40871.87	0	0	0
P56545	C-terminal CTBP2	13677.41	15006.65	8985.994	0	0	0
P56557	Transmem TMEM50B	11549.29	11682.12	10890.54	0	0	0
P56937	3-keto-ste HSD17B7	1256.486	1499.652	2645.867	0	0	0
P56945	Breast can BCAR1	7359.77	6212.994	10226.47	0	0	0
P57075	Ubiquitin-. UBASH3A	43901.38	41053.14	53359.55	0	0	0
P46776	60S riboso RPL27A	205687.1	223068.4	105892.8	363245.3	0	244713.4
P46778	60S riboso RPL21	23628	18268	34718.98	44947.46	0	25222.69
P46781	40S riboso RPS9	371010.7	385607	268532.7	286528.7	0	212652.6
P57087	Junctional JAM2	11042.74	16100.74	15944.3	0	0	0
P57088	Transmem TMEM33	8883.316	8810.409	13973.12	0	0	0
P57737	Coronin-7 CORO7	2259.995	2835.891	6766.76	0	0	0
P57764	Gasdermin GSDMD	6468.649	13605.81	30500.58	0	0	0
P46940	Ras GTPas IQGAP1	206817.8	191442.2	343876.6	946158.3	3378706	751005.9
P46952	3-hydroxy HAAO	16414.87	18426.04	6201.363	154607	233416.2	0
P58546	Myotroph MTPN	30099.94	27258.39	35445.8	0	0	0
P47755	F-actin-ca CAPZA2	150258.7	148949.1	229287.4	257106.1	340079.7	255140.5
P59768	Guanine n GNG2	339911.8	313211	566716.3	0	0	0
P47914	60S riboso RPL29	146736.9	152126.2	60263.1	226760.7	0	122028.7
P47929	Galectin-7 LGALS7	4985.737	0	5102.817	82412.69	0	124450
P60468	Protein tra SEC61B	9423.656	11179.21	3903.255	0	0	0

P48059	LIM and se LIMS1	164800.2	154452.4	201332.8	267761.3	131554.8	389170.4
P60510	Serine/thr PPP4C	9426.898	4120.085	4344.487	0	0	0
P60520	Gamma-a GABARAPI	14195.19	13962.18	14164.89	0	0	0
P60604	Ubiquitin-i UBE2G2	8614.627	7617.266	12310.54	0	0	0
P60903	Protein S1(S100A10	782025	755549.8	1195689	0	0	0
P60983	Glia matur. GMFB	29419.54	26630.63	39309.7	0	0	0
P48506	Glutamate GCLC	12460.11	13546.16	19879.5	0	54635.28	29257.06
P48507	Glutamate GCLM	35689.2	32286.39	39522.09	93683.2	25525.57	118412.3
P48509	CD151 ant CD151	384212	424301.2	328369.4	86873.29	0	162621.3
P61020	Ras-relate RAB5B	17672.65	18105.4	21135.43	0	0	0
P48643	T-complex CCT5	97919.22	65380.64	101349.8	68410.31	0	74324.78
P48723	Heat shock HSPA13	35562.96	36097.67	53989.14	112141.1	196403.3	101769.1
P61077	Ubiquitin-i UBE2D3	32069.92	72961.16	48171.49	0	0	0
P61081	NEDD8-cc UBE2M	77411.71	72389.8	100483.5	0	0	0
P61086	Ubiquitin-i UBE2K	26469.47	22986.27	55630.14	0	0	0
P61088	Ubiquitin-i UBE2N	46687.12	52892.16	77636.83	0	0	0
P61106	Ras-relate RAB14	37781.15	36871.46	48741.04	0	0	0
P61163	Alpha-cen ACTR1A	50357.7	51844.55	50325.66	0	0	0
P61221	ATP-bindin ABCE1	29727.36	28764.5	25065.03	0	0	0
P61289	Proteasom PSME3	18631.65	21467.79	13977.15	0	0	0
P49189	4-trimethy ALDH9A1	81253.1	82450.52	92533.8	52866.31	0	39805
P61421	V-type prc ATP6V0D1	18778.42	18016.28	17889.11	0	0	0
P61586	Transformi RHOA	93241.48	73980.32	116610	0	0	0
P49327	Fatty acid : FASN	217309.7	232029.5	229623.2	341196.7	296635.1	22849.91
P49368	T-complex CCT3	308107.6	306094	341551.4	251895.5	307944.7	226285.9
P61587	Rho-relate RND3	6497.795	5466.614	5207.243	0	0	0
P61604	10 kDa he: HSPE1	32018	34054.38	42578.58	0	0	0
P61619	Protein tra SEC61A1	6663.01	7837.294	6776.063	0	0	0
P61758	Prefoldin s VBP1	31541.43	27317.17	42313.09	0	0	0
P61764	Syntaxin-k STXBP1	20198.56	19960.84	21370.84	0	0	0
P49591	Serine--tR SARS	93888.92	91465.41	98191.13	165330.3	0	69157.27
P49721	Proteasom PSMB2	71701.84	61875.44	72971.74	107652.7	153592.3	124003.8
P61916	Epididyma NPC2	16345.09	13338.96	23471.23	0	0	0
P49746	Thrombosj THBS3	283854.8	220796.7	408942.7	3353682	1933116	1242553
P49747	Cartilage c COMP	69784.41	69747.28	349692.9	474714.5	842766	542616.3
P61923	Coatomer COPZ1	5580.958	6086.813	8075.971	0	0	0
P61960	Ubiquitin- UFM1	10821.85	14487.15	28855.33	0	0	0
P61962	DDB1- anc DCAF7	11960.69	10709.65	11372.91	0	0	0
P61964	WD repeat WDR5	25261.8	18144.53	16351.94	0	0	0
P61966	AP-1 comj AP1S1	16982.58	17486.79	19916.15	0	0	0
P61970	Nuclear tra NUTF2	64126.98	63756.66	73643.37	0	0	0
P62070	Ras-relate RRAS2	17562.11	18562.51	23575.04	0	0	0
P62079	Tetraspani TSPAN5	56319.42	55485.53	86566.67	0	0	0
P62166	Neuronal c NCS1	20113.65	20547.51	22685.95	0	0	0
P49915	GMP synth GMPS	58365.38	57296.22	55565.98	55682.5	28037.98	64366.95
P62256	Ubiquitin-i UBE2H	4287.955	9812.297	2310.735	0	0	0
P62310	U6 snRNA- LSM3	20339.66	19963.06	29165.41	0	0	0
P50281	Matrix met MMP14	134830.9	131625.7	134057.6	14407011	17113416	6649655
P50395	Rab GDP c GDI2	231033.7	202362	321550.6	201159.8	289885.8	165554.2
P62314	Small nuck SNRPD1	31085.33	42300.02	7226.25	0	0	0
P50454	Serpin H1 SERPINH1	30753.14	35664.64	36074.35	92115.6	0	58914.52
P62633	Cellular nu CNBP	102435.1	55230.22	70264.36	0	0	0
P50502	Hsc70-inte ST13	264813.5	237619.4	194156.1	174720	113459.3	144820.3
P50570	Dynamin-i DNMT2	37010.73	38766.23	48542.33	42013.88	14185.54	80349.38
P50583	Bis(5-nuck NUDT2	9257.771	9418.944	9589.846	10972.29	0	12644.83
P62745	Rho-relate RHOB	54018.13	12010.79	33645.27	0	0	0
P62829	60S riboso RPL23	45953.24	48349.4	38978.86	0	0	0
P62841	40S riboso RPS15	11929.44	22812.79	16882.06	0	0	0

P62847	40S riboso RPS24	30956.59	40958.77	25587.2	0	0	0
P50914	60S riboso RPL14	252452.9	264865.3	186519	535075.2	0	202625.1
P50990	T-complex CCT8	229560.6	237334.2	230056.9	67177.52	69977.49	176332.5
P50991	T-complex CCT4	258301.8	283041.5	289086.8	129441.5	52399.73	139428.4
P50995	Annexin A: ANXA11	163057.7	145161.8	165783.3	111385.3	81562.49	167797.1
P62873	Guanine n: GNB1	284624.6	273680.9	386391	0	0	0
P62877	E3 ubiquitin RBX1	11183.37	10929.03	16532.46	0	0	0
P51149	Ras-related RAB7A	365097.2	338397.2	395138.5	167883.9	150092	231399.6
P62899	60S riboso RPL31	25302.77	47838.88	30493.73	0	0	0
P62993	Growth factor GRB2	27766.52	24206.17	34414.82	0	0	0
P63098	Calcineurin PPP3R1	17361.15	13813.44	20925.62	0	0	0
P63167	Dynein light DYNLL1	12718.85	11841.34	13776.6	0	0	0
P63173	60S riboso RPL38	20017.94	19311.39	14827.22	0	0	0
P51570	Galactokinase GALK1	169987	164680.3	175596.4	216940	0	310678.4
P63208	S-phase kinase SKP1	69414.9	66211.55	93469.97	0	0	0
P63218	Guanine n: GNG5	16986.04	16074.72	37694.84	0	0	0
P63279	SUMO-core UBE2I	21117.86	20619.77	31071.85	0	0	0
P67809	Nuclease-: YBX1	195770.4	194485.1	180076.5	0	0	0
P67812	Signal peptide SEC11A	6633.227	7820.768	5486.982	0	0	0
P68036	Ubiquitin-: UBE2L3	38776.43	23636.84	58451.66	0	0	0
P68402	Platelet-actin PAFAH1B2	13272.98	16997.81	25270.09	0	0	0
P68431	Histone H4: HIST1H3A	6374.089	5021.167	3338.413	0	0	0
P78310	Coxsackievirus CXADR	41898.45	34091.84	66307.45	0	0	0
P78344	Eukaryotic EIF4G2	11930.11	13465.5	14622.6	0	0	0
P51884	Lumican LUM	339998.2	344257.8	563295.1	5233277	7073753	2957281
P52209	6-phosphogluconate PGD	71013.89	69272.2	97301.21	0	60463.39	59889.23
P78347	General transcription factor GTF2I	5411.717	5227.475	4295.052	0	0	0
P78356	Phosphatidylinositol PIP4K2B	8641.333	7790.498	14203.75	0	0	0
P78536	Disintegrin ADAM17	24983.58	26988.07	21523.62	0	0	0
P78552	Interleukin IL13RA1	8257.205	8377.972	9350.97	0	0	0
P80748	Ig lambda chain V-III	9491.523	9978.835	2001.447	0	0	0
P83916	Chromobaculum CBX1	9477.684	9858.854	8512.734	0	0	0
P84022	Mother's against SMAD3	24582.65	13853.09	16466.05	0	0	0
P84085	ADP-ribosylated ARF5	85975.64	46499.98	57432.45	0	0	0
P84090	Enhancer core ERH	55949.42	54271.52	45938.7	0	0	0
P52758	Ribonuclease HRSP12	10223.92	8689.965	14667.98	62007.31	80021.64	37036.96
P98095	Fibulin-2 FBLN2	21180.06	24639.91	18258.77	0	0	0
P98155	Very low-density lipoprotein VLDLR	8927.825	8145.469	7273.809	0	0	0
P98172	Ephrin-B1 EFNB1	30992.56	20445.37	18888.58	0	0	0
P98194	Calcium-transporter ATP2C1	27045.52	23144.19	21392.2	0	0	0
P52907	F-actin-capping CAPZA1	117869.5	120490.6	161563.3	78834.39	117225.8	123305.7
P98198	Phospholipase ATP8B2	28447.51	28371.54	12262.9	0	0	0
Q00013	55 kDa erythropoietin MPP1	3977.201	7799.492	7374.944	0	0	0
Q00169	Phosphatidylinositol PITPNA	7673.637	6940.384	12870.58	0	0	0
Q00266	S-adenosylmethionine MAT1A	43106.35	34631.12	33588.27	0	0	0
P53396	ATP-citrate lyase ACLY	126373.7	115657.3	117692.7	127618.5	70695.2	122859
Q00341	Vigilin HDLBP	23349.25	22100.34	28369.11	0	0	0
P53621	Coatomer COPA	34805.76	36077.06	21965.48	51662.27	0	17481.03
P53634	Dipeptidyl aminopeptidase CTSC	33635.88	33650.98	43511.28	291105.8	605369.6	322451.3
Q00526	Cyclin-dependent kinase CDK3	4820.437	8636.947	9198.14	0	0	0
P53680	AP-2 complex component AP2S1	30577.08	41022.87	25567.02	12192.28	0	14399.82
Q00534	Cyclin-dependent kinase CDK6	6429.215	8147.403	8211.726	0	0	0
Q00535	Cyclin-dependent kinase CDK5	3578.271	3121.568	4474.208	0	0	0
P53999	Activated transcription factor SUB1	244295.2	260762.6	119705.3	345443.1	0	240084.3
Q00537	Cyclin-dependent kinase CDK17	1941.907	2738.908	3257.318	0	0	0
Q00577	Transcription factor PURA	27286.56	22113.76	21444.48	0	0	0
Q00688	Peptidyl-prolyl isomerase FKBP3	5833.529	4763.223	3894.688	0	0	0
P54289	Voltage-dependent calcium channel CACNA2D	30687.76	26941.38	40209.64	130190.4	168615.8	75846.95

P54577	Tyrosine--YARS	33345.53	2597259	32830.61	0	25972.88	2.32E+08
Q00796	Sorbitol deSORD	39712.84	41174.2	44800.88	0	0	0
Q01581	Hydroxym: HMGCS1	29839.33	33187.05	36807.48	0	0	0
P54652	Heat shock HSPA2	2799094	2624288	2855912	1022708	834494.4	1333530
Q01629	Interferon-IFITM2	49659.79	50208.68	78297.64	0	0	0
Q01650	Large neut SLC7A5	1544282	1548549	2022650	0	0	0
Q01658	Protein Dr: DR1	49356.98	52504.41	137379.8	0	0	0
Q01804	OTU dom: OTUD4	2479.686	1923.643	989.8536	0	0	0
Q01970	1-phosph: PLCB3	15470.7	13795.43	24127.11	0	0	0
P55001	Microfibrill MFAP2	22838.52	22230.18	23558.48	57025.92	132073.6	59632.9
Q01974	Tyrosine-p: ROR2	4255.131	6867.131	7471.636	0	0	0
Q02153	Guanylate GUCY1B3	14675.82	18462.65	19501.29	0	0	0
Q02241	Kinesin-lik KIF23	35640.09	34634.77	52395.99	0	0	0
P55072	Transition: VCP	208869.2	246085	226186.3	601210.6	702868.1	434573.7
Q02539	Histone H1: HIST1H1A	29230.06	23183.98	21965.39	0	0	0
Q02790	Peptidyl-p FKBP4	18838.3	18710.59	26329	0	0	0
Q02880	DNA topoi: TOP2B	9519.52	24103.52	13812.35	0	0	0
Q02952	A-kinase a: AKAP12	21661.3	17938.3	33195.74	0	0	0
P55263	Adenosine ADK	114325.5	112659.1	111706.3	81258.3	74845.74	107763.4
Q03113	Guanine ni: GNA12	12542.13	11630.2	13000.63	0	0	0
P55287	Cadherin-: CDH11	21221.06	20868.62	26778.57	51290.77	137032.8	63581.63
P55290	Cadherin-: CDH13	86514.29	89178.95	106688.3	313293	335220.8	271303.9
Q03135	Caveolin-1: CAV1	49801.3	38941.48	30954.54	0	0	0
Q03169	Tumor nec: TNFAIP2	9441.659	15747.92	13469.66	0	0	0
P55854	Small ubiq: SUMO3	72409.99	62518.33	83618.88	0	83022.21	36787.14
P55884	Eukaryotic EIF3B	100046.6	102631.6	85463.94	49992.45	0	58704.16
Q03405	Urokinase: PLAUR	37957.46	29353.16	19375.38	0	0	0
Q03426	Mevalonat: MVK	3060.028	4143.624	2559.769	0	0	0
Q04206	Transcripti: RELA	9677.088	43465.7	55967.3	0	0	0
Q04446	1,4-alpha-: GBE1	9296.224	8129.502	23696.59	0	0	0
Q04637	Eukaryotic EIF4G1	23497.92	24912.9	21964.65	0	0	0
Q04771	Activin rec: ACVR1	50576.96	20167.28	27060.86	0	0	0
Q04837	Single-str: SSBP1	11791.84	9495.281	6929.41	0	0	0
Q05193	Dynamin-: DNMT1	15916.64	18250.12	11605.54	0	0	0
Q05209	Tyrosine-p: PTPN12	26430.68	20493.28	18714.88	0	0	0
Q05397	Focal adhe: PTK2	34720.14	23841.25	25256.91	0	0	0
Q05639	Elongation: EEF1A2	32318.18	32447.59	38297.73	0	0	0
Q06124	Tyrosine-p: PTPN11	10643.82	8546.729	14464.34	0	0	0
Q06265	Exosome c: EXOSC9	5086.363	5558.501	4150.975	0	0	0
Q06481	Amyloid-li: APLP2	6410.346	5409.487	4345.679	0	0	0
P59998	Actin-relat: ARPC4	249874.6	237209.4	354580.4	0	83282.08	79696.24
P60033	CD81 antiç: CD81	2264153	2234010	2169285	1900062	1581627	3493846
P60174	Triosephos: TPI1	678878.6	626835.3	991046.4	612185.1	791724.8	478278.5
P60228	Eukaryotic EIF3E	55120.23	59291.51	45022.38	0	34705.58	46802.96
Q07021	Compleme: C1QBP	29585.56	28431.63	26344.92	0	0	0
Q07157	Tight junct: TJP1	26440.83	24159.29	38287.58	0	0	0
Q07617	Sperm-ass: SPAG1	3765.446	3983.072	5258.069	0	0	0
Q07666	KH domair: KHDRBS1	6043.299	6993.355	1747.872	0	0	0
P60660	Myosin ligi: MYL6	473478.3	421733.7	541712	710507.8	645990.9	834062.3
P60709	Actin, cyto: ACTB	8306266	7673752	12711323	6261976	7845540	5209281
P60763	Ras-relate: RAC3	1412418	1198774	1551266	487732.5	501458.9	874617.4
P60842	Eukaryotic EIF4A1	466063.7	472286.1	470121.8	274392.6	309223.2	259137.9
P60866	40S riboso: RPS20	77727.14	81608.74	61044.38	43334.54	0	43740.13
P60900	Proteasom: PSMA6	56304.93	52630.92	68522.83	89078.78	82337.61	75443.92
Q07812	Apoptosis: BAX	15684.89	10051.16	19003.87	0	0	0
P60953	Cell divisio: CDC42	367073	274962.9	346188.7	141234.6	55109.74	193880.1
P60981	Destrin: DSTN	204466.3	229561.6	348448.2	240116	0	247415.7
Q07889	Son of sev: SOS1	818.0301	6595.234	3505.18	0	0	0

P61011	Signal reccSRP54	16192.19	9884.493	5759.597	145157.8	0	217647.1
P61019	Ras-relateRAB2A	144540.7	136556.5	161998	87045.52	160335.3	91564.16
Q07955	Serine/arg SRSF1	921710.8	1043658	378045.3	0	0	0
P61026	Ras-relateRAB10	323828	135113	384223	103561.3	122831.8	244707.1
Q07960	Rho GTPas ARHGAP1	10814.76	13480.34	12032.03	0	0	0
Q08170	Serine/arg SRSF4	85782.57	76502.96	50862.01	0	0	0
Q08209	Serine/thre PPP3CA	103086.7	99674.59	149403.1	0	0	0
Q08257	Quinone o CRYZ	15213.94	6851.561	15632.59	0	0	0
Q08357	Sodium-d SLC20A2	6493.748	4923.041	7053.871	0	0	0
P61160	Actin-relat ACTR2	92364.25	80032.26	139454.6	62835.01	0	45822.85
Q08722	Leukocyte CD47	180651.2	165147.1	227806.1	0	0	0
P61204	ADP-ribos ARF3	686003.3	659186.8	802882.4	417896.3	304944.6	432398.3
Q08752	Peptidyl-p PPID	18114.7	19749.57	23401.04	0	0	0
P61224	Ras-relateRAB1B	853035.8	1228178	884614.1	951262.6	1428546	480165.9
P61247	40S riboso RPS3A	155590.8	173382.8	114953.1	145218.5	46896.07	115120.1
Q08AM6	Protein VA VAC14	3897.213	4536.425	2936.546	0	0	0
P61313	60S riboso RPL15	91136	116475.2	39098.43	206750.1	0	139648.8
P61353	60S riboso RPL27	72665.48	78650.88	45424.78	160842	0	185503.7
Q08J23	tRNA (cytc NSUN2	10190.02	9880.332	8480.155	0	0	0
Q09161	Nuclear ca NCBP1	6612.779	5319.141	3738.969	0	0	0
Q0VDD5	Putative ur MIR22HG	203542.5	240626.2	180242	0	0	0
Q0VGL1	Ragulator LAMTOR4	6287.393	4660.851	8647.431	0	0	0
Q10472	Polypeptid GALNT1	19768.61	18910.97	32561.94	0	0	0
Q10570	Cleavage e CPSF1	5666.282	6084.238	3198.475	0	0	0
Q11201	CMP-N-ac ST3GAL1	5867.836	6530.405	5163.793	0	0	0
P61769	Beta-2-mi B2M	104950	74140.42	1193.943	876844.1	1359867	630079.4
Q12765	Secernin-1SCRN1	7155.82	7393.664	16621.33	0	0	0
Q12768	WASH con KIAA0196	5915.526	8264.139	6312.391	0	0	0
Q12788	Transducir TBL3	4749.503	6414.063	10986.88	0	0	0
Q12791	Calcium-a KCNMA1	17795.77	23224.46	29799.59	0	0	0
Q12792	Twinfilin-1 TWF1	8906.845	12461.61	15326.67	0	0	0
Q12846	Syntaxin-4 STX4	25785.73	24730.61	31967.07	0	0	0
Q12874	Splicing fa SF3A3	7202.278	8268.058	3549.892	0	0	0
P61978	Heterogen HNRNPK	133521.7	134589.7	100552.3	0	95889.98	23617.05
P61981	14-3-3 prc YWHAG	165001.6	134472.2	219822	155837.7	175087.5	149514.7
Q12882	Dihydropy DPYD	15880.52	16302.93	17004.67	0	0	0
Q12888	Tumor sup TP53BP1	5427.911	5902.348	1150.987	0	0	0
P62140	Serine/thre PPP1CB	48339.89	44690.18	50031.48	40180.05	0	35705.42
P62158	Calmodulin CALM1	1110708	1105094	1828927	782175.1	927278.9	665159.1
Q12904	Aminoacyl AIMP1	22196.39	27367.34	23712.67	0	0	0
P62191	26S protea PSMC1	77827.06	71952.92	67634.19	45534.24	39560.24	69532.2
P62195	26S protea PSMC5	36273.57	38672.57	26407.71	42887.3	0	39157.28
P62241	40S riboso RPS8	319590.3	346412.7	159933.3	472493.3	241984.1	265366.6
P62249	40S riboso RPS16	230308.6	172288.6	193441.8	234529.9	0	221601.8
Q12905	Interleukin ILF2	29180.77	23694.54	11821.64	0	0	0
P62258	14-3-3 prc YWHAE	371341.7	339160.8	546925.9	211570.7	366755.4	138827.3
P62263	40S riboso RPS14	64726.42	64307.91	47048.61	105136.9	93636.84	129242.1
P62266	40S riboso RPS23	59321.99	62918.16	56709.07	45551.25	0	49588.64
P62269	40S riboso RPS18	182014.2	177608.3	191635.7	140462.4	90347.64	163563.9
P62277	40S riboso RPS13	127128.5	159899.8	100940.8	87283.6	61189.55	75518.88
P62280	40S riboso RPS11	126793.2	117254.8	105167.8	93967.92	0	81768.91
Q12906	Interleukin ILF3	25150.01	34278.34	7064.656	0	0	0
Q12913	Receptor-i PTPRJ	10773.2	9901.982	14581.26	0	0	0
P62318	Small nucl SNRPD3	46787.97	88635.14	42434.32	53257.95	0	39733.36
P62328	Thymosin l TMSB4X	82036.78	73117.81	116081.2	0	411711.1	180083
Q12923	Tyrosine-p PTPN13	7528.565	8747.129	9292.16	0	0	0
P62333	26S protea PSMC6	65621.28	82515.06	72809.11	172746	0	111203.6
P62424	60S riboso RPL7A	209469.4	255667.9	186044.7	193385.7	110345.1	151183.5

Q12929	Epidermal EPS8	100961.2	80993.3	114584.2	0	0	0
P62701	40S riboso RPS4X	138205.1	139312.4	109688.5	172884.6	0	134552.5
P62736	Actin, aorti ACTA2	548728.9	530288.8	1049626	546390	757150.4	623295.3
Q12933	TNF recept TRAF2	15973.71	13430.38	17251.39	0	0	0
P62750	60S riboso RPL23A	11953.64	15716.67	7375.229	10187.77	0	14947.42
P62753	40S riboso RPS6	104304.9	157759	84708.96	419110.5	0	225311.6
Q12959	Disks large DLG1	57845.76	52103.75	72697.6	0	0	0
P62820	Ras-relate RAB1A	761452.4	722068.8	803454.1	1081687	1032340	1383776
P62826	GTP-bindin RAN	548323.8	732248.3	517796.3	471053.1	268026.7	583597.5
Q12965	Unconvent MYO1E	15590.95	15985	23911.02	0	0	0
P62834	Ras-relate RAP1A	77803.75	76960.89	100064.6	73275.25	0	85352.38
Q12974	Protein tyr PTP4A2	19912.91	19621.44	25576.17	0	0	0
Q12979	Active bre ABR	12718.85	10801.68	19178.74	0	0	0
P62851	40S riboso RPS25	73965.57	92578.59	43569.58	84136.37	26728.56	52238.82
P62854	40S riboso RPS26	208360.3	248839.6	162813.4	192189.6	0	243160.2
P62857	40S riboso RPS28	232946.6	225485.5	181367.1	83164.5	116205.3	56583.36
Q13033	Striatin-3 STRN3	6306.36	5893.258	5518.831	0	0	0
Q13042	Cell divisio CDC16	8421.574	7687.512	6437.223	0	0	0
P62879	Guanine ni GNB2	984430.4	819323.8	717252.8	418117.8	285086.9	422605.3
Q13043	Serine/thre STK4	15820.18	8071.883	15525.77	0	0	0
P62906	60S riboso RPL10A	92718.16	96800.05	56416.5	167471.6	0	140242.3
P62917	60S riboso RPL8	123168.8	123725.4	39325.03	244910.3	147052.3	161696.1
P62937	Peptidyl-p PPIA	1087356	997014.1	1425700	679068.9	738548	484851.5
P62942	Peptidyl-p FKBP1A	169861.2	136780.7	213474	718601.1	951429	469706.2
P62979	Ubiquitin- RPS27A	5099582	5105820	4240466	5457158	5896259	4741509
Q13045	Protein flic FLII	15513.62	16346.26	16067.17	0	0	0
Q13085	Acetyl-CoA ACACA	7852.91	9199.259	11648.72	0	0	0
P63010	AP-2 com AP2B1	84410.16	95368.83	76487.34	145662	0	64156.13
Q13094	Lymphocy LCP2	22176.35	16172.72	19233.03	0	0	0
P63104	14-3-3 prc YWHAZ	352528.9	937419.9	349835.6	217797.2	353191.5	247508.4
Q13107	Ubiquitin c USP4	12359.24	14007.08	14208.46	0	0	0
Q13131	5-AMP-ac PRKAA1	6448.778	7426.789	9113.768	0	0	0
Q13136	Liprin-alph PPFIA1	14709.78	13728.03	21068.03	0	0	0
Q13144	Translatio EIF2B5	19884.04	20194.07	6446.848	0	0	0
P63244	Guanine ni GNB2L1	115148.2	110514.2	85009.52	67212.32	0	58400.58
P63261	Actin, cyto ACTG1	903698.5	491855.3	1446895	359404.6	364770.3	0
Q13148	TAR DNA- TARDBP	19499.89	6978.813	6905.722	0	0	0
P67775	Serine/thre PPP2CA	217209.2	210649.9	251401.9	162806.2	142829.9	141568.3
Q13151	Heterogen HNRNPA0	2055.61	3493.148	1596.132	0	0	0
Q13155	Aminoacyl AIMP2	30485.62	33597.08	20732.09	0	0	0
P67870	Casein kin CSNK2B	95598.55	95250.91	59535.55	134752.7	0	78242.53
P67936	Tropomyo TPM4	262844.4	256518.8	544563.2	664716.5	824317.3	424795.4
Q13162	Peroxiredc PRDX4	8650.604	8515.068	14754.13	0	0	0
P68104	Elongation EEF1A1	3942794	3736230	4361231	2665316	2023420	2707649
P68363	Tubulin al TUBA1B	3362645	3339254	3432030	14435993	5758159	17968256
P68366	Tubulin al TUBA4A	666493.9	1022577	645128.3	4405745	4899424	10116559
P68371	Tubulin be TUBB4B	1712206	1737906	1875408	3311132	1586903	4510178
P68400	Casein kin CSNK2A1	49039.04	59507.79	46704.65	55528.15	35800.42	76615.82
Q13177	Serine/thre PAK2	9385.888	9299.092	11992.25	0	0	0
Q13228	Selenium- SELENBP1	13106.55	12931.21	16694.16	0	0	0
P69891	Hemoglob HBG1	57698404	59194588	65844792	1.62E+08	1.78E+08	1.57E+08
P69905	Hemoglob HBA1	15120860	15161891	15981636	44398616	40482928	43246024
Q13243	Serine/arg SRSF5	24780.68	20258.02	857.2128	0	0	0
Q13247	Serine/arg SRSF6	60876.8	83825.65	29709.93	0	0	0
Q13253	Noggin NOG	6125.506	7023.557	5747.992	0	0	0
Q13257	Mitotic spi MAD2L1	14489.52	11811.25	17037.81	0	0	0
P78371	T-complex CCT2	199933.8	197306.7	292616.2	177742.1	0	187005.8
P78527	DNA-depe PRKDC	68223.75	71884.11	56132.75	1202790	2386365	812444.3

Q13263	Transcripti	TRIM28	22689.57	26243.76	22829.2	0	0	0
Q13275	Semaphori	SEMA3F	9449.039	10473.02	11080.53	0	0	0
Q13277	Syntaxin-3	STX3	28145.52	23487.63	30642.04	0	0	0
Q13283	Ras GTPas	G3BP1	6546.523	13067.23	13310.66	0	0	0
P80723	Brain acid	BASP1	386895.4	377844.3	473241.6	378723.9	700093.6	450837.5
Q13325	Interferon-	IFIT5	1376.459	1528.321	5081.794	0	0	0
P83731	60S riboso	RPL24	27128.7	31608.39	25025.12	51250.79	0	32660.62
Q13330	Metastasis	MTA1	4791	4352.086	3185.976	0	0	0
Q13336	Urea trans	SLC14A1	65588.03	62890.46	91716.67	0	0	0
Q13393	Phospholi	PLD1	4615.377	7637.301	8329.848	0	0	0
Q13409	Cytoplasm	DYNC1I2	21543.29	20528.88	9802.272	0	0	0
P84095	Rho-relate	RHOG	81384.47	71083.22	85271.27	14677.78	0	33250.8
P84098	60S riboso	RPL19	81134.97	55936.31	17506.41	613335.1	0	167605.1
P84103	Serine/arg	SRSF3	339983.8	371819.7	144856	280170.1	250698.9	235834.3
Q13427	Peptidyl-p	PPIG	8437.237	5547.305	2611.67	0	0	0
Q13428	Treacle pr	TCOF1	43256.65	46054.19	7993.466	0	0	0
Q13433	Zinc trans	SLC39A6	9566.092	19310.46	7106.128	0	0	0
Q13435	Splicing fa	SF3B2	27231.93	32228.3	14372.25	0	0	0
Q13442	28 kDa he	PDAP1	49257.66	50476.81	45964.31	0	0	0
P98196	Probable	ATP11A	144849	21498.12	90181.98	8535011	11612708	4439523
Q13443	Disintegrin	ADAM9	47770.24	46735.8	52688.35	0	0	0
Q13444	Disintegrin	ADAM15	3986.941	4284.9	5861.261	0	0	0
Q13459	Unconvent	MYO9B	4785.067	4668.145	5208.304	0	0	0
Q13464	Rho-assoc	ROCK1	11037.74	7972.538	7898.896	0	0	0
Q13488	V-type pr	TCIRG1	5958.338	3255.531	4299.775	0	0	0
Q13496	Myotubula	MTM1	1091.871	1900.819	2654.231	0	0	0
Q13501	Sequestos	SQSTM1	34764.61	29954.15	20323.43	0	0	0
Q13526	Peptidyl-p	PIN1	11696.75	6528.196	18236.41	0	0	0
Q13547	Histone de	HDAC1	317615.8	98075.88	206514	0	0	0
Q13557	Calcium/c	CAMK2D	7994.315	7274.088	7213.42	0	0	0
Q00610	Clathrin he	CLTC	459018.9	743264.8	464109	470776.2	624443.8	568830.6
Q13561	Dynactin s	DCTN2	19478.39	16298.95	24364.97	0	0	0
Q13571	Lysosomal	LAPTM5	71012.19	66172.79	48899.15	0	0	0
Q01082	Spectrin b	SPTBN1	18335.95	16940.55	21154.18	6173.706	0	32380.52
Q01105	Protein SE	SET	341997	312042.9	458960.2	133960	0	74832.05
Q01130	Serine/arg	SRSF2	266856.4	278609.9	109174.8	246599.6	0	162563
Q01433	AMP dearr	AMPD2	14964.91	15279.52	15407.08	47425.62	0	46546.25
Q01469	Fatty acid-	FABP5	171474.9	159167	262782.3	266190.1	151779.6	124789.8
Q01518	Adenylyl c	CAP1	268417.9	272568.7	441957	157799.9	137914.4	166223.9
Q13576	Ras GTPas	IQGAP2	27265.83	11846.9	11835.63	0	0	0
Q01628	Interferon-	IFITM3	79181.66	54240.28	42606.88	27576.04	0	46307.61
Q13595	Transform	TRA2A	82499.55	50670.96	18737.39	0	0	0
Q13596	Sorting ne	SNX1	2596.782	4764.724	6865.409	0	0	0
Q13614	Myotubula	MTMR2	2890.883	2342.466	6934.577	0	0	0
Q13616	Cullin-1	CUL1	17173.32	16882.03	17999.52	0	0	0
Q01813	ATP-depe	PFKP	97262.92	91299.45	105617.1	63212.09	0	74323.12
Q13617	Cullin-2	CUL2	5099.464	8108.946	8667.766	0	0	0
Q13618	Cullin-3	CUL3	23142.63	15015.48	18306.56	0	0	0
Q13620	Cullin-4B	CUL4B	14701.87	17578.73	13121.96	0	0	0
Q13625	Apoptosis-	TP53BP2	23190.28	22885.28	22694.89	0	0	0
Q02388	Collagen a	COL7A1	56072.99	56289.65	80009.25	0	154853.2	126489.6
Q13630	GDP-L-fuc	TSTA3	12924.02	15424.65	12641.72	0	0	0
Q13636	Ras-relate	RAB31	36362.21	34998.18	48319.7	0	0	0
Q13641	Trophobla	TPBG	213375.6	223098.3	246401.7	0	0	0
Q13671	Ras and R	RIN1	5460.17	6391.134	2323.35	0	0	0
Q02878	60S riboso	RPL6	91139.05	94211.09	50891.07	123840.5	24586.78	26101.67
Q13683	Integrin al	ITGA7	7649.879	9743.175	6333.205	0	0	0
Q13769	THO comp	THOC5	10714.14	9993.153	7075.831	0	0	0

Q13795	ADP-ribos ARFRP1	5159.46	6810.15	1554.772	0	0	0
Q13838	Spliceoson DDX39B	13641.22	14529.86	12745.37	0	0	0
Q13867	Bleomycin BLMH	12594.87	14489.61	37945.67	0	0	0
Q13868	Exosome c EXOSC2	14709.57	15188.72	9302.155	0	0	0
Q13873	Bone morç BMPR2	10467.11	8792.08	11046.12	0	0	0
Q13884	Beta-1-syr SNTB1	15769	36198.67	49350.43	0	0	0
Q13895	Bystin BYSL	6839.925	6204.212	3810.124	0	0	0
Q13907	Isopentenyl IDI1	16420.2	14386.74	3433.1	0	0	0
Q14008	Cytoskeleton CKAP5	6834.426	6575.007	5697.65	0	0	0
Q04756	Hepatocyte HGFAC	211044.9	204460.3	192643	572580.1	1077806	727438.1
Q14108	Lysosome SCARB2	51524.03	49736.98	42046.32	0	0	0
Q14117	Dihydrops DPYS	19849.94	13935.17	17180.38	0	0	0
Q04917	14-3-3 prc YWHAH	64248.84	57576.86	68259	41405.19	0	52227.13
Q14118	Dystroglyc DAG1	51265.57	46025.11	61486.84	0	0	0
Q14126	Desmoglei DSG2	76505.94	72828.38	102846.3	0	0	0
Q14137	Ribosome BOP1	6852.337	10731.47	33879.18	0	0	0
Q05519	Serine/arg SRSF11	50723.66	52638.27	18514.46	133929	128881.6	91454.57
Q14141	Septin-6 6-Sep	14100.21	14247.41	14824.75	0	0	0
Q05682	Caldesmor CALD1	8461.098	15113.6	35594	0	32964.65	26461.6
Q14151	Scaffold at SAFB2	11043.75	12959.95	16104.91	0	0	0
Q14155	Rho guanil ARHGEF7	7230.102	9582.597	10746.97	0	0	0
Q14157	Ubiquitin-UBAP2L	5352.042	8077.32	5201.564	0	0	0
Q06210	Glutamine GFPT1	25121.25	27214.49	27257.38	77428.16	286029.8	26590.38
Q14160	Protein scr SCRIB	123489.6	122193.7	195887.7	0	0	0
Q14166	Tubulin--t TTLL12	35160.82	34090.29	34774.5	0	0	0
Q14168	MAGUK p5 MPP2	3430.611	14101.21	22119.69	0	0	0
Q14185	Dedicator DOCK1	16422.34	14825.54	15821.67	0	0	0
Q06830	Peroxioredc PRDX1	369681.3	364806.7	449453.4	861762.8	1150091	615647
Q07020	60S riboso RPL18	235707.1	231169.6	105662.1	295541.5	0	165165.9
Q14192	Four and a FHL2	15598.64	13827.44	17524.43	0	0	0
Q14195	Dihydrops DPYSL3	35201.73	35841	49687.38	0	0	0
Q14203	Dynactin s DCTN1	6452.169	6383.625	5376.186	0	0	0
Q14232	Translator EIF2B1	9650.458	11583.24	11743.6	0	0	0
Q14240	Eukaryotic EIF4A2	18591.46	17667.19	17981.08	0	0	0
Q14247	Src substr CTTN	220649.5	214598	501613.9	0	0	0
Q14258	E3 ubiquiti TRIM25	25275.52	24340.35	26973.68	0	0	0
Q07954	Prolow-de LRP1	43090.22	64238.64	63097.29	206711	227710.2	205834.2
Q14315	Filamin-C FLNC	7977.33	7902.232	8743.206	0	0	0
Q14376	UDP-gluc GALE	9680.829	9975.189	11402.07	0	0	0
Q14393	Growth arr GAS6	22810.64	21439.09	14509.48	0	0	0
Q14439	Probable GPR176	8436.834	5234.296	3299.643	0	0	0
Q14444	Caprin-1 CAPRIN1	7966.06	8861.236	7547.573	0	0	0
Q14498	RNA-bind RBM39	46828.93	48470.13	25365.08	0	0	0
Q08380	Galectin-3 LGALS3BP	203123.4	185112.7	272642.6	902531.9	560760.2	1261738
Q08431	Lactadheri MFGE8	1000397	842718.5	911776.3	1901814	1495151	3789209
Q08629	Testican-1 SPOCK1	39974.76	44829.16	35437.27	370466.2	697844.5	330086.3
Q14517	Protocadh FAT1	12637.84	11719.73	20603.77	0	0	0
Q14566	DNA replic MCM6	10508.76	10455.18	8541.804	0	0	0
Q14642	Type I inos INPP5A	13925.96	13643.91	19551.93	0	0	0
Q14651	Plastin-1 PLS1	9975.862	9763.255	19201.56	0	0	0
Q14676	Mediator c MDC1	36873.62	39309.5	34100.64	0	0	0
Q09666	Neuroblas AHNAK	390440.3	392851.6	675920.4	0	165102.5	56424.61
Q14677	Clathrin ini CLINT1	10017.9	8567.649	13342.8	0	0	0
Q14683	Structural SMC1A	20203.96	22984.89	15515.45	0	0	0
Q10469	Alpha-1,6- MGAT2	25950.63	29375.61	19065.32	0	866996.6	322290.1
Q10471	Polypeptid GALNT2	14372.26	17920.44	14094.11	54223.19	0	57685.2
Q14690	Protein RR PDCD11	6615.506	6205.679	5117.433	0	0	0
Q10567	AP-1 comj AP1B1	27426.45	27953.01	29503.9	0	30350.18	56866.69

Q14699	Raftlin RFTN1	15802.12	16092.68	14883.74	0	0	0
Q10588	ADP-ribos BST1	19692.74	18369.91	20810.74	51451.12	0	41807.05
Q14703	Membrane MBTPS1	3891.881	5123.036	10448.01	0	0	0
Q14714	Sarcospan SSPN	2734.541	6724.199	13177.58	0	0	0
Q14739	Lamin-B re LBR	9494.121	11385.46	11439.53	0	0	0
Q14839	Chromodc CHD4	13219.42	12456.99	6655.924	0	0	0
Q14847	LIM and SLASP1	138604.8	132084.5	248924.5	0	0	0
Q14914	Prostaglan PTGR1	24029.77	43776.57	33483.94	0	0	0
Q12805	EGF-conta EFEMP1	36864.52	27698.49	56085.87	555236.3	873508.7	402843.4
Q12841	Follistatin- FSTL1	17141.81	15877.98	22746.36	864688.6	1442083	576107.3
Q14978	Nucleolar iNOLC1	28220.95	25939.52	19750.88	0	0	0
Q12860	Contactin- CNTN1	21278.18	19869.25	31399.99	289396.3	354674.5	136727.6
Q14993	Collagen a COL19A1	14480.7	17777.56	12982.17	0	0	0
Q14997	Proteasom PSME4	5895.626	6075.881	4714.917	0	0	0
Q14999	Cullin-7 CUL7	8386.02	8453.055	10937.12	0	0	0
Q14C86	GTPase-ac GAPVD1	16098.17	16078.3	14148.03	0	0	0
Q15003	Condensin NCAPH	13263.86	15088.57	9876.595	0	0	0
Q15004	PCNA-asss KIAA0101	3733.166	3657.378	4345.878	0	0	0
Q15007	Pre-mRNA WTAP	4913.632	4698.881	3487.959	0	0	0
Q12907	Vesicular ir LMAN2	51683.3	57538.39	52148.07	175740	104373	145558.8
Q15012	Lysosomal LAPTM4A	46368.78	42586.77	31130.47	0	0	0
Q15020	Squamous SART3	14189.64	16470.76	10436.09	0	0	0
Q15021	Condensin NCAPD2	5913.429	6881.395	4662.57	0	0	0
Q12931	Heat shock TRAP1	3055582	2845150	2386111	1655165	1377226	1700805
Q15029	116 kDa U- EFTUD2	52292.75	57434.89	45372.76	0	0	0
Q15036	Sorting ne: SNX17	20970.8	19468.96	23368.12	0	0	0
Q15050	Ribosome RRS1	965.6576	1106.348	696.4004	0	0	0
Q15052	Rho guanin ARHGEF6	10085.22	10143.82	9402.115	0	0	0
Q15056	Eukaryotic EIF4H	24094.83	24758.11	30491.76	0	0	0
Q15057	Arf-GAP w ACAP2	10854.28	13771.5	14897.36	0	0	0
Q15059	Bromodomain BRD3	13192.58	17455.71	8780.166	0	0	0
Q15061	WD repeat WDR43	6716.51	26168.81	9056.915	0	0	0
Q15084	Protein dis PDIA6	27962.42	36383.01	46223.87	0	0	0
Q15125	3-beta-hy EBP	16823.77	15928.22	15322.33	0	0	0
Q13093	Platelet-ac PLA2G7	6003.296	5081.754	6684.496	36724.54	58812.06	30298.66
Q15172	Serine/thre PPP2R5A	8071.211	9038.232	12887.63	0	0	0
Q13103	Secreted p SPP2	141027.7	127317.2	124840.9	384678.6	352302.3	443168.6
Q15181	Inorganic i PPA1	44188.05	44445.97	65135.79	0	0	0
Q15185	Prostaglan PTGES3	249297.8	248688.4	199271.4	0	0	0
Q15208	Serine/thre STK38	13013.6	12921.69	15701.88	0	0	0
Q15233	Non-POU NONO	31588.17	34981.61	26989.76	0	0	0
Q15257	Serine/thre PPP2R4	16841.16	17603.37	17321.91	0	0	0
Q15262	Receptor-i PTPRK	69120.03	74674.98	66674.93	0	0	0
Q15283	Ras GTPase RASA2	9508.781	4722.561	7105.528	0	0	0
Q15293	Reticulocal RCN1	4698.721	5803.677	6156.824	0	0	0
Q15334	Lethal(2) g LLGL1	65264.85	66020.46	106842.6	0	0	0
Q15349	Ribosomal RPS6KA2	11312.94	11836.1	17639.24	0	0	0
Q13200	26S protea PSMD2	85401.16	83002.69	84619.37	94136.73	49600.45	109541.2
Q13219	Pappalysin PAPPB	4972.723	0	1464.519	18977.96	0	45076.86
Q15369	Transcripti TCEB1	31011.35	15191	11507.4	0	0	0
Q15382	GTP-bindin RHEB	61003.13	53207.25	57081.76	0	0	0
Q15386	Ubiquitin-i UBE3C	7343.572	5142.666	5977.036	0	0	0
Q15393	Splicing fa SF3B3	64059.85	67212.89	47055.41	0	0	0
Q15417	Calponin-i CNN3	23135.63	25446.6	49861.25	0	0	0
Q15418	Ribosomal RPS6KA1	6352.942	6126.812	4041.037	0	0	0
Q15427	Splicing fa SF3B4	26233.12	24450.93	30257.31	0	0	0
Q15435	Protein ph PPP1R7	25532.56	24804.43	29882.62	0	0	0
Q15436	Protein tra SEC23A	8376.358	6619.107	8240.235	0	0	0

Q13308	Inactive tyrosine PTK7	123926.7	115996	120693.9	213580	294510.3	145318.2
Q15459	Splicing factor SF3A1	3653.578	8031.493	6553.081	0	0	0
Q15477	Helicase subunit SKIV2L	3011.925	4673.124	3897.174	0	0	0
Q15599	Sodium(+)/Hydrogen(+) SLC9A3R2	52665.44	48659.47	83561.6	0	0	0
Q13347	Eukaryotic translation initiation factor 3I	29885.41	36846.54	44015.07	33469.04	0	40554.53
Q15631	Translin TSN	20891.42	21317.42	31329.23	0	0	0
Q15642	Cdc42-interacting protein TRIP10	6061.376	6914.662	7188.185	0	0	0
Q13418	Integrin-linked ILK	233781.8	195149	243470	268917.5	116830.2	371684.4
Q15648	Mediator complex MED1	6038.228	11780.06	13213.11	0	0	0
Q15654	Thyroid receptor TRIP6	8522.094	8245.201	16327.58	0	0	0
Q15691	Microtubule-associated MAPRE1	37297.3	38919.23	44222.97	0	0	0
Q15717	ELAV-like protein ELAVL1	23174.34	22413.95	21099.25	0	0	0
Q15751	Probable EGF receptor HERC1	5717.45	4748.274	2796.853	0	0	0
Q15785	Mitochondrial TOMM34	55633.92	60167.26	70685.52	0	0	0
Q15797	Mother's against SMAD1	20125.79	27128.49	27204.39	0	0	0
Q15813	Tubulin-specific TBCE	4867.779	5402.365	7188.197	0	0	0
Q15819	Ubiquitin-conjugating UBE2V2	68494.98	73565.41	187043.7	0	0	0
Q15836	Vesicle-associated VAMP3	13226.08	11804.25	7851.62	0	0	0
Q15904	V-type proton-ATPase ATP6AP1	10776.83	7790.543	9102.737	0	0	0
Q15942	Zyxin ZYX	45495.3	57934.78	81822.59	0	0	0
Q13509	Tubulin-binding TUBB3	97626.84	81842.2	93033.99	719906	0	1048418
Q16186	Proteasome subunit ADRM1	4415.601	8653.398	17402.81	0	0	0
Q16204	Coiled-coil protein CDC6	16809.82	8757.823	12407.75	0	0	0
Q16222	UDP-N-acetyl UAP1	27514.11	19891.95	26681.69	0	0	0
Q16512	Serine/threonine PKN1	21860.33	22339.64	30500	0	0	0
Q16513	Serine/threonine PKN2	17737.93	16415.62	24066.13	0	0	0
Q16537	Serine/threonine PPP2R5E	9141.616	9076.03	10622.84	0	0	0
Q16539	Mitogen-activated MAPK14	18362.56	17895.94	20015.35	0	0	0
Q16543	Hsp90 co-chaperone CDC37	33546.54	31123.38	25823.23	0	0	0
Q16563	Synaptophysin SYPL1	88001.02	80759.55	85747.84	0	0	0
Q16576	Histone-binding RBBP7	17136.04	15355	16659.28	0	0	0
Q16625	Occludin OCLN	10094.18	10436.26	12611.31	0	0	0
Q16643	Drebrin DBN1	51819.81	71721.58	123847.7	0	0	0
Q16719	Kynureninase KYNU	9566.494	9611.841	10580.82	0	0	0
Q16739	Ceramide glucosyltransferase UGCG	7673.938	7354.747	3080.993	0	0	0
Q16769	Glutaminylation QPCT	22083.31	23228.07	25491.25	0	0	0
Q16774	Guanylate cyclase GUK1	7374.766	7422.213	6065.132	0	0	0
Q13637	Ras-related protein RAB32	43448.86	42389.47	45210.95	65917.03	0	64449.97
Q16832	Discoidin domain-containing DDR2	12222.59	12159.04	13273.49	0	0	0
Q13642	Four and a half LIM1	126865.4	114403.1	152389.6	545492.3	0	757147.1
Q16851	UTP-glucose-1-phosphate UGP2	12532.58	15523.57	22866.57	0	0	0
Q16878	Cysteine dioxygenase CDO1	225610.9	240676.5	294552.6	0	0	0
Q13740	CD166 antigen ALCAM	14448.88	14165.7	14962.63	0	149907.5	66167.41
Q13748	Tubulin-binding TUBA3C	620763.3	653958.3	671195.7	1258749	0	1384352
Q16881	Thioredoxin TXNRD1	24407.96	17884.15	31637.95	0	0	0
Q27J81	Inverted form of INF2	7557.149	923.6736	2030.312	0	0	0
Q29980	MHC class II MICB	20960.38	19077.13	22041.46	0	0	0
Q29983	MHC class II MICA	39612.16	41439.2	61975.28	0	0	0
Q29RF7	Sister chromatid PDS5A	10255.1	5375.631	8705.196	0	0	0
Q2M2I8	AP2-associated AAK1	18615.39	15990.42	17261.49	0	0	0
Q2M389	WASH co-factor KIAA1033	3058.755	3360.302	2212.3	0	0	0
Q2TAY7	WD40 repeat SMU1	6571.458	4340.929	5250.715	0	0	0
Q32P44	Echinoderm EML3	1844.468	13633.07	8695.381	0	0	0
Q3LXA3	Triokinase TKFC	10301.48	11915.09	10156.08	0	0	0
Q3MHD2	Protein LSI LSM12	15504.35	17657.36	10741.85	0	0	0
Q14019	Coactosin COTL1	100722.1	81799.01	188775.6	177453.7	0	203258.5
Q14103	Heterogeneous HNRNPD	60618.78	48594.37	43685.11	43171.5	0	32162.7
Q3SXY8	ADP-ribosylation ARL13B	20030.88	19849.47	39080.25	0	0	0

Q3ZCW2	Galectin-rcLGALSL	26645.23	24818.19	25916.68	0	0	0
Q460N5	Poly [ADP- PARP14	20869.17	19752.26	19218.99	0	0	0
Q4J6C6	Prolyl endcPREPL	3268.745	3366.94	3536.262	0	0	0
Q4KMP7	TBC1 dom TBC1D10B	19658.54	17370.51	23322.77	0	0	0
Q4KMQ1	Taperin TPRN	6291.441	4246.048	8983.271	0	0	0
Q4KMQ2	Anoctamin ANO6	35829.95	36361.25	50734.63	0	0	0
Q502W6	von Willeb VWA3B	24565.65	32861.23	45875.48	0	0	0
Q14152	Eukaryotic EIF3A	113940	128619.6	82929.8	3388728	0	1656833
Q52LJ0	Protein FA FAM98B	10077.9	10161.61	6048.731	0	0	0
Q53EZ4	Centrosom CEP55	28827.03	30292.12	31927.26	0	0	0
Q53GA4	Pleckstrin I PHLDA2	39577.85	38921.38	52656.02	0	0	0
Q53GL0	Pleckstrin I PLEKHO1	3677.602	3424.646	4676.094	0	0	0
Q53GS9	U4/U6.U5 USP39	10164.66	9475.546	4016.197	0	0	0
Q53H96	Pyrroline-5-PYCRL	7338.724	5632.588	5445.278	0	0	0
Q58FF6	Putative h HSP90AB4	118283.4	120671.1	72917.73	0	0	0
Q5BJH7	Protein YIF YIF1B	6009.244	6546.346	3676.095	0	0	0
Q5GLZ8	Probable E HERC4	7130.156	7938.428	8267.823	0	0	0
Q14204	Cytoplasm DYNC1H1	101711.7	105263.7	69637.78	141071.6	87666.41	197685.1
Q5H9R7	Serine/thr PPP6R3	70894.15	119783.4	90525.76	0	0	0
Q5HYA8	Meckelin TMEM67	4247.429	4150.209	6004.827	0	0	0
Q5HYW2	NHS-like r NHSL2	17700.8	15827.18	21739.93	0	0	0
Q14254	Flotillin-2 FLOT2	54538.17	52137.87	49025.42	35988.51	0	63282.87
Q5JSH3	WD repeat WDR44	10113.93	8081.917	11896.71	0	0	0
Q14289	Protein-tyl PTK2B	34229.44	32297.6	36673.69	61265.67	105555.6	0
Q5JTH9	RRP12-like RRP12	3141.191	4016.716	2870.685	0	0	0
Q14344	Guanine n GNA13	690708.7	660471.3	747481.8	2337526	0	389962.7
Q5JVF3	PCI domain PCID2	3998.144	4184.255	5556.536	0	0	0
Q5KU26	Collectin-1 COLEC12	46149.21	40634.93	32602.85	0	0	0
Q5M775	Cytospin-1 SPECC1	3214.488	2793.568	3535.006	0	0	0
Q5QJ74	Tubulin-sr TBCEL	17326.99	19821.63	19201.74	0	0	0
Q5SSJ5	Heterochr HP1BP3	10549.03	12442.57	3865.686	0	0	0
Q14515	SPARC-like SPARCL1	11211.58	37078.3	37302.19	0	102401	55028.52
Q5SYE7	NHS-like r NHSL1	6127.531	64227.97	6867.1	0	0	0
Q14520	Hyaluronai HABP2	55603.11	45712.02	44277.13	56901.07	56525.19	55130.77
Q5T0F9	Coiled-coi CC2D1B	3988.246	3635.974	4036.952	0	0	0
Q5T447	E3 ubiquiti HECTD3	10633.61	9892.487	9419.937	0	0	0
Q5T5C0	Syntaxin-1c STXBP5	8214.012	8319.558	8233.401	0	0	0
Q14644	Ras GTPas RASA3	28170.25	26175.04	39810.78	439620.3	0	44306.38
Q5T9L3	Protein wn WLS	64940.93	71269.27	63326.98	0	0	0
Q5TDH0	Protein DC DDI2	11415.64	11142.5	22619.88	0	0	0
Q5VT25	Serine/thr CDC42BPA	2625.417	4056.312	5612.059	0	0	0
Q5VUB5	Protein FA FAM171A1	5318.387	4051.038	2709.771	0	0	0
Q5VVQ6	Ubiquitin t YOD1	15898.31	12243.61	17270.29	0	0	0
Q14697	Neutral alr GANAB	52816.67	52090.02	56604.18	112382.4	128031.8	87484.97
Q5VW32	BRO1 dom BROX	60627.39	51412.38	55414.49	0	0	0
Q5VW38	Protein GP GPR107	20081.63	19027.77	14108.86	0	0	0
Q5VZE5	N-alpha-a NAA35	3364.009	5490.119	3201.396	0	0	0
Q5W0Z9	Probable r ZDHHC20	21077.79	23072.17	25331.82	0	0	0
Q5W111	SPRY dom SPRYD7	15096.27	15129.54	13990.31	0	0	0
Q14766	Latent-trar LTBP1	14850.12	13559.65	5923.006	380742.7	551262.3	152547.7
Q5XPI4	E3 ubiquiti RNF123	17191.52	17426.03	19316.61	0	0	0
Q5ZPR3	CD276 ant CD276	77015.65	54645.25	93246.5	0	0	0
Q63HN8	E3 ubiquiti RNF213	1247.162	1868.189	1692.073	0	0	0
Q14974	Importin sr KPNB1	132628.3	145004.2	175215.2	39158.12	57689.78	46835.98
Q63HR2	Tensin-2 TNS2	10053.47	7056.249	3232.733	0	0	0
Q63ZY3	KN motif a KANK2	6885.137	6592.286	9263.696	0	0	0
Q658P3	Metallorec STEAP3	95010.95	88576.06	68832.55	0	0	0
Q658Y4	Protein FA FAM91A1	14255.49	18571.59	13885.77	0	0	0

Q66K14	TBC1 dom	TBC1D9B	6714.057	14493.74	7881.688	0	0	0
Q66K74	Microtubu	MAP1S	7440.309	7944.176	3950.4	0	0	0
Q68CZ2	Tensin-3	TNS3	102540.2	97686.96	134435.5	0	0	0
Q68D91	Metallo-b	MBLAC2	14611.79	13665.82	18642.61	0	0	0
Q15008	26S protea	PSMD6	49545.91	50245.13	40096.43	61890.34	42058.74	51917.22
Q68EM7	Rho GTPas	ARHGAP1	18897.48	18854.17	26190.6	0	0	0
Q6B0K9	Hemoglob	HBM	20886.21	19514.47	21458.22	0	0	0
Q6EMK4	Vasorin	VASN	8385.917	3796.985	2985.923	0	0	0
Q6FI81	Anamorsin	CIAPIN1	1545.944	1712.322	3005.282	0	0	0
Q6GQQ9	OTU dom	OTUD7B	9546.088	10664.38	16438.39	0	0	0
Q6GTS8	Probable c	PM20D1	27863.14	26693.42	27542.05	0	0	0
Q6IAA8	Ragulator	LAMTOR1	20649.4	18171.95	18916.33	0	0	0
Q6IBS0	Twinfilin-2	TWF2	24108.86	23446.28	35509.88	0	0	0
Q6IQ22	Ras-relate	RAB12	29888.2	28959.29	36526.39	0	0	0
Q6KC79	Nipped-B-	NIPBL	5363.561	6852.577	3930.799	0	0	0
Q6NYC1	Bifunction	JMJD6	6295.228	6639.286	2982.786	0	0	0
Q6NYC8	Phostensin	PPP1R18	29871.64	27042.6	50825.45	0	0	0
Q6NZI2	Polymeras	PTRF	8699.894	9158.295	9448.443	0	0	0
Q6P1N0	Coiled-coi	CC2D1A	11219.58	17449.51	11198.32	0	0	0
Q6P2E9	Enhancer c	EDC4	4953.392	4000.801	15217.54	0	0	0
Q6P2Q9	Pre-mRNA	PRPF8	22316.23	24747.62	20146.97	0	0	0
Q6P3W7	SCY1-like	SCYL2	5895.401	4494.778	4302.296	0	0	0
Q6P4E1	Protein CA	CASC4	8869.728	7962.333	7355.316	0	0	0
Q6P4Q7	Metal tran	CNNM4	5501.483	5863.047	8625.515	0	0	0
Q6P9B6	TLD doma	TLDC1	16705.82	17704.34	23730.18	0	0	0
Q6P9G4	Transmem	TMEM154	18451.91	20203.4	5876.98	0	0	0
Q6P9H4	Connector	CNKS3	8395.259	7894.581	9077.4	0	0	0
Q6PCB8	Embigin	EMB	19084.64	7295.752	11782.37	0	0	0
Q6PD62	RNA polyn	CTR9	10539.43	20812.19	7911.038	0	0	0
Q15286	Ras-relate	RAB35	738441.8	749854.8	881235.4	1079379	660415.8	1388577
Q6PGP7	Tetratric	TTC37	4803.649	4829.156	8547.51	0	0	0
Q6PJF5	Inactive rh	RHBDF2	19173.35	9073.929	12601.19	0	0	0
Q6PKG0	La-related	LARP1	6332.169	6219.319	6401.341	0	0	0
Q15365	Poly(rC)-b	PCBP1	234502.9	247431	285779.1	186053.2	118090.2	167179.7
Q15366	Poly(rC)-b	PCBP2	175835.6	190685.2	186484.1	345370.9	181962	339339.1
Q6R327	Rapamycin	RICTOR	9587.392	9685.73	7760.741	0	0	0
Q6T4R5	Nance-Ho	NHS	8316.918	8566.456	10438.57	0	0	0
Q6UWE0	E3 ubiquiti	LRSAM1	15135.49	3395.724	3574.393	0	0	0
Q15392	Delta(24)-	DHCR24	55039.53	53684.1	54870.96	175281.1	0	129490.3
Q6UWP2	Dehydroge	DHRS11	10774.46	11036.66	11853.84	0	0	0
Q15404	Ras suppre	RSU1	110439.3	113133.3	178604.7	101374.4	126301.4	109636.1
Q6UX71	Plexin dom	PLXDC2	8897.155	8971.698	13485.46	0	0	0
Q6V1X1	Dipeptidyl	DPP8	10779.82	18122.06	9086.33	0	0	0
Q6XZF7	Dynamamin	DNMBP	10798.3	10261.44	14611.24	0	0	0
Q6ZMP0	Thrombos	THSD4	2191.242	2392.867	2468.762	0	0	0
Q6ZNJ1	Neurobea	NBEAL2	5436.259	7295.914	7218.775	0	0	0
Q6ZNL6	FYVE, Rho	FGD5	12565.56	8986.272	15209.91	0	0	0
Q6ZRP7	Sulfhydryl	QSOX2	4757.859	4845.566	4442.45	0	0	0
Q6ZS17	Protein FA	FAM65A	10860.57	10081.73	10884.18	0	0	0
Q15555	Microtubu	MAPRE2	68753.94	65937.28	67279.62	78771.14	77669.15	111437.9
Q6ZUX7	Lipoma	HMLHFPL2	41101.64	37486.04	31888.36	0	0	0
Q70E73	Ras-associ	RAPH1	6290.958	5249.756	6804.438	0	0	0
Q70J99	Protein un	UNC13D	7773.262	9352.535	8739.52	0	0	0
Q7KYR7	Butyrophili	BTN2A1	28887.16	20224.89	27983.48	0	0	0
Q7KZF4	Staphylocc	SND1	50074.56	49801.93	39042.32	0	0	0
Q7KZI7	Serine/thre	MARK2	25364.89	24573.93	35510.05	0	0	0
Q7L014	Probable A	DDX46	31512.71	32919.09	19603.57	0	0	0
Q7L0J3	Synaptic v	SV2A	22636.96	19121.39	26068.3	0	0	0

Q7L1Q6	Basic leucic BZW1	56372.99	59793.59	46320.61	0	0	0
Q15758	Neutral an SLC1A5	2018390	1918981	2289039	488744.4	489888.5	781771.8
Q7L2E3	Putative A DHX30	5923.446	6424.324	5160.593	0	0	0
Q7L2H7	Eukaryotic EIF3M	43948.49	65199.28	54705.4	0	0	0
Q7L5N1	COP9 sign COPS6	11365.12	22447.35	22836.28	0	0	0
Q7L7X3	Serine/thre TAOK1	13496.2	11402.26	13245.99	0	0	0
Q7LBR1	Charged r CHMP1B	23440.18	73547.36	22493.55	0	0	0
Q7RTV0	PHD finger PHF5A	21346.99	28261.7	7339.565	0	0	0
Q15907	Ras-relate RAB11B	440335.2	468052.1	388200.1	73445.16	207065.8	366701.8
Q7RTY0	Monocarb SLC16A13	2533.268	2577.934	3842.507	0	0	0
Q7Z2H8	Proton-co SLC36A1	1252.655	2165.473	6569.088	0	0	0
Q7Z2K8	G protein- GPRIN1	16342.24	15256.67	18112.87	0	0	0
Q7Z2W4	Zinc finger ZC3HAV1	26784.86	27871.71	27133.72	0	0	0
Q7Z392	Trafficking TRAPPC11	2131.937	1732.51	1275.82	0	0	0
Q7Z3C6	Autophagy ATG9A	9681.845	5836.919	9083.06	0	0	0
Q16394	Exostosin- EXT1	20189.79	20375.79	21053.38	64458.87	57028.74	56867.5
Q16401	26S protea PSMD5	18499.94	18852.59	13568.96	80363.08	23702.31	33219.02
Q7Z403	Transmem TMC6	8311.614	6970.059	3837.077	0	0	0
Q7Z460	CLIP-assoc CLASP1	16102.52	15001.21	12867.15	0	0	0
Q7Z478	ATP-depe DHX29	5541.296	3530.326	7153.124	0	0	0
Q7Z4F1	Low-densi LRP10	28144.54	25052.53	13581.7	0	0	0
Q7Z4V5	Hepatoma HDGFRP2	13960.36	21665.68	7319.987	0	0	0
Q16555	Dihydrops DPYSL2	86903.97	84780.83	83086.52	94712.34	68673.52	77048.34
Q7Z4W1	L-xylulose DCXR	58733.74	60323.14	60259.91	0	0	0
Q7Z5N4	Protein sid SDK1	15893.67	15565.91	14012.65	0	0	0
Q7Z698	Sprouty-re SPRED2	35669.04	36371.25	52219.83	0	0	0
Q7Z6B7	SLIT-ROB SRGAP1	15153.7	15642.06	18239.17	0	0	0
Q7Z7H5	Transmem TMED4	7016.906	8724.449	3679.998	0	0	0
Q16658	Fascin FSCN1	137177.4	135453.7	304312.4	79565.14	53311.13	56508.36
Q7Z7M0	Multiple e MEGF8	5043.241	2708.731	6126.258	0	0	0
Q86SF2	N-acetylga GALNT7	5250.213	6021.815	8775.036	0	0	0
Q86SJ2	Amphoteri AMIGO2	45261.34	54695.13	51656.71	0	0	0
Q86SQ4	G-protein GPR126	7319.909	6916.075	5849.604	0	0	0
Q86T03	Type 1 phc TMEM55B	27901.24	42390.7	16926.13	0	0	0
Q86TI2	Dipeptidyl DPP9	11681.92	10644.83	13915.16	0	0	0
Q86TU7	Histone-ly SETD3	4822.518	4615.417	5112.898	0	0	0
Q86TV6	Tetratricop TTC7B	4623.236	4906.98	9055.571	0	0	0
Q86U42	Polyadeny PABPN1	16005.02	17346.22	17991.92	0	0	0
Q86UU1	Pleckstrin I PHLDB1	3123.682	2205.214	2678.47	0	0	0
Q86V21	Acetoacety AACS	5151.462	5104.508	5940.252	0	0	0
Q86V81	THO comp ALYREF	13467.83	20728.77	10294.41	0	0	0
Q86VE9	Serine incc SERINC5	265941.9	243539	237895.4	0	0	0
Q86VI3	Ras GTPas IQGAP3	15404.59	15653.04	23794.29	0	0	0
Q86VI4	Lysosomal LAPTM4B	651191.2	601529.1	432611.2	0	0	0
Q86VN1	Vacuolar p VPS36	6565.634	5081.421	6681.357	0	0	0
Q86VR8	Four-joint FJX1	1401.115	2779.801	2183.877	0	0	0
Q31612	HLA class I HLA-B	359980.4	455615.6	353766.4	638216.1	901350.4	427994.2
Q32P28	Prolyl 3-hy P3H1	14946.96	11432.02	14977.16	58860.05	0	42562.89
Q86VY9	Transmem TMEM200	30449.07	21662.38	20348.61	0	0	0
Q86W42	THO comp THOC6	16593.2	15351.71	12156.94	0	0	0
Q86W92	Liprin-bet PPFIBP1	33262.36	41346.45	51689.85	0	0	0
Q86W11	Fibrocystin PKHD1L1	7676.961	10747.3	14704.53	0	0	0
Q3SY69	Mitochondc ALDH1L2	56335.4	67228.56	83847.07	504748.3	1442816	1403507
Q86WR7	Proline an PROSER2	6298.49	5025.818	14499.37	0	0	0
Q86WV6	Stimulator TMEM173	3249.979	2155.916	2826.181	0	0	0
Q86X55	Histone-ar CARM1	10379.26	10021.42	8206.015	0	0	0
Q86XF0	Dihydrofol DHFRL1	14237.18	15770.26	20209.32	0	0	0
Q86XP3	ATP-depe DDX42	7194.622	6434.997	4994.624	0	0	0

Q86XS8	E3 ubiquitin RNF130	17608.36	16566.32	18828.75	0	0	0
Q86Y82	Syntaxin-1 STX12	34790.43	19304.44	57403.21	0	0	0
Q86YP4	Transcripti GATAD2A	3143.99	3288.982	523.2585	0	0	0
Q8IUC4	Rhopilin- RHPN2	1831.384	1809.213	2151.323	0	0	0
Q8IUE6	Histone H2 HIST2H2AI	10966.49	17401.47	10840.47	0	0	0
Q8IUR7	Armadillo ARMCM8	9645.065	6193.39	5781.775	0	0	0
Q8IUW5	RELT-like RELL1	55587.01	49450.78	67107.74	0	0	0
Q53H76	Phospholip PLA1A	30486.97	32540.47	23849.08	0	99442.86	74261.45
Q8IV08	Phospholip PLD3	39586.21	39567.57	28046.19	0	0	0
Q562R1	Beta-actin ACTBL2	2711024	2577813	3086805	539130.9	3083245	1032835
Q8IVB5	LIX1-like pLIX1L	7560.939	6073.504	9433.476	0	0	0
Q58FF8	Putative hHSP90AB2	192923.2	198778.2	205194.9	83086.01	73887.04	78047.16
Q8IVF2	Protein A AHNAK2	34485.64	22002.95	50728.6	0	0	0
Q8IVF7	Formin-like FMNL3	11486.85	9416.323	14986.93	0	0	0
Q8IVM0	Coiled-coil CCDC50	25051.98	24282.24	35812.38	0	0	0
Q8IWA0	WD repeat WDR75	5505.955	5381.858	3098.596	0	0	0
Q8IWB7	WD repeat WDFY1	5841.452	5442.887	5171.579	0	0	0
Q8IWE4	DCN1-like DCUN1D3	8859.692	8739.169	9591.86	0	0	0
Q8IWT6	Volume-reg LRRC8A	11426.67	11564.21	17779.37	0	0	0
Q8IWW6	Rho GTPase ARHGAP11	5032.885	4403.142	3388.333	0	0	0
Q8IWX8	Calcium hCCHERP	4588.649	3967.427	2923.311	0	0	0
Q8IX12	Cell division CCAR1	7422.248	7700.941	7656.106	0	0	0
Q8IX30	Signal pep SCUBE3	10678.87	10455.93	4155.957	0	0	0
Q8IXI1	Mitochondrion RHOT2	240763.3	228740.5	270504.1	0	0	0
Q8IXL6	Extracellular FAM20C	2564.157	3799.673	3300.944	0	0	0
Q8IXU6	Solute carrier SLC35F2	17613.99	15110.52	16970.84	0	0	0
Q8IY95	Transmembrane TMEM192	25997.18	39417.94	35361.88	0	0	0
Q5T4S7	E3 ubiquitin UBR4	19635.91	21727.48	14699.45	69927.66	15165.43	67587.99
Q8IYB3	Serine/arginine SRRM1	15956.77	16637.81	4841.752	0	0	0
Q8IYI6	Exocyst core EXOC8	20225.02	16647.39	12666.18	0	0	0
Q5TBA9	Protein kinase FRY	54093.49	19223.11	18974.5	0	61508.5	418833.3
Q8IYS1	Peptidase PM20D2	3114.379	2706.137	3209.949	0	0	0
Q8IYS2	Uncharacterized KIAA2013	13268.06	22682.84	14812.46	0	0	0
Q8IYT4	Katanin p6 KATNAL2	90147.38	97268.84	82444.41	0	0	0
Q5VU43	Myomegalin PDE4DIP	14192.94	21453.64	35444.99	1001814	1436005	595991.9
Q8IZ07	Ankyrin repeat ANKRD13A	5291.96	4348.515	9668.521	0	0	0
Q8IZA0	Dyslexia-associated KIAA0319L	15480.2	15089.85	13660.06	0	0	0
Q8IZJ1	Netrin receptor UNC5B	6119.264	6510.854	3533.388	0	0	0
Q8IZL8	Proline-4-hydroxylase PELP1	26369.62	31814.58	16502.91	0	0	0
Q8IZP0	Abl interaction ABI1	69861.79	85521.7	105164.4	0	0	0
Q8N122	Regulatory RPTOR	7335.686	7193.532	2414.086	0	0	0
Q8N163	Cell cycle regulator CCAR2	9198.424	9635.979	10108.51	0	0	0
Q8N1F7	Nuclear pore NUP93	12989.82	12845.04	9978.461	0	0	0
Q8N1G2	Cap-specific CMTR1	2933.091	3948.191	3664.214	0	0	0
Q8N1G4	Leucine-rich LRRC47	15651.99	17548.99	17079.71	0	0	0
Q8N2S1	Latent-transmembrane LTBP4	7030.929	6873.277	13286.05	0	0	0
Q8N357	Solute carrier SLC35F6	2204.316	5210.135	2790.725	0	0	0
Q8N392	Rho GTPase ARHGAP18	4551.702	3762.312	6520.587	0	0	0
Q8N3C0	Activating ASCC3	5280.598	5315.109	3879.665	0	0	0
Q8N3D4	EH domain EHBP1L1	5445.779	5695.876	8352.172	0	0	0
Q8N3F8	MICAL-like MICALL1	4475.257	3325.959	3188.697	0	0	0
Q8N3R9	MAGUK protein MPP5	8222.575	7204.714	108849.7	0	0	0
Q8N3T6	Transmembrane TMEM132C	1841.611	1670.638	28028.12	0	0	0
Q8N474	Secreted factor SFRP1	67652.82	81170.71	60501.33	0	0	0
Q8N4C8	Misshapen MINK1	39620.69	33436.54	35413.53	0	0	0
Q6DD88	Atlastin-3 ATL3	4465.811	2455.183	3798.445	56015	0	46711.82
Q8N5I2	Arrestin domain ARDC1	48317.32	45154.8	32078.52	0	0	0
Q8N6T3	ADP-ribosylation ARFGAP1	7290.766	4160.327	10016.93	0	0	0

Q8N7H5	RNA polyn PAF1	5131.237	3253.929	1275.955	0	0	0
Q8N7R7	Cyclin-Y-li CCNYL1	12407.58	13524.55	19842.83	0	0	0
Q8N8S7	Protein en: ENAH	8603.139	7062.888	13542.5	0	0	0
Q8N8Z6	Discoidin, DCBLD1	6141.101	5347.271	6195.25	0	0	0
Q8N9N7	Leucine-ric LRR C57	24624.28	27231.98	40890.06	0	0	0
Q8N9N8	Probable F E1F1AD	6521.992	5296.616	3450.709	0	0	0
Q8NAV1	Pre-mRNA PRPF38A	9921.031	15377.96	18271.9	0	0	0
Q8NB49	Phospholig ATP11C	9283.43	8195.662	10838.54	0	0	0
Q8NB90	Spermatoç SPATA5	51552.62	37428.05	87013.38	0	0	0
Q8NBF2	NHL repea NHLRC2	22592	14654.01	12240.43	0	0	0
Q8NBJ5	Procollage COLGALT1	6582.072	4421.815	4171.344	0	0	0
Q8NBM8	Prenylcyst PCYOX1L	23979.83	24469.19	23081.23	0	0	0
Q8NBN3	Transmem TMEM87A	14133.86	10524.54	7811.938	0	0	0
Q8NBW4	Sodium-c SLC38A9	31045.86	28493.28	34427.41	0	0	0
Q8NBZ7	UDP-gluc UXS1	10013.4	9991.188	11413.7	0	0	0
Q8NC42	E3 ubiquiti RNF149	74010.84	72143.84	51491.83	0	0	0
Q6P9B9	Integrator INTS5	29238.96	19192.09	37773.66	464583.6	674871.1	286240.6
Q8NC51	Plasminog SERBP1	30835.13	32637.35	28308.8	0	0	0
Q8NC54	Keratinocy KCT2	5980.244	6221.582	5136.369	0	0	0
Q8NC67	Neuropilin NETO2	12705.37	14969.61	17295.59	0	0	0
Q8NCA5	Protein FA FAM98A	21218.26	20203.28	18275.78	0	0	0
Q8NCH0	Carbohydr CHST14	18185.18	18430.19	16290.25	0	0	0
Q8ND76	Cyclin-Y CCNY	13468.99	12901.82	19779.36	0	0	0
Q8NDI1	EH domair EHBP1	4104.931	3311.195	3313.539	0	0	0
Q8NDZ4	Deleted in C3orf58	6902.771	8379.669	5920.829	0	0	0
Q8NE01	Metal tran: CNM3	20438.21	21945.91	30873.63	0	0	0
Q8NE71	ATP-bindin ABCF1	29559.97	35926.52	18045.48	0	0	0
Q8NEM2	SHC SH2 c SHCBP1	4181.965	5048.333	4211.88	0	0	0
Q8NEU8	DCC-inter: APPL2	8264.419	8006.804	7447.754	0	0	0
Q8NEW0	Zinc trans SLC30A7	7858.385	7014.553	10172	0	0	0
Q8NFA0	Ubiquitin c USP32	10047.35	9407.953	10547.77	0	0	0
Q8NFH3	Nucleopor NUP43	10675.28	8444.484	10051.13	0	0	0
Q8NFH5	Nucleopor NUP35	1734.313	1808.341	1300.939	0	0	0
Q8NFH8	RaBP1-as: REPS2	7468.835	7814.442	9894.865	0	0	0
Q8NFJ5	Retinoic ac GPRC5A	164960	154269.5	127247.2	0	0	0
Q8NI27	THO comp: THOC2	17747.68	12668.85	9313.665	0	0	0
Q8NI36	WD repeat WDR36	5108.176	6889.809	3855.516	0	0	0
Q8TAA9	Vang-like VANG1	38807.78	35999.7	42244.71	0	0	0
Q8TAF3	WD repeat WDR48	16468.1	12864.15	23408.86	0	0	0
Q8TAG9	Exocyst co EXOC6	17023.13	16261.38	14458.8	0	0	0
Q8TAT6	Nuclear pr NPLOC4	10648.44	9978.748	10671.51	0	0	0
Q8TB03	Uncharact: CXorf38	3184.127	3603.971	3489.968	0	0	0
Q8TB68	Proline-ric PRR7	5974.524	4199.083	2640.065	0	0	0
Q8TB96	T-cell imm ITFG1	3831.199	4048.355	3276.108	0	0	0
Q8TBC4	NEDD8-ac UBA3	8982.181	11721.85	17293.94	0	0	0
Q8TBF2	Prostamid: FAM213B	10491.63	9052.496	10981.67	0	0	0
Q8TBX8	Phosphatic PIP4K2C	17238.99	21692.64	31228.25	0	0	0
Q8TBZ3	WD repeat WDR20	10159.11	8872.169	14153.92	0	0	0
Q8TC12	Retinol del RDH11	15678.2	17826.76	12567.94	0	0	0
Q8TCT8	Signal pep SPPL2A	24550.69	21412.15	18998.05	0	0	0
Q8TCT9	Minor hist: HM13	39872.13	43675.57	35783.84	0	0	0
Q8TCZ2	CD99 antiç CD99L2	85005.45	76869.64	87572.28	0	0	0
Q8TD16	Protein bic BICD2	5821.073	7205.237	8085.82	0	0	0
Q8TD19	Serine/thr: NEK9	26060.79	26705.19	27772.92	0	0	0
Q7LDG7	RAS guany RASGRP2	16575.7	15836.37	14896.46	54803.99	0	63936.05
Q8TD55	Pleckstrin I PLEKHO2	13855.63	12217.66	18402.67	0	0	0
Q8TDM6	Disks large DLG5	3752.32	3298.742	5177.073	0	0	0
Q8TDN6	Ribosome BRX1	10623.22	12178.1	7309.393	0	0	0

