

Protein	Description	Gene	h_143B_1	h_143B_2	h_143B_3	Osteoblast	Osteoblast	Osteoblast
A0A0A6YY	Protein TM	TMED7-TM	7993.159	8374.977	7469.542	0	0	0
A0A0B4J2	Peptidyl-p	PPIAL4C	54159.09	49421.54	47170.47	0	0	0
A2RU67	Uncharacter	KIAA1467	7393.105	7569.978	11194.29	0	0	0
A3KN83	Protein str	SBNO1	1279.061	38612.84	1348.947	0	0	0
A5YKK6	CCR4-NO	CNOT1	5659.091	6161.538	4830.499	0	0	0
A6NCE7	Microtubu	MAP1LC3E	46301.66	49457.35	50493.6	0	0	0
A6NHR9	Structural	SMCHD1	2005.118	1664.383	598.8105	0	0	0
A6NKD9	Coiled-coi	CCDC85C	4775.521	6575.546	3380.49	0	0	0
A7MBM2	Protein dis	DISP2	1857.641	2258.144	2458.747	0	0	0
A8MWD9	Putative sr	SNRPGP15	29416.54	33156.51	24874.19	42343.49	523188.7	0
B1ALY0	Protein PA	PALM2-A	32981.47	19687.77	26341.13	0	0	0
B4DGG1	Uncharacter	Uncharacter	33128.54	36413.04	32495.15	0	0	0
B4E1Z4	Uncharacter	Uncharacter	270678.5	262296.3	389110.5	4228377	5263997	1517109
B5ME19	Eukaryotic	EIF3CL	47817.4	49077.27	47513.58	128058	63098.57	104513.3
B9A064	Immunogly	IGLL5	400331.6	547239.7	193385.9	5589226	8012192	4820024
C9J1V9	HCG20432	EEF1E1-BL	11084.35	9337.505	17418.6	0	0	0
E7EVH7	Uncharacter	Uncharacter	25366.14	25269.9	23379.42	0	0	0
E9PSI1	Uncharacter	Uncharacter	26436.31	22717.94	23413.15	0	0	0
F2Z307	Protein AT	ATP6V1G2	13754.68	10619.81	12069.17	0	0	0
H3BMM5	Uncharacter	Uncharacter	6605.287	6420.453	6455.261	0	0	0
H3BU86	Protein ST	STX16-NP	16283.99	15811.5	15155.82	0	0	0
I3L0A0	HCG20447	TMEM189	247570.3	244125.7	241102.8	50509.09	0	50917.48
MOQZK8	Uncharacter	Uncharacter	25841.48	11436.78	24890.66	0	0	0
MOR2C6	Uncharacter	Uncharacter	21188.6	27654.83	19783.99	0	0	0
O00139	Kinesin-lik	KIF2A	20052.39	13921.74	18846.99	0	0	0
O00151	PDZ and L	PDLIM1	62069.79	66124.42	62069.66	76848.63	0	47939.38
O00154	Cytosolic	ACOT7	31515	59043.22	62844.92	0	0	0
O00159	Unconvent	MYO1C	492748.1	512426.1	393205.4	85332.45	0	133874.4
O00161	Synaptoso	SNAP23	281644	387292.7	376689	0	0	0
O00170	AH recept	AIP	18191.9	18666.39	19043.83	0	0	0
O00186	Syntaxin-b	STXBP3	110305.1	122633.7	105747.4	0	0	0
O00203	AP-3 com	AP3B1	9730.424	106386.2	16708.73	129934.9	18222068	3270287
O00214	Galectin-8	LGALS8	8117.868	9897.013	8515.79	0	0	0
O00220	Tumor nec	TNFRSF10	23590.62	42691.88	45223.38	0	0	0
O00231	26S protea	PSMD11	17450.16	20194.05	25352.68	85492.82	0	73611.55
O00233	26S protea	PSMD9	17982.27	17413.63	18037.73	0	0	0
O00244	Copper tra	ATOX1	22701.68	29539.88	25684.7	0	0	0
O00299	Chloride ir	CLIC1	3007079	3015737	2570873	148484.3	148296	154672.1
O00303	Eukaryotic	EIF3F	25888.85	25804.24	29065.37	68613.09	0	77429.93
O00308	NEDD4-lik	WWP2	6393.567	4527.512	8081.101	0	0	0
O00329	Phosphatic	PIK3CD	1877.708	3994.923	4450.339	0	0	0
O00391	Sulfhydryl	QSOX1	102190.7	112191.5	135421.9	1010303	1379340	784346.1
O00401	Neural Wis	WASL	263818.2	30201.01	240329.3	0	0	0
O00410	Importin-5	IPO5	55320.82	66511.67	64487.22	68267	0	46220.8
O00442	RNA 3-ter	RTCA	4930.489	6204.446	6636.592	0	0	0
O00443	Phosphatic	PIK3C2A	19825.8	16373.34	18385.19	0	0	0
O00468	Agrin	AGRN	431814.1	502798.6	469434.5	583264.7	734229.8	570367
O00469	Procollage	PLOD2	8786.131	7154.838	9761.852	195423.5	219409.1	167949.8
O00471	Exocyst co	EXOC5	46877.32	44669.63	40182.28	0	0	0
O00487	26S protea	PSMD14	45467.95	45447.12	53917.02	145536.8	0	164732.9
O00499	Myc box-c	BIN1	14756.88	15499.33	11794.2	0	0	0
O00505	Importin si	KPNA3	36249.28	36918.63	21276.03	0	0	0
O00506	Serine/thr	STK25	32328.1	32284.47	27900.79	0	0	0
O00522	Krev intera	KRIT1	9224.692	8900.951	9190.264	0	0	0
O00541	Pescadillo	PES1	3863.396	4677.577	7891.264	0	0	0
O00560	Syntenin-1	SDCBP	1880159	1673640	1704755	354369.2	0	338963.3
O00567	Nucleolar	NOP56	6719.899	8900.477	8623.729	0	0	0

O00592	Podocalyxi	PODXL	92810.95	71734.74	49423	0	0	0
O00622	Protein CY	CYR61	31409.86	26731.8	38166.04	802018.5	495080.8	812536.9
O00629	Importin s	KPNA4	7896.183	16136.03	14880.06	0	0	0
O00754	Lysosomal	MAN2B1	41559.8	41785.77	51557.95	213196	275519.8	149103.6
O00762	Ubiquitin-	UBE2C	26382.65	29787.42	13508.75	0	0	0
O00764	Pyridoxal	kPDXK	29973.6	22081.25	21343.04	0	0	0
O14493	Claudin-4	CLDN4	11470.3	20203.97	15107.01	0	0	0
O14530	Thioredoxi	TXNDC9	9904.99	8884.696	7584.938	0	0	0
O14578	Citron Rho	CIT	3654.218	6761.543	5796.103	0	0	0
O14579	Coatomer	COPE	9315.512	10334.98	13650.64	0	0	0
O14672	Disintegrin	ADAM10	1486793	1396104	1445178	291035.2	0	319522.6
O14737	Programm	PDCD5	17614.31	16982.56	13768.65	0	0	0
O14744	Protein arc	PRMT5	59354.33	60820.38	66415.69	0	0	0
O14745	Na(+)/H(+)	SLC9A3R1	406796.3	405541.8	350551.9	0	0	0
O14763	Tumor nec	TNFRSF10I	51770.76	48952.66	45504.51	0	0	0
O14786	Neuropilin	NRP1	66758.85	68377.22	70892.08	60399.73	88702.34	73123.23
O14787	Transporti	TNPO2	27572.7	23643.96	26271.06	0	0	0
O14817	Tetraspani	TSPAN4	2301838	2046621	2131781	256016	0	479146.7
O14818	Proteasom	PSMA7	145089.8	142440.7	164870.3	86836.34	98504.18	79160.2
O14907	Tax1-bind	TAX1BP3	99077.92	80741.05	74241.05	0	0	0
O14908	PDZ doma	GIPC1	121106.5	119885.5	115684.3	0	0	0
O14910	Protein lin	LIN7A	111926	89221.92	84594.01	0	0	0
O14920	Inhibitor o	IKBKB	24726.93	19408.38	285881.8	0	0	0
O14929	Histone ac	HAT1	2300.368	7051.301	6962.613	0	0	0
O14936	Peripheral	CASK	29567.47	26580.55	25892.1	0	0	0
O14939	Phospholiğ	PLD2	14761.33	14558.16	9806.649	0	0	0
O14950	Myosin reğ	MYL12B	47927.96	53905.22	53146.63	313671.6	241507	219710.3
O14960	Leukocyte	LECT2	32310.58	24385.49	41790.8	0	0	0
O14964	Hepatocyt	HGS	31276.61	28453.29	32439.52	0	0	0
O14976	Cyclin-G-ε	GAK	3933.976	4413.537	7530.735	0	0	0
O14979	Heterogen	HNRNPDL	10741.81	10653.11	6081.136	0	0	0
O14980	Exportin-1	XPO1	19077.78	18660.2	20490.96	0	0	0
O15013	Rho guanin	ARHGEF1C	29349.88	27595.82	3667.655	0	0	0
O15020	Spectrin bε	SPTBN2	24925.48	25439.17	21851.5	0	0	0
O15027	Protein tra	SEC16A	7079.452	12219.29	6005.842	0	2417486	764338.8
O15031	Plexin-B2	PLXNB2	28191.05	29023.56	29966.91	63621.37	83108.97	36291.48
O15040	Tectonin b	TECPR2	1116.685	1736.284	2045.288	0	0	0
O15067	Phosphoril	PFAS	35028.22	38792.56	37054.05	0	0	0
O15072	A disintegr	ADAMTS3	7670.618	4801.088	8852.308	0	0	0
O15084	Serine/thrε	ANKRD28	3871.416	3711.872	4447.469	0	0	0
O15118	Niemann-	NPC1	53572.03	60472.76	61604.42	0	0	0
O15144	Actin-relat	ARPC2	246650	238801.6	215517.2	0	392752.4	67848.52
O15145	Actin-relat	ARPC3	221417.7	202080	184260.9	41038.46	0	24972.87
O15160	DNA-direc	POLR1C	6920.024	4515.089	9315.346	0	0	0