Q8TDW0	Volume-re	LRR8C	22997.29	23162.01	32785.68	0	0	0
Q8TDX7	Serine/thr	NEK7	3459.009	3066.995	3439.357	0	0	0
Q7Z304	MAM dom	MAMDC2	21875.88	20710.3	317298.5	43753.21	0	349404.8
Q8TDZ2	Protein-m	MICAL1	3166.489	3909.513	2670.681	0	0	0
Q8TED0	U3 small n	UTP15	7053.79	8227.048	6567.469	0	0	0
Q8TEQ6	Gem-asso	GEMIN5	11153.05	10040.55	7811.883	0	0	0
Q8TEW0	Partitionin	PARD3	14059.4	14557.54	14199.14	0	0	0
Q7Z406	Myosin-14	MYH14	320288.7	349401.3	306795.3	1153926	730364.6	1417264
Q8TEX9	Importin-4	IPO4	17694.64	14128.64	14231.82	0	0	0
Q8TF42	Ubiquitin-	UBASH3B	28703.12	27512.11	43691.95	0	0	0
Q8WTT2	Nucleolar	NOC3L	3512.555	4712.228	9669.605	0	0	0
Q8WTV0	Scavenger	SCARB1	108469	107361.3	108554.6	0	0	0
Q8WTW3	Conserved	COG1	3501.375	3505.94	2322.939	0	0	0
Q8WU20	Fibroblast	FRS2	8974.537	6464.613	8446.042	0	0	0
Q8WUA8	Tsukushin	TSKU	13688.73	19031.79	18674.46	0	0	0
Q8WUM9	Sodium-d	SLC20A1	73818.08	51309.45	67609.1	0	0	0
Q7Z6Z7	E3 ubiquiti	HUWE1	60994.16	66353.71	77919.45	15995571	20045522	4963382
Q8WUW1	Protein BR	BRK1	70149.48	70841.47	100683.2	0	0	0
Q8WUY9	DEP doma	DEPDC1B	10624.82	10551.55	13890.07	0	0	0
Q8WV24	Pleckstrin	PHLDA1	66913.79	78646.25	94558.9	0	0	0
Q8WV41	Sorting ne	SNX33	16883.66	7532.675	7924.902	0	0	0
Q8WV99	AN1-type	ZFAND2B	17573.03	17726.52	18669.04	0	0	0
Q8WVC0	RNA polyn	LEO1	8412.687	9620.613	5553.549	0	0	0
Q8WVJ2	NudC dom	NUDCD2	13208.47	14631.06	15010.38	0	0	0
Q8WVM8	Sec1 famil	SCFD1	21786.71	22507.72	20746.25	0	0	0
Q8WVQ1	Soluble cal	CANT1	4527.753	9467.354	3729.167	0	0	0
Q8WVY7	Ubiquitin-	UBLCP1	3459.103	2833.829	10436.5	0	0	0
Q8WWI1	LIM domai	LMO7	6133.027	6521.175	9276.872	0	0	0
Q86UD1	Out at first	OAF	45990.47	50371.55	66511.36	168282.2	209887.3	114285.3
Q86UP2	Kinectin	KTN1	63464.95	65930.43	66135.98	148453.7	0	87126.7
Q8WWN8	Arf-GAP w	ARAP3	4496.64	4457.355	4957.386	0	0	0
Q86UX7	Fermitin fa	FERMT3	227208	213998.6	170866.5	165117.6	152384.8	175049.1
Q8WXE1	ATR-intera	ATRIP	26567.3	22592.32	22802.62	0	0	0
Q8WXI9	Transcripti	GATAD2B	9598.513	8427.312	6507.846	0	0	0
Q8WYA6	Beta-cater	CTNBL1	7146.089	7814.575	4007.495	0	0	0
Q8WYP5	Protein EL	AHCTF1	1126.65	1675.09	621.4644	0	0	0
Q8WZA0	Protein LZ	LIZIC	4564.262	5241.396	7953.197	0	0	0
Q92522	Histone H1	H1FX	22214.67	30553.68	20215.1	0	0	0
Q86VP6	Cullin-assc	CAND1	60373.52	46189.01	42175.93	66374.02	0	80426.06
Q92530	Proteasom	PSMF1	19066.44	16694.98	30950.3	0	0	0
Q92536	Y+L aminc	SLC7A6	351194.9	337087.3	443533.3	0	0	0
Q92538	Golgi-spec	GBF1	8071.018	7504.921	9425.6	0	0	0
Q92541	RNA polyn	RTF1	14931.6	17016.22	11809.28	0	0	0
Q92556	Engulfmen	ELMO1	3982.614	3884.584	4505.398	0	0	0
Q92558	Wiskott-AI	WASF1	8474.707	6756.051	6266.339	0	0	0
Q92572	AP-3 com	AP3S1	13193.03	16214.55	9322.09	0	0	0
Q92597	Protein NC	NDRG1	34199.36	32534.34	46032.8	0	0	0
Q92598	Heat shock	HSPH1	24714.3	24434.9	32800.77	0	0	0
Q92599	Septin-8	8-Sep	12280.72	11593.77	14280.75	0	0	0
Q92600	Cell differe	RQCD1	127335.5	90962.89	110871.3	0	0	0
Q92619	Minor hist	HMHA1	9533.672	6367.459	8522.978	0	0	0
Q92621	Nuclear pc	NUP205	3595.547	2509.84	1156.04	0	0	0
Q86YQ8	Copine-8	CPNE8	134115.9	127139.6	141888.4	66077.84	48093.49	86873.32
Q92636	Protein FA	NSMAF	2113.639	2302.329	3282.281	0	0	0
Q92688	Acidic leuc	ANP32B	107619.1	109155	69133.98	0	0	0
Q92692	Nectin-2	PVRL2	91121.48	76733.95	88382.25	0	0	0
Q92729	Receptor-I	PTPRU	4238.087	3553.649	4309.733	0	0	0
Q92734	Protein TF	ITFG	33577.46	28501.59	41986.89	0	0	0

Q8IUX7	Adipocyte AEBP1	137172.6	143937	119331.2	177514.9	237493.7	176406.4
Q92738	USP6 N-te USP6NL	9678.539	9297.609	12277.1	0	0	0
Q92747	Actin-relat ARPC1A	25165.04	24606.69	38414.86	0	0	0
Q92769	Histone de HDAC2	53008.58	56187.07	30428.24	0	0	0
Q92783	Signal tran STAM	69658.77	69276.68	94961.81	0	0	0
Q92841	Probable / DDX17	17820.46	18522.98	9160.651	0	0	0
Q92882	Osteoclast OSTF1	22086.29	17629.66	31914.63	0	0	0
Q92888	Rho guanil ARHGEF1	23925.87	27528.47	29466.38	0	0	0
Q92890	Ubiquitin f UFD1L	16287.5	14297.09	18353.24	0	0	0
Q92905	COP9 sign COPS5	5711.21	4834.3	5269.148	0	0	0
Q92922	SWI/SNF c SMARCC1	10330.85	11549.84	18467.61	0	0	0
Q92925	SWI/SNF-r SMARCD2	5658.135	4623.839	10081.2	0	0	0
Q92945	Far upstre: KHSRP	23672.75	24030.88	15505.69	0	0	0
Q92990	Glomulin GLMN	6319.883	4262.318	4350.828	0	0	0
Q93009	Ubiquitin c USP7	11743.94	10804.96	8317.204	0	0	0
Q93034	Cullin-5 CUL5	9134.299	9536.664	6553.915	0	0	0
Q93052	Lipoma-pr LPP	19532.69	17349.85	23901.88	0	0	0
Q93096	Protein tyr PTP4A1	8568.901	8707.148	11018.89	0	0	0
Q93100	Phosphoryl PHKB	7132.696	6169.924	4507.42	0	0	0
Q969E2	Secretory c SCAMP4	55310	47271.1	36264.92	0	0	0
Q969G3	SWI/SNF-r SMARCE1	16265.4	15616.08	9353.822	0	0	0
Q969Q5	Ras-relate RAB24	11155.04	11077.37	8590.994	0	0	0
Q969U7	Proteasom PSMG2	5702.322	4397.524	4737.713	0	0	0
Q969W9	Protein TM PMEPA1	30682.2	30205.61	23809.1	0	0	0
Q8IZ83	Aldehyde c ALDH16A1	29669.15	21633.26	18815.41	41232.11	0	42253.07
Q969X6	Cirhin CIRH1A	7985.827	27786.67	17360.36	0	0	0
Q96A54	Adiponect ADIPOR1	12745.97	9546.962	3522.512	0	0	0
Q96A65	Exocyst co EXOC4	30864.88	32110.35	49254.91	0	0	0
Q96A72	Protein m: MAGOHB	23909.42	22275.8	18160.26	0	0	0
Q8N0Y7	Probable p PGAM4	19069.98	17847.98	23424	0	153991.7	309154.7
Q96AC1	Fermitin fa FERMT2	171534.2	146288.5	201489.9	0	0	0
Q96AE4	Far upstre: FUBP1	12484.43	13618.47	12761.7	0	0	0
Q96AG4	Leucine-ric LRRC59	22962.75	27856.09	26114.11	0	0	0
Q96B97	SH3 doma SH3KBP1	15036.67	15785.91	42478.34	0	0	0
Q96BD0	Solute carr SLCO4A1	76529.99	67238.26	51095.47	0	0	0
Q96BJ3	Axin intera AIDA	21047.04	17168.91	25876.1	0	0	0
Q96BM9	ADP-ribos ARL8A	42474.27	38108.96	68900.05	0	0	0
Q96BN8	Ubiquitin t OTULIN	8983.417	7137.097	10830.98	0	0	0
Q96BX8	MOB kinas MOB3A	16874.76	16079.12	18407.94	0	0	0
Q96BY6	Dedicator DOCK10	39282.75	38406.33	44592.64	0	0	0
Q96CC6	Inactive rh RHBDF1	8726.35	8443.931	7903.354	0	0	0
Q96CN7	Isochorism ISOC1	8373.777	8862.796	12648.83	0	0	0
Q96CS3	FAS-assoc FAF2	10596.34	11512.2	10191.67	0	0	0
Q96CS7	Pleckstrin I PLEKHB2	45661.48	36050.22	26665.82	0	0	0
Q96CW5	Gamma-tu TUBGCP3	10185.99	11226.86	9639.325	0	0	0
Q96D31	Calcium re ORAI1	50965.76	51576.68	71554.55	0	0	0
Q96D71	RalBP1-as: REPS1	10553.91	10869.53	11784.7	0	0	0
Q96DG6	Carboxym: CMBL	5437.176	1091.718	3843.628	0	0	0
Q96DI7	U5 small n SNRNP40	15172.15	8912.098	5463.456	0	0	0
Q96DM3	Uncharact: C18orf8	3164.67	3428.196	3123.302	0	0	0
Q8N884	Cyclic GMF MB21D1	35513.79	31871.68	72108.81	514410.3	727557.6	332782.3
Q96DX4	RING finge RSPRY1	18897.08	17356.95	24548.72	0	0	0
Q96EC8	Protein YIF YIPF6	19232.59	15569.33	9797.78	0	0	0
Q96EE3	Nucleopor SEH1L	14613.23	5113.558	4157.011	0	0	0
Q96EP5	DAZ-assoc DAZAP1	7338.844	9914.963	14601.37	0	0	0
Q96EY5	Multivesic: MVB12A	72434.38	28687.29	37142.63	0	0	0
Q96F85	CB1 canna CNRIP1	24515.98	23599.95	35078.1	0	0	0
Q96FN4	Copine-2 CPNE2	9528.918	9225.148	9933.703	0	0	0

Q96FQ6	Protein S1(S100A16	60383.35	58903.04	74828.5	0	0	0
Q96FS4	Signal-ind SIPA1	3493.377	2871.315	2735.39	0	0	0
Q96FV9	THO comp THOC1	15560.28	17328.54	17263.55	0	0	0
Q96FX8	p53 apopt PERP	46400.06	43933.99	47621.37	0	0	0
Q96FZ7	Charged r CHMP6	52147.76	43714.54	71630.66	0	0	0
Q96G03	Phosphogl PGM2	13672.5	15284.84	21401.44	0	0	0
Q96GD4	Aurora kin AURKB	11343.62	12404.68	13934.18	0	0	0
Q96GK7	Fumarylac FAHD2A	6054.449	5852.121	8169.256	0	0	0
Q96GQ7	Probable / DDX27	13672.74	14107.7	7410.95	0	0	0
Q96GR4	Probable r ZDHHC12	7734.715	7643.873	5845.864	0	0	0
Q96HU8	GTP-bindir DIRAS2	46711.43	7019.507	2403.889	0	0	0
Q96I15	Selenocyst SCLY	13786.74	12461.93	11033.44	0	0	0
Q96IF1	LIM domai AJUBA	5590.648	7523.461	8362.357	0	0	0
Q96II8	Leucine-ri LRCH3	3381.435	3296.437	4928.855	0	0	0
Q96IJ6	Mannose- GMPPA	2395.254	7156.668	4310.745	0	0	0
Q96IU4	Alpha/bet ABHD14B	7235.172	8117.436	13110.59	0	0	0
Q96IY4	Carboxype CPB2	131504.7	125389.6	120452	0	0	0
Q96J01	THO comp THOC3	11286.98	10762.21	13729.69	0	0	0
Q96J84	Kin of IRRE KIRREL	56970	47048.29	47018.98	0	0	0
Q96J92	Serine/thre WNK4	4609.357	8657.886	8078.791	0	0	0
Q96JA1	Leucine-ri LRIG1	736.4464	1878.412	1128.768	0	0	0
Q96JB2	Conserved COG3	5306.538	2621.012	4625.399	0	0	0
Q96JD6	1,5-anhydi AKR1E2	41565.2	40585.66	54365.59	0	0	0
Q96K17	Transcripti BTF3L4	21725.56	21883.5	17372.41	0	0	0
Q96K76	Ubiquitin c USP47	1230.644	3048.281	35350.47	0	0	0
Q96KB5	Lymphokir PBK	199855.2	11712.79	13379.03	0	0	0
Q96KG7	Multiple e MEGF10	36533.83	32041.54	27144.72	0	0	0
Q8NG11	Tetraspani TSPAN14	173510.4	212406.8	141087.5	83921.62	0	106427.6
Q8NHP8	Putative pl PLBD2	10807.25	7981.512	13833.77	46761.61	49197.2	33544.15
Q96KP4	Cytosolic r CNDP2	86259.41	82858.7	88929.2	0	0	0
Q8NI35	InaD-like r INADL	18144512	9643799	6247485	2.11E+08	3.29E+08	1.42E+08
Q96LD4	Tripartite r TRIM47	2477.84	3657.405	4452.69	0	0	0
Q96MC5	Uncharact C16orf45	4680.055	2832.755	4358.175	0	0	0
Q96ME1	F-box/LRR FBXL18	51923.01	28290.23	49223.05	0	0	0
Q96N06	Spermatoc SPATA33	3854.678	3471.041	3898.671	0	0	0
Q96N67	Dedicator DOCK7	7853.039	7041.515	8487.271	0	0	0
Q8TAV4	Stomatin-l STOML3	349798.6	321213.4	260446.1	0	377093.6	1059369
Q96NE9	FERM dom FRMD6	29245.13	23245.09	39538.72	0	0	0
Q8TB61	Adenosine SLC35B2	66083.02	68278.52	40722.78	44509.49	30410.88	32111.28
Q96NT5	Proton-co SLC46A1	21028.65	21231.43	19093.78	0	0	0
Q96NY7	Chloride ir CLIC6	273157	303535.4	472309.2	0	0	0
Q96P48	Arf-GAP w ARAP1	6212.117	10481.85	11712.37	0	0	0
Q96P70	Importin-ξ IPO9	10732.15	8944.57	24003.53	0	0	0
Q96PD2	Discoidin, DCBLD2	103719.1	101036.3	143300.3	0	0	0
Q96PK6	RNA-bindir RBM14	4395.721	3813.266	3068.921	0	0	0
Q96PU5	E3 ubiquiti NEDD4L	33040.43	28732.4	32981.86	0	0	0
Q96PY5	Formin-lik FMNL2	60582.43	51114.04	73747.29	0	0	0
Q96Q11	CCA tRNA TRNT1	8474.393	5710.918	13341.05	0	0	0
Q96Q45	Transmem TMEM237	21634.21	17681.37	24365.63	0	0	0
Q96QD8	Sodium-co SLC38A2	918167.4	944374.6	862359.7	0	0	0
Q96QR8	Transcripti PURB	21035.86	16180.76	18121.65	0	0	0
Q96QZ0	Pannexin- PANX3	23343.31	5144.432	14593.28	0	0	0
Q96QZ7	Membrane MAGI1	2317.935	787.1924	4829.706	0	0	0
Q96RD7	Pannexin- PANX1	1150.272	6087.118	5519.665	0	0	0
Q96RF0	Sorting ne SNX18	13565.69	12425.19	15014.98	0	0	0
Q96RN5	Mediator c MED15	2452.515	2755.789	2301.835	0	0	0
Q96RS6	NudC domr NUDCD1	9982.767	10296.37	11432.29	0	0	0
Q96RT1	Protein LA ERBB2IP	31256.55	34580.85	51762.71	0	0	0

Q96S44	TP53-reguTP53RK	12261.99	14770.21	17344.46	0	0	0
Q96S59	Ran-bindir RANBP9	3055.379	3391.22	2093.285	0	0	0
Q96S97	Myeloid-a MYADM	305653.2	207836.9	309283.6	0	0	0
Q96S99	Pleckstrin I PLEKHF1	12568.58	10308.72	7433.265	0	0	0
Q96SB3	Neurabin- PPP1R9B	15433.66	13659.76	19036.01	0	0	0
Q96SB4	SRSF protea SRPK1	10881.96	12796.06	10421.35	0	0	0
Q96SI9	Spermatid STRBP	33295.74	40343.36	11885.82	0	0	0
Q96SL1	Disrupted DIRC2	11743.94	11632.13	6070.729	0	0	0
Q96ST2	Protein IW IWS1	10713.89	21978.78	7306.751	0	0	0
Q96ST3	Paired am SIN3A	15900.53	16450.04	13762.11	0	0	0
Q96SU4	Oxysterol- OSBPL9	7941.246	6775.397	13191.32	0	0	0
Q96SZ5	2-aminoet ADO	5748.188	7959.869	7819.654	0	0	0
Q96T76	MMS19 nu MMS19	7869.999	8107.1	7753.045	0	0	0
Q99417	C-Myc-bir MYCBP	8490.861	8054.208	8086.952	0	0	0
Q99426	Tubulin-fo TBCB	19273.51	7689.787	6700.472	0	0	0
Q99447	Ethanolam PCYT2	12865.81	11267.05	12314.95	0	0	0
Q99459	Cell divisio CDC5L	5708.811	6081.973	6043.014	0	0	0
Q99460	26S protea PSMD1	65426.32	69066.34	55788.15	0	0	0
Q99519	Sialidase-1 NEU1	11058.89	15303.5	14948.86	0	0	0
Q99523	Sortilin SORT1	2116.586	1877.222	3002.243	0	0	0
Q99569	Plakophilin PKP4	5161.44	4461.318	7015.27	0	0	0
Q99570	Phosphoin PIK3R4	2863.261	3197.049	2851.063	0	0	0
Q8WWA0	Intellectin- ITLN1	82041.69	78335.63	59873.21	287552.2	253904.9	260935.5
Q99575	Ribonuclea POP1	5511.742	5449.672	5876.28	0	0	0
Q8WWI5	Choline tra SLC44A1	346666.9	260675.9	356884.6	519212.8	0	161801.5
Q99584	Protein S1(S100A13	131367.4	104131.2	97529.36	0	0	0
Q8WWU7	Intellectin- ITLN2	161541.3	164322.2	114308.1	313265.5	289193	540924.7
Q8WWZ4	ATP-bindir ABCA10	168880.8	140295.5	245273.2	1579875	2874770	1343837
Q8WWZ8	Oncoprotea OIT3	53612.04	58316.43	60526.45	197604.7	277849.5	190872.4
Q99615	DnaJ homa DNAJC7	8087.322	7866.131	16978.38	0	0	0
Q99622	Protein C1 C12orf57	18042.54	13538.2	18178.97	0	0	0
Q99627	COP9 sign COPS8	36567.59	38300.77	49118.36	0	0	0
Q99650	Oncostatin OSMR	18366.55	16403.53	17691.43	0	0	0
Q99653	Calcineurin CHP1	28136.17	28363.83	41903.65	0	0	0
Q99661	Kinesin-lik KIF2C	5992.635	9658.852	6086.154	0	0	0
Q92499	ATP-depea DDX1	22036.04	22049.02	22422.44	61581.58	0	46923.38
Q92520	Protein FA FAM3C	45781.71	44649.64	52691.59	0	119390.1	58729.86
Q99717	Mothers a SMAD5	3084.181	7291.982	8749.203	0	0	0
Q99729	Heterogen HNRNPAB	27045.63	27691.98	18743.16	0	0	0
Q99733	Nucleoson NAP1L4	26657.54	19354.43	21576.74	0	0	0
Q99747	Gamma-sc NAPG	24444.54	24251.85	41702.14	0	0	0
Q99755	Phosphatic PIP5K1A	53986.06	54898.48	84721.83	0	0	0
Q92544	Transmem TM9SF4	20596.01	22302.39	15691.1	23876.97	0	36278.88
Q99828	Calcium ar CIB1	20429.15	13522.62	17386.02	0	0	0
Q99848	Probable r EBNA1BP2	16019.32	15685.37	8209.728	0	0	0
Q99986	Serine/thre VRK1	12978.75	14505.4	8867.467	0	0	0
Q9BPX3	Condensin NCAPG	109489.6	124109.5	116987.2	0	0	0
Q9BPX5	Actin-relat ARPC5L	73668.12	72963.02	113370.5	0	0	0
Q9BQ04	RNA-bindir RBM4B	12296.88	9096.91	7494.352	0	0	0
Q9BQ24	Zinc finger ZFYVE21	7878.321	19121.04	8955.988	0	0	0
Q92614	Unconvent MYO18A	40208.54	37603.04	46302.46	631656.5	889543.4	285507.7
Q92616	Translator GCN1L1	212681.7	15922.23	346190.3	13711688	21284766	3531866
Q9BQ69	O-acetyl- MACROD1	1483.413	1599.322	1220.25	0	0	0
Q9BQA1	Methyloso WDR77	71879	71213.38	77484.79	0	0	0
Q92626	Peroxidasii PXDN	108370.9	195716.3	131743.4	874253.5	959492.4	1894679
Q9BQG0	Myb-bindir MYBBP1A	24285.5	28825.6	5523.074	0	0	0
Q9BQL6	Fermitin fa FERMT1	56659.25	54377.59	114971.3	0	0	0
Q9BR76	Coronin-1 CORO1B	46576.74	56853	101639	0	0	0

Q9BRF8	Serine/thr CPPED1	12269.04	10448.35	13905.6	0	0	0
Q9BRG1	Vacuolar p VPS25	32255.74	26739.88	34330.48	0	0	0
Q9BRP4	Proteasom PAAF1	7885.272	6802.409	9194.381	0	0	0
Q92743	Serine pro: HTRA1	70276.41	75960.31	84138.48	5173575	2761369	8269728
Q9BRX2	Protein pe PELO	16045.5	16710.43	11349.36	0	0	0
Q9BS18	Anaphase- ANAPC13	6602.929	6474.33	6896.489	0	0	0
Q9BS26	Endoplasr ERP44	13829.96	16311.88	13939.76	0	0	0
Q92820	Gamma-gl GGH	45413.65	44208.32	46868.76	19831.76	0	23583.55
Q9BSA4	Protein tw: TTYH2	30290.73	34068.1	26892.92	0	0	0
Q9BSL1	Ubiquitin-: UBAC1	4836.579	3909.605	3465.323	0	0	0
Q9BSQ5	Cerebral c: CCM2	12442.24	9410.826	12387.68	0	0	0
Q9BT78	COP9 sign COPS4	33942.94	34275.81	37344.77	0	0	0
Q92896	Golgi app: GLG1	52326.96	49041.71	51994.74	53510.26	0	34039.91
Q9BT88	Synaptota: SYT11	13359.3	8217.35	15699.44	0	0	0
Q9BTE1	Dynactin s DCTN5	20193.16	11652.75	16855.29	0	0	0
Q9BTE3	Mini-chrom MCMBP	5559.062	8630.244	6402.785	0	0	0
Q92930	Ras-relate: RAB8B	117440.9	112928.3	152051.1	42334.47	0	62894.6
Q9BTM9	Ubiquitin-: URM1	28308.56	27998.97	44456.38	0	0	0
Q92954	Proteoglyc PRG4	48656.82	77436.68	30285.48	142148.6	195878	91801.29
Q92974	Rho guanil ARHGEF2	8787.801	10965.49	2368.939	39711.62	0	79506.39
Q9BTT0	Acidic leuc ANP32E	39869.88	71202.56	39820.94	0	0	0
Q93008	Probable c USP9X	14090.4	15222.38	11509.95	85802.86	33276.18	78836.37
Q9BTT6	Leucine-ric LRRC1	13408.67	3016.898	18640.53	0	0	0
Q9BTU6	Phosphatic PI4K2A	23907.72	19134.39	18170.36	0	0	0
Q9BTW9	Tubulin-sp TBCD	9339.146	10358.19	12658.14	0	0	0
Q93063	Exostosin- EXT2	20419.48	19351.59	17784.43	70040.61	0	37517.64
Q9BTY2	Plasma alp FUCA2	592866.7	623940.7	1643400	0	0	0
Q9BU40	Chordin-lil CHRDL1	10595.1	10052.98	12133.55	0	0	0
Q9BU89	Deoxyhyp: DOHH	8751.364	10232.62	7950.521	0	0	0
Q9BUJ2	Heterogen HNRNPUL	9405.467	9712.619	5127.247	0	0	0
Q9BUL8	Programm PDCD10	80323.82	71057.88	100981.4	0	0	0
Q969P0	Immunogly IGSF8	79490.76	68376.35	72269.86	119654.4	85423.12	160093.8
Q9BUN8	Derlin-1 DERL1	17595.67	20561.04	15838.89	0	0	0
Q9BUQ8	Probable A DDX23	5770.354	5255.137	2534.253	0	0	0
Q9BV20	Methylthio MRI1	3491.246	3411.318	3603.739	0	0	0
Q9BV38	WD repeat WDR18	20843.92	22566.56	17627.64	0	0	0
Q9BV57	1,2-dihydr ADI1	14092	14146.39	21786.31	0	0	0
Q9BV68	E3 ubiquiti RNF126	15790.87	13432.39	15283.75	0	0	0
Q9BV86	N-termina NTMT1	11470.15	11653.17	20939.38	0	0	0
Q9BVC4	Target of r MLST8	3544.242	3158.288	5590.117	0	0	0
Q9BVC6	Transmem TMEM109	51579	57898.98	39726.79	0	0	0
Q9BVG4	Protein PB PBDC1	4389.065	11505.41	5269.974	0	0	0
Q9BVG9	Phosphatic PTDSS2	2304.24	6188.473	6224.803	0	0	0
Q9BVI4	Nucleolar r NOC4L	2109.854	2411.51	2020.308	0	0	0
Q9BVJ7	Dual speci DUSP23	2453.843	2635.534	1960.658	0	0	0
Q9BVK6	Transmem TMED9	98288.7	99935.09	118719	0	0	0
Q9BVQ7	Spermatoc SPATA5L1	3839.246	4182.724	5407.701	0	0	0
Q9BWJ5	Splicing fa SF3B5	5940.652	10380.51	1790.886	0	0	0
Q9BWU0	Kanadaptir SLC4A1AP	4566.999	3333.533	2919.651	0	0	0
Q9BX67	Junctional JAM3	51032.95	47992.1	51829.5	0	0	0
Q9BX79	Stimulated STRA6	19627.76	22237.86	26925.36	0	0	0
Q9BxB5	Oxysterol- OSBPL10	6457.648	10083.68	11469.78	0	0	0
Q9BXD5	N-acetylne NPL	4273.808	5978.918	6587.499	0	0	0
Q9BXF6	Rab11 fam RAB11FIP5	5741.27	2650.448	2802.086	0	0	0
Q9BXI6	TBC1 dom TBC1D10A	17140.15	16080.75	29715.96	0	0	0
Q96CX2	BTB/POZ c KCTD12	33078.05	29637.84	37240.19	114435	111293.4	69247.63
Q96D15	Reticulocal RCN3	49814.34	41908.15	55531.49	436612.4	604471.3	194022.6
Q9BXJ9	N-alpha-a NAA15	19800.29	25339.22	26584.43	0	0	0

Q9BXP2	Solute carr	SLC12A9	10381.76	5132.728	4283.613	0	0	0
Q9BXP5	Serrate	RNSRRT	10653.92	14455.13	8247.732	0	0	0
Q9BXS4	Transmem	TMEM59	11119.83	24937.56	35880.29	0	0	0
Q9BXY0	Protein M/	MAK16	15138.66	10187.25	4977.069	0	0	0
Q9BY32	Inosine tri	ITPA	10191.96	10995.76	15688.82	0	0	0
Q9BY44	Eukaryotic	EIF2A	14756.68	14222.47	13439.86	0	0	0
Q9BY67	Cell adhesi	CADM1	31050.8	30696.33	39167.73	0	0	0
Q96EG1	Arylsulfata	ARSG	15810.27	16115.43	15874.29	47078.93	48014.05	25521.71
Q9BY89	Uncharact	KIAA1671	7779.787	8617.284	6701.293	0	0	0
Q9BYG5	Partitionin	PARD6B	4634.469	3570.312	8098.584	0	0	0
Q9BYI3	Hyccin	FAM126A	7516.124	8859.037	12330.6	0	0	0
Q9BYN0	Sulfiredoxi	SRXN1	2016.413	2155.211	3207.275	0	0	0
Q9BZ29	Dedicator	DOCK9	14567.56	13695.99	18035.76	0	0	0
Q9BZ67	FERM dom	FRMD8	15789.83	14054.96	21322.69	0	0	0
Q9BZE4	Nucleolar	GTPBP4	11971.24	13133.04	8469.084	0	0	0
Q9BZE9	Tether con	ASPSR1	6799.454	5563.841	9787.058	0	0	0
Q9BZF1	Oxysterol-	OSBPL8	6750.529	3702.242	5882.025	0	0	0
Q9BZF9	Uveal auto	UACA	4443.284	3639.464	5871.018	0	0	0
Q9BZG1	Ras-relate	RAB34	78934.63	76714.1	98503.43	0	0	0
Q9BZG8	Diphthami	DPH1	2724.017	2604.82	3247.377	0	0	0
Q9BZH6	WD repeat	WDR11	7647.59	11433.43	4102.1	0	0	0
Q9BZI7	Regulator	UPF3B	6851.712	7520.003	7278.3	0	0	0
Q96HC4	PDZ and L	PDLIM5	45919.21	38936.74	89698.97	0	13015.1	19338.67
Q9BZK7	F-box-like	TBL1XR1	5099.737	5144.294	4210.226	0	0	0
Q9BZL1	Ubiquitin-	UBL5	12053.48	11909.73	16882.2	0	0	0
Q96I24	Far upstre	FUBP3	6489.468	5501.287	4890.458	423461.2	0	619744.4
Q9BZM6	NKG2D lig	ULBP1	4950.468	5390.424	6362.496	0	0	0
Q9BZQ8	Protein Nil	FAM129A	18031.39	16697.78	20440.54	0	0	0
Q9BZX2	Uridine-cy	UCK2	6315.175	5608.141	5834.434	0	0	0
Q9C004	Protein spr	SPRY4	48453.16	44224.35	40698.18	0	0	0
Q9C005	Protein dp	DPY30	26199.25	25799.2	25003.78	0	0	0
Q9C0B5	Palmitoylr	ZDHHC5	29738.83	28059.43	34826.46	0	0	0
Q9C0C4	Semaphori	SEMA4C	42795.4	42153.95	46127.95	0	0	0
Q9C0D5	Protein TA	TANC1	5436.657	4837.166	7316.542	0	0	0
Q9C0D9	Ethanolam	EPT1	42278.93	42589.27	33980	0	0	0
Q9C0E2	Exportin-4	XPO4	6026.855	6192.9	5419.949	0	0	0
Q9C0H5	Rho GTPas	ARHGAP39	5063.998	7719.295	10303.84	0	0	0
Q9GZM5	Protein YIF	YIPF3	31897.38	37557.69	26383.57	0	0	0
Q9GZM7	Tubulointe	TINAGL1	8609.109	14658.76	10930.79	0	0	0
Q9GZN8	UPF0687 p	C20orf27	824.4708	981.3009	1460.621	0	0	0
Q9GZU7	Carboxy-t	CTDSP1	24463.37	19739.08	14758.14	0	0	0
Q9GZZ9	Ubiquitin-	UBA5	7990.736	8890.16	9693.619	0	0	0
Q9H013	Disintegrin	ADAM19	6651.948	7802.226	7050.504	0	0	0
Q9H074	Polyadeny	PAIP1	7723.494	9570.511	10557.64	0	0	0
Q9H0B6	Kinesin lig	KLC2	4257.406	4067.445	4166.071	0	0	0
Q9H0D6	5-3 exorib	XRN2	16851.77	21749.08	2786.082	0	0	0
Q9H0M0	NEDD4-lik	WWP1	12572.34	10315.91	10906.9	0	0	0
Q9H0N0	Ras-relate	RAB6C	26328.28	27326.59	20899.84	0	0	0
Q9H0R3	Transmem	TMEM222	4266.667	3108.975	5991.756	0	0	0
Q9H0U4	Ras-relate	RAB1B	45609.24	51816.52	46482.49	0	0	0
Q9H0W9	Ester hydr	C11orf54	13342.92	14570.79	21002.97	0	0	0
Q9H1A4	Anaphase-	ANAPC1	3490.324	6697.322	5476.623	0	0	0
Q9H1C7	Cysteine-r	CYSTM1	85483.52	59439.18	77927.76	0	0	0
Q9H1Y0	Autophagy	ATG5	3085.262	3613.35	3335.772	0	0	0
Q96PD5	N-acetylm	PGLYRP2	29602.44	37498.02	62592.26	217558.9	382687	0
Q9H228	Sphingosir	S1PR5	1467.994	1372.06	2696.863	0	0	0
Q9H246	Uncharact	C1orf21	8759.93	6397.176	7960.266	0	0	0
Q9H2C0	Gigaxonin	GAN	4535.474	4945.435	5908.704	0	0	0

Q9H2D6	TRIO and FTRIOBP	2437.508	3733.758	6269.424	0	0	0
Q9H2G2	STE20-like SLK	17928.54	16712.4	20607.6	0	0	0
Q9H2H9	Sodium-cc SLC38A1	246537	220698.6	245616.7	0	0	0
Q9H2K8	Serine/thr TAOK3	14439.18	14182.98	30225.77	0	0	0
Q9H2U1	ATP-depe DHX36	3205.194	3142.522	3315.082	0	0	0
Q9H2U2	Inorganic p PPA2	71322.14	72376.36	98233.95	0	0	0
Q9H3G5	Probable s CPVL	101614	74919.85	150852.9	0	0	0
Q9H3K6	BolA-like p BOLA2	9832.254	11042	19699.47	0	0	0
Q96RI0	Proteinase F2RL3	16705.34	16067.62	19691.26	49568.36	0	105924.1
Q9H3S7	Tyrosine-p PTPN23	20122.29	21647.15	18359.93	0	0	0
Q9H3U1	Protein un UNC45A	15290.32	15785.68	15551.16	0	0	0
Q9H3Z4	DnaJ homc DNAJC5	7166.563	5363.898	7216.924	0	0	0
Q9H425	Uncharact C1orf198	7255.816	6845.253	9650.933	0	0	0
Q9H444	Charged n CHMP4B	95478.88	71291.14	99633.53	0	0	0
Q9H497	Torsin-3A TOR3A	5993.278	5205.476	6499.339	0	0	0
Q9H4A4	Amino pep RNPEP	32209.15	32321.18	37481.41	0	0	0
Q9H4G0	Band 4.1-l EPB41L1	6236.564	17338.63	17349.04	0	0	0
Q9H5V8	CUB doma CDCP1	10760.55	8950.704	14247.56	0	0	0
Q9H6W3	Bifunctionc NO66	996.1663	1170.585	1123.201	0	0	0
Q9H6X2	Anthrax to ANTXR1	23491.2	23466.14	23335.38	0	0	0
Q9H6Y7	E3 ubiquiti RNF167	13591.86	16544.78	21898.37	0	0	0
Q9H773	dCTP pyro DCTPP1	15702.49	15643.72	44890.79	0	0	0
Q9H7B2	Ribosome RPF2	15564.14	9235.477	5949.634	0	0	0
Q9H7B4	Histone-ly SMYD3	5828.68	4445.806	6844.807	0	0	0
Q9H7D7	WD repeat WDR26	5008.757	5681.716	1820.152	0	0	0
Q9H7F0	Probable c ATP13A3	33913.26	28281.92	36434.48	0	0	0
Q96TA1	Niban-like FAM129B	82587.64	85984.13	127287.2	1247459	0	671176.1
Q9H7F4	Transmem TMEM185I	3408.514	3275.234	2586.145	0	0	0
Q9H832	Ubiquitin-i UBE2Z	26314.51	25694.15	21359.61	0	0	0
Q99436	Proteasom PSMB7	100538.1	88102.8	100162.8	126185.6	98506.67	112890.4
Q9H8M7	Protein FA FAM188A	9322.11	12623.87	10306.43	0	0	0
Q9H8M9	Protein evc EVA1A	166207.5	166741.4	103202.2	0	0	0
Q9H8S9	MOB kinas MOB1A	17636.75	15895.84	22224.54	0	0	0
Q99497	Protein de PARK7	101614.5	85813.69	135469.3	158832.8	163500.6	132105.1
Q9H8W4	Pleckstrin I PLEKHF2	14213.49	13185.04	4903.514	0	0	0
Q9H910	Hematolog HN1L	19756.1	18928.72	29265.4	0	0	0
Q99536	Synaptic v VAT1	100377.9	88002.14	116159.9	73252.43	58272.39	64052.93
Q9H944	Mediator c MED20	4023.259	4034.983	4281.912	0	0	0
Q9H9A5	CCR4-NO CNOT10	9886.713	11407.58	10093.91	0	0	0
Q9H9A6	Leucine-ric LRRC40	8431.376	8833.139	11921.64	0	0	0
Q9H9E3	Conserved COG4	5947.83	6264.277	3841.633	0	0	0
Q9H9H4	Vacuolar p VPS37B	54459.36	49888.48	41316.81	0	0	0
Q9H9Q2	COP9 sign COPS7B	7811.026	8586.972	9631.835	0	0	0
Q9H9T3	Elongator p ELP3	6564.75	6471.128	11096.16	0	0	0
Q9HAB3	Solute carr SLC52A2	115538.6	98621.13	99222.49	0	0	0
Q9HAB8	Phosphop PPCS	7517.42	4369.017	5087.411	0	0	0
Q9HAC8	Ubiquitin c UBTD1	48204.7	42815.11	56584.13	0	0	0
Q9HAT8	E3 ubiquiti PELI2	10963.44	8588.635	9555.296	0	0	0
Q9HAU0	Pleckstrin I PLEKHA5	8233.063	9305.866	10202.72	0	0	0
Q9HAU4	E3 ubiquiti SMURF2	6509.241	6200.986	5117.864	0	0	0
Q9HAV4	Exportin-5 XPO5	6177.788	6255.026	6340.976	0	0	0
Q9HB07	UPF0160 p C12orf10	5112.812	11747.02	18393.07	0	0	0
Q9HB09	Bcl-2-like BCL2L12	18430.57	12357.69	11586.77	0	0	0
Q99805	Transmem TM9SF2	123273.6	131695	85097.27	84320.18	32916.44	64334.05
Q9HB40	Retinoid-ir SCPEP1	3769.89	5014.701	5276.076	0	0	0
Q9HB71	Calcyclin-k CACYBP	15310.82	18120.69	23062.44	0	0	0
Q9HB90	Ras-relate RRAGC	6992.417	7989.989	6059.884	0	0	0
Q99961	Endophilin SH3GL1	53816.27	52338.59	58708.3	39432.07	0	30842.87

Q9HBH0	Rho-relate RHO	19408.22	20466.42	28309.11	0	0	0
Q9HC07	Transmem TMEM165	33924.18	34903.84	20083.89	0	0	0
Q9HCE7	E3 ubiquitin SMURF1	2427.503	1871.404	1989.704	0	0	0
Q9HCM4	Band 4.1-l EPB41L5	22778.71	31826.88	19554.28	0	0	0
Q9HCN3	Transmem TMEM8A	23722.33	24862.88	25175.18	0	0	0
Q9HCP0	Casein kinase CSNK1G1	15963.26	14090.14	22108.43	0	0	0
Q9HD45	Transmem TM9SF3	52450.31	55264.78	34483.27	0	0	0
Q9HD67	Unconventional MYO10	61132.07	60828.48	63076.65	0	0	0
Q9NP58	ATP-binding ABCB6	4097.238	5266.816	3596.313	0	0	0
Q9NP72	Ras-relate RAB18	24507.93	25870.64	24472.75	0	0	0
Q9BRA2	Thioredoxin TXNDC17	49435.05	45556.94	58842.83	25577.71	121196.9	42447.66
Q9NPA8	Transcriptin ENY2	7153.618	10283.59	10315.15	0	0	0
Q9NPD3	Exosome core EXOSC4	12480.38	12033.12	12228.31	0	0	0
Q9NPF0	CD320 antigen CD320	24454.86	24037.1	34917.17	0	0	0
Q9NPF4	Probable transcription OSGEP	17491.89	23953.14	13115.84	0	0	0
Q9NPH2	Inositol-3-phosphatase ISYNA1	6008.207	5439.536	7025.771	0	0	0
Q9NPI0	Transmem TMEM138	12410.03	8657.609	14905.79	0	0	0
Q9NPI6	mRNA-decapping DCP1A	536.9897	412.2356	840.9872	0	0	0
Q9BSJ8	Extended synaptotagmin ESYT1	10739.38	13456.54	11629.92	39546.98	0	82468.09
Q9NPQ8	Synembryonin RIC8A	8247.146	7838.88	6867.752	0	0	0
Q9NPR2	Semaphorin SEMA4B	2009.788	1566.175	2138.677	0	0	0
Q9NQ79	Cartilage alpha CRTAC1	3121.662	4885.547	4962.829	0	0	0
Q9NQ84	G-protein GPRC5C	102897.5	97993.22	89223.8	0	0	0
Q9NQ88	Fructose-2-phosphate TIGAR	13755.02	9748.123	23714.14	0	0	0
Q9NQG5	Regulation RPRD1B	2807.441	4416.42	1952.679	0	0	0
Q9NQR4	Omega-3 fatty acid NIT2	5903.269	7013.18	11208.82	0	0	0
Q9NQS3	Nectin-3 PVRL3	10774.42	9448.872	15373.31	0	0	0
Q9NQT4	Exosome core EXOSC5	2297.903	4199.405	3421.733	0	0	0
Q9NQX7	Integral membrane ITM2C	174892.1	157210.4	125656.5	0	0	0
Q9NR09	Baculoviral BIRC6	10866.22	3618.52	4312.604	0	0	0
Q9NR12	PDZ and LIM domain PDLIM7	180561.6	192235.9	419042.1	0	0	0
Q9NR19	Acetyl-coenzyme ACSS2	20809.72	26984.62	18259.09	0	0	0
Q9NRA1	Platelet-derived PDGFC	32476.45	10009.15	20101.36	0	0	0
Q9BUF5	Tubulin beta TUBB6	414805.8	405173	408387.5	6209379	2288837	5673297
Q9NRA2	Sialin SLC17A5	8141.671	8620.832	8186.576	0	0	0
Q9NRG9	Aladin AAAS	4750.313	4523.604	2727.958	0	0	0
Q9NRN7	L-amino acid AASDHPP	4388.606	4048.695	3081.015	0	0	0
Q9NRR3	CDC42 small CDC42SE2	31105.19	30870.77	40097.24	0	0	0
Q9NRR8	CDC42 small CDC42SE1	29426.12	14727.26	20290.29	0	0	0
Q9NRV9	Heme-binding HEBP1	22120.32	20906.09	20242.13	0	0	0
Q9NRW1	Ras-relate RAB6B	613691.4	897842.9	325646.3	0	0	0
Q9NRW7	Vacuolar protein VPS45	15425.25	14051.47	27830.21	0	0	0
Q9NRX1	RNA-binding PNO1	1689.398	2036.278	1160.115	0	0	0
Q9BVA1	Tubulin beta TUBB2B	493459.8	510924.8	461248.3	1458404	1150398	3119961
Q9NRX4	14 kDa phosphatase PHPT1	7991.733	8120.101	6065.141	0	0	0
Q9NS15	Latent transcription LTBP3	2777.536	2071.073	1872.188	0	0	0
Q9NS86	LanC-like protein LANCL2	6031.197	6388.264	4675.945	0	0	0
Q9NSD9	Phenylalanine FARSB	19120.98	19405.32	17343.01	0	0	0
Q9NT62	Ubiquitin-like ATG3	15721.18	19391.42	20730.75	0	0	0
Q9NTI5	Sister chromatid PDS5B	5348.014	5579.3	4921.931	0	0	0
Q9NTJ3	Structural protein SMC4	13292.35	16640.6	10631.83	0	0	0
Q9NTJ5	Phosphatidylcholine SACM1L	5032.916	4071.638	6570.13	0	0	0
Q9NTK5	Obg-like protein OLA1	33241.28	44128.47	43622.56	0	0	0
Q9NU22	Midasin MDN1	7351.79	6668.534	6609.999	0	0	0
Q9NUE0	Palmitoyltransferase ZDHHC18	4701.044	3287.592	3651.584	0	0	0
Q9NUM4	Transmem TMEM106I	50998.5	51789.91	53180.1	0	0	0
Q9BX97	Plasma membrane PLVAP	0	16328.84	23547.55	65092.79	0	56856.02
Q9NUP9	Protein kinase LIN7C	108743.3	102944	165848.4	0	0	0

Q9NUQ8	ATP-binding ABCF3	15280.9	15611.08	10339.96	0	0	0
Q9NUQ9	Protein FA FAM49B	108397.3	123905.9	150930.5	0	0	0
Q9NUU7	ATP-dependent DDX19A	19448.46	24842.94	22381.18	0	0	0
Q9NUY8	TBC1 domain TBC1D23	2241.355	2245.937	2337.142	0	0	0
Q9NV58	E3 ubiquitin RNF19A	7143.758	7106.857	5621.427	0	0	0
Q9NV70	Exocyst complex EXOC1	7478.32	8552.736	12287.71	0	0	0
Q9NV96	Cell cycle protein TMEM30A	37623	34886.86	35247.09	0	0	0
Q9NVE7	Pantothenic PANK4	9349.404	10041.23	11827.64	0	0	0
Q9NVJ2	ADP-ribosyl ARL8B	21858.58	15244.78	16559.78	0	0	0
Q9NVM1	Protein evinc EVA1B	146273.5	126110.5	117672.6	0	0	0
Q9NVP1	ATP-dependent DDX18	10258.7	13793.32	7929.596	0	0	0
Q9NVQ4	Fas apoptotic FAIM	6985.146	6835.385	5344.009	0	0	0
Q9NVS9	Pyridoxine PNPO	3251.558	3459.978	4667.753	0	0	0
Q9NVT9	Armadillo domain ARMC1	3025.666	3244.324	2833.888	0	0	0
Q9NW97	Transmembrane TMEM51	28143.32	26869.78	20220.97	0	0	0
Q9NWD8	Transmembrane TMEM248	10348.32	8948.173	7337.46	0	0	0
Q9NWS0	PIH1 domain PIH1D1	3862.223	7953.465	7804.64	0	0	0
Q9NWX6	Probable trans THG1L	3880.917	3307.944	4698.413	0	0	0
Q9NX24	H/ACA ribonucleoprotein NHP2	15912.33	17569.76	11077.32	0	0	0
Q9NX57	Ras-related RAB20	12448.3	12342.8	9815.563	0	0	0
Q9NX62	Inositol multikinase IMPAD1	44578.64	41458.09	31751.81	0	0	0
Q9NXF1	Testis-expressed TEX10	7719.39	10951.13	6069.325	0	0	0
Q9NXH9	tRNA (guanine) TRMT1	2114.025	1639.318	17972.5	0	0	0
Q9NXU5	ADP-ribosyl ARL15	8232.834	10453.56	10703.03	0	0	0
Q9NY26	Zinc transporter SLC39A1	1399.058	1462.025	1194.608	0	0	0
Q9NY33	Dipeptidyl DPP3	24254.15	20251.42	29695.45	0	0	0
Q9NY35	Claudin domain CLDND1	92143.61	93675.03	98523.23	0	0	0
Q9NY97	N-acetyltransferase B3GNT2	3295.085	2193.113	4579.078	0	0	0
Q9BZL6	Serine/threonine PRKD2	13493.78	22917.74	25407.42	17198.17	0	25297.49
Q9NYB9	Abl interaction ABI2	72113.45	70175.77	83880.69	0	0	0
Q9NYK5	39S ribosome MRPL39	2001.965	2004.666	2292.308	0	0	0
Q9NYL2	Mitogen-activated ZAK	11070.47	6351.114	8971.176	0	0	0
Q9NYL9	Tropomodulin TMOD3	20124.99	18815.74	13330.43	0	0	0
Q9NYM9	BET1-like protein BET1L	9545.07	9325.443	7833.571	0	0	0
Q9NYT0	Pleckstrin- PLEK2	9162.631	4201.121	13303.1	0	0	0
Q9NZB2	Constitutively FAM120A	10339.18	10544.73	6232.245	0	0	0
Q9NZD2	Glycolipid GLTP	14276.68	9131.831	12927.26	0	0	0
Q9NZD8	Maspardin SPG21	7555.707	13013.31	8902.619	0	0	0
Q9NZJ4	Sacsin SACS	2511.147	2381.496	1749.786	0	0	0
Q9NZL4	Hsp70-binding HSPBP1	15787.79	20660.3	26300.5	0	0	0
Q9NZL9	Methionine MAT2B	16124.38	10527.95	13647.28	0	0	0
Q9NZN5	Rho guanine ARHGEF12	14344.88	13512.57	18012.36	0	0	0
Q9NZQ3	NCK-interacting NCKIPSD	8389.267	7946.715	12991.95	0	0	0
Q9NZQ7	Programmable CD274	19090.67	18373.2	29603.71	0	0	0
Q9GZX5	Zinc finger ZNF350	75187.68	37343.64	549379.6	0	50420504	27278870
Q9NZR2	Low-density LRP1B	53652.04	48209.3	29922.33	0	0	0
Q9NZT2	Opioid receptor OGFR	9213.34	9675.744	9725.084	0	0	0
Q9NZV1	Cysteine-rich CRIM1	11466.25	7415.335	9418.397	0	0	0
Q9NZW5	MAGUK protein MPP6	104955.6	109762.3	168916.3	0	0	0
Q9NZZ3	Charged residue CHMP5	126970.7	115832.5	112177	0	0	0
Q9P0K7	Ankyrin repeat RAI14	4076.129	3193.573	9055.415	0	0	0
Q9P0M6	Core histone H2AFY2	30912.14	31753.04	9569.057	0	0	0
Q9P0V3	SH3 domain SH3BP4	68998.48	68491.56	81692.06	0	0	0
Q9P0V9	Septin-10 10-Sep	15907.21	14362.84	29123.93	0	0	0
Q9P1F3	Costar for ABRACL	33339.91	25922.86	96952.87	0	0	0
Q9P206	Uncharacterized KIAA1522	2220.069	2039.025	1279.439	0	0	0
Q9P258	Protein RC RCC2	53020.53	54340.09	32612.67	0	0	0
Q9P270	SLAIN motif SLAIN2	14578.03	13672.23	16794.43	0	0	0

Q9P273	Teneurin-3 TENM3	7558.307	4827.65	12037.94	0	0	0
Q9P287	BRCA2 and BCCIP	7823.381	8754.104	10978.46	0	0	0
Q9H299	SH3 domain SH3BGR13	99406.48	85571.26	308345.6	470359	690882.8	355954
Q9P289	Serine/threonine STK26	65078.55	62072.19	67456.63	0	0	0
Q9P210	Cleavage site CPSF2	607566.7	32400.87	402499.1	0	0	0
Q9P2J5	Leucine-rich LARS	18826.53	19506.21	19116.81	0	0	0
Q9P2P6	Star-related STARD9	28842.53	42730.47	30552.03	0	0	0
Q9UBB4	Ataxin-10 ATXN10	15494.08	19953.09	8632.034	0	0	0
Q9UBB6	Neurochorion NCDN	4276.531	3497.901	4284.457	0	0	0
Q9UBC2	Epidermal EPS15L1	6768.992	6964.585	13674.44	0	0	0
Q9UBF8	Phosphatidylinositol PI4KB	2321.448	2038.671	3166.524	0	0	0
Q9UBH6	Xenotropic XPR1	10942.2	9578.389	8816.36	0	0	0
Q9UBP9	PTB domain GULP1	9656.21	10619.27	10999.43	0	0	0
Q9UBQ0	Vacuolar protein VPS29	24545.4	21849.51	25385.51	0	0	0
Q9UBQ5	Eukaryotic EIF3K	53923.41	49676.66	42876.96	0	0	0
Q9UBS4	DnaJ homolog DNAJB11	19736.93	23690.67	22826.3	0	0	0
Q9UBT2	SUMO-actin UBA2	13838.1	15031.11	16548.53	0	0	0
Q9UBW8	COP9 signal COPS7A	5081.251	3343.693	4133.796	0	0	0
Q9UDY4	DnaJ homolog DNAJB4	3001.214	4197.842	3847.875	0	0	0
Q9H4B7	Tubulin beta TUBB1	203541.6	183397.6	304742.6	3927363	1112367	5073463
Q9H4F8	SPARC-related SMOC1	13612.74	15965.35	13338.2	154725.4	0	79816.55
Q9UEY8	Gamma-aminobutyrate ADD3	14011.61	15068.19	22188.5	0	0	0
Q9H4G4	Golgi-associated GLIPR2	81750.34	69491.4	103958.5	121954.1	179785.7	145865.8
Q9UG63	ATP-binding ABCF2	15879.47	15207.28	15855.75	0	0	0
Q9UGH3	Solute carrier SLC23A2	30804.94	26326.54	28127.75	0	0	0
Q9UGI8	Testin TES	6743.383	7959.904	12186.72	0	0	0
Q9UGJ0	5-AMP-activated PRKAG2	9487.798	9070.77	10861.9	0	0	0
Q9UGJ1	Gamma-tubulin TUBGCP4	5555.166	5277.444	5712.394	0	0	0
Q9UGQ3	Solute carrier SLC2A6	15077.43	15502.07	11026.27	0	0	0
Q9UH17	DNA double-strand break APOBEC3E	6900.87	7369.958	5425.729	0	0	0
Q9UHA4	Ragulator subunit LAMTOR3	11707.28	12126.56	16582.26	0	0	0
Q9UHB6	LIM domain LIMA1	26955.28	24577.5	45880.77	0	0	0
Q9UHB9	Signal receptor SRP68	15377.81	19273.56	10223.08	0	0	0
Q9UHD1	Cysteine aminochord C1	51868.78	37217.52	11422.89	0	0	0
Q9UHD2	Serine/threonine TBK1	1566.805	1099.78	1641.567	0	0	0
Q9UHE8	Metalloregulator STEAP1	33058.97	31424.49	76406.95	0	0	0
Q9H853	Putative tubulin TUBA4B	912512.8	875492.2	858057.8	4566328	1709119	5628501
Q9UHI6	Probable transcription factor DDX20	9960.892	5756.188	1269.205	0	0	0
Q9UHR4	Brain-specific BAIAP2L1	27770.41	23843.79	31421.62	0	0	0
Q9UHV9	Prefoldin subunit PFDN2	19673.46	15400.6	17054.78	0	0	0
Q9UHW9	Solute carrier SLC12A6	3745.142	5794.336	35425.55	0	0	0
Q9UHX1	Poly(U)-binding PUF60	51616.43	63539.29	56712.16	0	0	0
Q9UHY7	Enolase-phosphoenolpyruvate ENOPH1	6483.075	5815.424	11460.61	0	0	0
Q9UHY8	Fasciculation FEZ2	1562.258	2639.59	1036.628	0	0	0
Q9UI10	Translation initiation EIF2B4	16441.72	19353.27	8517.958	0	0	0
Q9UI12	V-type proton-activated ATP6V1H	12750	14761.07	8999.884	0	0	0
Q9UI26	Importin-1 IPO11	8554.873	8279.121	7824.343	0	0	0
Q9UI30	Multifunctional TRMT112	16830.08	18384.4	21864.26	0	0	0
Q9UIA9	Exportin-7 XPO7	7154.179	7691.866	5402.095	0	0	0
Q9UIK4	Death-associated DAPK2	28402.23	29705.14	35696.49	0	0	0
Q9UIQ6	Leucyl-cysteine LNPEP	48562.99	48752.7	41771.02	0	0	0
Q9UIW2	Plexin-A1 PLXNA1	65356.93	38674.73	80432.85	0	0	0
Q9UJ68	Mitochondrial MSRA	4216.338	3731.81	5129.247	0	0	0
Q9UJU6	Drebrin-like DBNL	21835.04	23729.56	39009.36	0	0	0
Q9UJV9	Probable transcription factor DDX41	6386.313	5654.598	4219.83	0	0	0
Q9HAV0	Guanine nucleotide GNB4	13812.84	14585.75	14475.94	43964.9	0	72563.13
Q9UJW0	Dynactin subunit DCTN4	5178.122	3969.191	1667.226	0	0	0
Q9UJX2	Cell division CDC23	13283.63	14771.9	5989.815	0	0	0

Q9UJX3	Anaphase-ANAPC7	11404.1	8555.256	9028.102	0	0	0
Q9UK41	Vacuolar p VPS28	68520.65	64245.3	72722.86	0	0	0
Q9UK76	Hematoloç HN1	19639.78	15227.88	23620.01	0	0	0
Q9UKD2	mRNA turr MRT04	41643.38	47639.65	20797.58	0	0	0
Q9UKE5	TRAF2 and TNIK	11175.04	9416.789	6687.591	0	0	0
Q9HBI1	Beta-parvi PARVB	114543.8	69598.54	137259.8	0	84116.48	156210.9
Q9UKF6	Cleavage ε CPSF3	3499.21	6256.283	5377.02	0	0	0
Q9UKJ5	Cysteine-r CHIC2	12224.71	14651.47	12524.09	0	0	0
Q9UKK9	ADP-sugaı NUDT5	30546.93	29633.67	34004.59	0	0	0
Q9UKM9	RNA-bindı RALY	13740.29	12424.13	4848.058	0	0	0
Q9UKS6	Protein kin PACSIN3	14877.66	13233.09	17144.23	0	0	0
Q9UKV3	Apoptotic ACIN1	13482.98	13872.29	7687.141	0	0	0
Q9UKZ9	Procollage PCOLCE2	13493.06	7653.859	7196.064	0	0	0
Q9UL15	BAG family BAG5	57689.69	65809.48	43993.59	0	0	0
Q9UL26	Ras-relateı RAB22A	58495.89	54477.64	57345.39	0	0	0
Q9UL46	Proteasom PSME2	15792	21600.95	25715.99	0	0	0
Q9NP79	Vacuolar p VTA1	59260.18	67527.2	71396.95	0	72524.54	61220.77
Q9UL54	Serine/threı TAOK2	3590.896	3968.603	4561.062	0	0	0
Q9ULC4	Malignant MCTS1	2396.597	2389.778	2479.76	0	0	0
Q9ULC8	Probable ç ZDHHC8	6318.376	5484.327	8297.088	0	0	0
Q9ULF5	Zinc transç SLC39A10	41662.43	39636.21	32505.31	0	0	0
Q9NPG4	Protocadh PCDH12	20010.56	15297.36	27033.37	0	215536.9	24885
Q9ULH1	Arf-GAP wı ASAP1	8962.503	5589.185	2652.986	0	0	0
Q9ULK4	Mediator cı MED23	1956.592	2566.705	1344.604	0	0	0
Q9ULP9	TBC1 domı TBC1D24	2638.443	2697.394	3076.484	0	0	0
Q9ULT8	E3 ubiquitiı HECTD1	10887.98	11771.37	14238.15	0	0	0
Q9ULV4	Coronin-1 CORO1C	51550.62	43802.27	32271.58	0	0	0
Q9ULX3	RNA-bindı NOB1	7124.901	5177.372	6389.497	0	0	0
Q9UM54	Unconventı MYO6	2958.54	1183.602	7426.537	0	0	0
Q9UMR5	Lysosomal PPT2	3688.288	3316.292	4489.829	0	0	0
Q9UMS4	Pre-mRNA PRPF19	41165.73	38003.17	17855.34	0	0	0
Q9UMX0	Ubiquilin-ı UBQLN1	8414.053	9539.752	12122.37	0	0	0
Q9UMY4	Sorting neı SNX12	4590.651	5073.751	2661.85	0	0	0
Q9UN42	Protein AT ATP1B4	212630.7	254336.4	261382	0	0	0
Q9UN70	Protocadh PCDHGC3	66787.59	58168.84	50933.5	0	0	0
Q9UN86	Ras GTPası G3BP2	7883.289	7229.499	5686.884	0	0	0
Q9UNF0	Protein kin PACSIN2	28505.19	28047.2	28290.34	0	0	0
Q9NQW7	Xaa-Pro aıı XPNPEP1	34960.92	33615.92	35918.04	0	30603.16	24009.25
Q9UNH7	Sorting neı SNX6	17288.59	16320.45	31480.04	0	0	0
Q9UNK0	Syntaxin-8 STX8	13094.6	5842.75	16298.55	0	0	0
Q9UNK4	Group IID ıı PLA2G2D	16985.97	25896.92	16757.77	0	0	0
Q9UNN5	FAS-assoc FAF1	7352.114	9194.362	13817.29	0	0	0
Q9UNN8	Endothelia PROCR	10504.95	15854.78	14896.15	0	0	0
Q9NR31	GTP-bindıı SAR1A	55313.78	55141.13	84428.92	94917.96	95572.46	164484.4
Q9UNQ0	ATP-bindıı ABCG2	10987.69	10114.38	12186.49	0	0	0
Q9UNQ2	Probable cı DIMT1	2345.733	2288.563	2366.27	0	0	0
Q9UNS2	COP9 signı COPS3	26218.49	12015.04	15175.66	0	0	0
Q9UNX4	WD repeatı WDR3	4696.885	6047.251	2914.371	0	0	0
Q9UNY4	Transcriptıı TTF2	647.9667	606.8552	1230.109	0	0	0
Q9UNZ2	NSFL1 cofıı NSFL1C	6877.656	7025.665	7024.483	0	0	0
Q9UP38	Frizzled-1 FZD1	5328.637	5364.108	3735.022	0	0	0
Q9UPN3	Microtubuıı MACF1	8862.91	9158.979	10046.38	0	0	0
Q9UPT5	Exocyst coıı EXOC7	11125.06	12704.72	18785.99	0	0	0
Q9UPU5	Ubiquitin cıı USP24	4194.098	4856.782	4726.059	0	0	0
Q9UPY3	Endoribonııı DICER1	1920.612	1791.641	967.1083	0	0	0
Q9UPY5	Cystine/glıı SLC7A11	85184.68	83623.2	121864.4	0	0	0
Q9NRY6	Phospholiğııı PLSCR3	19379.75	18727.71	37508.18	1263432	0	474169.8
Q9UQ13	Leucine-riııı SHOC2	6544.505	8333.119	15793.33	0	0	0

Q9UQ35	Serine/arg SRRM2	19972.09	22991.02	7160.061	0	0	0
Q9UQ49	Sialidase-3 NEU3	1415.581	2129.246	1889.548	0	0	0
Q9UQB8	Brain-spec BAIAP2	67170.27	60987.17	82162.27	0	0	0
Q9UQE7	Structural i SMC3	16065.52	15875.64	19949.67	0	0	0
Q9Y223	Bifunctional GNE	28223.34	24175.44	15219.06	0	0	0
Q9Y224	UPF0568 p C14orf166	9194.65	10984.41	8895.224	0	0	0
Q9Y225	RING finger RNF24	5535.966	4991.042	1859.168	0	0	0
Q9Y266	Nuclear miNUDC	24990.1	28379.74	40688.74	0	0	0
Q9Y277	Voltage-dependent VDAC3	7485.912	11429.98	11310.21	0	0	0
Q9Y287	Integral membrane ITM2B	90322.21	87319.08	63450.31	0	0	0
Q9Y295	Developmental DRG1	8450.423	9905.567	11685.4	0	0	0
Q9Y296	Trafficking TRAPPC4	9274.052	9382.205	14397.4	0	0	0
Q9Y2D4	Exocyst component EXOC6B	11172.06	11047.88	9724.313	0	0	0
Q9Y2D5	A-kinase anchor AKAP2	38587.55	35300.59	78126.91	0	0	0
Q9Y2E4	Disco-integrin DIP2C	4076.285	3885.497	3855.079	0	0	0
Q9Y2H0	Disks large DLGAP4	6341.595	8876.048	8472.754	0	0	0
Q9Y2H1	Serine/threonine STK38L	4651.881	5399.29	7060.002	0	0	0
Q9Y2I8	WD repeat WDR37	8808.397	8647.377	13376.6	0	0	0
Q9Y2L1	Exosome component DIS3	5674.29	6076.147	2821.758	0	0	0
Q9Y2P8	RNA 3-terminal RCL1	7642.699	8138.83	6085.356	0	0	0
Q9Y2U9	Kelch domain KLHDC2	2232.269	2769.281	2783.35	0	0	0
Q9Y2V2	Calcium-regulated CARHSP1	18703.29	16239.64	21623.92	0	0	0
Q9Y2W1	Thyroid hormone THRAP3	21631.22	20228.45	18651.69	0	0	0
Q9Y2W2	WW domain WBP11	6662.145	8207.435	4291.764	0	0	0
Q9Y2X3	Nucleolar protein NOP58	35232.93	41130.2	20431.04	0	0	0
Q9Y2Z0	Protein SG SUGT1	7326.081	8253.566	2826.663	0	0	0
Q9Y303	Putative N AMDHD2	12274.93	11299.2	13856.11	0	0	0
Q9Y316	Protein MEMO1	21555.1	20723.59	23585.18	0	0	0
Q9Y333	U6 snRNA LSM2	23145.59	20409.79	21465.82	0	0	0
Q9Y365	PCTP-like STARD10	9991.161	10955.24	10362.16	0	0	0
Q9Y371	Endophilin SH3GLB1	7638.683	5684.112	7891.767	0	0	0
Q9Y383	Putative RILUC7L2	18840.34	14957.79	15809.56	0	0	0
Q9Y397	Palmitoyltransferase ZDHHC9	7154.45	3457.151	5540.795	0	0	0
Q9Y3A5	Ribosome SBDS	16161.34	15213.77	15902.97	0	0	0
Q9Y3A6	Transmembrane TMED5	11175.97	10655.92	8074.798	0	0	0
Q9Y3B4	Splicing factor SF3B6	26659.84	24161.05	36615.6	0	0	0
Q9Y3B8	Oligoribonuclease REXO2	13819.55	16703.34	13680.78	0	0	0
Q9Y3D0	Mitotic spindle FAM96B	7677.434	9920.827	12289.98	0	0	0
Q9Y3D6	Mitochondrial FIS1	3474.034	7831.838	6761.915	0	0	0
Q9Y3E1	Hepatoma HDGFRP3	6900.028	14208.34	5743.88	0	0	0
Q9Y3E7	Charged residue CHMP3	28037.32	25242.7	30632.49	0	0	0
Q9Y3F4	Serine-threonine STRAP	26826.28	24649.07	20547.83	0	0	0
Q9Y3I0	tRNA-splicing RTCB	31752.18	31808.12	31192.38	0	0	0
Q9Y3I1	F-box only FBXO7	15806.59	12017.37	20924.47	0	0	0
Q9Y3T9	Nucleolar protein NOC2L	9633.896	12354.52	5819.675	0	0	0
Q9Y446	Plakophilin PKP3	7463.934	6525.536	9012.44	0	0	0
Q9Y450	HBS1-like HBS1L	9326.996	14588.18	37415.01	0	0	0
Q9Y487	V-type proton ATP6V0A2	7057.419	6990.709	5500.22	0	0	0
Q9Y4A5	Transforming TRRAP	2609.876	3608.908	1368.857	0	0	0
Q9Y4B5	Microtubule MTCL1	4402.279	2321.349	3894.444	0	0	0
Q9Y4C2	TRPM8 channel TCAFI	10085.95	9845.835	11049.09	0	0	0
Q9NZN3	EH domain EHD3	390964.2	329930.6	402656	157525	161339	250372.8
Q9Y4D1	Dishevelled DAAM1	19290.79	16194.87	16940.38	0	0	0
Q9Y4D7	Plexin-D1 PLXND1	4233.472	1583.527	5062.01	0	0	0
Q9Y4E8	Ubiquitin conjugase USP15	6779.261	9090.363	6331.83	0	0	0
Q9Y4G6	Talin-2 TLN2	3620.685	7447.867	11526.06	0	0	0
Q9Y4I1	Unconventional MYO5A	7797.313	8092.473	3278.995	0	0	0
Q9NZT1	Calmodulin CALML5	2712.424	2593.861	0	735275.8	0	546168.8

Q9Y4L1	Hypoxia up HYOU1	37257.07	31451.16	31320.3	0	0	0
Q9Y4P1	Cysteine p ATG4B	12952.66	17766.55	15980.51	0	0	0
Q9Y4R8	Telomere I TELO2	1567.351	4520.45	3541.742	0	0	0
Q9Y4W2	Ribosomal LAS1L	11449.38	31039.67	7876.046	0	0	0
Q9Y4X5	E3 ubiquitin ARIH1	7286.161	6792.354	4221.693	0	0	0
Q9Y530	O-acetyl- OARD1	6745.291	6142.663	6983.768	0	0	0
Q9Y547	Intraflagell HSPB11	8216.804	7644.542	9902.666	0	0	0
Q9Y561	Low-densi LRP12	435.3206	686.7251	2445.06	0	0	0
Q9Y570	Protein ph PPME1	6488.008	7535.052	9955.345	0	0	0
Q9Y5G0	Protocadherin PCDHGB5	72866.19	102699.5	74338.3	0	0	0
Q9Y5K5	Ubiquitin c UCHL5	26626.44	21144.44	50154.2	0	0	0
Q9P265	Disco-integrin DIP2B	90560.94	77177.22	27733.71	0	109252.7	417751.8
Q9Y5K6	CD2-associated CD2AP	41073.7	34556.86	39868.05	0	0	0
Q9Y5K8	V-type proton ATP6V1D	3363.417	4543.113	6185.585	0	0	0
Q9Y5L0	Transporter TNPO3	6517.321	11054.12	11986.29	0	0	0
Q9Y5M8	Signal receptor SRPRB	9879.026	9435.423	7917.188	0	0	0
Q9P2B2	Prostaglandin PTGFRN	252608.2	227290.3	222765.4	429118	349189.3	619980.5
Q9Y5P4	Collagen type COL4A3BP	9625.08	14939.53	6095.318	0	0	0
Q9Y5P6	Mannose-6-phosphate GMPPB	6717.916	5467.522	8140.43	0	0	0
Q9Y5Q8	General transcription factor GTF3C5	5255.182	5980.972	2614.165	0	0	0
Q9Y5Q9	General transcription factor GTF3C3	2640.629	2842.061	1812.125	0	0	0
Q9Y5R8	Trafficking TRAPPC1	4780.878	3381.582	4767.15	0	0	0
Q9Y5S2	Serine/threonine CDC42BPB	18680.97	18699.29	25788.82	0	0	0
Q9Y5S9	RNA-binding RBM8A	10583.36	11716.52	6995.354	0	0	0
Q9UBF2	Coatomer COPG2	10554.55	11686.05	11996.82	40402.85	85860.48	28727.37
Q9Y5X3	Sorting nexin SNX5	19062.63	18952.5	21344.51	0	0	0
Q9Y5X9	Endothelial LIPG	20066.05	19212.71	25347.01	0	0	0
Q9Y5Y0	Feline leukocyte FLVCR1	11849.7	13341.11	15783.42	0	0	0
Q9Y5Z4	Heme-binding HEBP2	6879.25	7759.283	8834.741	0	0	0
Q9Y606	tRNA pseudouracil PUS1	3351.872	1746.709	8401.955	0	0	0
Q9Y613	FH1/FH2 domain FHOD1	14161.51	13925.01	16585.63	0	0	0
Q9UBR2	Cathepsin CTSZ	26062.27	26083.67	43016.21	533875.4	626240.5	226822.2
Q9Y617	Phosphoserine PSAT1	75571.71	71579.92	65468.96	0	0	0
Q9Y624	Junctional F11R	15552.92	14322.15	22466.36	0	0	0
Q9UBV8	Peflin PEF1	34786.64	30165.56	30045.02	21869.42	0	57074.88
Q9Y639	Neuroplasin NPTN	114053	98921.77	143937.2	0	0	0
Q9UBX5	Fibulin-5 FBLN5	7356.063	7994.052	9551.635	0	85261.71	59463.8
Q9UDY2	Tight junction TJP2	51066.09	54275.73	61803.04	32899.14	0	46084.13
Q9Y653	G-protein GPR56	13332.99	11888.44	11345.13	0	0	0
Q9Y678	Coatomer COPG1	27347.23	24485.52	23796.25	0	0	0
Q9Y6D5	Brefeldin A AARFGEF2	5151.97	7917.854	7435.773	0	0	0
Q9Y6E0	Serine/threonine STK24	46109.2	47766.27	49048.25	0	0	0
Q9Y6M4	Casein kinase CSNK1G3	42375.44	42320.24	49827.24	0	0	0
Q9Y6M5	Zinc transporter SLC30A1	30852.83	29156.51	34534.61	0	0	0
Q9Y6M7	Sodium bicarbonate SLC4A7	85714.52	76757.44	81214.41	0	0	0
Q9Y6W5	Wiskott-Aldrich WASF2	31215.91	29360.03	26326.17	0	0	0
Q9Y6Y8	SEC23-interacting SEC23IP	15963.75	15277.22	15503.23	0	0	0
P17301	Integrin alpha ITGA2	767513.1	785731.1	970905.2	50015.98	51923	45628.58
P26006	Integrin alpha ITGA3	1418164	1282748	1363060	65444	95352.14	98118.67
P08195	4F2 cell-surface SLC3A2	2418343	2359517	3298207	224560.8	200606.7	295840.9
P05023	Sodium/potassium ATP1A1	1143400	1113538	1695458	73673.88	208159.9	112211
P11166	Solute carrier SLC2A1	3220119	3038320	3253443	389148.1	203733	585202.5
P62805	Histone H4 HIST1H4A	17725896	18606074	26169028	1319124	5238356	2664199
Q9UHD8	Septin-9 9-Sep	126456.9	131367.1	219652.8	69914.99	25911.91	65536.16
P19338	Nucleolin NCL	1372812	1294508	668611.2	228344.8	130208.5	161819.3
P39060	Collagen alpha COL18A1	1292395	1161471	1248117	152962.1	246012.4	199019.7
P07947	Tyrosine-phosphatase YES1	175107.3	168687.3	192488.1	25294.37	0	33762.27
P0C0S8	Histone H2 HIST1H2A	16857260	18518462	19147556	1617089	4094493	3721678

Q9Y2A7	Nck-associ NCKAP1	92695.18	94651.48	109446.6	18227.92	0	16128.25
P07355	Annexin A: ANXA2	4702163	4581006	6323468	943532.4	759536.7	1043306
P62330	ADP-ribos ARF6	284563.2	275373.2	386130.4	68841.8	0	42646.13
Q5TEC6	Histone H ₂ : HIST2H3P	17955280	16804618	13234686	2510084	2961339	3398035
Q06323	Proteasom PSME1	50929.96	51767.05	67013.4	15101.39	0	6016.05
P05556	Integrin β : ITGB1	2524848	2305220	2817792	460622.6	438754.5	536648.9
Q7L576	Cytoplasm CYFIP1	130264.9	125245.2	139131.9	22524.39	21223.2	30570.35
P35241	Radixin RDX	2331139	2132193	3719661	590720.6	0	491819.5
Q99808	Equilibrativ SLC29A1	301567.4	274409.1	318957.7	47406.21	0	73315.46
Q8WUM4	Programm PDCD6IP	510166.1	487439.6	521111.1	88995.02	59865.63	160786.5
Q9UID3	Vacuolar p VPS51	7049	4722.007	7755.131	0	103561.2	74403.73
O75954	Tetraspani TSPAN9	276055.7	250521.3	238216.4	40375.2	0	65267.51
P35613	Basigin BSG	1000650	1036354	1261135	111841.6	370525.9	229997.5
P06899	Histone H ₂ : HIST1H2B1	884625.8	1155184	1243283	100599.7	344947.4	268551.1
Q9NQH7	Probable XPNPEP3	1347180	1368770	1014047	277034.8	278955.9	274383.6
P07910	Heterogen HNRNPC	262481.3	265506.8	219167.8	53965.45	64064.68	49368.46
P07737	Profilin-1 PFN1	1362523	1490871	2413250	570275.9	414578.3	246133.2
Q15102	Platelet-ac PAFAH1B3	139071.2	141275.9	154006.4	0	38401.33	29813.59
P13612	Integrin α : ITGA4	106080	103023.8	99833.48	0	27137.66	22112.88
P23528	Cofilin-1 CFL1	1072062	1144262	1699778	353840.9	230560.1	369754.2
P11142	Heat shock HSPA8	2142964	2009889	2392907	505054.3	444828.1	651406.8
P00441	Superoxid ϵ SOD1	103538	80701.97	143781.4	497276.2	522567.7	300515.3
Q76LX8	A disintegr ADAMTS1:	83956.8	79791.93	88720.79	333701	390530.8	298895.4
P02042	Hemoglob HBD	62963804	55685136	5651221	1.64E+08	1.74E+08	1.67E+08
Q12884	Prolyl end ϵ FAP	54246.72	53377.14	60085.74	232141.7	228566.4	229654.2
O95445	Apolipop α : APOM	679111.4	616984.2	630787.3	2831498	3249384	1914968
P11717	Cation-inc IGF2R	88431.32	96854.97	88997.86	424402.3	403580.5	348016.4
O43505	Beta-1,4- ϵ B4GAT1	31918.36	28246.16	32451.37	163779.5	137959.4	101226.5
P22626	Heterogen HNRNPA2	59449.28	58511.17	57703.97	286667.9	283283.8	208013.1
Q9NQC3	Reticulon- RTN4	199397.7	231236	162325.9	990735.6	831440.5	818230.7
Q9UKU9	Angiopoie ANGPTL2	11324.54	10651.24	11744.76	103427.5	0	205318.1
P11362	Fibroblast FGFR1	37516.85	22701.74	26479.6	118196.1	179770.2	90240.34
Q6YHK3	CD109 ant CD109	84161.85	77969.13	117264.5	443494.6	511132.1	318346.5
P07225	Vitamin K- PROS1	506502.8	499388.5	505405.3	2482576	2928418	1551278
P01344	Insulin-like IGF2	328239.8	312452.3	416989.9	1340448	2355847	1486736
Q02818	Nucleobin ϵ NUCB1	24912.48	25748.55	33990.87	134929.5	173293.9	115882
Q15493	Regucalcin RGN	42209.29	37593.59	61970.07	175878.1	294994	258608.3
O43286	Beta-1,4- ϵ B4GALT5	53203.26	52680.75	71916.67	295101.6	376298.9	244293.5
P20908	Collagen α COL5A1	137241.4	148345.2	168522.8	727181.1	987781.4	637353.9
P05452	Tetranectin CLEC3B	609272.6	530378.4	327860.1	2183074	2862270	2648154
O00754	Lysosomal MAN2B1	38154.37	36078.63	42585.57	213196	275519.8	149103.6
P02656	Apolipop α : APOC3	313106.1	290007	328424	1624285	2062006	1517510
Q02809	Procollage PLOD1	15960.79	31915.6	31394.7	138342.7	165899.1	140330.6
O95197	Reticulon- RTN3	18295.41	17544.29	12127.12	104513.2	61486.48	103020
O00391	Sulfhydryl QSOX1	208641.1	214637.2	122032.6	1010303	1379340	784346.1
Q14624	Inter- α : ITIH4	32244.22	34254.26	47027.65	210113.4	258568	202851.2
Q9UM47	Neurogeni NOTCH3	22023.17	16615.4	23354.2	0	120623.2	54712.08
P12111	Collagen α COL6A3	1709215	2282623	2275002	8482742	12983499	16302902
Q06033	Inter- α : ITIH3	700481.4	690665.7	1123821	5470790	6167389	3656485
P16930	Fumarylac ϵ FAH	19621.73	12686.22	20351.3	110371	138357.7	78087.6
Q8IUL8	Cartilage ir CILP2	16682.08	24541.64	44959.87	212758	166226.9	168581.3
P10643	Compleme C7	134286.8	135793.8	174461.7	805346.6	1131515	930895.1
Q9UN37	Vacuolar p VPS4A	54627.77	54264.81	57122.13	50112.12	35106.15	57587.57
P01008	Antithromb SERPINC1	4766346	4003508	5519488	30211412	40719696	21346772
P05543	Thyroxine- SERPINA7	190778.1	182085.8	306934.1	1435918	1952742	1097828
P19823	Inter- α : ITIH2	4788535	4935901	5673047	34503536	42908024	26339244
P11177	Pyruvate d PDHB	37435.7	2773.796	62267.68	216935.8	314982.9	160104.5
P12110	Collagen α COL6A2	1476718	1840149	1831700	8113221	12491387	14542009

Q93088	Betaine--r BHMT	29350.78	31528.52	30788.92	216999.3	266992.1	143047.1
P36955	Pigment e; SERPINF1	1068730	1009033	1109932	6594453	9604032	5833403
Q9UNM6	26S protea PSMD13	42130.59	41753.69	71032.75	56780.98	0	61337.15
P13591	Neural cell NCAM1	59334.34	54645.97	74095.45	405040.1	585858.6	315098.7
P01621	Ig kappa chain V-III re	55183.97	56574.87	77534.22	490984.3	452385.6	392804
Q9UNP9	Peptidyl-p PPIE	156001.9	131365.4	161764.3	318547.6	381440.6	282898.7
P19827	Inter-alpha; ITIH1	505180.7	447682.1	701345.1	3924111	5111713	2982691
Q9H6B4	CXADR-lik CLMP	633731.9	34850.95	853204.8	4471939	0	3086545
O75144	ICOS ligand ICOSLG	28463.61	27953.37	48256.99	261061.1	344439.5	174962.5
Q9UBG0	C-type mannose MRC2	16117.55	15776.69	22344.95	98426.73	154751.3	156549.5
P04745	Alpha-amyloid AMY1A	70288.57	67731.78	114492.6	620849.6	870071.3	442593.3
Q06828	Fibromodulin FMOD	52577.25	50839.21	84825.63	472282	639771.8	355573.4
Q9UK55	Protein Z--r SERPINA10	22693.47	64934.28	61235.3	349665.4	471716.7	349283.9
P04278	Sex hormone SHBG	103391.1	103848.4	144360.9	784091.8	1257457	741959.2
Q9Y5C1	Angiopoietin ANGPTL3	17972.7	10048.6	9539.013	113178.1	0	92974.05
P26927	Hepatocyte MST1	56215.62	48484.9	74624.18	496300.6	651340.6	337064.9
Q15582	Transforming TGFB1	452542.8	441187.7	532175	3156945	4577377	4117508
Q8NBS9	Thioredoxin TXNDC5	6293.403	7270.03	8989.331	59496.86	79353.56	49275.71
P05090	Apolipoprotein APOD	149765.5	148953.4	90016.27	709488.9	1354631	1194718
Q9UQ16	Dynamin-1 DNMT3	35334.26	31251.9	43131.11	97435.65	63464.75	119591.4
P30086	Phosphatidylethanolamine PEBP1	35021.92	74831.73	125280.8	864857.3	749178.4	378717.7
P01034	Cystatin-C CST3	34679.86	27897.74	79011.68	478651.9	357385.6	371644
Q9UQ80	Proliferating cell PA2G4	50469.41	47872.56	48229.82	13828.51	0	30537.7
Q9NPH3	Interleukin IL1RAP	61980.45	55907.94	66007.57	534726.8	630523.4	404219
P0C0L4	Complement C4A	476880.3	453851.1	462934.9	3976250	4735114	3259220
Q9NRN5	Olfactory receptor OLFML3	37414.19	37948.1	29066.78	246114.2	344209.4	317987
Q13822	Ectonucleoside ENPP2	23506.57	21434.17	27245.82	174375.2	226232	231670.7
Q13163	Dual specific MAP2K5	2658685	2525683	4508393	27340140	38997316	18936590
Q9Y230	RuvB-like 1 RUVBL2	105767	88974.45	98925.13	15991016	32627920	83068.62
Q9Y240	C-type lectin CLEC11A	0	4778.633	4941.86	101042.9	0	52002
Q9Y262	Eukaryotic EIF3L	60401.45	71224.59	52972.09	21255.54	0	20137.19
Q9Y265	RuvB-like 1 RUVBL1	92255.51	86076.27	72619.86	91734.94	0	177367.7
P13798	Acylamino acid APEH	19463.6	19356.99	28110.1	203079	255145	130696.7
Q16610	Extracellular matrix ECM1	31899.64	29564.35	26759.29	209460.7	256405.7	324061.6
Q9Y281	Cofilin-2 CFL2	458942.9	382561.2	561567.9	682974.3	457304.1	446995.5
Q16853	Membrane associated AOC3	86636.41	82270.02	153491.5	1155179	1155577	600363.4
P00488	Coagulation factor F13A1	362438.1	395478	350410.1	2800774	2963346	4349714
Q14764	Major vault MVP	86076.75	97860.55	78336.94	765741.1	804876	841241
Q15063	Periostin POSTN	194967.5	200896.5	210273.8	1602861	2226877	1816469
P20849	Collagen alpha COL9A1	14502.1	9040.732	19211.5	141804.7	173300.7	92944.56
Q16674	Melanoma MIA	10735.96	9039.338	12475.61	89204.71	140415.5	80642.96
Q7KZ85	Transcriptin SUPT6H	418647.8	15683663	15164988	1.03E+08	1.32E+08	80323176
P05155	Plasma protein SERPING1	322328.6	286477.8	818767.6	4814396	6697312	3028103
P62995	Transforming TRA2B	77612.43	84689.4	38056.85	530145.9	843934.4	670002.1
P04003	C4b-binding protein C4BPA	109084.7	154685	119106	1036900	1155821	1730243
Q9Y2J2	Band 4.1-like EPB41L3	23678.55	34923.91	53992.3	0	1999146	902620.4
O60888	Protein Cu CUTA	107220.1	211805.8	362041.8	2194230	2946819	1880132
O00469	Procollagen PLOD2	17670.58	19193.98	19255.42	195423.5	219409.1	167949.8
Q9BY76	Angiopoietin ANGPTL4	11198.43	14809.25	10297.15	119535.9	91896.05	168165.9
P28065	Proteasome PSMB9	4626.196	3201.66	0	48954.49	0	34380
P27635	60S ribosome RPL10	42354.66	34087.36	1541.579	370579.1	0	196406.8
O43852	Calumenin CALU	18922.84	19827.75	16235.58	217148.3	230224.7	153953.6
Q96CG8	Collagen type I CTHRC1	4457.928	6510.347	9945.789	76020.31	64791.75	88464.18
P35443	Thrombospondin THBS4	316100.3	293761.5	508770.1	4121698	5082330	3146594
Q8WUJ3	Cell migration CEMIP	12105.5	13122.13	11033.34	146531.9	116685.5	141083.8
P78539	Sushi repeat SRPX	24620.93	28695.16	27634.35	389804.3	232763.3	283262.5
P02774	Vitamin D-binding GC	2663630	2426236	3618333	30924030	44400800	23247808
P55285	Cadherin-1 CDH6	21522.69	21891.8	25694.04	263199.5	355019.1	180554.9

P01024	Complement C3	1460696	1432789	1867558	19360314	23938682	11885536
P35908	Keratin, type KRT2	236661.3	403122.5	399706.5	3921650	4317927	3845191
P02649	Apolipoprotein APOE	195431.7	199100.2	161136.3	2960874	2121512	1423429
P03956	Interstitial MMP1	18279.94	16823.75	8387.482	245802.8	156423.7	120538.1
P04275	von Willebrand factor VWF	14095.51	11979.37	10231.3	174714.3	137147.3	129039.4
P48740	Mannan-binding protein MASP1	33494.48	44638.31	43197.39	544179.4	468809.7	546199.8
Q9H583	Heat shock protein HEATR1	45517.79	62335.66	3029.333	460353.1	0	492470
P02100	Hemoglobin HBE1	4799.589	5216.321	2722.854	47252.03	70522.69	49799.61
O60462	Neuropilin NRP2	2505.032	0	9190.39	95607.87	100312.9	46468.12
Q8N1N4	Keratin, type KRT78	6412.556	2070.525	8043.26	100808.7	71649.63	60882.41
P07942	Laminin subunit LAMB1	89765.6	93028.2	98464.92	1245133	1898862	1111659
P04114	Apolipoprotein APOB	239361.6	241222.1	120166.7	3385774	3458774	2642429
Q9Y6C2	EMILIN-1 EMILIN1	15354.67	13681.09	29355.27	256856.4	238170.1	430163.6
P02753	Retinol-binding protein RBP4	394573.4	344734.2	623915.1	7708837	8963601	5013635
P07093	Glia-derived protein SERPINE2	28262.34	32126.51	27248.47	457769.6	469718.5	506453.9
Q15113	Procollagen PCOLCE	282623.8	267152.7	291200.6	4340181	5408422	4506807
Q9Y3U8	60S ribosomal protein RPL36	61049.11	54447.64	60845.18	88326.1	0	59096.22
P23142	Fibulin-1 FBLN1	227986.9	229035.9	272713	4094277	5281919	3169619
Q9P2D3	Heat shock protein HEATR5B	120032.4	119397.9	108155.2	1624527	2242156	2293727
P35527	Keratin, type KRT9	51162.33	74707.61	69306.51	1450968	1080219	952070.8
Q9Y490	Talin-1 TLN1	405767	389809.6	492111.8	683451.7	546153.9	838229.5
P02461	Collagen alpha COL3A1	164195	146874.8	189176.3	2539115	3970310	2653301
B9A064	Immunoglobulin IGLL5	509497.2	383514.8	91080.27	5589226	8012192	4820024
Q16270	Insulin-like growth factor binding protein IGFBP7	71933.32	67457.21	52883.11	1170431	1688007	859752.2
Q9UGM3	Deleted in DMBT1	53977.32	52301.11	86360.84	1620548	1058128	1228339
Q9Y4K0	Lysyl oxidase LOXL2	30834.38	20582.17	58229.82	642683.1	872959.6	732888.2
P11047	Laminin subunit LAMC1	43141.76	45385.11	33458.88	769181.1	1185000	722636.9
P16035	Metalloproteinase TIMP2	34051.12	26987.55	44401.63	674719.6	1076181	594139.3
Q99715	Collagen alpha COL12A1	327865	352253.7	559795.8	9335523	8199789	12020047
Q8NBJ4	Golgi marker GOLM1	11156.83	11130.53	20891.48	317513.1	487378.2	232587.2
O60687	Sushi repeat SRPX2	6443.053	11361.23	0	290020.5	141376.2	212756.8
P16112	Aggrecan ACAN	19339	16733.25	28792.94	482052.2	648320.6	522338.6
Q14112	Nidogen-2 NID2	12229.89	12323.13	16664.03	272059	382887.5	446308
P07996	Thrombospondin THBS1	4647480	4451297	5842345	1.2E+08	1.42E+08	1.49E+08
P35442	Thrombospondin THBS2	526720.4	488022.5	670270.8	12761292	16182934	18263486
P39059	Collagen alpha COL15A1	14759.98	12442.76	17309.9	299284.7	425056.8	527137.8
P12109	Collagen alpha COL6A1	896933.5	1014577	1008699	26611642	37608784	19312486
Q9HDC9	Adipocyte APMAP	151889.5	192749.3	112607	5043623	4710812	3572824
P24821	Tenascin TNC	50235.55	49699.26	35778.46	1014257	1299209	1850307
P04216	Thy-1 marker THY1	23922.44	12514.2	16217.75	475917.8	514798.4	711335.2
P22105	Tenascin-like TNXB	3617.019	4243.569	5928.853	133076.1	178456.4	164121.3
O00622	Protein C CYR61	17677.45	17802.88	23535.44	802018.5	495080.8	812536.9
P08476	Inhibin beta INHBA	0	5197.681	10939.9	277860.4	344188.5	247076.1
Q96RW7	Hemicentin HMCN1	2002061	1316392	456945.7	47601024	65044392	31404530
Q9Y2X7	ARF GTPase GIT1	39463	0	5839.761	832881.3	749694.8	1166966
P98160	Basement membrane HSPG2	11533.94	12189.61	15455.77	403314.8	502427	701589.1
P02679	Fibrinogen FGG	14396.19	8738.482	0	652600.9	323055.3	578729.3
P12107	Collagen alpha COL11A1	13401.54	9105.533	13808.45	437364.8	787103.4	418072.1
P21810	Biglycan BGN	142554.8	163235.5	32047.4	3712922	6318149	5764266
P00747	Plasminogen PLG	65799.84	42791.73	28070.79	2657273	3331337	1611935
Q06203	Amidophorin PPAT	48048.98	40914.59	50149.23	2732075	3298194	1831235
O76061	Stanniocalcin STC2	9554.738	9937.08	15004.1	538649.4	736076.5	779267.9
Q7Z7G0	Target of rapamycin ABI3BP	6613.879	4360.13	7665.847	423851.2	473071.2	380172.4
Q9Y5X1	Sorting nexin SNX9	24642.95	29898.77	24666.11	49476.39	0	45505.39
P01591	Immunoglobulin JCHAIN	19459.84	22383.03	25127.09	1552234	1854049	1286563
P13611	Versican alpha VCAN	28559.2	12516.74	10714.16	1117257	1469838	1261549
P02768	Serum albumin ALB	1.79E+08	1.7E+08	2.76E+08	1.87E+10	1.72E+10	1.31E+10
Q03181	Peroxisomal protein PPARD	1275666	1065821	1048503	95690448	1.2E+08	55573584

P28300	Protein-lys LOX	0	4308.46	5109.609	363726.5	517392.3	254507.6
P26022	Pentraxin- PTX3	40049.98	40606.29	67100.88	5258973	5900698	4052882
O94823	Probable γ ATP10B	9190.244	4980.997	0	592786.6	886658.8	752521.8
P05121	Plasminog. SERPINE1	29257.05	30834.24	26161.72	3233969	3739385	2250639
Q9Y625	Glypican- ϵ GPC6	20526.23	20956.32	23768.65	0	39932.67	69858.97
P02452	Collagen a COL1A1	553586.2	476121.7	462167.4	43402192	60887532	57844964
P02765	Alpha-2-I AHSG	5372146	4324859	1555995	5.4E+08	4.82E+08	2.35E+08
P08123	Collagen a COL1A2	178706.1	155650.4	196682.5	16283200	22820206	22035850
Q9Y696	Chloride ir CLIC4	141049.3	125251.3	224734.3	28295.85	0	84226.45
P08253	72 kDa typ MMP2	37986.8	41034.19	57607.25	4767561	7582943	4855409
P05231	Interleukin IL6	3590.816	0	4072.08	417961.8	593040.3	466689.3
P02751	Fibronectin FN1	1397371	1967063	1319067	1.76E+08	2.1E+08	2.49E+08
Q9Y6E2	Basic leucic BZW2	27060.27	24717.64	26923.99	1457851	3367015	0
Q9Y6G9	Cytoplasm DYNC1LI1	13511.71	13941.69	13648.13	127102.4	0	36341.48
Q16363	Laminin su LAMA4	1498.716	3211.397	1837.063	413254.1	400325.9	458215.7
P02458	Collagen a COL2A1	74464.75	75385.46	69313.3	20690848	19684960	9763341
Q7Z3U7	Protein MCMON2	14614.68	8191.886	26182.75	4238394	4733293	2830150
P17936	Insulin-like IGFBP3	1548.717	0	5417.156	2017370	1273004	1964008
Q9NR30	Nucleolar DDX21	60305.28	71457.16	41317.84	59828184	63204688	35631700

MNNG.vs.(	MNNG.vs.(	MNNG.vs.(	MNNG.vs.(	MNNG.vs.(	GO_NUM	GO_Descri	KEGG_Des	KEGG_EC
#NAME?	0	#NAME?	Significant down	--	--	collagen, t	--	--
#NAME?	0	#NAME?	Significant down		1	Molecular decorin	--	--
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#NAME?	0	#NAME?	Significant down		3	Cellular Cc C-X-C mo	--	--
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#NAME?	0	#NAME?	Significant down		3	Cellular Cc C-X-C mo	--	--
#NAME?	0	#NAME?	Significant down	--	--	--	--	--
#NAME?	0	#NAME?	Significant down	--	--	stonin-1/2	--	--
#NAME?	0	#NAME?	Significant down		4	Molecular lysyl oxidase	1.4.3.-	--
#NAME?	0	#NAME?	Significant down		2	Molecular --	--	--
#NAME?	0	#NAME?	Significant down		3	Molecular a disintegr	3.4.24.-	--
0.249628	0.539458	-2.00215	Nonsignifi	--	--	small nucle	--	--
Inf	0	Inf	Significant up		1	Molecular rRNA smal	2.1.1.260	--
Inf	0	Inf	Significant up	--	--	WAS prote	--	--
0.0481	0.088742	-4.37782	Nonsignifi		2	Molecular componen	3.4.21.47	--
1.446866	0.244285	0.532932	Nonsignifi		5	Molecular translation	--	--
Inf	0	Inf	Significant up		2	Biological p24 family	--	--
Inf	0	Inf	Significant up		3	Biological peptidylpr	5.2.1.8	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular --	--	--
Inf	0	Inf	Significant up	--	--	CCR4-NO	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		4	Molecular --	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
2.872213	0.059345	1.522163	Nonsignifi	--	--	transmemt	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	integrin al	--	--
Inf	0	Inf	Significant up	--	--	eukaryotic	--	--
Inf	0	Inf	Significant up		2	Molecular nicotinate	2.4.2.19	--
0.400422	0.072391	-1.32041	Nonsignifi		2	Molecular --	--	--
Inf	0	Inf	Significant up		1	Molecular kinesin lig	--	--
2.543277	0.033159	1.346689	Nonsignifi		4	Molecular myosin I	--	--
Inf	0	Inf	Significant up		2	Biological transmemt	--	--
Inf	0	Inf	Significant up	--	--	V-type H+	--	--
Inf	0	Inf	Significant up		4	Biological peptidyl-d	3.4.15.1	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.019544	0.332989	-5.67715	Nonsignifi		3	Biological AP-3 com	--	--
Inf	0	Inf	Significant up		2	Biological interleukin	--	--
Inf	0	Inf	Significant up		2	Biological vacuolar p	--	--
0.673281	0.013608	-0.57072	Nonsignifi		1	Molecular 26S protea	--	--
Inf	0	Inf	Significant up		1	Cellular Cc syntaxin 1	--	--
Inf	0	Inf	Significant up	--	--	gamma-gl	4.3.2.9	--
Inf	0	Inf	Significant up		4	Molecular seryl-tRNA	6.1.1.11	--
4.460394	0.081902	2.157171	Nonsignifi		1	Molecular chloride in	--	--
0.146893	0.102786	-2.76716	Nonsignifi		2	Molecular tumor necr	--	--
0.895633	0.341696	-0.15902	Nonsignifi		1	Molecular translation	--	--
Inf	0	Inf	Significant up		2	Molecular deoxyribor	3.1.22.1	--
Inf	0	Inf	Significant up		4	Molecular kinesin far	--	--
Inf	0	Inf	Significant up	--	--	acyl-coenz	3.1.2.2	--
Inf	0	Inf	Significant up	--	--	synaptosol	--	--
0.858789	0.60891	-0.21962	Nonsignifi		1	Molecular importin-5	--	--

Inf		0	Inf	Significant up	--	--	AH receptor	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		2	Biological syntaxin-b	--
Inf		0	Inf	Significant up		1	Molecular galectin-8	--
0.332384	0.001407	-1.58908	Nonsignifi	None		4	Molecular agrin	--
Inf		0	Inf	Significant up		2	Molecular tumor necr	--
Inf		0	Inf	Significant up		1	Molecular 26S protea	--
0.376506	0.060234	-1.40926	Nonsignifi	None		1	Molecular 26S protea	--
Inf		0	Inf	Significant up		2	Biological copper ch	--
Inf		0	Inf	Significant up	--	--	transcriptic	--
Inf		0	Inf	Significant up		2	Molecular NEDD4-like	2.3.2.26
Inf		0	Inf	Significant up		1	Molecular phosphatic	2.7.1.153
Inf		0	Inf	Significant up		1	Molecular Wiskott-AI	--
Inf		0	Inf	Significant up	--	--	RNA 3'-ter	6.5.1.4
3.893783	0.000529	1.961173	Nonsignifi	None		1	Molecular syntenin-1	--
Inf		0	Inf	Significant up		3	Molecular phosphatic	2.7.1.154
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		3	Cellular Cc exocyst co	--
Inf		0	Inf	Significant up		2	Molecular amphiphys	--
Inf		0	Inf	Significant up		5	Molecular --	--
Inf		0	Inf	Significant up		3	Molecular serine/thre	2.7.11.1
Inf		0	Inf	Significant up		2	Biological ubiquitin c	3.4.19.12
Inf		0	Inf	Significant up	--	--	Krev intera	--
Inf		0	Inf	Significant up		2	Cellular Cc pescadillo	--
Inf		0	Inf	Significant up	--	--	nucleolar p	--
Inf		0	Inf	Significant up	--	--	podocalyxin	--
Inf		0	Inf	Significant up		5	Molecular --	--
2.590595	0.004646	1.373283	Nonsignifi	None	--	--	disintegrin	3.4.24.81
Inf		0	Inf	Significant up	--	--	ubiquitin-c	2.3.2.23
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		3	Molecular citron Rho	2.7.11.1
Inf		0	Inf	Significant up	--	--	coatome	--
Inf		0	Inf	Significant up	--	--	carboxy-te	3.1.3.16
Inf		0	Inf	Significant up		1	Molecular --	--
1.651825	0.007507	0.724061	Nonsignifi	None		1	Cellular Cc neuropilin	--
Inf		0	Inf	Significant up		5	Molecular ATP-binding	--
2.148915	0.017583	1.103608	Nonsignifi	None		1	Cellular Cc tetraspanin	--
1.036084	0.74677	0.051141	Nonsignifi	None		5	Molecular 20S protea	3.4.25.1
Inf		0	Inf	Significant up		1	Molecular programm	--
Inf		0	Inf	Significant up		2	Biological type II prot	2.1.1.320
Inf		0	Inf	Significant up		1	Molecular Na(+)/H(+)	--
Inf		0	Inf	Significant up		2	Molecular tumor necr	--
Inf		0	Inf	Significant up		1	Molecular tripeptidyl	3.4.14.9
Inf		0	Inf	Significant up		1	Molecular transcriptic	--
0.778375	0.16124	-0.36146	Nonsignifi	None		1	Molecular myosin reg	--
Inf		0	Inf	Significant up		4	Molecular kinesin fan	--
Inf		0	Inf	Significant up		2	Biological transportir	--
Inf		0	Inf	Significant up		1	Molecular --	--
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
Inf		0	Inf	Significant up		2	Molecular phospholip	3.1.4.4
0.005605	0.306517	-7.47906	Nonsignifi	None	--	--	COPII coat	--
0.396352	0.111351	-1.33514	Nonsignifi	None		2	Molecular plexin B	--

Inf		0	Inf	Significant up	--	--	--	--
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-a
Inf		0	Inf	Significant up		1	Molecular	heterogen
0.556906	0.477973	-0.84449	Nonsignifi	None		4	Cellular	Cc actin relate
4.248635	0.056141	2.086999	Nonsignifi	None		4	Cellular	Cc actin relate
Inf		0	Inf	Significant up		2	Biological	exportin-1
Inf		0	Inf	Significant up		2	Molecular	Rho guanin
Inf		0	Inf	Significant up		1	Molecular	spectrin be
Inf		0	Inf	Significant up		3	Molecular	U2-associ
Inf		0	Inf	Significant up		1	Molecular	synaptojar
0.211323	0.062377	-2.24248	Nonsignifi	None		5	Molecular	laminin, al
Inf		0	Inf	Significant up	--	--	--	phosphoril
Inf		0	Inf	Significant up		1	Molecular	serine/thre
0.259201	0.007279	-1.94786	Nonsignifi	None		1	Cellular	Cc ER-deriv
Inf		0	Inf	Significant up		1	Cellular	Cc Niemann-
Inf		0	Inf	Significant up		2	Molecular	DNA-direc
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	carboxy-te
Inf		0	Inf	Significant up		3	Molecular	Eph recept
Inf		0	Inf	Significant up		3	Biological	prefoldin k
0.791478	0.619169	-0.33738	Nonsignifi	None		1	Molecular	syntaxin 7
Inf		0	Inf	Significant up	--	--	--	--
3.496078	0.002582	1.805737	Nonsignifi	None		2	Cellular	Cc MFS trans
Inf		0	Inf	Significant up		1	Cellular	Cc --
Inf		0	Inf	Significant up		1	Molecular	protein O-
Inf		0	Inf	Significant up		3	Molecular	phosphom
Inf		0	Inf	Significant up		3	Molecular	midline 1
Inf		0	Inf	Significant up	--	--	--	high mobil
Inf		0	Inf	Significant up		1	Molecular	protein ph
Inf		0	Inf	Significant up		2	Biological	importin-E
2.007927	0.007694	1.005707	Nonsignifi	None		3	Biological	--
Inf		0	Inf	Significant up		2	Cellular	Cc MFS trans
Inf		0	Inf	Significant up		3	Molecular	solute carr
0.572042	0.232763	-0.80581	Nonsignifi	None		4	Cellular	Cc 26S protea
Inf		0	Inf	Significant up		2	Cellular	Cc synaptobre
Inf		0	Inf	Significant up		4	Cellular	Cc actin relate
Inf		0	Inf	Significant up		3	Molecular	3-phosphph
0.104489	0.311247	-3.25858	Nonsignifi	None		1	Molecular	--
0.777256	0.171623	-0.36354	Nonsignifi	None		1	Molecular	heterogen
Inf		0	Inf	Significant up		2	Molecular	Arf-GAP w
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	U4/U6 sm
Inf		0	Inf	Significant up		3	Molecular	G protein-
Inf		0	Inf	Significant up	--	--	--	dynein lig
Inf		0	Inf	Significant up		1	Molecular	--
Inf		0	Inf	Significant up		2	Cellular	Cc protein tra
Inf		0	Inf	Significant up		1	Biological	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	--
Inf		0	Inf	Significant up		3	Biological	peptidyl-p
Inf		0	Inf	Significant up	--	--	--	aflatoxin B
Inf		0	Inf	Significant up		5	Molecular	erythrocyt
Inf		0	Inf	Significant up		5	Cellular	Cc ragulator c
Inf		0	Inf	Significant up		2	Biological	exportin-T
Inf		0	Inf	Significant up		3	Biological	protein spi
Inf		0	Inf	Significant up	--	--	--	mitochondr

Inf	0	Inf	Significant up	--	--	trafficking	--
Inf	0	Inf	Significant up		1 Biological	charged m	--
Inf	0	Inf	Significant up		1 Cellular Cc	tetraspanin	--
0.000144	0.493396	-12.7655	Nonsignifi	None	4 Biological	AP-1 com	--
Inf	0	Inf	Significant up		1 Molecular	pleiotropic	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Molecular	cell cycle a	--
Inf	0	Inf	Significant up	--	--	phosphatic	3.1.3.4
Inf	0	Inf	Significant up		2 Molecular	cytohesin	--
Inf	0	Inf	Significant up		1 Molecular	5'-AMP-ac	--
Inf	0	Inf	Significant up		3 Molecular	syntaxin 6	--
0.331658	0.130386	-1.59223	Nonsignifi	None	1 Molecular	--	--
0.803487	0.088019	-0.31565	Nonsignifi	None	3 Molecular	adenosylh	3.3.1.1
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
Inf	0	Inf	Significant up		3 Cellular Cc	origin recc	--
Inf	0	Inf	Significant up		2 Cellular Cc	cohesin co	--
Inf	0	Inf	Significant up		3 Molecular	pre-mRNA	3.6.4.13
Inf	0	Inf	Significant up		3 Molecular	protocadh	--
Inf	0	Inf	Significant up		3 Molecular	--	--
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		1 Molecular	TBC1 dom	--
1.231192	0.0561	0.300055	Nonsignifi	None	1 Molecular	sorting ne	--
Inf	0	Inf	Significant up		3 Molecular	frizzled 6	--
Inf	0	Inf	Significant up		5 Molecular	nucleoside	2.7.4.6
Inf	0	Inf	Significant up	--	--	non-syndr	--
Inf	0	Inf	Significant up		2 Molecular	long-chair	6.2.1.3
Inf	0	Inf	Significant up		3 Molecular	syntaxin 6	--
Inf	0	Inf	Significant up	--	--	--	--
0.647016	0.085562	-0.62813	Nonsignifi	None	2 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	heterogen	--
Inf	0	Inf	Significant up		1 Molecular	pre-mRNA	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		4 Molecular	diaphanou	--
Inf	0	Inf	Significant up		1 Cellular Cc	tetraspanin	--
Inf	0	Inf	Significant up		2 Cellular Cc	exocyst co	--
Inf	0	Inf	Significant up	--	--	perilipin-3	--
Inf	0	Inf	Significant up		2 Cellular Cc	MFS transp	--
3.826674	0.06188	1.936091	Nonsignifi	None	1 Molecular	catenin (ca	--
Inf	0	Inf	Significant up	--	--	type I prot	2.1.1.319
Inf	0	Inf	Significant up		5 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		2 Molecular	translation	--
Inf	0	Inf	Significant up		2 Biological	sorting ne	--
1.870911	0.183914	0.903741	Nonsignifi	None	1 Molecular	histone H2	--
1.093385	0.856104	0.128801	Nonsignifi	None	2 Molecular	H/ACA rib	5.4.99.-
0.385424	0.051541	-1.37548	Nonsignifi	None	1 Molecular	translation	--
Inf	0	Inf	Significant up		6 Cellular Cc	--	--
Inf	0	Inf	Significant up		2 Biological	solute carr	--
Inf	0	Inf	Significant up		2 Cellular Cc	--	--
Inf	0	Inf	Significant up		1 Molecular	putative tri	--

Inf	0	Inf	Significant up	2	Molecular	DnaJ hom	--
Inf	0	Inf	Significant up	3	Biological	prefoldin s	--
Inf	0	Inf	Significant up	2	Molecular	SLIT-ROBC	--
2.19702	0.025322	1.135548	Nonsignifi	1	Molecular	--	--
Inf	0	Inf	Significant up	2	Molecular	plexin A	--
Inf	0	Inf	Significant up	--	--	immunogl	--
0.148558	0.352637	-2.7509	Nonsignifi	4	Molecular	Rho-assoc	2.7.11.1
Inf	0	Inf	Significant up	3	Molecular	frizzled 1/	--
Inf	0	Inf	Significant up	2	Molecular	phospholi	3.6.3.1
Inf	0	Inf	Significant up	--	--	CLIP-assoc	--
Inf	0	Inf	Significant up	2	Molecular	huntingtin	--
Inf	0	Inf	Significant up	--	--	obscurin-li	--
0.432412	0.004413	-1.20952	Nonsignifi	--	--	DnaJ hom	--
Inf	0	Inf	Significant up	--	--	protein TIF	--
Inf	0	Inf	Significant up	1	Molecular	low density	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	2	Biological	ubiquitin c	3.4.19.12
1.578733	0.027444	0.658767	Nonsignifi	1	Molecular	--	--
Inf	0	Inf	Significant up	2	Molecular	semaphori	--
Inf	0	Inf	Significant up	3	Biological	tubulin-sp	--
Inf	0	Inf	Significant up	1	Molecular	vacuolar p	--
0.483425	0.137065	-1.04864	Nonsignifi	1	Molecular	histone H2	--
0.886674	0.702641	-0.17352	Nonsignifi	1	Molecular	filamin	--
Inf	0	Inf	Significant up	--	--	mannose-	--
Inf	0	Inf	Significant up	3	Molecular	tripartite r	--
Inf	0	Inf	Significant up	2	Cellular	Cc MFS trans	--
Inf	0	Inf	Significant up	--	--	citrate synt	2.3.3.1
Inf	0	Inf	Significant up	2	Cellular	Cc vesicle trar	--
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	1	Molecular	FUS-intera	--
Inf	0	Inf	Significant up	1	Molecular	heat shock	--
Inf	0	Inf	Significant up	1	Cellular	Cc claudin	--
0.929043	0.833193	-0.10618	Nonsignifi	1	Molecular	barrier-to	--
Inf	0	Inf	Significant up	2	Molecular	tumor nec	--
Inf	0	Inf	Significant up	--	--	splicing fac	--
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	3	Molecular	mediator c	--
Inf	0	Inf	Significant up	--	--	nucleopho	--
Inf	0	Inf	Significant up	1	Molecular	lysophosph	3.1.1.5
0.044695	0.05958	-4.48374	Nonsignifi	--	--	type 2A ph	--
Inf	0	Inf	Significant up	2	Molecular	pre-mRNA	3.6.4.13
Inf	0	Inf	Significant up	2	Cellular	Cc --	--
Inf	0	Inf	Significant up	--	--	nuclear po	--
Inf	0	Inf	Significant up	--	--	protein XR	--
Inf	0	Inf	Significant up	--	--	cartilage-a	--
Inf	0	Inf	Significant up	4	Molecular	transient r	--
Inf	0	Inf	Significant up	2	Molecular	renin rece	--
Inf	0	Inf	Significant up	1	Molecular	translation	--
Inf	0	Inf	Significant up	3	Molecular	translation	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	1	Molecular	26S protea	--
0.471169	0.325655	-1.08568	Nonsignifi	1	Biological	isocitrate c	1.1.1.42
1.51722	0.460897	0.60143	Nonsignifi	4	Biological	formyltetr	1.5.1.6
0.153	0.089261	-2.7084	Nonsignifi	--	--	PRA1 famil	--
Inf	0	Inf	Significant up	2	Molecular	STE24 end	3.4.24.84
Inf	0	Inf	Significant up	6	Molecular	triple funct	2.7.11.1

Inf	0	Inf	Significant up		1	Molecular	multiple PI	--
Inf	0	Inf	Significant up		3	Molecular	carboxype	3.4.17.22
Inf	0	Inf	Significant up		3	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	ribosome l	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	regulator c	--
Inf	0	Inf	Significant up		4	Molecular	signal recc	--
Inf	0	Inf	Significant up	--	--	--	dimethylar	3.5.3.18
Inf	0	Inf	Significant up		4	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up		4	Molecular	protein kin	2.7.11.13
Inf	0	Inf	Significant up		2	Biological	glucosamii	2.6.1.16
Inf	0	Inf	Significant up		4	Biological	protein tra	--
Inf	0	Inf	Significant up		1	Cellular Cc	calcium pe	--
Inf	0	Inf	Significant up		2	Molecular	FERM, Rho	--
Inf	0	Inf	Significant up		4	Biological	AP-2 com	--
Inf	0	Inf	Significant up		3	Molecular	E3 ubiquiti	2.3.2.26
0.421239	0.010427	-1.24729	Nonsignifi	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	splicing fac	--
0.393994	0.3224	-1.34376	Nonsignifi		3	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	aflatoxin B	--
0.492015	0.15752	-1.02323	Nonsignifi		2	Molecular	serine prot	3.4.21.-
Inf	0	Inf	Significant up		5	Cellular Cc	ubiquitin c	2.3.2.27
Inf	0	Inf	Significant up		2	Biological	elongator	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Cellular Cc	vesicle-ass	--
Inf	0	Inf	Significant up		1	Molecular	sorting ne	--
Inf	0	Inf	Significant up		4	Molecular	kinesin far	--
Inf	0	Inf	Significant up	--	--	--	myotubula	--
Inf	0	Inf	Significant up	--	--	--	golgi SNAI	--
Inf	0	Inf	Significant up	--	--	--	vesicle-ass	--
Inf	0	Inf	Significant up	--	--	--	SNARE-as	--
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		5	Molecular	ATP-bindin	--
Inf	0	Inf	Significant up		4	Molecular	structural r	--
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-l	--
Inf	0	Inf	Significant up		1	Molecular	lysophosph	3.1.1.5
Inf	0	Inf	Significant up		2	Biological	phosphoar	5.4.2.3
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	--	--
Inf	0	Inf	Significant up		2	Cellular Cc	proteasom	--
Inf	0	Inf	Significant up		4	Molecular	--	--
Inf	0	Inf	Significant up		5	Molecular	latrophilin	--
Inf	0	Inf	Significant up		2	Molecular	DNA-direct	2.7.7.6
Inf	0	Inf	Significant up		1	Molecular	STAM-bin	3.4.19.12
Inf	0	Inf	Significant up		1	Molecular	protein ph	--
Inf	0	Inf	Significant up		4	Molecular	E3 ubiquiti	2.3.2.26
0.104222	0.058375	-3.26227	Nonsignifi		1	Biological	pantethein	3.5.1.92
0.068165	0.070404	-3.87483	Nonsignifi		1	Biological	pantethein	3.5.1.92
Inf	0	Inf	Significant up	--	--	--	synaptoso	--
Inf	0	Inf	Significant up	--	--	--	double-str	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	BCL2-asso	--
Inf	0	Inf	Significant up		2	Molecular	BCL2-asso	--
1.078285	0.722774	0.108739	Nonsignifi		4	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up		1	Molecular	echinoderr	--
Inf	0	Inf	Significant up		3	Molecular	serine/thre	2.7.11.1

Inf	0	Inf	Significant up		1 Cellular Cc tetraspanin	--
Inf	0	Inf	Significant up	--	--	protein-di:1.8.4.2
0.562534	0.002757	-0.82999	Nonsignifi		3 Molecular mitogen-a	2.7.11.1
Inf	0	Inf	Significant up		1 Molecular EGF-conta	--
Inf	0	Inf	Significant up		3 Molecular p21-activa	2.7.11.1
Inf	0	Inf	Significant up	--	--	actin-like p --
0.211992	0.086731	-2.23792	Nonsignifi	--	--	dimethylar 3.5.3.18
Inf	0	Inf	Significant up		1 Biological alcohol de	1.1.1.1
0.016661	0.074512	-5.90735	Nonsignifi	--	--	-- --
Inf	0	Inf	Significant up		3 Biological glutamate	1.4.1.3
Inf	0	Inf	Significant up		4 Molecular dihydrofol	1.5.1.3
Inf	0	Inf	Significant up		5 Molecular cytochrom	--
Inf	0	Inf	Significant up		1 Biological hypoxanth	2.4.2.8
0.93641	0.599405	-0.09479	Nonsignifi		2 Molecular L-lactate d	1.1.1.27
0.900994	0.041773	-0.15041	Nonsignifi		3 Biological retinal deh	1.2.1.36
Inf	0	Inf	Significant up		2 Biological aspartate ε	2.6.1.1
Inf	0	Inf	Significant up	--	--	adenylate 2.7.4.3
0.429063	0.139894	-1.22074	Nonsignifi		2 Molecular cytochrom	1.6.2.2
0.276166	0.011317	-1.85639	Nonsignifi		3 Molecular glutathion	1.8.1.7
Inf	0	Inf	Significant up		2 Molecular urokinase	3.4.21.73
Inf	0	Inf	Significant up		4 Molecular tissue plas	3.4.21.68
0.16727	0.060098	-2.57975	Nonsignifi		3 Molecular ceruloplas	1.16.3.1
Inf	0	Inf	Significant up	--	--	alpha-1-a --
0.289538	0.003703	-1.78817	Nonsignifi		2 Molecular purine-nur	2.4.2.1
Inf	0	Inf	Significant up		2 Molecular GTPase HF	--
Inf	0	Inf	Significant up		2 Molecular low-densit	--
1.793633	0.021954	0.842885	Nonsignifi		6 Molecular epidermal	2.7.10.1
2.09047	0.019071	1.063827	Nonsignifi		2 Molecular phosphogl	2.7.2.3
Inf	0	Inf	Significant up	--	--	thyroglob --
0.895551	0.615752	-0.15915	Nonsignifi		5 Molecular coagulatio	3.4.21.5
0.12617	0.269782	-2.98656	Nonsignifi		2 Molecular haptoglob	--
0.607428	0.184535	-0.71921	Nonsignifi		5 Molecular coagulatio	3.4.21.22
1.530429	0.075762	0.613937	Nonsignifi		5 Molecular coagulatio	3.4.21.6
Inf	0	Inf	Significant up	--	--	-- --
Inf	0	Inf	Significant up	--	--	-- --
Inf	0	Inf	Significant up	--	--	compleme --
Inf	0	Inf	Significant up		1 Molecular compleme	--
Inf	0	Inf	Significant up		4 Molecular RAF proto	2.7.11.1
0.352842	0.002702	-1.5029	Nonsignifi		3 Molecular alpha-2-r	--
Inf	0	Inf	Significant up	--	--	glucosylce 3.2.1.45
0.05096	0.113814	-4.29449	Nonsignifi		3 Molecular compleme	--
0.025354	0.063164	-5.30167	Nonsignifi		1 Molecular metallope	--
Inf	0	Inf	Significant up		2 Molecular alpha-L-fu	3.2.1.51
0.076895	0.050358	-3.70097	Nonsignifi		1 Molecular kininogen	--
Inf	0	Inf	Significant up		1 Molecular cystatin-A	--
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
Inf	0	Inf	Significant up		2 Molecular thymidine	2.7.1.21
Inf	0	Inf	Significant up		1 Molecular --	--
0.081163	0.054446	-3.62304	Nonsignifi	--	--	-- --
Inf	0	Inf	Significant up	--	--	argininosu 4.3.2.1
Inf	0	Inf	Significant up	--	--	thymidylat 2.1.1.45
Inf	0	Inf	Significant up		3 Biological solute carr	--
1.686527	0.006017	0.754055	Nonsignifi		2 Biological major histc	--
0.569654	0.293324	-0.81184	Nonsignifi		2 Biological major histc	--
Inf	0	Inf	Significant up		3 Cellular Cc sodium/pc	--
Inf	0	Inf	Significant up		2 Molecular fructose-b	4.1.2.13
Inf	0	Inf	Significant up	--	--	integrin be --

Inf	0	Inf	Significant up		1	Molecular	ubiquitin c	--
Inf	0	Inf	Significant up	--	--	--	intercellula	--
0.074519	0.078969	-3.74626	Nonsignifi		2	Molecular	collagen, t	--
0.088486	0.06645	-3.4984	Nonsignifi		2	Molecular	type I kera	--
0.088768	0.055116	-3.49381	Nonsignifi		2	Molecular	type II ker	--
0.08734	0.086211	-3.51722	Nonsignifi		4	Cellular	Cc apolipop	--
Inf	0	Inf	Significant up		2	Molecular	lupus La p	--
Inf	0	Inf	Significant up		6	Molecular	classical pr	2.7.11.13
0.040602	0.138776	-4.62231	Nonsignifi		5	Molecular	fibrinogen	--
Inf	0	Inf	Significant up		2	Molecular	type I kera	--
Inf	0	Inf	Significant up		2	Molecular	type II ker	--
Inf	0	Inf	Significant up		2	Molecular	uroporphyr	4.1.1.37
0.143631	0.123422	-2.79956	Nonsignifi	--	--	--	beta-2-gly	--
Inf	0	Inf	Significant up		6	Molecular	insulin rec	2.7.10.1
Inf	0	Inf	Significant up		3	Molecular	tyrosine-p	2.7.10.2
Inf	0	Inf	Significant up		1	Biological	alpha-gala	3.2.1.22
Inf	0	Inf	Significant up		3	Molecular	--	--
0.085626	0.083793	-3.54582	Nonsignifi		1	Cellular	Cc alpha-feto	--
Inf	0	Inf	Significant up		4	Molecular	translation	--
0.00859	0.477526	-6.8631	Nonsignifi	--	--	--	transferrin	--
0.109035	0.051731	-3.19714	Nonsignifi	--	--	--	lactotransf	3.4.21.-
0.065136	0.098438	-3.94041	Nonsignifi	--	--	--	hemopexir	--
0.017256	0.154394	-5.85673	Nonsignifi		2	Biological	ferritin ligh	--
0.088911	0.113385	-3.4915	Nonsignifi		2	Biological	ferritin hea	1.16.3.2
0.136084	0.148904	-2.87744	Nonsignifi		2	Molecular	plasma kal	3.4.21.34
Inf	0	Inf	Significant up		1	Molecular	creatine kin	2.7.3.2
Inf	0	Inf	Significant up		1	Molecular	lipoproteir	3.1.1.34
0.142538	0.178831	-2.81058	Nonsignifi		3	Molecular	vitronectin	--
0.063938	0.158327	-3.96718	Nonsignifi		3	Molecular	catalase	1.11.1.6
Inf	0	Inf	Significant up	--	--	--	microsom	3.3.2.9
Inf	0	Inf	Significant up		1	Molecular	diazepam-	--
Inf	0	Inf	Significant up		3	Molecular	glutathion	1.11.1.9
1.407358	0.076078	0.492989	Nonsignifi		2	Molecular	fructose-b	4.1.2.13
Inf	0	Inf	Significant up		4	Cellular	Cc histone H1	--
0.962507	0.791076	-0.05513	Nonsignifi		2	Molecular	annexin A1	--
Inf	0	Inf	Significant up	--	--	--	carbonic a	4.2.1.1
Inf	0	Inf	Significant up		3	Molecular	tyrosine-p	2.7.10.2
Inf	0	Inf	Significant up		2	Biological	fumarate f	4.2.1.2
Inf	0	Inf	Significant up		6	Molecular	insulin-like	2.7.10.1
Inf	0	Inf	Significant up	--	--	--	decay acce	--
Inf	0	Inf	Significant up		5	Molecular	ATP-bindin	3.6.3.44
0.051048	0.212575	-4.292	Nonsignifi		2	Molecular	type II ker	--
0.039872	0.053261	-4.64847	Nonsignifi		2	Molecular	type II ker	--
Inf	0	Inf	Significant up		2	Molecular	6-phospho	2.7.1.11
Inf	0	Inf	Significant up		2	Molecular	asparagine	6.3.5.4
1.664496	0.025767	0.735086	Nonsignifi		1	Biological	glyceraldel	1.2.1.12
Inf	0	Inf	Significant up		2	Molecular	neprilysin	3.4.24.11
Inf	0	Inf	Significant up		4	Molecular	proto-onc	2.7.10.1
0.280051	0.010585	-1.83624	Nonsignifi	--	--	--	heat shock	--
Inf	0	Inf	Significant up	--	--	--	melanoma	--
0.143868	0.14318	-2.79718	Nonsignifi		4	Molecular	oligosacch	--
3.102968	0.000218	1.633649	Nonsignifi		5	Molecular	guanine nt	--
Inf	0	Inf	Significant up		1	Biological	acetyl-CoA	2.3.1.16
Inf	0	Inf	Significant up		3	Biological	signal recc	--
Inf	0	Inf	Significant up		1	Molecular	U1 small n	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		5	Molecular	clathrin lig	--
0.038797	0.058019	-4.68789	Nonsignifi	--	--	--	integrin be	--

Inf	0	Inf	Significant up		5	Molecular	clathrin lig	--
Inf	0	Inf	Significant up		2	Molecular	annexin A2	--
Inf	0	Inf	Significant up		4	Molecular	poly [ADP-ribose]	2.4.2.30
0.063473	0.064258	-3.97771	Nonsignificant	None	5	Molecular	complement C3	3.4.21.45
0.251299	0.132336	-1.99252	Nonsignificant	None	--	--	coagulation factor	--
Inf	0	Inf	Significant up		2	Molecular	leukotriene 4-epoxide synthase	3.3.2.6
Inf	0	Inf	Significant up		1	Molecular	histone H2A	--
Inf	0	Inf	Significant up		1	Molecular	F-box protein 1	--
0.640903	0.600175	-0.64182	Nonsignificant	None	--	--	large subunit of RNA polymerase II	--
0.974441	0.794879	-0.03735	Nonsignificant	None	--	--	large subunit of RNA polymerase II	--
1.779133	0.026631	0.831175	Nonsignificant	None	2	Cellular	Cc large subunit of RNA polymerase II	--
Inf	0	Inf	Significant up		2	Molecular	Ras-related protein 1	--
Inf	0	Inf	Significant up		1	Molecular	60 kDa SS-RP	--
Inf	0	Inf	Significant up		4	Molecular	A-Raf protein	2.7.11.1
0.141484	0.096078	-2.82129	Nonsignificant	None	--	--	heparin cofactor	--
Inf	0	Inf	Significant up		1	Biological	pyruvate dehydrogenase	2.3.1.12
Inf	0	Inf	Significant up		3	Molecular	receptor tyrosine kinase	3.1.3.48
Inf	0	Inf	Significant up		2	Molecular	cathepsin B	3.4.16.5
Inf	0	Inf	Significant up	--	--	--	S-formylglutathione hydrolase	3.1.2.12
0.715904	0.373821	-0.48216	Nonsignificant	None	1	Molecular	myosin light chain 1	--
0.044212	0.056623	-4.4994	Nonsignificant	None	2	Molecular	collagen, type I	--
Inf	0	Inf	Significant up		1	Molecular	chaperonin 19.1	--
Inf	0	Inf	Significant up		1	Molecular	lysosomal enzyme	3.1.3.2
Inf	0	Inf	Significant up		5	Molecular	erythrocyte membrane protein	--
0.377684	0.154018	-1.40475	Nonsignificant	None	--	--	cholinesterase	3.1.1.8
Inf	0	Inf	Significant up		3	Molecular	--	--
0.234668	0.058945	-2.09131	Nonsignificant	None	--	--	gelsolin	--
Inf	0	Inf	Significant up		2	Molecular	Ras-related protein 2	--
0.106657	0.098467	-3.22895	Nonsignificant	None	4	Cellular	Cc apolipoprotein B	--
Inf	0	Inf	Significant up		1	Cellular	Cc lysosomal enzyme	--
Inf	0	Inf	Significant up		4	Molecular	DNA topoisomerase	5.99.1.2
2.116782	0.070887	1.081873	Nonsignificant	None	--	--	enolase	4.2.1.11
0.613857	0.395475	-0.70402	Nonsignificant	None	2	Biological	glycogen phosphorylase	2.4.1.1
0.434941	0.006845	-1.20111	Nonsignificant	None	3	Molecular	glucose-6-phosphate dehydrogenase	5.3.1.9
2.167467	0.016688	1.11601	Nonsignificant	None	1	Molecular	nucleophosmin	--
4.284285	0.126525	2.099054	Nonsignificant	None	--	--	tropomyosin	--
1.660077	0.000976	0.73125	Nonsignificant	None	--	--	integrin alpha 1	--
Inf	0	Inf	Significant up		5	Molecular	DNA topoisomerase	5.99.1.3
0.290707	0.001029	-1.78236	Nonsignificant	None	1	Biological	hexosaminidase	3.2.1.52
Inf	0	Inf	Significant up		3	Molecular	cyclin-dependent kinase 2	2.7.11.22
Inf	0	Inf	Significant up		3	Molecular	ribose-phosphate isomerase	2.7.6.1
Inf	0	Inf	Significant up		2	Molecular	proliferating cell nuclear antigen	--
Inf	0	Inf	Significant up		3	Molecular	histidyl-tRNA synthetase	6.1.1.21
0.039792	0.230087	-4.65139	Nonsignificant	None	--	--	fatty acid synthase	--
1.924884	0.013301	0.944771	Nonsignificant	None	2	Molecular	L-lactate dehydrogenase	1.1.1.27
Inf	0	Inf	Significant up		1	Biological	nucleoprotein	--
Inf	0	Inf	Significant up		1	Molecular	creatine kinase	2.7.3.2
0.398029	0.006037	-1.32906	Nonsignificant	None	1	Biological	protein disulfide isomerase	5.3.4.1
Inf	0	Inf	Significant up		1	Molecular	creatine kinase	2.7.3.2
0.371496	0.019985	-1.42858	Nonsignificant	None	2	Molecular	cathepsin L	3.4.23.5
Inf	0	Inf	Significant up		3	Molecular	tyrosine phosphatase	2.7.10.2
0.706405	0.495484	-0.50143	Nonsignificant	None	1	Molecular	tubulin beta chain	--
Inf	0	Inf	Significant up		3	Molecular	ATP-dependent protein kinase	--
Inf	0	Inf	Significant up		3	Molecular	ATP-dependent protein kinase	--
0.277097	0.010256	-1.85154	Nonsignificant	None	1	Biological	saposin	--
0.328634	0.001988	-1.60544	Nonsignificant	None	1	Biological	hexosaminidase	3.2.1.52
Inf	0	Inf	Significant up		1	Biological	protein disulfide isomerase	5.3.4.1
0.421723	0.167839	-1.24563	Nonsignificant	None	--	--	--	--

1.260525	0.594213	0.334025	Nonsignifi	None	8	Molecular	--	--
0.274991	0.052478	-1.86255	Nonsignifi	None	4	Molecular	cathepsin	13.4.22.1
2.244697	0.003485	1.166521	Nonsignifi	None	4	Molecular	molecular	--
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
Inf	0	Inf	Significant	up	2	Molecular	glycogen s	2.4.1.11
Inf	0	Inf	Significant	up	--	--	cAMP-dep	--
Inf	0	Inf	Significant	up	3	Cellular	Cc transcriptic	3.6.4.12
Inf	0	Inf	Significant	up	1	Molecular	protein kin	--
Inf	0	Inf	Significant	up	1	Biological	--	--
0.288495	0.033603	-1.79338	Nonsignifi	None	2	Molecular	annexin A	--
Inf	0	Inf	Significant	up	3	Molecular	carboxype	3.4.17.12
Inf	0	Inf	Significant	up	--	--	alcohol de	1.1.1.2
Inf	0	Inf	Significant	up	--	--	small nucle	--
Inf	0	Inf	Significant	up	4	Molecular	matrix met	3.4.24.35
2.178816	0.000132	1.123545	Nonsignifi	None	4	Molecular	molecular	--
Inf	0	Inf	Significant	up	1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	1	Molecular	junction pl	--
Inf	0	Inf	Significant	up	--	--	poliovirus	--
Inf	0	Inf	Significant	up	3	Molecular	interferon	--
0.282967	0.090681	-1.8213	Nonsignifi	None	1	Biological	pleckstrin	--
0.654904	0.248079	-0.61064	Nonsignifi	None	2	Molecular	collagen, t	--
Inf	0	Inf	Significant	up	3	Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant	up	--	--	membrane	--
2.107292	0.039533	1.075391	Nonsignifi	None	--	--	integrin al	--
0.671136	0.010472	-0.57532	Nonsignifi	None	2	Molecular	vimentin	--
0.079929	0.1139	-3.64513	Nonsignifi	None	--	--	alpha-2-a	--
0.503549	0.401945	-0.98979	Nonsignifi	None	2	Molecular	type I kera	--
0.781458	0.161345	-0.35576	Nonsignifi	None	2	Molecular	annexin A	--
0.076695	0.336533	-3.70472	Nonsignifi	None	2	Molecular	type I kera	--
0.658054	0.51252	-0.60372	Nonsignifi	None	4	Molecular	small subu	--
1.556035	0.197839	0.637875	Nonsignifi	None	1	Cellular	Cc CD63 anti	--
Inf	0	Inf	Significant	up	5	Molecular	nucleoside	2.7.4.6
Inf	0	Inf	Significant	up	--	--	NAD(P)H c	1.6.5.2
0.843187	0.617082	-0.24608	Nonsignifi	None	1	Molecular	glutathion	2.5.1.18
Inf	0	Inf	Significant	up	--	--	replication	--
Inf	0	Inf	Significant	up	3	Molecular	integrin be	--
1.229099	0.443545	0.297601	Nonsignifi	None	1	Molecular	galectin-1	--
0.563776	0.048758	-0.82681	Nonsignifi	None	--	--	high mobil	--
Inf	0	Inf	Significant	up	--	--	beta-galac	3.2.1.23
0.017747	0.052965	-5.8163	Nonsignifi	None	4	Molecular	--	--
4.777866	0.180252	2.256366	Nonsignifi	None	--	--	tropomyos	--
Inf	0	Inf	Significant	up	1	Molecular	NCK adapt	--
Inf	0	Inf	Significant	up	3	Molecular	NADPH-fe	1.6.2.4
Inf	0	Inf	Significant	up	5	Molecular	phosphatic	3.1.4.11
0.199573	0.085885	-2.32501	Nonsignifi	None	2	Molecular	platelet-d	2.7.10.1
0.500221	0.000412	-0.99936	Nonsignifi	None	1	Molecular	heterogen	--
Inf	0	Inf	Significant	up	1	Biological	stathmin	--
Inf	0	Inf	Significant	up	1	Molecular	cold shock	--
0.734237	0.194807	-0.44568	Nonsignifi	None	2	Molecular	fructose-b	4.1.2.13
Inf	0	Inf	Significant	up	2	Molecular	Ras homol	--
Inf	0	Inf	Significant	up	--	--	high mobil	--
Inf	0	Inf	Significant	up	2	Biological	aspartate	2.6.1.1
Inf	0	Inf	Significant	up	6	Molecular	classical pr	2.7.11.13
0.688405	0.193718	-0.53867	Nonsignifi	None	--	--	heat shock	--
Inf	0	Inf	Significant	up	--	--	gap juncti	--
Inf	0	Inf	Significant	up	--	--	upstream-	--

Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		3	Molecular	S-adenosyl
1.107622	0.839364	0.147466	Nonsignifi	None		2	Molecular	Ras-relate
Inf		0	Inf	Significant up		2	Molecular	CTP synth
Inf		0	Inf	Significant up		1	Molecular	26S protea
Inf		0	Inf	Significant up		2	Molecular	tyrosine-p
0.251978	0.007365	-1.98863	Nonsignifi	None		1	Biological	thioredoxi
Inf		0	Inf	Significant up		4	Molecular	large subu
Inf		0	Inf	Significant up		2	Molecular	receptor-t
0.301013	0.012743	-1.7321	Nonsignifi	None		1	Molecular	tissue fact
Inf		0	Inf	Significant up	--	--		2,3-bisphc
Inf		0	Inf	Significant up	--	--		regulator c
0.015601	0.119318	-6.00219	Nonsignifi	None		2	Molecular	hyaluronar
0.521471	0.193312	-0.93934	Nonsignifi	None	--	--		heat shock
Inf		0	Inf	Significant up		5	Molecular	--
Inf		0	Inf	Significant up		3	Biological	DNA-repa
Inf		0	Inf	Significant up		3	Molecular	cadherin 2
Inf		0	Inf	Significant up		2	Molecular	hexokinase
1.378855	0.243541	0.46347	Nonsignifi	None		3	Cellular	Cc MFS trans
Inf		0	Inf	Significant up		3	Molecular	DNA-direct
Inf		0	Inf	Significant up		2	Molecular	tumor necr
Inf		0	Inf	Significant up		3	Molecular	eukaryotic
0.508063	0.413974	-0.97692	Nonsignifi	None		2	Biological	glycogen p
Inf		0	Inf	Significant up	--	--		spermidine
Inf		0	Inf	Significant up		4	Biological	solute carr
Inf		0	Inf	Significant up		3	Molecular	casein kin
Inf		0	Inf	Significant up		2	Molecular	Ras-relate
Inf		0	Inf	Significant up		2	Molecular	Ras-relate
0.278788	0.442661	-1.84276	Nonsignifi	None		4	Molecular	--
Inf		0	Inf	Significant up		5	Molecular	atrial natri
1.050644	0.766596	0.071274	Nonsignifi	None		1	Biological	--
Inf		0	Inf	Significant up		2	Molecular	lamin B
Inf		0	Inf	Significant up	--	--		interleukin
2.434621	0.004143	1.283697	Nonsignifi	None		2	Molecular	polyadeny
Inf		0	Inf	Significant up	--	--		calpastatin
Inf		0	Inf	Significant up		2	Molecular	IMP dehyd
Inf		0	Inf	Significant up		2	Molecular	Ras GTPas
Inf		0	Inf	Significant up	--	--		--
Inf		0	Inf	Significant up		3	Molecular	cell divisio
Inf		0	Inf	Significant up		1	Molecular	glutathioni
0.352236	1.02E-05	-1.50539	Nonsignifi	None		1	Molecular	coagulatio
1.072589	0.811778	0.101097	Nonsignifi	None		2	Molecular	IMP dehyd
Inf		0	Inf	Significant up		3	Molecular	V-type H+
Inf		0	Inf	Significant up		2	Molecular	V-type H+
0.066911	0.22085	-3.90162	Nonsignifi	None		2	Molecular	annexin A
Inf		0	Inf	Significant up		1	Molecular	cysteine ar
5.610941	0.181379	2.488243	Nonsignifi	None		1	Molecular	actinin alp
Inf		0	Inf	Significant up		1	Biological	neurofibro
0.40013	0.024181	-1.32146	Nonsignifi	None		2	Molecular	Xaa-Pro di
Inf		0	Inf	Significant up		5	Molecular	glycerol-3
Inf		0	Inf	Significant up		1	Molecular	catechol O
0.582792	0.217747	-0.77895	Nonsignifi	None		1	Cellular	Cc lysosomal
0.048518	0.499292	-4.36532	Nonsignifi	None		1	Molecular	ribonuclea
0.255496	0.067341	-1.96863	Nonsignifi	None		3	Molecular	bone morp
Inf		0	Inf	Significant up	--	--		oxysterol-I
Inf		0	Inf	Significant up		4	Molecular	rRNA 2'-O
Inf		0	Inf	Significant up		3	Molecular	--
2.70264	0.003893	1.434369	Nonsignifi	None		1	Molecular	elongation

0.066825	0.095197	-3.90346	Nonsignifi	None	2	Molecular	type I kera	--
0.066075	0.167582	-3.91976	Nonsignifi	None	2	Molecular	type II ker	--
Inf	0	Inf	Significant	up	1	Biological	--	--
Inf	0	Inf	Significant	up	--	--	acetylcholi	3.1.1.7
Inf	0	Inf	Significant	up	7	Molecular	--	--
Inf	0	Inf	Significant	up	4	Molecular	E3 ubiquiti	2.3.2.27
0.096048	0.154053	-3.38011	Nonsignifi	None	2	Molecular	plastin-2	--
0.778892	0.533998	-0.3605	Nonsignifi	None	2	Molecular	plastin-3	--
Inf	0	Inf	Significant	up	3	Molecular	protein kin	2.7.11.11
Inf	0	Inf	Significant	up	3	Molecular	transcripti	--
Inf	0	Inf	Significant	up	1	Molecular	tubulin gai	--
0.502627	0.034336	-0.99244	Nonsignifi	None	--	--	enolase	4.2.1.11
Inf	0	Inf	Significant	up	1	Molecular	--	--
1.112839	0.732515	0.154244	Nonsignifi	None	--	--	phenylpyr	5.3.2.1
Inf	0	Inf	Significant	up	2	Molecular	Janus kina	2.7.10.2
Inf	0	Inf	Significant	up	3	Molecular	receptor-t	3.1.3.48
Inf	0	Inf	Significant	up	2	Molecular	receptor-t	3.1.3.48
0.09654	0.070264	-3.37274	Nonsignifi	None	2	Molecular	nidogen (e	--
Inf	0	Inf	Significant	up	3	Molecular	receptor-t	3.1.3.48
2.276421	0.00118	1.186767	Nonsignifi	None	4	Molecular	pyruvate k	2.7.1.40
0.681338	0.001793	-0.55356	Nonsignifi	None	4	Molecular	heat shock	--
Inf	0	Inf	Significant	up	1	Molecular	translation	--
Inf	0	Inf	Significant	up	1	Molecular	1D-myo-i	2.7.1.127
Inf	0	Inf	Significant	up	--	--	dTMP kina	2.7.4.9
Inf	0	Inf	Significant	up	3	Biological	interleukin	--
2.504202	0.047672	1.324351	Nonsignifi	None	--	--	aldehyde r	1.1.1.21
0.420634	0.000457	-1.24936	Nonsignifi	None	2	Molecular	aminopept	3.4.11.2
Inf	0	Inf	Significant	up	2	Molecular	elongation	--
0.293144	0.001919	-1.77032	Nonsignifi	None	3	Molecular	carboxype	3.4.17.3
Inf	0	Inf	Significant	up	--	--	--	--
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-adrei	2.7.11.15
Inf	0	Inf	Significant	up	3	Molecular	coagulatio	--
1.100099	0.73321	0.137634	Nonsignifi	None	4	Molecular	small subu	--
Inf	0	Inf	Significant	up	3	Molecular	DNA replic	3.6.4.12
Inf	0	Inf	Significant	up	--	--	--	--
0.692009	0.23684	-0.53114	Nonsignifi	None	2	Molecular	CD44 antiç	--
Inf	0	Inf	Significant	up	1	Molecular	bromodon	--
Inf	0	Inf	Significant	up	--	--	DnaJ hom	--
Inf	0	Inf	Significant	up	4	Molecular	F-type H+	--
Inf	0	Inf	Significant	up	3	Molecular	DNA (cyto	2.1.1.37
2.887379	0.022976	1.529761	Nonsignifi	None	4	Cellular	Cc histone H1	--
2.436644	0.040643	1.284895	Nonsignifi	None	4	Cellular	Cc histone H1	--
1.969325	0.104446	0.977701	Nonsignifi	None	4	Cellular	Cc histone H1	--
Inf	0	Inf	Significant	up	5	Molecular	threonyl-tl	6.1.1.3
Inf	0	Inf	Significant	up	--	--	FK506-bin	5.2.1.8
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
Inf	0	Inf	Significant	up	4	Molecular	replication	--
2.237799	0.001525	1.162081	Nonsignifi	None	--	--	heat shock	--
Inf	0	Inf	Significant	up	--	--	AP endon	4.2.99.18
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
Inf	0	Inf	Significant	up	3	Molecular	20S protea	3.4.25.1
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		4	Molecular	receptor-t	3.1.3.48
1.669672	0.060644	0.739565	Nonsignifi	None	4	Molecular	calpain-2	3.4.22.53
Inf	0	Inf	Significant up		3	Molecular	--	--
Inf	0	Inf	Significant up		1	Biological	myo-inosit	3.1.3.25
1.605811	0.028513	0.683302	Nonsignifi	None	2	Molecular	ATP-depei	3.6.4.13
0.975083	0.649134	-0.0364	Nonsignifi	None	2	Molecular	6-phosphc	2.7.1.11
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
1.610659	9.64E-05	0.687651	Nonsignifi	None	1	Molecular	T-complex	--
Inf	0	Inf	Significant up		1	Molecular	SHC-trans	--
0.143232	0.050986	-2.80357	Nonsignifi	None	3	Biological	--	--
Inf	0	Inf	Significant up		2	Molecular	elongation	--
3.2697	0.006692	1.709158	Nonsignifi	None	1	Molecular	ADP-ribos	--
0.648436	0.63098	-0.62496	Nonsignifi	None	--	--	large subu	--
0.353301	0.084906	-1.50103	Nonsignifi	None	2	Biological	vinculin	--
Inf	0	Inf	Significant up		2	Molecular	--	--
0.68509	0.515354	-0.54563	Nonsignifi	None	3	Molecular	large subu	--
Inf	0	Inf	Significant up	--	--	--	D-dopach	4.1.1.84
Inf	0	Inf	Significant up		1	Molecular	anaphase-	--
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	--
Inf	0	Inf	Significant up		3	Biological	solute carr	--
Inf	0	Inf	Significant up		2	Molecular	DNA-direc	2.7.7.6
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
Inf	0	Inf	Significant up		3	Molecular	solute carr	--
Inf	0	Inf	Significant up		2	Molecular	DnaJ hom	--
Inf	0	Inf	Significant up		4	Molecular	RAC serine	2.7.11.1
Inf	0	Inf	Significant up		1	Molecular	--	--
0.036331	0.412442	-4.78264	Nonsignifi	None	2	Molecular	translation	--
Inf	0	Inf	Significant up	--	--	--	beta-arres	--
Inf	0	Inf	Significant up		2	Molecular	syntaxin 1f	--
Inf	0	Inf	Significant up		1	Molecular	cystathioni	4.4.1.1
0.612754	0.041894	-0.70662	Nonsignifi	None	3	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant up		4	Molecular	large subu	--
0.307974	0.00199	-1.69912	Nonsignifi	None	3	Molecular	--	--
0.164835	0.064886	-2.60091	Nonsignifi	None	1	Molecular	osteoglyci	--
Inf	0	Inf	Significant up		3	Molecular	tumor nec	--
Inf	0	Inf	Significant up		2	Molecular	long-chair	6.2.1.3
Inf	0	Inf	Significant up		3	Molecular	cadherin 5	--
Inf	0	Inf	Significant up		2	Molecular	dUTP pyro	3.6.1.23
Inf	0	Inf	Significant up		5	Molecular	ATP-bindii	--
Inf	0	Inf	Significant up	--	--	--	--	--
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
Inf	0	Inf	Significant up		1	Molecular	glycine hyc	2.1.2.1
Inf	0	Inf	Significant up		1	Molecular	glycine hyc	2.1.2.1
Inf	0	Inf	Significant up	--	--	--	--	--
0.706301	0.065637	-0.50165	Nonsignifi	None	1	Molecular	filamin	--
Inf	0	Inf	Significant up	--	--	--	profilin	--
1.319816	0.029686	0.400336	Nonsignifi	None	1	Biological	aconitate f	4.2.1.3
3.340552	0.002552	1.740087	Nonsignifi	None	2	Biological	5'-nucleot	3.1.3.5

Inf		0	Inf	Significant up	--	--	prohibitin	--
Inf		0	Inf	Significant up	--	--	serpin B	--
3.119808	0.006786	1.641457	Nonsignifi	None		1	Cellular Cc CD9 antigen	--
Inf		0	Inf	Significant up		3	Cellular Cc merlin	--
0.202752	0.146493	-2.30221	Nonsignifi	None		2	Molecular transglutar	2.3.2.13
Inf		0	Inf	Significant up		5	Molecular replication	--
Inf		0	Inf	Significant up		1	Molecular replication	--
Inf		0	Inf	Significant up		1	Molecular replication	--
Inf		0	Inf	Significant up		4	Molecular large subu	--
Inf		0	Inf	Significant up		4	Molecular transcriptic	--
Inf		0	Inf	Significant up		1	Molecular prostaglan	1.14.99.1
0.86438	0.823314	-0.21026	Nonsignifi	None		1	Molecular ubiquitin-ε	6.2.1.45
0.761896	0.573529	-0.39233	Nonsignifi	None		3	Molecular glutathion	1.11.1.9
3.791231	0.053732	1.922666	Nonsignifi	None		5	Molecular nucleoside	2.7.4.6
Inf		0	Inf	Significant up		3	Molecular histamine	--
Inf		0	Inf	Significant up	--	--	cystathioni	4.2.1.22
Inf		0	Inf	Significant up		1	Molecular actinin alpl	--
0.056642	0.092682	-4.14199	Nonsignifi	None		3	Biological --	--
Inf		0	Inf	Significant up	--	--	adducin	--
Inf		0	Inf	Significant up		2	Molecular RNA-bindin	--
Inf		0	Inf	Significant up	--	--	nuclear po	--
2.678116	0.044599	1.421218	Nonsignifi	None	--	--	integrin al	--
0.445292	0.007734	-1.16718	Nonsignifi	None		1	Molecular splicing fac	--
Inf		0	Inf	Significant up	--	--	protein DE	--
0.756188	0.357956	-0.40318	Nonsignifi	None		3	Biological peptidyl-p	5.2.1.8
Inf		0	Inf	Significant up		4	Molecular protein ph	3.1.3.16
1.279866	0.355744	0.355992	Nonsignifi	None		1	Molecular small subu	--
Inf		0	Inf	Significant up		2	Molecular --	--
Inf		0	Inf	Significant up	--	--	gap junctio	--
Inf		0	Inf	Significant up		1	Molecular ADP-ribos	--
Inf		0	Inf	Significant up		3	Molecular mitogen-a	2.7.12.2
0.155005	0.141906	-2.68961	Nonsignifi	None		3	Molecular receptor-t	3.1.3.48
1.667799	0.000223	0.737946	Nonsignifi	None		3	Molecular adenosylh	3.3.1.1
Inf		0	Inf	Significant up		1	Biological V-type H+	--
Inf		0	Inf	Significant up		3	Molecular coproporp	1.3.3.3
Inf		0	Inf	Significant up		1	Molecular --	--
Inf		0	Inf	Significant up		5	Molecular bone mor	2.7.11.30
1.048304	0.713666	0.068057	Nonsignifi	None		3	Molecular ribonucleo	1.17.4.1
0.148587	0.10766	-2.75062	Nonsignifi	None		5	Molecular laminin,	al
Inf		0	Inf	Significant up		5	Molecular activin rec	2.7.11.30
Inf		0	Inf	Significant up		5	Molecular TGF-beta	2.7.11.30
Inf		0	Inf	Significant up		1	Molecular --	--
Inf		0	Inf	Significant up		1	Molecular lymphotox	--
Inf		0	Inf	Significant up		2	Molecular GMP redu	1.7.1.7
Inf		0	Inf	Significant up		3	Molecular phospholi	1.11.1.12
Inf		0	Inf	Significant up		3	Biological signal rec	--
Inf		0	Inf	Significant up		5	Molecular TGF-beta	2.7.11.30
Inf		0	Inf	Significant up		1	Molecular --	--
Inf		0	Inf	Significant up	--	--	electron tr	--
0.303735	0.295478	-1.71911	Nonsignifi	None		5	Molecular laminin,	al
1.319488	0.051368	0.399979	Nonsignifi	None	--	--	small subu	--
Inf		0	Inf	Significant up		1	Molecular heterogen	--
Inf		0	Inf	Significant up	--	--	lysosomal	3.1.1.13
Inf		0	Inf	Significant up		3	Molecular V-type H+	3.6.3.14
0.799687	0.459866	-0.32249	Nonsignifi	None		5	Molecular 20S protea	3.4.25.1
0.449504	0.017398	-1.15359	Nonsignifi	None		5	Molecular 20S protea	3.4.25.1
0.646632	0.152984	-0.62898	Nonsignifi	None		5	Molecular 20S protea	3.4.25.1
0.98256	0.83595	-0.02538	Nonsignifi	None		5	Molecular 20S protea	3.4.25.1