O15162	Phospholiğ	PLSCR1	307399.5	320640.4	333306.6	0	0	0
O15194	CTD small	CTDSPL	21404.81	24641.34	38072.25	0	0	0
O15212	Prefoldin s	PFDN6	32749.12	33827.16	29033.36	0	0	0
O15230	Laminin su	LAMA5	32244.85	31447.8	26635.21	36579.36	58980.03	29751.91
O15240	Neurosecr	VGF	46353.84	52465.38	58302.65	0	0	0
O15258	Protein RE	RER1	15171.03	16741.17	7118.131	0	0	0
O15260	Surfeit loc	SURF4	7608.559	13304.32	10221.85	143168.2	0	117005.4
O15305	Phosphom	PMM2	11799.75	14337.3	10627.97	0	0	0
O15347	High mobi	HMGB3	5236.456	4848.144	5192.243	0	0	0
O15394	Neural cell	NCAM2	12620.12	12263.63	12853.2	0	0	0
O15397	Importin-ξ	IPO8	4392.891	4769.096	3789.777	0	0	0
O15400	Syntaxin-7	STX7	87556.81	88488.77	82097.2	43829.52	82294.27	171820.5
O15403	Monocarbo	SLC16A6	4068.613	2701.972	3098.658	0	0	0
O15427	Monocarbo	SLC16A3	125788.4	139132.8	119110.3	169751.5	181709.3	233618.8

O15431	High affinity SLC31A1	54419.09	47661.28	47297.89	0	0	0
O15498	Synaptobrevin YKT6	72272.98	73806.71	68583.47	0	0	0
O15511	Actin-related ARPC5	90044.46	80380.41	87323.72	0	0	0
O15554	Intermediate KCNN4	10866.09	10933.28	7637.92	0	0	0
O43150	Arf-GAP w ASAP2	7971.25	11278.64	9219.929	0	0	0
O43175	D-3-phospho PHGDH	935284.6	983616.5	942149.6	102313.8	88738.13	116331.9
O43237	Cytoplasmic DYNC1L2	8422.508	7863.323	7398.911	0	0	0
O43242	26S proteasome PSMD3	29359.27	31893.26	39662.57	132062.8	0	60403.45
O43252	Bifunctional PAPSS1	11569.37	7636.98	16594.77	0	0	0
O43264	Centromere ZW10	8628.369	7679.44	4534.014	0	0	0
O43286	Beta-1,4-galactosyl B4GALT5	63537.86	67290.68	82264.95	295101.6	376298.9	244293.5
O43294	Transforming TGFB1I1	6876.101	6991.599	6280.562	158149.4	0	56003.31
O43390	Heterogeneous HNRNP	14073.14	17087.68	15948.03	40704.81	0	41427.71
O43396	Thioredoxin TXNL1	5948.153	7494.109	6173.866	0	0	0
O43399	Tumor protein TPD52L2	165197.1	169411.3	147129.3	0	0	0
O43427	Acidic fibronectin FIBP	10147.77	9279.934	9148.632	0	0	0
O43447	Peptidyl-prolyl PPIH	3545.695	3657.883	3064.594	0	0	0
O43488	Aflatoxin B AKR7A2	17842.16	17108.73	16866.82	0	0	0
O43491	Band 4.1-like EPB41L2	254123.8	294683.6	248357.8	0	0	0
O43505	Beta-1,4-galactosyl B4GAT1	25632.99	24278.47	32845.58	163779.5	137959.4	101226.5
O43592	Exportin-1 TXPOT	20730.08	10134.48	11033.42	0	0	0
O43597	Protein sproutin SPRY2	16109.55	16650.93	18533.52	0	0	0
O43617	Trafficking TRAPPC3	26973.75	30227.04	26685.42	0	0	0
O43633	Charged residue CHMP2A	155905.7	121182.9	131958.2	0	0	0
O43657	Tetraspanin TSPAN6	84235.96	90925.66	85150.26	0	0	0
O43681	ATPase ASASNA1	24759.89	26949.09	26032.53	0	0	0
O43684	Mitotic chromosome BUB3	44268.69	43755.64	36580.73	0	0	0
O43688	Phospholipase PLPP2	87265.38	72379.66	80303.39	0	0	0
O43739	Cytohesin-3 CYTH3	33095.4	23310.06	20974.6	0	0	0
O43741	5-AMP-activated PRKAB2	6507.164	8322.603	5220.972	0	0	0
O43747	AP-1 component AP1G1	14062.76	16652.02	2742555	0	2675926	2.56E+08
O43752	Syntaxin-6 STX6	16446.01	18733.75	13551.36	0	0	0
O43765	Small glutathione SGTA	11646.24	11604.59	14563.32	0	0	0
O43795	Unconventional MYO1B	366613.9	396807.7	310267	0	0	0
O43809	Cleavage site NUDT21	7545.716	20260.28	8004.012	0	0	0
O43813	LanC-like protein LANCL1	112361	107325.6	112150.4	0	0	0
O43847	Nardilysin NRD1	21404.26	18675.99	16607.79	0	0	0
O43852	Calumenin CALU	3814.591	4377.7	4270.342	217148.3	230224.7	153953.6
O43854	EGF-like repeat EDIL3	217768.8	217354.5	210261.1	1517839	1147329	2769120
O43865	Adenosyltransferase AHCYL1	179673.4	165787.2	171644.6	199581.1	166282.1	224099
O43913	Origin recognition ORC5	3360.269	3652.171	3272.511	0	0	0
O43924	Retinal rod PDE6D	6795.793	6123.401	6591.685	0	0	0
O60231	Putative protein DHX16	1577.489	2331.302	2090.322	0	0	0
O60245	Protocadherin PCDH7	8314.455	6577.306	5831.016	0	0	0
O60256	Phosphoribosyl PRPSAP2	4891.893	23494.28	5273.12	0	0	0
O60264	SWI/SNF-related SMARCA5	16529.11	10841.96	16258.25	0	0	0
O60271	C-Jun-aminotransferase SPAG9	10120.42	5512.823	7864.258	0	0	0
O60291	E3 ubiquitin ligase MGRN1	27566.71	28688.36	27899.65	0	0	0
O60341	Lysine-specific KDM1A	3323.557	3925.754	3716.112	0	0	0
O60343	TBC1 domain TBC1D4	2422.238	2388.578	3790.196	0	0	0
O60353	Frizzled-6 FZD6	31608.21	28092.22	24697.22	0	0	0
O60361	Putative nuclear NME2P1	90223.64	91692.07	150707.4	0	0	0
O60443	Non-syndromic DFNA5	26619.08	24721.69	24607.32	0	0	0
O60462	Neuropilin NRP2	46458.38	42156.69	35249.66	95607.87	100312.9	46468.12
O60488	Long-chain ACSL4	825809.5	785422.8	727459.5	0	0	0
O60493	Sorting nexin SNX3	50854.57	51831.98	48839.49	29374.17	0	24071.7
O60502	Protein O-mannosyltransferase MGEA5	8243.77	5228.258	5900.311	0	0	0
O60503	Adenylate ADCY9	10958.37	8940.839	9398.204	0	0	0

O60506	Heterogen SYNCRIP	7679.208	7072.797	13618.71	0	0	0
O60568	Procollage PLOD3	5745.654	6024.239	8426.503	27799.45	0	36297.83
O60610	Protein dia DIAPH1	12919.81	14644.92	14697.13	0	0	0
O60645	Exocyst co EXOC3	25658.99	21046.72	22432.11	0	0	0
O60664	Perilipin-3 PLIN3	32132.99	31556.29	16764.33	0	0	0
O60669	Monocarb SLC16A7	15161.6	18564.82	15798.88	0	0	0
O60671	Cell cycle c RAD1	3403.961	3487.325	2428.936	0	0	0
O60678	Protein arc PRMT3	12240.22	9192.637	7942.693	0	0	0
O60684	Importin si KPNA6	33680.9	23851.64	25497.56	0	0	0
O60687	Sushi repe SRPX2	2365.562	7686.472	21443.59	290020.5	141376.2	212756.8
O60711	Leupaxin LPXN	11459.67	15892.06	5224.333	0	0	0
O60716	Catenin de CTNND1	222976	227997.7	197685.2	9478.817	0	32046.69
O60739	Eukaryotic EIF1B	38295	35505.86	36967.15	0	0	0
O60749	Sorting ne: SNX2	22076.19	22636.16	22300.53	0	0	0
O60763	General ve USO1	14632.47	14710.45	15360.29	0	0	0
O60779	Thiamine t SLC19A2	15422.89	17880.53	14957.89	0	0	0
O60784	Target of MTOM1	14259.53	12864.45	15207.14	0	0	0
O60814	Histone H2 HIST1H2B1	8442991	8670687	8037664	1926069	11448047	5566483
O60832	H/ACA rib DKC1	8464.182	5600.883	8677.977	34582.58	23718.96	0
O60841	Eukaryotic EIF5B	5208.155	4382.07	3256.48	55386.78	0	34832.05
O60869	Endothelia EDF1	6728.935	5428.117	7197.682	0	0	0
O60884	DnaJ homc DNAJA2	118860.5	86104.19	43013.79	0	0	0
O60888	Protein Cu CUTA	304398.7	279582.8	293128.6	2194230	2946819	1880132
O60925	Prefoldin s PFDN1	24535.97	36312.82	19414.83	0	0	0
O75044	SLIT-ROBC SRGAP2	77574.19	73334.09	56867.02	0	0	0
O75051	Plexin-A2 PLXNA2	66675.44	65456.93	59254.69	0	0	0
O75054	Immunoglu IGSF3	85276.37	85587.66	86761.16	0	0	0
O75083	WD repeat WDR1	451494.8	399227.7	295588.8	84703.58	250799.3	241404.9
O75084	Frizzled-7 FZD7	49996.3	66492.63	64801.22	0	0	0