0.068568	0.059692	-3.86631	Nonsignifi	None		1 Molecular collagen, t	--
Inf	0	Inf	Significant up		--	-- molecular	--
Inf	0	Inf	Significant up			2 Molecular ATP-depe	3.6.4.13
2.173565	0.147041	1.120063	Nonsignifi	None		3 Cellular Cc moesin	--
Inf	0	Inf	Significant up			3 Molecular small subu	--
1.047909	0.870684	0.067513	Nonsignifi	None		1 Molecular splicing fac	--
1.143027	0.27103	0.192859	Nonsignifi	None		4 Molecular large subu	--
0.304235	0.017676	-1.71674	Nonsignifi	None	--	-- high mobil	--
Inf	0	Inf	Significant up			2 Cellular Cc oligosacch	--
0.04158	0.506313	-4.58797	Nonsignifi	None		4 Molecular valyl-tRNA	6.1.1.9
1.464064	0.037369	0.549979	Nonsignifi	None		3 Molecular elongation	--
Inf	0	Inf	Significant up			2 Molecular flap endon	3.-.-.-
Inf	0	Inf	Significant up			1 Molecular interleukin	--
0.66606	0.451407	-0.58627	Nonsignifi	None	--	-- erythrocyt	--
1.02683	0.95193	0.038198	Nonsignifi	None	--	-- 14-3-3 pr	--
Inf	0	Inf	Significant up			1 Molecular ADP-ribos	--
Inf	0	Inf	Significant up			2 Molecular signal tran	--
Inf	0	Inf	Significant up			2 Biological ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up	--	--	-- replication	--
Inf	0	Inf	Significant up			1 Molecular translation	--
1.455084	0.010785	0.541102	Nonsignifi	None		1 Cellular Cc CD82 anti	--
1.067948	0.849362	0.094842	Nonsignifi	None		5 Molecular --	--
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
Inf	0	Inf	Significant up			2 Biological solute carr	--
1.039674	0.818401	0.056131	Nonsignifi	None		5 Molecular 20S protea	3.4.25.1
Inf	0	Inf	Significant up			6 Molecular atypical pr	2.7.11.13
Inf	0	Inf	Significant up	--	--	-- centractin	--
0.828742	0.119622	-0.271	Nonsignifi	None		3 Molecular 20S protea	3.4.25.1
Inf	0	Inf	Significant up			1 Molecular --	--
Inf	0	Inf	Significant up			2 Molecular signal tran	--
Inf	0	Inf	Significant up			2 Molecular ATP-depe	3.6.4.13
Inf	0	Inf	Significant up			1 Molecular phosphatic	2.7.1.153
Inf	0	Inf	Significant up			1 Molecular phosphatic	2.7.1.153
Inf	0	Inf	Significant up			3 Molecular serine/thre	2.7.11.1
0.274844	0.140897	-1.86332	Nonsignifi	None		4 Biological connective	--
1.003156	0.989536	0.004545	Nonsignifi	None		3 Molecular Eph recept	2.7.10.1
Inf	0	Inf	Significant up			1 Molecular phosphatic	2.7.1.67
Inf	0	Inf	Significant up	--	--	-- histidine a	4.3.1.3
Inf	0	Inf	Significant up	--	--	-- leucine-ric	--
0.900563	0.818289	-0.1511	Nonsignifi	None	--	-- transketol	2.2.1.1
0.032325	0.072388	-4.95119	Nonsignifi	None		2 Molecular non-recep	2.7.10.2
Inf	0	Inf	Significant up	--	--	-- --	--
2.552843	0.007314	1.352105	Nonsignifi	None		1 Molecular myristoylat	--
Inf	0	Inf	Significant up			2 Molecular endothelin	3.4.24.71
0.957424	0.858573	-0.06277	Nonsignifi	None		4 Molecular --	--
1.597781	0.104104	0.676069	Nonsignifi	None		1 Molecular peroxiredc	1.11.1.15
Inf	0	Inf	Significant up	--	--	-- melanoma	--
1.912407	0.01169	0.935389	Nonsignifi	None		3 Molecular large subu	--
0.770325	0.652057	-0.37646	Nonsignifi	None	--	-- --	--
Inf	0	Inf	Significant up	--	--	-- matrin 3	--
0.418997	0.000421	-1.25499	Nonsignifi	None		1 Biological protein dis	5.3.4.1
Inf	0	Inf	Significant up			3 Molecular DNA mism	--
Inf	0	Inf	Significant up			3 Molecular G protein-	2.7.11.16
Inf	0	Inf	Significant up			1 Biological Ran-bindir	--
Inf	0	Inf	Significant up	--	--	-- nicotinami	2.4.2.12
Inf	0	Inf	Significant up			2 Cellular Cc voltage-d	--
Inf	0	Inf	Significant up			3 Molecular c-Jun N-te	2.7.11.24

0.545682	0.447461	-0.87387	Nonsignifi	None		1 Molecular	--	--
Inf	0	Inf	Significant up			1 Molecular	antigen KI	--
Inf	0	Inf	Significant up	--		--	phosphory	--
1.623713	0.036919	0.699297	Nonsignifi	None		1 Molecular	coronin-1	--
Inf	0	Inf	Significant up			3 Molecular	Ran GTPas	--
0.14026	0.429199	-2.83382	Nonsignifi	None	--	--	protein S1	--
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	--
2.897135	0.00081	1.534627	Nonsignifi	None	--	--	syndecan	--
Inf	0	Inf	Significant up			1 Molecular	proto-onc	--
Inf	0	Inf	Significant up			1 Molecular	--	--
Inf	0	Inf	Significant up			6 Molecular	Notch 1	--
1.444337	0.043481	0.530407	Nonsignifi	None		3 Molecular	--	--
1.949547	0.084037	0.963139	Nonsignifi	None	--	--	14-3-3 pr	--
0.62078	0.056606	-0.68785	Nonsignifi	None		1 Molecular	stress-ind	--
Inf	0	Inf	Significant up			3 Molecular	mitogen-a	2.7.12.2
0.066321	0.189525	-3.91439	Nonsignifi	None	--	4 Molecular	peroxired	1.11.1.15
Inf	0	Inf	Significant up	--		--	small subu	--
0.207768	0.338507	-2.26696	Nonsignifi	None	--	--	4-hydroxy	1.13.11.27
Inf	0	Inf	Significant up	--		--	microtubu	--
Inf	0	Inf	Significant up			1 Biological	glucosami	3.5.99.6
Inf	0	Inf	Significant up			2 Molecular	--	--
Inf	0	Inf	Significant up			3 Molecular	dolichyl-di	2.4.99.18
Inf	0	Inf	Significant up			3 Biological	aldehyde c	1.2.1.5
Inf	0	Inf	Significant up			3 Molecular	solute carr	--
0.76762	0.783504	-0.38154	Nonsignifi	None		4 Molecular	kinesin far	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up			3 Molecular	solute carr	--
Inf	0	Inf	Significant up			4 Molecular	prolyl olig	3.4.21.26
Inf	0	Inf	Significant up			3 Molecular	malate de	1.1.1.40
Inf	0	Inf	Significant up	--		--	lanosterol	5.4.99.7
Inf	0	Inf	Significant up	--		--	26S protea	--
0.136943	0.186203	-2.86835	Nonsignifi	None	--	--	ribonuclea	3.1.27.-
Inf	0	Inf	Significant up			3 Molecular	casein kin	2.7.11.1
Inf	0	Inf	Significant up			3 Molecular	casein kin	2.7.11.1
Inf	0	Inf	Significant up			1 Biological	isocitrate c	1.1.1.42
0.491278	0.003373	-1.02539	Nonsignifi	None		3 Cellular Cc	glypican 1	--
Inf	0	Inf	Significant up			1 Molecular	phosphatic	2.7.1.153
0.063776	0.43115	-3.97084	Nonsignifi	None		1 Molecular	catenin be	--
Inf	0	Inf	Significant up			2 Cellular Cc	--	--
Inf	0	Inf	Significant up			5 Molecular	CD97 anti	--
Inf	0	Inf	Significant up			1 Molecular	paxillin	--
Inf	0	Inf	Significant up			4 Molecular	large subu	--
Inf	0	Inf	Significant up			1 Cellular Cc	lectin, mar	--
Inf	0	Inf	Significant up			1 Molecular	elongation	--
Inf	0	Inf	Significant up			3 Biological	--	--
Inf	0	Inf	Significant up	--		--	cytochrom	1.16.5.1
Inf	0	Inf	Significant up	--		--	signal recc	--
Inf	0	Inf	Significant up	--		--	cysteinyl-t	6.1.1.16
Inf	0	Inf	Significant up			7 Molecular	DNA replic	3.6.4.12
Inf	0	Inf	Significant up			4 Molecular	very long c	1.3.8.9
Inf	0	Inf	Significant up			2 Molecular	RNA-bind	--
Inf	0	Inf	Significant up			1 Molecular	numb	--
Inf	0	Inf	Significant up			1 Biological	translation	--
0.066458	0.059018	-3.91141	Nonsignifi	None		1 Molecular	fibrillin 1	--
0.52659	0.03739	-0.92525	Nonsignifi	None	--	--	--	--
0.272681	0.052759	-1.87471	Nonsignifi	None		3 Molecular	myosin he	--

1.992166	0.027908	0.994338	Nonsignifi	None	4	Molecular	myosin he	--	
0.153793	0.076873	-2.70094	Nonsignifi	None	3	Molecular	tyrosine ki	2.7.10.1	
0.34851	0.467259	-1.52073	Nonsignifi	None	5	Molecular	coatomer	--	
Inf	0	Inf	Significant	up	--	--	histidine tr	--	
Inf	0	Inf	Significant	up	--	--	regulator c	--	
Inf	0	Inf	Significant	up		3	Molecular	glycogen s	2.7.11.26
Inf	0	Inf	Significant	up		1	Molecular	estrone su	2.8.2.4
Inf	0	Inf	Significant	up	--	--	5'-nucleot	3.1.3.5	
Inf	0	Inf	Significant	up		5	Molecular	guanine n	--
1.912028	0.122447	0.935104	Nonsignifi	None	3	Molecular	glutaredox	--	
Inf	0	Inf	Significant	up		3	Molecular	guanine n	--
0.176287	0.050328	-2.504	Nonsignifi	None	1	Molecular	insulin-like	--	
Inf	0	Inf	Significant	up		3	Biological	solute carr	--
0.859886	0.147299	-0.21778	Nonsignifi	None	1	Molecular	26S protea	--	
0.008391	0.05714	-6.89687	Nonsignifi	None	1	Biological	chitinase-	--	
Inf	0	Inf	Significant	up		2	Molecular	--	--
Inf	0	Inf	Significant	up	--	--	kinetochor	--	
Inf	0	Inf	Significant	up		3	Molecular	--	--
Inf	0	Inf	Significant	up	--	--	--	--	
Inf	0	Inf	Significant	up		1	Molecular	palmitoyl-	3.1.2.22
Inf	0	Inf	Significant	up		1	Molecular	fragile X m	--
0.586311	0.341013	-0.77026	Nonsignifi	None	3	Molecular	large subu	--	
Inf	0	Inf	Significant	up		2	Molecular	Ras-relate	--
0.523679	0.131272	-0.93325	Nonsignifi	None	2	Biological	phosphogl	5.4.2.2	
Inf	0	Inf	Significant	up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		5	Molecular	phosphatic	3.1.4.11
Inf	0	Inf	Significant	up		2	Biological	--	--
Inf	0	Inf	Significant	up		4	Molecular	SWI/SNF-r	3.6.4.-
Inf	0	Inf	Significant	up		3	Cellular Cc	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		1	Biological	caveolin 2	--
Inf	0	Inf	Significant	up		1	Cellular Cc	--	--
Inf	0	Inf	Significant	up		4	Molecular	chloride ct	--
0.601613	0.085488	-0.73309	Nonsignifi	None	1	Molecular	transgelin	--	
0.552428	0.367689	-0.85614	Nonsignifi	None	1	Biological	transaldol	2.2.1.2	
Inf	0	Inf	Significant	up		4	Molecular	chloride ct	--
Inf	0	Inf	Significant	up		2	Cellular Cc	vesicle-ass	--
Inf	0	Inf	Significant	up		4	Molecular	ribosomal	2.7.11.1
Inf	0	Inf	Significant	up	--	--	hepatoma	--	
Inf	0	Inf	Significant	up		1	Molecular	heterogen	--
Inf	0	Inf	Significant	up		5	Molecular	importin si	--
Inf	0	Inf	Significant	up		5	Molecular	importin si	--
0.235597	0.067466	-2.08561	Nonsignifi	None	4	Molecular	large subu	--	
Inf	0	Inf	Significant	up		1	Molecular	--	--
Inf	0	Inf	Significant	up		3	Biological	solute carr	--
Inf	0	Inf	Significant	up		1	Molecular	Arf-GAP d	--
Inf	0	Inf	Significant	up		1	Molecular	heterogen	--
Inf	0	Inf	Significant	up		2	Cellular Cc	transcripti	--
3.760672	0.001779	1.91099	Nonsignifi	None	1	Molecular	T-complex	--	
2.377137	0.34593	1.249225	Nonsignifi	None	1	Molecular	nicotinami	2.1.1.1	
0.568795	0.317396	-0.81402	Nonsignifi	None	3	Molecular	large subu	--	
Inf	0	Inf	Significant	up		3	Molecular	DNA mism	--
Inf	0	Inf	Significant	up		2	Molecular	hexokinase	2.7.1.1
Inf	0	Inf	Significant	up		1	Cellular Cc	ephrin-B	--
0.501184	0.059625	-0.99659	Nonsignifi	None	2	Molecular	malate de	1.1.1.37	
Inf	0	Inf	Significant	up		2	Molecular	thimet olic	3.4.24.15

Inf		0	Inf	Significant up		1	Molecular	high mobil	--
0.143696	0.107125	-2.79891	Nonsignifi	None		4	Molecular	wingless-t	--
Inf		0	Inf	Significant up		5	Molecular	biliverdin r	1.3.1.24
Inf		0	Inf	Significant up		2	Molecular	serine/thre	3.1.3.16
0.4602	0.002835	-1.11967	Nonsignifi	None		4	Molecular	glycyl-tRN	6.1.1.14
0.854012	0.493659	-0.22767	Nonsignifi	None		4	Molecular	isoleucyl-t	6.1.1.5
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	methionyl	3.4.11.18
Inf		0	Inf	Significant up		5	Molecular	clathrin he	--
Inf		0	Inf	Significant up		4	Molecular	solute carr	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	chloride cl	--
Inf		0	Inf	Significant up		5	Molecular	arginyl-tR	6.1.1.19
Inf		0	Inf	Significant up		2	Molecular	Ataxin-3	3.4.22.-
Inf		0	Inf	Significant up		2	Biological	ubiquitin c	3.4.19.12
Inf		0	Inf	Significant up	--	--	--	5'-AMP-ac	--
Inf		0	Inf	Significant up		2	Molecular	branched-	2.6.1.42
Inf		0	Inf	Significant up		4	Molecular	UV excision	--
0.532435	0.038507	-0.90932	Nonsignifi	None		4	Molecular	large subu	--
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
2.384072	0.007396	1.253428	Nonsignifi	None		2	Molecular	solute carr	--
0.326967	0.009411	-1.61278	Nonsignifi	None		1	Molecular	platelet-ac	--
Inf		0	Inf	Significant up		1	Cellular	Cc	--
Inf		0	Inf	Significant up		5	Molecular	solute carr	--
Inf		0	Inf	Significant up	--	--	--	26S protea	--
Inf		0	Inf	Significant up		1	Molecular	uncharacte	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		3	Molecular	coagulatio	--
0.112109	0.056955	-3.15702	Nonsignifi	None		1	Cellular	Cc	--
0.347338	0.204496	-1.52559	Nonsignifi	None		3	Biological	peptidyl-p	5.2.1.8
Inf		0	Inf	Significant up		2	Molecular	afadin	--
Inf		0	Inf	Significant up	--	--	--	caspase 6	3.4.22.59
Inf		0	Inf	Significant up	--	--	--	U4/U6 sm	--
Inf		0	Inf	Significant up		1	Molecular	heterogen	--
Inf		0	Inf	Significant up		1	Biological	ribosomal	--
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		3	Biological	C-terminal	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	breast can	--
Inf		0	Inf	Significant up		1	Molecular	ubiquitin-	3.1.3.48
0.586277	0.146719	-0.77035	Nonsignifi	None	--	--	--	large subu	--
0.727897	0.395502	-0.45819	Nonsignifi	None		4	Molecular	large subu	--
1.369109	0.19221	0.453237	Nonsignifi	None		3	Molecular	small subu	--
Inf		0	Inf	Significant up	--	--	--	junctional	--
Inf		0	Inf	Significant up		1	Cellular	Cc transmem	--
Inf		0	Inf	Significant up		1	Molecular	coronin-7	--
Inf		0	Inf	Significant up	--	--	--	gasdermin	--
0.146209	0.229269	-2.7739	Nonsignifi	None		2	Molecular	Ras GTPas	--
0.070515	0.134174	-3.82592	Nonsignifi	None		3	Molecular	3-hydroxy	1.13.11.6
Inf		0	Inf	Significant up	--	--	--	--	--
0.620062	0.04895	-0.68952	Nonsignifi	None		2	Cellular	Cc capping pr	--
Inf		0	Inf	Significant up		3	Molecular	guanine nt	--
0.686424	0.391646	-0.54283	Nonsignifi	None		4	Molecular	large subu	--
0.048769	0.133986	-4.35788	Nonsignifi	None		1	Molecular	galectin-7	--
Inf		0	Inf	Significant up	--	--	--	protein tra	--

0.660234	0.303805	-0.59895	Nonsignifi	None		1 Molecular	--	--
Inf	0	Inf	Significant	up		1 Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significant	up	--	--	GABA(A) r	--
Inf	0	Inf	Significant	up	--	--	ubiquitin-(	2.3.2.23
Inf	0	Inf	Significant	up	--	--	calpactin-	--
Inf	0	Inf	Significant	up		2 Molecular	--	--
0.36464	0.074601	-1.45545	Nonsignifi	None		2 Molecular	glutamate-	6.3.2.2
0.452391	0.258347	-1.14436	Nonsignifi	None	--	--	glutamate-	--
3.037828	0.011448	1.60304	Nonsignifi	None		1 Cellular Cc	CD151 ant	--
Inf	0	Inf	Significant	up		2 Molecular	Ras-relate	--
1.236088	0.341987	0.305781	Nonsignifi	None		1 Molecular	T-complex	--
0.306229	0.036088	-1.70732	Nonsignifi	None	--	--	stress 70 p	--
Inf	0	Inf	Significant	up	--	--	ubiquitin-(	2.3.2.23
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	--
Inf	0	Inf	Significant	up	--	--	centractin	--
Inf	0	Inf	Significant	up		2 Molecular	ATP-bindin	--
Inf	0	Inf	Significant	up		1 Cellular Cc	proteasom	--
1.843342	0.010083	0.882324	Nonsignifi	None		3 Biological	--	--
Inf	0	Inf	Significant	up	--	--	V-type H+	--
Inf	0	Inf	Significant	up		2 Molecular	Ras homol	--
1.027669	0.956771	0.039376	Nonsignifi	None		2 Biological	fatty acid s	2.3.1.85
1.215776	0.101731	0.281877	Nonsignifi	None		1 Molecular	T-complex	--
Inf	0	Inf	Significant	up		2 Molecular	Rho family	--
Inf	0	Inf	Significant	up		2 Cellular Cc	chaperonir	--
Inf	0	Inf	Significant	up		2 Biological	protein tra	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up		2 Biological	syntaxin-b	--
0.806142	0.718905	-0.31089	Nonsignifi	None		4 Molecular	seryl-tRNA	6.1.1.11
0.536145	0.012773	-0.89931	Nonsignifi	None		3 Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant	up	--	--	Niemann-	--
0.139921	0.093657	-2.83731	Nonsignifi	None		3 Molecular	thrombos	--
0.26301	0.035633	-1.92681	Nonsignifi	None		3 Molecular	thrombos	--
Inf	0	Inf	Significant	up	--	--	coatomer	--
Inf	0	Inf	Significant	up	--	--	ubiquitin-f	--
Inf	0	Inf	Significant	up		1 Molecular	WD repeat	--
Inf	0	Inf	Significant	up		1 Molecular	COMPASS	--
Inf	0	Inf	Significant	up	--	--	AP-1 com	--
Inf	0	Inf	Significant	up		2 Cellular Cc	--	--
Inf	0	Inf	Significant	up		2 Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		1 Cellular Cc	tetraspanir	--
Inf	0	Inf	Significant	up		1 Molecular	neuronal c	--
1.15626	0.554538	0.209466	Nonsignifi	None		4 Molecular	GMP synth	6.3.5.2
Inf	0	Inf	Significant	up	--	--	ubiquitin-(	2.3.2.23
Inf	0	Inf	Significant	up	--	--	U6 snRNA	--
0.010493	0.056801	-6.57444	Nonsignifi	None		4 Molecular	matrix met	3.4.24.80
1.149782	0.559335	0.20136	Nonsignifi	None		2 Molecular	Rab GDP c	--
Inf	0	Inf	Significant	up	--	--	small nucle	--
0.452414	0.240003	-1.14429	Nonsignifi	None	--	--	serpin pep	--
Inf	0	Inf	Significant	up		2 Molecular	cellular nu	--
1.608752	0.031726	0.685942	Nonsignifi	None		1 Molecular	suppressor	--
0.910439	0.844721	-0.13537	Nonsignifi	None		2 Molecular	dynamin G	3.6.5.5
0.797912	0.210682	-0.3257	Nonsignifi	None		1 Molecular	bis(5'-nucl	3.6.1.17
Inf	0	Inf	Significant	up		2 Molecular	Ras homol	--
Inf	0	Inf	Significant	up		3 Molecular	large subu	--
Inf	0	Inf	Significant	up		3 Molecular	small subu	--

Inf	0	Inf	Significant up		4	Molecular	small subu	--
0.636064	0.370727	-0.65276	Nonsignifi	None	4	Molecular	large subu	--
2.22322	0.070031	1.15265	Nonsignifi	None	1	Molecular	T-complex	--
2.584838	0.004287	1.370074	Nonsignifi	None	1	Molecular	T-complex	--
1.313956	0.221576	0.393917	Nonsignifi	None	2	Molecular	annexin A7	--
Inf	0	Inf	Significant up		1	Molecular	guanine nu	--
Inf	0	Inf	Significant up		1	Molecular	RING-box	--
1.999785	0.003482	0.999845	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		3	Molecular	large subu	--
Inf	0	Inf	Significant up		1	Molecular	growth fac	--
Inf	0	Inf	Significant up		1	Molecular	serine/thre	--
Inf	0	Inf	Significant up		2	Biological	dynein ligh	--
Inf	0	Inf	Significant up		4	Molecular	large subu	--
0.644738	0.294048	-0.63321	Nonsignifi	None	1	Molecular	galactokin	2.7.1.6
Inf	0	Inf	Significant up		1	Biological	S-phase ki	--
Inf	0	Inf	Significant up		3	Molecular	guanine nu	--
Inf	0	Inf	Significant up	--	--	--	ubiquitin- α	--
Inf	0	Inf	Significant up		1	Molecular	Y-box-bin	--
Inf	0	Inf	Significant up	--	--	--	signal pep	3.4.21.89
Inf	0	Inf	Significant up	--	--	--	ubiquitin- α	2.3.2.23
Inf	0	Inf	Significant up	--	--	--	platelet-ac	3.1.1.47
Inf	0	Inf	Significant up		1	Molecular	histone H3	--
Inf	0	Inf	Significant up	--	--	--	coxsackiev	--
Inf	0	Inf	Significant up		2	Molecular	translation	--
0.08173	0.058695	-3.61299	Nonsignifi	None	1	Molecular	lumican	--
1.316062	0.170704	0.396228	Nonsignifi	None	3	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	transcripti	--
Inf	0	Inf	Significant up		2	Molecular	1-phosphat	2.7.1.149
Inf	0	Inf	Significant up	--	--	--	disintegrin	3.4.24.86
Inf	0	Inf	Significant up	--	--	--	interleukin	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Cellular	Cc chromobo	--
Inf	0	Inf	Significant up		1	Cellular	Cc mothers a	--
Inf	0	Inf	Significant up		1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant up		3	Biological	--	--
0.187539	0.057429	-2.41474	Nonsignifi	None	--	--	2-iminobu	3.5.99.10
Inf	0	Inf	Significant up		2	Molecular	fibulin 1/2	--
Inf	0	Inf	Significant up		2	Molecular	very low-d	--
Inf	0	Inf	Significant up		1	Cellular	Cc ephrin-B	--
Inf	0	Inf	Significant up		2	Molecular	Ca ²⁺ -tran	3.6.3.8
1.252242	0.247516	0.324513	Nonsignifi	None	2	Cellular	Cc capping pr	--
Inf	0	Inf	Significant up		2	Molecular	phospholip	3.6.3.1
Inf	0	Inf	Significant up		1	Molecular	55 kDa ery	--
Inf	0	Inf	Significant up		2	Cellular	Cc --	--
Inf	0	Inf	Significant up		2	Molecular	S-adenosy	2.5.1.6
1.120032	0.526098	0.16354	Nonsignifi	None	3	Molecular	ATP citrate	2.3.3.8
Inf	0	Inf	Significant up		1	Molecular	--	--
0.895226	0.812639	-0.15968	Nonsignifi	None	6	Molecular	coatomer	--
0.090898	0.065884	-3.45961	Nonsignifi	None	2	Biological	cathepsin	3.4.14.1
Inf	0	Inf	Significant up		3	Molecular	cyclin-dep	2.7.11.22
2.435986	0.048693	1.284506	Nonsignifi	None	--	--	AP-2 com	--
Inf	0	Inf	Significant up		3	Molecular	cyclin-dep	2.7.11.22
Inf	0	Inf	Significant up		3	Molecular	cyclin-dep	2.7.11.22
0.71134	0.311623	-0.49139	Nonsignifi	None	2	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	cyclin-dep	2.7.11.22
Inf	0	Inf	Significant up	--	--	--	transcripti	--
Inf	0	Inf	Significant up	--	--	--	FK506-bin	5.2.1.8
0.261145	0.072589	-1.93708	Nonsignifi	None	--	--	voltage-d	--

0.007652	0.502368	-7.03003	Nonsignifi	None		5 Molecular	tyrosyl-tRN	6.1.1.1
Inf	0	Inf	Significant	up		1 Biological	L-iditol 2-	1.1.1.14
Inf	0	Inf	Significant	up		2 Molecular	hydroxyme	2.3.3.10
2.594794	0.000463	1.37562	Nonsignifi	None	--	--	heat shock	--
Inf	0	Inf	Significant	up		2 Biological	interferon	--
Inf	0	Inf	Significant	up		3 Biological	solute carr	--
Inf	0	Inf	Significant	up	--	--	down-regu	--
Inf	0	Inf	Significant	up	--	--	OTU dom	3.4.19.12
Inf	0	Inf	Significant	up		7 Molecular	phosphatic	3.1.4.11
0.275908	0.13468	-1.85774	Nonsignifi	None		1 Cellular Cc	--	--
Inf	0	Inf	Significant	up		3 Molecular	receptor ty	2.7.10.1
Inf	0	Inf	Significant	up		6 Molecular	guanylate	4.6.1.2
Inf	0	Inf	Significant	up		4 Molecular	kinesin far	--
0.391763	0.043568	-1.35195	Nonsignifi	None		1 Molecular	transitiona	--
Inf	0	Inf	Significant	up		4 Cellular Cc	histone H1	--
Inf	0	Inf	Significant	up		1 Molecular	FK506-bin	5.2.1.8
Inf	0	Inf	Significant	up		5 Molecular	DNA topoi	5.99.1.3
Inf	0	Inf	Significant	up		2 Biological	A-kinase a	--
1.283564	0.130902	0.360156	Nonsignifi	None	--	--	adenosine	2.7.1.20
Inf	0	Inf	Significant	up		5 Molecular	guanine nu	--
0.27339	0.149598	-1.87097	Nonsignifi	None		3 Molecular	cadherin 1	--
0.306997	0.000427	-1.7037	Nonsignifi	None		3 Molecular	cadherin 1	--
Inf	0	Inf	Significant	up		1 Biological	caveolin 1	--
Inf	0	Inf	Significant	up		2 Cellular Cc	tumor necr	--
1.216083	0.54343	0.282242	Nonsignifi	None	--	--	small ubiq	--
1.767256	0.012018	0.821511	Nonsignifi	None		1 Molecular	translation	--
Inf	0	Inf	Significant	up	--	--	plasminog	--
Inf	0	Inf	Significant	up		1 Molecular	mevalonat	2.7.1.36
Inf	0	Inf	Significant	up		1 Molecular	transcripti	--
Inf	0	Inf	Significant	up		3 Molecular	1,4-alpha-	2.4.1.18
Inf	0	Inf	Significant	up		2 Molecular	translation	--
Inf	0	Inf	Significant	up		5 Molecular	activin rec	2.7.11.30
Inf	0	Inf	Significant	up		1 Molecular	single-str	--
Inf	0	Inf	Significant	up		2 Molecular	dynamain G	3.6.5.5
Inf	0	Inf	Significant	up		2 Molecular	tyrosine-p	3.1.3.48
Inf	0	Inf	Significant	up		6 Molecular	focal adhe	2.7.10.2
Inf	0	Inf	Significant	up		1 Molecular	elongation	--
Inf	0	Inf	Significant	up		2 Molecular	tyrosine-p	3.1.3.48
Inf	0	Inf	Significant	up	--	--	exosome c	--
Inf	0	Inf	Significant	up		3 Molecular	amyloid-lil	--
3.442848	0.025518	1.783602	Nonsignifi	None		4 Cellular Cc	actin relate	--
0.955833	0.878223	-0.06517	Nonsignifi	None		1 Cellular Cc	CD81 anti	--
1.220261	0.396102	0.287189	Nonsignifi	None		2 Molecular	triosephos	5.3.1.1
1.304028	0.178743	0.382975	Nonsignifi	None		1 Molecular	translation	--
Inf	0	Inf	Significant	up		1 Cellular Cc	compleme	--
Inf	0	Inf	Significant	up		1 Molecular	tight juncti	--
Inf	0	Inf	Significant	up		1 Molecular	sperm-ass	--
Inf	0	Inf	Significant	up		1 Molecular	KH domair	--
0.655962	0.01826	-0.60832	Nonsignifi	None		1 Molecular	myosin ligl	--
1.485305	0.150448	0.57076	Nonsignifi	None	--	--	actin beta/	--
2.233307	0.009305	1.159182	Nonsignifi	None		2 Molecular	Ras-relate	--
1.671273	0.005544	0.740948	Nonsignifi	None		2 Molecular	translation	--
1.68729	0.041557	0.754708	Nonsignifi	None	--	--	small subu	--
0.718863	0.020383	-0.47621	Nonsignifi	None		5 Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant	up		1 Biological	apoptosis	--
2.532451	0.015379	1.340535	Nonsignifi	None		2 Molecular	cell divisio	--
1.069983	0.785676	0.097588	Nonsignifi	None		2 Molecular	destrin (ac	--
Inf	0	Inf	Significant	up		5 Molecular	son of seve	--

0.0585	0.131015	-4.09541	Nonsignifi	None	4	Molecular	signal recc	3.6.5.4
1.307278	0.235295	0.386566	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significan	up	1	Molecular	splicing fa	--
1.789776	0.227451	0.839779	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significan	up	1	Biological	Rho GTPas	--
Inf	0	Inf	Significan	up	1	Molecular	splicing fa	--
Inf	0	Inf	Significan	up	1	Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significan	up	1	Biological	NADPH2:q	1.6.5.5
Inf	0	Inf	Significan	up	3	Molecular	solute carr	--
1.913352	0.132906	0.936102	Nonsignifi	None	--	--	actin-relat	--
Inf	0	Inf	Significan	up	--	--	CD47 antiç	--
1.859418	0.005192	0.894851	Nonsignifi	None	1	Molecular	ADP-ribos	--
Inf	0	Inf	Significan	up	4	Biological	peptidyl-p	5.2.1.8
1.037012	0.911741	0.052433	Nonsignifi	None	2	Molecular	Ras-relate	--
1.444911	0.249366	0.53098	Nonsignifi	None	3	Molecular	small subu	--
Inf	0	Inf	Significan	up	--	--	vacuole m	--
0.474808	0.099708	-1.07458	Nonsignifi	None	3	Molecular	large subu	--
0.378699	0.006815	-1.40088	Nonsignifi	None	4	Molecular	large subu	--
Inf	0	Inf	Significan	up	1	Molecular	tRNA (cytc	2.1.1.203
Inf	0	Inf	Significan	up	3	Molecular	nuclear ca	--
Inf	0	Inf	Significan	up	--	--	--	--
Inf	0	Inf	Significan	up	--	--	ragulator c	--
Inf	0	Inf	Significan	up	--	--	polypeptid	2.4.1.41
Inf	0	Inf	Significan	up	2	Molecular	cleavage a	--
Inf	0	Inf	Significan	up	2	Biological	beta-galac	2.4.99.4
0.062887	0.050176	-3.99109	Nonsignifi	None	--	--	beta-2-mi	--
Inf	0	Inf	Significan	up	2	Biological	secernin	--
Inf	0	Inf	Significan	up	1	Cellular	Cc WASH con	--
Inf	0	Inf	Significan	up	3	Molecular	U3 small n	--
Inf	0	Inf	Significan	up	5	Molecular	potassium	--
Inf	0	Inf	Significan	up	2	Molecular	twinfilin	--
Inf	0	Inf	Significan	up	2	Molecular	syntaxin 4	--
Inf	0	Inf	Significan	up	--	--	splicing fa	--
2.05658	0.130694	1.040247	Nonsignifi	None	1	Molecular	heterogen	--
1.080876	0.646074	0.112201	Nonsignifi	None	--	--	14-3-3 prc	--
Inf	0	Inf	Significan	up	3	Cellular	Cc dihydropy	1.3.1.2
Inf	0	Inf	Significan	up	--	--	tumor sup	--
1.25682	0.034182	0.329778	Nonsignifi	None	1	Molecular	serine/thre	3.1.3.16
1.703321	0.091732	0.76835	Nonsignifi	None	1	Molecular	calmodulir	--
Inf	0	Inf	Significan	up	1	Molecular	aminoacyl	--
1.406059	0.095294	0.491657	Nonsignifi	None	1	Molecular	26S protea	--
0.823567	0.246542	-0.28004	Nonsignifi	None	1	Molecular	26S protea	--
0.842926	0.612631	-0.24652	Nonsignifi	None	--	--	small subu	--
0.87115	0.281083	-0.19901	Nonsignifi	None	3	Molecular	small subu	--
Inf	0	Inf	Significan	up	--	--	interleukin	--
1.753361	0.125485	0.810123	Nonsignifi	None	--	--	14-3-3 prc	--
0.536812	0.01347	-0.89751	Nonsignifi	None	3	Molecular	small subu	--
1.253938	0.022251	0.326465	Nonsignifi	None	4	Molecular	small subu	--
1.397806	0.076264	0.483164	Nonsignifi	None	5	Molecular	small subu	--
1.732066	0.042778	0.792494	Nonsignifi	None	4	Molecular	small subu	--
1.324768	0.054196	0.40574	Nonsignifi	None	4	Molecular	small subu	--
Inf	0	Inf	Significan	up	--	--	interleukin	--
Inf	0	Inf	Significan	up	3	Molecular	receptor-t	3.1.3.48
1.275083	0.561913	0.350591	Nonsignifi	None	--	--	small nucle	--
0.305552	0.323773	-1.71051	Nonsignifi	None	2	Molecular	thymosin,	--
Inf	0	Inf	Significan	up	3	Molecular	tyrosine-p	--
0.518743	0.063943	-0.94691	Nonsignifi	None	1	Molecular	26S protea	--
1.431439	0.106496	0.517466	Nonsignifi	None	--	--	large subu	--

Inf	0	Inf	Significant up		1 Molecular	epidermal	--
0.839643	0.285123	-0.25215	Nonsignifi		1 Molecular	small subu	--
1.104735	0.728892	0.143701	Nonsignifi	--	--	actin, aorti	--
Inf	0	Inf	Significant up		2 Molecular	TNF recept	2.3.2.27
0.929521	0.820721	-0.10544	Nonsignifi		3 Molecular	large subu	--
0.358743	0.076007	-1.47898	Nonsignifi		4 Molecular	small subu	--
Inf	0	Inf	Significant up		1 Molecular	disks large	--
0.653832	0.022902	-0.61301	Nonsignifi		2 Molecular	Ras-relate	--
1.359643	0.236873	0.443227	Nonsignifi		2 Molecular	GTP-bindin	--
Inf	0	Inf	Significant up		4 Molecular	myosin I	--
1.070974	0.636839	0.098924	Nonsignifi		2 Molecular	Ras-relate	--
Inf	0	Inf	Significant up		2 Molecular	protein tyr	3.1.3.48
Inf	0	Inf	Significant up		4 Molecular	active bree	--
1.288221	0.513903	0.36538	Nonsignifi	--	--	small subu	--
0.949449	0.787121	-0.07484	Nonsignifi		4 Molecular	small subu	--
2.499673	0.005601	1.32174	Nonsignifi		4 Molecular	small subu	--
Inf	0	Inf	Significant up		1 Molecular	striatin 1/3	--
Inf	0	Inf	Significant up	--	--	anaphase-	--
2.239283	0.006655	1.163037	Nonsignifi		1 Molecular	guanine nu	--
Inf	0	Inf	Significant up		4 Molecular	serine/thre	--
0.532821	0.034295	-0.90828	Nonsignifi	--	--	large subu	--
0.51696	0.097687	-0.95188	Nonsignifi		4 Molecular	large subu	--
1.845008	0.023974	0.883627	Nonsignifi		3 Biological	peptidyl-p	5.2.1.8
0.243075	0.057107	-2.04053	Nonsignifi	--	--	FK506-bin	5.2.1.8
0.897542	0.282057	-0.15595	Nonsignifi		4 Molecular	small subu	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		3 Molecular	--	--
0.814249	0.576369	-0.29646	Nonsignifi		4 Biological	AP-2 com	--
Inf	0	Inf	Significant up		1 Molecular	lymphocyt	--
2.003409	0.242275	1.002457	Nonsignifi	--	--	14-3-3 pr	--
Inf	0	Inf	Significant up		3 Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up		3 Molecular	5'-AMP- α	2.7.11.11
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	translation	--
1.648832	0.047448	0.721445	Nonsignifi		1 Molecular	guanine nu	--
2.616724	0.1685	1.387762	Nonsignifi	--	--	actin beta/	--
Inf	0	Inf	Significant up		1 Molecular	--	--
1.518905	0.005779	0.603031	Nonsignifi		1 Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significant up		1 Molecular	heterogen	--
Inf	0	Inf	Significant up	--	--	aminoacyl	--
0.783695	0.442703	-0.35164	Nonsignifi		2 Cellular Cc	casein kin	--
0.555915	0.131962	-0.84706	Nonsignifi	--	--	tropomyos	--
Inf	0	Inf	Significant up		4 Molecular	peroxiredc	1.11.1.15
1.627857	0.00577	0.702974	Nonsignifi		1 Molecular	elongation	--
0.265547	0.123444	-1.91296	Nonsignifi		1 Molecular	tubulin alp	--
0.120185	0.088653	-3.05667	Nonsignifi		1 Molecular	tubulin alp	--
0.56605	0.249617	-0.821	Nonsignifi		1 Molecular	tubulin bet	--
0.924422	0.750592	-0.11338	Nonsignifi		3 Molecular	casein kin	2.7.11.1
Inf	0	Inf	Significant up		3 Molecular	p21-activa	2.7.11.1
Inf	0	Inf	Significant up		1 Molecular	selenium-t	--
0.367692	0.000115	-1.44343	Nonsignifi		2 Molecular	hemoglob	--
0.361081	2.18E-05	-1.46961	Nonsignifi		2 Molecular	hemoglob	--
Inf	0	Inf	Significant up		1 Molecular	splicing fac	--
Inf	0	Inf	Significant up		1 Molecular	splicing fac	--
Inf	0	Inf	Significant up	--	--	noggin	--
Inf	0	Inf	Significant up	--	--	mitotic spi	--
1.260883	0.325927	0.334435	Nonsignifi		1 Molecular	T-complex	--
0.044584	0.097545	-4.48733	Nonsignifi		7 Molecular	DNA-depe	2.7.11.1

Inf	0	Inf	Significant up	3	Molecular	tripartite n	2.3.2.27
Inf	0	Inf	Significant up	1	Molecular	semaphori	--
Inf	0	Inf	Significant up	2	Molecular	syntaxin 1f	--
Inf	0	Inf	Significant up	3	Molecular	--	--
0.809321	0.394444	-0.30522	Nonsignifi	--	--	brain acid	--
Inf	0	Inf	Significant up	1	Molecular	--	--
0.665481	0.152879	-0.58753	Nonsignifi	--	--	large subu	--
Inf	0	Inf	Significant up	3	Molecular	metastasis	--
Inf	0	Inf	Significant up	3	Molecular	solute carr	--
Inf	0	Inf	Significant up	2	Molecular	phospholi	3.1.4.4
Inf	0	Inf	Significant up	3	Molecular	dynein inte	--
3.306851	0.008195	1.725458	Nonsignifi	2	Molecular	Ras homol	--
0.131959	0.368902	-2.92184	Nonsignifi	4	Molecular	large subu	--
1.117329	0.698964	0.160053	Nonsignifi	1	Molecular	splicing fac	--
Inf	0	Inf	Significant up	3	Biological	peptidyl-p	5.2.1.8
Inf	0	Inf	Significant up	--	--	Treacher C	--
Inf	0	Inf	Significant up	4	Cellular Cc	solute carr	--
Inf	0	Inf	Significant up	1	Cellular Cc	splicing fac	--
Inf	0	Inf	Significant up	--	--	--	--
0.010433	0.05976	-6.58264	Nonsignifi	2	Molecular	phospholi	3.6.3.1
Inf	0	Inf	Significant up	2	Molecular	disintegrin	3.4.24.-
Inf	0	Inf	Significant up	2	Molecular	disintegrin	3.4.24.-
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	2	Molecular	V-type H+	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	2	Molecular	sequestosc	--
Inf	0	Inf	Significant up	2	Molecular	peptidyl-p	5.2.1.8
Inf	0	Inf	Significant up	--	--	histone de	3.5.1.98
Inf	0	Inf	Significant up	5	Molecular	calcium/ca	2.7.11.17
1.001408	0.994375	0.002029	Nonsignifi	5	Molecular	clathrin he	--
Inf	0	Inf	Significant up	--	--	dynactin 2	--
Inf	0	Inf	Significant up	1	Cellular Cc	lysosomal-	--
0.97578	0.97735	-0.03537	Nonsignifi	1	Molecular	spectrin be	--
3.553776	0.023059	1.829353	Nonsignifi	2	Cellular Cc	template-	--
1.066636	0.87102	0.093068	Nonsignifi	1	Molecular	splicing fac	--
0.323866	3.45E-06	-1.62653	Nonsignifi	1	Molecular	AMP dearr	3.5.4.6
1.093347	0.771247	0.128751	Nonsignifi	--	--	fatty acid-	--
2.127868	0.09041	1.089409	Nonsignifi	2	Molecular	adenylyl cy	--
Inf	0	Inf	Significant up	2	Molecular	Ras GTPas	--
1.588342	0.257341	0.667522	Nonsignifi	2	Biological	interferon	--
Inf	0	Inf	Significant up	1	Molecular	transforme	--
Inf	0	Inf	Significant up	2	Biological	sorting ne	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	2	Biological	cullin 1	--
1.425959	0.022794	0.511933	Nonsignifi	2	Molecular	6-phosphc	2.7.1.11
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	1	Molecular	apoptosis-	--
0.455842	0.013835	-1.13339	Nonsignifi	2	Molecular	collagen, t	--
Inf	0	Inf	Significant up	2	Molecular	GDP-L-fuc	1.1.1.271
Inf	0	Inf	Significant up	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	1	Biological	Ras and R	--
1.353593	0.595122	0.436794	Nonsignifi	4	Molecular	large subu	--
Inf	0	Inf	Significant up	--	--	integrin al	--
Inf	0	Inf	Significant up	--	--	THO comp	--

Inf		0	Inf	Significant up		1	Molecular	ADP-ribos	--
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 mor	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	isopenten	5.3.3.2
Inf		0	Inf	Significant up	--	--	--	cytoskelet	--
0.255758	0.058418	-1.96715	Nonsignifi	None		4	Molecular	hepatocyt	3.4.21.-
Inf		0	Inf	Significant up		1	Cellular Cc	lysosome r	--
Inf		0	Inf	Significant up		1	Molecular	dihydropy	3.5.2.2
1.353412	0.062257	0.436602	Nonsignifi	None	--	--	--	14-3-3 pr	--
Inf		0	Inf	Significant up		2	Biological	dystroglyc	--
Inf		0	Inf	Significant up		3	Molecular	desmoglei	--
Inf		0	Inf	Significant up		2	Molecular	ribosome l	--
0.344026	0.011181	-1.53941	Nonsignifi	None		1	Molecular	splicing fa	--
Inf		0	Inf	Significant up		1	Molecular	septin 6/8	--
0.663777	0.423772	-0.59123	Nonsignifi	None	--	--	--	caldesmon	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		3	Molecular	Rho guanin	--
Inf		0	Inf	Significant up	--	--	--	--	--
0.20406	0.32219	-2.29294	Nonsignifi	None		2	Biological	glucosami	2.6.1.16
Inf		0	Inf	Significant up		1	Molecular	protein scr	--
Inf		0	Inf	Significant up		1	Biological	tubulin--t	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		1	Molecular	dedicator	--
0.450596	0.037379	-1.15009	Nonsignifi	None		4	Molecular	peroxiredc	1.11.1.15
0.828492	0.627764	-0.27144	Nonsignifi	None	--	--	--	large subu	--
Inf		0	Inf	Significant up		1	Molecular	four and a	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up	--	--	--	dynactin 1	--
Inf		0	Inf	Significant up		1	Biological	translation	--
Inf		0	Inf	Significant up		2	Molecular	translation	--
Inf		0	Inf	Significant up		1	Molecular	cortactin	--
Inf		0	Inf	Significant up		1	Molecular	tripartite n	2.3.2.27
0.266185	9.38E-05	-1.9095	Nonsignifi	None		2	Molecular	low-densit	--
Inf		0	Inf	Significant up		1	Molecular	filamin	--
Inf		0	Inf	Significant up	--	--	--	UDP-gluc	5.1.3.2
Inf		0	Inf	Significant up		2	Molecular	growth arr	--
Inf		0	Inf	Significant up		3	Molecular	G protein-	--
Inf		0	Inf	Significant up	--	--	--	caprin-1	--
Inf		0	Inf	Significant up		1	Molecular	RNA-bind	--
0.242522	0.074273	-2.04381	Nonsignifi	None		2	Molecular	galectin-3	--
0.38336	0.171269	-1.38323	Nonsignifi	None		1	Molecular	lactadherin	--
0.085985	0.06717	-3.53977	Nonsignifi	None		4	Molecular	sparc/oste	--
Inf		0	Inf	Significant up		4	Molecular	protocadh	--
Inf		0	Inf	Significant up		3	Molecular	DNA replic	3.6.4.12
Inf		0	Inf	Significant up	--	--	--	inositol-1,	3.1.3.56
Inf		0	Inf	Significant up		2	Molecular	plastin-1	--
Inf		0	Inf	Significant up		1	Molecular	mediator c	--
4.391373	0.061747	2.134672	Nonsignifi	None	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		4	Molecular	structural r	--
0.041701	0.283801	-4.58378	Nonsignifi	None		4	Cellular Cc	alpha-1,6-	2.4.1.143
0.276338	0.000283	-1.85549	Nonsignifi	None	--	--	--	polypeptid	2.4.1.41
Inf		0	Inf	Significant up		3	Molecular	rRNA biog	--
0.64883	0.45397	-0.62409	Nonsignifi	None		4	Biological	AP-1 com	--

Inf		0	Inf	Significant up	--	--	--	--
0.420863	0.005343	-1.24858	Nonsignifi	None		1	Molecular	--
Inf		0	Inf	Significant up		2	Molecular	membrane 3.4.21.112
Inf		0	Inf	Significant up		1	Cellular Cc	sarcospan --
Inf		0	Inf	Significant up		1	Cellular Cc	lamin-B re --
Inf		0	Inf	Significant up		5	Molecular	chromodo 3.6.4.12
Inf		0	Inf	Significant up		2	Molecular	-- --
Inf		0	Inf	Significant up		1	Biological	-- --
0.065871	0.053849	-3.92421	Nonsignifi	None		1	Molecular	EGF-conta --
0.019344	0.065842	-5.69198	Nonsignifi	None		1	Molecular	-- --
Inf		0	Inf	Significant up	--	--	--	--
0.092914	0.066909	-3.42795	Nonsignifi	None		1	Molecular	contactin 1--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	proteasom --
Inf		0	Inf	Significant up		2	Biological	cullin 7 --
Inf		0	Inf	Significant up		1	Biological	-- --
Inf		0	Inf	Significant up		2	Cellular Cc	condensin --
Inf		0	Inf	Significant up		2	Biological	-- --
Inf		0	Inf	Significant up		2	Cellular Cc	-- --
0.379094	0.049875	-1.39937	Nonsignifi	None		1	Cellular Cc	lectin, mar --
Inf		0	Inf	Significant up		1	Cellular Cc	lysosomal- --
Inf		0	Inf	Significant up		1	Molecular	-- --
Inf		0	Inf	Significant up	--	--	--	condensin --
1.750792	0.005943	0.808008	Nonsignifi	None		4	Molecular	TNF recept --
Inf		0	Inf	Significant up		1	Molecular	116 kDa U --
Inf		0	Inf	Significant up		1	Molecular	sorting ne --
Inf		0	Inf	Significant up		2	Cellular Cc	regulator c --
Inf		0	Inf	Significant up		3	Molecular	Rho guanil --
Inf		0	Inf	Significant up		1	Molecular	-- --
Inf		0	Inf	Significant up		1	Molecular	Arf-GAP w --
Inf		0	Inf	Significant up		1	Molecular	bromodon --
Inf		0	Inf	Significant up		1	Molecular	U3 small n --
Inf		0	Inf	Significant up		1	Biological	protein dis 5.3.4.1
Inf		0	Inf	Significant up		3	Cellular Cc	cholestenc 5.3.3.5
0.141213	0.052559	-2.82406	Nonsignifi	None		2	Molecular	platelet-ac 3.1.1.47
Inf		0	Inf	Significant up		3	Cellular Cc	serine/thre --
0.333166	0.000634	-1.58569	Nonsignifi	None		2	Cellular Cc	-- --
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
Inf		0	Inf	Significant up		3	Molecular	Ras GTPas --
Inf		0	Inf	Significant up		1	Molecular	-- --
Inf		0	Inf	Significant up		1	Molecular	lethal(2) gi --
Inf		0	Inf	Significant up		4	Molecular	ribosomal 2.7.11.1
0.998993	0.996655	-0.00145	Nonsignifi	None	--	--	--	26S protea --
0.100496	0.16016	-3.31479	Nonsignifi	None	--	--	--	pappalysin 3.4.24.79
Inf		0	Inf	Significant up		1	Biological	transcripti --
Inf		0	Inf	Significant up		2	Molecular	Ras homol --
Inf		0	Inf	Significant up		1	Molecular	ubiquitin- p 2.3.2.26
Inf		0	Inf	Significant up		2	Molecular	splicing fac --
Inf		0	Inf	Significant up		1	Molecular	-- --
Inf		0	Inf	Significant up		4	Molecular	ribosomal 2.7.11.1
Inf		0	Inf	Significant up		1	Molecular	splicing fac --
Inf		0	Inf	Significant up	--	--	--	protein ph --
Inf		0	Inf	Significant up		4	Biological	protein tra --

0.551901	0.151554	-0.85752	Nonsignifi	None	2 Molecular	PTK7 prote	2.7.10.1
Inf	0	Inf	Significant up		3 Molecular	splicing fac	--
Inf	0	Inf	Significant up		2 Molecular	antiviral he	3.6.4.-
Inf	0	Inf	Significant up		1 Molecular	Na(+)/H(+)	--
0.997403	0.988008	-0.00375	Nonsignifi	None	1 Molecular	translation	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	thyroid ho	--
0.887737	0.72636	-0.1718	Nonsignifi	None	2 Molecular	integrin-lir	2.7.11.1
Inf	0	Inf	Significant up		3 Molecular	mediator c	--
Inf	0	Inf	Significant up		1 Molecular	thyroid rec	--
Inf	0	Inf	Significant up		2 Molecular	microtubu	--
Inf	0	Inf	Significant up		1 Molecular	ELAV-like	--
Inf	0	Inf	Significant up		2 Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up		1 Molecular	mitochondr	--
Inf	0	Inf	Significant up		1 Cellular	Cc mothers a	--
Inf	0	Inf	Significant up		1 Molecular	tubulin-sp	--
Inf	0	Inf	Significant up	--	--	ubiquitin- α	--
Inf	0	Inf	Significant up		2 Cellular	Cc vesicle-ass	--
Inf	0	Inf	Significant up		1 Biological	V-type H+	--
Inf	0	Inf	Significant up		1 Molecular	zyxin	--
0.102735	0.129726	-3.283	Nonsignifi	None	1 Molecular	tubulin bet	--
Inf	0	Inf	Significant up		2 Cellular	Cc 26S protea	--
Inf	0	Inf	Significant up	--	--	coiled-coil	--
Inf	0	Inf	Significant up		2 Biological	--	--
Inf	0	Inf	Significant up		5 Molecular	protein kin	2.7.11.13
Inf	0	Inf	Significant up		5 Molecular	protein kin	2.7.11.13
Inf	0	Inf	Significant up		3 Cellular	Cc serine/thre	--
Inf	0	Inf	Significant up		3 Molecular	p38 MAP k	2.7.11.24
Inf	0	Inf	Significant up		1 Molecular	cell division	--
Inf	0	Inf	Significant up		1 Cellular	Cc	--
Inf	0	Inf	Significant up		1 Molecular	histone-bi	--
Inf	0	Inf	Significant up		1 Cellular	Cc occludin	--
Inf	0	Inf	Significant up		2 Molecular	--	--
Inf	0	Inf	Significant up	--	--	kynurenin α	3.7.1.3
Inf	0	Inf	Significant up	--	--	ceramide ζ	2.4.1.80
Inf	0	Inf	Significant up	--	--	glutaminyl	2.3.2.5
Inf	0	Inf	Significant up	--	--	guanylate	2.7.4.8
0.670156	0.000374	-0.57743	Nonsignifi	None	2 Molecular	Ras-relate	--
Inf	0	Inf	Significant up		2 Molecular	discoidin c	2.7.10.1
0.201467	0.124476	-2.31139	Nonsignifi	None	1 Molecular	four and a	--
Inf	0	Inf	Significant up		2 Biological	UTP--gluc	2.7.7.9
Inf	0	Inf	Significant up		2 Molecular	cysteine di	1.13.11.20
0.134451	0.267997	-2.89485	Nonsignifi	None	--	activated k	--
0.490817	0.000917	-1.02674	Nonsignifi	None	1 Molecular	tubulin alp	--
Inf	0	Inf	Significant up		5 Molecular	thioredoxin	1.8.1.9
Inf	0	Inf	Significant up		4 Molecular	--	--
Inf	0	Inf	Significant up	--	--	MHC class	--
Inf	0	Inf	Significant up	--	--	MHC class	--
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	--
Inf	0	Inf	Significant up		1 Molecular	echinoderr	--
Inf	0	Inf	Significant up		2 Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--
0.650179	0.224338	-0.62109	Nonsignifi	None	2 Molecular	--	--
1.353066	0.18182	0.436233	Nonsignifi	None	1 Molecular	heterogen	--
Inf	0	Inf	Significant up		1 Molecular	ADP-ribos	--

Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	poly [ADP-2.4.2.30	
Inf	0	Inf	Significant up		4	Molecular	Function:serine-type e	
Inf	0	Inf	Significant up	--	--		TBC1 dom	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	anoctamin	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.043007	0.219169	-4.53929	Nonsignifi		1	Molecular	translation	--
Inf	0	Inf	Significant up	--	--		protein FA	--
Inf	0	Inf	Significant up	--	--		centrosom	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	U4/U6.U5	--
Inf	0	Inf	Significant up	--	--		pyrroline-1.5.1.2	
Inf	0	Inf	Significant up		4	Molecular	molecular	--
Inf	0	Inf	Significant up	--	--		protein tra	--
Inf	0	Inf	Significant up		1	Molecular	E3 ubiquiti	2.3.2.26
0.648683	0.21279	-0.62442	Nonsignifi		5	Molecular	dynein hea	--
Inf	0	Inf	Significant up	--	--		serine/thre	--
Inf	0	Inf	Significant up		3	Biological	meckelin	--
Inf	0	Inf	Significant up	--	--	--	--	--
1.045628	0.895448	0.06437	Nonsignifi	--	--		flotillin	--
Inf	0	Inf	Significant up		1	Molecular	WD repeat	--
0.41242	0.269274	-1.27781	Nonsignifi		6	Molecular	focal adhe	2.7.10.2
Inf	0	Inf	Significant up	--	--		ribosomal	--
0.512966	0.618899	-0.96307	Nonsignifi		5	Molecular	guanine nt	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--		collectin st	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	Function:protein bindi	
Inf	0	Inf	Significant up		4	Cellular Cc	--	--
0.362457	0.095743	-1.46412	Nonsignifi		4	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.863757	0.161807	-0.2113	Nonsignifi		3	Molecular	hyaluronar	3.4.21.-
Inf	0	Inf	Significant up		1	Molecular	coiled-coil	--
Inf	0	Inf	Significant up		1	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up		1	Molecular	syntaxin-b	--
0.129711	0.479802	-2.94662	Nonsignifi		3	Molecular	Ras GTPas	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	DNA dam	--
Inf	0	Inf	Significant up		5	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	ubiquitin t	3.1.2.-
0.492562	0.040771	-1.02162	Nonsignifi		1	Biological	alpha 1,3-	3.2.1.84
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Cellular Cc	--	--
Inf	0	Inf	Significant up	--	--		N-alpha-a	--
Inf	0	Inf	Significant up	--	--		palmitoyltr	2.3.1.225
Inf	0	Inf	Significant up		1	Molecular	--	--
0.031656	0.093705	-4.98137	Nonsignifi		1	Molecular	latent tran	--
Inf	0	Inf	Significant up		1	Molecular	Kip1 ubiqu	2.3.2.27
Inf	0	Inf	Significant up	--	--		immune cc	--
Inf	0	Inf	Significant up		1	Molecular	--	--
3.151694	0.001692	1.656127	Nonsignifi		2	Biological	importin st	--
Inf	0	Inf	Significant up		1	Molecular	tensin	--
Inf	0	Inf	Significant up		1	Molecular	--	--
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	--	--	microtubu	--
Inf	0	Inf	Significant up		1 Molecular	tensin	--
Inf	0	Inf	Significant up	--	--	--	--
0.897484	0.46455	-0.15604	Nonsignifi		1 Molecular	26S protea	--
Inf	0	Inf	Significant up		3 Molecular	Rho GTPas	--
Inf	0	Inf	Significant up		2 Molecular	hemoglobi	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		5 Cellular Cc	--	--
Inf	0	Inf	Significant up		2 Molecular	OTU dom	3.4.19.12
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	--	--	cohesin lo	--
Inf	0	Inf	Significant up	--	--	histone arg	1.14.11.-
Inf	0	Inf	Significant up		1 Molecular	phostensir	--
Inf	0	Inf	Significant up	--	--	polymeras	--
Inf	0	Inf	Significant up		1 Molecular	coiled-coil	--
Inf	0	Inf	Significant up	--	--	enhancer c	--
Inf	0	Inf	Significant up		4 Molecular	pre-mRNA	--
Inf	0	Inf	Significant up		3 Molecular	SCY1-like	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	metal trans	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	4 Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Molecular	RNA polyn	--
0.757433	0.306411	-0.40081	Nonsignifi		2 Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1 Molecular	superkiller	--
Inf	0	Inf	Significant up		2 Molecular	--	--
Inf	0	Inf	Significant up	--	--	la-related	--
1.628847	0.017794	0.703851	Nonsignifi		1 Molecular	poly(rC)-b	--
0.638079	0.189059	-0.64819	Nonsignifi		1 Molecular	poly(rC)-b	--
Inf	0	Inf	Significant up	--	--	rapamycin	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Molecular	E3 ubiquiti	2.3.2.27
0.357852	0.146214	-1.48257	Nonsignifi		3 Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--
1.192301	0.408892	0.253748	Nonsignifi		1 Molecular	--	--
Inf	0	Inf	Significant up		1 Cellular Cc	--	--
Inf	0	Inf	Significant up		2 Biological	dipeptidyl-	3.4.14.5
Inf	0	Inf	Significant up		4 Molecular	dynammin-k	--
Inf	0	Inf	Significant up		3 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		3 Molecular	FYVE, Rho	--
Inf	0	Inf	Significant up		3 Molecular	thiol oxida	1.8.3.2
Inf	0	Inf	Significant up	--	--	--	--
0.753965	0.185176	-0.40743	Nonsignifi		2 Molecular	microtubu	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Biological	--	--
Inf	0	Inf	Significant up		1 Molecular	protein un	--
Inf	0	Inf	Significant up		1 Molecular	butyrophili	--
Inf	0	Inf	Significant up	--	--	staphylocc	--
Inf	0	Inf	Significant up		3 Molecular	MAP/micr	2.7.11.1
Inf	0	Inf	Significant up		2 Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		3 Cellular Cc	MFS trans	--

Inf	0	Inf	Significant up	1	Molecular	--	--
3.536919	0.000541	1.822493	Nonsignifi	2	Molecular	solute carr	--
Inf	0	Inf	Significant up	3	Molecular	ATP-depei	3.6.4.13
Inf	0	Inf	Significant up	1	Molecular	translation	--
Inf	0	Inf	Significant up	1	Molecular	COP9 sign	--
Inf	0	Inf	Significant up	3	Molecular	thousand ε	2.7.11.1
Inf	0	Inf	Significant up	1	Biological	charged m	--
Inf	0	Inf	Significant up	--	--	PHD finger	--
2.00334	0.069583	1.002408	Nonsignifi	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up	2	Cellular Cc	MFS transp	--
Inf	0	Inf	Significant up	--	--	solute carr	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	1	Molecular	poly [ADP-2.4.2.30	
Inf	0	Inf	Significant up	--	--	trafficking	--
Inf	0	Inf	Significant up	--	--	autophagy	--
0.345485	0.003796	-1.53331	Nonsignifi	3	Biological	--	--
0.37092	0.241256	-1.43082	Nonsignifi	1	Biological	26S protea	--
Inf	0	Inf	Significant up	1	Cellular Cc	transmemt	--
Inf	0	Inf	Significant up	--	--	CLIP-assoc	--
Inf	0	Inf	Significant up	3	Molecular	ATP-depei	3.6.4.13
Inf	0	Inf	Significant up	1	Molecular	low-densit	--
Inf	0	Inf	Significant up	--	--	--	--
1.05963	0.598266	0.083561	Nonsignifi	1	Molecular	dihdropyri	--
Inf	0	Inf	Significant up	--	--	L-xylulose	1.1.1.10
Inf	0	Inf	Significant up	1	Molecular	protein sid	--
Inf	0	Inf	Significant up	3	Biological	sprouty-re	--
Inf	0	Inf	Significant up	2	Molecular	SLIT-ROBC	--
Inf	0	Inf	Significant up	2	Biological	p24 family	--
3.046411	0.144683	1.607111	Nonsignifi	1	Molecular	fascin 1/2	--
Inf	0	Inf	Significant up	2	Molecular	--	--
Inf	0	Inf	Significant up	--	--	polypeptid	2.4.1.41
Inf	0	Inf	Significant up	1	Molecular	Function:protein bindi	
Inf	0	Inf	Significant up	4	Molecular	G protein-	--
Inf	0	Inf	Significant up	2	Molecular	phosphatic	3.1.3.78
Inf	0	Inf	Significant up	2	Biological	dipeptidyl-	3.4.14.5
Inf	0	Inf	Significant up	1	Molecular	histone-ly	2.1.1.43
Inf	0	Inf	Significant up	1	Molecular	tetratricop	--
Inf	0	Inf	Significant up	1	Molecular	polyadeny	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	2	Molecular	acetoacety	6.2.1.16
Inf	0	Inf	Significant up	1	Molecular	THO comp	--
Inf	0	Inf	Significant up	1	Cellular Cc	--	--
Inf	0	Inf	Significant up	2	Molecular	Ras GTPas	--
Inf	0	Inf	Significant up	1	Cellular Cc	lysosomal-	--
Inf	0	Inf	Significant up	2	Molecular	ESCRT-II c	--
Inf	0	Inf	Significant up	--	--	four-jointe	--
0.594321	0.131886	-0.75069	Nonsignifi	2	Biological	major histc	--
0.271839	0.00973	-1.87917	Nonsignifi	2	Molecular	leucine prc	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	1	Molecular	THO comp	--
Inf	0	Inf	Significant up	1	Molecular	--	--
Inf	0	Inf	Significant up	1	Molecular	--	--
0.061894	0.07577	-4.01406	Nonsignifi	4	Biological	formyltetra	1.5.1.6
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	2	Biological	transmemt	--
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	ATP-depei	3.6.4.13

Inf	0	Inf	Significant up		2	Molecular	E3 ubiquitin	2.3.2.27
Inf	0	Inf	Significant up		1	Molecular	syntaxin 12	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		1	Biological	--	--
Inf	0	Inf	Significant up		1	Molecular	histone H2	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.333427	0.010185	-1.58456	Nonsignificant	--	--	--	phospholipase	3.1.1.-
Inf	0	Inf	Significant up		1	Molecular	phospholipase	3.1.4.4
1.799197	0.193195	0.847353	Nonsignificant	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	LIX1-like p	--
2.539766	1.08E-05	1.344696	Nonsignificant		4	Molecular	molecular	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		4	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	NET1-assc	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	DCN1-like	--
Inf	0	Inf	Significant up		1	Molecular	volume-re	--
Inf	0	Inf	Significant up		2	Molecular	Rho GTPase	--
Inf	0	Inf	Significant up		3	Molecular	calcium hc	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	mitochondrial	3.6.5.-
Inf	0	Inf	Significant up	--	--	--	extracellular	2.7.11.1
Inf	0	Inf	Significant up		2	Biological	solute carrier	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.367189	0.212097	-1.4454	Nonsignificant		1	Molecular	E3 ubiquitin	2.3.2.27
Inf	0	Inf	Significant up		1	Biological	serine/arginine	--
Inf	0	Inf	Significant up	--	--	--	exocyst complex	--
0.128091	0.449069	-2.96476	Nonsignificant	--	--	--	--	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	katanin p6	3.6.4.3
0.023433	0.055264	-5.41531	Nonsignificant		1	Cellular	Cc myomegalin	--
Inf	0	Inf	Significant up	--	--	--	ankyrin repeat	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	netrin receptor	--
Inf	0	Inf	Significant up	--	--	--	proline-, gamma	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	regulatory	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Cellular	Cc nuclear pore	--
Inf	0	Inf	Significant up		3	Molecular	cap1 methyl	2.1.1.57
Inf	0	Inf	Significant up		3	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	latent transition	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up		1	Biological	Rho GTPase	--
Inf	0	Inf	Significant up		2	Molecular	activating	3.6.4.12
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	MICAL-like	--
Inf	0	Inf	Significant up		1	Molecular	MAGUK p150	--
Inf	0	Inf	Significant up	--	--	--	transmembrane	--
Inf	0	Inf	Significant up		1	Molecular	secreted from	--
Inf	0	Inf	Significant up		3	Molecular	misshapen	2.7.11.1
0.069566	0.058117	-3.84547	Nonsignificant		2	Molecular	atlastin	3.6.5.-
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	ADP-ribosyl	--

Inf	0	Inf	Significant up		3	Biological	RNA polyn	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	enabled	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	probable F	--
Inf	0	Inf	Significant up	--	--	pre-mRNA	--	--
Inf	0	Inf	Significant up		2	Molecular	phospholip	3.6.3.1
Inf	0	Inf	Significant up		1	Molecular	AAA family	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	collagen b	2.4.1.50	
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up		1	Cellular Cc	--	--
Inf	0	Inf	Significant up	--	--	solute carr	--	--
Inf	0	Inf	Significant up		1	Molecular	UDP-gluct	4.1.1.35
Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti	2.3.2.27
0.060465	0.057528	-4.04776	Nonsignifi	None	--	--	integrator	--
Inf	0	Inf	Significant up	--	--	plasminog	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	1	Molecular	--	--
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		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	metal trans	--	--
Inf	0	Inf	Significant up	--	2	Molecular	ATP-bindin	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	DCC-inter	--
Inf	0	Inf	Significant up		4	Biological	solute carr	--
Inf	0	Inf	Significant up		4	Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up		1	Molecular	nuclear po	--
Inf	0	Inf	Significant up	--	--	nuclear po	--	--
Inf	0	Inf	Significant up		1	Molecular	RaBP1-as	--
Inf	0	Inf	Significant up		3	Molecular	G protein-	--
Inf	0	Inf	Significant up	--	--	THO comp	--	--
Inf	0	Inf	Significant up		3	Molecular	U3 small n	--
Inf	0	Inf	Significant up		2	Biological	vang-like	--
Inf	0	Inf	Significant up		1	Molecular	WD repeat	--
Inf	0	Inf	Significant up		2	Cellular Cc	exocyst co	--
Inf	0	Inf	Significant up	--	--	nuclear pr	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	integrin al	--	--
Inf	0	Inf	Significant up		4	Molecular	ubiquitin- ϵ	6.2.1.45
Inf	0	Inf	Significant up	--	--	prostamid	1.11.1.20	
Inf	0	Inf	Significant up		2	Molecular	1-phosph	2.7.1.149
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	retinol deh	1.1.1.300	
Inf	0	Inf	Significant up		2	Molecular	signal pep	3.4.23.-
Inf	0	Inf	Significant up		2	Molecular	minor hist	3.4.23.-
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Cellular Cc	protein bic	--
Inf	0	Inf	Significant up		3	Molecular	NIMA (nev	2.7.11.1
0.265614	0.063749	-1.9126	Nonsignifi	None	4	Molecular	RAS guany	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	ribosome l	--	--

Inf	0	Inf	Significant up		1	Molecular	volume-re	--
Inf	0	Inf	Significant up		3	Molecular	NIMA (nev	2.7.11.1
0.610246	0.684298	-0.71254	Nonsignifi	None	1	Cellular	Cc	--
Inf	0	Inf	Significant up		3	Molecular	F-actin mc	1.14.13.22!
Inf	0	Inf	Significant up		3	Molecular	U3 small n	--
Inf	0	Inf	Significant up		1	Molecular	gem assoc	--
Inf	0	Inf	Significant up		1	Molecular	partitionin	--
0.295765	0.060105	-1.75748	Nonsignifi	None	3	Molecular	myosin he	--
Inf	0	Inf	Significant up		3	Molecular	importin-4	--
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-ε	3.1.3.48
Inf	0	Inf	Significant up	--	--	--	nucleolar c	--
Inf	0	Inf	Significant up		1	Cellular	Cc scavenger	--
Inf	0	Inf	Significant up	--	--	--	conserved	--
Inf	0	Inf	Significant up		1	Molecular	fibroblast ε	--
Inf	0	Inf	Significant up		1	Molecular	tsukushi (le	--
Inf	0	Inf	Significant up		3	Molecular	solute carr	--
0.005006	0.094503	-7.64213	Nonsignifi	None	1	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up	--	--	--	chromosor	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	sorting ne	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		3	Biological	RNA polyn	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Biological	sec1 family	--
Inf	0	Inf	Significant up		2	Molecular	soluble cal	3.6.1.6
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-l	3.1.3.16
Inf	0	Inf	Significant up		2	Molecular	F-box prot	--
0.330738	0.017956	-1.59624	Nonsignifi	None	--	--	--	--
0.553332	0.335754	-0.85378	Nonsignifi	None	--	--	kinectin	--
Inf	0	Inf	Significant up		3	Molecular	Arf-GAP w	--
1.242658	0.094203	0.313429	Nonsignifi	None	--	--	kindlin 3	--
Inf	0	Inf	Significant up	--	--	--	ATR intera	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	beta-cater	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		4	Cellular	Cc histone H1	--
0.675469	0.07419	-0.56604	Nonsignifi	None	--	--	cullin-asso	--
Inf	0	Inf	Significant up	--	--	--	proteasom	--
Inf	0	Inf	Significant up		3	Biological	solute carr	--
Inf	0	Inf	Significant up		2	Molecular	golgi-spec	--
Inf	0	Inf	Significant up		1	Molecular	RNA polyn	--
Inf	0	Inf	Significant up	--	--	--	engulfmen	--
Inf	0	Inf	Significant up		1	Molecular	WAS prote	--
Inf	0	Inf	Significant up	--	--	--	AP-3 com	--
Inf	0	Inf	Significant up	--	--	--	protein NC	--
Inf	0	Inf	Significant up	--	--	--	heat shock	--
Inf	0	Inf	Significant up		1	Molecular	septin 6/8/	--
Inf	0	Inf	Significant up	--	--	--	CCR4-NO	--
Inf	0	Inf	Significant up		1	Biological	Rho GTPas	--
Inf	0	Inf	Significant up		1	Cellular	Cc nuclear po	--
2.005246	0.004928	1.003779	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	factor assc	--
Inf	0	Inf	Significant up	--	--	--	acidic leuc	--
Inf	0	Inf	Significant up	--	--	--	poliovirus	--
Inf	0	Inf	Significant up		4	Molecular	receptor-t	3.1.3.48
Inf	0	Inf	Significant up		1	Molecular	protein TF	--

0.677089	0.041368	-0.56258	Nonsignifi	None		3	Molecular	adipocyte	--
Inf	0	Inf	Significant up		--	--		USP6 N-te	--
Inf	0	Inf	Significant up			1	Molecular	actin relat	--
Inf	0	Inf	Significant up		--	--		histone de	3.5.1.98
Inf	0	Inf	Significant up			2	Molecular	signal tran	--
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 guan	--
Inf	0	Inf	Significant up			1	Biological	ubiquitin fi	--
Inf	0	Inf	Significant up			1	Molecular	COP9 sign	3.4.-.-
Inf	0	Inf	Significant up			1	Molecular	SWI/SNF r	--
Inf	0	Inf	Significant up			1	Molecular	SWI/SNF-r	--
Inf	0	Inf	Significant up			1	Molecular	far upstrea	--
Inf	0	Inf	Significant up		--	--	--	--	--
Inf	0	Inf	Significant up			3	Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up			2	Biological	cullin 5	--
Inf	0	Inf	Significant up			1	Molecular	lipoma-pr	--
Inf	0	Inf	Significant up			2	Biological	protein tyr	3.1.3.48
Inf	0	Inf	Significant up		--	--	--	phosphory	--
Inf	0	Inf	Significant up		--	2	Biological	secretory c	--
Inf	0	Inf	Significant up		--	--	--	SWI/SNF-r	--
Inf	0	Inf	Significant up		--	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		--	--	--	proteasom	--
Inf	0	Inf	Significant up		--	--	--	--	--
0.559922	0.022326	-0.8367	Nonsignifi	None		3	Biological	--	--
Inf	0	Inf	Significant up			1	Molecular	U3 small n	--
Inf	0	Inf	Significant up			1	Cellular	Cc adiponecti	--
Inf	0	Inf	Significant up			3	Cellular	Cc exocyst co	--
Inf	0	Inf	Significant up			1	Cellular	Cc protein m	--
0.086858	0.223718	-3.5252	Nonsignifi	None	--	--	--	2,3-bisphc	5.4.2.11
Inf	0	Inf	Significant up		--	--	--	kindlin 2	--
Inf	0	Inf	Significant up			1	Molecular	far upstrea	--
Inf	0	Inf	Significant up			1	Molecular	--	--
Inf	0	Inf	Significant up			1	Molecular	SH3 doma	--
Inf	0	Inf	Significant up			4	Molecular	solute carr	--
Inf	0	Inf	Significant up		--	--	--	--	--
Inf	0	Inf	Significant up			1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant up		--	--	--	ubiquitin tl	3.4.19.12
Inf	0	Inf	Significant up		--	--	--	--	--
Inf	0	Inf	Significant up		--	--	--	dedicator c	--
Inf	0	Inf	Significant up			2	Molecular	--	--
Inf	0	Inf	Significant up			2	Molecular	--	--
Inf	0	Inf	Significant up			1	Molecular	FAS-assoc	--
Inf	0	Inf	Significant up		--	--	--	--	--
Inf	0	Inf	Significant up			5	Biological	gamma-tu	--
Inf	0	Inf	Significant up		--	--	--	calcium rel	--
Inf	0	Inf	Significant up			1	Molecular	RalBP1-as	--
Inf	0	Inf	Significant up			1	Molecular	carboxyme	3.1.1.45
Inf	0	Inf	Significant up			1	Molecular	Prp8 bindi	--
Inf	0	Inf	Significant up		--	--	--	--	--
0.088582	0.050795	-3.49685	Nonsignifi	None	--	--	--	cyclic GMF	2.7.7.86
Inf	0	Inf	Significant up			1	Molecular	--	--
Inf	0	Inf	Significant up			1	Cellular	Cc --	--
Inf	0	Inf	Significant up			1	Molecular	nucleopori	--
Inf	0	Inf	Significant up			1	Molecular	RNA-bind	--
Inf	0	Inf	Significant up			1	Cellular	Cc ESCRT-I	cc --
Inf	0	Inf	Significant up		--	--	--	--	--
Inf	0	Inf	Significant up			1	Molecular	--	--

Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	signal-indu	--
Inf	0	Inf	Significant up		2	Molecular	THO comp	--
Inf	0	Inf	Significant up		1	Cellular Cc	TP53 apop	--
Inf	0	Inf	Significant up		1	Biological	charged m	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up		3	Molecular	aurora kin	2.7.11.1
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up	--	--	--	palmitoyltr	2.3.1.225
Inf	0	Inf	Significant up		2	Molecular	DIRAS fam	--
Inf	0	Inf	Significant up	--	--	--	selenocyst	4.4.1.16
Inf	0	Inf	Significant up		1	Molecular	LIM domai	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Biological	mannose-	2.7.7.13
Inf	0	Inf	Significant up	--	--	--	abhydrola	--
Inf	0	Inf	Significant up		4	Molecular	carboxype	3.4.17.20
Inf	0	Inf	Significant up		1	Molecular	THO comp	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		4	Molecular	WNK lysin	2.7.11.1
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		3	Cellular Cc	conserved	--
Inf	0	Inf	Significant up	--	--	--	1,5-anhyd	1.1.1.263
Inf	0	Inf	Significant up	--	--	--	nascent pc	--
Inf	0	Inf	Significant up		2	Biological	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up		3	Molecular	PDZ-bindi	2.7.12.2
Inf	0	Inf	Significant up	--	--	--	--	--
1.845748	0.063298	0.884205	Nonsignifi	None	1	Cellular Cc	tetraspanir	--
0.251906	0.003296	-1.98904	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		2	Biological	cytosolic n	3.4.13.18
0.049901	0.057586	-4.3248	Nonsignifi	None	1	Molecular	InaD-like	--
Inf	0	Inf	Significant up		2	Cellular Cc	tripartite n	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	F-box and	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	dedicator	--
0.432293	0.442663	-1.20992	Nonsignifi	None	--	--	erythrocyt	--
Inf	0	Inf	Significant up	--	--	--	FERM dom	--
1.635818	0.083643	0.710012	Nonsignifi	None	1	Biological	solute carr	--
Inf	0	Inf	Significant up		2	Cellular Cc	MFS trans	--
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- ϵ	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	RNA-bindi	--
Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up		4	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	solute carr	--
Inf	0	Inf	Significant up	--	--	--	transcripti	--
Inf	0	Inf	Significant up		1	Cellular Cc	pannexin 2	--
Inf	0	Inf	Significant up		1	Molecular	atrophin-1	--
Inf	0	Inf	Significant up		1	Cellular Cc	pannexin 1	--
Inf	0	Inf	Significant up		2	Molecular	sorting ne	--
Inf	0	Inf	Significant up		3	Molecular	mediator c	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	erbb2-inte	--

Inf		0	Inf	Significant up		2	Molecular	TP53 regul	2.7.11.1
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		1	Cellular Cc	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		1	Molecular	neurabin	--
Inf		0	Inf	Significant up		3	Molecular	serine/thre	2.7.11.1
Inf		0	Inf	Significant up	--	--	--	spermatid	--
Inf		0	Inf	Significant up	--	--	--	MFS transp	--
Inf		0	Inf	Significant up		1	Cellular Cc	transcripti	--
Inf		0	Inf	Significant up	--	--	--	paired am	--
Inf		0	Inf	Significant up	--	--	--	oxysterol-I	--
Inf		0	Inf	Significant up		1	Biological	cysteamin	1.13.11.19
Inf		0	Inf	Significant up	--	--	--	DNA repai	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	tubulin-fol	--
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	--
Inf		0	Inf	Significant up	--	--	--	sialidase-1	3.2.1.18
Inf		0	Inf	Significant up	--	--	--	sortilin	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		4	Molecular	phosphoin	2.7.11.1
0.274492	9.52E-05	-1.86516	Nonsignifi	None	--	--	--	intelectin	--
Inf		0	Inf	Significant up		3	Biological	ribonuclea	3.1.26.5
0.943913	0.89935	-0.08327	Nonsignifi	None	--	--	--	solute carr	--
Inf		0	Inf	Significant up	--	--	--	--	--
0.384973	0.045713	-1.37717	Nonsignifi	None	--	--	--	intelectin	--
0.09562	0.066167	-3.38655	Nonsignifi	None		2	Molecular	ATP-bindin	--
0.258814	0.027077	-1.95001	Nonsignifi	None	--	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	DnaJ hom	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	COP9 sign	--
Inf		0	Inf	Significant up		1	Molecular	oncostatin	--
Inf		0	Inf	Significant up		1	Molecular	calcineurin	--
Inf		0	Inf	Significant up		4	Molecular	kinesin fan	--
0.40863	0.142884	-1.29113	Nonsignifi	None		3	Molecular	ATP-depe	3.6.4.13
0.53568	0.401664	-0.90056	Nonsignifi	None	--	--	--	--	--
Inf		0	Inf	Significant up		1	Cellular Cc	mothers a	--
Inf		0	Inf	Significant up		1	Molecular	heterogen	--
Inf		0	Inf	Significant up		2	Cellular Cc	nucleosom	--
Inf		0	Inf	Significant up	--	--	--	gamma-sc	--
Inf		0	Inf	Significant up		2	Molecular	1-phosph	2.7.1.68
0.649308	0.139767	-0.62303	Nonsignifi	None		1	Cellular Cc	transmem	--
Inf		0	Inf	Significant up		1	Molecular	calcium an	--
Inf		0	Inf	Significant up	--	--	--	rRNA-proc	--
Inf		0	Inf	Significant up	--	--	--	vaccinia re	2.7.11.1
Inf		0	Inf	Significant up		--	--	condensin	--
Inf		0	Inf	Significant up		4	Cellular Cc	actin relat	--
Inf		0	Inf	Significant up		2	Molecular	RNA-bindi	--
Inf		0	Inf	Significant up		1	Molecular	--	--
0.068696	0.08507	-3.86362	Nonsignifi	None		4	Molecular	myosin XV	--
0.014919	0.13302	-6.06673	Nonsignifi	None	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	methyloso	--
0.116894	0.077489	-3.09673	Nonsignifi	None		1	Molecular	peroxidase	1.11.1.7
Inf		0	Inf	Significant up		2	Molecular	DNA polyr	2.7.7.7
Inf		0	Inf	Significant up	--	--	--	kindlin 1	--
Inf		0	Inf	Significant up		1	Molecular	coronin-1	--

Inf	0	Inf	Significant up		1	Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significant up	--	--		ESCRT-II c	--
Inf	0	Inf	Significant up		1	Molecular	proteasom	--
0.014217	0.079141	-6.13628	Nonsignifi	None	4	Biological	HtrA serine	3.4.21.-
Inf	0	Inf	Significant up	--	--		protein pe	--
Inf	0	Inf	Significant up	--	--		anaphase-	--
Inf	0	Inf	Significant up		1	Biological	endoplasm	--
2.095893	0.000811	1.067565	Nonsignifi	None	2	Biological	gamma-gl	3.4.19.9
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up	--	--		Kip1 ubiqu	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		1	Molecular	COP9 sign	--
1.167814	0.587911	0.22381	Nonsignifi	None	1	Cellular Cc	golgi appa	--
Inf	0	Inf	Significant up		1	Molecular	synaptotax	--
Inf	0	Inf	Significant up	--	--		dynactin 5	--
Inf	0	Inf	Significant up	--	--		--	--
2.422779	0.024176	1.276663	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		2	Cellular Cc	ubiquitin r	--
0.363818	0.050889	-1.45871	Nonsignifi	None	3	Molecular	--	--
0.123707	0.226851	-3.015	Nonsignifi	None	2	Molecular	Rho guanin	--
Inf	0	Inf	Significant up	--	--		acidic leuc	--
0.206263	0.085674	-2.27744	Nonsignifi	None	2	Biological	ubiquitin c	3.4.19.12
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	--
0.35674	0.279145	-1.48706	Nonsignifi	None	3	Biological	--	--
Inf	0	Inf	Significant up		2	Molecular	alpha-L-fu	3.2.1.51
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--		deoxyhypu	1.14.99.29
Inf	0	Inf	Significant up		1	Molecular	heterogen	--
Inf	0	Inf	Significant up	--	--		programm	--
0.602832	0.151581	-0.73017	Nonsignifi	None	--	--	immunogl	--
Inf	0	Inf	Significant up	--	--		Derlin-1	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		1	Biological	methylthio	5.3.1.23
Inf	0	Inf	Significant up		1	Molecular	pre-rRNA-	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti	2.3.2.27
Inf	0	Inf	Significant up		2	Biological	protein N-	2.1.1.244
Inf	0	Inf	Significant up		1	Molecular	target of r	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		1	Biological	phosphatic	2.7.8.29
Inf	0	Inf	Significant up	--	--		U3 small n	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up		2	Biological	p24 family	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--		splicing fac	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--		junctional	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up	--	--		oxysterol-l	--
Inf	0	Inf	Significant up		2	Biological	N-acetylIn	4.1.3.3
Inf	0	Inf	Significant up		1	Molecular	Rab11 fam	--
Inf	0	Inf	Significant up	--	--		TBC1 dom	--
0.338862	0.043973	-1.56123	Nonsignifi	None	1	Biological	BTB/POZ c	--
0.119224	0.092953	-3.06826	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	N-alpha-a	--

Inf	0	Inf	Significant up		5	Molecular	solute carr	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	protein M	--
Inf	0	Inf	Significant up		1	Molecular	inosine tri	3.6.1.-
Inf	0	Inf	Significant up	--	--	--	translation	--
Inf	0	Inf	Significant up	--	--	--	cell adhesi	--
0.396303	0.08066	-1.33532	Nonsignifi		2	Biological	arylsulfata	3.1.6.-
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	partitionin	--
Inf	0	Inf	Significant up	--	--	--	protein FA	--
Inf	0	Inf	Significant up	--	--	--	sulfiredoxi	1.8.98.2
Inf	0	Inf	Significant up	--	--	--	dedicator c	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	nucleolar C	--
Inf	0	Inf	Significant up		1	Molecular	tether con	--
Inf	0	Inf	Significant up	--	--	--	oxysterol-l	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up	--	--	--	2-(3-amin	2.5.1.108
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	regulator c	--
3.596797	0.134695	1.846713	Nonsignifi		2	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	transducin	--
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-l	--
0.010788	0.119653	-6.53442	Nonsignifi		1	Molecular	far upstrea	--
Inf	0	Inf	Significant up	--	--	--	UL16 bindi	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	uridine kin	2.7.1.48
Inf	0	Inf	Significant up		3	Biological	protein spi	--
Inf	0	Inf	Significant up	--	--	--	protein dp	--
Inf	0	Inf	Significant up	--	--	--	palmitoyltr	2.3.1.225
Inf	0	Inf	Significant up		2	Molecular	semaphori	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Biological	ethanolam	2.7.8.1
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	Rho GTPas	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	carboxy-te	3.1.3.16
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-l	--
Inf	0	Inf	Significant up		2	Molecular	disintegrin	3.4.24.-
Inf	0	Inf	Significant up		2	Molecular	polyadeny	--
Inf	0	Inf	Significant up		1	Molecular	kinesin lig	--
Inf	0	Inf	Significant up		2	Molecular	5'-3' exor	3.1.13.-
Inf	0	Inf	Significant up		2	Molecular	NEDD4-lik	2.3.2.26
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up	--	--	--	transmem	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Cellular Cc	--	--
Inf	0	Inf	Significant up		1	Cellular Cc	anaphase-	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Cellular Cc	autophagy	--
0.144044	0.193605	-2.79542	Nonsignifi		2	Molecular	peptidogly	--
Inf	0	Inf	Significant up		3	Molecular	sphingosin	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	kelch-like	--

Inf	0	Inf	Significant up	--	--	--	--
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 ε 2.7.11.1
Inf	0	Inf	Significant up		3	Molecular	ATP-depe 3.6.4.13
Inf	0	Inf	Significant up		4	Molecular	inorganic p 3.6.1.1
Inf	0	Inf	Significant up		2	Molecular	vitellogen 3.4.16.-
Inf	0	Inf	Significant up	--	--	--	--
0.224938	0.278039	-2.1524	Nonsignifi		3	Molecular	coagulatio --
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	--	--		DnaJ homc --
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1	Biological	charged m --
Inf	0	Inf	Significant up		1	Molecular	-- --
Inf	0	Inf	Significant up		2	Molecular	aminopept 3.4.11.6
Inf	0	Inf	Significant up		5	Molecular	erythrocyt --
Inf	0	Inf	Significant up	--	--		CUB doma --
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	anthrax to --
Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti 2.3.2.27
Inf	0	Inf	Significant up		1	Molecular	dCTP diph 3.6.1.12
Inf	0	Inf	Significant up	--	--		ribosome p --
Inf	0	Inf	Significant up		1	Molecular	SET and M --
Inf	0	Inf	Significant up		1	Molecular	Function:protein bindi
Inf	0	Inf	Significant up		5	Molecular	cation-trar 3.6.3.-
0.102802	0.204902	-3.28206	Nonsignifi	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--		ubiquitin-ε 2.3.2.23
0.855505	0.144278	-0.22515	Nonsignifi		3	Molecular	20S protea 3.4.25.1
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--		MOB kinas --
0.710542	0.067513	-0.49301	Nonsignifi	--	--		protein DJ 3.5.1.124
Inf	0	Inf	Significant up		1	Molecular	-- --
Inf	0	Inf	Significant up	--	--	--	--
1.55713	0.017105	0.638889	Nonsignifi		1	Biological	-- --
Inf	0	Inf	Significant up		3	Molecular	mediator c --
Inf	0	Inf	Significant up	--	--		CCR4-NO ⁻ --
Inf	0	Inf	Significant up		1	Molecular	-- --
Inf	0	Inf	Significant up	--	--		conserved --
Inf	0	Inf	Significant up	--	--		ESCRT-I cc --
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		3	Cellular	Cc riboflavin t --
Inf	0	Inf	Significant up	--	--		phosphop 6.3.2.51
Inf	0	Inf	Significant up		2	Molecular	-- --
Inf	0	Inf	Significant up		1	Biological	pellino 2.3.2.27
Inf	0	Inf	Significant up		1	Molecular	-- --
Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti 2.3.2.26
Inf	0	Inf	Significant up	--	--		exportin-5 --
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
1.872912	0.063328	0.905283	Nonsignifi		1	Cellular	Cc transmemt --
Inf	0	Inf	Significant up		2	Molecular	serine cart 3.4.16.-
Inf	0	Inf	Significant up	--	--		calcyclin bi --
Inf	0	Inf	Significant up		1	Molecular	Ras-relate --
1.563982	0.016356	0.645224	Nonsignifi		2	Molecular	endophilin --

Inf	0	Inf	Significant up		2	Molecular	Ras homol	--	
Inf	0	Inf	Significant up	--	--	--	--	--	
Inf	0	Inf	Significant up		2	Molecular	E3 ubiquiti	2.3.2.26	
Inf	0	Inf	Significant up	--	--	--	--	--	
Inf	0	Inf	Significant up	--	--	--	--	--	
Inf	0	Inf	Significant up		4	Molecular	casein kin	2.7.11.1	
Inf	0	Inf	Significant up		1	Cellular	Cc transmem	--	
Inf	0	Inf	Significant up		6	Molecular	myosin X	--	
Inf	0	Inf	Significant up		5	Molecular	ATP-bindin	--	
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--	
0.812985	0.728694	-0.2987	Nonsignifi	None	--	--	--	--	
Inf	0	Inf	Significant up	--	--		enhancer c	--	
Inf	0	Inf	Significant up	--	--		exosome c	--	
Inf	0	Inf	Significant up		1	Molecular	CD320 ant	--	
Inf	0	Inf	Significant up	--	--		N6-L-thre	2.3.1.234	
Inf	0	Inf	Significant up		3	Molecular	myo-inosit	5.5.1.4	
Inf	0	Inf	Significant up	--	--	--	--	--	
Inf	0	Inf	Significant up		3	Biological	mRNA-dec	3.-.-.-	
0.195745	0.262098	-2.35295	Nonsignifi	None		2	Molecular	--	
Inf	0	Inf	Significant up	--	--	--	--	--	
Inf	0	Inf	Significant up		2	Molecular	semaphori	--	
Inf	0	Inf	Significant up		1	Molecular	--	--	
Inf	0	Inf	Significant up		3	Molecular	G protein-	--	
Inf	0	Inf	Significant up	--	--		fructose-2	3.1.3.46	
Inf	0	Inf	Significant up	--	--		regulator c	--	
Inf	0	Inf	Significant up		1	Biological	omega-an	3.5.1.3	
Inf	0	Inf	Significant up	--	--		poliovirus	--	
Inf	0	Inf	Significant up	--	--		exosome c	--	
Inf	0	Inf	Significant up	--	--		integral m	--	
Inf	0	Inf	Significant up		3	Molecular	baculovira	2.3.2.23	
Inf	0	Inf	Significant up		2	Molecular	--	--	
Inf	0	Inf	Significant up		2	Molecular	acetyl-Co/	6.2.1.1	
Inf	0	Inf	Significant up		2	Molecular	platelet de	--	
0.086679	0.072259	-3.52818	Nonsignifi	None		1	Molecular	tubulin bet	--
Inf	0	Inf	Significant up		2	Cellular	Cc MFS trans	--	
Inf	0	Inf	Significant up		1	Molecular	aladin	--	
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	--	--	--	--	--	
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--	
Inf	0	Inf	Significant up		2	Biological	vacuolar p	--	
Inf	0	Inf	Significant up	--	--		RNA-bindi	--	
0.255838	0.145742	-1.9667	Nonsignifi	None		1	Molecular	tubulin bet	--
Inf	0	Inf	Significant up	--	--		phosphohi	3.9.1.3	
Inf	0	Inf	Significant up		1	Molecular	latent tran	--	
Inf	0	Inf	Significant up	--	--	--	--	--	
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	phosphatic	3.1.3.-	
Inf	0	Inf	Significant up		1	Molecular	obg-like A	--	
Inf	0	Inf	Significant up		2	Molecular	midasin	--	
Inf	0	Inf	Significant up	--	--		palmitoyltr	2.3.1.225	
Inf	0	Inf	Significant up	--	--	--	--	--	
0.326993	0.017346	-1.61267	Nonsignifi	None	--	--	plasmalem	--	
Inf	0	Inf	Significant up		1	Molecular	protein lin	--	

Inf	0	Inf	Significant up		2	Molecular	ATP-binding	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	ATP-dep	3.6.4.13
Inf	0	Inf	Significant up	--	--			
Inf	0	Inf	Significant up	--	--		E3 ubiquitin	2.3.2.27
Inf	0	Inf	Significant up		2	Cellular	Cc exocyst co	--
Inf	0	Inf	Significant up		1	Cellular	Cc	--
Inf	0	Inf	Significant up		3	Molecular	type II pan	2.7.1.33
Inf	0	Inf	Significant up		1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	ATP-dep	3.6.4.13
Inf	0	Inf	Significant up		1	Biological	--	--
Inf	0	Inf	Significant up		3	Molecular	pyridoxam	1.4.3.5
Inf	0	Inf	Significant up		1	Molecular	armadillo r	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	tRNA(His)	2.7.7.79
Inf	0	Inf	Significant up	--	--		H/ACA ribo	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Biological	--	--
Inf	0	Inf	Significant up	--	--	--	pre-rRNA	--
Inf	0	Inf	Significant up		4	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	ADP-ribos	--
Inf	0	Inf	Significant up		4	Cellular	Cc solute carr	--
Inf	0	Inf	Significant up	--	--	--	dipeptidyl-	3.4.14.4
Inf	0	Inf	Significant up		1	Cellular	Cc	--
Inf	0	Inf	Significant up		3	Biological	N-acetylla	2.4.1.149
0.969808	0.915618	-0.04423	Nonsignifi	None	4	Molecular	protein kin	2.7.11.13
Inf	0	Inf	Significant up		2	Molecular	abl interac	--
Inf	0	Inf	Significant up	--	--	--	large subu	--
Inf	0	Inf	Significant up		3	Molecular	sterile alph	2.7.11.25
Inf	0	Inf	Significant up		2	Molecular	tropomod	--
Inf	0	Inf	Significant up	--	--	--	blocked e	--
Inf	0	Inf	Significant up		1	Biological	pleckstrin	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		4	Cellular	Cc	--
Inf	0	Inf	Significant up	--	--	--	maspardin	--
Inf	0	Inf	Significant up		1	Molecular	sacsin	--
Inf	0	Inf	Significant up	--	--	--	hsp70-inte	--
Inf	0	Inf	Significant up	--	--	--	S-adenosy	2.5.1.6
Inf	0	Inf	Significant up		4	Molecular	Rho guan	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	programm	--
0.005679	0.185214	-7.46008	Nonsignifi	None	3	Molecular	KRAB dom	--
Inf	0	Inf	Significant up		2	Molecular	low-densit	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up		5	Biological	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Biological	charged m	--
Inf	0	Inf	Significant up		1	Molecular	--	--
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	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	SLAIN mot	--

Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up	--	--	protein BC	--	--
0.325155	0.048797	-1.6208	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up	--	--	cleavage a	--	--
Inf	0	Inf	Significant up		4	Molecular	leucyl-tRN	6.1.1.4
Inf	0	Inf	Significant up		6	Molecular	StAR-relat	--
Inf	0	Inf	Significant up	--	--	ataxin-10	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	epidermal	--
Inf	0	Inf	Significant up		1	Molecular	phosphatic	2.7.1.67
Inf	0	Inf	Significant up		1	Cellular Cc	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	vacuolar p	--	--
Inf	0	Inf	Significant up	--	--	translation	--	--
Inf	0	Inf	Significant up	--	--	DnaJ hom	--	--
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-I	6.2.1.45
Inf	0	Inf	Significant up		1	Molecular	COP9 sign	--
Inf	0	Inf	Significant up	--	--	DnaJ hom	--	--
0.068394	0.116256	-3.86999	Nonsignifi	None	1	Molecular	tubulin bet	--
0.121986	0.221954	-3.03521	Nonsignifi	None	4	Molecular	--	--
Inf	0	Inf	Significant up	--	--	adducin	--	--
0.570145	0.030612	-0.8106	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	ATP-bindin	--
Inf	0	Inf	Significant up		4	Molecular	solute carr	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	5'-AMP-ac	--	--
Inf	0	Inf	Significant up		5	Biological	gamma-tu	--
Inf	0	Inf	Significant up		3	Cellular Cc	MFS trans	--
Inf	0	Inf	Significant up		1	Molecular	C->U-edit	3.5.4.-
Inf	0	Inf	Significant up		1	Biological	ragulator c	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		4	Molecular	signal recc	--
Inf	0	Inf	Significant up	--	--	cysteine ar	--	--
Inf	0	Inf	Significant up		3	Molecular	TANK-binc	2.7.11.10
Inf	0	Inf	Significant up	--	--	metallored	1.16.1.-	--
0.222284	0.118716	-2.16952	Nonsignifi	None	1	Molecular	tubulin alp	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		2	Molecular	BAI1-asso	--
Inf	0	Inf	Significant up		3	Biological	prefoldin s	--
Inf	0	Inf	Significant up		5	Molecular	solute carr	--
Inf	0	Inf	Significant up		1	Molecular	poly(U)-bi	--
Inf	0	Inf	Significant up	--	--	enolase-pl	3.1.3.77	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Biological	translation	--
Inf	0	Inf	Significant up		1	Biological	V-type H+	--
Inf	0	Inf	Significant up		2	Biological	--	--
Inf	0	Inf	Significant up	--	--	multifuncti	--	--
Inf	0	Inf	Significant up		2	Biological	exportin-7	--
Inf	0	Inf	Significant up		3	Molecular	death-assc	2.7.11.1
Inf	0	Inf	Significant up		2	Molecular	cystinyl arr	3.4.11.3
Inf	0	Inf	Significant up		2	Molecular	plexin A	--
Inf	0	Inf	Significant up		2	Molecular	peptide-m	1.8.4.11
Inf	0	Inf	Significant up		3	Molecular	drebrin-lik	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
0.245289	0.200064	-2.02745	Nonsignifi	None	1	Molecular	guanine nt	--
Inf	0	Inf	Significant up		1	Cellular Cc	dynactin 4	--
Inf	0	Inf	Significant up		3	Molecular	anaphase-	--

Inf	0	Inf	Significant up		1	Molecular	anaphase-	--
Inf	0	Inf	Significant up	--	--		ESCRT-I	cc --
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		2	Cellular	Cc mRNA turr	--
Inf	0	Inf	Significant up		3	Molecular	TRAF2 and	2.7.11.1
0.891567	0.749015	-0.16558	Nonsignifi	None	1	Molecular	parvin	--
Inf	0	Inf	Significant up	--	--		cleavage a	3.1.27.-
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	heterogen	--
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		1	Molecular	BCL2-asso	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Cellular	Cc proteasom	--
0.987869	0.904989	-0.01761	Nonsignifi	None	--	--	vacuolar p	--
Inf	0	Inf	Significant up		3	Molecular	thousand	2.7.11.1
Inf	0	Inf	Significant up		1	Molecular	PUA doma	--
Inf	0	Inf	Significant up	--	--		palmitoyltr	2.3.1.225
Inf	0	Inf	Significant up		4	Cellular	Cc solute carr	--
0.172866	0.486438	-2.53227	Nonsignifi	None	3	Molecular	protocadh	--
Inf	0	Inf	Significant up		2	Molecular	Arf-GAP w	--
Inf	0	Inf	Significant up	--	--		mediator c	--
Inf	0	Inf	Significant up	--	--		TBC1 dom	--
Inf	0	Inf	Significant up		3	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up		1	Molecular	coronin-1	--
Inf	0	Inf	Significant up	--	--		RNA-bind	--
Inf	0	Inf	Significant up		3	Molecular	myosin VI	--
Inf	0	Inf	Significant up		1	Molecular	palmitoyl-	3.1.2.22
Inf	0	Inf	Significant up		3	Molecular	pre-mRNA	2.3.2.27
Inf	0	Inf	Significant up		1	Molecular	ubiquilin	--
Inf	0	Inf	Significant up		1	Molecular	sorting ne	--
Inf	0	Inf	Significant up		3	Cellular	Cc sodium/pc	--
Inf	0	Inf	Significant up		3	Molecular	protocadh	--
Inf	0	Inf	Significant up		3	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	protein kin	--
1.275594	0.063027	0.351169	Nonsignifi	None	1	Molecular	Xaa-Pro ar	3.4.11.9
Inf	0	Inf	Significant up		1	Molecular	sorting ne	--
Inf	0	Inf	Significant up		1	Molecular	syntaxin 8	--
Inf	0	Inf	Significant up		3	Molecular	secretory	3.1.1.4
Inf	0	Inf	Significant up		1	Molecular	FAS-assoc	--
Inf	0	Inf	Significant up	--	--		protein C r	--
0.549007	0.100167	-0.8651	Nonsignifi	None	1	Molecular	GTP-bind	3.6.5.-
Inf	0	Inf	Significant up		3	Molecular	ATP-bind	--
Inf	0	Inf	Significant up	--	--		18S rRNA	(2.1.1.183
Inf	0	Inf	Significant up		1	Molecular	COP9 sign	--
Inf	0	Inf	Significant up		1	Molecular	U3 small n	--
Inf	0	Inf	Significant up		2	Molecular	transcript	3.6.4.-
Inf	0	Inf	Significant up		1	Molecular	UBX doma	--
Inf	0	Inf	Significant up		3	Molecular	frizzled 1/	--
Inf	0	Inf	Significant up		4	Molecular	microtuble	--
Inf	0	Inf	Significant up		2	Cellular	Cc 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	--
0.029011	0.27849	-5.10723	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	leucine-ric	--

Inf	0	Inf	Significant up	--	--	serine/argi	--
Inf	0	Inf	Significant up	--	--	sialidase-23.2.1.18	
Inf	0	Inf	Significant up		2 Molecular	BAI1-asso	--
Inf	0	Inf	Significant up		4 Molecular	structural r	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	RLL motif c	--
Inf	0	Inf	Significant up		2 Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		2 Cellular Cc	voltage-de	--
Inf	0	Inf	Significant up	--	--	integral m	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		2 Biological	trafficking	--
Inf	0	Inf	Significant up		2 Cellular Cc	exocyst co	--
Inf	0	Inf	Significant up	--	--	A-kinase a	--
Inf	0	Inf	Significant up		2 Molecular	--	--
Inf	0	Inf	Significant up		1 Biological	--	--
Inf	0	Inf	Significant up		4 Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up	--	--	exosome c	3.1.13.-
Inf	0	Inf	Significant up	--	--	RNA 3'-ter	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up	--	--	thyroid ho	--
Inf	0	Inf	Significant up		1 Biological	WW doma	--
Inf	0	Inf	Significant up	--	--	nucleolar p	--
Inf	0	Inf	Significant up	--	--	suppressor	--
Inf	0	Inf	Significant up		1 Molecular	N-acetylgl	3.5.1.25
Inf	0	Inf	Significant up	--	--	MEMO1 fa	--
Inf	0	Inf	Significant up	--	--	U6 snRNA	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		2 Molecular	endophilin	--
Inf	0	Inf	Significant up		3 Molecular	RNA-bindi	--
Inf	0	Inf	Significant up	--	--	palmitoyltr	2.3.1.225
Inf	0	Inf	Significant up		1 Biological	ribosome r	--
Inf	0	Inf	Significant up		2 Biological	p24 family	--
Inf	0	Inf	Significant up		1 Molecular	pre-mRNA	--
Inf	0	Inf	Significant up	--	--	oligoribon	3.1.-.-
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	mitochondr	--
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	--
Inf	0	Inf	Significant up	--	--	nucleolar c	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	elongation	--
Inf	0	Inf	Significant up		2 Molecular	V-type H+	--
Inf	0	Inf	Significant up		2 Molecular	transforma	--
Inf	0	Inf	Significant up		2 Cellular Cc	--	--
Inf	0	Inf	Significant up	--	--	--	--
1.973784	0.00811	0.980964	Nonsignifi		1 Molecular	EH domain	--
Inf	0	Inf	Significant up		4 Molecular	dishevellec	--
Inf	0	Inf	Significant up		2 Molecular	plexin D	--
Inf	0	Inf	Significant up		3 Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up		5 Cellular Cc	talins	--
Inf	0	Inf	Significant up		4 Molecular	myosin V	--
0.004141	0.093657	-7.91585	Nonsignifi		1 Molecular	calmodulir	--

Inf	0	Inf	Significant up	--	--	hypoxia up	--
Inf	0	Inf	Significant up	--	--	cysteine pr	3.4.22.-
Inf	0	Inf	Significant up	--	--	telomere l	--
Inf	0	Inf	Significant up	--	--	ribosomal	--
Inf	0	Inf	Significant up	--	--	ariadne-1	2.3.2.27
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	heat shock	--
Inf	0	Inf	Significant up		1 Molecular	low-densit	--
Inf	0	Inf	Significant up	--	--	protein ph	3.1.1.89
Inf	0	Inf	Significant up		3 Molecular	protocadh	--
Inf	0	Inf	Significant up		3 Molecular	ubiquitin c	3.4.19.12
0.247274	0.418364	-2.01582	Nonsignifi	None	2 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	CD2-assoc	--
Inf	0	Inf	Significant up	--	--	V-type H+	--
Inf	0	Inf	Significant up	--	--	transportir	--
Inf	0	Inf	Significant up	--	--	signal recc	--
0.502517	0.100078	-0.99275	Nonsignifi	None	--	prostaglan	--
Inf	0	Inf	Significant up		1 Molecular	collagen ty	--
Inf	0	Inf	Significant up		2 Biological	mannose-	2.7.7.13
Inf	0	Inf	Significant up	--	--	general tra	--
Inf	0	Inf	Significant up		1 Molecular	general tra	--
Inf	0	Inf	Significant up		2 Biological	trafficking	--
Inf	0	Inf	Significant up		5 Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up		1 Molecular	RNA-bindi	--
0.2209	0.147088	-2.17854	Nonsignifi	None	5 Molecular	coatomer	--
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 Cc	MFS trans	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		4 Biological	tRNA pseu	5.4.99.12
Inf	0	Inf	Significant up	--	--	--	--
0.068613	0.070096	-3.86537	Nonsignifi	None	2 Biological	cathepsin	3.4.18.1
Inf	0	Inf	Significant up	--	--	phosphose	2.6.1.52
Inf	0	Inf	Significant up	--	--	junctional	--
0.80223	0.734282	-0.31791	Nonsignifi	None	1 Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--
0.114708	0.125723	-3.12396	Nonsignifi	None	1 Molecular	fibulin 5	--
1.410804	0.085196	0.496517	Nonsignifi	None	1 Molecular	tight juncti	--
Inf	0	Inf	Significant up		4 Molecular	G protein-	--
Inf	0	Inf	Significant up		5 Molecular	coatomer	--
Inf	0	Inf	Significant up		2 Molecular	brefeldin A	--
Inf	0	Inf	Significant up		3 Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up		4 Molecular	casein kin	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		1 Molecular	WAS prote	--
Inf	0	Inf	Significant up		2 Molecular	--	--
17.10504	0.006625	4.09635	Significant up	--	--	integrin al	--
15.69618	6.31E-06	3.972341	Significant up	--	--	integrin al	--
11.20107	0.014359	3.485565	Significant up		2 Molecular	solute carr	--
10.03032	0.00358	3.326296	Significant up		2 Molecular	sodium/pc	3.6.3.9
8.074029	2.74E-05	3.013289	Significant up		3 Cellular Cc	MFS trans	--
6.777616	0.003675	2.760778	Significant up	--	--	histone H4	--
2.959021	0.034223	1.56512	Nonsignifi	None	1 Molecular	septin 3/9/	--
6.410657	0.049871	2.680472	Significant up		1 Molecular	nucleolin	--
6.190667	2.50E-05	2.630095	Significant up		4 Molecular	collagen, t	--
6.05388	0.000598	2.59786	Significant up		3 Molecular	tyrosine-p	2.7.10.2
5.779898	0.000128	2.531044	Significant up		1 Molecular	histone H2	--

5.759145	0.001277	2.525855	Significant up	--	--	NCK-associ	--
5.682631	0.015149	2.506559	Significant up		2 Molecular	annexin A2	--
5.657215	0.01158	2.500092	Significant up		1 Molecular	ADP-ribos	--
5.41122	0.000833	2.435954	Significant up		1 Molecular	histone H3	--
5.357671	0.008875	2.421606	Significant up		1 Cellular	Cc proteasom	--
5.325711	0.000166	2.412974	Significant up	--	--	integrin be	--
5.310185	2.85E-05	2.408762	Significant up	--	--	cytoplasmic	--
5.039377	0.042892	2.333246	Significant up		3 Cellular	Cc radixin	--
4.942135	0.001153	2.305134	Significant up		3 Molecular	solute carr	--
4.90467	0.000217	2.294156	Significant up		1 Molecular	programm	--
0.073146	0.110233	-3.77308	Nonsignifi	--	--	vacuolar p	--
4.826289	0.001306	2.270914	Significant up		1 Cellular	Cc tetraspanin	--
4.629844	0.001464	2.210964	Significant up	--	--	basigin	--
4.597537	0.002736	2.200861	Significant up		1 Molecular	histone H2	--
4.491946	0.013809	2.167341	Significant up		2 Molecular	Xaa-Pro ar	3.4.11.9
4.463334	0.000243	2.158122	Significant up		1 Molecular	heterogen	--
4.27839	0.017372	2.097068	Significant up	--	--	profilin	--
4.244952	0.000506	2.085748	Significant up	--	--	platelet-ac	3.1.1.47
4.181845	0.000122	2.06414	Significant up	--	--	integrin al	--
4.104261	0.008275	2.037122	Significant up		2 Molecular	cofilin	--
4.087805	0.000209	2.031326	Significant up	--	--	heat shock	--
0.248433	0.010351	-2.00907	Significant down		3 Biological	superoxide	1.15.1.1
0.246763	0.010105	-2.0188	Significant down		2 Molecular	a disintegr	3.4.24.87
0.245891	0.002245	-2.02391	Significant down		2 Molecular	hemoglobi	--
0.24293	2.01E-07	-2.04139	Significant down		2 Biological	fibroblast	3.4.21.-
0.240985	0.035652	-2.05298	Significant down	--	--	--	--
0.233235	0.005186	-2.10014	Significant down		4 Molecular	insulin-like	--
0.229836	0.028875	-2.12132	Significant down	--	--	beta-1,4-g	2.4.1.-
0.2258	0.015932	-2.14688	Significant down		1 Molecular	heterogen	--
0.224571	0.000317	-2.15475	Significant down	--	--	reticulon-4	--
0.072812	0.217679	-3.77968	Nonsignifi	--	--	--	--
0.22333	0.019985	-2.16275	Significant down		2 Molecular	fibroblast	3.2.7.10.1
0.219483	0.004586	-2.18782	Significant down		3 Molecular	CD109 ant	--
0.217069	0.046407	-2.20377	Significant down		3 Molecular	protein S	--
0.204066	0.047885	-2.29289	Significant down		2 Molecular	insulin-like	--
0.199601	0.002722	-2.32481	Significant down		1 Molecular	nucleobinc	--
0.194348	0.005552	-2.36329	Significant down	--	--	gluconolac	3.1.1.17
0.19417	0.003219	-2.3646	Significant down	--	--	beta-1,4-g	2.4.1.-
0.193048	0.025749	-2.37297	Significant down		1 Molecular	collagen, t	--
0.190747	0.000671	-2.39027	Significant down	--	--	C-type lec	--
0.183153	0.041097	-2.44888	Significant down		5 Molecular	lysosomal	3.2.1.24
0.179011	0.013107	-2.48188	Significant down		4 Cellular	Cc apolipop	--
0.178309	0.000293	-2.48755	Significant down		2 Molecular	procollage	1.14.11.4
0.178302	0.032668	-2.4876	Significant down	--	--	reticulon-3	--
0.171806	0.0076	-2.54115	Significant down		3 Molecular	thiol oxida	1.8.3.2
0.169055	0.000505	-2.56443	Significant down		2 Molecular	--	--
0.235711	0.289982	-2.08491	Nonsignifi		6 Molecular	Notch 3	--
0.165925	0.042689	-2.5914	Significant down		1 Molecular	collagen, t	--
0.164434	0.005021	-2.60442	Significant down		2 Molecular	--	--
0.161128	0.032327	-2.63372	Significant down		4 Molecular	fumarylac	3.7.1.2
0.157394	0.000889	-2.66755	Significant down	--	--	--	--
0.155014	0.012315	-2.68953	Significant down		1 Molecular	compleme	--
1.16252	0.362255	0.217256	Nonsignifi		1 Molecular	vacuolar p	--
0.154851	0.042643	-2.69105	Significant down	--	--	antithromk	--
0.151521	0.007288	-2.72241	Significant down	--	--	thyroxine-	--
0.148408	0.02506	-2.75236	Significant down		2 Molecular	inter-alpha	--
0.148083	0.015359	-2.75552	Significant down	--	--	pyruvate d	1.2.4.1
0.146488	0.033675	-2.77114	Significant down	--	--	collagen, t	--

0.146192	0.038335	-2.77406	Significant down	--	--	betaine-hc	2.1.1.5
0.144686	0.031914	-2.78901	Significant down	--	--	pigment e	--
0.874362	0.598273	-0.1937	Nonsignifi	None	1 Molecular	26S protea	--
0.144009	0.04208	-2.79577	Significant down		1 Molecular	neural cell	--
0.141668	0.000203	-2.81941	Significant down	--	--	--	--
0.456951	0.00419	-1.12989	Nonsignifi	None	4 Biological	peptidyl-p	5.2.1.8
0.137638	0.028756	-2.86105	Significant down		2 Molecular	inter-alpha	--
0.134223	0.012406	-2.89729	Significant down		1 Molecular	adipocyte-	--
0.134118	0.041847	-2.89843	Significant down	--	--	inducible T	--
0.132379	0.023792	-2.91726	Significant down	--	--	mannose r	--
0.130598	0.043791	-2.9368	Significant down		3 Molecular	alpha-amy	3.2.1.1
0.128263	0.033463	-2.96282	Significant down		1 Molecular	fibromodu	--
0.127161	0.001366	-2.97527	Significant down	--	--	serpin pep	--
0.126316	0.038342	-2.9849	Significant down	--	--	--	--
0.121465	0.001656	-3.04139	Significant down	--	--	angiopoiet	--
0.120781	0.039958	-3.04953	Significant down		2 Molecular	--	--
0.120311	0.013865	-3.05516	Significant down	--	--	transformi	--
0.119881	0.023903	-3.06032	Significant down		1 Biological	thioredoxi	--
0.119286	0.037527	-3.0675	Significant down	--	--	apolipoprc	--
0.39116	0.027007	-1.35417	Nonsignifi	None	2 Molecular	dynamin C	3.6.5.5
0.117995	0.017046	-3.08321	Significant down	--	--	--	--
0.117241	0.00102	-3.09246	Significant down		1 Molecular	cystatin-C	--
2.202454	0.190355	1.139112	Nonsignifi	None	--	--	--
0.117171	0.019405	-3.09332	Significant down		2 Molecular	interleukin	--
0.116424	0.014277	-3.10254	Significant down		3 Molecular	compleme	--
0.114971	0.011179	-3.12066	Significant down	--	--	--	--
0.114169	0.008974	-3.13076	Significant down		7 Molecular	ectonuclec	3.1.4.39
0.113666	0.047852	-3.13713	Significant down		4 Molecular	mitogen-a	2.7.12.2
0.00603	0.228045	-7.37366	Nonsignifi	None	2 Molecular	RuvB-like	3.6.4.12
0.063514	0.209877	-3.97678	Nonsignifi	None	--	C-type lec	--
2.973117	0.009458	1.571976	Nonsignifi	None	3 Molecular	translation	--
0.6217	0.218276	-0.68571	Nonsignifi	None	2 Molecular	RuvB-like	--
0.11365	0.039648	-3.13733	Significant down		2 Biological	acylamino	3.4.19.1
0.111685	0.01946	-3.16249	Significant down		2 Cellular Cc	--	--
0.883951	0.544512	-0.17796	Nonsignifi	None	2 Molecular	cofilin	--
0.110747	0.041169	-3.17466	Significant down		5 Molecular	primary-ar	1.4.3.21
0.109585	0.025699	-3.18988	Significant down		2 Molecular	coagulatio	2.3.2.13
0.108744	5.82E-06	-3.201	Significant down	--	--	major vaul	--
0.107353	0.011634	-3.21956	Significant down	--	--	--	--
0.104777	0.033209	-3.2546	Significant down	--	--	collagen, t	--
0.103947	0.037908	-3.26608	Significant down	--	--	melanoma	--
0.099114	0.003835	-3.33476	Significant down		2 Molecular	transcripti	--
0.098184	0.015189	-3.34837	Significant down	--	--	C1 inhibitc	--
0.098019	0.019016	-3.3508	Significant down		1 Molecular	transforme	--
0.097599	0.030919	-3.357	Significant down	--	--	compleme	--
0.025868	0.235502	-5.27268	Nonsignifi	None	5 Molecular	erythrocyt	--
0.097002	0.002886	-3.36584	Significant down		1 Biological	periplasmi	--
0.096297	0.007041	-3.37637	Significant down		2 Molecular	procollage	1.14.11.4
0.09564	0.035485	-3.38624	Significant down	--	--	angiopoiet	--
0.093933	0.035616	-3.41222	Significant down		3 Molecular	20S protea	3.4.25.1
0.091694	0.030928	-3.44703	Significant down		3 Molecular	large subu	--
0.091441	0.016153	-3.45101	Significant down		1 Molecular	--	--
0.091218	0.000586	-3.45454	Significant down	--	--	--	--
0.090573	0.020277	-3.46478	Significant down		3 Molecular	thrombos	--
0.089688	0.005388	-3.47894	Significant down	--	--	cell migrat	3.2.1.35
0.089366	0.027117	-3.48413	Significant down	--	--	--	--
0.088343	0.039639	-3.50074	Significant down		1 Cellular Cc	vitamin D-	--
0.086518	0.040253	-3.53085	Significant down		3 Molecular	cadherin 6	--

0.086275	0.040817	-3.53491	Significant down		3 Molecular compleme --
0.086017	1.93E-05	-3.53924	Significant down		2 Molecular type II kerat --
0.085411	0.046628	-3.54943	Significant down		4 Cellular Cc apolipoprc --
0.083195	0.049399	-3.58737	Significant down		4 Molecular matrix met 3.4.24.7
0.082345	0.010345	-3.60217	Significant down		1 Molecular von Willeb --
0.077816	0.002414	-3.68379	Significant down		2 Molecular mannan-b 3.4.21.-
0.077582	0.000437	-3.68814	Significant down	--	-- U3 small n --
0.076019	0.018875	-3.7175	Significant down		2 Molecular hemoglobi --
0.072376	0.044032	-3.78835	Significant down		1 Cellular Cc neuropilin --
0.070825	0.024082	-3.8196	Significant down		2 Molecular type II kerat --
0.066091	0.032081	-3.91941	Significant down	--	-- laminin, be --
0.063324	0.006641	-3.98111	Significant down		2 Molecular apolipoprc --
0.063112	0.041155	-3.98593	Significant down		1 Molecular -- --
0.062862	0.027781	-3.99168	Significant down	--	-- retinol-bin --
0.061116	0.000959	-4.0323	Significant down	--	-- glia-derive --
0.058994	0.005445	-4.0833	Significant down	--	-- -- --
0.797446	0.276316	-0.32654	Nonsignifi	None	4 Molecular large subu --
0.058166	0.0232	-4.10369	Significant down		1 Molecular fibulin 1/2 --
0.056422	0.012068	-4.14759	Significant down	--	-- -- --
0.056033	0.017939	-4.15759	Significant down		2 Molecular type I kera --
0.622723	0.044806	-0.68334	Nonsignifi	None	5 Cellular Cc talin --
0.054596	0.024304	-4.19507	Significant down		2 Molecular collagen, t --
0.053421	0.024728	-4.22645	Significant down	--	-- -- --
0.051712	0.039676	-4.27337	Significant down		4 Biological -- --
0.049306	0.017262	-4.34209	Significant down		2 Molecular deleted in --
0.048764	0.000466	-4.35805	Significant down		4 Molecular lysyl oxidat 1.4.3.-
0.045571	0.028455	-4.45573	Significant down	--	-- laminin, ga --
0.044963	0.037505	-4.47511	Significant down		1 Molecular Function:metalloendo
0.041952	0.013804	-4.57511	Significant down		1 Molecular collagen, t --
0.041619	0.047225	-4.58661	Significant down	--	-- -- --
0.04146	0.033987	-4.59215	Significant down	--	-- sushi repe --
0.039248	0.00856	-4.67125	Significant down		2 Molecular aggrecan --
0.037427	0.020069	-4.73976	Significant down		2 Molecular nidogen (e --
0.036384	0.004201	-4.78055	Significant down		4 Molecular thrombos --
0.035694	0.010918	-4.80819	Significant down		4 Molecular thrombos --
0.035568	0.025747	-4.81328	Significant down		3 Molecular collagen, t --
0.034959	0.036995	-4.8382	Significant down	--	-- collagen, t --
0.034309	0.010446	-4.86527	Significant down		2 Biological adipocyte --
0.032594	0.031775	-4.93926	Significant down		1 Molecular tenascin --
0.030936	0.016947	-5.01458	Significant down	--	-- Thy-1 cell --
0.028991	0.007361	-5.10828	Significant down		1 Molecular tenascin --
0.027974	0.022389	-5.15975	Significant down		4 Biological cysteine ric --
0.027851	0.004725	-5.1661	Significant down		2 Molecular inhibin, be --
0.026209	0.040291	-5.2538	Significant down		1 Molecular hemicentir --
0.024715	0.012356	-5.33849	Significant down		1 Molecular G protein- --
0.024375	0.026997	-5.35843	Significant down		1 Molecular heparan su --
0.022325	0.036627	-5.48518	Significant down		5 Molecular fibrinogen --
0.022109	0.046665	-5.4992	Significant down		1 Molecular collagen, t --
0.021388	0.022601	-5.54702	Significant down		1 Molecular biglycan --
0.017981	0.038066	-5.79741	Significant down		2 Molecular plasminog 3.4.21.7
0.017695	0.026442	-5.82048	Significant down		1 Biological amidopho: 2.4.2.14
0.016795	0.011854	-5.89586	Significant down		2 Molecular -- --
0.014596	0.004027	-6.09833	Significant down		1 Molecular -- --
0.555951	0.004363	-0.84697	Nonsignifi	None	2 Molecular sorting ne --
0.014271	0.011108	-6.13081	Significant down	--	-- -- --
0.013457	0.006347	-6.21553	Significant down		3 Molecular versican cc --
0.012768	0.010694	-6.29135	Significant down		1 Cellular Cc serum albu --
0.012495	0.041554	-6.32253	Significant down		4 Cellular Cc peroxisom --

0.01244	0.03917	-6.32888	Significant down		2	Molecular	protein-lys	1.4.3.13
0.009713	0.011419	-6.68589	Significant down	--	--	--	--	--
0.009524	0.012987	-6.71424	Significant down		2	Molecular	phospholip	3.6.3.1
0.009351	0.019976	-6.74067	Significant down	--	--	--	plasminog	--
0.396212	0.268694	-1.33565	Nonsignifi		3	Cellular	Cc glypican	6 --
0.009201	0.009991	-6.76392	Significant down		2	Molecular	collagen, t	--
0.008948	0.047018	-6.80418	Significant down		1	Molecular	--	--
0.008686	0.010243	-6.84714	Significant down		1	Molecular	collagen, t	--
2.90926	0.096865	1.540652	Nonsignifi	--	--	--	chloride in	--
0.007941	0.025378	-6.9765	Significant down		4	Molecular	matrix met	3.4.24.24
0.007779	0.011202	-7.00628	Significant down		3	Molecular	interleukin	--
0.007385	0.01002	-7.08111	Significant down		2	Molecular	fibronectin	--
0.010874	0.242261	-6.52291	Nonsignifi		1	Molecular	--	--
0.167648	0.374545	-2.57649	Nonsignifi	--	--	--	dynein lig	--
0.005148	0.001712	-7.60178	Significant down		5	Molecular	laminin, al	--
0.004371	0.041217	-7.83779	Significant down		2	Molecular	collagen, t	--
0.004151	0.020519	-7.91233	Significant down	--	--	--	--	--
0.001989	0.018288	-8.97404	Significant down		3	Biological	insulin-like	--
0.001091	0.025966	-9.84032	Significant down		5	Molecular	ATP-depe	3.6.4.13

KEGG_ko	COG_Func	COG_Func	COG_Class	IPR_Term
ko04151	P Autotransf	UW	Intracellular	IPR002035 [von Willebrand factor, type A] ; IPR008160
ko04350	T Leucine-rich	K	Transcripti	IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04062	C --	--	--	IPR001811 [Chemokine interleukin-8-like domain]
--	--	--	--	IPR007455 [Serglycin]
ko04060	C --	--	--	IPR001811 [Chemokine interleukin-8-like domain]
ko04062	C --	--	--	IPR001811 [Chemokine interleukin-8-like domain]
ko04062	C --	--	--	IPR001811 [Chemokine interleukin-8-like domain]
--	--	--	--	IPR004978 [Stanniocalcin]
ko04062	C --	--	--	IPR001811 [Chemokine interleukin-8-like domain]
--	Autotransf	UW	Intracellular	IPR008160 [Collagen triple helix repeat]
--	--	--	--	IPR022699 [Stonin-2, N-terminal] ; IPR028565[Mu hom
--	--	--	--	IPR001190 [SRCR domain] ; IPR001695[Lysyl oxidase]
--	Secreted tr	O	Posttransla	IPR000859 [CUB domain] ; IPR001254[Serine proteases
--	--	--	--	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IF
ko03040	S Small nucl	K	Transcripti	IPR001163 [LSM domain, eukaryotic/archaea-type]
ko03008	R rRNA pseu	J	Translatior	IPR005304 [Ribosomal biogenesis, methyltransferase, E
ko04144	E --	--	--	IPR021854 [WASH1, WAHD domain]
ko04610	C Secreted tr	O	Posttransla	IPR000436 [Sushi/SCR/CCP domain] ; IPR001254[Serine
ko03013	R --	--	--	IPR000717 [Proteasome component (PCI) domain] ; IPR
--	--	--	--	IPR009038 [GOLD domain]
--	Peptidyl-p	O	Posttransla	IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans is
--	--	--	--	IPR013106 [Immunoglobulin V-set domain]
--	Predicted IR		General fu	IPR026937 [Strawberry notch, helicase C domain]
--	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
ko03018	R --	--	--	IPR007196 [CCR4-Not complex component, Not1, C-ter
--	--	--	--	IPR004241 [Autophagy protein Atg8 ubiquitin-like]
ko00630	G Ribonucle	F	Nucleotide	IPR006357 [HAD-superfamily hydrolase, subfamily IIA]
--	--	--	--	IPR010935 [SMCs flexible hinge]
--	--	--	--	IPR019359 [CCDC85 family]
--	Uncharacter	S	Function u	--
--	Sterol des	I	Lipid trans	IPR000608 [Ubiquitin-conjugating enzyme E2] ; IPR019
--	--	--	--	--
--	--	--	--	--
--	--	--	--	--
ko00760	N Nicotinate	H	Coenzyme	IPR002638 [Quinolinate phosphoribosyl transferase, C-
--	--	--	--	IPR001478 [PDZ domain] ; IPR001781[Zinc finger, LIM-
ko05132	S Tfp pilus a	NW	Cell motilit	IPR011990 [Tetratricopeptide-like helical domain] ; IPR
--	--	--	--	IPR000048 [IQ motif, EF-hand binding site] ; IPR001609
--	--	--	--	IPR004240 [Nonaspanin (TM9SF)] ; IPR005024[Snf7 fam
ko00190	C --	--	--	--
ko04614	R Oligoendo	E	Amino acid	IPR001548 [Peptidase M2, peptidyl-dipeptidase A]
--	--	--	--	IPR021852 [Domain of unknown function DUF3456]
ko04142	L --	--	--	IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
ko04060	C Galactose-	G	Carbohydr	IPR005849 [Galactose-1-phosphate uridyl transferase,
--	--	--	--	IPR001619 [Sec1-like protein]
ko03050	P --	--	--	IPR000717 [Proteasome component (PCI) domain]
ko04130	S --	--	--	IPR006011 [Syntaxin, N-terminal domain]
ko00480	G Cation trar	P	Inorganic i	--
ko00970	A Seryl-tRN	J	Translatior	IPR002314 [Aminoacyl-tRNA synthetase, class II (G/ P/
--	Glutathion	O	Posttransla	IPR004045 [Glutathione S-transferase, N-terminal]
ko04060	C --	--	--	IPR000488 [Death domain] ; IPR001368[TNFR/NGFR cy
ko03013	R --	--	--	IPR000555 [JAB1/MPN/MOV34 metalloenzyme domain
ko04142	L --	--	--	IPR004947 [Deoxyribonuclease II]
--	--	--	--	IPR001752 [Kinesin motor domain]
ko00062	F Acyl-CoA	II	Lipid trans	IPR006683 [Thioesterase domain]
ko04130	S --	--	--	IPR000928 [SNAP-25]
--	--	--	--	IPR000357 [HEAT repeat]

--	--	--	--	IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
--	GTPase	R	General fu	--
--	--	--	--	IPR001619 [Sec1-like protein]
--	--	--	--	IPR001079 [Galectin, carbohydrate recognition domain
ko04512 E	--	--	--	IPR000082 [SEA domain] ; IPR000742[EGF-like domain]
ko04210 A	--	--	--	IPR000488 [Death domain] ; IPR001368[TNFR/NGFR cy
--	Membrane	OK	Posttransla	IPR001478 [PDZ domain]
ko03050 P	Proteasom	O	Posttransla	IPR000555 [JAB1/MPN/MOV34 metalloenzyme domain
ko04978 N	--	--	--	IPR006121 [Heavy metal-associated domain, HMA]
--	Transcripti	K	Transcripti	IPR005100 [Transcription elongation factor Spt5, NGN
ko04120 U	--	--	--	IPR000569 [HECT domain] ; IPR001202[WW domain]
ko00562 Ir	--	--	--	IPR000341 [Phosphatidylinositol 3-kinase Ras-binding
ko04062 C	Acyl transf	Q	Secondary	IPR000095 [CRIB domain] ; IPR000697[WH1/EVH1 dom
--	RNA 3'-ter	A	RNA proce	IPR013791 [RNA 3'-terminal phosphate cyclase, insert
--	--	--	--	IPR001478 [PDZ domain]
ko00562 Ir	--	--	--	IPR000008 [C2 domain] ; IPR000341[Phosphatidylinosit
--	--	--	--	IPR006921 [Interferon-related developmental regulato
--	--	--	--	--
--	--	--	--	IPR009976 [Exocyst complex component Sec10-like]
ko04144 E	--	--	--	IPR001452 [SH3 domain] ; IPR004148[BAR domain]
--	--	--	--	IPR000225 [Armadillo] ; IPR002652[Importin-alpha, imp
--	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
--	--	--	--	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04015 R	Ankyrin rej	T	Signal tran	IPR019748 [FERM central domain] ; IPR032022[KRIT, N-
--	--	--	--	IPR001357 [BRCT domain] ; IPR010613[Pescadillo]
ko03008 R	RNA proce	J	Translatior	IPR002687 [Nop domain] ; IPR012974[NOP5, N-termin
--	--	--	--	IPR013836 [CD34/Podocalyxin]
--	--	--	--	IPR000225 [Armadillo] ; IPR002652[Importin-alpha, imp
ko05010 A	--	--	--	IPR001762 [Disintegrin domain] ; IPR002870[Peptidase
ko04120 U	Ubiquitin-	O	Posttransla	IPR000608 [Ubiquitin-conjugating enzyme E2]
ko00750 V	Pyridoxal/	H	Coenzyme	IPR013749 [Pyridoxamine kinase/Phosphomethylpyrim
ko05225 H	--	--	--	IPR001606 [ARID DNA-binding domain] ; IPR033388[S'
--	Negative r	O	Posttransla	IPR013766 [Thioredoxin domain]
--	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR001180[Citron
--	--	--	--	--
--	TFIIF-inter	K	Transcripti	IPR004274 [FCP1 homology domain]
--	ATP-depe	O	Posttransla	IPR010448 [Torsin]
ko04360 A	Phage-rel	X	Mobilome	IPR000421 [Coagulation factor 5/8 C-terminal domain]
ko02010 A	ABC-type	R	General fu	IPR003439 [ABC transporter-like] ; IPR011527[ABC tran
--	--	--	--	IPR018499 [Tetraspanin/Peripherin]
ko03050 P	20S protea	O	Posttransla	IPR000426 [Proteasome alpha-subunit, N-terminal dor
--	DNA-bind	R	General fu	IPR002836 [PDCD5-related protein]
ko03013 R	Predicted IR		General fu	IPR025799 [Protein arginine N-methyltransferase]
ko04530 T	Periplasmic	O	Posttransla	IPR001478 [PDZ domain] ; IPR015098[EBP50, C-termin
ko04210 A	--	--	--	IPR000488 [Death domain] ; IPR001368[TNFR/NGFR cy
ko04142 L	Serine pro	O	Posttransla	IPR015366 [Peptidase S53, activation domain]
ko03040 S	Endonucle	R	General fu	IPR001202 [WW domain] ; IPR002713[FF domain]
ko04510 F	Ca ²⁺ -bind	T	Signal tran	IPR002048 [EF-hand domain] ; IPR015070[DJBP, EF-ha
--	--	--	--	IPR001752 [Kinesin motor domain]
--	--	--	--	IPR001494 [Importin-beta, N-terminal domain]
--	--	--	--	IPR001478 [PDZ domain]
--	--	--	--	IPR001478 [PDZ domain]
--	--	--	--	IPR001478 [PDZ domain] ; IPR014775[L27 domain, C-ter
ko05034 A	--	--	--	IPR019467 [Histone acetyl transferase HAT1 N-termina
--	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR001478[PDZ do
ko00564 G	Phosphatic	I	Lipid trans	IPR001683 [Phox homologous domain] ; IPR001736[Ph
--	--	--	--	IPR024298 [Ancestral coatomer element 1, Sec16/Sec3
ko04360 A	DNA-bind	R	General fu	IPR001627 [Sema domain] ; IPR002165[Plexin repeat] ;

--	Murein DCM	Cell wall/r	IPR016047	[Peptidase M23]
ko04144 E	--	--	IPR000306	[FYVE zinc finger] ; IPR002014[VHS domain]
ko04022 c	Chromoso D	Cell cycle c	IPR020683	[Ankyrin repeat-containing domain] ; IPR03
--	Serine/threT	Signal tran	IPR000719	[Protein kinase domain] ; IPR014020[Tensin
--	RNA recogJ	Translatior	IPR000504	[RNA recognition motif domain]
ko04144 E	--	--	IPR007188	[Actin-related protein 2/3 complex subunit
ko04144 E	--	--	IPR007204	[Actin-related protein 2/3 complex subunit
ko03008 R	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
--	--	--	IPR000219	[Dbl homology (DH) domain]
--	--	--	IPR001715	[Calponin homology domain] ; IPR002017[S
ko03040 S	RNA recogJ	Translatior	IPR000061	[SWAP/Surp] ; IPR000504[RNA recognition
ko00562 Ir	--	--	IPR002013	[SAC domain] ; IPR005135[Endonuclease/ex
ko01100 N	UncharactS	Function u	IPR000034	[Laminin IV] ; IPR001791[Laminin G domain]
ko00230 P	PhosphorilF	Nucleotide	IPR010918	[AIR synthase-related protein, C-terminal d
--	Chromoso D	Cell cycle c	IPR002110	[Ankyrin repeat] ; IPR020683[Ankyrin repeat
--	UncharactS	Function u	IPR002995	[Surfeit locus 4]
ko04142 L	Predicted eR	General fu	IPR000731	[Sterol-sensing domain] ; IPR003392[Protein
ko00230 P	DNA-directK	Transcripti	IPR011262	[DNA-directed RNA polymerase, insert dom
--	UncharactS	Function u	IPR005552	[Scramblase]
--	TFIIF-inter.K	Transcripti	IPR004274	[FCP1 homology domain]
ko04360 A	Ankyrin rejT	Signal tran	IPR001090	[Ephrin receptor ligand binding domain] ; IF
--	Prefoldin, (O	Posttransla	IPR002777	[Prefoldin beta-like]
ko04130 S	--	--	IPR000727	[Target SNARE coiled-coil homology doma
--	--	--	--	--
ko05230 C	Predicted iG	Carbohydr	IPR011701	[Major facilitator superfamily]
--	--	--	IPR004932	[Retrieval of early ER protein Rer1]
ko00514 C	Predicted (O	Posttransla	IPR001440	[Tetratricopeptide repeat 1] ; IPR011990[Tet
ko00051 F	HydroxymHR	Coenzyme	IPR005002	[Phosphomannomutase]
ko04120 U	--	--	IPR000315	[B-box-type zinc finger] ; IPR003877[SPRY c
--	--	--	IPR009071	[High mobility group box domain]
--	Serine/threT	Signal tran	IPR001932	[PPM-type phosphatase domain]
--	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
ko00260 G	PhosphoglHR	Coenzyme	IPR006139	[D-isomer specific 2-hydroxyacid dehydrog
--	Sugar pho G	Carbohydr	IPR011701	[Major facilitator superfamily]
ko01524 P	--	--	IPR007274	[Ctr copper transporter]
ko03050 P	--	--	IPR000717	[Proteasome component (PCI) domain] ; IPF
ko04130 S	--	--	IPR001388	[Synaptobrevin] ; IPR010908[Longin domain
ko04144 E	--	--	IPR006789	[Actin-related protein 2/3 complex subunit
ko01524 P	PASTA dorM	Cell wall/r	IPR000719	[Protein kinase domain] ; IPR033931[PDK1-
--	--	--	IPR001781	[Zinc finger, LIM-type]
--	RNA recogJ	Translatior	IPR000504	[RNA recognition motif domain]
ko04144 E	Ankyrin rejT	Signal tran	IPR001164	[Arf GTPase activating protein] ; IPR001452[
--	Cytochromo Cl	Energy prc	IPR001199	[Cytochrome b5-like heme/steroid binding
ko03040 S	WD40 repR	General fu	IPR001680	[WD40 repeat] ; IPR014906[Pre-mRNA proc
--	--	--	IPR000276	[G protein-coupled receptor, rhodopsin-like
ko04145 P	--	--	IPR022780	[Dynein family light intermediate chain]
ko00230 P	ATP sulfurP	Inorganic i	IPR024951	[Sulphate adenylyltransferase catalytic dom
--	--	--	IPR009361	[RZZ complex, subunit Zw10]
--	Thiol-disulO	Posttransla	IPR010400	[PITH domain] ; IPR013766[Thioredoxin dor
--	--	--	IPR007327	[Tumour protein D52]
--	--	--	IPR008614	[Acidic fibroblast growth factor intracellular
ko03040 S	Peptidyl-p O	Posttransla	IPR002130	[Cyclophilin-type peptidyl-prolyl cis-trans i
ko00980 N	Predicted eR	General fu	IPR023210	[NADP-dependent oxidoreductase domain]
--	--	--	IPR007477	[SAB domain] ; IPR008379[Band 4.1, C-term
ko04150 r	--	--	IPR024135	[Ragulator complex protein LAMTOR5]
ko03013 R	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
ko05206 N	--	--	IPR007875	[Sprouty]
--	Predicted II	Lipid trans	IPR007379	[Tim44-like domain]

--	--	--	--	IPR007194	[Transport protein particle (TRAPP) compon
ko04144	E	--	--	IPR005024	[Snf7 family]
--	--	--	--	IPR018499	[Tetraspanin/Peripherin]
ko04142	L	--	--	IPR002553	[Clathrin/coatomer adaptor, adaptin-like, N
ko03040	S	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
--		Anion-trar	P	Inorganic i	IPR025723 [Anion-transporting ATPase-like domain]
ko04110	C	Predicted	IT	Signal tran	IPR001680 [WD40 repeat]
ko00561	G	--	--	--	IPR000326 [Phosphatidic acid phosphatase type 2/halc
ko04072	P	Guanine-n	R	General fu	IPR000904 [Sec7 domain] ; IPR001849[Pleckstrin homo
ko04068	F	Carbohydr	GT	Carbohydr	IPR006828 [Association with the SNF1 complex (ASC) c
ko04130	S	--	--	--	IPR000727 [Target SNARE coiled-coil homology doma
--	--	--	--	--	IPR000421 [Coagulation factor 5/8 C-terminal domain]
ko00270	C	S-adenosy	H	Coenzyme	IPR000043 [Adenosylhomocysteinase] ; IPR015878[S-a
--		Tetratricop	R	General fu	IPR001440 [Tetratricopeptide repeat 1] ; IPR019734[Tet
--	--	--	--	--	IPR000048 [IQ motif, EF-hand binding site] ; IPR001609
ko03015	r	--	--	--	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
ko04110	C	--	--	--	IPR020796 [Origin recognition complex, subunit 5]
ko04110	C	--	--	--	IPR006909 [Rad21/Rec8-like protein, C-terminal, eukar
ko03040	S	HrpA-like	J	Translatior	IPR001650 [Helicase, C-terminal] ; IPR007502[Helicase-
--		Large exo	U	Intracellula	IPR002126 [Cadherin] ; IPR013164[Cadherin, N-termin
--		Phosphoril	FE	Nucleotide	IPR005946 [Ribose-phosphate diphosphokinase] ; IPRC
--		Uncharact	S	Function u	IPR000330 [SNF2-related, N-terminal domain] ; IPR001
--	--	--	--	--	IPR019143 [JNK/Rab-associated protein-1, N-terminal]
ko04120	U	--	--	--	--
--		Monoamir	E	Amino acid	IPR002937 [Amine oxidase] ; IPR007526[SWIRM domai
ko04919	T	--	--	--	IPR000195 [Rab-GTPase-TBC domain] ; IPR006020[PTE
ko04144	E	--	--	--	IPR001683 [Phox homologous domain]
ko04150	r	--	--	--	IPR000539 [Frizzled protein] ; IPR020067[Frizzled doma
ko00230	P	Nucleoside	F	Nucleotide	IPR001564 [Nucleoside diphosphate kinase]
--	--	--	--	--	IPR007677 [Gasdermin]
ko00061	F	Long-chain	I	Lipid trans	IPR000873 [AMP-dependent synthetase/ligase]
ko04130	S	--	--	--	IPR000727 [Target SNARE coiled-coil homology doma
ko04931	Ir	N-acetyl-k	G	Carbohydr	IPR011496 [Beta-N-acetylglucosaminidase]
ko00310	L	Glycosyltra	M	Cell wall/r	IPR005123 [Oxoglutarate/iron-dependent dioxygenase
--		RNA reco	J	Translatior	IPR000504 [RNA recognition motif domain]
ko03040	S	Predicted	IT	Signal tran	IPR001680 [WD40 repeat]
ko00533	G	Glycosyltra	G	Carbohydr	IPR027791 [Galactosyltransferase, C-terminal] ; IPR0279
--	--	--	--	--	IPR000357 [HEAT repeat]
ko04510	F	Transcripti	K	Transcripti	IPR009408 [Formin Homology 1] ; IPR010465[DRF auto
--	--	--	--	--	IPR018499 [Tetraspanin/Peripherin]
--	--	--	--	--	IPR010326 [Exocyst complex component EXOC3/Sec6]
--	--	--	--	--	IPR004279 [Perilipin]
--		Predicted	G	Carbohydr	IPR011701 [Major facilitator superfamily]
ko04015	R	--	--	--	IPR000225 [Armadillo]
--		Predicted	IR	General fu	--
--	--	--	--	--	IPR000225 [Armadillo] ; IPR002652[Importin-alpha, im
--	--	--	--	--	IPR001781 [Zinc finger, LIM-type]
ko03013	R	Translatior	J	Translatior	IPR001950 [SUI1 domain]
ko04144	E	--	--	--	IPR001683 [Phox homologous domain] ; IPR005329[So
ko05034	A	--	--	--	IPR007125 [Histone H2A/H2B/H3]
ko03008	R	Glutamate	E	Amino acid	IPR002478 [PUA domain] ; IPR002501[Pseudouridine sy
ko03013	R	Translatior	J	Translatior	IPR004161 [Translation elongation factor EFTu-like, do
--	--	--	--	--	IPR006953 [Vesicle tethering protein Uso1/P115-like, t
ko04977	V	--	--	--	IPR002666 [Reduced folate carrier]
--	--	--	--	--	IPR002014 [VHS domain] ; IPR004152[GAT domain]
--		Archaeal ri	J	Translatior	IPR001387 [Cro/C1-type helix-turn-helix domain] ; IPR

ko04141 P DnaJ-class O	Posttransla IPR001305 [Heat shock protein DnaJ, cysteine-rich don
-- -- --	-- IPR002777 [Prefoldin beta-like]
ko04360 A -- --	-- IPR000198 [Rho GTPase-activating protein domain] ; IF
-- Predicted IT	Signal tran IPR001680 [WD40 repeat]
ko04360 A Streptogra V	Defense m IPR001627 [Sema domain] ; IPR002165[Plexin repeat] ;
-- -- --	-- IPR013106 [Immunoglobulin V-set domain]
ko04022 c Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR015008[Rho bi
ko04150 r -- --	-- IPR000539 [Frizzled protein] ; IPR020067[Frizzled dom
-- Magnesiur P	Inorganic i IPR008250 [P-type ATPase, A domain] ; IPR032630[P-i
-- -- --	-- IPR024395 [CLASP N-terminal domain]
-- -- --	-- IPR002558 [I/LWEQ domain] ; IPR011417[AP180 N-terr
-- Uncharact R	General fu IPR013098 [Immunoglobulin I-set]
-- DnaJ-class O	Posttransla IPR001623 [DnaJ domain] ; IPR025640[Domain of unkn
-- Tetratricop R	General fu IPR025697 [CLU domain] ; IPR028275[Clustered mitoch
ko04150 r Glucose/ar G	Carbohydr IPR000033 [LDLR class B repeat] ; IPR002172[Low-dens
-- -- --	-- --
-- -- --	-- IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
-- Ca2+ -bind T	Signal tran IPR002048 [EF-hand domain]
ko04360 A -- --	-- IPR001627 [Sema domain] ; IPR002165[Plexin repeat] ;
-- -- --	-- IPR004226 [Tubulin binding cofactor A]
ko04144 E AAA+ -typ MDT	Cell wall/r IPR003959 [ATPase, AAA-type, core] ; IPR007330[MIT]
ko04217 N O-acetyl- /J	Translatior IPR002589 [Macro domain] ; IPR007125[Histone H2A/H
ko04010 N Uncharact S	Function u IPR001715 [Calponin homology domain] ; IPR017868[F
-- -- --	-- IPR006603 [PQ-loop repeat]
-- DNA-bind R	General fu IPR000315 [B-box-type zinc finger] ; IPR001258[NHL re
-- -- --	-- IPR011701 [Major facilitator superfamily]
ko00020 C Citrate syn C	Energy prc IPR002020 [Citrate synthase]
ko04130 S -- --	-- IPR001388 [Synaptobrevin] ; IPR010908[Longin domain
ko03040 S -- --	-- IPR001202 [VW domain] ; IPR002713[FF domain]
ko04144 E -- --	-- IPR028934 [Vacuolar protein sorting protein 26 related
-- -- --	-- IPR000313 [PWWP domain] ; IPR021567[Lens epitheliu
ko03040 S RNA recog J	Translatior IPR000504 [RNA recognition motif domain]
-- -- --	-- IPR009643 [Heat shock factor binding 1]
ko04514 C -- --	-- IPR004031 [PMP-22/EMP/MP20/Claudin superfamily]
-- -- --	-- IPR004122 [Barrier- to-autointegration factor, BAF]
ko04060 C -- --	-- IPR000488 [Death domain] ; IPR001368[TNFR/NGFR cy
ko03040 S -- --	-- IPR015016 [Splicing factor 3B subunit 1]
-- -- --	-- IPR002059 [Cold-shock protein, DNA-binding] ; IPR02
-- -- --	-- IPR007018 [Mediator complex, subunit Med6]
-- -- --	-- IPR024057 [Nucleoplasmin core domain]
ko00564 G Predicted R	General fu IPR003140 [Phospholipase/carboxylesterase/thioestera
-- -- --	-- IPR007303 [TIP41-like protein]
ko03040 S Replicative L	Replicatio IPR001650 [Helicase, C-terminal] ; IPR004179[Sec63 dc
-- -- --	-- IPR002014 [VHS domain] ; IPR004152[GAT domain]
ko03013 R -- --	-- IPR007187 [Nucleoporin, Nup133/Nup155-like, C-term
-- -- --	-- IPR012945 [Tubulin binding cofactor C-like domain]
-- -- --	-- --
ko04750 Ir Chromoso D	Cell cycle c IPR005821 [Ion transport domain] ; IPR020683[Ankyrin
ko04614 R -- --	-- IPR012493 [Renin receptor-like]
ko03013 R RNA recog J	Translatior IPR000504 [RNA recognition motif domain] ; IPR02467
ko03013 R -- --	-- IPR013906 [Eukaryotic translation initiation factor 3 sub
-- -- --	-- IPR007084 [BRICHOS domain]
-- Ankyrin rej T	Signal tran IPR002110 [Ankyrin repeat] ; IPR020683[Ankyrin repeat
ko00020 C Isocitrate c C	Energy prc IPR024084 [Isopropylmalate dehydrogenase-like dom
ko00670 C Acyl-CoA C	Energy prc IPR002376 [Formyl transferase, N-terminal] ; IPR00579
-- -- --	-- IPR004895 [Prenylated rab acceptor PRA1]
ko00900 T Zn-depend O	Posttransla IPR001915 [Peptidase M48] ; IPR032456[CAAX prenyl p
-- PASTA dor M	Cell wall/r IPR000219 [Dbl homology (DH) domain] ; IPR000719[P

ko04530 T -- --	-- IPR001478 [PDZ domain] ; IPR015132[L27-2] ; IPR0320
-- Bacillopep O	Posttransla IPR000834 [Peptidase M14, carboxypeptidase A]
-- Glutaredox O	Posttransla IPR002109 [Glutaredoxin] ; IPR013766[Thioredoxin don
-- -- --	-- IPR028364 [Ribosomal protein L1/ribosomal biogenesis
-- WD40 rep R	General fu IPR001680 [WD40 repeat]
-- -- --	-- IPR016137 [RGS domain]
ko03060 P Tetratricop R	General fu IPR013699 [Signal recognition particle, SRP72 subunit,
-- N-Dimethy E	Amino acid --
ko04914 P Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR022165[Polo ki
ko04015 R Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR001849[Pleckst
ko00250 A Glucosami M	Cell wall/r IPR001347 [Sugar isomerase (SIS)]
ko04141 P -- --	-- IPR006895 [Zinc finger, Sec23/Sec24-type] ; IPR006896
-- -- --	-- IPR003864 [Calcium-dependent channel, 7TM region, i
ko04015 R -- --	-- IPR000219 [Dbl homology (DH) domain] ; IPR001849[P
ko04144 E -- --	-- IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
ko04120 U -- --	-- IPR000569 [HECT domain] ; IPR002004[Polyadenylate-l
-- -- --	-- IPR025481 [Cell morphogenesis protein C-terminal] ; IPR000504
-- -- --	-- IPR000504 [RNA recognition motif domain] ; IPR00690
-- -- --	-- IPR002126 [Cadherin]
ko00980 N Predicted R	General fu IPR023210 [NADP-dependent oxidoreductase domain]
-- V8-like Glu E	Amino acid IPR001254 [Serine proteases, trypsin domain]
ko04120 U -- --	-- IPR003613 [U box domain] ; IPR019474[Ubiquitin conj
-- -- --	-- IPR006849 [Elongator complex subunit lki3]
-- -- --	-- --
ko04130 S -- --	-- IPR001388 [Synaptobrevin]
ko04144 E -- --	-- IPR001683 [Phox homologous domain]
-- -- --	-- IPR001752 [Kinesin motor domain]
-- -- --	-- IPR001194 [DENN domain] ; IPR001849[Pleckstrin hom
ko04130 S -- --	-- --
ko04979 C -- --	-- IPR000535 [Major sperm protein (MSP) domain]
-- -- --	-- IPR028119 [Snapin/Pallidin/Snn1]
ko04514 C -- --	-- IPR013106 [Immunoglobulin V-set domain]
ko00030 P 6-phospho G	Carbohydr IPR006148 [Glucosamine/galactosamine-6-phosphate
ko00230 P ATP sulfur P	Inorganic i IPR024951 [Sulphate adenylyltransferase catalytic dom
ko01522 E ABC-type V	Defense m IPR003439 [ABC transporter-like] ; IPR011527[ABC tran
Chromoso D	Cell cycle c IPR003395 [RecF/RecN/SMC, N-terminal] ; IPR010935[
ko04136 A Molybdop H	Coenzyme IPR000594 [THIF-type NAD/FAD binding fold] ; IPR032
ko00564 G Predicted R	General fu IPR003140 [Phospholipase/carboxylesterase/thioestera
ko00520 A Phosphom G	Carbohydr IPR005843 [Alpha-D-phosphohexomutase, C-terminal
-- -- --	-- IPR019317 [Brain protein l3]
-- Uncharact S	Function u IPR013538 [Activator of Hsp90 ATPase homologue 1-li
-- -- --	-- IPR016565 [Proteasome assembly chaperone 1]
-- -- --	-- IPR010472 [Formin, FH3 domain] ; IPR010473[Formin, (
-- -- --	-- IPR000203 [GPS motif] ; IPR000832[GPCR, family 2, sec
ko00230 P DNA-direct K	Transcripti IPR000722 [RNA polymerase, alpha subunit] ; IPR00706
ko04144 E Proteasom O	Posttransla IPR000555 [JAB1/MPN/MOV34 metalloenzyme domair
ko04910 Ir -- --	-- IPR005036 [CBM21 (carbohydrate binding type-21) do
ko04120 U Alpha-tub DZ	Cell cycle c IPR000408 [Regulator of chromosome condensation, R
ko00770 P Predicted R	General fu IPR003010 [Carbon-nitrogen hydrolase]
ko00770 P Predicted R	General fu IPR003010 [Carbon-nitrogen hydrolase]
ko04130 S -- --	-- --
-- -- --	-- IPR014720 [Double-stranded RNA-binding domain] ; I
-- -- --	-- IPR007919 [Uncharacterised protein family UPF0220]
ko04141 P -- --	-- --
-- -- --	-- IPR001202 [WW domain] ; IPR003103[BAG domain]
-- Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR024678[Serine/
-- WD40 rep R	General fu IPR001680 [WD40 repeat] ; IPR005108[HELP]
ko04390 H PASTA dor M	Cell wall/r IPR000719 [Protein kinase domain] ; IPR015940[Ubiqui

--	--	--	--	IPR018499 [Tetraspanin/Peripherin]
ko00480	G Thiol:disulf	O	Posttransla	--
ko04010	N Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR001180[Citron
--	--	--	--	IPR001881 [EGF-like calcium-binding domain] ; IPR026
ko04012	E Serine/thre	T	Signal tran	IPR000095 [CRIB domain] ; IPR000719[Protein kinase d
ko05225	H Actin-relat	Z	Cytoskelet	IPR004000 [Actin family]
--	N-Dimethy	E	Amino acid	--
ko00010	G Zn-depende	R	General fu	IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
--	--	--	--	IPR013111 [EGF-like domain, extracellular]
ko00220	A Glutamate	E	Amino acid	IPR006096 [Glutamate/phenylalanine/leucine/valine de
ko00670	C Dihydrofol	H	Coenzyme	IPR001796 [Dihydrofolate reductase domain]
ko00190	C Heme/cop	C	Energy prc	IPR002429 [Cytochrome c oxidase subunit II-like C-ter
ko00230	P Hypoxanth	F	Nucleotide	IPR000836 [Phosphoribosyltransferase domain]
ko00010	G Malate/lac	C	Energy prc	IPR001236 [Lactate/malate dehydrogenase, N-termina
ko00830	R Acyl-CoA	C	Energy prc	IPR015590 [Aldehyde dehydrogenase domain]
ko00220	A Aspartate/	E	Amino acid	IPR004839 [Aminotransferase, class I/classII]
ko00230	P Adenylate	F	Nucleotide	--
ko00520	A Ferredoxin	C	Energy prc	IPR001433 [Oxidoreductase FAD/NAD(P)-binding] ; IPR
ko00480	G Pyruvate/2	C	Energy prc	IPR004099 [Pyridine nucleotide-disulphide oxidoreduc
ko04064	N Secreted tr	O	Posttransla	IPR000001 [Kringel] ; IPR001254[Serine proteases, tryps
ko04371	A Secreted tr	O	Posttransla	IPR000001 [Kringel] ; IPR000083[Fibronectin, type I] ; IP
ko00860	P Multicopp	DPM	Cell cycle c	IPR001117 [Multicopper oxidase, type 1] ; IPR011706[N
ko04610	C Serine pro	O	Posttransla	IPR023796 [Serpine domain]
ko00230	P Purine nuc	F	Nucleotide	IPR000845 [Nucleoside phosphorylase domain]
ko01521	E GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
ko04144	E Glucose/ar	G	Carbohydr	IPR000033 [LDLR class B repeat] ; IPR001881[EGF-like c
ko01521	E Serine/thre	T	Signal tran	IPR000494 [Receptor L-domain] ; IPR001245[Serine-th
ko00010	G 3-phosph	G	Carbohydr	IPR001576 [Phosphoglycerate kinase]
ko04918	T Carboxyles	I	Lipid trans	IPR000716 [Thyroglobulin type-1] ; IPR002018[Carboxy
ko04080	N Secreted tr	O	Posttransla	IPR000001 [Kringel] ; IPR000294[Gamma-carboxygluta
--	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
--	--	--	--	IPR003597 [Immunoglobulin C1-set]
--	--	--	--	IPR003597 [Immunoglobulin C1-set]
ko04610	C Type V sec	MU	Cell wall/r	IPR001073 [C1q domain] ; IPR008160[Collagen triple h
ko04610	C --	--	--	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IP
ko01521	E HEAT repe	R	General fu	IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko04610	C Uncharact	R	General fu	IPR001599 [Alpha-2-macroglobulin] ; IPR002890[Alph
ko00511	C O-Glycosy	M	Cell wall/r	IPR033452 [Glycosyl hydrolase family 30, beta sandwic
ko04610	C Uncharact	R	General fu	IPR000020 [Anaphylatoxin/fibulin] ; IPR001599[Alpha-2
ko04066	H --	--	--	IPR001820 [Protease inhibitor I35 (TIMP)]
ko00511	C Alpha-L-ft	G	Carbohydr	IPR000933 [Glycoside hydrolase, family 29] ; IPR031919
ko04610	C ABC-type	P	Inorganic i	IPR000010 [Cystatin domain]
--	--	--	--	IPR000010 [Cystatin domain]
ko00564	G --	--	--	IPR003386 [Lecithin:cholesterol/phospholipid:diacylgly
ko00330	A Acetylornit	E	Amino acid	IPR005814 [Aminotransferase class-III]
ko00240	P Thymidine	F	Nucleotide	IPR001267 [Thymidine kinase]
--	--	--	--	IPR000010 [Cystatin domain]
--	--	--	--	IPR013106 [Immunoglobulin V-set domain]
ko00220	A Argininosu	E	Amino acid	IPR022761 [Fumarate lyase, N-terminal] ; IPR029419[Ar
ko00240	P Thymidylat	F	Nucleotide	IPR023451 [Thymidylate synthase/dCMP hydroxymethy
ko04970	S --	--	--	IPR011531 [Bicarbonate transporter, C-terminal] ; IPR0
ko04144	E --	--	--	IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC
ko04144	E --	--	--	IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC
ko04022	c --	--	--	IPR000402 [Sodium/potassium-transporting ATPase su
ko00010	G Fructose-k	G	Carbohydr	IPR000741 [Fructose-bisphosphate aldolase, class-I]
ko04015	R Secreted p	R	General fu	IPR002369 [Integrin beta subunit, VWA domain] ; IPR0

ko04622 R -- --	-- IPR000626 [Ubiquitin domain]
ko04064 N -- --	-- IPR013768 [Intercellular adhesion molecule, N-termina
ko04151 P Autotransp UW	Intracellular IPR001442 [Collagen IV, non-collagenous] ; IPR008160
-- -- --	-- IPR001664 [Intermediate filament protein]
-- DNA repair L	Replication IPR001664 [Intermediate filament protein] ; IPR032444[
ko03320 P -- --	-- IPR000074 [Apolipoprotein A/E]
ko05322 S -- --	-- IPR000504 [RNA recognition motif domain] ; IPR00663
ko01521 E Serine/thre T	Signal trans IPR000008 [C2 domain] ; IPR000719[Protein kinase dor
ko04610 C -- --	-- IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
-- -- --	-- IPR001664 [Intermediate filament protein]
-- -- --	-- IPR001664 [Intermediate filament protein] ; IPR032444[
ko00860 P Uroporphyrin H	Coenzyme IPR000257 [Uroporphyrinogen decarboxylase (URO-D)
ko04979 C -- --	-- IPR000436 [Sushi/SCR/CCP domain] ; IPR015104[Beta-
ko04010 N Ankyrin repeat T	Signal trans IPR000494 [Receptor L-domain] ; IPR001245[Serine-th
ko04071 S TolB amino R	General fu IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
ko00052 G Alpha-galact G	Carbohydr IPR002241 [Glycoside hydrolase, family 27]
ko04110 C Predicted , R	General fu IPR000719 [Protein kinase domain]
ko04390 H -- --	-- IPR014760 [Serum albumin, N-terminal]
ko01521 E -- --	-- IPR001040 [Translation Initiation factor eIF- 4e]
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	Posttransl IPR001254 [Serine proteases, trypsin domain] ; IPR0036
ko00330 A Protein-arr O	Posttransl IPR022413 [ATP:guanido phosphotransferase, N-termi
ko00561 G Ca2+ -bind Q	Secondary IPR001024 [PLAT/LH2 domain] ; IPR013818[Lipase/vitel
ko04151 P -- --	-- IPR001212 [Somatomedin B domain] ; IPR018487[Hem
ko00380 T Catalase P	Inorganic i IPR010582 [Catalase immune-responsive domain] ; IPR
ko00980 N Pimeloyl- A HR	Coenzyme IPR010497 [Epoxide hydrolase, N-terminal]
ko03320 P Acyl-CoA- I	Lipid trans IPR000582 [Acyl-CoA-binding protein, ACBP]
ko00480 G Glutathion VI	Defense m IPR000889 [Glutathione peroxidase]
ko00010 G Fructose-k G	Carbohydr IPR000741 [Fructose-bisphosphate aldolase, class-I]
-- -- --	-- IPR005818 [Linker histone H1/H5, domain H15]
-- -- --	-- IPR018502 [Annexin repeat]
ko00910 N Carbonic a P	Inorganic i IPR001148 [Alpha carbonic anhydrase]
ko04062 C Serine/thre T	Signal trans IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
ko00020 C Fumarate l C	Energy prc IPR018951 [Fumarase C, C-terminal] ; IPR022761[Fuma
ko01521 E Ankyrin repeat T	Signal trans IPR000494 [Receptor L-domain] ; IPR001245[Serine-th
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain]
ko02010 A ABC-type V	Defense m IPR003439 [ABC transporter-like] ; IPR011527[ABC tran
-- DNA repair L	Replication IPR001664 [Intermediate filament protein] ; IPR032444[
-- Uncharacter S	Function u IPR001664 [Intermediate filament protein] ; IPR032444[
ko00010 G 6-phospho G	Carbohydr IPR000023 [Phosphofructokinase domain]
ko00250 A Asparagine E	Amino acid IPR001962 [Asparagine synthase] ; IPR017932[Glutamir
ko00010 G Glyceralde G	Carbohydr IPR020828 [Glyceraldehyde 3-phosphate dehydrogen
ko04614 R Predicted r O	Posttransl IPR008753 [Peptidase M13, N-terminal domain] ; IPR0
ko01521 E Ankyrin repeat T	Signal trans IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko04010 N Molecular O	Posttransl IPR002068 [Alpha crystallin/Hsp20 domain]
-- -- --	-- IPR001156 [Transferrin-like domain]
ko00510 N -- --	-- IPR007676 [Ribophorin I]
ko04015 R -- --	-- IPR001019 [Guanine nucleotide binding protein (G-prc
ko00071 F Acetyl-CoA I	Lipid trans IPR020616 [Thiolase, N-terminal] ; IPR020617[Thiolase,
ko03060 P Signal rec U	Intracellular IPR002778 [Signal recognition particle, SRP19 subunit]
ko03040 S -- --	-- IPR013085 [Zinc finger, U1-C type]
-- -- --	-- IPR000566 [Lipocalin/cytosolic fatty-acid binding dom
ko04142 L -- --	-- IPR000996 [Clathrin light chain]
ko04015 R Secreted p R	General fu IPR002369 [Integrin beta subunit, VWA domain] ; IPR0

ko04142 L' -- --	-- IPR000996 [Clathrin light chain]
-- Tfp pilus a: NW	Cell motilit IPR018502 [Annexin repeat]
ko03410 B WGR dom. K	Transcripti IPR001357 [BRCT domain] ; IPR001510[Zinc finger, PAF
ko04610 C Secreted tr O	Posttransla IPR001190 [SRCR domain] ; IPR001254[Serine protease
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain]
ko00590 A Aminopep E	Amino acid IPR014782 [Peptidase M1, membrane alanine aminope
ko04217 N -- --	-- IPR007125 [Histone H2A/H2B/H3] ; IPR032454[Histone
-- -- --	-- IPR001810 [F-box domain] ; IPR003877[SPRY domain]
ko03010 R -- --	-- --
ko03010 R -- --	-- --
ko03010 R Ribosomal J	Translatior IPR001790 [Ribosomal protein L10P]
-- GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko05322 S Secreted p R	General fu IPR008858 [TROVE domain]
ko01521 E Ankyrin rej T	Signal tran IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko04610 C Serine pro: O	Posttransla IPR023796 [Serpine domain]
ko00010 G Pyruvate/2 C	Energy prc IPR000089 [Biotin/lipoyl attachment] ; IPR001078[2-ox
ko04514 C Protein tyr T	Signal tran IPR000242 [PTP type protein phosphatase] ; IPR003961
ko04142 L' Carboxype E	Amino acid IPR001563 [Peptidase S10, serine carboxypeptidase]
ko01200 C S-formylgl V	Defense m IPR000801 [Putative esterase]
-- Ca2+ -binc T	Signal tran IPR002048 [EF-hand domain]
ko04974 P Autotransp UW	Intracellula IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[\
ko03018 R Chaperoni O	Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
ko00740 R -- --	-- IPR000560 [Histidine phosphatase superfamily, clade-2
-- -- --	-- IPR007477 [SAB domain] ; IPR008379[Band 4.1, C-term
-- Carboxylest I	Lipid trans IPR002018 [Carboxylesterase, type B] ; IPR014788[Acet
ko00240 P Orotate pl F	Nucleotide IPR000836 [Phosphoribosyltransferase domain] ; IPR00
ko04666 F -- --	-- IPR007123 [Gelsolin-like domain]
ko04014 R GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko04975 F Chromoso D	Cell cycle c IPR000074 [Apolipoprotein A/E]
ko04140 A -- --	-- IPR002000 [Lysosome-associated membrane glycopro
-- DNA topoi L	Replicatio IPR008336 [DNA topoisomerase I, DNA binding, eukan
ko00010 G Enolase G	Carbohydr IPR020810 [Enolase, C-terminal TIM barrel domain] ; IF
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
ko01524 P DNA gyrase L	Replicatio IPR002205 [DNA topoisomerase, type IIA, subunit A/C-
ko00511 C N-acetyl-k G	Carbohydr IPR015883 [Glycoside hydrolase family 20, catalytic dor
ko01522 E Serine/thre T	Signal tran IPR000719 [Protein kinase domain]
ko00030 P Phosphoril FE	Nucleotide IPR005946 [Ribose-phosphate diphosphokinase] ; IPRC
ko03030 D DNA polyr L	Replicatio IPR022648 [Proliferating cell nuclear antigen, PCNA, N-
ko00970 A Histidyl-tr J	Translatior IPR000738 [WHEP-TRS domain] ; IPR004154[Anticodor
ko03320 P -- --	-- --
ko00010 G Malate/lac C	Energy prc IPR001236 [Lactate/malate dehydrogenase, N-termina
ko03013 R -- --	-- IPR012929 [Nucleoprotein TPR/MLP1]
ko00330 A Protein-ar: O	Posttransla IPR022413 [ATP:guanido phosphotransferase, N-termi
ko04141 P Negative r: O	Posttransla IPR013766 [Thioredoxin domain]
ko00330 A Protein-ar: O	Posttransla IPR022413 [ATP:guanido phosphotransferase, N-termi
ko04071 S -- --	-- IPR012848 [Aspartic peptidase, N-terminal] ; IPR03312:
ko01521 E Serine/thre T	Signal tran IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
ko04145 P -- --	-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko03450 N -- --	-- IPR003034 [SAP domain] ; IPR005160[Ku70/Ku80 C-ter
ko03450 N -- --	-- IPR005160 [Ku70/Ku80 C-terminal arm] ; IPR005161[Ku
ko04142 L' -- --	-- IPR003119 [Saposin A-type domain] ; IPR007856[Sapo
ko00511 C N-acetyl-k G	Carbohydr IPR015883 [Glycoside hydrolase family 20, catalytic dor
ko04141 P Negative r: O	Posttransla IPR013766 [Thioredoxin domain]
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
ko00330 A Proline 4-HJO	Translatior IPR005123 [Oxoglutarate/iron-dependent dioxygenase
-- -- --	-- IPR018105 [Translationally controlled tumour protein]
ko00860 P Delta-amir H	Coenzyme IPR001731 [Delta-aminolevulinic acid dehydratase]
ko00500 S Glycosyltra M	Cell wall/r IPR008631 [Glycogen synthase]
ko04910 Ir cAMP-bin T	Signal tran IPR000595 [Cyclic nucleotide-binding domain] ; IPR003
ko03022 B -- --	-- IPR003196 [Transcription initiation factor IIF, beta subu
ko04141 P Cell divisio D	Cell cycle c IPR002048 [EF-hand domain] ; IPR009011[Mannose-6-
ko00900 T Geranylgei H	Coenzyme IPR000092 [Polyprenyl synthetase]
-- -- --	-- IPR018502 [Annexin repeat]
-- Murein trix M	Cell wall/r IPR000834 [Peptidase M14, carboxypeptidase A]
ko00010 G Aldo/keto Q	Secondary IPR023210 [NADP-dependent oxidoreductase domain]
ko03040 S -- --	-- IPR001163 [LSM domain, eukaryotic/archaea-type]
ko01522 E Predicted i O	Posttransla IPR000562 [Fibronectin, type II, collagen-binding] ; IPR
ko04141 P Molecular O	Posttransla IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
-- -- --	-- IPR000504 [RNA recognition motif domain]
ko05200 P -- --	-- IPR000225 [Armadillo]
ko04514 C -- --	-- IPR013106 [Immunoglobulin V-set domain] ; IPR01316
ko04060 C -- --	-- IPR003961 [Fibronectin type III] ; IPR021126[Interferon
-- -- --	-- IPR000591 [DEP domain] ; IPR001849[Pleckstrin homol
ko04151 P Autotransx UW	Intracellular IPR001442 [Collagen IV, non-collagenous] ; IPR008160
-- -- --	-- IPR001578 [Peptidase C12, ubiquitin carboxyl-terminal
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain]
ko04145 P Cytolysin, i U	Intracellular IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
ko05169 E -- --	-- IPR001664 [Intermediate filament protein] ; IPR006821[
ko04610 C Serine proi O	Posttransla IPR023796 [Serpine domain]
-- -- --	-- IPR001664 [Intermediate filament protein]
-- -- --	-- IPR018502 [Annexin repeat]
-- -- --	-- IPR001664 [Intermediate filament protein]
ko03010 R Ribosomal J	Translatior IPR001865 [Ribosomal protein S2] ; IPR032281[40S ribc
ko04142 L -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko00230 P Nucleoside F	Nucleotide IPR001564 [Nucleoside diphosphate kinase]
ko00130 U Putative N.R	General fu IPR003680 [Flavodoxin-like fold]
ko00480 G Glutathion O	Posttransla IPR004045 [Glutathione S-transferase, N-terminal] ; IPF
ko03030 D -- --	-- IPR014892 [Replication protein A, C-terminal]
ko04151 P Secreted p R	General fu IPR002369 [Integrin beta subunit, VWA domain] ; IPR00
-- -- --	-- IPR001079 [Galectin, carbohydrate recognition domain
ko03410 B -- --	-- IPR009071 [High mobility group box domain]
ko00052 G Beta-galac G	Carbohydr IPR025300 [Beta-galactosidase jelly roll domain] ; IPR0
-- -- --	-- IPR002350 [Kazal domain] ; IPR015369[Follistatin/Ostec
ko04260 C Cell divisio D	Cell cycle c IPR000533 [Tropomyosin]
ko04012 E -- --	-- IPR000980 [SH2 domain] ; IPR001452[SH3 domain]
-- Cytochrom QV	Secondary IPR001433 [Oxidoreductase FAD/NAD(P)-binding] ; IPR
ko00562 Ir -- --	-- IPR000008 [C2 domain] ; IPR000909[Phosphatidylinosit
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
ko04010 N -- --	-- IPR000956 [Stathmin family]
ko04530 T Cold shock K	Transcripti IPR002059 [Cold-shock protein, DNA-binding]
ko00010 G Fructose-k G	Carbohydr IPR000741 [Fructose-bisphosphate aldolase, class-I]
ko04910 Ir GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- -- --	-- --
ko00220 A Aspartate/ E	Amino acid IPR004839 [Aminotransferase, class I/classII]
ko01521 E Serine/thre T	Signal tran IPR000008 [C2 domain] ; IPR000719[Protein kinase dor
ko03040 S Molecular O	Posttransla IPR013126 [Heat shock protein 70 family]
ko04540 G -- --	-- IPR013092 [Connexin, N-terminal] ; IPR013124[Gap jur
-- -- --	-- IPR009071 [High mobility group box domain] ; IPR0292

ko00120 P Aldo/keto Q	Secondary IPR023210 [NADP-dependent oxidoreductase domain]
ko00270 C -- --	-- IPR001985 [S-adenosylmethionine decarboxylase]
ko04010 M GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko00240 P CTP synthase F	Nucleotide IPR017456 [CTP synthase, N-terminal] ; IPR017926[Glut
ko03050 P ATP-dependent O	Posttranslational IPR003959 [ATPase, AAA-type, core]
ko04520 A Protein tyrosine T	Signal transduction IPR000242 [PTP type protein phosphatase]
ko04621 N Negative regulatory O	Posttranslational IPR013766 [Thioredoxin domain]
ko03010 R Ribosomal J	Translation IPR001780 [Ribosomal protein L35A]
-- Protein tyrosine T	Signal transduction IPR000242 [PTP type protein phosphatase]
ko04610 C -- --	-- IPR002223 [Pancreatic trypsin inhibitor Kunitz domain]
ko00010 G Phosphoglycyl G	Carbohydrate IPR013078 [Histidine phosphatase superfamily, clade-1
-- Alpha-tubulin DZ	Cell cycle control IPR000408 [Regulator of chromosome condensation, R
-- -- --	-- IPR000538 [Link domain] ; IPR013106[Immunoglobulin
ko03060 P Molecular O	Posttranslational IPR013126 [Heat shock protein 70 family]
ko03030 D ATP-dependent L	Replication IPR012308 [DNA ligase, ATP-dependent, N-terminal] ;
ko03410 B -- --	-- IPR001357 [BRCT domain] ; IPR002706[DNA-repair pr
ko04514 C Large exoribonuclease U	Intracellular IPR000233 [Cadherin, cytoplasmic domain] ; IPR002126
ko00010 G Hexokinase G	Carbohydrate IPR022672 [Hexokinase, N-terminal] ; IPR022673[Hexol
-- Predicted transmembrane G	Carbohydrate IPR005828 [Major facilitator, sugar transporter-like]
ko00230 P DNA-directed K	Transcription IPR000783 [RNA polymerase, subunit H/Rpb5 C-termir
ko04010 M -- --	-- IPR000488 [Death domain] ; IPR001368[TNFR/NGFR cy
ko04141 P Serine/threonine T	Signal transduction IPR000719 [Protein kinase domain] ; IPR014720[Double
ko00500 S Glucan phosphorylase G	Carbohydrate IPR000811 [Glycosyl transferase, family 35]
ko00270 C Spermidine E	Amino acids --
ko04024 c. NhaP-type P	Inorganic ion IPR006153 [Cation/H+ exchanger] ; IPR032103[Sodium
ko03008 R Serine/threonine T	Signal transduction IPR000719 [Protein kinase domain]
ko04144 E GTPase SAR	General function IPR001806 [Small GTPase superfamily]
-- GTPase SAR	General function IPR001806 [Small GTPase superfamily]
ko00030 P Glucose-6-phosphate G	Carbohydrate IPR022674 [Glucose-6-phosphate dehydrogenase, NA
ko00230 P Signal transduction T	Signal transduction IPR001054 [Adenylyl cyclase class-3/4/guanylyl cyclase
ko00010 G Zn-dependent R	General function IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
ko04210 A -- --	-- IPR001322 [Lamin Tail Domain] ; IPR001664[Intermedia
ko04060 C -- --	-- IPR020438 [Interleukin-11]
ko03013 R RNA recognition J	Translation IPR000504 [RNA recognition motif domain] ; IPR00200
-- -- --	-- IPR001259 [Proteinase inhibitor I27, calpastatin]
ko00230 P CBS domain T	Signal transduction IPR000644 [CBS domain] ; IPR001093[IMP dehydrogen
ko04010 M -- --	-- IPR000008 [C2 domain] ; IPR000980[SH2 domain] ; IPR
-- -- --	-- IPR004931 [Prothymosin/parathymosin]
-- Serine/threonine T	Signal transduction IPR000719 [Protein kinase domain]
ko00480 G Glutathione O	Posttranslational IPR004045 [Glutathione S-transferase, N-terminal] ; IPF
ko04610 C Multicopper DPM	Cell cycle control IPR000421 [Coagulation factor 5/8 C-terminal domain]
ko00230 P CBS domain T	Signal transduction IPR000644 [CBS domain] ; IPR001093[IMP dehydrogen
ko00190 C Archaeal/v C	Energy production IPR000194 [ATPase, F1/V1/A1 complex, alpha/beta sub
ko00190 C -- --	-- IPR004907 [ATPase, V1 complex, subunit C]
-- -- --	-- IPR018502 [Annexin repeat]
-- -- --	-- IPR001781 [Zinc finger, LIM-type]
ko04510 F -- --	-- IPR001715 [Calponin homology domain] ; IPR002017[S
ko01521 E -- --	-- IPR001251 [CRAL-TRIO lipid binding domain] ; IPR0016
-- Xaa-Pro amide E	Amino acids IPR000994 [Peptidase M24] ; IPR007865[Aminopeptida
ko00564 G Glycerol-3-phosphate C	Energy production IPR006109 [Glycerol-3-phosphate dehydrogenase, NA
ko00140 S Predicted transmembrane R	General function IPR002935 [O-methyltransferase, family 3]
ko04140 A -- --	-- IPR002000 [Lysosome-associated membrane glycoprotein
-- Leucine-rich K	Transcription IPR001611 [Leucine-rich repeat]
-- Tfp pilus assembly NW	Cell motility IPR000859 [CUB domain] ; IPR001506[Peptidase M12A]
-- -- --	-- IPR000648 [Oxysterol-binding protein] ; IPR001849[Ple
ko03008 R Fibrillarin J	Translation IPR000692 [Fibrillarin]
ko00230 P Phosphorylation F	Nucleotide IPR002376 [Formyl transferase, N-terminal] ; IPR010916
ko04152 A Translation J	Translation IPR000640 [Translation elongation factor EFG, V domai

--	--	--	--	IPR001664	[Intermediate filament protein]
--	--	--	--	IPR001664	[Intermediate filament protein] ; IPR032444[
ko00230	P	Phosphoril	F	Nucleotide	IPR000031 [PurE domain] ; IPR028923[SAICAR synthetase]
ko00564	G	Carboxylesterase	I	Lipid trans	IPR002018 [Carboxylesterase, type B] ; IPR014788[Acetyl-CoA synthetase]
ko00230	P	Predicted	R	General fu	IPR001212 [Somatomedin B domain] ; IPR001604[DNA topoisomerase]
ko04012	E	--	--	--	IPR003153 [Adaptor protein Cbl, N-terminal helical] ; IPR001715 [Calponin homology domain] ; IPR002048[EF-hand domain] ; IPR001715 [Calponin homology domain] ; IPR002048[EF-hand domain]
--	--	--	--	--	IPR001715 [Calponin homology domain] ; IPR002048[EF-hand domain]
--	--	--	--	--	IPR001715 [Calponin homology domain] ; IPR002048[EF-hand domain]
ko01522	E	WD40 repeat	R	General fu	IPR000719 [Protein kinase domain]
--	--	DNA-directed	K	Transcripti	IPR001222 [Zinc finger, TFIIIS-type] ; IPR003618[Transcription factor]
ko05165	H	Cell division	D	Cell cycle c	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[Cell cycle]
ko00010	G	Enolase	G	Carbohydr	IPR020810 [Enolase, C-terminal TIM barrel domain] ; IPR002048 [EF-hand domain] ; IPR013787[S100/CaBP-1]
--	--	--	--	--	IPR002048 [EF-hand domain] ; IPR013787[S100/CaBP-1]
ko00350	T	Phenylpyruvate	Q	Secondary	IPR001398 [Macrophage migration inhibitory factor]
ko01521	E	PASTA domain	M	Cell wall/r	IPR001245 [Serine-threonine/tyrosine-protein kinase catalytic domain]
--	--	Protein tyrosine	T	Signal tran	IPR000242 [PTP type protein phosphatase] ; IPR003961 [PTP type protein phosphatase]
--	--	Protein tyrosine	T	Signal tran	IPR000242 [PTP type protein phosphatase]
--	--	Glucose/arabinose	G	Carbohydr	IPR000033 [LDLR class B repeat] ; IPR000716[Thyroglobulin]
--	--	Protein tyrosine	T	Signal tran	IPR000242 [PTP type protein phosphatase] ; IPR001148 [PTP type protein phosphatase]
ko00010	G	Phosphohistidine	T	Signal tran	IPR015793 [Pyruvate kinase, barrel] ; IPR015795[Pyruvate kinase]
ko04141	P	Molecular	O	Posttransla	IPR001404 [Heat shock protein Hsp90 family] ; IPR003504 [RNA recognition motif domain]
ko03013	R	--	--	--	IPR000504 [RNA recognition motif domain]
ko00562	Ir	--	--	--	IPR005522 [Inositol polyphosphate kinase]
ko00240	P	Thymidylate	F	Nucleotide	--
ko04060	C	--	--	--	IPR015319 [Interleukin-4 receptor alpha, N-terminal]
ko00040	P	Aldo/keto	Q	Secondary	IPR023210 [NADP-dependent oxidoreductase domain]
ko00480	G	Aminopeptidase	E	Amino acid	IPR014782 [Peptidase M1, membrane alanine aminopeptidase]
--	--	--	--	--	IPR014038 [Translation elongation factor EF1B, beta/delta]
--	--	Bacillopeptidase	O	Posttransla	IPR000834 [Peptidase M14, carboxypeptidase A]
ko00730	T	Protein-tyrosine	T	Signal tran	IPR023485 [Phosphotyrosine protein phosphatase I subfamily]
ko00230	P	DNA-directed	K	Transcripti	IPR000684 [RNA polymerase II, heptapeptide repeat, epsilon]
ko04068	F	Serine/threonine	T	Signal tran	IPR000719 [Protein kinase domain]
ko04062	C	Serine/threonine	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR001849[Pleckstrin]
ko04015	R	--	--	--	IPR000276 [G protein-coupled receptor, rhodopsin-like]
ko03010	R	Ribosomal	J	Translatio	IPR005324 [Ribosomal protein S5, C-terminal] ; IPR013787[S100/CaBP-1]
ko03030	D	DNA replic	L	Replicatio	IPR001208 [MCM domain] ; IPR027925[MCM N-terminal]
ko00270	C	3-mercapt	P	Inorganic i	IPR001763 [Rhodanese-like domain]
ko04512	E	--	--	--	IPR000538 [Link domain]
--	--	--	--	--	IPR001487 [Bromodomain] ; IPR027353[NET domain]
--	--	--	--	--	IPR001487 [Bromodomain] ; IPR027353[NET domain]
ko04141	P	DnaJ-class	O	Posttransla	IPR001623 [DnaJ domain] ; IPR002939[Chaperone DnaJ]
ko00190	C	FoF1-type	C	Energy prc	IPR000194 [ATPase, F1/V1/A1 complex, alpha/beta subunit]
ko00270	C	Site-specif	L	Replicatio	IPR001025 [Bromo adjacent homology (BAH) domain]
--	--	--	--	--	IPR005818 [Linker histone H1/H5, domain H15]
--	--	--	--	--	IPR005818 [Linker histone H1/H5, domain H15]
--	--	--	--	--	IPR005818 [Linker histone H1/H5, domain H15]
ko00970	A	Threonyl-tRNA	J	Translatio	IPR002314 [Aminoacyl-tRNA synthetase, class II (G/ P/)]
--	--	FKBP-type	O	Posttransla	IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomerase]
ko01521	E	Serine/threonine	T	Signal tran	IPR000719 [Protein kinase domain]
--	--	PASTA domain	M	Cell wall/r	IPR000719 [Protein kinase domain] ; IPR001772[Kinase]
ko03030	D	ssDNA-bir	L	Replicatio	IPR004365 [OB-fold nucleic acid binding domain, AA-tRNA]
ko03040	S	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko03410	B	Exonuclease	L	Replicatio	IPR005135 [Endonuclease/exonuclease/phosphatase]
--	--	--	--	--	IPR001084 [Microtubule associated protein, tubulin-binding]
ko01521	E	--	--	--	IPR000198 [Rho GTPase-activating protein domain] ; IPR001353 [Proteasome, subunit alpha/beta]
ko03050	P	20S proteas	O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta]
ko03050	P	20S proteas	O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta]
ko00230	P	DNA polyr	L	Replicatio	IPR006133 [DNA-directed DNA polymerase, family B, epsilon]
ko01521	E	Outer men	M	Cell wall/r	IPR000719 [Protein kinase domain]

ko04514 C Protein tyr T	Signal tran IPR000242 [PTP type protein phosphatase] ; IPR000998
ko04141 P Serine pro O	Posttransla IPR001300 [Peptidase C2, calpain, catalytic domain] ; IF
ko00330 A Leucyl ami E	Amino acic IPR000819 [Peptidase M17, leucyl aminopeptidase, C-t
ko00562 Ir Archaeal fr G	Carbohydr IPR000760 [Inositol monophosphatase-like]
ko03040 S Superfamil L	Replicatio IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DI
ko00010 G 6-phospho G	Carbohydr IPR000023 [Phosphofructokinase domain]
ko04360 A Ankyrin rej T	Signal tran IPR001090 [Ephrin receptor ligand binding domain] ; IF
ko04520 A Protein tyr T	Signal tran IPR000242 [PTP type protein phosphatase] ; IPR00098C
-- Chaperoni O	Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
ko01521 E -- --	-- IPR000980 [SH2 domain] ; IPR006020[PTB/PI domain]
-- -- --	-- IPR000716 [Thyroglobulin type-1] ; IPR000867[Insulin-
ko05168 H -- --	-- IPR014038 [Translation elongation factor EF1B, beta/de
-- GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko03010 R Ribosomal J	Translatio IPR012988 [Ribosomal protein L30, N-terminal] ; IPR01
ko04510 F -- --	-- IPR006077 [Vinculin/alpha-catenin]
-- Predicted e R	General fu IPR003719 [Phenazine biosynthesis PhzF protein]
ko03010 R Ribosomal J	Translatio IPR001063 [Ribosomal protein L22/L17]
-- Phenylpyru Q	Secondary IPR001398 [Macrophage migration inhibitory factor]
ko04110 C Tetratricop R	General fu IPR001440 [Tetratricopeptide repeat 1] ; IPR019734[Tet
-- -- --	-- IPR022676 [Myristoyl-CoA:protein N-myristoyltransfera
ko01521 E Ankyrin rej 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 n -- --	-- IPR000938 [CAP Gly-rich domain] ; IPR032108[CLIP1, z
ko05206 M Amino acic E	Amino acic IPR002293 [Amino acid/polyamine transporter I] ; IPR0
ko00230 P DNA-direc K	Transcripti IPR007120 [DNA-directed RNA polymerase, subunit 2,
-- -- --	-- IPR018203 [GDP dissociation inhibitor]
ko04910 Ir cAMP-bin T	Signal tran IPR000595 [Cyclic nucleotide-binding domain] ; IPR00
ko00220 A Carbamoyl EF	Amino acic IPR002474 [Carbamoyl-phosphate synthase, small sub
ko00230 P Ribonuclec F	Nucleotide IPR000358 [Ribonucleotide reductase small subunit fan
-- 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
-- -- --	-- IPR002048 [EF-hand domain] ; IPR013787[S100/CaBP-
ko03013 R Translatio J	Translatio IPR002735 [Translation initiation factor IF2/IF5]
ko04010 M -- --	-- IPR011021 [Arrestin-like, N-terminal] ; IPR011022[Arre
ko04130 S -- --	-- IPR000727 [Target SNARE coiled-coil homology doma
ko00260 G Cystathion E	Amino acic IPR000277 [Cys/Met metabolism, pyridoxal phosphate-
ko03050 P 20S protea O	Posttransla IPR001353 [Proteasome, subunit alpha/beta]
ko03010 R Ribosomal J	Translatio IPR020040 [Ribosomal protein L6, alpha-beta domain]
-- Uncharact e R	General fu IPR001599 [Alpha-2-macroglobulin] ; IPR002890[Alph
-- Leucine-ric K	Transcripti IPR001611 [Leucine-rich repeat]
ko04060 C -- --	-- IPR006052 [Tumour necrosis factor domain]
ko00061 F Long-chain I	Lipid trans IPR000873 [AMP-dependent synthetase/ligase]
ko04514 C Large exo U	Intracellul IPR000233 [Cadherin, cytoplasmic domain] ; IPR002126
ko00240 P dUTPase FV	Nucleotide IPR008180 [Deoxyuridine triphosphate nucleotidohydr
ko01523 A ABC-type V	Defense m IPR003439 [ABC transporter-like] ; IPR011527[ABC tran
-- -- --	-- IPR013787 [S100/CaBP-9k-type, calcium binding, subc
ko00510 N -- --	-- IPR001382 [Glycoside hydrolase family 47]
ko03030 D DNA replic L	Replicatio IPR001208 [MCM domain] ; IPR027925[MCM N-termin
ko03030 D DNA replic L	Replicatio IPR001208 [MCM domain] ; IPR027925[MCM N-termin
ko00260 G Glycine/sei E	Amino acic IPR001085 [Serine hydroxymethyltransferase]
ko00260 G Glycine/sei E	Amino acic IPR001085 [Serine hydroxymethyltransferase]
ko00590 A Lysophosph I	Lipid trans IPR000073 [Alpha/beta hydrolase fold-1] ; IPR023214[t
ko04010 M Autotrans U	Intracellul IPR001715 [Calponin homology domain] ; IPR017868[F
ko04015 R -- --	-- IPR005455 [Profilin]
ko00020 C Aconitase C	Energy prc IPR000573 [Aconitase A/isopropylmalate dehydratase s
ko00230 P 2',3'-cyclic FV	Nucleotide IPR004843 [Calcineurin-like phosphoesterase domain,

--	Regulator	O	Posttransla	IPR001107	[Band 7 domain]
ko05146	A Serine pro	O	Posttransla	IPR023796	[Serp domain]
ko04640	H --	--	--	IPR018499	[Tetraspanin/Peripherin]
ko04390	H --	--	--	IPR011259	[Ezrin/radixin/moesin, C-terminal] ; IPR0189
ko05016	H --	--	--	IPR001102	[Transglutaminase, N-terminal] ; IPR002931
ko03030	D --	--	--	IPR013970	[Replication factor A protein 3]
ko03030	D DNA polyr	L	Replicatio	IPR003959	[ATPase, AAA-type, core] ; IPR013748[Repli
ko03030	D DNA polyr	L	Replicatio	IPR003959	[ATPase, AAA-type, core] ; IPR013748[Repli
ko03010	R --	--	--	IPR002671	[Ribosomal protein L22e]
ko03022	B --	--	--	IPR008851	[Transcription initiation factor IIF, alpha sub
ko00590	A Cytochrom	QV	Secondary	IPR000742	[EGF-like domain] ; IPR019791[Haem perox
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]
ko04020	C --	--	--	IPR000276	[G protein-coupled receptor, rhodopsin-lik
ko00260	G CBS doma	T	Signal tran	IPR000644	[CBS domain] ; IPR001926[Tryptophan synt
ko05412	A --	--	--	IPR001715	[Calponin homology domain] ; IPR002017[S
--	--	--	--	IPR000716	[Thyroglobulin type-1] ; IPR000867[Insulin-
--	Ribulose-5	G	Carbohydr	IPR001303	[Class II aldolase/adducin N-terminal]
ko05202	T RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain] ; IPR00187
ko03013	R --	--	--	--	--
ko04151	P Cytolysin,	U	Intracellul	IPR013517	[FG-GAP repeat] ; IPR013649[Integrin alpha
--	RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain] ; IPR01297
--	--	--	--	IPR014876	[DEK, C-terminal]
--	Peptidyl-p	O	Posttransla	IPR002130	[Cyclophilin-type peptidyl-prolyl cis-trans i
ko04010	M Serine/thre	T	Signal tran	IPR001932	[PPM-type phosphatase domain] ; IPR0129
ko03010	R Ribosomal	J	Translatio	IPR004044	[K Homology domain, type 2]
ko00430	T Gamma-gl	E	Amino acid	IPR000101	[Gamma-glutamyltranspeptidase]
--	--	--	--	IPR013092	[Connexin, N-terminal]
--	GTPase SAR		General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
ko01521	E Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
ko05120	E Protein tyr	T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR001148
ko00270	C S-adenosy	H	Coenzyme	IPR000043	[Adenosylhomocysteinase] ; IPR015878[S-a
ko00190	C Archaeal/v	C	Energy prc	IPR002842	[ATPase, V1/A1 complex, subunit E]
ko00860	P Copropor	H	Coenzyme	IPR001260	[Coproporphyrinogen III oxidase, aerobic]
--	ADP-ribos	F	Nucleotide	IPR000086	[NUDIX hydrolase domain]
ko04060	C Serine/thre	T	Signal tran	IPR000472	[Activin types I and II receptor domain] ; IP
ko00230	P Ribonucle	F	Nucleotide	IPR000788	[Ribonucleotide reductase large subunit, C-
ko04151	P DNA repai	L	Replicatio	IPR000034	[Laminin IV] ; IPR001791[Laminin G domain]
ko04060	C Serine/thre	T	Signal tran	IPR000472	[Activin types I and II receptor domain] ; IP
ko04010	M Serine/thre	T	Signal tran	IPR000472	[Activin types I and II receptor domain] ; IP
--	Ribosome	J	Translatio	IPR006073	[GTP binding domain]
ko04060	C --	--	--	IPR001368	[TNFR/NGFR cysteine-rich region]
ko00230	P IMP dehyd	F	Nucleotide	IPR001093	[IMP dehydrogenase/GMP reductase]
ko00480	G Glutathion	VI	Defense m	IPR000889	[Glutathione peroxidase]
ko03060	P --	--	--	IPR003210	[Signal recognition particle, SRP14 subunit]
ko04010	M Serine/thre	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
--	Ca ²⁺ -bind	T	Signal tran	IPR002048	[EF-hand domain]
--	Electron tr	C	Energy prc	IPR014730	[Electron transfer flavoprotein, alpha/beta-s
ko04151	P Chromoso	D	Cell cycle	IPR000034	[Laminin IV] ; IPR001791[Laminin G domain]
ko03010	R Ribosomal	J	Translatio	IPR004038	[Ribosomal protein L7Ae/L30e/S12e/Gadd4
ko03040	S RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain] ; IPR01260
ko00100	S Lysophosp	I	Lipid trans	IPR000073	[Alpha/beta hydrolase fold-1]
ko00190	C Archaeal/v	C	Energy prc	IPR000194	[ATPase, F1/V1/A1 complex, alpha/beta su
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	Intracellular IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160[
ko03018 R Molecular O	Posttransl IPR013126 [Heat shock protein 70 family]
ko03013 R Superfamil L	Replicator IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
ko04530 T -- --	-- IPR011259 [Ezrin/radixin/moesin, C-terminal] ; IPR0189
ko03010 R Ribosomal J	Translator IPR001266 [Ribosomal protein S19e]
ko03040 S RNA recog J	Translator IPR000504 [RNA recognition motif domain]
ko03010 R Ribosomal J	Translator IPR001380 [Ribosomal protein L13e]
-- -- --	-- IPR009071 [High mobility group box domain]
ko00510 N -- --	-- IPR005013 [Dolichyl-diphosphooligosaccharide--prote
ko00970 A Tfp pilus a: NW	Cell motilit IPR002300 [Aminoacyl-tRNA synthetase, class Ia] ; IPRC
ko05134 L Glutathion O	Posttransl IPR001662 [Translation elongation factor EF1B, gamma
ko03030 D 5'-3' exon L	Replicator IPR006085 [XPG N-terminal] ; IPR006086[XPG-I domain
ko04060 C -- --	-- IPR003961 [Fibronectin type III] ; IPR010457[Immunogl
-- Regulator O	Posttransl IPR001107 [Band 7 domain]
ko04110 C -- --	-- IPR023410 [14-3-3 domain]
-- GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko01521 E -- --	-- IPR000980 [SH2 domain] ; IPR013799[STAT transcriptio
ko04137 N -- --	-- IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko03030 D DNA polyr L	Replicator --
ko03013 R Translator J	Translator IPR004161 [Translation elongation factor EFTu-like, do
ko04115 p -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko00240 P Carbamoyl EF	Amino acid IPR002474 [Carbamoyl-phosphate synthase, small subu
-- Ribosomal J	Translator IPR000182 [GNAT domain]
ko05120 E PASTA dor M	Cell wall/r IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
ko01523 A -- --	-- IPR002666 [Reduced folate carrier]
ko03050 P 20S protea O	Posttransl IPR000426 [Proteasome alpha-subunit, N-terminal dor
ko04015 R Serine/thre T	Signal tran IPR000270 [PB1 domain] ; IPR000719[Protein kinase dc
-- Actin-relat Z	Cytoskelet IPR004000 [Actin family]
ko03050 P 20S protea O	Posttransl IPR001353 [Proteasome, subunit alpha/beta]
-- -- --	-- IPR003887 [LEM domain] ; IPR013146[LEM-like domair
ko04012 E -- --	-- IPR000980 [SH2 domain] ; IPR013799[STAT transcriptio
ko03018 R Superfamil L	Replicator IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
ko00562 Ir -- --	-- IPR000341 [Phosphatidylinositol 3-kinase Ras-binding
ko00562 Ir -- --	-- IPR000341 [Phosphatidylinositol 3-kinase Ras-binding
ko01521 E -- --	-- IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic
ko04371 A -- --	-- IPR000867 [Insulin-like growth factor-binding protein,
ko04010 N Ankyrin rej T	Signal tran IPR001090 [Ephrin receptor ligand binding domain] ; IF
ko00562 Ir -- --	-- IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic
ko00340 H Histidine a E	Amino acid IPR001106 [Aromatic amino acid lyase]
-- -- --	-- IPR002885 [Pentatricopeptide repeat] ; IPR033443[Pent
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
-- -- --	-- IPR024613 [Huntingtin, middle-repeat]
ko04666 F -- --	-- IPR002101 [Myristoylated alanine-rich C-kinase substr
-- Predicted r O	Posttransl IPR008753 [Peptidase M13, N-terminal domain] ; IPR0
ko01100 N Alkyl hydr V	Defense m IPR000866 [Alkyl hydroperoxide reductase subunit C/ T
ko04146 P Peroxiredc O	Posttransl IPR013740 [Redoxin]
-- -- --	-- IPR013106 [Immunoglobulin V-set domain] ; IPR01315
ko03010 R Ribosomal J	Translator IPR020783 [Ribosomal protein L11, C-terminal] ; IPR02
ko00240 P Adenylate F	Nucleotide --
-- -- --	-- --
ko04141 P Negative r O	Posttransl IPR013766 [Thioredoxin domain]
ko01524 P DNA mism L	Replicator IPR000432 [DNA mismatch repair protein MutS, C-tern
ko04062 C Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR016137[RGS dc
ko05166 H -- --	-- IPR000156 [Ran binding domain]
ko00760 N Nicotinic a H	Coenzyme IPR007229 [Nicotinate phosphoribosyltransferase famil
ko04020 C -- --	-- IPR027246 [Eukaryotic porin/Tom40]
ko01522 E PASTA dor M	Cell wall/r IPR000719 [Protein kinase domain]

--	--	--	--	IPR002048	[EF-hand domain]
--	Forkhead	εT	Signal tran	IPR000253	[Forkhead-associated (FHA) domain] ; IPR000253
ko04020	C	Glucoamylase	Carbohydr	IPR011613	[Glycoside hydrolase family 15/Phosphorylase]
ko04145	P	Membrane	Cell wall/r	IPR001680	[WD40 repeat] ; IPR015048[Domain of unknown function]
ko03013	R	Leucine-rich	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR009109[Ran-GTPase]
ko04657	IL	--	--	IPR013787	[S100/CaBP-9k-type, calcium binding, subdomain]
--	Superfamil	L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DFG motif]
--	16S rRNA	(J	Translatio	IPR001678	[SAM-dependent methyltransferase RsmB/I]
ko04010	M	--	--	IPR000980	[SH2 domain] ; IPR001452[SH3 domain] ; IPR000980
ko04512	E	--	--	IPR027789	[Syndecan/Neurexin domain]
ko04010	M	--	--	IPR000980	[SH2 domain] ; IPR001452[SH3 domain] ; IPR000980
--	Ubiquitin	O	Posttransla	IPR000626	[Ubiquitin domain] ; IPR021925[Protein of unknown function]
ko01522	E	Ankyrin re	Signal tran	IPR000742	[EGF-like domain] ; IPR000800[Notch domain]
ko00230	P	AICAR tra	Nucleotide	IPR002695	[AICARFT/IMPCHase bienzyme] ; IPR011607
ko04110	C	--	--	IPR023410	[14-3-3 domain]
ko05020	P	Uncharact	Function u	IPR011990	[Tetratricopeptide-like helical domain] ; IPR011990
ko04010	M	Serine/thr	Signal tran	IPR000719	[Protein kinase domain]
--	Alkyl hydr	V	Defense m	IPR000866	[Alkyl hydroperoxide reductase subunit C/1]
ko03010	R	--	--	IPR005326	[Plectin/S10, N-terminal]
ko00130	U	4-hydroxy	Amino acid	IPR004360	[Glyoxalase/fosfomycin resistance/dioxygenase]
--	--	--	--	IPR000102	[Neuraxin/MAP1B repeat]
ko00520	A	6-phosph	Carbohydr	IPR006148	[Glucosamine/galactosamine-6-phosphate]
--	--	--	--	IPR000433	[Zinc finger, ZZ-type] ; IPR001715[Calponin]
ko00510	N	Asparagin	Posttransla	IPR003674	[Oligosaccharyl transferase, STT3 subunit]
ko00010	G	Acyl-CoA	Energy prc	IPR015590	[Aldehyde dehydrogenase domain]
--	Na+-depe	R	General fu	IPR000175	[Sodium:neurotransmitter symporter]
ko04144	E	--	--	IPR001752	[Kinesin motor domain]
--	Uncharact	S	Function u	IPR014044	[CAP domain]
--	Na+-depe	R	General fu	IPR000175	[Sodium:neurotransmitter symporter]
ko04614	R	Prolyl olig	Amino acid	IPR001375	[Peptidase S9, prolyl oligopeptidase, catalytic domain]
ko00620	P	Malic enzy	Energy prc	IPR012301	[Malic enzyme, N-terminal domain] ; IPR012301
ko00100	S	Squalene c	Lipid trans	IPR032696	[Squalene cyclase, C-terminal] ; IPR032697[
ko03050	P	--	--	IPR033464	[CSN8/PSMD8/EIF3K]
--	--	--	--	IPR023412	[Ribonuclease A-domain]
ko04310	V	Serine/thr	Signal tran	IPR000719	[Protein kinase domain]
ko04340	H	Serine/thr	Signal tran	IPR000719	[Protein kinase domain]
ko00020	C	Isocitrate c	Energy prc	IPR024084	[Isopropylmalate dehydrogenase-like domain]
ko05205	P	--	--	IPR001863	[Glypican]
ko00562	I	--	--	IPR000341	[Phosphatidylinositol 3-kinase Ras-binding domain]
ko04015	R	--	--	IPR000225	[Armadillo]
--	--	--	--	IPR001666	[Phosphatidylinositol transfer protein]
--	--	--	--	IPR000203	[GPS motif] ; IPR000832[GPCR, family 2, second extracellular loop]
ko04062	C	--	--	IPR001781	[Zinc finger, LIM-type]
ko03010	R	Ribosomal	Translatio	IPR008195	[Ribosomal protein L34Ae]
ko04141	P	--	--	IPR005052	[Legume-like lectin]
--	Translator	J	Translatio	IPR004160	[Translation elongation factor EFTu/EF1A, C-terminal domain]
ko00010	G	Acyl-CoA	Energy prc	IPR015590	[Aldehyde dehydrogenase domain]
--	--	--	--	IPR006593	[Cytochrome b561/ferric reductase transmembrane domain]
ko03060	P	--	--	--	--
ko00970	A	Cysteiny	Translatio	IPR032678	[tRNA synthetases class I, catalytic domain]
ko03030	D	DNA replic	Replicatio	IPR001208	[MCM domain] ; IPR008045[DNA replicatio
ko00071	F	Acyl-CoA	Lipid trans	IPR006091	[Acyl-CoA oxidase/dehydrogenase, central domain]
ko03040	S	ABC-type	Inorganic i	IPR000504	[RNA recognition motif domain] ; IPR002480
ko04330	N	--	--	IPR006020	[PTB/PI domain] ; IPR010449[NUMB domain]
ko03013	R	Translator	Translatio	IPR000649	[Initiation factor 2B-related]
--	--	--	--	IPR001881	[EGF-like calcium-binding domain] ; IPR017171
ko00500	S	Glycogen	Carbohydr	IPR029436	[Eukaryotic glycogen debranching enzyme, catalytic domain]
ko04530	T	Chromoso	Cell cycle c	IPR001609	[Myosin head, motor domain] ; IPR002928[

ko04530 T Chromoso D	Cell cycle c IPR000048 [IQ motif, EF-hand binding site] ; IPR001608
-- Serine/thrε T	Signal tran IPR001245 [Serine-threonine/tyrosine-protein kinase c
-- WD40 repε R	General fu IPR001680 [WD40 repeat] ; IPR006692[Coatomer, WD ;
-- Diadenosir FGR	Nucleotide IPR001310 [Histidine triad (HIT) protein]
-- -- --	-- IPR016137 [RGS domain]
ko04062 C Formylglyc O	Posttransla IPR000719 [Protein kinase domain]
ko00140 S -- --	-- IPR000863 [Sulfotransferase domain]
ko00230 P Chromoso D	Cell cycle c IPR008380 [HAD-superfamily hydrolase, subfamily IG, t
ko04015 R -- --	-- IPR001019 [Guanine nucleotide binding protein (G-prc
-- Glutaredo> O	Posttransla IPR002109 [Glutaredoxin]
ko04014 R -- --	-- IPR015898 [G-protein gamma-like domain]
-- Leucine-rich K	Transcripti IPR000372 [Leucine-rich repeat N-terminal domain] ; I
-- Sulfate per P	Inorganic i IPR002645 [STAS domain] ; IPR011547[SLC26A/Sulp tra
ko03050 P ATP-deper O	Posttransla IPR003959 [ATPase, AAA-type, core]
-- Chitinase, i G	Carbohydr IPR001223 [Glycoside hydrolase family 18, catalytic dor
-- -- --	-- IPR001478 [PDZ domain] ; IPR001781[Zinc finger, LIM-
-- -- --	-- IPR019527 [RZZ complex, subunit KNTC1/ROD, C-term
ko05202 T Forkhead ε T	Signal tran IPR000719 [Protein kinase domain]
-- ATP-, malt K	Transcripti IPR000409 [BEACH domain] ; IPR010508[Domain of un
ko00062 F, -- --	-- IPR002472 [Palmitoyl protein thioesterase]
ko03013 R -- --	-- IPR004088 [K Homology domain, type 1] ; IPR008395[A
ko03010 R Ribosomal J	Translatior IPR002136 [Ribosomal protein L4/L1e] ; IPR025755[60S
ko04014 R GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko00010 G Phosphogl G	Carbohydr IPR005843 [Alpha-D-phosphohexomutase, C-terminal
ko05162 M GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko00562 Ir -- --	-- IPR000008 [C2 domain] ; IPR000909[Phosphatidylinosit
ko04010 M Protein-tyl T	Signal tran IPR000340 [Dual specificity phosphatase, catalytic dom
ko05225 H Uncharactε S	Function u IPR000330 [SNF2-related, N-terminal domain] ; IPR001
ko04141 P -- --	-- IPR008417 [B-cell receptor-associated protein 29/31]
ko00983 D SAM-deper QR	Secondary IPR008854 [TPMT family]
ko05168 H N-acetylne M	Cell wall/m IPR006652 [Kelch repeat type 1]
ko04144 E -- --	-- IPR001612 [Caveolin]
-- -- --	-- IPR001614 [Myelin proteolipid protein PLP]
-- Nucleotide T	Signal tran IPR000644 [CBS domain] ; IPR001807[Chloride channel
-- -- --	-- IPR000557 [Calponin repeat] ; IPR001715[Calponin hor
ko00030 P Transaldol. G	Carbohydr IPR001585 [Transaldolase/Fructose-6-phosphate aldol
-- Nucleotide T	Signal tran IPR000644 [CBS domain] ; IPR001807[Chloride channel
ko04130 S -- --	-- IPR001388 [Synaptobrevin] ; IPR010908[Longin domair
ko04010 M Cell divisio D	Cell cycle c IPR000719 [Protein kinase domain] ; IPR017892[Protein
-- -- --	-- IPR000313 [PWWP domain]
ko03040 S RNA recog J	Translatior IPR000504 [RNA recognition motif domain] ; IPR02466
ko05164 Ir -- --	-- IPR000225 [Armadillo] ; IPR002652[Importin-alpha, imp
ko05164 Ir -- --	-- IPR000225 [Armadillo] ; IPR002652[Importin-alpha, imp
ko03010 R Ribosomal J	Translatior IPR000597 [Ribosomal protein L3]
-- -- --	-- IPR000225 [Armadillo]
-- Amino acid E	Amino acid IPR002293 [Amino acid/polyamine transporter I] ; IPR0
ko05164 Ir -- --	-- IPR001164 [Arf GTPase activating protein]
-- -- --	-- IPR000504 [RNA recognition motif domain] ; IPR01299
ko03022 B -- --	-- IPR004855 [Transcription factor IIA, alpha/beta subunit
-- Chaperoni O	Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
ko00760 N -- --	-- IPR000940 [Methyltransferase, NNMT/PNMT/TEMT]
ko03010 R Ribosomal J	Translatior IPR005822 [Ribosomal protein L13]
ko01524 P DNA mism L	Replicatior IPR000313 [PWWP domain] ; IPR000432[DNA mismatch
ko00010 G Hexokinase G	Carbohydr IPR022672 [Hexokinase, N-terminal] ; IPR022673[Hexol
ko04360 A -- --	-- IPR001799 [Ephrin receptor-binding domain]
ko00020 C Malate/lac C	Energy prc IPR001236 [Lactate/malate dehydrogenase, N-termina
ko04614 R Zn-depend E	Amino acid IPR001567 [Peptidase M3A/M3B catalytic domain]

ko05202 T -- --	-- IPR017956 [AT hook, DNA-binding motif]
ko04150 r -- --	-- IPR005817 [Wnt]
ko00860 P Predicted cR	General fu IPR000683 [Oxidoreductase, N-terminal] ; IPR015249[B
ko04010 N Diadenosin	Signal tran IPR001440 [Tetratricopeptide repeat 1] ; IPR004843[Cal
ko00970 A Glycyl-tRN	Translatior IPR000738 [WHEP-TRS domain] ; IPR002314[Aminoacy
ko00970 A Isoleucyl-t	Translatior IPR002300 [Aminoacyl-tRNA synthetase, class Ia] ; IPRC
-- Chromoso D	Cell cycle c IPR033756 [Flagellum site-determining protein YlxH/ F
-- Methionin	Translatior IPR000994 [Peptidase M24] ; IPR031615[MYND-like zir
ko04142 L -- --	-- IPR000547 [Clathrin, heavy chain/VPS, 7-fold repeat] ; I
-- UncharacteR	General fu IPR001734 [Sodium/solute symporter]
-- -- --	-- --
ko03013 R -- --	-- --
ko00970 A Arginyl-tR	Translatior IPR001278 [Arginine-tRNA ligase] ; IPR005148[Arginyl
ko04141 P -- --	-- IPR003903 [Ubiquitin interacting motif] ; IPR006155[Jos
-- -- --	-- IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04068 F CBS doma T	Signal tran IPR000644 [CBS domain]
ko00270 C Branched- EH	Amino acid IPR001544 [Aminotransferase class IV]
ko03420 N Ubiquitin O	Posttransla IPR000626 [Ubiquitin domain] ; IPR015360[XPC-bindin
ko03010 R Ribosomal J	Translatior IPR001854 [Ribosomal protein L29]
ko04360 A Ankyrin rejT	Signal tran IPR001090 [Ephrin receptor ligand binding domain] ; IF
ko04360 A Ankyrin rejT	Signal tran IPR001090 [Ephrin receptor ligand binding domain] ; IF
-- Na ⁺ /H ⁺ -c C	Energy prc IPR001991 [Sodium:dicarboxylate symporter]
ko00565 E WD40 rep	General fu IPR001680 [WD40 repeat] ; IPR006594[LIS1 homology
-- -- --	-- IPR004031 [PMP-22/EMP/MP20/Claudin superfamily]
ko04970 S Amino acid E	Amino acid IPR004841 [Amino acid permease/ SLC12A domain] ; IF
ko03050 P -- --	-- IPR002035 [von Willebrand factor, type A] ; IPR003903[
-- Ribosome-J	Translatior IPR004095 [TGS] ; IPR006073[GTP binding domain] ; IP
-- -- --	-- IPR013151 [Immunoglobulin]
ko04080 N -- --	-- IPR000276 [G protein-coupled receptor, rhodopsin-lik
-- -- --	-- IPR014760 [Serum albumin, N-terminal]
-- Peptidyl-p O	Posttransla IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans is
ko04014 R -- --	-- IPR000159 [Ras-associating (RA) domain] ; IPR000253[I
ko04210 A -- --	-- --
ko03008 R Ribosomal J	Translatior IPR004038 [Ribosomal protein L7Ae/L30e/S12e/Gadd4
-- -- --	-- IPR000504 [RNA recognition motif domain] ; IPR01299
-- -- --	-- IPR010301 [Nucleolar, Nop52]
ko00450 S Methionyl-J	Translatior IPR000738 [WHEP-TRS domain] ; IPR004046[Glutathior
ko03008 R Translatior J	Translatior IPR002769 [Translation initiation factor IF6]
ko04310 V Lactate del CHR	Energy prc IPR006139 [D-isomer specific 2-hydroxyacid dehydrog
-- -- --	-- IPR007919 [Uncharacterised protein family UPF0220]
ko00100 S NAD(P)-de IQR	Lipid trans IPR002347 [Short-chain dehydrogenase/reductase SDF
ko04015 R -- --	-- IPR001452 [SH3 domain] ; IPR014928[Serine rich protei
-- Broad spec G	Carbohydr IPR001452 [SH3 domain] ; IPR013078[Histidine phosph
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
ko04514 C -- --	-- IPR013106 [Immunoglobulin V-set domain]
-- -- --	-- IPR005344 [Per33/Pom33 family]
-- WD40 rep	General fu IPR001680 [WD40 repeat] ; IPR015048[Domain of unkn
ko04621 N -- --	-- IPR007677 [Gasdermin]
ko04520 A -- --	-- IPR000048 [IQ motif, EF-hand binding site] ; IPR000593
ko00380 T Mannose- G	Carbohydr IPR010329 [3-hydroxyanthranilic acid dioxygenase]
-- Predicted IT	Signal tran IPR020683 [Ankyrin repeat-containing domain]
ko04144 E -- --	-- IPR002189 [F-actin-capping protein subunit alpha]
ko04014 R -- --	-- IPR015898 [G-protein gamma-like domain]
ko03010 R -- --	-- IPR002673 [Ribosomal protein L29e]
-- WGR dom.K	Transcripti IPR001079 [Galectin, carbohydrate recognition domain
ko03060 P -- --	-- IPR016482 [Protein transport protein SecE/Sec61-beta

--	--	--	--	IPR001781	[Zinc finger, LIM-type]
ko04922	G	Diadenosin	T	Signal tran	IPR004843 [Calcineurin-like phosphoesterase domain,
ko04068	F	--	--	--	IPR004241 [Autophagy protein Atg8 ubiquitin-like]
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608 [Ubiquitin-conjugating enzyme E2]
--	--	--	--	--	IPR013787 [S100/CaBP-9k-type, calcium binding, subc
--	--	--	--	--	IPR002108 [Actin-depolymerising factor homology do
ko00270	C	--	--	--	IPR004308 [Glutamate-cysteine ligase catalytic subunit
ko00270	C	Aldo/keto	Q	Secondary	IPR023210 [NADP-dependent oxidoreductase domain]
--	--	--	--	--	IPR018499 [Tetraspanin/Peripherin]
ko04014	R	GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
--		Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
--		Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608 [Ubiquitin-conjugating enzyme E2]
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 SAR		General fu	IPR001806 [Small GTPase superfamily]
--		Actin-relat	Z	Cytoskelet	IPR004000 [Actin family]
--		Translator	J	Translator	IPR003439 [ABC transporter-like] ; IPR007209[RNase L
ko03050	P	--	--	--	IPR003185 [Proteasome activator pa28, N-terminal dor
ko00010	G	Acyl-CoA	C	Energy prc	IPR015590 [Aldehyde dehydrogenase domain]
ko00190	C	--	--	--	IPR002843 [ATPase, V0 complex, c/d subunit]
ko04014	R	GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
ko00061	F	NADP-dep	C	Energy prc	IPR001031 [Thioesterase] ; IPR009081[Phosphopanteth
--		Chaperoni	O	Posttransla	IPR002423 [Chaperonin Cpn60/TCP-1 family]
--		GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
--		Co-chaper	O	Posttransla	IPR020818 [GroES chaperonin family]
ko03060	P	Preprotein	U	Intracellular	IPR002208 [SecY/SEC61-alpha family] ; IPR019561[Trar
--	--	--	--	--	IPR004127 [Prefoldin alpha-like]
ko04721	S	--	--	--	IPR001619 [Sec1-like protein]
ko00970	A	Seryl-tRNA	J	Translator	IPR002314 [Aminoacyl-tRNA synthetase, class II (G/ P/
ko03050	P	20S protea	O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta]
ko04142	L	--	--	--	IPR003172 [MD-2-related lipid-recognition domain]
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
--	--	--	--	--	IPR022775 [AP complex, mu/sigma subunit]
--	--	--	--	--	IPR005375 [Ubiquitin-fold modifier 1]
--		Uncharact	R	General fu	IPR001680 [WD40 repeat]
--		WD40 rep	R	General fu	IPR001680 [WD40 repeat]
ko04142	L	--	--	--	IPR022775 [AP complex, mu/sigma subunit]
--	--	--	--	--	IPR002075 [Nuclear transport factor 2]
ko04010	M	GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
--	--	--	--	--	IPR018499 [Tetraspanin/Peripherin]
--		Ca2+ -binc	T	Signal tran	IPR002048 [EF-hand domain]
ko00230	P	GMP synth	F	Nucleotide	IPR001674 [GMP synthase, C-terminal] ; IPR017926[Glu
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608 [Ubiquitin-conjugating enzyme E2]
ko03018	R	Small nucl	K	Transcripti	IPR001163 [LSM domain, eukaryotic/archaea-type]
ko04668	T	Predicted	O	Posttransla	IPR001818 [Peptidase M10, metallopeptidase] ; IPR002
--	--	--	--	--	IPR018203 [GDP dissociation inhibitor]
ko03040	S	--	--	--	IPR001163 [LSM domain, eukaryotic/archaea-type]
--		Serine pro	O	Posttransla	IPR023796 [Serp domain]
--	--	--	--	--	IPR001878 [Zinc finger, CCHC-type]
--		Tetratricop	R	General fu	IPR019734 [Tetratricopeptide repeat]
ko04072	P	--	--	--	IPR000375 [Dynamin central domain] ; IPR001849[Plecl
ko00230	P	8-oxo-dG	V	Defense m	IPR000086 [NUDIX hydrolase domain]
--		GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
ko03010	R	Ribosomal	J	Translator	IPR000218 [Ribosomal protein L14P]
ko03010	R	Ribosomal	J	Translator	IPR002222 [Ribosomal protein S19/S15]

ko03010 R Ribosomal J	Translatior IPR001976 [Ribosomal protein S24e]
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]
ko04014 R WD40 rep: R	General fu IPR001680 [WD40 repeat]
ko03420 N -- --	-- IPR024766 [Zinc finger, RING-H2-type]
ko04137 N GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03010 R Ribosomal J	Translatior IPR000054 [Ribosomal protein L31e]
ko01521 E -- --	-- IPR000980 [SH2 domain] ; IPR001452[SH3 domain]
ko04010 N Ca2+ -binc T	Signal tran IPR002048 [EF-hand domain]
ko04962 V -- --	-- IPR001372 [Dynein light chain, type 1/2]
ko03010 R -- --	-- IPR002675 [Ribosomal protein L38e]
ko00052 G Galactokin G	Carbohydr IPR006204 [GHMP kinase N-terminal domain] ; IPR013
ko04110 C -- --	-- IPR016072 [SKP1 component, dimerisation] ; IPR01607:
ko04014 R -- --	-- IPR015898 [G-protein gamma-like domain]
ko03013 R Ubiquitin- O	Posttransla IPR000608 [Ubiquitin-conjugating enzyme E2]
-- Cold shock K	Transcripti IPR002059 [Cold-shock protein, DNA-binding]
ko03060 P Signal pep U	Intracellula IPR019759 [Peptidase S24/S26A/S26B]
ko04120 U Ubiquitin- O	Posttransla IPR000608 [Ubiquitin-conjugating enzyme E2]
ko00565 E Lysophosp E	Amino acic IPR013830 [SGNH hydrolase-type esterase domain]
ko05034 A -- --	-- IPR007125 [Histone H2A/H2B/H3]
ko05416 V -- --	-- IPR013106 [Immunoglobulin V-set domain] ; IPR01315
ko03013 R -- --	-- IPR003307 [W2 domain] ; IPR003890[MIF4G-like, type :
ko05205 P Leucine-rich K	Transcripti IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko00030 P 6-phospho G	Carbohydr IPR006114 [6-phosphogluconate dehydrogenase, C-te
ko03022 B -- --	-- IPR004212 [GTF2I-like repeat]
ko00562 Ir -- --	-- IPR002498 [Phosphatidylinositol-4-phosphate 5-kinase
ko04330 N -- --	-- IPR001762 [Disintegrin domain] ; IPR002870[Peptidase
ko04060 C -- --	-- IPR015321 [Type I cytokine receptor, cytokine-binding
-- -- --	-- IPR013106 [Immunoglobulin V-set domain]
-- -- --	-- IPR008251 [Chromo shadow domain] ; IPR023780[Chrc
ko04068 F -- --	-- IPR001132 [SMAD domain, Dwarfing-type] ; IPR003619[
ko04144 E GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
-- -- --	-- IPR000781 [Enhancer of rudimentary]
-- Enamine d V	Defense m IPR006175 [YjgF/YER057c/UK114 family]
-- -- --	-- IPR000020 [Anaphylatoxin/fibulin] ; IPR001881[EGF-like
-- Glucose/ar G	Carbohydr IPR000033 [LDLR class B repeat] ; IPR001881[EGF-like c
ko04360 A -- --	-- IPR001799 [Ephrin receptor-binding domain]
-- Magnesiur P	Inorganic i IPR004014 [Cation-transporting P-type ATPase, N-terr
ko04144 E -- --	-- IPR002189 [F-actin-capping protein subunit alpha]
-- Magnesiur P	Inorganic i IPR008250 [P-type ATPase, A domain] ; IPR032630[P-1
-- Guanylate F	Nucleotide IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
-- -- --	-- IPR001666 [Phosphatidylinositol transfer protein]
ko00270 C S-adenosyl H	Coenzyme IPR022628 [S-adenosylmethionine synthetase, N-termi
ko00020 C Citrate syn C	Energy prc IPR002020 [Citrate synthase] ; IPR003781[CoA-binding
-- -- --	-- IPR004088 [K Homology domain, type 1]
-- Predicted IT	Signal tran IPR001680 [WD40 repeat] ; IPR006692[Coatomer, WD :
ko04142 L Cysteine p O	Posttransla IPR000668 [Peptidase C1A, papain C-terminal] ; IPR014
-- Serine/thre T	Signal tran IPR000719 [Protein kinase domain]
ko04144 E -- --	-- IPR022775 [AP complex, mu/sigma subunit]
ko04110 C PASTA dom M	Cell wall/r IPR000719 [Protein kinase domain]
ko04360 A Predicted , R	General fu IPR000719 [Protein kinase domain]
-- -- --	-- IPR003173 [Transcriptional coactivator p15 (PC4)]
-- Predicted , R	General fu IPR000719 [Protein kinase domain]
-- -- --	-- IPR006628 [Purine-rich element binding protein family
-- FKBP-type O	Posttransla IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
ko04010 N Secreted p R	General fu IPR002035 [von Willebrand factor, type A] ; IPR013608[

ko00970 A Tryptophan J	Translation IPR002305 [Aminoacyl-tRNA synthetase, class Ic] ; IPRC
ko00040 P Threonine ER	Amino acid IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
ko00072 S 3-hydroxy I	Lipid trans IPR013528 [Hydroxymethylglutaryl-coenzyme A synthase
ko03040 S Molecular O	Posttranslational IPR013126 [Heat shock protein 70 family]
-- -- --	-- IPR007593 [CD225/Dispanin family]
ko04150 n Amino acid E	Amino acid IPR002293 [Amino acid/polyamine transporter I]
-- -- --	-- IPR003958 [Transcription factor CBF/NF-Y/archaeal his
-- -- --	-- IPR003323 [OTU domain]
ko00562 Ir -- --	-- IPR000008 [C2 domain] ; IPR000909 [Phosphatidylinosit
-- -- --	-- IPR003582 [ShKT domain] ; IPR008673 [Microfibril-asso
-- Ankyrin repeat T	Signal transduction IPR000001 [Kringle] ; IPR001245 [Serine-threonine/tyro
ko00230 P GAF domain T	Signal transduction IPR001054 [Adenylyl cyclase class-3/4/guanylyl cyclase
ko05206 I -- --	-- IPR001752 [Kinesin motor domain] ; IPR032384 [Kinesin
ko04141 P ATP-dependent O	Posttranslational IPR003338 [CDC48, N-terminal subdomain] ; IPR00395
-- -- --	-- IPR005818 [Linker histone H1/H5, domain H15]
ko04915 E FKBP-type O	Posttranslational IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
ko01524 P DNA gyrase L	Replication IPR002205 [DNA topoisomerase, type IIA, subunit A/C-
-- -- --	-- IPR001573 [Protein kinase A anchoring, WSK motif] ; IP
ko00230 P Sugar or n G	Carbohydrate IPR011611 [Carbohydrate kinase PfkB]
ko04010 I -- --	-- IPR001019 [Guanine nucleotide binding protein (G-pro
-- Large exon U	Intracellular IPR000233 [Cadherin, cytoplasmic domain] ; IPR002126
-- Large exon U	Intracellular IPR002126 [Cadherin] ; IPR014868 [Cadherin prodomain
ko04144 E -- --	-- IPR001612 [Caveolin]
-- -- --	-- IPR010326 [Exocyst complex component EXOC3/Sec6]
ko03013 R -- --	-- IPR022617 [Rad60/SUMO-like domain]
ko03013 R -- --	-- IPR000504 [RNA recognition motif domain] ; IPR013970
ko04610 C -- --	-- IPR016054 [Ly-6 antigen/uPA receptor-like]
ko00900 T Mevalonate I	Lipid trans IPR006204 [GHMP kinase N-terminal domain] ; IPR013
ko01523 A -- --	-- IPR011539 [Rel homology domain (RHD), DNA-binding
ko00500 S 1,4-alpha-G	Carbohydrate IPR004193 [Glycoside hydrolase, family 13, N-terminal]
ko03013 R -- --	-- IPR003307 [W2 domain] ; IPR003890 [MIF4G-like, type 1
ko04060 C Serine/threonine T	Signal transduction IPR000472 [Activin types I and II receptor domain] ; IPR
ko03030 D Single-strand L	Replication IPR000424 [Primosome PriB/single-strand DNA-binding
ko04072 P -- --	-- IPR000375 [Dynamin central domain] ; IPR001849 [Pleck
-- Protein tyrosine T	Signal transduction IPR000242 [PTP type protein phosphatase]
ko01522 E Ankyrin repeat T	Signal transduction IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko03013 R Translation J	Translation IPR004160 [Translation elongation factor EFTu/EF1A, C
ko04014 R Protein tyrosine T	Signal transduction IPR000242 [PTP type protein phosphatase] ; IPR000980
ko03018 R Exosome c J	Translation IPR001247 [Exoribonuclease, phosphorolytic domain 1]
-- -- --	-- IPR002223 [Pancreatic trypsin inhibitor Kunitz domain]
ko04144 E -- --	-- IPR008384 [Actin-related protein 2/3 complex subunit
ko04662 B -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko00010 G Triosephosphate G	Carbohydrate IPR000652 [Triosephosphate isomerase]
ko03013 R -- --	-- IPR000717 [Proteasome component (PCI) domain] ; IPR
ko05168 H -- --	-- IPR003428 [Mitochondrial glycoprotein]
ko04520 A -- --	-- IPR000906 [ZU5 domain] ; IPR001478 [PDZ domain] ; IPR
-- Tetratricopeptide R	General function IPR001440 [Tetratricopeptide repeat 1] ; IPR019734 [Tet
-- -- --	-- IPR004088 [K Homology domain, type 1] ; IPR032335 [S
ko04270 V Ca ²⁺ -binding T	Signal transduction IPR002048 [EF-hand domain]
ko04015 R Actin-related Z	Cytoskeleton IPR004000 [Actin family]
ko04010 I GTPase SAR	General function IPR001806 [Small GTPase superfamily]
ko03013 R Superfamily L	Replication IPR001650 [Helicase, C-terminal] ; IPR011545 [DEAD/DF
ko03010 R Ribosomal J	Translation IPR027486 [Ribosomal protein S10 domain]
ko03050 P 20S proteasome O	Posttranslational IPR000426 [Proteasome alpha-subunit, N-terminal domain
ko01521 E -- --	-- IPR026298 [Blc2 family]
ko04010 I GTPase SAR	General function IPR001806 [Small GTPase superfamily]
-- -- --	-- IPR002108 [Actin-depolymerising factor homology domain
ko01521 E Anaerobic F	Nucleotide IPR000219 [Dbl homology (DH) domain] ; IPR000651 [R

ko03060 P Signal recc U	Intracellular IPR000897 [Signal recognition particle, SRP54 subunit,
ko04152 A GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03040 S RNA recog J	Translatior IPR000504 [RNA recognition motif domain]
ko04144 E GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- -- --	-- IPR000198 [Rho GTPase-activating protein domain] ; IF
ko03040 S RNA recog J	Translatior IPR000504 [RNA recognition motif domain]
ko04010 N Diadenosir T	Signal tran IPR004843 [Calcineurin-like phosphoesterase domain,
-- NADPH:qu CR	Energy prc IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
-- Phosphate P	Inorganic i IPR001204 [Phosphate transporter]
ko04530 T Actin-relat Z	Cytoskelet IPR004000 [Actin family]
ko04512 E -- --	-- IPR013147 [CD47 transmembrane] ; IPR013270[CD47 ir
ko04144 E GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko04217 N Peptidyl-p O	Posttransla IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans i:
ko04010 N GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03010 R Ribosomal J	Translatior IPR001593 [Ribosomal protein S3Ae]
ko05166 H -- --	-- IPR021841 [Vacuolar protein 14 C-terminal Fig4-bindir
ko03010 R Ribosomal J	Translatior IPR000439 [Ribosomal protein L15e]
ko03010 R -- --	-- IPR001141 [Ribosomal protein L27e] ; IPR005824[KOW
-- 16S rRNA (J	Translatior IPR001678 [SAM-dependent methyltransferase RsmB/I
ko03013 R -- --	-- IPR003890 [MIF4G-like, type 3] ; IPR015172[MIF4G-like
-- -- --	-- --
ko04150 r -- --	-- --
ko00512 N Glycosyltra G	Carbohydr IPR000772 [Ricin B, lectin domain] ; IPR001173[Glycosy
ko03015 r -- --	-- IPR004871 [Cleavage/polyadenylation specificity factor
ko00512 N -- --	-- IPR001675 [Glycosyl transferase family 29]
ko04612 A -- --	-- IPR003597 [Immunoglobulin C1-set]
-- Dipeptidas E	Amino acid IPR005322 [Peptidase C69, dipeptidase A]
ko04144 E -- --	-- IPR019393 [WASH complex, subunit strumpellin]
ko03008 R Predicted IT	Signal tran IPR001680 [WD40 repeat] ; IPR013934[Small-subunit p
ko04022 c Voltage-g; P	Inorganic i IPR003929 [Potassium channel, BK, alpha subunit] ; IPR
-- -- --	-- IPR002108 [Actin-depolymerising factor homology do
ko04130 S -- --	-- IPR000727 [Target SNARE coiled-coil homology doma
ko03040 S -- --	-- IPR021966 [Splicing factor SF3a60 binding domain] ; IP
ko03040 S -- --	-- IPR004088 [K Homology domain, type 1] ; IPR012987[F
ko04110 C -- --	-- IPR023410 [14-3-3 domain]
ko00240 P NAD-depe F	Nucleotide IPR005720 [Dihydroorotate dehydrogenase domain] ; I
ko04621 N -- --	-- IPR015125 [Tumour suppressor p53-binding protein-1
ko03015 r Diadenosir T	Signal tran IPR004843 [Calcineurin-like phosphoesterase domain,
ko04014 R Ca2+ -binc T	Signal tran IPR002048 [EF-hand domain]
-- tRNA-binc J	Translatior IPR002547 [tRNA-binding 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]
-- -- --	-- IPR006561 [DZF domain]
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[4C
-- -- --	-- IPR006561 [DZF domain] ; IPR014720[Double-strandec
ko04520 A Protein tyr T	Signal tran IPR000242 [PTP type protein phosphatase] ; IPR003961
ko03040 S -- --	-- IPR001163 [LSM domain, eukaryotic/archaea-type]
ko04810 R -- --	-- IPR001152 [Beta-thymosin]
ko04210 A Protein tyr T	Signal tran IPR000242 [PTP type protein phosphatase] ; IPR001478
ko03050 P ATP-depei O	Posttransla IPR003959 [ATPase, AAA-type, core]
ko03010 R Ribosomal J	Translatior IPR004038 [Ribosomal protein L7Ae/L30e/S12e/Gadd4