O75110	Probable p ATP9A	1277.209	599.4937	4043.401	0	0	0
O75116	Rho- assoc ROCK2	14323.71	21131.6	18824.28	112059.3	0	34732.52
O75122	CLIP- assoc CLASP2	4080.457	2818.037	2593.865	0	0	0
O75144	ICOS ligand ICOSLG	25495.6	25266.5	28274.08	261061.1	344439.5	174962.5
O75147	Obscurin-1 OBSL1	45007.11	42795.21	30378.39	0	0	0
O75153	Clustered r CLUH	17473.47	20921.9	21532.65	0	0	0
O75165	DnaJ homc DNAJC13	6987.304	10666.54	6737.802	19961.42	16769.07	23090.7
O75204	Transmem TMEM127	10215.22	9690.163	9619.627	0	0	0
O75317	Ubiquitin c USP12	31176.63	30265.9	39584.24	0	0	0
O75326	Semaphori SEMA7A	20940.14	21660.84	20623.16	0	0	0
O75340	Programm PDCD6	816212.9	791242.1	818194.8	145949.9	185389.6	256656.5
O75347	Tubulin-sp TBCA	100825	93530.41	93579.23	0	0	0
O75351	Vacuolar p VPS4B	71295.52	68976.48	70149.84	0	0	0
O75352	Mannose- MPDU1	2943.214	2086.349	3105.327	0	0	0
O75367	Core histoi H2AFY	117443.3	115041.1	110990.7	165873.2	295734.2	158213.8
O75369	Filamin-B FLNB	86157.18	93663.46	73542.5	63724.9	0	124895.7
O75382	Tripartite r TRIM3	16109.4	15364.02	17906.78	0	0	0
O75387	Large neut SLC43A1	79255.02	47911.55	46716.92	0	0	0
O75400	Pre-mRNA PRPF40A	18866.91	7127.216	12323.7	0	0	0
O75436	Vacuolar p VPS26A	21945	19083.99	18648.71	0	0	0
O75487	Glypican-4 GPC4	46651.32	46474.89	40416.48	0	0	0
O75506	Heat shock HSBP1	9260.093	9112.402	11449.73	0	0	0
O75508	Claudin-1: CLDN11	285084.6	302909.5	362481.4	0	0	0
O75531	Barrier-to- BANF1	273813.2	235604.5	199810.8	180065.9	400535.2	0
O75533	Splicing fa SF3B1	20216.28	22035.95	24386.97	0	0	0
O75534	Cold shock CSDE1	24467.15	20719.57	20695.36	0	0	0
O75608	Acyl-prote LYPLA1	34985.28	33242.77	27940.45	0	0	0
O75643	U5 small n SNRNP20C	19096.32	17137.16	18467.23	0	0	0
O75663	TIP41-like TIPRL	419035.5	7873.451	1184877	2873284	3123115	5899021

O75674	TOM1-like TOM1L1	47839.9	47595.71	45077.2	0	0	0
O75694	Nuclear pore NUP155	10252.88	10335.18	9769.436	0	0	0
O75695	Protein XR RP2	94008.13	94204.63	83889.5	0	0	0
O75718	Cartilage-α CRTAP	5807.982	4998.809	12309.03	0	0	0
O75762	Transient receptor TRPA1	2088.396	1893.382	2053.721	0	0	0
O75787	Renin receptor ATP6AP2	2289.143	3077.091	6436.844	0	0	0
O75822	Eukaryotic EIF3J	28103.36	25174.82	28083.11	0	0	0
O75832	26S proteasome PSMD10	115945.4	87012.84	227191	0	0	0
O75844	CAAX prenylation ZMPSTE24	2755.402	2095.041	1425.124	0	0	0
O75874	Isocitrate dehydrogenase IDH1	52908.31	52814.7	47006.22	33301.76	45359.41	120190.2
O75891	Cytosolic 1 ALDH1L1	13062.45	24405.61	29848.32	84823.53	0	31407.48
O75915	PRA1 family ARL6IP5	5775.765	5522.641	0	81814.47	0	64194.84
O75954	Tetraspanin TSPAN9	109962.9	105825.7	100250.5	40375.2	0	65267.51
O75962	Triple function TRIO	13794.72	15064.02	9326.92	0	0	0
O75970	Multiple PIMPDZ	12692.42	14008.79	14143.15	0	0	0
O75976	Carboxypeptidase CPD	20511.66	22332.1	20430.87	0	0	0
O76003	Glutaredoxin GLRX3	59345.54	58078.28	51881.02	0	0	0
O76061	Stanniocalcin STC2	7025.187	8811.929	18068.65	538649.4	736076.5	779267.9
O76076	WNT1-inducible WISP2	1911.733	1804.991	2709.133	39972.79	77585.02	0
O76081	Regulator of G-protein signaling RGS20	15439.6	14258.48	9535.395	0	0	0
O76094	Signal receptor SRP72	7984.225	3545.824	6661.597	0	0	0
O94760	N(G),N(G)-DDAH1	130324.2	129442.1	129732.4	0	0	0
O94804	Serine/threonine kinase STK10	169523.2	161062.7	143089.8	0	0	0
O94806	Serine/threonine kinase PRKD3	22733.34	27322.37	25216.75	0	0	0
O94808	Glutamine gamma-glutamyl transaminase GFPT2	16581.99	15594.05	14080.3	0	0	0
O94813	Slit homologue SLIT2	29712.35	37899.26	36407.82	276861.3	0	360025
O94823	Probable G-protein coupled receptor ATP10B	4767.847	4598.514	3854.079	592786.6	886658.8	752521.8
O94887	FERM, Rho GTPase FARP2	32286	19352.96	20922.97	0	0	0
O94906	Pre-mRNA processing PRPF6	4145.307	5083.658	1748.565	0	0	0
O94915	Protein furin FRYL	21956.22	22449.06	22192.48	38147.28	0	30633.2
O94973	AP-2 complex component AP2A2	33317.96	30175.25	30005.32	0	0	0
O94985	Calsynenin CLSTN1	24642.96	23627.83	34600.38	69439.66	140893.7	0
O95084	Serine protease PRSS23	23006.49	25789.04	24347.65	191351.6	205617.8	377140.4
O95155	Ubiquitin chain UBE4B	2216.948	2821.402	1723.402	0	0	0
O95163	Elongator complex IKBKAP	8255.947	7309.521	9624.156	0	0	0
O95164	Ubiquitin chain UBL3	55260.66	39020.12	33667.33	0	0	0
O95183	Vesicle-associated VAMP5	71848.59	68370.65	67712.73	0	0	0
O95197	Reticulon-3 RTN3	17223.72	25834.18	25544.69	104513.2	61486.48	103020
O95214	Leptin receptor LEPROTL1	18226.08	15837.05	24004.56	0	0	0
O95219	Sorting nexin SNX4	7933.151	8054.277	7585.353	0	0	0
O95235	Kinesin-like KIF20A	4355.309	6203.38	3171.926	0	0	0
O95248	Myotubularin SBF1	9124.306	8917.305	9217.787	0	0	0
O95249	Golgi SNARE GOSR1	11327.15	9469.666	12819.52	0	0	0
O95297	Myelin protein MPZL1	173390.3	181341.1	156814	0	0	0
O95336	6-phosphogluconate PGLS	22041.75	23601.72	22669	0	0	0
O95340	Bifunctional PAPSS2	8322.408	11592.92	13415.63	0	0	0
O95347	Structural protein SMC2	8454.838	7400.808	6388.485	0	0	0
O95352	Ubiquitin chain ATG7	4651.106	17806.05	89564.23	0	0	0
O95372	Acyl-protein lyase LYPLA2	4203.006	5164.434	6566.631	0	0	0
O95376	E3 ubiquitin ligase ARIH2	7533.676	6746.592	7693.298	0	0	0
O95394	Phosphoglucomutase PGM3	6321.671	5977.571	5219.906	0	0	0
O95415	Brain protein BRI3	19641.93	18784.44	20189.66	0	0	0
O95433	Activator core AHSA1	66228.97	61561.89	60313.95	0	0	0
O95445	Apolipoprotein APOM	755016.3	721332.6	908426.3	2831498	3249384	1914968
O95456	Proteasome PSMG1	6840.35	7900.076	6416.914	0	0	0
O95466	Formin-like FMNL1	8733.605	8497.285	7354.605	0	0	0
O95486	Protein transmembrane SEC24A	5675.006	4011.985	7253.047	0	0	0
O95490	Adhesion (ADGRL2)	74098.21	69244.74	73553.73	0	0	0

O95497	Pantethein VNN1	143899.2	207705.6	357785.1	1422246	2069474	916991.6
O95498	Vascular n VNN2	146547	129311.4	210314.3	1526596	2430510	953240.3
O95602	DNA-direc POLR1A	1206.216	1363.455	7034.791	0	0	0
O95630	STAM-bin STAMBP	12763.77	13623.41	15076.52	0	0	0
O95685	Protein ph PPP1R3D	2857.299	3279.203	3200.989	0	0	0
O95714	E3 ubiquiti HERC2	3725.115	4939.885	5961.314	0	0	0
O95721	Synaptoso SNAP29	24012.1	27857.36	34864.92	0	0	0
O95747	Serine/thre OXSR1	90018.73	96439.33	88504.94	69762.28	40671.55	78193.48
O95772	MLN64 N- STARD3NL	55847.78	56279.86	39740.84	0	0	0
O95807	Transmem TMEM50A	42355.21	42462.34	64391.47	0	0	0
O95816	BAG family BAG2	20388.48	28922.74	27320.45	0	0	0