-- -- --
ko03010 R Ribosomal J
ko04270 V Actin-relat Z
ko04010 N -- --
ko03010 R Ribosomal J
ko01521 E Ribosomal J
ko04390 H Guanylate F
ko05134 L GTPase SAR
ko03008 R GTPase SAR
-- -- --
ko04010 N GTPase SAR
-- Protein-tyl T
-- -- --
ko03010 R -- --
ko03010 R Ribosomal J
ko03010 R Ribosomal J
Predicted IT
ko04110 C Tetratricop R
ko04014 R WD40 repe R
ko04010 N Serine/thre T
ko03010 R Ribosomal J
ko03010 R Ribosomal J
ko04217 N Peptidyl-p O
-- FKBP-type O
ko03010 R Ubiquitin O
-- Leucine-rich K
ko00061 F Biotin carb I
ko04144 E Predicted IT
ko04015 R -- --
ko04110 C -- --
-- Ubiquitin (O
ko04068 F Serine/thre T
-- -- --
ko03013 R NDP-suga JM
ko05162 N Uncharact R
ko04015 R Actin-relat Z
-- RNA recog J
ko03015 n Diadenosir T
-- RNA recog J
-- -- --
ko03008 R -- --
ko04260 C Chromoso D
Alkyl hydr V
ko03013 R Translator J
ko04145 P -- --
ko04145 P -- --
ko04145 P -- --
ko03008 R PASTA dor M
ko04010 N Serine/thre T
-- DNA-bind R
-- -- --
ko05143 A Hemoglob C
ko03040 S RNA recog J
ko03040 S RNA recog J
ko04350 T -- --
ko04110 C -- --
-- Chaperoni O
ko03450 N -- --

-- IPR001452 [SH3 domain] ; IPR013625[Tensin/EPS8 pho
Translator IPR002942 [RNA-binding S4 domain] ; IPR005824[KOV
Cytoskelet IPR004000 [Actin family]
-- IPR001293 [Zinc finger, TRAF-type] ; IPR018957[Zinc fir
Translator IPR005633 [Ribosomal protein L23/L25, N-terminal] ; IF
Translator IPR001377 [Ribosomal protein S6e]
Nucleotide IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
General fu IPR001806 [Small GTPase superfamily]
General fu IPR001806 [Small GTPase superfamily]
-- IPR001452 [SH3 domain] ; IPR001609[Myosin head, mc
General fu IPR001806 [Small GTPase superfamily]
Signal tran IPR000242 [PTP type protein phosphatase]
-- IPR000008 [C2 domain] ; IPR000198[Rho GTPase-activ
-- IPR004977 [Ribosomal protein S25]
Translator IPR000892 [Ribosomal protein S26e]
Translator IPR000289 [Ribosomal protein S28e]
Signal tran IPR001680 [WD40 repeat] ; IPR013258[Striatin, N-termi
General fu --
General fu IPR001680 [WD40 repeat]
Signal tran IPR000719 [Protein kinase domain] ; IPR024205[Mst1 S
Translator IPR028364 [Ribosomal protein L1/ribosomal biogenesis
Translator IPR022666 [Ribosomal Proteins L2, RNA binding doma
Posttransla IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans is
Posttransla IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
Posttransla IPR000626 [Ubiquitin domain] ; IPR002906[Ribosomal p
Transcripti IPR001611 [Leucine-rich repeat] ; IPR007123[Gelsolin-I
Lipid trans IPR000022 [Carboxyl transferase] ; IPR000089[Biotin/lip
Signal tran IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
-- IPR000980 [SH2 domain] ; IPR001660[Sterile alpha mot
-- IPR023410 [14-3-3 domain]
Posttransla IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
Signal tran IPR000719 [Protein kinase domain] ; IPR032270[AMPK,
-- IPR001660 [Sterile alpha motif domain]
Translator IPR001451 [Hexapeptide repeat] ; IPR003307[W2 doma
General fu IPR001680 [WD40 repeat]
Cytoskelet IPR004000 [Actin family]
Translator IPR000504 [RNA recognition motif domain]
Signal tran IPR004843 [Calcineurin-like phosphoesterase domain,
Translator IPR000504 [RNA recognition motif domain]
-- IPR004046 [Glutathione S-transferase, C-terminal] ; IPR
-- IPR000704 [Casein kinase II, regulatory subunit]
Cell cycle c IPR000533 [Tropomyosin]
Defense m IPR000866 [Alkyl hydroperoxide reductase subunit C/ 1
Translator IPR004160 [Translation elongation factor EFTu/EF1A, C
-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316]
-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316]
-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316]
Cell wall/r IPR000719 [Protein kinase domain]
Signal tran IPR000095 [CRIB domain] ; IPR000719[Protein kinase d
General fu IPR008826 [Selenium-binding protein]
-- IPR000971 [Globin]
Energy prc IPR000971 [Globin]
Translator IPR000504 [RNA recognition motif domain]
Translator IPR000504 [RNA recognition motif domain]
-- --
-- IPR003511 [HORMA domain]
Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
-- IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic c

--	--	--	--	IPR000315	[B-box-type zinc finger] ; IPR001841[Zinc fi
ko04360 A	--	--	--	IPR001627	[Sema domain]
ko04130 S	--	--	--	IPR000727	[Target SNARE coiled-coil homology doma
--	RNA recogJ		Translation	IPR000504	[RNA recognition motif domain] ; IPR00207
--	--	--	--	IPR008408	[Brain acid soluble protein 1]
--	4-amino-4M		Cell wall/r	IPR011990	[Tetratricopeptide-like helical domain] ; IPR
ko03010 R	Ribosomal J		Translation	IPR000988	[Ribosomal protein L24e-related]
--	--	--	--	IPR000679	[Zinc finger, GATA-type] ; IPR000949[ELM2
--	Urea transJ		Amino acid	IPR004937	[Urea transporter]
ko00564 G	Phosphatic I		Lipid trans	IPR001683	[Phox homologous domain] ; IPR001736[Ph
ko04145 P	Predicted IT		Signal tran	IPR001680	[WD40 repeat] ; IPR025956[Cytoplasmic dyr
ko05100 B	GTPase SAR		General fu	IPR001806	[Small GTPase superfamily]
ko03010 R	Ribosomal J		Translation	IPR000196	[Ribosomal protein L19/L19e]
ko03040 S	RNA recogJ		Translation	IPR000504	[RNA recognition motif domain]
--	Peptidyl-p O		Posttransla	IPR002130	[Cyclophilin-type peptidyl-prolyl cis-trans i
ko03008 R	--	--	--	IPR003993	[Treacher Collins syndrome, treacle]
--	Zinc transP		Inorganic i	IPR003689	[Zinc/iron permease]
ko03040 S	--	--	--	IPR003034	[SAP domain] ; IPR006568[PSP, proline-rich
--	--	--	--	IPR019380	[Casein kinase substrate, phosphoprotein PI
--	Magnesiur P		Inorganic i	IPR008250	[P-type ATPase, A domain] ; IPR032630[P-1
--	--	--	--	IPR001590	[Peptidase M12B, ADAM/reprolysin] ; IPR00
--	--	--	--	IPR001590	[Peptidase M12B, ADAM/reprolysin] ; IPR00
--	--	--	--	IPR000048	[IQ motif, EF-hand binding site] ; IPR00015
ko04022 c	Serine/threT		Signal tran	IPR000719	[Protein kinase domain] ; IPR015008[Rho bi
ko00190 C	Archaeal/v C		Energy prc	IPR002490	[V-type ATPase, VO complex, 116kDa subu
ko00562 Ir	--	--	--	IPR004182	[GRAM domain] ; IPR010569[Myotubularin-
ko04137 Ir	--	--	--	IPR000270	[PB1 domain] ; IPR000433[Zinc finger, ZZ-ty
ko04622 R	Parvulin-lil O		Posttransla	IPR000297	[Peptidyl-prolyl cis-trans isomerase, PpiC-t
ko04110 C	Acetoin uti BQ		Chromatin	IPR023801	[Histone deacetylase domain]
ko04012 E	Serine/threT		Signal tran	IPR000719	[Protein kinase domain] ; IPR013543[Calciur
ko04142 L	--	--	--	IPR000547	[Clathrin, heavy chain/VPS, 7-fold repeat] ;
ko04962 V	--	--	--	--	
ko04142 L	--	--	--	IPR004687	[Lysosomal-associated transmembrane pro
--	--	--	--	IPR001715	[Calponin homology domain] ; IPR002017[S
--	--	--	--	IPR002164	[Nucleosome assembly protein (NAP)]
ko03040 S	RNA recogJ		Translation	IPR000504	[RNA recognition motif domain]
ko00230 P	Adenosine F		Nucleotide	IPR001365	[Adenosine/AMP deaminase domain]
ko03320 P	--	--	--	IPR000566	[Lipocalin/cytosolic fatty-acid binding dom
--	--	--	--	IPR013912	[Adenylate cyclase-associated CAP, C-term
ko04810 R	--	--	--	IPR000048	[IQ motif, EF-hand binding site] ; IPR00059
--	--	--	--	IPR007593	[CD225/Dispanin family]
ko03040 S	RNA recogJ		Translation	IPR000504	[RNA recognition motif domain]
ko04144 E	--	--	--	IPR001683	[Phox homologous domain] ; IPR005329[So
ko00562 Ir	--	--	--	IPR004182	[GRAM domain] ; IPR010569[Myotubularin-
ko04110 C	--	--	--	IPR001373	[Cullin, N-terminal] ; IPR019559[Cullin prote
ko00010 G	6-phospho G		Carbohydr	IPR000023	[Phosphofructokinase domain]
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
ko04390 H	Chromoso D		Cell cycle c	IPR001452	[SH3 domain] ; IPR020683[Ankyrin repeat-c
ko04974 P	AutotransUW		Intracellul	IPR002035	[von Willebrand factor, type A] ; IPR002223[
ko00051 F	Nucleoside M		Cell wall/r	IPR001509	[NAD-dependent epimerase/dehydratase]
ko04144 E	GTPase SAR		General fu	IPR001806	[Small GTPase superfamily]
--	Leucine-rich K		Transcripti	IPR000372	[Leucine-rich repeat N-terminal domain] ; I
ko04014 R	--	--	--	IPR000159	[Ras-associating (RA) domain] ; IPR003123[
ko03010 R	--	--	--	IPR000915	[60S ribosomal protein L6E] ; IPR005568[Rib
ko04151 P	Cytolysin, U		Intracellul	IPR013517	[FG-GAP repeat] ; IPR013649[Integrin alpha
ko03013 R	--	--	--	IPR019163	[THO complex, subunit 5]

--	GTPase SAR	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
ko03013	R Superfamil L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/D
--	Aminopep E	Amino acid	IPR004134	[Peptidase C1B, bleomycin hydrolase]
ko03018	R Exosome c J	Translatio	IPR004088	[K Homology domain, type 1] ; IPR025721[E
ko04060	C Serine/thre T	Signal tran	IPR000472	[Activin types I and II receptor domain] ; IP
--	--	--	IPR001478	[PDZ domain] ; IPR001849[Pleckstrin homol
--	--	--	IPR007955	[Bystin]
ko00900	T Isopentenyl I	Lipid trans	IPR000086	[NUDIX hydrolase domain]
--	--	--	IPR024395	[CLASP N-terminal domain]
--	Secreted tr O	Posttransla	IPR000001	[Krigle] ; IPR000083[Fibronectin, type I] ; IP
ko04142	L --	--	IPR002159	[CD36 family]
ko00240	P Dihydroor F	Nucleotide	IPR006680	[Amidohydrolase-related]
ko04110	C --	--	IPR023410	[14-3-3 domain]
ko04512	E --	--	IPR008465	[Dystroglycan]
ko05412	A Large exo U	Intracellul	IPR002126	[Cadherin]
--	Predicted , R	General fu	IPR001680	[WD40 repeat] ; IPR012953[BOP1, N-termin
--	--	--	IPR000504	[RNA recognition motif domain]
ko05100	B --	--	IPR030379	[Septin-type guanine nucleotide-binding (C
ko04270	V Cell divisio D	Cell cycle c	IPR006018	[Caldesmon/lymphocyte specific protein]
--	RNA recog J	Translatio	IPR000504	[RNA recognition motif domain] ; IPR00303
ko04810	R --	--	IPR000219	[Dbl homology (DH) domain] ; IPR001715[C
--	--	--	IPR022166	[Protein of unknown function DUF3697, ubi
ko00250	A Glucosami M	Cell wall/r	IPR001347	[Sugar isomerase (SIS)]
ko04390	H Leucine-rich K	Transcripti	IPR001478	[PDZ domain] ; IPR001611[Leucine-rich rep
--	--	--	IPR004344	[Tubulin-tyrosine ligase/Tubulin polyglutar
--	Guanylate F	Nucleotide	IPR001478	[PDZ domain] ; IPR008145[Guanylate kinase
ko04510	Fi --	--	IPR001452	[SH3 domain] ; IPR010703[Dedicator of cytc
ko04146	P Alkyl hydr V	Defense m	IPR000866	[Alkyl hydroperoxide reductase subunit C/ 1
ko03010	R --	--	IPR021131	[Ribosomal protein L18e/L15P]
ko04380	C --	--	IPR001781	[Zinc finger, LIM-type]
--	Dihydroor F	Nucleotide	IPR006680	[Amidohydrolase-related]
ko04962	V Uncharact S	Function u	IPR000938	[CAP Gly-rich domain] ; IPR022157[Dynein ;
ko03013	R Translatio J	Translatio	IPR000649	[Initiation factor 2B-related]
ko03013	R Superfamil L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/D
ko04530	T --	--	IPR001452	[SH3 domain] ; IPR003134[Hs1/Cortactin]
ko04064	N --	--	IPR003877	[SPRY domain] ; IPR006574[SPRY-associated
ko04979	C Glucose/ar G	Carbohydr	IPR000033	[LDLR class B repeat] ; IPR001881[EGF-like c
ko04010	N Uncharact S	Function u	IPR001715	[Calponin homology domain] ; IPR017868[F
ko00052	G UDP-gluc M	Cell wall/r	IPR016040	[NAD(P)-binding domain]
ko01521	E --	--	IPR000294	[Gamma-carboxyglutamic acid-rich (GLA) c
--	--	--	IPR000276	[G protein-coupled receptor, rhodopsin-lik
--	--	--	IPR022070	[Cytoplasmic activation/proliferation-associ
--	RNA recog J	Translatio	IPR000504	[RNA recognition motif domain] ; IPR02912
--	--	--	IPR001190	[SRCR domain] ; IPR011705[BTB/Kelch-asso
--	--	--	IPR000421	[Coagulation factor 5/8 C-terminal domain]
--	--	--	IPR000716	[Thyroglobulin type-1] ; IPR002350[Kazal d
--	Large exo U	Intracellul	IPR000742	[EGF-like domain] ; IPR001791[Laminin G d
ko03030	D DNA replic L	Replicatio	IPR001208	[MCM domain] ; IPR027925[MCM N-termin
ko00562	Ir --	--	--	--
--	--	--	IPR001715	[Calponin homology domain] ; IPR002048[E
--	--	--	IPR000253	[Forkhead-associated (FHA) domain] ; IPR0
--	Ca ²⁺ -binc Q	Secondary	--	--
--	--	--	IPR013809	[ENTH domain]
ko04110	C Chromoso D	Cell cycle c	IPR003395	[RecF/RecN/SMC, N-terminal] ; IPR010935[
ko00510	N --	--	IPR007754	[N-acetylglucosaminyltransferase II]
ko00512	N Glycosyltra G	Carbohydr	IPR000772	[Ricin B, lectin domain] ; IPR001173[Glycosy
--	Predicted IR	General fu	IPR003029	[S1 domain] ; IPR008847[Suppressor of fork
ko04142	L Predicted IT	Signal tran	IPR002553	[Clathrin/coatomer adaptor, adaptin-like, N

--	--	--	--	IPR028169	[Raftlin family]
ko00760	N	--	--	--	IPR003193 [ADP-ribosyl cyclase (CD38/157)]
ko04141	P	Serine protease	O	Posttranslational	IPR000209 [Peptidase S8/S53 domain]
--	--	--	--	--	IPR007237 [CD20-like family]
--	--	Protein-S-Oxidation	O	Posttranslational	IPR001171 [Ergosterol biosynthesis ERG4/ERG24] ; IPR0000330 [SNF2-related, N-terminal domain] ; IPR000900 [Nebulin repeat] ; IPR001452[SH3 domain] ;
ko05165	H	Uncharacterized	S	Secondary	IPR013149 [Alcohol dehydrogenase, C-terminal]
--	--	--	--	--	IPR001881 [EGF-like calcium-binding domain] ; IPR026
--	--	--	--	--	IPR002350 [Kazal domain] ; IPR015369[Follistatin/Osteonectin]
--	--	--	--	--	IPR007718 [SRP40, C-terminal]
ko04514	C	Sugar lactose	G	Carbohydrate	IPR003961 [Fibronectin type III] ; IPR013098[Immunoglobulin-like fold]
--	--	Autotransporter	UW	Intracellular	IPR008160 [Collagen triple helix repeat]
ko03050	P	--	--	--	IPR021843 [Protein of unknown function DUF3437] ; IPR001373 [Cullin, N-terminal] ; IPR004939[APC10/DOA10]
ko04120	U	--	--	--	IPR001936 [Ras GTPase-activating protein] ; IPR003123 [Condensin complex subunit 2/barren]
--	--	--	--	--	IPR022816 [Condensin complex subunit 2/barren]
--	--	--	--	--	IPR031444 [PCNA-associated factor]
--	--	--	--	--	IPR029732 [WTAP/Mum2 family]
ko04141	P	--	--	--	IPR005052 [Legume-like lectin]
ko04142	L	--	--	--	IPR004687 [Lysosomal-associated transmembrane protein]
--	--	RNA recognition	J	Translational	IPR000504 [RNA recognition motif domain] ; IPR008661 [Condensin complex subunit 1, N-terminal]
--	--	--	--	--	IPR024324 [Condensin complex subunit 1, N-terminal]
--	--	Molecular chaperone	O	Posttranslational	IPR001404 [Heat shock protein Hsp90 family]
ko03040	S	Translational	J	Translational	IPR000640 [Translation elongation factor EFG, V domain]
--	--	--	--	--	IPR001683 [Phox homologous domain]
--	--	--	--	--	IPR007023 [Ribosomal biogenesis regulatory protein]
ko04810	R	--	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR001452[SH3 domain]
--	--	RNA recognition	J	Translational	IPR000504 [RNA recognition motif domain]
ko04144	E	SUMO ligase	L	Replication	IPR001164 [Arf GTPase activating protein] ; IPR001849[Arf GTPase activating protein]
--	--	--	--	--	IPR001487 [Bromodomain] ; IPR027353[NET domain]
ko03008	R	Predicted	R	General function	IPR001680 [WD40 repeat] ; IPR007148[Small-subunit p190]
ko04141	P	Negative regulation	O	Posttranslational	IPR013766 [Thioredoxin domain]
ko00100	S	--	--	--	IPR007905 [Emopamil-binding protein]
ko00565	E	Predicted	R	General function	IPR005065 [Platelet-activating factor acetylhydrolase-like]
ko03015	r	--	--	--	IPR002554 [Protein phosphatase 2A, regulatory B subunit]
--	--	--	--	--	IPR010892 [Secreted phosphoprotein 24]
ko00190	C	Inorganic pyrophosphatase	CP	Energy process	IPR008162 [Inorganic pyrophosphatase]
ko00590	A	--	--	--	IPR007052 [CS domain]
--	--	Serine/threonine phosphorylation	T	Signal transduction	IPR000719 [Protein kinase domain] ; IPR017892[Protein kinase domain]
--	--	RNA recognition	J	Translational	IPR000504 [RNA recognition motif domain] ; IPR012971 [RNA recognition motif domain]
ko04931	Ir	--	--	--	IPR004327 [Phosphotyrosyl phosphatase activator, PTPase]
--	--	Protein tyrosine phosphorylation	T	Signal transduction	IPR000242 [PTP type protein phosphatase] ; IPR000998 [PTP type protein phosphatase]
ko04010	N	--	--	--	IPR000008 [C2 domain] ; IPR001562[Zinc finger, Btk motif]
--	--	--	--	--	IPR002048 [EF-hand domain]
ko04390	H	--	--	--	IPR001680 [WD40 repeat] ; IPR013577[Lethal giant larva protein]
ko04010	N	Cell division	D	Cell cycle control	IPR000719 [Protein kinase domain] ; IPR017892[Protein kinase domain]
ko03050	P	--	--	--	IPR002015 [Proteasome/cyclosome repeat]
--	--	PKD repeat	S	Function unknown	IPR000436 [Sushi/SCR/CCP domain] ; IPR008754[Peptide repeat]
ko04066	H	--	--	--	IPR016073 [SKP1 component, POZ domain]
ko04072	P	GTPase SAR	R	General function	IPR001806 [Small GTPase superfamily]
ko04120	U	--	--	--	IPR000569 [HECT domain]
ko03040	S	--	--	--	IPR004871 [Cleavage/polyadenylation specificity factor]
--	--	--	--	--	IPR000557 [Calponin repeat] ; IPR001715[Calponin homology domain]
ko04010	N	Cell division	D	Cell cycle control	IPR000719 [Protein kinase domain] ; IPR017892[Protein kinase domain]
ko03040	S	RNA recognition	J	Translational	IPR000504 [RNA recognition motif domain]
--	--	Leucine-rich repeat	K	Transcription	--
ko04141	P	--	--	--	IPR006895 [Zinc finger, Sec23/Sec24-type] ; IPR006896 [Zinc finger, Sec23/Sec24-type]

--	PASTA domain	Cell wall/r	IPR001245	[Serine-threonine/tyrosine-protein kinase c
ko03040 S	--	--	IPR000061	[SWAP/Surp] ; IPR000626[Ubiquitin domain
ko03018 R	Superfamily L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DI
ko04960 A	Periplasmic O	Posttransla	IPR001478	[PDZ domain] ; IPR015098[EBP50, C-termin
ko03013 R	WD40 repeat R	General fu	IPR001680	[WD40 repeat]
--	--	--	IPR002848	[Translin family]
ko04910 Ir	--	--	IPR001060	[FCH domain] ; IPR001452[SH3 domain]
ko03320 P	Ankyrin repeat T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
ko01522 E	--	--	IPR019680	[Mediator complex, subunit Med1]
ko04621 N	--	--	IPR001781	[Zinc finger, LIM-type]
--	--	--	IPR001715	[Calponin homology domain] ; IPR004953[E
ko04152 A	RNA recognition J	Translatio	IPR000504	[RNA recognition motif domain]
ko04120 U	Alpha-tubulin DZ	Cell cycle c	IPR000408	[Regulator of chromosome condensation, R
--	Serine/threonine T	Signal tran	IPR001440	[Tetratricopeptide repeat 1]
ko04350 T	--	--	IPR001132	[SMAD domain, Dwarfina-type] ; IPR003619[
--	Leucine-rich K	Transcripti	IPR000626	[Ubiquitin domain] ; IPR000938[CAP Gly-rich
--	--	--	IPR000608	[Ubiquitin-conjugating enzyme E2]
ko04130 S	--	--	IPR001388	[Synaptobrevin]
ko00190 C	--	--	IPR008388	[ATPase, V1 complex, subunit S1]
ko04510 F	--	--	IPR001781	[Zinc finger, LIM-type]
ko04145 P	--	--	IPR003008	[Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko03050 P	--	--	IPR006773	[26S proteasome complex ubiquitin recepto
ko05200 P	--	--	IPR019152	[Protein of unknown function DUF2046]
ko00520 A	UDP-N-acetyl G	Carbohydr	IPR002618	[UDPGP family]
ko04151 P	Serine/threonine T	Signal tran	IPR000719	[Protein kinase domain] ; IPR011072[HR1 rh
ko04151 P	Serine/threonine T	Signal tran	IPR000719	[Protein kinase domain] ; IPR011072[HR1 rh
ko03015 r	--	--	IPR002554	[Protein phosphatase 2A, regulatory B subu
ko01522 E	Serine/threonine T	Signal tran	IPR000719	[Protein kinase domain]
ko04151 P	--	--	IPR013855	[Cdc37, N-terminal domain] ; IPR013873[Cc
--	--	--	IPR008253	[Marvel domain]
--	WD40 repeat R	General fu	IPR001680	[WD40 repeat] ; IPR022052[Histone-binding
ko04514 C	--	--	IPR008253	[Marvel domain] ; IPR010844[Occludin hom
--	--	--	IPR002108	[Actin-depolymerising factor homology do
ko00380 T	Kynureninase E	Amino acid	IPR000192	[Aminotransferase class V domain]
ko00600 S	Glycosyltransferase N	Cell motilit	IPR025993	[Ceramide glucosyltransferase]
--	Zn-dependent O	Posttransla	IPR007484	[Peptidase M28]
ko00230 P	Guanylate kinase F	Nucleotide	IPR008145	[Guanylate kinase/L-type calcium channel b
--	GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
--	Ankyrin repeat T	Signal tran	IPR000421	[Coagulation factor 5/8 C-terminal domain]
ko04630 J	--	--	IPR001781	[Zinc finger, LIM-type]
ko00040 P	UDP-N-acetyl G	Carbohydr	IPR002618	[UDPGP family]
ko00270 C	Predicted r R	General fu	IPR010300	[Cysteine dioxygenase type I]
ko04514 C	--	--	IPR013162	[CD80-like, immunoglobulin C2-set]
ko04145 P	--	--	IPR003008	[Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko00450 S	Pyruvate/2 C	Energy pro	IPR002109	[Glutaredoxin] ; IPR004099[Pyridine nucleot
--	--	--	IPR003124	[WH2 domain] ; IPR010472[Formin, FH3 do
ko05167 K	--	--	IPR003597	[Immunoglobulin C1-set] ; IPR011161[MHC
ko05167 K	--	--	IPR003597	[Immunoglobulin C1-set] ; IPR011161[MHC
--	--	--	--	--
--	Serine/threonine T	Signal tran	IPR000719	[Protein kinase domain]
ko04144 E	--	--	IPR028191	[WASH complex subunit 7, N-terminal] ; IPR
--	Predicted IT	Signal tran	IPR001680	[WD40 repeat]
--	WD40 repeat R	General fu	IPR001680	[WD40 repeat] ; IPR005108[HELP]
ko00051 F	Dihydroxyacetate G	Carbohydr	IPR004006	[DhaK domain] ; IPR004007[DhaL domain]
--	--	--	IPR019181	[Anticodon-binding domain]
--	--	--	IPR002108	[Actin-depolymerising factor homology do
--	RNA recognition J	Translatio	IPR000504	[RNA recognition motif domain] ; IPR01295
--	GTPase SAR	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]

--	--	--	--	IPR001079	[Galectin, carbohydrate recognition domain
--	O-acetyl-/J			Translatior	IPR002589 [Macro domain] ; IPR012317[Poly(ADP-ribo
endopeptid	Protease II E			Amino acid	IPR001375 [Peptidase S9, prolyl oligopeptidase, catalyt
--	Membrane M			Cell wall/r	IPR000195 [Rab-GTPase-TBC domain]
--	--	--		--	IPR025903 [Phostensin/Taperin N-terminal domain] ; I
--	--	--		--	IPR007632 [Anoctamin] ; IPR032394[Anoctamin, dimeri
--	Secreted p R			General fu	IPR002035 [von Willebrand factor, type A] ; IPR032770[
ko03013 R	16S rRNA IJ			Translatior	IPR000717 [Proteasome component (PCI) domain]
--	--	--		--	IPR018797 [Uncharacterised protein family FAM98]
--	--	--		--	IPR022008 [TSG101 and ALIX binding domain of CEP5
--	--	--		--	--
--	--	--		--	IPR001849 [Pleckstrin homology domain]
ko03040 S	--	--		--	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko00330 A	Pyrroline-5E			Amino acid	IPR028939 [Pyrroline-5-carboxylate reductase, catalytic
ko04141 P	Molecular O			Posttransla	IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
--	--	--		--	IPR005578 [Yif1 family]
ko04120 U	Alpha-tub DZ			Cell cycle c	IPR000408 [Regulator of chromosome condensation, R
ko04145 P	--	--		--	IPR004273 [Dynein heavy chain domain] ; IPR011704[A
--	--	--		--	IPR007587 [SIT4 phosphatase-associated protein famil
--	--	--		--	IPR019170 [Meckelin]
--	--	--		--	IPR024845 [Nance-Horan syndrome protein family]
ko04910 Ir	UncharactS			Function u	IPR001107 [Band 7 domain] ; IPR031905[Flotillin, C-ter
--	WD40 repR			General fu	IPR001680 [WD40 repeat]
ko04020 C	Serine/threT			Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
--	--	--		--	IPR012978 [Uncharacterised domain NUC173]
ko04022 c	--	--		--	IPR001019 [Guanine nucleotide binding protein (G-prc
--	--	--		--	IPR000717 [Proteasome component (PCI) domain]
ko04145 P	Type V sec MU			Cell wall/r	IPR001304 [C-type lectin-like] ; IPR008160[Collagen tri
--	--	--		--	IPR001715 [Calponin homology domain]
ng (GO:00	--	--		--	IPR000626 [Ubiquitin domain]
--	--	--		--	IPR005818 [Linker histone H1/H5, domain H15]
--	--	--		--	IPR002350 [Kazal domain] ; IPR015369[Follistatin/Ostec
--	--	--		--	IPR024845 [Nance-Horan syndrome protein family]
--	Secreted tr O			Posttransla	IPR000001 [Krigle] ; IPR000742[EGF-like domain] ; IPR
--	--	--		--	IPR000008 [C2 domain]
--	--	--		--	IPR000569 [HECT domain] ; IPR004939[APC10/DOC dc
--	WD40 repR			General fu	IPR001680 [WD40 repeat] ; IPR013577[Lethal giant larv
ko04014 R	--	--		--	IPR000008 [C2 domain] ; IPR001562[Zinc finger, Btk mc
--	--	--		--	--
--	--	--		--	IPR000626 [Ubiquitin domain] ; IPR019103[Aspartic pe
--	Serine/threT			Signal tran	IPR000719 [Protein kinase domain] ; IPR001180[Citron
--	--	--		--	IPR018890 [Uncharacterised protein family FAM171]
ko04141 P	--	--		--	IPR003323 [OTU domain]
ko00510 N	Alpha-glucG			Carbohydr	IPR000322 [Glycoside hydrolase family 31] ; IPR025887
--	--	--		--	IPR004328 [BRO1 domain]
--	--	--		--	IPR009637 [Lung seven transmembrane receptor-like]
--	--	--		--	IPR007244 [NatC N(alpha)-terminal acetyltransferase, I
--	--	--		--	IPR001594 [Palmitoyltransferase, DHHC domain]
--	--	--		--	IPR003877 [SPRY domain]
ko04350 T	--	--		--	IPR001881 [EGF-like calcium-binding domain] ; IPR017
--	--	--		--	IPR003877 [SPRY domain]
ko04514 C	--	--		--	IPR013106 [Immunoglobulin V-set domain]
--	--	--		--	IPR018957 [Zinc finger, C3HC4 RING-type]
ko03013 R	--	--		--	IPR001494 [Importin-beta, N-terminal domain]
--	--	--		--	IPR000980 [SH2 domain] ; IPR013625[Tensin/EPS8 pho
--	Ankyrin rejT			Signal tran	IPR002110 [Ankyrin repeat] ; IPR020683[Ankyrin repeat
ko04115 p	Predicted cR			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]
ko03050 P	--	--	--	IPR000717 [Proteasome component (PCI) domain] ; IPF
ko04530 T	--	--	--	IPR000198 [Rho GTPase-activating protein domain] ; IF
--	Hemoglob C		Energy prc	IPR000971 [Globin]
--	Leucine-rich K		Transcripti	IPR000742 [EGF-like domain] ; IPR001611[Leucine-rich
--	--	--	--	IPR007785 [Anamorsin] ; IPR013216[Methyltransferase
--	--	--	--	IPR002653 [Zinc finger, A20-type] ; IPR003323[OTU do
--	Acetylornit E		Amino acic	IPR002933 [Peptidase M20] ; IPR011650[Peptidase M20
ko04150 nr	--	--	--	IPR028209 [LAMTOR1/MEH1]
--	--	--	--	IPR002108 [Actin-depolymerising factor homology do
--	GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
--	16S rRNA IJ		Translatior	IPR024986 [Sister chromatid cohesion C-terminal dom
--	Ribosomal J		Translatior	IPR003347 [JmjC domain]
--	--	--	--	IPR025903 [Phostensin/Taperin N-terminal domain] ; IF
--	--	--	--	IPR026752 [Cavin family]
--	--	--	--	IPR000008 [C2 domain]
ko03018 R	--	--	--	IPR032401 [Enhancer of mRNA-decapping protein 4, V
ko03040 S	--	--	--	IPR000555 [JAB1/MPN/MOV34 metalloenzyme domain
--	Serine/thre T		Signal tran	IPR000719 [Protein kinase domain]
--	--	--	--	--
--	Hemolysin R		General fu	IPR000644 [CBS domain] ; IPR002550[Domain of unknc
--	--	--	--	IPR006571 [TLDc domain]
--	--	--	--	IPR028064 [Transmembrane protein 154]
--	--	--	--	IPR001478 [PDZ domain] ; IPR001660[Sterile alpha mot
--	--	--	--	IPR013098 [Immunoglobulin I-set] ; IPR013151[Immun
--	Putative Zr R		General fu	IPR019734 [Tetratricopeptide repeat]
ko04144 E	GTPase SAR		General fu	IPR001806 [Small GTPase superfamily]
ko03018 R	Predicted rR		General fu	IPR019734 [Tetratricopeptide repeat]
--	Membrane O		Posttransla	IPR022241 [Rhomboid serine protease] ; IPR022764[Pe
--	--	--	--	IPR006630 [RNA-binding protein Lupus La]
ko03040 S	--	--	--	IPR004088 [K Homology domain, type 1]
ko04216 F	--	--	--	IPR004088 [K Homology domain, type 1]
ko04150 nr	--	--	--	IPR028267 [Rapamycin-insensitive companion of mTO
--	--	--	--	IPR024845 [Nance-Horan syndrome protein family]
--	Leucine-rich K		Transcripti	IPR001611 [Leucine-rich repeat] ; IPR001660[Sterile alp
ko00100 S	FAD/FMN- C		Energy prc	IPR006094 [FAD linked oxidase, N-terminal]
--	NADP-dep C		Energy prc	IPR002347 [Short-chain dehydrogenase/reductase SDF
--	Leucine-rich K		Transcripti	IPR001611 [Leucine-rich repeat]
--	Serine pro O		Posttransla	IPR002165 [Plexin repeat]
--	Dipeptidyl E		Amino acic	IPR001375 [Peptidase S9, prolyl oligopeptidase, catalyt
--	--	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR001452[S
--	--	--	--	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IF
--	WD40 rep R		General fu	IPR000409 [BEACH domain] ; IPR001680[WD40 repeat]
--	--	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR000306[F
--	--	--	--	IPR013766 [Thioredoxin domain] ; IPR017905[ERV/ALR
--	--	--	--	IPR031780 [FAM65, N-terminal]
--	--	--	--	IPR001715 [Calponin homology domain] ; IPR004953[E
--	--	--	--	IPR019372 [Lipoma HMGIC fusion partner-like protein]
--	--	--	--	IPR000159 [Ras-associating (RA) domain] ; IPR001849[I
--	--	--	--	IPR000008 [C2 domain] ; IPR019558[Mammalian uncoc
--	--	--	--	IPR003877 [SPRY domain] ; IPR006574[SPRY-associate
ko05169 E	Endonucle L		Replicatio	IPR002999 [Tudor domain] ; IPR016071[Staphylococcal
--	PASTA dom M		Cell wall/r	IPR000719 [Protein kinase domain] ; IPR001772[Kinase
ko03040 S	Superfamil L		Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DT
ko04512 E	Predicted zG		Carbohydr	IPR001646 [Pentapeptide repeat] ; IPR005828[Major fa

--	--	--	--	IPR003307	[W2 domain]
ko04974	P	Na ⁺ /H ⁺ -c C	Energy prc	IPR001991	[Sodium:dicarboxylate symporter]
--	--	HrpA-like J	Translatior	IPR001650	[Helicase, C-terminal] ; IPR007502[Helicase-
--	--	--	--	IPR000717	[Proteasome component (PCI) domain]
--	--	--	--	IPR000555	[JAB1/MPN/MOV34 metalloenzyme domain]
ko04010	N	Serine/threT	Signal tran	IPR000719	[Protein kinase domain]
ko04144	E	--	--	IPR005024	[Snf7 family]
ko03040	S	--	--	IPR005345	[PHF5-like]
ko04144	E	GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
--	--	Predicted :G	Carbohydr	IPR011701	[Major facilitator superfamily]
--	--	--	--	IPR013057	[Amino acid transporter, transmembrane dc
--	--	--	--	IPR032745	[G protein-regulated inducer of neurite out
--	--	--	--	IPR004170	[WWE domain] ; IPR012317[Poly(ADP-ribos
--	--	--	--	IPR021773	[Foie gras liver health family 1] ; IPR025876[
ko04136	A	--	--	IPR007241	[Autophagy-related protein 9]
ko00534	G	--	--	IPR004263	[Exostosin-like] ; IPR015338[Exostosin , C-te
--	--	--	--	IPR019538	[26S proteasome non-ATPase regulatory su
--	--	--	--	IPR012496	[TMC]
--	--	--	--	IPR024395	[CLASP N-terminal domain]
--	--	HrpA-like J	Translatior	IPR001650	[Helicase, C-terminal] ; IPR007502[Helicase-
--	--	--	--	IPR000859	[CUB domain] ; IPR002172[Low-density lipo
--	--	--	--	IPR000313	[PWWP domain] ; IPR021567[Lens epitheliu
ko04360	A	DihydroorF	Nucleotide	IPR006680	[Amidohydrolase-related]
ko00040	P	NAD(P)-dεIQR	Lipid trans	--	--
--	--	Phage-relεX	Mobilome	IPR003961	[Fibronectin type III] ; IPR013098[Immunogl
--	--	--	--	IPR000697	[WH1/EVH1 domain] ; IPR007875[Sprouty]
ko04360	A	--	--	IPR000198	[Rho GTPase-activating protein domain] ; IF
--	--	--	--	IPR009038	[GOLD domain]
--	--	--	--	IPR022768	[Fascin domain]
--	--	N-acetyl-εM	Cell wall/r	IPR000859	[CUB domain] ; IPR001881[EGF-like calcium
ko00512	N	UncharactεR	General fu	IPR000772	[Ricin B, lectin domain] ; IPR001173[Glycosy
ng (GO:00		Leucine-richK	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR013151[Immunog
--	--	--	--	IPR000203	[GPS motif] ; IPR000832[GPCR, family 2, sec
ko04070	P	--	--	IPR019178	[Phosphatidylinositol 4,5-bisphosphate 4-p
--	--	Dipeptidyl E	Amino aci	IPR001375	[Peptidase S9, prolyl oligopeptidase, catalyt
ko00310	L	--	--	IPR001214	[SET domain] ; IPR015353[Rubisco LSMT, su
--	--	TetratricopeR	General fu	IPR019734	[Tetratricopeptide repeat]
ko03015	n	RNA recogJ	Translatior	IPR000504	[RNA recognition motif domain]
--	--	--	--	IPR001849	[Pleckstrin homology domain]
ko00280	V	Acyl-coen: l	Lipid trans	IPR000873	[AMP-dependent synthetase/ligase] ; IPR03
ko03013	R	RNA recogJ	Translatior	IPR000504	[RNA recognition motif domain] ; IPR02571
--	--	--	--	IPR005016	[Serine incorporator/TMS membrane protei
ko04810	R	--	--	IPR000048	[IQ motif, EF-hand binding site] ; IPR00059
ko04142	L	--	--	IPR004687	[Lysosomal-associated transmembrane pro
ko04144	E	--	--	IPR007286	[EAP30] ; IPR021648[Vacuolar protein sortin
--	--	--	--	--	--
ko04144	E	--	--	IPR003597	[Immunoglobulin C1-set] ; IPR010579[MHC
--	--	--	--	IPR005123	[Oxoglutarate/iron-dependent dioxygenase
--	--	--	--	IPR018787	[Protein of unknown function DUF2371, TM
ko03013	R	UncharactεR	General fu	IPR001680	[WD40 repeat]
--	--	--	--	IPR001660	[Sterile alpha motif domain]
--	--	Plastocyan C	Energy prc	IPR002909	[IPT domain] ; IPR011658[PA14 domain] ; IP
ko00670	C	Acyl-CoA l C	Energy prc	IPR002376	[Formyl transferase, N-terminal] ; IPR00579
--	--	--	--	--	--
ko04621	N	--	--	IPR029158	[Stimulator of interferon genes protein]
ko01522	E	Predicted IR	General fu	IPR020989	[Histone-arginine methyltransferase CARM
ko00670	C	Dihydrofol H	Coenzyme	IPR001796	[Dihydrofolate reductase domain]
ko03040	S	Superfamil L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DI

--	--	--	--	IPR001841 [Zinc finger, RING-type] ; IPR003137[PA do
ko04145 P	--	--	--	IPR000727 [Target SNARE coiled-coil homology doma
--	--	--	--	IPR000679 [Zinc finger, GATA-type] ; IPR032346[Transc
--	--	--	--	IPR004328 [BRO1 domain] ; IPR011072[HR1 rho-bindir
ko04217 N	--	--	--	IPR007125 [Histone H2A/H2B/H3] ; IPR032454[Histone
--	--	--	--	IPR000225 [Armadillo]
--	--	--	--	IPR022248 [TNF receptor family, RELT]
ko04014 R Ca ²⁺ -binc Q			Secondary	IPR013818 [Lipase/vitellogenin]
ko00564 G Phosphatic I			Lipid trans	IPR001736 [Phospholipase D/Transphosphatidylase] ; II
--	Actin-relat Z		Cytoskelet	IPR004000 [Actin family]
--	--	--	--	IPR029270 [Limb expression 1]
ko04141 P Molecular O			Posttransla	IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
--	--	--	--	--
--	--	--	--	IPR010472 [Formin, FH3 domain] ; IPR010473[Formin, (
--	--	--	--	IPR029311 [Coiled-coil domain-containing protein 50,
ko03008 R WD40 rep R			General fu	IPR001680 [WD40 repeat]
--	Uncharact R		General fu	IPR000306 [FYVE zinc finger] ; IPR001680[WD40 repeat
--	--	--	--	IPR005176 [Potentiating neddylation domain]
--	Leucine-rich K		Transcripti	IPR001611 [Leucine-rich repeat] ; IPR021040[LRR8, p
--	--	--	--	IPR000198 [Rho GTPase-activating protein domain] ; IF
ko03040 S	--	--	--	IPR000061 [SWAP/Surp] ; IPR000467[G-patch domain]
--	--	--	--	IPR003034 [SAP domain] ; IPR025223[S1-like RNA binc
--	--	--	--	IPR000859 [CUB domain] ; IPR001881[EGF-like calcium
ko04137 N	--	--	--	IPR001806 [Small GTPase superfamily] ; IPR013566[EF
--	--	--	--	IPR009581 [FAM20, C-terminal]
--	Permease GER		Carbohydr	IPR009262 [Solute carrier family 35 member SLC35F1/F
--	--	--	--	IPR029399 [TMEM192 family]
ko05165 H	--	--	--	IPR003126 [Zinc finger, UBR-type] ; IPR025704[E3 ubiq
ko03013 R	--	--	--	IPR002483 [PWI domain]
--	--	--	--	IPR032403 [Exocyst component Exo84, C-terminal]
--	--	--	--	IPR025481 [Cell morphogenesis protein C-terminal] ; IF
--	Metal-dep R		General fu	IPR002933 [Peptidase M20] ; IPR011650[Peptidase M2(
--	--	--	--	IPR018795 [Protein of unknown function DUF2152]
--	AAA+-typ MDT		Cell wall/r	IPR003959 [ATPase, AAA-type, core] ; IPR006594[LIS1 I
--	--	--	--	IPR010630 [Neuroblastoma breakpoint family (NBPF) d
--	Ankyrin rep T		Signal tran	IPR021832 [Ankyrin repeat domain-containing protein
--	Uncharact S		Function u	--
ko04360 A	--	--	--	IPR000488 [Death domain] ; IPR000884[Thrombosponc
--	--	--	--	IPR012583 [Pre-rRNA-processing protein RIX1, N-term
--	--	--	--	IPR001452 [SH3 domain] ; IPR012849[Abl-interactor, h
ko04136 A Predicted IT			Signal tran	IPR000357 [HEAT repeat] ; IPR001680[WD40 repeat] ; II
--	--	--	--	IPR025223 [S1-like RNA binding domain] ; IPR025954[I
ko03013 R	--	--	--	IPR007231 [Nucleoporin interacting component Nup9
--	--	--	--	IPR000467 [G-patch domain] ; IPR002877[Ribosomal R
--	Phenylalan J		Translatior	IPR001611 [Leucine-rich repeat] ; IPR005146[B3/B4 tRN
--	--	--	--	IPR001881 [EGF-like calcium-binding domain] ; IPR017
--	Permease GER		Carbohydr	IPR009262 [Solute carrier family 35 member SLC35F1/F
--	--	--	--	IPR000198 [Rho GTPase-activating protein domain]
--	Replicative L		Replicatio	IPR001650 [Helicase, C-terminal] ; IPR004179[Sec63 dc
--	--	--	--	IPR001715 [Calponin homology domain] ; IPR019448[E
--	--	--	--	IPR001715 [Calponin homology domain] ; IPR001781[Z
ko04390 H Guanylate F			Nucleotide	IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
--	--	--	--	IPR031435 [Transmembrane protein TMEM132, N-term
ko04310 V	--	--	--	IPR018933 [Netrin module, non-TIMP type] ; IPR02006
--	Serine/thre T		Signal tran	IPR000719 [Protein kinase domain] ; IPR001180[Citron
--	--	--	--	IPR003191 [Guanylate-binding protein, C-terminal] ; IP
--	--	--	--	IPR011021 [Arrestin-like, N-terminal] ; IPR011022[Arres
ko04144 E	--	--	--	IPR001164 [Arf GTPase activating protein]

--	--	--	--	IPR007133	[RNA polymerase II associated factor Paf1]
--	--	--	--	IPR006671	[Cyclin, N-terminal]
ko04360	A	Membrane M	Cell wall/r	IPR000697	[WH1/EVH1 domain] ; IPR014885[VASP tetr
--	--	--	--	IPR000421	[Coagulation factor 5/8 C-terminal domain]
--	Leucine-rich	K	Transcripti	IPR001611	[Leucine-rich repeat]
--	--	--	--	IPR006196	[RNA-binding domain, S1, IF1 type]
ko03040	S	--	--	IPR005037	[Pre-mRNA-splicing factor 38] ; IPR024767[
--	Magnesium	P	Inorganic i	IPR008250	[P-type ATPase, A domain] ; IPR032630[P-i
ko03008	R	ATP-depe	Posttransla	IPR003959	[ATPase, AAA-type, core]
--	DNA-bind	R	General fu	IPR001258	[NHL repeat] ; IPR012336[Thioredoxin-like f
ko00310	L	Glycosyltra	Cell wall/r	IPR002654	[Glycosyl transferase, family 25]
--	--	--	--	IPR010795	[Prenylcysteine lyase]
--	--	--	--	IPR009637	[Lung seven transmembrane receptor-like]
ko04150	rr	--	--	IPR013057	[Amino acid transporter, transmembrane dc
ko00520	A	Nucleoside	Cell wall/r	IPR016040	[NAD(P)-binding domain] ; IPR021761[UDP
--	--	--	--	IPR001841	[Zinc finger, RING-type] ; IPR003137[PA do
--	--	--	--	IPR029444	[Integrator complex subunit 5, C-terminal] ;
--	--	--	--	IPR006861	[Hyaluronan/mRNA-binding protein] ; IPR0
--	--	--	--	--	--
--	--	--	--	IPR000859	[CUB domain] ; IPR002172[Low-density lipo
--	--	--	--	IPR018797	[Uncharacterised protein family FAM98]
ko00532	G	Putative Zr	General fu	IPR005331	[Sulfotransferase]
--	--	--	--	IPR006671	[Cyclin, N-terminal]
--	--	--	--	IPR001715	[Calponin homology domain] ; IPR019448[E
--	--	--	--	IPR022049	[FAM69, protein-kinase domain]
--	Hemolysin	R	General fu	IPR000644	[CBS domain]
--	ATPase co	R	General fu	IPR003439	[ABC transporter-like] ; IPR032781[ABC-trar
--	--	--	--	--	--
--	--	--	--	IPR001849	[Pleckstrin homology domain] ; IPR006020[I
--	Co/Zn/Cd	P	Inorganic i	IPR002524	[Cation efflux protein]
--	--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko03013	R	WD40 rep	General fu	IPR001680	[WD40 repeat]
ko03013	R	--	--	IPR007846	[RNA-recognition motif (RRM) Nup35-type
--	--	--	--	IPR000261	[EH domain]
--	--	--	--	IPR017978	[GPCR family 3, C-terminal]
ko03013	R	--	--	IPR021418	[THO complex, subunitTHOC2, C-terminal]
ko03008	R	WD40 rep	General fu	IPR001680	[WD40 repeat] ; IPR007319[Small-subunit p
ko04310	V	--	--	IPR009539	[Vang-like protein]
ko03460	F	WD40 rep	General fu	IPR001680	[WD40 repeat] ; IPR021772[Protein of unknc
--	--	--	--	IPR007225	[Exocyst complex component EXOC6/Sec15
ko04141	P	--	--	IPR007716	[NPL4, zinc-binding putative] ; IPR007717[N
--	--	--	--	IPR027897	[Protein of unknown function DUF4559]
--	--	--	--	--	--
--	Ca ²⁺ -bind	Q	Secondary	--	--
ko04120	U	Ubiquitin	Posttransla	IPR000594	[THIF-type NAD/FAD binding fold] ; IPR014
ko00590	A	Peroxi	Posttransla	IPR032801	[Peroxi
ko00562	Ir	--	--	IPR002498	[Phosphatidylinositol-4-phosphate 5-kinas
--	WD40 rep	R	General fu	IPR001680	[WD40 repeat]
ko00830	R	NAD(P)-de	Lipid trans	IPR002347	[Short-chain dehydrogenase/reductase SDF
--	--	--	--	IPR003137	[PA domain] ; IPR007369[Peptidase A22B, si
--	--	--	--	IPR007369	[Peptidase A22B, signal peptide peptidase]
--	--	--	--	IPR022078	[CD99 antigen-like protein 2]
--	--	--	--	IPR018477	[Bicaudal-D protein, microtubule-associat
--	Alpha-tub	DZ	Cell cycle c	IPR000408	[Regulator of chromosome condensation, R
ko04010	M	--	--	IPR000651	[Ras-like guanine nucleotide exchange fact
--	--	--	--	IPR001849	[Pleckstrin homology domain]
--	Uncharact	S	Function u	IPR001478	[PDZ domain] ; IPR006907[Domain of unknc
--	--	--	--	IPR007109	[Brix domain]

--	Leucine-rich	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR021040[LRRC8, p
ko04621	N PASTA dom	Cell wall/r	IPR000719	[Protein kinase domain]
--	Phage-rel	Mobilome	IPR000998	[MAM domain]
--	--	--	IPR001715	[Calponin homology domain] ; IPR001781[Z
ko03008	R WD40 rep	General fu	IPR001680	[WD40 repeat] ; IPR018983[U3 small nucleo
ko03013	R Predicted IT	Signal tran	IPR001680	[WD40 repeat] ; IPR024977[Anaphase-prom
ko04015	R --	--	IPR001478	[PDZ domain] ; IPR021922[Domain of unknc
ko04530	T --	--	IPR001609	[Myosin head, motor domain] ; IPR002928[
--	--	--	IPR000357	[HEAT repeat] ; IPR001494[Importin-beta, N
--	Broad spec	Carbohydr	IPR001452	[SH3 domain] ; IPR013078[Histidine phosph
--	--	--	IPR005612	[CCAAT-binding factor] ; IPR011501[Nuclec
ko04145	P --	--	IPR002159	[CD36 family]
--	--	--	--	--
ko04722	N --	--	IPR002404	[IRS-type PTB domain]
--	Leucine-rich	Transcripti	IPR001611	[Leucine-rich repeat]
--	Phosphate P	Inorganic i	IPR001204	[Phosphate transporter]
ko04120	U --	--	IPR000569	[HECT domain] ; IPR004170[WWE domain] ;
ko04810	R --	--	--	--
--	--	--	IPR000198	[Rho GTPase-activating protein domain] ; IF
--	Periplasmic	Cell wall/r	--	--
--	--	--	IPR001452	[SH3 domain] ; IPR001683[Phox homologou
--	--	--	IPR000058	[Zinc finger, AN1-type]
--	U3 small n	Function u	IPR007149	[Leo1-like protein]
--	--	--	IPR007052	[CS domain]
--	--	--	IPR001619	[Sec1-like protein]
ko00230	P --	--	IPR009283	[Apyrase]
--	--	--	IPR000626	[Ubiquitin domain] ; IPR004274[FCP1 homo
ko04520	A --	--	IPR001478	[PDZ domain] ; IPR001715[Calponin homol
--	--	--	IPR026315	[Out at first protein]
--	--	--	--	--
ko04015	R Predicted ,R	General fu	IPR000159	[Ras-associating (RA) domain] ; IPR000198[
ko04611	P --	--	IPR001849	[Pleckstrin homology domain] ; IPR019748[
ko03460	F --	--	--	--
--	--	--	IPR000679	[Zinc finger, GATA-type] ; IPR032346[Transc
ko03040	S --	--	IPR013180	[Beta-catenin-like protein 1, N-terminal]
--	--	--	IPR025151	[ELYS-like domain] ; IPR032040[ELYS, beta-
--	--	--	IPR009428	[Beta-catenin-interacting ICAT]
--	--	--	IPR005818	[Linker histone H1/H5, domain H15]
--	--	--	IPR013932	[TATA-binding protein interacting (TIP20)]
ko03050	P --	--	IPR013886	[PI31 proteasome regulator, C-terminal] ; IF
--	Amino acid	Amino acid	IPR002293	[Amino acid/polyamine transporter I]
ko04144	E Guanine-n	General fu	IPR000904	[Sec7 domain] ; IPR032691[Guanine nucleot
--	--	--	IPR004343	[Plus-3 domain]
ko04062	C --	--	IPR001849	[Pleckstrin homology domain] ; IPR006816[
ko04520	A --	--	IPR003124	[WH2 domain]
ko04142	L --	--	IPR022775	[AP complex, mu/sigma subunit]
--	Pimeloyl- β	Coenzyme	IPR004142	[NDRG]
ko04141	P Molecular O	Posttransla	IPR013126	[Heat shock protein 70 family]
ko05100	B --	--	IPR030379	[Septin-type guanine nucleotide-binding (C
ko03018	R --	--	--	--
--	--	--	IPR000198	[Rho GTPase-activating protein domain]
ko03013	R --	--	IPR021827	[Nucleoporin Nup186/Nup192/Nup205]
--	--	--	IPR000008	[C2 domain] ; IPR010734[Copine]
ko04071	S WD40 rep	General fu	IPR000409	[BEACH domain] ; IPR001680[WD40 repeat]
--	Leucine-rich	Transcripti	--	--
ko04514	C --	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
--	Protein tyr	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR000998
ko05200	P --	--	IPR000270	[PB1 domain]

--	Bacillopep	O	Posttransla	IPR000421	[Coagulation factor 5/8 C-terminal domain]
--	--	--	--	IPR000195	[Rab-GTPase-TBC domain]
ko04144	E	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
ko04110	C	Acetoin uti	BQ	Chromatin	IPR023801 [Histone deacetylase domain]
ko04144	E	--	--	--	IPR001452 [SH3 domain] ; IPR002014[VHS domain] ; IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DF
--	Superfamil	L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DF
--	Ankyrin re	T	Signal tran	IPR001452	[SH3 domain] ; IPR020683[Ankyrin repeat-c
ko04270	V	--	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR015212[R
ko04141	P	--	--	--	IPR004854 [Ubiquitin fusion degradation protein UFD1
--	Proteasom	O	Posttransla	IPR000555	[JAB1/MPN/MOV34 metalloenzyme domain
ko05225	H	--	--	--	IPR001005 [SANT/Myb domain] ; IPR007526[SWIRM dc
ko05225	H	--	--	--	IPR003121 [SWIB/MDM2 domain]
--	--	--	--	--	IPR004088 [K Homology domain, type 1] ; IPR015096[L
--	--	--	--	--	IPR013877 [YAP-binding/ALF4/Glomulin]
ko04068	F	Ubiquitin (O	Posttransla	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko04120	U	--	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
--	--	--	--	--	IPR001781 [Zinc finger, LIM-type]
--	Protein-tyl	T	Signal tran	IPR000340	[Dual specificity phosphatase, catalytic dom
ko04020	C	Glucosamyl G	Carbohydr	IPR011613	[Glycoside hydrolase family 15/Phosphoryla
--	--	--	--	--	IPR007273 [SCAMP]
ko05225	H	--	--	--	IPR009071 [High mobility group box domain]
--	GTPase SAR		General fu	IPR001806	[Small GTPase superfamily]
--	Predicted	/R	General fu	IPR019151	[Proteasome assembly chaperone 2]
--	--	--	--	--	--
--	Acyl-CoA	/C	Energy prc	IPR015590	[Aldehyde dehydrogenase domain]
ko03008	R	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
ko04152	A	Predicted	/U	Intracellular	IPR004254 [AdipoR/Haemolysin-III-related]
--	--	--	--	--	IPR007191 [Sec8 exocyst complex component specific
ko03013	R	--	--	--	IPR004023 [Mago nashi protein]
ko00010	G	Phosphogl	G	Carbohydr	IPR013078 [Histidine phosphatase superfamily, clade-1
--	--	--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR019748[F
--	Uncharact	S	Function u	IPR004088	[K Homology domain, type 1] ; IPR015096[L
--	Leucine-rich	K	Transcripti	IPR001611	[Leucine-rich repeat]
ko04144	E	--	--	--	IPR001452 [SH3 domain]
--	Sugar pho	G	Carbohydr	IPR002350	[Kazal domain] ; IPR004156[Organic anion t
--	--	--	--	--	IPR023421 [Axin interactor, dorsalization-associated pr
--	GTPase SAR		General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
--	--	--	--	--	IPR023235 [FAM105]
--	--	--	--	--	IPR005301 [MOB kinase activator family]
--	--	--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR010703[I
--	Membrane	O	Posttransla	IPR022241	[Rhomboid serine protease] ; IPR022764[Pe
--	Nicotinami	HR	Coenzyme	IPR000868	[Isochorismatase-like]
--	--	--	--	--	IPR001012 [UBX domain]
--	--	--	--	--	IPR001849 [Pleckstrin homology domain]
--	--	--	--	--	IPR007259 [Gamma-tubulin complex component prote
ko04020	C	--	--	--	IPR012446 [Calcium release-activated calcium channel
--	--	--	--	--	IPR000261 [EH domain]
ko01100	N	Dienelacto	Q	Secondary	IPR002925 [Dienelactone hydrolase]
ko03040	S	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
--	--	--	--	--	IPR009755 [Colon cancer-associated Mic1-like]
ko04623	C	--	--	--	IPR024810 [Mab-21 domain]
--	--	--	--	--	IPR003877 [SPRY domain]
--	--	--	--	--	IPR006977 [Yip1 domain]
ko03013	R	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
ko03015	n	RNA recog	J	Translatio	IPR000504 [RNA recognition motif domain]
ko04144	E	--	--	--	IPR018798 [Multivesicular body subunit 12]
--	--	--	--	--	IPR029204 [CB1 cannabinoid receptor-interacting prot
--	Ca2+-dep	R	General fu	IPR000008	[C2 domain] ; IPR010734[Copine]

--	--	--	--	IPR002048	[EF-hand domain] ; IPR013787[S100/CaBP-]	
ko04015	R	--	--	--	IPR000331 [Rap GTPase activating protein domain] ; IP	
ko03013	R	--	--	--	IPR000488 [Death domain] ; IPR021861[THO complex,	
ko04115	p	--	--	--	IPR004031 [PMP-22/EMP/MP20/Claudin superfamily]	
ko04144	E	--	--	--	IPR005024 [Snf7 family]	
ko00010	G	Phosphom	G	Carbohydr	IPR005843 [Alpha-D-phosphohexomutase, C-terminal	
--	--	PASTA	dor	M	Cell wall/r	IPR000719 [Protein kinase domain]
--	--	2-keto-4-	Q	Secondary	IPR011234 [Fumarylacetoacetase, C-terminal-related]	
--	--	Superfamil	L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df	
--	--	--	--	--	IPR001594 [Palmitoyltransferase, DHHC domain]	
--	--	GTPase	SAR	General fu	IPR001806 [Small GTPase superfamily]	
ko00450	S	Cysteine	st	E	Amino acic	IPR000192 [Aminotransferase class V domain]
ko04390	H	--	--	--	IPR001781 [Zinc finger, LIM-type]	
--	--	Leucine-ric	K	Transcripti	IPR001611 [Leucine-rich repeat] ; IPR001715[Calponin	
ko00051	F	NDP-suga	JM	Translatio	IPR001451 [Hexapeptide repeat] ; IPR005835[Nucleotic	
--	--	Fermentati	T	Signal tran	IPR000073 [Alpha/beta hydrolase fold-1]	
ko04610	C	Murein tri	M	Cell wall/r	IPR000834 [Peptidase M14, carboxypeptidase A] ; IPR0	
ko03013	R	WD40 rep	R	General fu	IPR001680 [WD40 repeat] ; IPR013979[Translation initia	
--	--	Outer men	M	Cell wall/r	IPR013098 [Immunoglobulin I-set] ; IPR013162[CD80-I	
--	--	PASTA	dor	M	Cell wall/r	IPR000719 [Protein kinase domain] ; IPR024678[Serine/
--	--	Leucine-ric	K	Transcripti	IPR000483 [Cysteine-rich flanking region, C-terminal] ;	
--	--	--	--	--	IPR007265 [Conserved oligomeric Golgi complex, subu	
--	--	Aldo/keto	Q	Secondary	IPR023210 [NADP-dependent oxidoreductase domain]	
--	--	--	--	--	IPR002715 [Nascent polypeptide-associated complex f	
--	--	--	--	--	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal	
--	--	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]	
--	--	--	--	--	IPR002049 [Laminin EGF domain] ; IPR013032[EGF-like	
--	--	--	--	--	IPR018499 [Tetraspanin/Peripherin]	
--	--	--	--	--	IPR007000 [Phospholipase B-like]	
ko00330	A	Acetylornit	E	Amino acic	IPR002933 [Peptidase M20] ; IPR011650[Peptidase M2C	
ko04390	H	--	--	--	IPR001478 [PDZ domain] ; IPR015132[L27-2]	
--	--	--	--	--	IPR000315 [B-box-type zinc finger]	
--	--	--	--	--	IPR022735 [Domain of unknown function DUF3585]	
--	--	--	--	--	IPR001810 [F-box domain]	
--	--	--	--	--	IPR027930 [Protein of unknown function DUF4609]	
--	--	--	--	--	IPR010703 [Dedicator of cytokinesis, C-terminal] ; IPR0	
--	--	Regulator	O	Posttransla	IPR001107 [Band 7 domain]	
ko04390	H	--	--	--	IPR018979 [FERM, N-terminal] ; IPR018980[FERM, C-te	
--	--	--	--	--	IPR013657 [UAA transporter]	
ko01523	A	Predicted	G	Carbohydr	IPR011701 [Major facilitator superfamily]	
--	--	Glutathion	O	Posttransla	--	
ko04144	E	--	--	--	IPR000159 [Ras-associating (RA) domain] ; IPR000198[	
--	--	--	--	--	IPR001494 [Importin-beta, N-terminal domain]	
--	--	--	--	--	IPR000421 [Coagulation factor 5/8 C-terminal domain]	
--	--	RNA recog	J	Translatio	IPR000504 [RNA recognition motif domain]	
ko04120	U	--	--	--	IPR000008 [C2 domain] ; IPR000569[HECT domain] ; IP	
--	--	Cell divisio	D	Cell cycle c	IPR010472 [Formin, FH3 domain] ; IPR010473[Formin, (	
ko03013	R	tRNA nuck	J	Translatio	IPR002646 [Poly A polymerase, head domain] ; IPR032	
--	--	--	--	--	IPR029409 [Transmembrane protein 237]	
ko04724	G	--	--	--	IPR013057 [Amino acid transporter, transmembrane dc	
--	--	--	--	--	IPR006628 [Purine-rich element binding protein family	
--	--	--	--	--	IPR000990 [Innexin]	
ko04015	R	Guanylate	F	Nucleotide	IPR001202 [WW domain] ; IPR001478[PDZ domain] ; IP	
ko04621	N	--	--	--	IPR000990 [Innexin]	
--	--	--	--	--	IPR001452 [SH3 domain] ; IPR001683[Phox homologou	
--	--	Uncharact	S	Function u	IPR019087 [Mediator of RNA polymerase II transcriptio	
--	--	--	--	--	IPR007052 [CS domain]	
ko04621	N	Leucine-ric	K	Transcripti	IPR001478 [PDZ domain] ; IPR001611[Leucine-rich rep	

--	tRNA A-37J	Translator	IPR010440 [Lipopolysaccharide kinase]
--	--	--	IPR003877 [SPRY domain] ; IPR006594[LIS1 homology
--	--	--	IPR008253 [Marvel domain]
--	--	--	IPR000306 [FYVE zinc finger] ; IPR001849[Pleckstrin ho
--	--	--	IPR001478 [PDZ domain]
ko05168	H PASTA dor M	Cell wall/r	IPR000719 [Protein kinase domain]
--	--	--	IPR006561 [DZF domain] ; IPR014720[Double-strandec
--	Predicted 3G	Carbohydr	--
--	U3 small n S	Function u	IPR017923 [Transcription factor IIS, N-terminal]
ko04919	T --	--	IPR003822 [Paired amphipathic helix] ; IPR013194[Histe
--	--	--	IPR000648 [Oxysterol-binding protein] ; IPR001849[Ple
ko00430	T --	--	IPR012864 [Cysteine oxygenase/2-aminoethanethiol di
--	--	--	IPR024687 [MMS19, C-terminal]
--	--	--	--
--	--	--	IPR000626 [Ubiquitin domain] ; IPR000938[CAP Gly-ric
ko00440	P Glycerol-3 M	Cell wall/r	IPR004821 [Cytidyltransferase-like domain]
ko03040	S --	--	IPR021786 [Pre-mRNA splicing factor component Cdc
ko03050	P Predicted IT	Signal tran	IPR002015 [Proteasome/cyclosome repeat]
ko00511	C Neuramini GM	Carbohydr	IPR011040 [Sialidases]
ko04142	L UncharacteR	General fu	IPR031777 [Sortilin, C-terminal] ; IPR031778[Sortilin, N-
--	--	--	IPR000225 [Armadillo]
ko04136	A WD40 repeR	General fu	IPR000719 [Protein kinase domain] ; IPR001680[WD40
--	--	--	--
ko03008	R --	--	IPR009723 [Ribonuclease P/MRP, subunit POP1] ; IPR0:
ko05231	C --	--	IPR007603 [Choline transporter-like]
--	--	--	IPR013787 [S100/CaBP-9k-type, calcium binding, subc
--	--	--	--
ko02010	A ABC-type V	Defense m	IPR003439 [ABC transporter-like]
--	--	--	IPR001507 [Zona pellucida domain]
--	TetratricopR	General fu	IPR001623 [DnaJ domain] ; IPR011990[Tetratricopeptid
--	--	--	IPR026317 [Protein C10]
--	--	--	IPR033464 [CSN8/PSMD8/EIF3K]
ko04060	C --	--	IPR003961 [Fibronectin type III]
--	--	--	IPR002048 [EF-hand domain]
--	--	--	IPR001752 [Kinesin motor domain]
--	Superfamil L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR003877[SPRY dor
--	--	--	--
ko04350	T --	--	IPR001132 [SMAD domain, Dwarf-in-type] ; IPR003619[
--	RNA recogJ	Translator	IPR000504 [RNA recognition motif domain] ; IPR01295
--	--	--	IPR002164 [Nucleosome assembly protein (NAP)]
--	--	--	--
ko00562	Ir --	--	IPR002498 [Phosphatidylinositol-4-phosphate 5-kinase
--	--	--	IPR004240 [Nonaspanin (TM9SF)]
--	Ca2+-bincT	Signal tran	IPR002048 [EF-hand domain]
--	--	--	IPR008610 [Eukaryotic rRNA processing]
--	Serine/threT	Signal tran	IPR000719 [Protein kinase domain]
--	--	--	IPR025977 [Nuclear condensin complex subunit 3, C-te
ko04144	E --	--	IPR006789 [Actin-related protein 2/3 complex subunit
--	RNA recogJ	Translator	IPR000504 [RNA recognition motif domain] ; IPR00187
--	--	--	IPR000306 [FYVE zinc finger] ; IPR032031[Zinc finger F
--	--	--	IPR001478 [PDZ domain] ; IPR001609[Myosin head, mc
--	Predicted IT	Signal tran	--
--	O-acetyl-/J	Translator	IPR002589 [Macro domain]
--	Predicted /R	General fu	IPR001680 [WD40 repeat]
--	Ca2+-bincQ	Secondary	IPR001007 [VWFC domain] ; IPR001611[Leucine-rich re
--	--	--	IPR007015 [DNA polymerase V]
--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR019748[
--	Membrane M	Cell wall/r	IPR001680 [WD40 repeat] ; IPR015048[Domain of unkn

--	3',5'-cyclic T	Signal tran	IPR004843	[Calcineurin-like phosphoesterase domain,
ko04144 E	--	--	IPR008570	[ESCRT-II complex, vps25 subunit]
--	WD40 repeat	General fu	IPR001680	[WD40 repeat]
--	Periplasmic O	Posttransla	IPR000867	[Insulin-like growth factor-binding protein,
ko03015 n	Stalled ribo	Translatio	IPR005140	[eRF1 domain 1/Pelota-like] ; IPR005141[eR
ko04110 C	--	--	IPR008401	[Apc13p]
--	Negative r	Posttransla	IPR013766	[Thioredoxin domain]
ko00790 F	Gamma-gl	Amino aci	IPR011697	[Peptidase C26]
--	--	--	IPR006990	[Tweety]
--	--	--	IPR015940	[Ubiquitin-associated domain]
--	--	--	IPR032375	[Cerebral cavernous malformations 2, harm
--	--	--	IPR000717	[Proteasome component (PCI) domain]
ko04514 C	--	--	IPR001893	[Cysteine-rich Golgi apparatus protein 1 rep
--	--	--	IPR000008	[C2 domain]
ko04962 V	Carbonic a	General fu	IPR001451	[Hexapeptide repeat]
--	--	--	IPR019140	[Mini-chromosome maintenance complex-
ko04530 T	GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
ko04122 S	--	--	IPR015221	[Ubiquitin-related modifier 1]
--	Leucine-rich	Transcripti	IPR001212	[Somatomedin B domain] ; IPR018487[Hem
ko04530 T	--	--	IPR000219	[Dbl homology (DH) domain]
--	--	--	--	--
--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
--	Leucine-rich	Transcripti	IPR001611	[Leucine-rich repeat]
ko00562 Ir	--	--	IPR000403	[Phosphatidylinositol 3-/4-kinase, catalytic
--	--	--	IPR022577	[Tubulin-specific chaperone D, C-terminal]
ko00534 G	--	--	IPR004263	[Exostosin-like] ; IPR015338[Exostosin , C-te
ko00511 C	Alpha-L-fu	Carbohydr	IPR000933	[Glycoside hydrolase, family 29] ; IPR031919
--	--	--	IPR001007	[VWFC domain]
--	HEAT repe	General fu	--	--
ko05164 Ir	--	--	IPR003034	[SAP domain] ; IPR003877[SPRY domain]
--	--	--	--	--
--	--	--	IPR013106	[Immunoglobulin V-set domain]
ko04141 P	--	--	--	--
ko03040 S	Superfamil	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DI
ko00270 C	Methylthio	Amino aci	IPR000649	[Initiation factor 2B-related]
--	Uncharact	General fu	IPR001680	[WD40 repeat] ; IPR026987[WD repeat-con
ko00270 C	Acireducto	Amino aci	IPR004313	[Acireductone dioxygenase ARD family]
--	--	--	IPR001841	[Zinc finger, RING-type]
--	Cyclopropyl	Lipid trans	IPR008576	[Alpha-N-methyltransferase NTM1]
ko04136 A	Predicted	General fu	IPR001680	[WD40 repeat]
--	--	--	--	--
--	--	--	IPR021148	[Polysaccharide biosynthesis domain]
ko00564 G	--	--	IPR004277	[Phosphatidyl serine synthase]
--	--	--	IPR005612	[CCAAT-binding factor]
--	Protein-ty	Signal tran	IPR000340	[Dual specificity phosphatase, catalytic dom
--	--	--	IPR009038	[GOLD domain]
--	ATP-depe	Posttransla	IPR003959	[ATPase, AAA-type, core]
ko03040 S	--	--	IPR009846	[Splicing factor 3B subunit 5/RDS3 complex
--	Forkhead	Signal tran	IPR000253	[Forkhead-associated (FHA) domain] ; IPR0
ko04514 C	--	--	IPR013106	[Immunoglobulin V-set domain]
--	--	--	--	--
--	--	--	IPR000648	[Oxysterol-binding protein]
ko00520 A	Dihydrodi	Amino aci	IPR002220	[DapA-like]
ko04144 E	--	--	IPR000008	[C2 domain] ; IPR019018[Rab-binding dom
--	--	--	IPR000195	[Rab-GTPase-TBC domain]
--	--	--	IPR003131	[Potassium channel tetramerisation-type BT
--	--	--	IPR002048	[EF-hand domain]
--	Tetratricop	General fu	IPR019734	[Tetratricopeptide repeat] ; IPR021183[N-te

--	Amino acid E	Amino acid IPR004841 [Amino acid permease/ SLC12A domain] ; IF
--	--	-- IPR007042 [Arsenite-resistance protein 2] ; IPR021933[
--	--	-- IPR022065 [Uncharacterised protein family, TMEM59]
--	--	-- IPR006958 [Mak16 protein] ; IPR029004[Ribosomal L28
ko00230 P	Inosine/xai F	Nucleotide IPR002637 [Ham1-like protein]
--	--	-- IPR013979 [Translation initiation factor, beta propellor-
ko04514 C	--	-- IPR013106 [Immunoglobulin V-set domain] ; IPR01316
ko04142 L	Arylsulfata P	Inorganic i IPR000917 [Sulfatase, N-terminal]
--	--	-- IPR032764 [Tankyrase 1-binding protein, C-terminal]
ko04015 R	--	-- IPR000270 [PB1 domain] ; IPR001478[PDZ domain]
--	--	-- IPR018619 [Hyccin]
--	Uncharact R	General fu IPR003115 [ParB/Sulfiredoxin]
--	--	-- IPR001849 [Pleckstrin homology domain] ; IPR010703[
--	--	-- IPR019748 [FERM central domain]
ko03008 R	GTP-binding R	General fu IPR010674 [Nucleolar GTP-binding protein 1, Rossman
ko05202 T	--	-- IPR001012 [UBX domain] ; IPR021569[TUG ubiquitin-li
--	--	-- IPR000648 [Oxysterol-binding protein] ; IPR001849[Ple
--	Ankyrin rej T	Signal tran IPR020683 [Ankyrin repeat-containing domain]
--	GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
--	Diphthami J	Translator IPR016435 [Diphthamide synthesis DPH1/DPH2]
--	WD40 rep R	General fu --
ko03013 R	--	-- IPR005120 [Regulator of nonsense-mediated decay, UI
--	--	-- IPR001478 [PDZ domain] ; IPR001781[Zinc finger, LIM-
ko04310 V	Predicted IT	Signal tran IPR001680 [WD40 repeat] ; IPR006594[LIS1 homology i
--	--	-- IPR000626 [Ubiquitin domain]
--	--	-- IPR004088 [K Homology domain, type 1]
ko04650 N	--	-- IPR011161 [MHC class I-like antigen recognition-like]
--	--	-- --
ko00240 P	Uridine kin F	Nucleotide IPR006083 [Phosphoribulokinase/uridine kinase]
--	--	-- IPR007875 [Sprouty]
--	--	-- IPR007858 [Dpy-30 motif]
--	--	-- IPR001594 [Palmitoyltransferase, DHHC domain]
ko04360 A	--	-- IPR001627 [Sema domain] ; IPR002165[Plexin repeat]
--	Ankyrin rej T	Signal tran IPR020683 [Ankyrin repeat-containing domain]
ko00440 P	--	-- IPR000462 [CDP-alcohol phosphatidyltransferase]
--	--	-- IPR014877 [CRM1 C-terminal domain]
--	--	-- IPR000198 [Rho GTPase-activating protein domain] ; IF
--	--	-- --
--	Cysteine p O	Posttransla IPR000668 [Peptidase C1A, papain C-terminal]
--	--	-- IPR026794 [Uncharacterised protein family UPF0687]
--	TFIIF-inter. K	Transcripti IPR004274 [FCP1 homology domain]
--	Molybdop H	Coenzyme IPR000594 [THIF-type NAD/FAD binding fold]
--	--	-- IPR001590 [Peptidase M12B, ADAM/reprolysin] ; IPR00
ko03013 R	--	-- IPR003890 [MIF4G-like, type 3] ; IPR009818[Ataxin-2, C
ko05132 S	Tfp pilus a: NW	Cell motilit IPR011990 [Tetratricopeptide-like helical domain]
ko03008 R	--	-- IPR004859 [Putative 5-3 exonuclease]
ko04120 U	--	-- IPR000008 [C2 domain] ; IPR000569[HECT domain] ; IP
--	GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
--	--	-- IPR008496 [Protein of unknown function DUF778]
ko05134 L	GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
--	--	-- IPR015021 [Domain of unknown function DUF1907]
ko04110 C	--	-- IPR024990 [Anaphase-promoting complex subunit 1]
--	--	-- IPR028144 [Cysteine-rich transmembrane CYSTM dom
ko04136 A	--	-- IPR007239 [Autophagy-related protein 5]
--	N-acetyl m M	Cell wall/r IPR002502 [N-acetylmuramoyl-L-alanine amidase don
ko04071 S	--	-- IPR000276 [G protein-coupled receptor, rhodopsin-lik
--	--	-- IPR027967 [Protein of unknown function DUF4612]
--	N-acetyl n M	Cell wall/r IPR000210 [BTB/POZ domain] ; IPR006652[Kelch repea

--	U3 small n S	Function u	IPR001849 [Pleckstrin homology domain]
ko04114	C Serine/thr T	Signal tran	IPR000719 [Protein kinase domain] ; IPR022165 [Polo ki
ko04724	G -- --	--	IPR013057 [Amino acid transporter, transmembrane dc
ko04010	N Serine/thr T	Signal tran	IPR000719 [Protein kinase domain]
ko03018	R HrpA-like J	Translatior	IPR001650 [Helicase, C-terminal] ; IPR007502 [Helicase-
ko00190	C Inorganic p CP	Energy prc	IPR008162 [Inorganic pyrophosphatase]
--	Carboxype E	Amino acic	IPR001563 [Peptidase S10, serine carboxypeptidase]
--	Acid stress T	Signal tran	IPR002634 [BoIA protein]
ko04015	R -- --	--	IPR000276 [G protein-coupled receptor, rhodopsin-lik
--	Protein tyr T	Signal tran	IPR000242 [PTP type protein phosphatase] ; IPR004328
--	Tetratricop R	General fu	IPR019734 [Tetratricopeptide repeat] ; IPR024660 [UNC
ko04141	P DnaJ-class O	Posttransla	IPR001623 [DnaJ domain]
--	-- --	--	IPR031600 [Domain of unknown function DUF4706]
ko04144	E -- --	--	IPR005024 [Snf7 family]
--	ATP-depei O	Posttransla	IPR010448 [Torsin]
--	Aminopep E	Amino acic	IPR014782 [Peptidase M1, membrane alanine aminope
--	-- --	--	IPR007477 [SAB domain] ; IPR008379 [Band 4.1, C-term
--	-- --	--	--
--	Ribosomal J	Translatior	IPR003347 [JmjC domain]
ko04621	N -- --	--	IPR002035 [von Willebrand factor, type A] ; IPR008399 [
--	-- --	--	IPR001841 [Zinc finger, RING-type] ; IPR003137 [PA do
ko00240	P NTP pyrop V	Defense m	IPR025984 [dCTP pyrophosphatase 1]
--	-- --	--	IPR007109 [Brix domain]
--	-- --	--	IPR001214 [SET domain] ; IPR002893 [Zinc finger, MYNI
ng (GO:00	WD40 rep R	General fu	IPR001680 [WD40 repeat]
--	Magnesiur P	Inorganic i	IPR004014 [Cation-transporting P-type ATPase, N-terr
--	-- --	--	--
--	-- --	--	IPR019396 [Transmembrane Fragile-X-F-associated pr
ko04120	U -- --	--	IPR000608 [Ubiquitin-conjugating enzyme E2]
ko03050	P 20S protea O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta] ; IPR0246
--	-- --	--	IPR025257 [Domain of unknown function DUF4205]
--	-- --	--	--
ko04390	H -- --	--	IPR005301 [MOB kinase activator family]
ko05012	P Putative in R	General fu	IPR002818 [DJ-1/PfpI]
--	-- --	--	IPR000306 [FYVE zinc finger] ; IPR001849 [Pleckstrin ho
--	-- --	--	IPR033335 [Microtubule-associated protein Jupiter/He
--	NADPH:qu CR	Energy prc	IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
--	-- --	--	IPR013921 [Mediator complex, subunit Med20]
ko03018	R -- --	--	--
--	Leucine-rich K	Transcripti	IPR001611 [Leucine-rich repeat]
--	-- --	--	IPR013167 [Conserved oligomeric Golgi complex, subu
ko04144	E -- --	--	IPR009851 [Modifier of rudimentary, Modr]
--	-- --	--	IPR000717 [Proteasome component (PCI) domain]
--	Histone ac KB	Transcripti	IPR000182 [GNAT domain] ; IPR007197 [Radical SAM] ;
--	-- --	--	IPR009357 [Solute carrier family 52, riboflavin transport
ko00770	P Phosphop H	Coenzyme	IPR007085 [DNA/pantothenate metabolism flavoprotei
--	Ubiquitin O	Posttransla	IPR000626 [Ubiquitin domain] ; IPR032752 [Ubiquitin-b
--	-- --	--	IPR006800 [Pellino family]
--	-- --	--	IPR001202 [WW domain] ; IPR001849 [Pleckstrin homol
ko04120	U -- --	--	IPR000008 [C2 domain] ; IPR000569 [HECT domain] ; IP
ko03013	R -- --	--	IPR013598 [Exportin-1/Importin-beta-like]
--	Uncharact S	Function u	IPR003226 [Metal-dependent protein hydrolase]
--	-- --	--	--
--	-- --	--	IPR004240 [Nonaspanin (TM9SF)]
--	Carboxype E	Amino acic	IPR001563 [Peptidase S10, serine carboxypeptidase]
ko04310	V -- --	--	IPR007052 [CS domain] ; IPR007699 [SGS domain] ; IPR
ko04140	A -- --	--	IPR006762 [Gtr1/RagA G protein]
ko04144	E -- --	--	IPR001452 [SH3 domain] ; IPR004148 [BAR domain]

--	GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
--	Putative C:R	General fu	IPR001727	[Gdt1 family]
ko04120 U	--	--	IPR000008	[C2 domain] ; IPR000569[HECT domain] ; IPR014847 [FERM adjacent (FA)] ; IPR018979[FERM, N-terminus]
--	--	--	IPR021910	[Protein of unknown function DUF3522]
--	--	--	IPR000719	[Protein kinase domain] ; IPR022247[Casein kinase II domain]
ko04340 H	Periplasmic U	--	IPR004240	[Nonaspanin (TM9SF)]
--	--	Translatio	IPR000048	[IQ motif, EF-hand binding site] ; IPR000155[EF-hand domain]
ko04666 F	HD superfamily	Posttransla	IPR003439	[ABC transporter-like] ; IPR011527[ABC transporter-like]
ko02010 A	ABC-type O	General fu	IPR001806	[Small GTPase superfamily]
--	GTPase SAR	--	IPR010357	[Protein of unknown function DUF953, thiorodocyclinase]
--	--	--	--	--
ko03018 R	Ribonuclease J	Translatio	IPR001247	[Exoribonuclease, phosphorolytic domain 1]
--	--	--	IPR002172	[Low-density lipoprotein (LDL) receptor class B type I domain]
--	tRNA A-37 J	Translatio	IPR000905	[Gcp-like domain]
ko00562 I	Myo-inositol	Lipid trans	IPR002587	[Myo-inositol-1-phosphate synthase] ; IPR002413 [Transmembrane protein 138]
--	--	--	IPR010334	[mRNA-decapping enzyme subunit 1] ; IPR000008 [C2 domain] ; IPR031468[Synaptotagmin-like]
ko03018 R	--	--	IPR019318	[Guanine nucleotide exchange factor, Ric8]
--	--	--	IPR001627	[Sema domain] ; IPR002165[Plexin repeat]
ko04360 A	--	Function u	IPR001881	[EGF-like calcium-binding domain] ; IPR011798 [GPCR family 3, C-terminal]
--	PKD repeat S	--	IPR013078	[Histidine phosphatase superfamily, clade-1]
ko00051 F	Broad specific G	--	IPR006903	[RNA polymerase II-binding domain] ; IPR003010 [Carbon-nitrogen hydrolase]
--	--	General fu	IPR003010	[Carbon-nitrogen hydrolase]
ko00250 A	Predicted :R	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
ko04514 C	--	Translatio	IPR001247	[Exoribonuclease, phosphorolytic domain 1]
ko03018 R	Ribonuclease J	--	IPR007084	[BRICHOS domain]
--	--	--	IPR000608	[Ubiquitin-conjugating enzyme E2] ; IPR001478 [PDZ domain] ; IPR001781[Zinc finger, LIM-domain]
ko04120 U	--	Lipid trans	IPR000873	[AMP-dependent synthetase/ligase] ; IPR0200072 [PDGF/VEGF domain] ; IPR000859[CUB domain]
--	--	--	IPR003008	[Tubulin/FtsZ, GTPase domain] ; IPR018316[Carbohydrate-binding domain]
ko00010 G	Acyl-coenzyme I	Carbohydr	IPR011701	[Major facilitator superfamily]
ko01521 E	--	General fu	IPR001680	[WD40 repeat]
ko04145 P	--	Coenzyme	IPR008278	[4'-phosphopantetheinyl transferase superfamily]
ko04142 L	Sugar phosphate G	--	IPR000095	[CRIB domain]
ko03013 R	WD40 repeat R	--	--	--
ko00770 P	Phosphoprotein H	Replicatio	IPR006917	[SOUL haem-binding protein]
--	--	General fu	IPR001806	[Small GTPase superfamily]
--	DNA gyrase L	--	IPR001619	[Sec1-like protein]
--	GTPase SAR	Translatio	--	--
ko04144 E	--	--	IPR003008	[Tubulin/FtsZ, GTPase domain] ; IPR018316[Janus]
--	rRNA processing J	--	IPR007702	[Janus]
ko04145 P	--	--	IPR001881	[EGF-like calcium-binding domain] ; IPR01316
--	--	Defense m	IPR007822	[Lanthionine synthetase C-like]
--	Lantibiotic V	Translatio	IPR005146	[B3/B4 tRNA-binding domain] ; IPR005147[Autophagy-related protein 3, N-terminal] ;
ko00970 A	Phenylalanine J	--	IPR007134	[Autophagy-related protein 3, N-terminal] ;
ko04136 A	--	--	--	--
--	--	Cell cycle c	IPR003395	[RecF/RecN/SMC, N-terminal] ; IPR010935[RecF/RecN/SMC, N-terminal]
ko00562 I	Chromosome D	--	IPR002013	[SAC domain]
--	--	Translatio	IPR006073	[GTP binding domain] ; IPR013029[Domain]
ko03008 R	Ribosome-J	Translatio	IPR011704	[ATPase, dynein-related, AAA domain]
--	Midasin, A J	--	IPR001594	[Palmitoyltransferase, DHHC domain]
--	--	--	IPR009790	[Protein of unknown function DUF1356, TM domain]
--	--	--	IPR009538	[PV-1]
--	--	--	IPR001478	[PDZ domain] ; IPR014775[L27 domain, C-terminal]

--	ATPase co R	General fu	IPR003439 [ABC transporter-like] ; IPR032781[ABC-trar
--	--	--	IPR009828 [Protein of unknown function DUF1394]
--	Superfamil L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
--	--	--	IPR000195 [Rab-GTPase-TBC domain] ; IPR001763[Rhc
--	--	--	IPR002867 [IBR domain]
--	--	--	IPR019160 [Exocyst complex component Sec3, C-termi
--	--	--	IPR005045 [CDC50/LEM3 family]
ko00770 P	UncharactS	Function u	IPR002791 [Domain of unknown function DUF89] ; IPR(
--	GTPase SAR	General fu	IPR006689 [Small GTPase superfamily, ARF/SAR type]
--	--	--	--
--	Superfamil L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
--	--	--	IPR010695 [Fas apoptotic inhibitory molecule 1]
ko00750 V	Pyridoxine. H	Coenzyme	IPR011576 [Pyridoxamine 5'-phosphate oxidase-like, F
--	--	--	IPR000225 [Armadillo]
--	--	--	IPR029265 [Transmembrane protein 51]
--	--	--	--
--	--	--	IPR012981 [PIH1 family]
--	tRNA(His) J	Translatio	IPR024956 [tRNAHis guanylyltransferase catalytic dom
ko03008 R	Ribosomal J	Translatio	IPR004038 [Ribosomal protein L7Ae/L30e/S12e/Gadd4
--	GTPase SAR	General fu	IPR001806 [Small GTPase superfamily]
ko00562 Ir	3'-Phosph P	Inorganic i	IPR000760 [Inositol monophosphatase-like]
--	--	--	IPR024679 [Pre-rRNA-processing protein IPI1/Testis-e
--	tRNA G26 J	Translatio	IPR000571 [Zinc finger, CCCH-type] ; IPR002905[tRNA
--	GTPase SAR	General fu	IPR006689 [Small GTPase superfamily, ARF/SAR type]
--	Zinc trans P	Inorganic i	IPR003689 [Zinc/iron permease]
--	--	--	--
--	--	--	IPR004031 [PMP-22/EMP/MP20/Claudin superfamily]
ko00533 G	--	--	IPR002659 [Glycosyl transferase, family 31]
ko04015 R	Serine/threT	Signal tran	IPR000719 [Protein kinase domain] ; IPR002219[Protein
ko04810 R	--	--	IPR001452 [SH3 domain] ; IPR012849[Abl-interactor, h
--	Threonyl-tJ	Translatio	--
ko04010 N	Ankyrin rejT	Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
--	Leucine-ricK	Transcripti	IPR004934 [Tropomodulin]
ko04130 S	--	--	--
--	--	--	IPR000591 [DEP domain] ; IPR001849[Pleckstrin homol
--	--	--	--
--	--	--	IPR014830 [Glycolipid transfer protein domain]
ko04144 E	Lysophosphl	Lipid trans	IPR000073 [Alpha/beta hydrolase fold-1]
--	Molecular O	Posttransla	IPR000626 [Ubiquitin domain] ; IPR007842[HEPN dom
ko04141 P	--	--	IPR013918 [Nucleotide exchange factor Fes1]
ko00270 C	dTDP-4-dM	Cell wall/r	IPR029903 [RmlD-like substrate binding domain]
ko04270 V	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR001478[P
--	--	--	IPR001452 [SH3 domain] ; IPR018556[Domain of unknc
ko04514 C	--	--	IPR013106 [Immunoglobulin V-set domain] ; IPR01316
--	FOG: Zn-fi R	General fu	IPR001909 [Krueppel-associated box] ; IPR007087[Zinc
--	Glucose/ar G	Carbohydr	IPR000033 [LDLR class B repeat] ; IPR000742[EGF-like c
--	Ubiquitin (O	Posttransla	IPR006757 [Opioid growth factor receptor (OGFr) cons
--	--	--	IPR000867 [Insulin-like growth factor-binding protein,
--	Guanylate F	Nucleotide	IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
ko04144 E	--	--	IPR005024 [Snf7 family]
--	Ankyrin rejT	Signal tran	IPR002110 [Ankyrin repeat] ; IPR020683[Ankyrin repeat
ko04217 N	O-acetyl-/J	Translatio	IPR002589 [Macro domain] ; IPR007125[Histone H2A/H
--	--	--	IPR000906 [ZU5 domain] ; IPR001452[SH3 domain] ; IP
--	--	--	IPR030379 [Septin-type guanine nucleotide-binding (C
--	--	--	IPR027817 [Costars domain]
--	--	--	--
--	Alpha-tub DZ	Cell cycle c	IPR000408 [Regulator of chromosome condensation, R
--	--	--	IPR026179 [SLAIN motif-containing protein]

--	DNA-bind R	General fu	IPR009471 [Teneurin intracellular, N-terminal] ; IPR028
--	--	--	IPR025602 [BCP1 family]
--	--	--	IPR006993 [SH3-binding, glutamic acid-rich protein]
--	Serine/threT	Signal tran	IPR000719 [Protein kinase domain]
ko03015 n	Predicted rR	General fu	IPR001279 [Metallo-beta-lactamase] ; IPR011108[Zn-d
ko00970 A	Leucyl-tRNJ	Translatior	IPR002300 [Aminoacyl-tRNA synthetase, class Ia] ; IPRC
--	--	--	IPR000253 [Forkhead-associated (FHA) domain] ; IPR0
--	--	--	IPR019156 [Ataxin-10 domain]
--	--	--	IPR008709 [Neurochondrin]
ko04144 E	UncharactS	Function u	IPR000261 [EH domain]
ko00562 Ir	--	--	IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic i
--	--	--	IPR004331 [SPX domain] ; IPR004342[EXS, C-terminal]
--	--	--	IPR006020 [PTB/PI domain]
ko04144 E	Predicted jR	General fu	IPR024654 [Calcineurin-like phosphoesterase domain,
--	--	--	IPR033464 [CSN8/PSMD8/EIF3K]
ko04141 P	DnaJ-class O	Posttransla	IPR001623 [DnaJ domain] ; IPR002939[Chaperone Dna.
ko04120 U	Molybdop H	Coenzyme	IPR000594 [THIF-type NAD/FAD binding fold] ; IPR028
--	--	--	IPR000717 [Proteasome component (PCI) domain]
--	DnaJ-class O	Posttransla	IPR001623 [DnaJ domain] ; IPR002939[Chaperone Dna.
ko04145 P	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
--	--	--	IPR000716 [Thyroglobulin type-1] ; IPR002350[Kazal dc
--	Ribulose-5 G	Carbohydr	IPR001303 [Class II aldolase/adducin N-terminal]
--	UncharactS	Function u	IPR014044 [CAP domain]
--	ATPase co R	General fu	IPR003439 [ABC transporter-like] ; IPR032781[ABC-trar
--	Xanthine/L 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]
--	--	--	IPR007259 [Gamma-tubulin complex component prote
--	Predicted iG	Carbohydr	IPR005828 [Major facilitator, sugar transporter-like]
--	--	--	IPR013158 [APOBEC-like, N-terminal]
ko04010 M	--	--	IPR015019 [Ragulator complex protein LAMTOR3]
--	--	--	IPR001781 [Zinc finger, LIM-type]
ko03060 P	--	--	IPR026258 [Signal recognition particle subunit SRP68]
--	--	--	IPR007051 [CHORD domain] ; IPR007052[CS domain]
ko04014 R	Serine/threT	Signal tran	IPR000719 [Protein kinase domain]
ko04978 M	--	--	IPR013130 [Ferric reductase transmembrane compone
ko04145 P	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain]
ko03013 R	Superfamil L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
--	--	--	IPR001452 [SH3 domain] ; IPR013606[IMD/I-BAR dom
--	Prefoldin, (O	Posttransla	IPR002777 [Prefoldin beta-like]
--	Amino acid E	Amino acid	IPR004841 [Amino acid permease/ SLC12A domain] ; If
ko03040 S	RNA recogJ	Translatior	IPR000504 [RNA recognition motif domain]
ko00270 C	Enolase-pl E	Amino acid	--
--	--	--	IPR011680 [Fasciculation and elongation protein zeta, l
ko03013 R	Translator J	Translatior	IPR000649 [Initiation factor 2B-related]
ko00190 C	--	--	IPR011987 [ATPase, V1 complex, subunit H, C-terminal
--	--	--	IPR001494 [Importin-beta, N-terminal domain]
--	--	--	IPR005651 [Uncharacterised protein family UPF0434/Tr
--	--	--	IPR001494 [Importin-beta, N-terminal domain]
ko04140 A	Serine/threT	Signal tran	IPR000719 [Protein kinase domain]
ko04614 R	Aminopep E	Amino acid	IPR014782 [Peptidase M1, membrane alanine aminope
ko04360 A	DNA-bind R	General fu	IPR001627 [Sema domain] ; IPR002165[Plexin repeat] ;
--	Peptide mO	Posttransla	IPR002569 [Peptide methionine sulfoxide reductase l
--	--	--	IPR001452 [SH3 domain] ; IPR002108[Actin-depolymer
--	Superfamil L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
ko04014 R	WD40 repeR	General fu	IPR001680 [WD40 repeat]
ko04962 V	--	--	IPR008603 [Dynactin subunit 4]
ko04110 C	TetratricopR	General fu	IPR007192 [Cdc23] ; IPR011990[Tetratricopeptide-like l

ko04110 C Predicted iR	General fu IPR019734 [Tetratricopeptide repeat]
ko04144 E -- --	-- IPR007143 [Vacuolar protein sorting-associated, VPS28]
-- -- --	-- IPR033335 [Microtubule-associated protein Jupiter/He
-- Ribosomal J	Translatior IPR001790 [Ribosomal protein L10P]
Serine/threT	Signal tran IPR000719 [Protein kinase domain] ; IPR001180[Citron
ko04510 F -- --	-- IPR001715 [Calponin homology domain]
ko03015 r RNA procEJ	Translatior IPR001279 [Metallo-beta-lactamase] ; IPR011108[Zn-d
-- -- --	-- IPR019383 [Golgin subfamily A member 7/ERF4]
ko00230 P 8-oxo-dG V	Defense m IPR000086 [NUDIX hydrolase domain]
-- RNA recogJ	Translatior IPR000504 [RNA recognition motif domain]
-- -- --	-- IPR001060 [FCH domain] ; IPR001452[SH3 domain]
ko03013 R -- --	-- IPR003034 [SAP domain] ; IPR032552[Acin1, RNSP1-SA
-- -- --	-- IPR000859 [CUB domain] ; IPR018933[Netrin module, r
-- -- --	-- IPR003103 [BAG domain]
ko04144 E GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03050 P -- --	-- IPR003185 [Proteasome activator pa28, N-terminal dor
ko04144 E -- --	-- --
ko04010 M Serine/threT	Signal tran IPR000719 [Protein kinase domain]
-- Predicted iJ	Translatior IPR002478 [PUA domain]
-- -- --	-- IPR001594 [Palmitoyltransferase, DHHC domain]
-- Zinc transP	Inorganic i IPR003689 [Zinc/iron permease]
-- Large exoU	IntracellulE IPR002126 [Cadherin] ; IPR013164[Cadherin, N-termin
ko04144 E Ankyrin rejT	Signal tran IPR001164 [Arf GTPase activating protein] ; IPR001452[
-- -- --	-- IPR021629 [Mediator complex, subunit Med23]
-- -- --	-- IPR000195 [Rab-GTPase-TBC domain] ; IPR006571[TLC
-- Ankyrin rejT	Signal tran IPR000569 [HECT domain] ; IPR010606[Mib-herc2] ; IPI
-- MembraneM	Cell wall/r IPR001680 [WD40 repeat] ; IPR015048[Domain of unkn
ko03008 R rRNA matUJ	Translatior IPR014881 [Nin one binding (NOB1) Zn-ribbon-like] ; I
-- -- --	-- IPR001609 [Myosin head, motor domain] ; IPR032412[M
ko00062 F Triacylglyc I	Lipid trans IPR002472 [Palmitoyl protein thioesterase]
ko03040 S Predicted iR	General fu IPR001680 [WD40 repeat] ; IPR003613[U box domain] ;
ko04141 P -- --	-- IPR000626 [Ubiquitin domain] ; IPR015940[Ubiquitin-a
ko04144 E -- --	-- IPR001683 [Phox homologous domain]
ko04022 c -- --	-- IPR000402 [Sodium/potassium-transporting ATPase su
-- Large exoU	IntracellulE IPR002126 [Cadherin] ; IPR013164[Cadherin, N-termin
-- RNA recogJ	Translatior IPR000504 [RNA recognition motif domain] ; IPR00207
-- -- --	-- IPR001060 [FCH domain] ; IPR001452[SH3 domain]
-- Xaa-Pro arE	Amino acic IPR000587 [Creatinase, N-terminal] ; IPR000994[Peptid
ko04144 E -- --	-- IPR001683 [Phox homologous domain] ; IPR015404[So
ko04130 S -- --	-- IPR000727 [Target SNARE coiled-coil homology doma
ko00564 G -- --	-- IPR016090 [Phospholipase A2 domain]
ko04217 N -- --	-- IPR001012 [UBX domain]
ko04610 C -- --	-- IPR011161 [MHC class I-like antigen recognition-like]
ko04141 P GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko01523 A Forkhead iT	Signal tran IPR003439 [ABC transporter-like] ; IPR013525[ABC-2 ty
-- 16S rRNA iJ	Translatior IPR001737 [Ribosomal RNA adenine methyltransferase
-- -- --	-- IPR000717 [Proteasome component (PCI) domain]
ko03008 R WD40 repR	General fu IPR001680 [WD40 repeat] ; IPR007148[Small-subunit p
ko04918 T Superfamil KL	Transcripti IPR000330 [SNF2-related, N-terminal domain] ; IPR001
ko04141 P -- --	-- IPR001012 [UBX domain] ; IPR012989[SEP domain]
ko04150 r -- --	-- IPR000539 [Frizzled protein] ; IPR020067[Frizzled domE
-- -- --	-- IPR001101 [Plectin repeat] ; IPR001715[Calponin homo
ko04910 Ir -- --	-- IPR004140 [Exocyst complex component Exo70]
-- -- --	-- IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko05206 M dsRNA-spK	Transcripti IPR000999 [Ribonuclease III domain] ; IPR001650[Helic
ko04216 F Amino acicE	Amino acic IPR002293 [Amino acid/polyamine transporter I]
-- UncharactS	Function u IPR005552 [Scramblase]
ko04014 R Leucine-richK	Transcripti IPR001611 [Leucine-rich repeat]

--	--	--	--	IPR013170	[mRNA splicing factor Cwf21 domain]
ko00511	C	Neuramini GM	Carbohydr	IPR011040	[Sialidases]
ko04520	A	--	--	IPR001452	[SH3 domain] ; IPR013606[IMD/I-BAR dom
ko04110	C	Chromoso D	Cell cycle c	IPR003395	[RecF/RecN/SMC, N-terminal] ; IPR010935[
ko00520	A	UDP-N-acM	Cell wall/r	IPR000600	[ROK family] ; IPR003331[UDP-N-acetylgluc
--	--	--	--	IPR019265	[Protein of unknown function UPF0568]
--	--	--	--	IPR001841	[Zinc finger, RING-type]
--	--	--	--	IPR007052	[CS domain] ; IPR025934[NudC N-terminal
ko04020	C	--	--	IPR027246	[Eukaryotic porin/Tom40]
--	--	--	--	IPR007084	[BRICHOS domain]
--	--	Ribosome-J	Translatior	IPR004095	[TGS] ; IPR006073[GTP binding domain] ; IP
--	--	--	--	IPR007233	[Trafficking protein particle complex subuni
--	--	--	--	IPR007225	[Exocyst complex component EXOC6/Sec15
--	--	--	--	IPR029304	[A-kinase anchor protein 2, C-terminal dor
--	--	Thioestera Q	Secondary	IPR000873	[AMP-dependent synthetase/ligase] ; IPR01
--	--	--	--	IPR005026	[SAPAP family]
--	--	Serine/threT	Signal tran	IPR000719	[Protein kinase domain] ; IPR017892[Protein
--	--	UncharactS	Function u	IPR001680	[WD40 repeat]
ko03018	R	ExoribonucK	Transcripti	IPR002716	[PIN domain] ; IPR033770[Exosome comple
ko03008	R	RNA 3'-terA	RNA proce	IPR013791	[RNA 3'-terminal phosphate cyclase, insert c
--	--	N-acetylneM	Cell wall/r	--	--
--	--	Cold shockK	Transcripti	IPR002059	[Cold-shock protein, DNA-binding]
--	--	--	--	IPR029199	[THRAP3/BCLAF1 family]
ko03040	S	--	--	IPR019007	[WW domain binding protein 11]
ko03008	R	RNA proceJ	Translatior	IPR002687	[Nop domain] ; IPR012974[NOP5, N-termin
ko04621	N	Serine/threT	Signal tran	IPR007052	[CS domain] ; IPR007699[SGS domain]
ko00520	A	N-acetylgl G	Carbohydr	IPR006680	[Amidohydrolase-related]
--	--	Predicted cR	General fu	IPR002737	[MEMO1 family]
ko03018	R	--	--	IPR001163	[LSM domain, eukaryotic/archaea-type]
--	--	--	--	IPR002913	[START domain]
ko04140	A	--	--	IPR001452	[SH3 domain] ; IPR004148[BAR domain]
--	--	--	--	IPR004882	[Luc7-related]
--	--	--	--	IPR001594	[Palmitoyltransferase, DHHC domain]
ko03008	R	Ribosome J	Translatior	IPR018978	[Ribosome maturation protein SBDS, C-terr
--	--	--	--	IPR009038	[GOLD domain]
ko03040	S	RNA recogJ	Translatior	IPR000504	[RNA recognition motif domain]
ko03008	R	OligoribonA	RNA proce	IPR013520	[Exonuclease, RNase T/DNA polymerase III]
--	--	Metal-sulfuO	Posttransla	IPR002744	[Domain of unknown function DUF59]
ko04137	N	--	--	IPR028058	[Fis1, N-terminal tetratricopeptide repeat] ;
--	--	--	--	IPR000313	[PWWP domain]
ko04144	E	--	--	IPR005024	[Snf7 family]
ko03013	R	Predicted IT	Signal tran	IPR001680	[WD40 repeat]
--	--	RNA-spliciJ	Translatior	IPR001233	[tRNA-splicing ligase, RtcB]
--	--	--	--	IPR001810	[F-box domain] ; IPR021625[PI31 proteason
--	--	--	--	IPR005343	[Nucleolar complex protein 2]
--	--	--	--	IPR000225	[Armadillo]
ko03015	n	Translator J	Translatior	IPR004160	[Translation elongation factor EFTu/EF1A, C
ko00190	C	Archaeal/vC	Energy prc	IPR002490	[V-type ATPase, V0 complex, 116kDa subu
ko05166	H	--	--	IPR000403	[Phosphatidylinositol 3-/4-kinase, catalytic c
--	--	UncharactS	Function u	IPR027881	[Protein SOGA] ; IPR027882[Domain of unki
--	--	MembraneM	Cell wall/r	IPR031161	[Peptidase family M60 domain]
ko04144	E	Replicator L	Replicator	IPR000261	[EH domain] ; IPR022812[Dynamin superfan
ko04310	V	--	--	IPR010472	[Formin, FH3 domain] ; IPR010473[Formin, c
--	--	Type V secMU	Cell wall/r	IPR001627	[Sema domain] ; IPR002165[Plexin repeat] ;
ko04137	N	Ubiquitin (O	Posttransla	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko04015	R	--	--	IPR002558	[I/LWEQ domain] ; IPR015009[Vinculin-binc
--	--	Phosphoer G	Carbohydr	IPR000048	[IQ motif, EF-hand binding site] ; IPR001609
ko04014	R	Ca2+-bincT	Signal tran	IPR002048	[EF-hand domain]

ko04141 P Molecular O	Posttransla IPR013126 [Heat shock protein 70 family]
ko04136 A -- --	-- IPR005078 [Peptidase C54]
ko03460 F -- --	-- IPR019337 [Telomere length regulation protein, conser
-- -- --	-- IPR007174 [Las1-like]
-- -- --	-- IPR002867 [IBR domain]
-- O-acetyl-/J	Translatior IPR002589 [Macro domain]
-- -- --	-- IPR000421 [Coagulation factor 5/8 C-terminal domain]
-- -- --	-- IPR000859 [CUB domain] ; IPR002172[Low-density lipo
-- Lysophosph I	Lipid trans IPR000073 [Alpha/beta hydrolase fold-1]
-- Large exoç U	Intracellulæ IPR002126 [Cadherin] ; IPR013164[Cadherin, N-terminæ
-- -- --	-- IPR001578 [Peptidase C12, ubiquitin carboxyl-terminal
-- Thioestera Q	Secondary IPR000873 [AMP-dependent synthetase/ligase] ; IPR01
ko05100 B -- --	-- IPR001452 [SH3 domain]
ko00190 C Archaeal/v C	Energy prc IPR002699 [ATPase, V1 complex, subunit D]
-- -- --	-- IPR013598 [Exportin-1/Importin-beta-like]
ko03060 P -- --	-- IPR019009 [Signal recognition particle receptor, beta si
-- -- --	-- IPR013106 [Immunoglobulin V-set domain]
-- -- --	-- IPR001849 [Pleckstrin homology domain] ; IPR002913[
ko00051 F NDP-suga JM	Translatior IPR001451 [Hexapeptide repeat] ; IPR005835[Nucleotic
-- -- --	-- IPR019136 [Transcription factor IIIC, subunit 5]
-- Predicted (O	Posttransla IPR019734 [Tetratricopeptide repeat]
-- -- --	-- IPR007233 [Trafficking protein particle complex subuni
-- Serine/thrç T	Signal tran IPR000719 [Protein kinase domain] ; IPR001180[Citron
ko03013 R RNA recog J	Translatior IPR000504 [RNA recognition motif domain]
-- -- --	-- IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
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]
-- DNA gyras L	Replicatior IPR006917 [SOUL haem-binding protein]
-- tRNA U38, J	Translatior IPR020097 [Pseudouridine synthase I, TruA, alpha/beta
-- -- --	-- IPR015425 [Formin, FH2 domain]
ko04142 L Cysteine p O	Posttransla IPR000668 [Peptidase C1A, papain C-terminal]
ko00260 G Phosphose HE	Coenzyme IPR000192 [Aminotransferase class V domain]
ko04514 C -- --	-- IPR013151 [Immunoglobulin]
-- -- --	-- IPR002048 [EF-hand domain]
-- -- --	-- --
-- -- --	-- IPR001881 [EGF-like calcium-binding domain] ; IPR026
ko04530 T -- --	-- IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
-- -- --	-- IPR000203 [GPS motif] ; IPR000832[GPCR, family 2, sec
-- -- --	-- IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
ko04144 E Guanine-n R	General fu IPR000904 [Sec7 domain] ; IPR015403[Sec7, C-termina
-- Serine/thrç T	Signal tran IPR000719 [Protein kinase domain]
ko04340 H Periplasmi U	Intracellulæ IPR000719 [Protein kinase domain] ; IPR022247[Casein
ko04978 N Co/Zn/Cd P	Inorganic i IPR002524 [Cation efflux protein]
-- -- --	-- IPR011531 [Bicarbonate transporter, C-terminal] ; IPR0
ko04520 A -- --	-- IPR003124 [WH2 domain]
-- -- --	-- IPR001660 [Sterile alpha motif domain] ; IPR004177[DC
ko04145 P Ca2+ -binc Q	Secondary IPR002035 [von Willebrand factor, type A] ; IPR013517[
ko04151 P Cytolysin, ç U	Intracellulæ IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
ko04150 n Glycosidas G	Carbohydr IPR006047 [Glycosyl hydrolase, family 13, catalytic dom
ko04022 c Magnesiur P	Inorganic i IPR004014 [Cation-transporting P-type ATPase, N-terr
ko04066 H Predicted ç G	Carbohydr IPR005828 [Major facilitator, sugar transporter-like]
ko05034 A -- --	-- --
ko05100 B Predicted (R	General fu IPR030379 [Septin-type guanine nucleotide-binding (C
ko05130 P RNA recog J	Translatior IPR000504 [RNA recognition motif domain]
ko04974 P Autotransç UW	Intracellulæ IPR008160 [Collagen triple helix repeat] ; IPR010363[Dc
ko04520 A Serine/thrç T	Signal tran IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
ko04217 N -- --	-- IPR007125 [Histone H2A/H2B/H3] ; IPR032454[Histone

ko04810 R -- --	-- IPR019137 [Nck-associated protein 1]
-- -- --	-- IPR018502 [Annexin repeat]
ko04014 R GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko05034 A -- --	-- IPR007125 [Histone H2A/H2B/H3]
ko03050 P -- --	-- IPR003185 [Proteasome activator pa28, N-terminal domain]
ko04015 R Secreted pR	General fu IPR002369 [Integrin beta subunit, VWA domain] ; IPR000808
ko03013 R -- --	-- IPR008081 [Cytoplasmic FMR1-interacting] ; IPR009828
ko04530 T -- --	-- IPR011259 [Ezrin/radixin/moesin, C-terminal] ; IPR0189
-- -- --	-- IPR002259 [Equilibrative nucleoside transporter]
ko04144 E -- --	-- IPR004328 [BRO1 domain] ; IPR025304[ALIX V-shaped domain]
-- -- --	-- --
-- -- --	-- IPR018499 [Tetraspanin/Peripherin]
-- -- --	-- --
ko05034 A -- --	-- IPR007125 [Histone H2A/H2B/H3]
-- Xaa-Pro arE	Amino acid IPR000994 [Peptidase M24] ; IPR007865[Aminopeptidase]
ko03040 S RNA recogJ	Translation IPR000504 [RNA recognition motif domain]
ko04015 R -- --	-- IPR005455 [Profilin]
ko00565 E LysophosphE	Amino acid IPR013830 [SGNH hydrolase-type esterase domain]
ko04151 P Cytolysin, iU	Intracellular IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha]
ko04360 A -- --	-- IPR002108 [Actin-depolymerising factor homology domain]
ko03040 S Molecular O	Posttranslational IPR013126 [Heat shock protein 70 family]
ko04146 P Cu/Zn sup P	Inorganic i IPR001424 [Superoxide dismutase, copper/zinc binding domain]
-- -- --	-- IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IPR000971
-- -- --	-- IPR000971 [Globin]
-- Dipeptidyl E	Amino acid IPR001375 [Peptidase S9, prolyl oligopeptidase, catalytic domain]
-- -- --	-- IPR022734 [Apolipoprotein M]
ko04142 L -- --	-- IPR000479 [Cation-independent mannose-6-phosphatase]
ko00515 N -- --	-- --
-- RNA recogJ	Translation IPR000504 [RNA recognition motif domain]
ko05010 A -- --	-- IPR003388 [Reticulon]
-- -- --	-- IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-terminal domain]
ko04010 N PASTA domM	Cell wall/m IPR001245 [Serine-threonine/tyrosine-protein kinase catalytic domain]
-- UncharacterR	General fu IPR001599 [Alpha-2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin]
ko04610 C -- --	-- IPR000294 [Gamma-carboxyglutamic acid-rich (GLA) domain]
ko04010 N -- --	-- IPR013576 [Insulin-like growth factor II E-peptide, C-terminal domain]
-- -- --	-- IPR002048 [EF-hand domain]
ko00030 P Sugar lactG	Carbohydr IPR013658 [SMP-30/Gluconolactonase/LRE-like region]
ko00512 N GlycosyltraG	Carbohydr IPR027791 [Galactosyltransferase, C-terminal] ; IPR027791
ko04974 P Autotransp UW	Intracellular IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160[C-terminal domain]
-- UncharacterR	General fu IPR001304 [C-type lectin-like]
ko00511 C Alpha-marG	Carbohydr IPR000602 [Glycoside hydrolase family 38, N-terminal domain]
ko03320 P -- --	-- IPR008403 [Apolipoprotein CIII]
ko00310 L GlycosyltraM	Cell wall/m IPR005123 [Oxoglutarate/iron-dependent dioxygenase]
ko05010 A -- --	-- IPR003388 [Reticulon]
-- -- --	-- IPR013766 [Thioredoxin domain] ; IPR017905[ERV/ALR domain]
-- Secreted pR	General fu IPR002035 [von Willebrand factor, type A] ; IPR010600[von Willebrand factor, type A]
ko01522 E Ankyrin rejT	Signal tran IPR000742 [EGF-like domain] ; IPR000800[Notch domain]
ko04151 P Transcripti K	Transcripti IPR002035 [von Willebrand factor, type A] ; IPR002223[von Willebrand factor, type A]
-- Secreted pR	General fu IPR002035 [von Willebrand factor, type A] ; IPR010600[von Willebrand factor, type A]
ko00350 T 2-keto-4-Q	Secondary IPR011234 [Fumarylacetoacetase, C-terminal-related]
-- UncharacterR	General fu IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IPR000436
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain] ; IPR000884[Thrombospondin type-1 (TSP1) repeat]
ko04144 E AAA+-typ MDT	Cell wall/m IPR003959 [ATPase, AAA-type, core] ; IPR007330[MIT domain]
ko04610 C Serine pro:O	Posttranslational IPR023796 [Serpine domain]
ko04918 T Serine pro:O	Posttranslational IPR023796 [Serpine domain]
-- Secreted pR	General fu IPR002035 [von Willebrand factor, type A] ; IPR010600[von Willebrand factor, type A]
ko00010 G Pyruvate/2 C	Energy proc IPR005475 [Transketolase-like, pyrimidine-binding domain]
ko04151 P Autotransp UW	Intracellular IPR002035 [von Willebrand factor, type A] ; IPR008160[C-terminal domain]

ko00260 G Methionine E	Amino acid IPR003726 [Homocysteine-binding domain]
ko04310 V Serine protease O	Posttranslational IPR023796 [Serpine domain]
ko03050 P -- --	-- IPR000717 [Proteasome component (PCI) domain]
ko04514 C Uncharacterized S	Function unknown IPR003961 [Fibronectin type III] ; IPR013098 [Immunoglobulin V-set domain]
-- -- --	-- IPR013106 [Immunoglobulin V-set domain]
ko03040 S Peptidyl-pyrophosphate O	Posttranslational IPR000504 [RNA recognition motif domain] ; IPR002131
-- Secreted periplasmic R	General function IPR002035 [von Willebrand factor, type A] ; IPR010600 [
-- -- --	-- IPR007110 [Immunoglobulin-like domain] ; IPR013106 [
ko04514 C -- --	-- IPR013106 [Immunoglobulin V-set domain] ; IPR01316
ko04145 P Ca ²⁺ -binding Q	Secondary IPR000562 [Fibronectin, type II, collagen-binding] ; IPR
ko00500 S Glycosylase G	Carbohydrate IPR006047 [Glycosyl hydrolase, family 13, catalytic dom
-- Leucine-rich K	Transcript IPR000372 [Leucine-rich repeat N-terminal domain] ; I
-- Serine protease O	Posttranslational IPR023796 [Serpine domain]
-- -- --	-- IPR001791 [Laminin G domain]
ko04979 C -- --	-- IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
-- Secreted transmembrane O	Posttranslational IPR000001 [Kringle] ; IPR001254 [Serine proteases, tryps
-- Uncharacterized R	General function IPR000782 [FAS1 domain]
ko04141 P Negative charge O	Posttranslational IPR013766 [Thioredoxin domain]
-- Bacterial lipoprotein M	Cell wall/membrane IPR000566 [Lipocalin/cytosolic fatty-acid binding dom
ko04072 P -- --	-- IPR000375 [Dynamin central domain] ; IPR001849 [Pleck
-- Uncharacterized R	General function IPR008914 [Phosphatidylethanolamine-binding protei
ko04970 S -- --	-- IPR000010 [Cystatin domain]
-- Methionine J	Translational IPR000994 [Peptidase M24]
ko04010 M -- --	-- IPR000157 [Toll/interleukin-1 receptor homology (TIR)
ko04610 C Uncharacterized R	General function IPR000020 [Anaphylatoxin/fibulin] ; IPR001599 [Alpha-2
-- -- --	-- IPR003112 [Olfactomedin-like domain]
ko00565 E Predicted J R	General function IPR001212 [Somatomedin B domain] ; IPR001604 [DNA
ko04010 M Serine/threonine T	Signal transduction IPR000270 [PB1 domain] ; IPR000719 [Protein kinase dc
-- DNA helicase K	Transcript IPR010339 [TIP49, C-terminal]
-- Spore coat M	Cell wall/membrane IPR001304 [C-type lectin-like]
-- -- --	-- IPR019382 [Translation initiation factor 3 complex subu
ko04310 V DNA helicase K	Transcript IPR010339 [TIP49, C-terminal]
-- Dipeptidyl E	Amino acid IPR001375 [Peptidase S9, prolyl oligopeptidase, catalyt
-- -- --	-- IPR008605 [Extracellular matrix protein 1]
ko04360 A -- --	-- IPR002108 [Actin-depolymerising factor homology do
ko00260 G Cu ²⁺ -concentrating Q	Secondary IPR015798 [Copper amine oxidase, C-terminal] ; IPR01
ko04610 C -- --	-- IPR001102 [Transglutaminase, N-terminal] ; IPR002931
-- Uncharacterized S	Function unknown IPR002499 [Major vault protein, N-terminal] ; IPR02187
-- Uncharacterized R	General function IPR000782 [FAS1 domain]
ko04151 P Autotransporter UW	Intracellular IPR008160 [Collagen triple helix repeat]
-- -- --	-- IPR011511 [Variant SH3 domain]
-- Transcript K	Transcript IPR000980 [SH2 domain] ; IPR003029 [S1 domain] ; IPR
ko04610 C Serine protease O	Posttranslational IPR023796 [Serpine domain]
ko03040 S RNA recogni J	Translational IPR000504 [RNA recognition motif domain]
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain]
-- -- --	-- IPR007477 [SAB domain] ; IPR008379 [Band 4.1, C-term
-- Uncharacterized P	Inorganic ion IPR004323 [Divalent ion tolerance protein, CutA]
ko00310 L Glycosyltransferase M	Cell wall/membrane IPR005123 [Oxoglutarate/iron-dependent dioxygenase
ko03320 P -- --	-- IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko03050 P 20S proteasome O	Posttranslational IPR001353 [Proteasome, subunit alpha/beta]
ko03010 R Ribosomal J	Translational IPR016180 [Ribosomal protein L10e/L16]
-- Ca ²⁺ -binding T	Signal transduction IPR002048 [EF-hand domain]
-- -- --	-- --
ko04145 P Alpha-tubulin DZ	Cell cycle control IPR001881 [EGF-like calcium-binding domain] ; IPR003
-- Plastocyanin C	Energy processing IPR019316 [G8 domain] ; IPR025155 [WxxW domain]
-- -- --	-- IPR000436 [Sushi/SCR/CCP domain] ; IPR003410 [HYR c
-- -- --	-- IPR014760 [Serum albumin, N-terminal] ; IPR015247 [Vi
-- Large exon U	Intracellular IPR000233 [Cadherin, cytoplasmic domain] ; IPR002126

ko04145 P Uncharacterized R	General function IPR000020 [Anaphylatoxin/fibulin] ; IPR001599[Alpha-2
-- Uncharacterized S	Function IPR001664 [Intermediate filament protein] ; IPR032444[
ko04979 C -- --	-- IPR000074 [Apolipoprotein A/E]
ko03320 P Predicted iO	Posttranslational IPR001818 [Peptidase M10, metallopeptidase] ; IPR002
ko04151 P Secreted pR	General function IPR001007 [VWFC domain] ; IPR001846[von Willebrand
ko04610 C Secreted trO	Posttranslational IPR000436 [Sushi/SCR/CCP domain] ; IPR000859[CUB c
ko03008 R -- --	-- IPR012954 [BP28, C-terminal domain] ; IPR022125[U3 s
-- -- --	-- IPR000971 [Globin]
-- Regulatory O	Posttranslational IPR000421 [Coagulation factor 5/8 C-terminal domain]
-- -- --	-- IPR001664 [Intermediate filament protein] ; IPR032444[
ko04151 P Uncharacterized S	Function IPR002049 [Laminin EGF domain] ; IPR008211[Laminin,
ko04975 F PPE-repeat S	Function IPR001747 [Lipid transport protein, N-terminal] ; IPR00
-- Chromosome D	Cell cycle IPR001073 [C1q domain] ; IPR008160[Collagen triple helix
-- -- --	-- IPR000566 [Lipocalin/cytosolic fatty-acid binding dom
-- Serine protease O	Posttranslational IPR023796 [Serp domain]
-- -- --	-- IPR000859 [CUB domain] ; IPR018933[Netrin module, r
ko03010 R -- --	-- IPR000509 [Ribosomal protein L36e]
-- -- --	-- IPR001881 [EGF-like calcium-binding domain] ; IPR026
-- -- --	-- --
-- -- --	-- IPR001664 [Intermediate filament protein]
ko04015 R -- --	-- IPR002558 [I/LWEQ domain] ; IPR015009[Vinculin-binc
ko04611 P Autotransport UW	Intracellular IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[\
-- -- --	-- IPR003597 [Immunoglobulin C1-set]
-- -- --	-- IPR000867 [Insulin-like growth factor-binding protein,
ko04970 S -- --	-- IPR000859 [CUB domain] ; IPR001190[SrcR domain] ; I
-- -- --	-- IPR001190 [SrcR domain] ; IPR001695[Lysyl oxidase]
ko04151 P Methyl-accepting NT	Cell motility IPR000034 [Laminin IV] ; IPR002049[Laminin EGF doma
peptidase i -- --	-- IPR001820 [Protease inhibitor I35 (TIMP)]
ko04974 P Cell division D	Cell cycle IPR002035 [von Willebrand factor, type A] ; IPR003961[
-- -- --	-- --
-- Outer membrane M	Cell wall/membrane IPR000436 [Sushi/SCR/CCP domain] ; IPR003410[HYR c
-- Spore coat M	Cell wall/membrane IPR000436 [Sushi/SCR/CCP domain] ; IPR000538[Link c
-- Glucose/arabinose G	Carbohydrate IPR000033 [LDLR class B repeat] ; IPR000716[Thyroglob
ko04015 R Alpha-tubulin DZ	Cell cycle IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IF
ko04145 P Alpha-tubulin DZ	Cell cycle IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IF
ko04974 P Autotransport UW	Intracellular IPR008160 [Collagen triple helix repeat] ; IPR010515[Cc
ko04151 P Autotransport UW	Intracellular IPR002035 [von Willebrand factor, type A] ; IPR008160[
-- Sugar lactose G	Carbohydrate IPR018119 [Strictosidine synthase, conserved region]
ko04151 P Phage-related X	Mobilome IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko04670 L -- --	-- IPR013151 [Immunoglobulin]
ko04151 P Phage-related X	Mobilome IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
-- -- --	-- IPR000867 [Insulin-like growth factor-binding protein,
ko04350 T -- --	-- IPR001111 [Transforming growth factor-beta, N-termi
-- Outer membrane M	Cell wall/membrane IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IF
ko04144 E Ankyrin repeat T	Signal transduction IPR001164 [Arf GTPase activating protein] ; IPR013724[
ko04512 E Outer membrane M	Cell wall/membrane IPR000034 [Laminin IV] ; IPR000742[EGF-like domain] ;
ko04610 C -- --	-- IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko04974 P Autotransport UW	Intracellular IPR000885 [Fibrillar collagen, C-terminal] ; IPR001791[L
-- Leucine-rich K	Transcript IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04080 N Secreted trO	Posttranslational IPR000001 [Kringle] ; IPR001254[Serine proteases, tryp
ko00230 P Glutamine F	Nucleotide IPR000836 [Phosphoribosyltransferase domain]
-- -- --	-- IPR004978 [Stanniocalcin]
-- -- --	-- IPR003961 [Fibronectin type III]
-- -- --	-- IPR001452 [SH3 domain] ; IPR001683[Phox homologou
-- -- --	-- IPR024110 [Immunoglobulin J chain]
ko04514 C Spore coat M	Cell wall/membrane IPR000436 [Sushi/SCR/CCP domain] ; IPR000538[Link c
ko04918 T -- --	-- IPR014760 [Serum albumin, N-terminal]
ko03320 P -- --	-- IPR000536 [Nuclear hormone receptor, ligand-binding

--	--	--	--	IPR001695 [Lysyl oxidase]
--	Autotransf	U	Intracellular	IPR001759 [Pentraxin-related]
--	Magnesium	P	Inorganic	IPR008250 [P-type ATPase, A domain] ; IPR032630[P-1
ko04066	H	Serine protease	Posttranslational	IPR023796 [Serpine domain]
--	--	--	--	IPR001863 [Glypican]
ko04151	P	Autotransf	Intracellular	IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[\
--	--	--	--	IPR000010 [Cystatin domain]
ko04151	P	Autotransf	Intracellular	IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160[(
--	Glutathione	O	Posttranslational	--
ko01522	E	Predicted	Posttranslational	IPR000562 [Fibronectin, type II, collagen-binding] ; IPR
ko01521	E	--	--	IPR003574 [Interleukin-6]
ko04151	P	Phage-related	Mobilome	IPR000083 [Fibronectin, type I] ; IPR000562[Fibronectin
--	--	--	--	IPR003307 [W2 domain]
ko04145	P	--	--	IPR022780 [Dynein family light intermediate chain]
ko04151	P	Methyl-accepting	Cell motility	IPR001791 [Laminin G domain] ; IPR002049[Laminin EC
ko04151	P	Autotransf	Intracellular	IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[\
--	--	--	--	IPR015403 [Sec7, C-terminal] ; IPR032629[Mon2, dimer
ko04115	p	--	--	IPR000716 [Thyroglobulin type-1] ; IPR000867[Insulin-
	Superfamily	L	Replicator	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DI

IPR001590[Peptidase M12B, ADAM/reprolysin] ; IPR002870[Peptidase M12B, propeptide] ; IPR010294

terminal] ; IPR024557[CCR4-Not complex, Not1 subunit, domain of unknown function DUF3819] ; IP

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

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

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

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

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

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

domain] ; 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, dc

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

:ratricopeptide-like helical domain] ; IPR019734[Tetratricopeptide repeat] ; IPR029489[O-GlcNAc tr

domain] ; IPR003961[Fibronectin type III] ; IPR006574[SPRY-associated] ; IPR027370[RING-type zinc

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

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

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 unknow

1650[Helicase, C-terminal] ; IPR015194[ISWI, HAND domain] ; IPR015195[SLIDE domain] ; IPR020838

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

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

ninal homology (ANTH) domain] ; IPR032422[Huntingtin-interacting protein 1, clathrin-binding do

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

3[Formyl transferase, C-terminal] ; IPR009081[Phosphopantetheine binding ACP domain] ; IPR01556

rotein kinase domain] ; IPR001251[CRAL-TRIO lipid binding domain] ; IPR001452[SH3 domain] ; IPF

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

rin homology domain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding dom

i[Sec23/Sec24, trunk domain] ; IPR006900[Sec23/Sec24, helical domain] ; IPR007123[Gelsolin-like d
putative phosphate] ; IPR027815[10TM putative phosphate transporter, cytosolic domain] ; IPR0328
leckstrin homology domain] ; IPR014847[FERM adjacent (FA)] ; IPR018979[FERM, N-terminal] ; IPR0
-terminal] ; IPR003164[Clathrin adaptor, alpha-adaptin, appendage, C-terminal subdomain] ; IPR0
binding protein/Hyperplastic disc protein] ; IPR024725[E3 ubiquitin ligase EDD, ubiquitin-associate
R025614[Cell morphogenesis protein N-terminal] ; IPR029473[Cell morphogenesis central region]

ology domain] ; IPR004182[GRAM domain] ; IPR005113[uDENN domain] ; IPR010569[Myotubularin

retin-like] ; IPR000922[D-galactoside/L-rhamnose binding SUEL lectin domain] ; IPR001879[GPCR, ·
56[RNA polymerase Rpb1, domain 3] ; IPR007080[RNA polymerase Rpb1, domain 1] ; IPR007081[RN

CC1] ; IPR000433[Zinc finger, ZZ-type] ; IPR000569[HECT domain] ; IPR001199[Cytochrome b5-like

hydrogenase, C-terminal] ; IPR006097[Glutamate/phenylalanine/leucine/valine dehydrogenase, dir

calcium-binding domain] ; IPR002172[Low-density lipoprotein (LDL) receptor class A repeat]
reonine/tyrosine-protein kinase catalytic domain] ; IPR006211[Furin-like cysteine-rich domain] ; IPR0

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

IPR002172[Low-density lipoprotein (LDL) receptor class A repeat] ; IPR020864[Membrane attack com
atalytic domain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding domain] ; I
α-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding] ; IPR011625[

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

12896[Integrin beta subunit, tail] ; IPR014836[Integrin beta subunit, cytoplasmic domain] ; IPR03376

nain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding domain] ; IPR017892[I
rminal globular domain] ; IPR012290[Fibrinogen, alpha/beta/gamma chain, coiled coil domain]

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

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

ise, NAD(P) binding domain] ; IPR020829[Glyceraldehyde 3-phosphate dehydrogenase, catalytic dc
atalytic domain] ; IPR001627[Sema domain] ; IPR002165[Plexin repeat] ; IPR002909[IPT domain]

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

3P-type] ; IPR004102[Poly(ADP-ribose) polymerase, regulatory domain] ; IPR008893[WGR domain] ;

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

atalytic domain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding domain] ; I

oacid dehydrogenase acyltransferase, catalytic domain] ; IPR004167[E3-binding domain]

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

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

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

-phosphate receptor binding domain] ; IPR028146[Glucosidase II beta subunit, N-terminal]

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

33644[Na-Ca exchanger/integrin-beta4] ; IPR003961[Fibronectin type III] ; IPR012896[Integrin beta

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

nain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding domain] ; IPR017892[I

IPR012309[DNA ligase, ATP-dependent, C-terminal] ; IPR012310[DNA ligase, ATP-dependent, cen

] ; IPR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001828[Receptor, lig

001452[SH3 domain] ; IPR001849[Pleckstrin homology domain] ; IPR001936[Ras GTPase-activating

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

.D-dependent, C-terminal] ; IPR011128[Glycerol-3-phosphate dehydrogenase, NAD-dependent, N

3[AIR synthase-related protein, C-terminal domain] ; IPR016188[PurM-like, N-terminal domain] ; IP
n] ; IPR004161[Translation elongation factor EFTu-like, domain 2] ; IPR005517[Translation elongatic

/RNA non-specific endonuclease] ; IPR002591[Type I phosphodiesterase/nucleotide pyrophosphatase
IPR014741[Adaptor protein Cbl, EF hand-like] ; IPR014742[Adaptor protein Cbl, SH2-like domain] ; I

ription elongation factor S-II, central domain] ; IPR017923[Transcription factor IIS, N-terminal]

ulin type-1] ; IPR001881[EGF-like calcium-binding domain] ; IPR003886[NIDO domain] ; IPR006601

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

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

subunit, nucleotide-binding domain] ; IPR000793[ATP synthase, alpha subunit, C-terminal] ; IPR004101
; IPR002857[Zinc finger, CXXC-type] ; IPR010506[DMAP1-binding domain] ; IPR022702[DNA (cytosine)

S/T)] ; IPR004095[TGS] ; IPR004154[Anticodon-binding] ; IPR012947[Threonyl/alanine tRNA synthetase

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

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

IPR002048[EF-hand domain] ; IPR022682[Peptidase C2, calpain, large subunit, domain III]

IPR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha motif

sterile alpha subunit, guanine nucleotide exchange domain] ; IPR018940[Elongation factor 1 beta central acidic

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

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

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

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

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

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

IPR003605[GS domain] ; IPR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR003605[GS domain]
terminal] ; IPR005144[ATP-cone domain] ; IPR013509[Ribonucleotide reductase large subunit, N-terminal] ; IPR005144[ATP-cone domain] ; IPR013509[Ribonucleotide reductase large subunit, N-terminal] ; IPR002049[Laminin EGF domain] ; IPR008211[Laminin, N-terminal] ; IPR009254[Laminin alpha, dc

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

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

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

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

homology domain] ; IPR002017[Spectrin repeat] ; IPR015153[EF-hand domain, type 1] ; IPR015154

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

1 licensing factor Mcm2] ; IPR027925[MCM N-terminal domain] ; IPR033762[MCM OB domain]
domain] ; IPR009075[Acyl-CoA dehydrogenase/oxidase C-terminal] ; IPR013786[Acyl-CoA dehydr

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

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

known function DUF1088] ; IPR023362[PH-BEACH domain] ; IPR031570[Domain of unknown function
agenet-like domain] ; IPR022034[Fragile X-related 1 protein, C-terminal core] ; IPR032172[Fragile X
] ; IPR005844[Alpha-D-phosphohexomutase, alpha/beta/alpha domain I] ; IPR005845[Alpha-D-phospho-
ol-specific phospholipase C, X domain] ; IPR001711[Phospholipase C, phosphatidylinositol-specific
L487[Bromodomain] ; IPR001650[Helicase, C-terminal] ; IPR006576[BRK domain] ; IPR014012[Helica

h repair protein MutS, C-terminal] ; IPR007695[DNA mismatch repair protein MutS-like, N-terminal

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

IPR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha motif]
IPR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha motif]

IPR013612[Amino acid permease, N-terminal] ; IPR018491[SLC12A transporter, C-terminal]

Forkhead-associated (FHA) domain] ; IPR001478[PDZ domain] ; IPR002710[Dilute domain]

dehydrogenase, catalytic domain] ; IPR006140[D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding site]

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

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

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

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]

750[GHMP kinase, C-terminal domain] ; IPR019539[Galactokinase galactose-binding domain]

calcium-binding domain] ; IPR002172[Low-density lipoprotein (LDL) receptor class A repeat]
ninal] ; IPR006068[Cation-transporting P-type ATPase, C-terminal] ; IPR008250[P-type ATPase, A c

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

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

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

9[ATPase, AAA-type, core] ; IPR004201[CDC48, domain 2] ; IPR015415[Vps4 oligomerisation, C-ter
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

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

; IPR011178[Amyloidogenic glycoprotein, copper-binding] ; IPR015849[Amyloidogenic glycoprotei

IPR008145[Guanylate kinase/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain]
tratricopeptide repeat] ; IPR025986[RNA-polymerase II-associated protein 3-like, C-terminal domai

as-like guanine nucleotide exchange factor, N-terminal] ; IPR001849[Pleckstrin homology domain]

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

rg domain] ; IPR032878[Vacuole morphology and inheritance protein 14, Fab1-binding region]

PR023753[FAD/NAD(P)-binding domain] ; IPR028261[Dihydropyrimidine dehydrogenase domain II]

3[PDZ domain] ; IPR018979[FERM, N-terminal] ; IPR018980[FERM, C-terminal PH-like domain] ; IPR

v] ; IPR013843[Ribosomal protein S4e, N-terminal] ; IPR013845[Ribosomal protein S4e, central region, C3HC4 RING-type] ; IPR032070[TNF receptor-associated factor, BIRC3 binding domain]

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

ating protein domain] ; IPR000219[Dbl homology (DH) domain] ; IPR001849[Pleckstrin homology domain]

amoyl attachment] ; IPR005479[Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain, N-terminal] ; IPR008152[Clathrin adaptor, alpha/beta/gamma-adaptin, appendage, Ig-like subdomain]

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

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

domain] ; IPR001005[SANT/Myb domain] ; IPR001025[Bromo adjacent homology (BAH) domain]
ospholipase D/Transphosphatidylase] ; IPR001849[Pleckstrin homology domain] ; IPR025202[Phosp

1762[Disintegrin domain] ; IPR002870[Peptidase M12B, propeptide] ; IPR006586[ADAM, cysteine-ri
1762[Disintegrin domain] ; IPR002870[Peptidase M12B, propeptide] ; IPR006586[ADAM, cysteine-ri
][Ras-associating (RA) domain] ; IPR000198[Rho GTPase-activating protein domain] ; IPR001609[M

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

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

[Pancreatic trypsin inhibitor Kunitz domain] ; IPR003961[Fibronectin type III] ; IPR008160[Collagen tr

IPR000562[Fibronectin, type II, collagen-binding] ; IPR000742[EGF-like domain] ; IPR001254[Serine p

calponin homology domain] ; IPR001849[Pleckstrin homology domain] ; IPR011511[Variant SH3 dor

α/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain] ; IPR014775[L27 domain, C
cytokinesis, C-terminal] ; IPR027007[DHR-1 domain] ; IPR032376[Dedicator of cytokinesis, N-terminal c

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

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

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

L650[Helicase, C-terminal] ; IPR009462[Domain of unknown function DUF1086] ; IPR009463[Domain

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

H3 domain] ; IPR001715[Calponin homology domain] ; IPR001849[Pleckstrin homology domain] ; If

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

i[Sec23/Sec24, trunk domain] ; IPR006900[Sec23/Sec24, helical domain] ; IPR007123[Gelsolin-like d

3AH box helicase domain] ; IPR012961[ATP-dependent RNA helicase Ski2, C-terminal] ; IPR025696[

ide-disulphide oxidoreductase, dimerisation domain] ; IPR023753[FAD/NAD(P)-binding domain]

028282[WASH complex subunit 7, central domain] ; IPR028283[WASH complex subunit 7, C-termi

.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

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

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

2019585[26S proteasome regulatory subunit Rpn7/COP9 signalosome complex subunit 1]

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

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

R, N-terminal domain] ; IPR029259[Rapamycin-insensitive companion of mTOR, phosphorylation-s

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

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

-binding domain] ; IPR002049[Laminin EGF domain] ; IPR002165[Plexin repeat] ; IPR024731[EGF do

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

3[Formyl transferase, C-terminal] ; IPR009081[Phosphopantetheine binding ACP domain] ; IPR01556

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

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

din type-1 (TSP1) repeat] ; IPR000906[ZU5 domain] ; IPR013098[Immunoglobulin I-set] ; IPR033772

;/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain] ; IPR014775[L27 domain, C
ninal] ; IPR031436[Transmembrane protein TMEM132, C-terminal] ; IPR031437[Transmembrane pro

hydrolase] ; IPR002048[EF-hand domain] ; IPR006615[Peptidase C19, ubiquitin-specific peptidase,

; IPR021726[THO complex, subunitTHOC2, N-terminal] ; IPR032302[THO complex subunit 2, N-terminal
processome, Utp21] ; IPR024977[Anaphase-promoting complex subunit 4, WD40 domain]

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

or, N-terminal] ; IPR001895[Ras guanine-nucleotide exchange factors catalytic domain] ; IPR002048
own function DUF622] ; IPR008145[Guanylate kinase/L-type calcium channel beta subunit]

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

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

ngy domain] ; IPR001781[Zinc finger, LIM-type] ; IPR031865[Domain of unknown function DUF4757

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

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

hydrolase] ; IPR002083[MATH/TRAF domain] ; IPR024729[Ubiquitin carboxyl-terminal hydrolase 7,

rotein, N-terminal] ; IPR025939[Axin interactor dorsalization-associated protein, C-terminal domain

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

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

ation factor, beta propellor-like domain] ; IPR024977[Anaphase-promoting complex subunit 4, WD

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

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

1762[Disintegrin domain] ; IPR002870[Peptidase M12B, propeptide] ; IPR006586[ADAM, cysteine-ri

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

ptidase, N-terminal] ; IPR015211[Peptidase M1, leukotriene A4 hydrolase/aminopeptidase C-terminal] ; IPR014847[FERM adjacent (FA)] ; IPR018979[FERM, N-terminal] ; IPR018980[FERM, C-terminal]

ninal] ; IPR006068[Cation-transporting P-type ATPase, C-terminal] ; IPR006544[P-type ATPase, subunit]

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

] [Ras-associating (RA) domain] ; IPR000857[MyTH4 domain] ; IPR001609[Myosin head, motor domain]
porter type 1, transmembrane domain] ; IPR032410[Mitochondrial ABC-transporter, N-terminal fi

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

]032[EGF-like, conserved site] ; IPR017878[TB domain] ; IPR026823[Complement C1r-like EGF domai

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

MN-binding domain] ; IPR019576[Pyridoxine 5'-phosphate oxidase, dimerisation, C-terminal]

domain] ; IPR001881[EGF-like calcium-binding domain] ; IPR002172[Low-density lipoprotein (LDL) i

;/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain] ; IPR014775[L27 domain, C

dependent metallo-hydrolase, RNA specificity domain] ; IPR022712[Beta-Casp domain] ; IPR025069

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

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

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

PR033411[Ribonuclease, PIN domain] ; IPR033461[Putative WW-binding domain and destruction b

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

rocessome, Utp12] ; IPR024977[Anaphase-promoting complex subunit 4, WD40 domain]

logy domain] ; IPR002017[Spectrin repeat] ; IPR002048[EF-hand domain] ; IPR003108[Gas2-related

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

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

hydrolase] ; IPR006615[Peptidase C19, ubiquitin-specific peptidase, DUSP domain] ; IPR028135[Ub
ling site-containing domain] ; IPR015224[Talin, central] ; IPR018979[FERM, N-terminal] ; IPR019748

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

homology (CNH) domain] ; IPR002219[Protein kinase C-like, phorbol ester/diacylglycerol-binding c
l-terminal] ; IPR013040[Coatomer, gamma subunit, appendage, Ig-like subdomain] ; IPR032154[Co:

l-terminal] ; IPR013040[Coatomer, gamma subunit, appendage, Ig-like subdomain] ; IPR032154[Co:
l] ; IPR032629[Mon2, dimerisation and cyclophilin-binding domain] ; IPR032691[Guanine nucleotide

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

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

12896[Integrin beta subunit, tail] ; IPR013111[EGF-like domain, extracellular] ; IPR014836[Integrin beta subunit, tail] ; IPR018980[FERM, C-terminal PH-like domain] ; IPR019748[FERM central domain]

alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding] ; IPR011625[alpha-2-macroglobulin, N-terminal] ; IPR000742[EGF-like domain] ; IPR001791[Laminin G domain] ; IPR001881[EGF-like calcium-binding domain]

domain] ; IPR011682[Glycosyl hydrolase family 38, C-terminal] ; IPR015341[Glycoside hydrolase family 38, C-terminal]

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

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

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

2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobu
/RNA non-specific endonuclease] ; IPR002591[Type I phosphodiesterase/nucleotide pyrophosphat:

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

327999[Death-like domain of Spt6] ; IPR028083[Spt6 acidic, N-terminal domain] ; IPR028088[Helix-

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

3367[Thrombospondin, type 3-like repeat] ; IPR008859[Thrombospondin, C-terminal] ; IPR024665[T

2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin
 factor, type D domain] ; IPR002035[von Willebrand factor, type A] ; IPR002919[Trypsin Inhibitor-like
 domain] ; IPR000859[CUB domain] ; IPR000998[MAM domain] ; IPR022579[Neuropilin, C-terminal]
 9454[Lipid transport, open beta-sheet] ; IPR015255[Vitellinogen, open beta-sheet] ; IPR022176[Apoc
 binding site-containing domain] ; IPR015224[Talin, central] ; IPR018979[FERM, N-terminal] ; IPR019748
 domain] ; IPR001881[EGF-like calcium-binding domain] ; IPR003886[NIDO domain] ; IPR006601
 IPR001007[VWFC domain] ; IPR003367[Thrombospondin, type 3-like repeat] ; IPR008859[Thrombospor
 IPR001007[VWFC domain] ; IPR001881[EGF-like calcium-binding domain] ; IPR003367[Thrombospor
 domain] ; IPR003961[Fibronectin type III] ; IPR013111[EGF-like domain, extracellular
 domain] ; IPR003961[Fibronectin type III] ; IPR013111[EGF-like domain, extracellular
 IGFBP] ; IPR001007[VWFC domain] ; IPR006208[Glycoprotein hormone subunit beta, cystine knot]
 IPR001881[EGF-like calcium-binding domain] ; IPR006605[G2 nidogen/fibulin G2F] ; IPR013098[Imm
 GIT, Spa2 homology (SHD) domain] ; IPR020683[Ankyrin repeat-containing domain] ; IPR022018[A
 IPR001791[Laminin G domain] ; IPR002049[Laminin EGF domain] ; IPR002172[Low-density lipoprote
 domain] ; IPR012290[Fibrinogen, alpha/beta/gamma chain, coiled coil domain]

domain] ; IPR000742[EGF-like domain] ; IPR001304[C-type lectin-like] ; IPR013106[Immunoglobulin

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

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

R032191[CCR4-NOT transcription complex subunit 1, CAF1-binding domain] ; IPR032193[CCR4-N

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

3 domain] ; IPR001263[Phosphoinositide 3-kinase, accessory (PIK) domain] ; IPR001683[Phox homol

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

80[Calcium permeable stress-gated cation channel 1, N-terminal transmembrane domain]

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

: heme/steroid binding domain] ; IPR004939[APC10/DOC domain] ; IPR010606[Mib-herc2] ; IPR021

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

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

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

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

subunit, tail] ; IPR013111[EGF-like domain, extracellular] ; IPR033760[Integrin beta N-terminal]

5[G2 nidogen/fibulin G2F] ; IPR024731[EGF domain] ; IPR026823[Complement C1r-like EGF domain]

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

ine-5)-methyltransferase 1, replication foci domain] ; IPR029063[S-adenosyl-L-methionine-depend

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

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

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

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

osphoinositide 3-kinase, accessory (PIK) domain] ; IPR002420[Phosphatidylinositol 3-kinase, C2 do
osphoinositide 3-kinase, accessory (PIK) domain] ; IPR002420[Phosphatidylinositol 3-kinase, C2 do
nycin binding domain] ; IPR024585[Domain of unknown function DUF3385, target of rapamycin pr
if domain] ; IPR003961[Fibronectin type III] ; IPR027936[Ephrin receptor, transmembrane domain]

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

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

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

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

-related 1 protein, C-terminal region 1] ; IPR032177[Fragile X-related 1 protein, C-terminal region :
osphohexomutase, alpha/beta/alpha domain II] ; IPR005846[Alpha-D-phosphohexomutase, alpha/
; Y domain] ; IPR015359[Phosphoinositide-specific phospholipase C, EF-hand-like domain]
se/SANT-associated domain] ; IPR014978[Glutamine-Leucine-Glutamine, QLQ] ; IPR029295[Snf2, A

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

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

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

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

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

n, heparin-binding] ; IPR019543[Beta-amyloid precursor protein C-terminal] ; IPR024329[Amyloido

; IPR001895[Ras guanine-nucleotide exchange factors catalytic domain] ; IPR007125[Histone H2A/I

.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

?6823[Complement C1r-like EGF domain] ; IPR032485[Domain of unknown function DUF5050]

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 L

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

domain] ; IPR014930[Myotonic dystrophy protein kinase, coiled coil] ; IPR017892[Protein kinase, C-t

IPR019580[Pre-mRNA-processing-splicing factor 8, U6-snRNA-binding] ; IPR019581[Pre-mRNA-process

ing factor 8, U6-snRNA-binding] ; IPR029451[Rapamycin-insensitive companion of mTOR, middle domain] ; IPR029452[Rapamycin

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/

ain] ; IPR001849[Pleckstrin homology domain] ; IPR019748[FERM central domain] ; IPR031971[Unco

receptor class A repeat] ; IPR026823[Complement C1r-like EGF domain] ; IPR032485[Domain of unk

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

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

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

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

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

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

lin, receptor-binding] ; IPR011625[Alpha-2-macroglobulin, N-terminal 2] ; IPR011626[Alpha-macroglobulin, cysteine rich domain] ; IPR014853[Uncharacterised domain, cysteine-rich] ; IPR032361[von Willebrand factor type A domain]

5[G2 nidogen/fibulin G2F] ; IPR024731[EGF domain] ; IPR026823[Complement C1r-like EGF domain] ; IPR026824[Complement C1s-like EGF domain] ; IPR008859[Thrombospondin, C-terminal] ; IPR024731[EGF domain]

RF GTPase-activating protein GIT1, C-terminal] ; IPR032352[Arf GTPase-activating protein GIT1/2, C-terminal] ; IPR007110[Immunoglobulin-like domain] ; IPR013098[Immunoglobulin-like domain, type 3-like repeat] ; IPR007110[Immunoglobulin-like domain] ; IPR013098[Immunoglobulin-like domain]

OT transcription complex subunit 1, TTP binding domain] ; IPR032194[CCR4-NOT transcription con

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

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

IPR007080[RNA polymerase Rpb1, domain 1] ; IPR007081[RNA polymerase Rpb1, domain 5] ; IPR0C

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

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

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

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] ;

cin-insensitive companion of mTOR, domain 5] ; IPR029453[Rapamycin-insensitive companion of n

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

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

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

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

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