O95817	BAG family BAG3	12977.5	4992.561	3143.377	0	0	0
O95819	Mitogen-a MAP4K4	296943.1	284808.5	274815.1	147520	156364.6	143849.4
O95834	Echinoderr EML2	35445.28	39737.57	49725.24	0	0	0
O95835	Serine/thre LATS1	7406.903	5952.674	6696.852	0	0	0
O95857	Tetraspani TSPAN13	40936.05	42881.48	57784.68	0	0	0
O95858	Tetraspani TSPAN15	52267.66	66397.14	55851.61	0	0	0
O95865	N(G),N(G)- DDAH2	101966.8	69399	93622.15	356854.1	272996.9	136166.9
O95881	Thioredoxi TXNDC12	1222.204	1454.758	1376.259	0	0	0
O95965	Integrin be ITGBL1	0	273.3481	616.4772	20498.62	25871.37	0
O96013	Serine/thre PAK4	41260.12	43590.66	36323.05	0	0	0
O96019	Actin-like ACTL6A	34163.12	39289.45	32833.77	0	0	0
P00338	L-lactate d LDHA	1402728	1407553	1524892	1417967	1133633	1244605
P00352	Retinal del ALDH1A1	7024.703	5677.931	13511.82	45905.95	0	46841.77
P00374	Dihydrofol DHFR	16597.99	18047.25	23501.3	0	0	0
P00387	NADH-cyt CYB5R3	13542.71	13552.66	12653	80357.67	32311.95	62279.48
P00390	Glutathion GSR	27035.6	24174.17	41769.09	110477.4	75510.74	66857.32
P00441	Superoxide SOD1	126947.7	132138.5	133320.7	497276.2	522567.7	300515.3
P00450	Ceruloplas CP	17258.51	18969.85	37665.18	90107.81	196353.4	135910.3
P00488	Coagulatic F13A1	218689.4	207763.7	258529.2	2800774	2963346	4349714
P00491	Purine nuc PNP	47749.01	50214.48	48374.4	109750.7	125599.8	85691.2
P00492	Hypoxanth HPRT1	70196.73	72960.51	73462.03	0	0	0
P00533	Epidermal EGFR	327690	318877.5	302814.7	60279.79	90307.98	53028.61
P00558	Phosphogl PGK1	460287.2	463929.5	427267	215485.5	104420.2	240834.3
P00568	Adenylate AK1	12220.04	14503.15	10397.76	0	0	0
P00734	Prothromb F2	2102351	2014787	2650318	7057864	3789778	6725526
P00738	Haptoglob HP	19262.71	17358.24	22627.18	242131.8	0	561067.6
P00740	Coagulatic F9	241345.5	236467	291182.4	694409.9	1086583	573202.1
P00742	Coagulatic F10	140995.7	136778.5	174987.3	532302.2	825313.4	527205
P00747	Plasminog PLG	30049.37	50542.73	41967.45	2657273	3331337	1611935
P00749	Urokinase- PLAU	64612.13	71144.77	84884.44	0	0	0
P00750	Tissue-typ PLAT	16486.23	17563.44	24696.89	0	0	0
P01008	Antithromb SERPINC1	3075163	3555323	5055003	30211412	40719696	21346772
P01023	Alpha-2-n A2M	87755872	84397112	99073416	1.29E+08	1.28E+08	96147840
P01024	Compleme C3	1818626	1698691	2116302	19360314	23938682	11885536
P01031	Compleme C5	78293.91	75965.98	98955.54	1889089	3999791	1238066
P01033	Metallopro TIMP1	45560.97	43955.09	64660.74	5632950	8258561	3181560
P01034	Cystatin-C CST3	0	13142.27	37289.65	478651.9	357385.6	371644
P01042	Kininogen- KNG1	751500.4	777435.9	1404809	10547805	16567593	8058223
P01112	GTPase H HHRAS	206987.9	184078.9	188463.7	0	0	0
P01130	Low-densi LDLR	35312.05	37909.39	33685.69	0	0	0
P01266	Thyroglob TG	39946.37	40027.64	58106.93	0	0	0
P01344	Insulin-like IGF2	204205.3	194215.7	254392.9	1340448	2355847	1486736
P01583	Interleukin IL1A	8201.05	7419.439	6583.353	0	0	0
P01591	Immunoglob JCHAIN	25265.86	23373.25	29376.03	1552234	1854049	1286563
P01621	Ig kappa chain V-III re	65450.5	61613.93	70577.98	490984.3	452385.6	392804
P01891	HLA class I HLA-A	359019.6	354224.2	332251.7	0	276833.3	308168.7
P01893	Putative H HLA-H	822733.6	771215.4	508418.7	367584.1	0	567797.1

P02042	Hemoglob HBD	29925040	40045292	46053936	1.64E+08	1.74E+08	1.67E+08
P02100	Hemoglob HBE1	2143.851	2364.205	1317.096	47252.03	70522.69	49799.61
P02452	Collagen a COL1A1	424782.5	424851.3	607705.7	43402192	60887532	57844964
P02458	Collagen a COL2A1	106178	90045.66	134282.7	20690848	19684960	9763341
P02461	Collagen a COL3A1	182361	173153.8	320679.3	2539115	3970310	2653301
P02462	Collagen a COL4A1	24374.47	37834.79	27592.59	237286	470051.9	201699.3
P02533	Keratin, ty KRT14	263107.2	476859.5	409342.8	1427313	3483941	2303723
P02538	Keratin, ty KRT6A	67239.31	156709.9	137018.7	462970.6	1042913	1003104
P02647	Apolipoprc APOA1	11565842	3896263	4477374	47196760	59620932	18950614
P02649	Apolipoprc APOE	64062.46	48715.43	36169.06	2960874	2121512	1423429
P02656	Apolipoprc APOC3	54020.49	65942.34	90416.66	1624285	2062006	1517510
P02675	Fibrinogen FGB	86718.77	49821.5	127161.9	204348.2	1194950	1453643
P02679	Fibrinogen FGG	28605.97	0	29118.03	652600.9	323055.3	578729.3
P02749	Beta-2-gly APOH	778721.2	798113.6	1121085	1993687	6668891	3616376
P02751	Fibronectir FN1	900942.7	891407.6	1164282	1.76E+08	2.1E+08	2.49E+08
P02753	Retinol-bir RBP4	454999.9	432352.8	1403791	7708837	8963601	5013635
P02765	Alpha-2-I AHSG	2453798	5962496	1779508	5.4E+08	4.82E+08	2.35E+08
P02768	Serum albu ALB	2.56E+08	2.41E+08	3.33E+08	1.87E+10	1.72E+10	1.31E+10
P02771	Alpha-fetc AFP	5221326	5154493	7359711	52023072	77304440	26327024
P02774	Vitamin D- GC	4231523	4142006	5554745	30924030	44400800	23247808
P02787	Serotransf TF	17217.92	20192.37	19104.04	5493981	0	217694.3
P02788	Lactotrans LTF	38254420	40907900	58653644	2.98E+08	4.57E+08	2.22E+08
P02790	Hemopexin HPX	67781.34	79466.01	94413.54	588119.3	1366101	553144.3
P02792	Ferritin lig FTL	211424.3	239087.5	484434.7	500452.6	3513572	4951271
P02794	Ferritin he FTH1	150147	159158	211612.5	1591932	886506.6	462145.6
P03952	Plasma kal KLKB1	101691.9	92893.97	133371.5	1166066	602828.3	283999.9
P03956	Interstitial MMP1	1464575	1355593	1949859	245802.8	156423.7	120538.1
P04003	C4b-bindin C4BPA	183297.4	196614.6	223487.8	1036900	1155821	1730243
P04004	Vitronectir VTN	3368242	2959434	4282778	19663492	6645257	37739532
P04040	Catalase CAT	11834.4	8108.995	17946.29	292154.1	0	179690.2
P04049	RAF proto- RAF1	45544.87	44522.12	51948.32	0	0	0
P04066	Tissue alpt FUCA1	11678.22	18640.9	7471.654	0	0	0
P04075	Fructose-k ALDOA	843655.3	808306.3	900088.3	613206.5	790384.3	514858.7
P04080	Cystatin-B CSTB	81326.05	89313.91	89391.77	0	0	0
P04083	Annexin A: ANXA1	284546.3	207539.5	235209.2	352890.1	339134	248198.2
P04114	Apolipoprc APOB	98188.14	99071.81	112893.3	3385774	3458774	2642429
P04180	Phosphatic LCAT	34041.27	40109.73	65642.16	0	0	0
P04216	Thy-1 mer THY1	0	0	0	475917.8	514798.4	711335.2
P04259	Keratin, ty KRT6B	260876.8	307446.1	199650.3	5356778	997069.3	1505684
P04264	Keratin, ty KRT1	698027.1	1292948	643146.9	10337758	19867054	10563592
P04275	von Willeb VWF	0	2014.66	2758.468	174714.3	137147.3	129039.4
P04278	Sex hormo SHBG	145808.5	160326.3	209430.7	784091.8	1257457	741959.2
P04350	Tubulin be TUBB4A	17924.69	16048.53	23192.81	0	0	0
P04406	Glyceralde GAPDH	1159782	1200191	1078160	1739243	1198381	1925284
P04424	Argininosu ASL	40306.52	40086.21	43394.62	0	0	0
P04745	Alpha-amyl AMY1A	95616.66	90819.88	118939.7	620849.6	870071.3	442593.3
P04792	Heat shock HSPB1	71246.21	65581.97	65709.02	191661.7	181669.6	147272.5
P04818	Thymidylat TYMS	99660.2	102065	73839.64	0	0	0
P04843	Dolichyl-d RPN1	9415.239	11874.61	14174.99	0	165713.3	110866.6
P04899	Guanine n: GNAI2	2964142	2855167	2762525	297261.3	258325.9	340356.3
P05023	Sodium/p: ATP1A1	1551442	1575169	1516954	73673.88	208159.9	112211
P05026	Sodium/p: ATP1B1	307469.8	165582.1	151217.5	0	0	0
P05062	Fructose-k ALDOB	8959.201	8816.631	8835.114	0	0	0
P05090	Apolipoprc APOD	73168.7	119438.7	128125.9	709488.9	1354631	1194718
P05106	Integrin be ITGB3	27424.83	29223.73	27533.29	186609.5	202846	380741.4
P05107	Integrin be ITGB2	150798.2	141683.7	137879.7	0	0	0
P05121	Plasminog SERPINE1	149925.9	155154	184755.9	3233969	3739385	2250639
P05155	Plasma prc SERPING1	715403	690601.5	986424.4	4814396	6697312	3028103

P05156	Complement CFI	159392.1	157450.3	187845.8	2456741	3263148	1261623
P05160	Coagulation F13B	18912.25	0	13314.34	112520.1	0	81283.26
P05231	Interleukin IL6	0	0	0	417961.8	593040.3	466689.3
P05362	Intercellular ICAM1	952106.4	948801.3	840351.1	0	0	0
P05386	60S acidic RPLP1	116879.6	87620.88	70062.41	949130.3	40380.62	721693.7
P05387	60S acidic RPLP2	107354.8	102074.9	88407.4	415662.4	0	328147.9
P05388	60S acidic RPLP0	65671.36	64505.79	67975.7	152766.5	92050.16	77703.5
P05452	Tetranectin CLEC3B	290133.1	296075.9	411210.6	2183074	2862270	2648154
P05455	Lupus La p SSB	8048.934	6934.504	7336.17	0	0	0
P05543	Thyroxine- SERPINA7	240195.5	225133.8	314042	1435918	1952742	1097828
P05546	Heparin cc SERPIND1	68810.05	90707.73	137420.5	428486.8	965370.8	444054.9
P05556	Integrin beta ITGB1	2191049	2154714	2276576	460622.6	438754.5	536648.9
P05771	Protein kinase PRKCB	5619.034	8110.264	7024.646	0	0	0
P05783	Keratin, type KRT18	8586.776	5278.095	1088.208	0	0	0
P05976	Myosin light MYL1	57483.55	23257.31	27088.58	0	108986.6	136927.6
P05997	Collagen alpha COL5A2	19578.41	22536.01	30371.6	451310	825428.4	403068.6
P06132	Uroporphyrin UROD	40026.72	41456.28	44788.65	0	0	0
P06213	Insulin receptor INSR	8405.239	8853.051	11618.61	0	0	0
P06241	Tyrosine-kinase FYN	21418.93	17818.09	26468.25	0	0	0
P06276	Cholinesterase BCHE	14313.07	16373.55	17201.73	24746.38	34684.11	0
P06396	Gelsolin GSN	987670.8	1002935	1350053	4862841	6779867	3406601
P06493	Cyclin-dependent CDK1	37492.29	41615.98	42065.89	0	0	0
P06727	Apolipoprotein APOA4	142675.3	81242.7	115726.9	617209.1	1151623	408372.7
P06730	Eukaryotic EIF4E	36173.83	35540.69	23596.29	0	0	0
P06732	Creatine kinase CKM	8739.011	9385.838	1517.276	0	0	0
P06733	Alpha-encodase ENO1	1885072	1793528	1717534	689404.8	773133.4	696294.7
P06737	Glycogen phosphorylase PYGL	70043.48	69501.11	81215.98	363014.7	57072.76	248760.7
P06744	Glucose-6-phosphate GPI	75093.37	78782.54	81592.7	131988.2	0	116845.9
P06748	Nucleophosmin NPM1	103783.8	132061.2	128843.7	358042.8	227261	254393.4
P06753	Tropomyosin TPM3	204739.2	212104.8	185968.5	56467.45	52839.91	0
P06756	Integrin alpha ITGAV	289998.4	274655.2	271357.1	101437.4	80761.59	92205.98
P06858	Lipoprotein LPL	16910.54	14110.7	24785.38	0	0	0
P06865	Beta-hexosaminidase HEXA	11529.59	10330.28	23735.75	92746.87	104162.4	0
P06899	Histone H2 HIST1H2B	789635.9	749447.3	801455.6	100599.7	344947.4	268551.1
P07093	Glia-derived SERPINE2	15610.3	16936.39	16990.62	457769.6	469718.5	506453.9
P07108	Acyl-CoA:DBI	80844.4	76384.92	74999.28	0	0	0
P07148	Fatty acid-binding FABP1	53338744	29009618	41069984	3125538	1.47E+09	7.85E+08
P07195	L-lactate dehydrogenase LDHB	449106.2	422736	464388.2	292822.7	226628.2	222021.7
P07203	Glutathione peroxidase GPX1	15710.06	15290.54	12018.55	0	0	0
P07204	Thrombospondin THBD	405387.7	161390.3	281107.1	0	0	0
P07225	Vitamin K-protein PROS1	183438.5	173999.3	243875.9	2482576	2928418	1551278
P07237	Protein disulfide isomerase P4HB	10307.21	10335.94	10993.46	64108.5	51358.36	45800.79
P07339	Cathepsin CTSD	20915.37	23786.34	28247.53	95830.89	96158.34	153021.5
P07355	Annexin A:ANXA2	7870237	8234866	7710950	943532.4	759536.7	1043306
P07437	Tubulin beta TUBB	1004115	1006875	913036.7	2073206	605203.6	2824406
P07451	Carbonic anhydrase CA3	14822.87	22819.92	18567.81	0	0	0
P07585	Decorin DCN	0	0	0	2122213	2781883	2407803
P07602	Prosaposin PSAP	48227.5	41231.77	53407.05	193225.8	300181.3	193927.3
P07686	Beta-hexosaminidase HEXB	15101.07	13045.63	24080.62	92746.98	104162.2	0
P07737	Profilin-1 PFN1	3129337	2909234	2673551	570275.9	414578.3	246133.2
P07738	Bisphosphoglycerate BPGM	6931.562	11131.41	13770.46	294303.5	293818.1	104174.7
P07814	Bifunctional EPRS	29443.65	28978.62	31746.55	66408.54	0	19529.06
P07858	Cathepsin CTSB	15052.99	22093.29	26290.55	141920.2	268427.5	225307
P07900	Heat shock protein HSP90AA1	1922161	1924894	1819638	815443.8	680620.6	839277.8
P07910	Heterogeneous nuclear HNRNPC	4781.046	3684.193	3313.813	53965.45	64064.68	49368.46
P07942	Laminin subunit LAMB1	453448.8	442634.1	428244.3	1245133	1898862	1111659
P07947	Tyrosine-kinase YES1	487135.3	488754.9	453963.4	25294.37	0	33762.27
P07948	Tyrosine-kinase LYN	107062.3	97078.45	83382.14	0	0	0

P07996	Thrombospondin 1	2431149	2440913	2908014	1.2E+08	1.42E+08	1.49E+08
P08069	Insulin-like growth factor 1R	43638.47	36668.27	37699.65	0	0	0
P08123	Collagen alpha 1(COL1A2)	130359.8	121527.6	187102.8	16283200	22820206	22035850
P08133	Annexin A1	622328.9	626200.9	570821	329509.4	533282.4	456115.5
P08174	Complement C5	177970.8	174258.5	169277.6	0	0	0
P08183	Multidrug resistance ABCB1	9950.797	12026.93	7922.902	0	0	0
P08195	4F2 cell surface SLC3A2	1379741	1384831	1328158	224560.8	200606.7	295840.9
P08237	ATP-dependent PFKM	24258.21	22442.38	22460.72	0	0	0
P08238	Heat shock protein 90A B1	386316.8	346622.3	365248.1	167274.3	171790.8	138891.1
P08243	Asparagine synthetase	32279.49	34293.61	38687.57	0	0	0
P08253	72 kDa type MMP2	26577.24	27735.48	35500.92	4767561	7582943	4855409
P08473	Neprilysin	42903.97	42343.38	52297.52	0	0	0
P08476	Inhibin beta	5202.885	5426.913	7889.681	277860.4	344188.5	247076.1
P08567	Pleckstrin	0	16334.44	20913.45	344736.1	182247.9	438759
P08572	Collagen alpha 1(COL4A2)	75983.08	77064.7	69640.48	241830.9	229149.3	99816.63
P08581	Hepatocyte growth factor	7994.305	10524.31	71355.48	0	0	0
P08582	Melanotransferrin	34414.27	35497.09	29926.24	0	0	0
P08648	Integrin alpha 1	635472.5	574154.8	543858.9	66235.57	110083.9	231015.3
P08670	Vimentin	75138.96	64626.21	55070.45	357802.6	337939.6	340517.4
P08697	Alpha-2-macroglobulin	5603241	5517329	3741123	17089592	52681304	25172122
P08727	Keratin, type I KRT19	16601.55	66265.41	18047.3	38018.48	38059.3	158347.7
P08758	Annexin A1	2059838	2081299	1897555	1117415	1359860	1536302
P08779	Keratin, type I KRT16	0	19418.03	28646.71	53910.55	292206.1	43204.13
P08865	40S ribosomal RPSA	63796.08	61946.65	65805.94	396736.2	0	188253.2
P08962	CD63 antigen	463847.2	811878.6	735731.3	963948.6	449293.1	1065170
P09110	3-ketoacyl-CoA ACAA1	2488.327	2452.436	4272.729	0	0	0
P09211	Glutathione S-transferase P1	150757.3	190189.9	198037.8	314307.7	226907.3	135854.6
P09341	Growth-regulated CXCL1	17354.26	20919.99	24863.8	7859904	7623940	2650093
P09382	Galectin-1	519623.6	548352.8	527650.9	295349.5	571497.9	327089.2
P09429	High mobility group B1	43504.48	18176.11	19529.45	466443.9	427932	389514.8
P09455	Retinol-binding RBP1	4772.824	4782.841	1824.119	0	0	0
P09471	Guanine nucleotide GNAO1	49665.95	53244.6	47142.61	0	0	0
P09486	SPARC	136526.2	131131.4	183241	4275316	7280123	3400598
P09493	Tropomyosin TPM1	251555	267459.2	242066.6	58146.41	51667.28	56522.45
P09496	Clathrin light chain CLTA	124195.8	181348.2	199592.3	0	0	0
P09497	Clathrin light chain CLTB	54789.19	67609.7	64464.85	0	0	0
P09525	Annexin A1	25849.92	29362.84	29040.56	0	0	0
P09619	Platelet-derived PDGFRB	0	0	0	49292.74	95045.67	44908.23
P09651	Heterogeneous nuclear HNRNPA1	51677.91	52966.61	56734.8	279193.2	0	259750.4
P09871	Complement C1S	109202.5	122693.1	136112.3	1130071	1684504	1021190
P09874	Poly (ADP-ribose) PARP1	5293.738	5286.859	6411.046	0	0	0
P09960	Leukotrien LTA4H	20801.59	27897.17	24127.6	0	0	0
P09972	Fructose-1,6-bisphosphate ALDOC	101157.9	103992	91365.46	116641	0	107956.1
P0C0L4	Complement C4A	298674.3	309157.8	394449.8	3976250	4735114	3259220
P0C0S8	Histone H2A HIST1H2A	15602849	10649732	27210384	1617089	4094493	3721678
P0C2W1	F-box/SPR domain FBXO45	2751.729	2422.619	2874.256	0	0	0
P0C7U0	Protein ELN	0	7163.189	168984.4	1443784	1512039	1313869
P0DMV8	Heat shock protein HSPA1A	243312.4	231179.2	234603.6	568768.5	437351.5	768514.4
P10114	Ras-related RAP2A	344807.7	321691.8	314188.3	0	0	0
P10124	Serine-glycine SRGN	166051.4	145038.2	146956.1	498227.2	710033.3	623048.3
P10145	Interleukin CXCL8	33740.48	30182.54	39200.91	1520724	1844316	669054.6
P10155	60 kDa SS-TROVE2	4528.78	4618.59	4435.701	0	0	0
P10301	Ras-related RRAS	430326.8	387204.4	362210.5	100126.1	245577.8	34837.4
P10398	Serine/threonine ARAF	33730.57	36973.12	29036.2	0	0	0
P10586	Receptor-interacting PTPRF	94778.95	33898.23	34760.39	0	0	0
P10599	Thioredoxin TXN	119432	79451.83	71937.59	225647.6	0	174902.8
P10619	Lysosomal CTSA	7339.859	2688.93	3341.48	0	0	0
P10643	Complement C7	112006.5	113351.7	156437	805346.6	1131515	930895.1

P10646	Tissue fact TFPI	1323.767	3789.917	2444.394	26564.4	0	37333.99
P10768	S-formylgl ESD	51937.04	66809.37	50399.13	0	0	0
P10809	60 kDa he: HSPD1	9852.661	7154.553	8767.29	0	0	0
P10915	Hyaluronai HAPLN1	0	2799.836	2176.817	0	269042.9	184374.5
P11021	78 kDa glu HSPA5	33478.75	30993.21	26532.06	71909.9	175954.1	114792.6
P11047	Laminin su LAMC1	262389.9	271018.7	264296.8	769181.1	1185000	722636.9
P11117	Lysosomal ACP2	32071.61	32710.78	36957.84	0	0	0
P11142	Heat shock HSPA8	2711343	2503239	2369818	505054.3	444828.1	651406.8
P11166	Solute carr SLC2A1	1562504	1545666	1366642	389148.1	203733	585202.5
P11169	Solute carr SLC2A3	263938.9	255152.6	224906.3	355022.8	277595.3	663835.8
P11171	Protein 4.1 EPB41	53520.95	53793.91	8764.718	0	0	0
P11172	Uridine 5-i UMP5	22926.34	23026.65	18945.69	0	0	0
P11177	Pyruvate d PDHB	42870.14	0	67750.9	216935.8	314982.9	160104.5
P11216	Glycogen i PYGB	127000.2	127686	136071.9	613863.8	0	279215.6
P11233	Ras-relate: RALA	457671	365657.6	304302.6	0	0	0
P11279	Lysosome- LAMP1	133474.3	128179.3	118083.7	0	0	0
P11362	Fibroblast FGFR1	23329.42	22214.34	27870.9	118196.1	179770.2	90240.34
P11387	DNA topoi TOP1	22284.46	25765.7	19806.12	0	0	0
P11388	DNA topoi TOP2A	8926.441	11906.63	8429.68	0	0	0
P11413	Glucose-6 G6PD	92559.41	91679.59	104564.1	134576.4	1334118	120024.2
P11717	Cation-inc IGF2R	154962.8	154212.1	154126.6	424402.3	403580.5	348016.4
P11766	Alcohol de ADH5	92025.27	91040.13	102111.9	81656.02	0	106451.5
P11802	Cyclin-de: CDK4	4719.658	5113.743	4752.214	0	0	0
P11908	Ribose-ph PRPS2	9574.733	10565.47	20884.52	0	0	0
P11940	Polyadeny PABPC1	45481.06	43053.52	43375.31	41435.05	0	25945.5
P12004	Proliferatin PCNA	20884.54	18280.86	17961.5	0	0	0
P12081	Histidine-- HARS	14505.27	14007.83	13090.62	0	0	0
P12107	Collagen a COL11A1	15887.71	13469.25	21892.9	437364.8	787103.4	418072.1
P12109	Collagen a COL6A1	434203.4	483034.6	548718.1	26611642	37608784	19312486
P12110	Collagen a COL6A2	688619.6	654839.3	920085.7	8113221	12491387	14542009
P12111	Collagen a COL6A3	715036.7	698176.7	992105.7	8482742	12983499	16302902
P12259	Coagulatic F5	398761.8	392911.9	516528.6	1771764	1797123	1716002
P12268	Inosine-5- IMPDH2	56762.98	57921.21	59285.85	22792.53	0	47820.7
P12277	Creatine ki CKB	238853.5	226218.7	199916.2	0	0	0
P12532	Creatine ki CKMT1A	47920.72	45394.53	44768.22	0	0	0
P12814	Alpha-acti ACTN1	1631021	1287272	1374860	420413	416863.5	151910.5
P12931	Proto-onc SRC	83000.48	93092.31	79166.42	0	0	0
P12955	Xaa-Pro di PEPD	33796.66	28352.3	37331.4	46923.04	77766.69	78194.5
P12956	X-ray repa XRCC6	16427.61	19146.33	18755.75	0	0	0
P13010	X-ray repa XRCC5	16091.96	18949.84	18863.23	0	0	0
P13473	Lysosome- LAMP2	343697.2	380650.7	371173	728902.3	929983.1	380651.4
P13489	Ribonucle: RNH1	82251	85903.07	78910.72	0	967384.4	25124.95
P13497	Bone mor: BMP1	30017.48	29325.88	32617.71	103323.3	84347.03	164019.7
P13535	Myosin-8 MYH8	59625.64	36620.27	9741.907	0	0	0
P13591	Neural cell NCAM1	113392.9	128736.4	147237.4	405040.1	585858.6	315098.7
P13611	Versican a: VCAN	31127.99	50309.82	38393.57	1117257	1469838	1261549
P13612	Integrin al: ITGA4	566738.1	567950.5	538285.1	0	27137.66	22112.88
P13639	Elongation EEF2	449379.5	438703.4	386822.8	212138.2	145287	229210.4
P13645	Keratin, ty: KRT10	843123.2	1505597	1372899	6469691	15882172	7045640
P13647	Keratin, ty: KRT5	32966	64063.03	48576.67	166713	787060.1	319471.8
P13667	Protein dis PDIA4	3922.58	2707.318	2276.746	0	0	0
P13693	Translatior TPT1	102736.8	58264.53	84410.52	0	0	0
P13716	Delta-amir ALAD	9837.738	15666.99	16303.73	0	0	0
P13796	Plastin-2 LCP1	122710.1	69666.71	114348.8	0	472448.1	298711
P13797	Plastin-3 PLS3	112406.4	146419.9	111424.1	165890.6	321151.1	164319.5
P13798	Acylamino APEH	29258.04	29893.95	26262.51	203079	255145	130696.7
P13807	Glycogen i GYS1	10076.19	10097.36	9165.446	0	0	0
P13861	cAMP-de: PRKAR2A	66728.89	68210.18	60731.44	0	0	0

P13929	Beta-enolase	ENO3	559387.3	548708.3	692914.4	656578.9	927322.9	666539
P13984	General transcription factor	GTF2F2	2834.801	3087.251	4863.234	0	0	0
P14174	Macrophage	MIF	525712	450931.8	457265.3	364194.1	633662.8	256857.4
P14314	Glucosyltransferase	PRKCSH	27319.32	9095.69	14914.35	0	0	0
P14324	Farnesyl pyrophosphatase	FDPS	21059.7	11718.15	12430.94	0	0	0
P14384	Carboxypeptidase	CPM	2186.68	3786.9	13141.27	0	0	0
P14543	Nidogen-1	NID1	228779.2	317012.5	253096.3	421199.3	854475.1	426171.2
P14550	Alcohol dehydrogenase	AKR1A1	34214.95	54229.03	56004.05	0	0	0
P14618	Pyruvate kinase	PKM	2174561	2260892	2197864	1522820	1172836	1636030
P14625	Endoplasmic reticulum	HSP90B1	45765.21	48207.66	46926.71	142014.2	153715.8	134359.1
P14678	Small nuclear	SNRPB	31999.81	27836.26	27744.16	0	0	0
P14780	Matrix metalloproteinase	MMP9	6336.946	17430.52	10845.83	0	0	0
P14866	Heterogeneous nuclear	HNRNPL	6017.602	5045.017	7643.668	0	0	0
P14923	Junction protein	JUP	12588.59	10982.74	14192.55	0	0	0
P15104	Glutamine	GLUL	11007.81	12486.19	12592.41	0	0	0
P15121	Aldose reductase	AKR1B1	48726.54	49559.36	48804.96	52623.18	0	40846.57
P15144	Aminopeptidase	ANPEP	4306041	4388485	3956607	465741.3	521707.7	541507.1
P15151	Poliovirus	PVR	64735.91	58565.63	121245.4	0	0	0
P15169	Carboxypeptidase	CPN1	21396.35	33184.99	33255.28	94620.27	80507.63	69497.42
P15260	Interferon	IFNGR1	19557.22	15729.27	16871.46	0	0	0
P15374	Ubiquitin	UCHL3	25528.55	24926.64	17886.82	0	0	0
P15529	Membrane	CD46	197972.2	194847.7	175000.7	0	0	0
P15531	Nucleoside	NME1	107885.9	98963.84	100219.9	0	0	0
P15559	NAD(P)H dehydrogenase	NQO1	8417.411	9093.737	10661.03	0	0	0
P15880	40S ribosome	RPS2	124284.2	120316.1	92468.32	167419.5	0	138721.3
P16035	Metalloproteinase	TIMP2	17206.84	10671.3	25151.07	674719.6	1076181	594139.3
P16070	CD44 antigen	CD44	1668030	1505488	1354908	706553.1	1354348	984418.4
P16112	Aggrecan	ACAN	26621.29	33737.57	28729.61	482052.2	648320.6	522338.6
P16333	Cytoplasmic	NCK1	32804.43	29480.92	27680.71	0	0	0
P16402	Histone H1	HIST1H1D	2712.008	7680.454	0	217047.5	397714.7	475124.5
P16403	Histone H1	HIST1H1C	4980.941	18165.04	12470.28	175510.3	210927.8	203434.3
P16885	1-phosphatase	PLCG2	10379.29	28057.75	14771.6	0	0	0
P16930	Fumarate hydratase	FAH	27265.81	30355.75	33457.72	110371	138357.7	78087.6
P16949	Stathmin	STMN1	108396.9	112730.4	95763.18	0	0	0
P16989	Y-box-binding	YBX3	14636.03	19148.17	12614.64	0	0	0
P17066	Heat shock	HSPA6	1825262	1810724	1629733	618722.8	544536.9	756627.7
P17081	Rho-related	RHOQ	6469.417	5571.474	7281.602	0	0	0
P17096	High mobility	HMGA1	3687.919	2192.117	6605.804	0	0	0
P17174	Aspartate aminotransferase	GOT1	52955.5	68428.13	69003.5	0	0	0
P17301	Integrin alpha	ITGA2	1009662	984344	883273.1	50015.98	51923	45628.58
P17302	Gap junction	GJA1	124116.2	129005.2	148090.5	0	0	0
P17516	Aldo-keto	AKR1C4	6832.339	4223.949	5983.1	0	0	0
P17655	Calpain-2	CAPN2	65544.27	64223.46	61648.42	10050.96	0	10921.24
P17812	CTP synthase	CTPS1	20776.92	20517.01	20301.43	0	0	0
P17844	Probable	DDX5	41271.52	40623.71	20131.07	68812.92	67227.61	67164.85
P17858	ATP-dependent	PFKL	45184.76	41476.06	38879.52	99858.99	0	103868.5
P17936	Insulin-like	IGFBP3	12576.61	6261.276	14508.17	2017370	1273004	1964008
P17948	Vascular endothelial	FLT1	31893.48	28433.65	24419.78	0	0	0
P17980	26S proteasome	PSMC3	60037.38	62950.76	63730.88	0	0	0
P17987	T-complex	TCP1	105662	104974.6	116663.7	130138.4	126603.8	117422.5
P18031	Tyrosine phosphatase	PTPN1	7576.963	8027.679	7217.724	0	0	0
P18065	Insulin-like	IGFBP2	27339.62	29786.61	45108.41	1135821	1632740	798135
P18077	60S ribosome	RPL35A	15435.44	12092.56	15573.57	0	0	0
P18085	ADP-ribosyl	ARF4	323125.1	320038.6	274515	62027.86	14358.39	78393.39
P18124	60S ribosome	RPL7	121444.8	115933.3	57083.38	445772.2	0	41926.02
P18206	Vinculin	VCL	161814.8	154140.2	166864.2	291263.1	587345.9	255023.1
P18433	Receptor-type	PTPRA	46711.7	43568.67	35359.64	0	0	0
P18621	60S ribosome	RPL17	69757.83	55763.35	45099.66	200641.6	20258.1	156001.8

P18669	Phosphogl PGAM1	259234.5	169318.6	279757.3	0	0	0
P18754	Regulator RCC1	2957.087	3815.347	4370.665	0	0	0
P18858	DNA ligase LIG1	1384.476	1375.96	1362.402	0	0	0
P19021	Peptidyl-g PAM	7053.125	7126.544	6897.303	0	0	0
P19022	Cadherin-;CDH2	52471.48	47255.59	39384.42	0	0	0
P19338	Nucleolin NCL	40349.73	41763.84	39259.07	228344.8	130208.5	161819.3
P19367	Hexokinase HK1	11184.95	12655.81	11544.51	0	0	0
P19387	DNA-direct POLR2C	6881.188	5007.706	6486.116	0	0	0
P19438	Tumor nec TNFRSF1A	9150.521	12225.68	21799.87	0	0	0
P19525	Interferon- EIF2AK2	16165.97	16077.09	4678.995	0	0	0
P19623	Spermidine SRM	32004.71	32804.76	27421.71	0	0	0
P19634	Sodium/hy SLC9A1	14338.58	14316.5	11894.72	0	0	0
P19784	Casein kinase CSNK2A2	20411.52	21254.77	19425.27	0	0	0
P19823	Inter-alpha; ITIH2	5457429	5426182	7400795	34503536	42908024	26339244
P19827	Inter-alpha; ITIH1	662811	564146.3	1614610	3924111	5111713	2982691
P20042	Eukaryotic EIF2S2	11076.61	11605.89	19061.28	75326.13	2296786	23276.21
P20337	Ras-related RAB3B	66199.8	77089.81	50154.52	0	0	0
P20338	Ras-related RAB4A	9708.833	11137.75	14655.8	0	0	0
P20340	Ras-related RAB6A	68230.97	110219	97305.55	0	0	0
P20594	Atrial natri NPR2	13676.73	14646.52	11647.71	0	0	0
P20618	Proteasome PSMB1	143259.1	131830.8	145013.1	158835	0	119417
P20700	Lamin-B1 LMNB1	13902.63	15405.05	14140.41	0	0	0
P20742	Pregnancy PZP	2207538	2024129	2813263	2856046	3205320	2454337
P20774	Mimetic OGN	37575.14	34131.71	21414.67	233844.1	343776.9	154995.6
P20849	Collagen a COL9A1	20810.83	19204.69	28521.77	141804.7	173300.7	92944.56
P20908	Collagen a COL5A1	29241.74	27993.36	31002.68	727181.1	987781.4	637353.9
P20936	Ras GTPase RASA1	5287.128	5815.677	6560.585	0	0	0
P20962	Parathyroid PTMS	6391.431	6924.742	7793.045	0	0	0
P21127	Cyclin-dependent CDK11B	36944.5	29310.46	36961.09	0	0	0
P21266	Glutathione GSTM3	28858.66	32648.62	34992.86	0	0	0
P21281	V-type proton ATP6V1B2	26225.77	27153.32	27066.87	0	0	0
P21283	V-type proton ATP6V1C1	7909.916	8167.086	7767.062	0	0	0
P21291	Cysteine aryl CSRP1	84980.58	87469.35	83442.97	0	0	0
P21333	Filamin-A FLNA	201938.9	180235.9	173953.5	690854.6	670321.5	765811.9
P21359	Neurofibrin NF1	35534.41	34734.56	30708.17	0	0	0
P21399	Cytoplasmic ACO1	61015.65	58294.36	57916.84	73739.38	0	88251.52
P21453	Sphingosine S1PR1	14079.01	13827.11	15699.31	4308854	6081246	2831802
P21589	5-nucleotide NT5E	155873	169958.6	178985.5	223716.3	251527.7	285565.7
P21810	Biglycan BGN	30743.75	26600.61	56474.4	3712922	6318149	5764266
P21926	CD9 antigen CD9	607472.4	654677.1	547520.1	202728.4	161303.1	221922
P21964	Catecholamine COMT	31365.35	29155.12	36800.98	0	0	0
P21980	Protein-glucosyl TGM2	1095.827	1504.6	0	73070.27	0	106890.9
P22059	Oxysterol-binding OSBP	19629.51	130455.3	5025.07	0	0	0
P22102	Trifunctional GART	92760.67	90326.3	81901.11	0	0	0
P22105	Tenascin-3 TNXB	2953.698	3181.553	3601.627	133076.1	178456.4	164121.3
P22234	Multifunctional PAICS	107100.2	107599.5	114188	0	0	0
P22303	Acetylcholine ACHE	27053.63	24330.06	17961.6	0	0	0
P22314	Ubiquitin-like UBA1	67495.34	71263.64	76378.48	58141.82	295258.8	75957.52
P22352	Glutathione GPX3	40674.96	40279.96	40938.83	102954.1	321520.5	142458.1
P22392	Nucleoside NME2	467219.2	448339.9	445903.1	0	99813.16	124463.2
P22413	Ectonucleotide ENPP1	44499.91	43136.04	37395.38	0	0	0
P22626	Heterogeneous HNRNPA2	24031.71	15001.14	26934.31	286667.9	283283.8	208013.1
P22692	Insulin-like IGFBP4	20808	11594.88	27173.2	527457.6	935729.9	311529.9
P22694	cAMP-dependent PRKACB	28895.26	36778.05	40155.65	0	0	0
P23142	Fibulin-1 FBLN1	186856.3	185248.1	266740.6	4094277	5281919	3169619
P23229	Integrin alpha ITGA6	174326.9	176936.4	172621.6	31793.19	50239.89	112400.1
P23246	Splicing factor SFPQ	58819.82	25059.12	50038.02	80971.68	0	99451.78
P23258	Tubulin gamma TUBG1	14128.34	15955.63	15677.27	0	0	0

P23284	Peptidyl-p PPIB	56336.99	58585.38	56272.42	66169.91	125086.5	121793.8
P23297	Protein S1(S100A1	30644.17	23398.02	33096.2	0	0	0
P23396	40S riboso RPS3	122006	115286	117659.4	285864.1	121836.6	192196.1
P23458	Tyrosine- γ JAK1	86524.32	82540.41	73327.55	0	0	0
P23468	Receptor-iPTPRD	58006.56	61018.37	56202.98	0	0	0
P23469	Receptor-iPTPRE	13283	16987.94	10073.65	0	0	0
P23470	Receptor-iPTPRG	40483.37	39884.71	36271.8	0	0	0
P23471	Receptor-iPTPRZ1	3769.577	3778.1	4271.455	15068.59	22215.65	0
P23526	Adenosylh AHCY	567316.3	588292.7	678983.9	433160.9	399695.3	450404.5
P23528	Cofilin-1 CFL1	3532851	3335559	2637645	353840.9	230560.1	369754.2
P23588	Eukaryotic EIF4B	3005.857	3767.909	3544.085	0	0	0
P23677	Inositol-tri ITPKA	3148.011	3628.016	4165.306	0	0	0
P23919	Thymidylat DTYMK	67149.72	67972.13	66070.04	0	0	0
P23921	Ribonuclec RRM1	61215.11	64621.39	77627.86	32617.52	0	40310.43
P24043	Laminin su LAMA2	45457.39	46769.24	46127.98	61991.2	66399.36	19241.04
P24386	Rab protei CHM	7081.992	8327.18	3284.627	0	0	0
P24394	Interleukin IL4R	16569.71	9633.532	13532.49	0	0	0
P24534	Elongation EEF1B2	92760.78	31003.77	87696.65	0	0	0
P24666	Low molec ACP1	69359.24	66307.55	73483.86	0	0	0
P24821	Tenascin TNC	119927.9	109347.5	148830.2	1014257	1299209	1850307
P24941	Cyclin-de γ CDK2	233664.1	235614.6	203436.6	0	0	0
P25098	Beta-adrer ADRBK1	15999.99	16007.92	15300.66	0	0	0
P25116	Proteinase F2R	43445.62	41304.69	36658.55	0	0	0
P25205	DNA replic MCM3	10900.69	11199.41	12168.09	0	0	0
P25325	3-mercapt MPST	21393.39	20527.61	23680.02	0	0	0
P25391	Laminin su LAMA1	81804.8	84088.16	85485.34	72692.16	21761.62	15202.79
P25398	40S riboso RPS12	14798.36	18930.99	16296.54	26241.1	0	29554.4
P25685	DnaJ homc DNAJB1	13751.73	13541.57	10256.79	0	0	0
P25786	Proteasom PSMA1	74368.35	67136.15	99074.22	155388.7	72433.41	176696.1
P25787	Proteasom PSMA2	42391.9	22565.85	54589.14	60645.3	0	71392.14
P25788	Proteasom PSMA3	56716.36	51097.89	67266.71	96510.58	48027.72	73604.73
P25789	Proteasom PSMA4	243925.5	241996.5	297530.6	183114.4	0	181164.6
P26006	Integrin al β ITGA3	548641.3	534405.8	476519.9	65444	95352.14	98118.67
P26022	Pentraxin- PTX3	175182.4	147850.2	217663.1	5258973	5900698	4052882
P26038	Moesin MSN	3311767	3245841	3067309	175839.6	143079.8	142847.2
P26232	Catenin al β CTNNA2	34102.47	37230.55	28735.49	0	0	0
P26358	DNA (cyto: DNMT1	6229.929	8609.217	9202.223	0	0	0
P26368	Splicing fa: U2AF2	7982.995	7939.718	7896.79	0	55446.54	27127.76
P26373	60S riboso RPL13	54178.68	47616.16	55531.46	109179.1	0	92670.12
P26583	High mobi HMGB2	6809.559	6310.305	7611.938	200395.9	0	265663.4
P26639	Threonine- TARS	64432.39	69404.98	71497.41	0	0	0
P26640	Valine--tR VARS	31031.32	30282.8	33440.88	34824.42	0	3077459
P26641	Elongation EEF1G	160334.8	166125.9	130297.1	143115.5	0	121053.2
P26927	Hepatocyt: MST1	58335.46	54299.87	77651.38	496300.6	651340.6	337064.9
P27105	Erythrocyt: STOM	185684.1	135528.2	153076.2	90858.41	377093.6	537546.1
P27348	14-3-3 prc YWHAQ	308826.7	292402.8	321685.1	0	81860.28	193102.2
P27361	Mitogen-a MAPK3	9732.484	8531.196	14843.14	0	0	0
P27448	MAP/micr: MARK3	31490.96	29735.19	26807.77	0	0	0
P27635	60S riboso RPL10	9308.512	27428.69	0	370579.1	0	196406.8
P27658	Collagen a COL8A1	3016.81	2566.205	0	106448	0	114843
P27694	Replicator RPA1	7552.458	8940.097	7204.613	0	0	0
P27695	DNA-(apu APEX1	4695.581	7964.373	8685.086	0	0	0
P27701	CD82 anti γ CD82	470344.4	464133.5	474329.4	336899.3	360719.3	285588.5
P27708	CAD prote CAD	121080.2	104121.2	151215.7	98922.84	36475.49	102711
P27816	Microtubu MAP4	4009.459	3360.061	4199.01	0	0	0
P27986	Phosphatic PIK3R1	12822.73	6281.726	9734.533	0	0	0
P28065	Proteasom PSMB9	3295.465	5542.842	981.8821	48954.49	0	34380
P28066	Proteasom PSMA5	116033.7	124084.2	142086.9	59979.58	0	88638.95

P28070	Proteasom	PSMB4	105795.1	70795.49	65547.66	0	0	0
P28072	Proteasom	PSMB6	113092.8	99943.1	108460.5	0	0	0
P28074	Proteasom	PSMB5	87010.83	97325.89	124769.8	88018.07	0	80479.29
P28340	DNA polyr	POLD1	126199	120325.3	303412.3	0	0	0
P28482	Mitogen-a	MAPK1	9663.09	10609.94	17198.35	0	0	0
P28827	Receptor-i	PTPRM	26400.93	39566.26	43332.05	0	0	0
P28838	Cytosol an	LAP3	8667.288	8859.294	9394.686	0	0	0
P29218	Inositol mc	IMPA1	22474.43	21583.66	20289.65	0	0	0
P29279	Connective	CTGF	250001.4	189784.3	271716	653843.9	183631.5	555122.1
P29317	Ephrin typ	EPHA2	183128.9	184250.1	165098.4	220922.2	122074	0
P29323	Ephrin typ	EPHB2	80847.69	84013.85	71628.56	0	0	0
P29353	SHC-trans	SHC1	1118.223	1321.258	3800.431	0	0	0
P29373	Cellular ret	CRABP2	28758.84	29583.01	42207.52	0	0	0
P29401	Transketol	TKT	76947.53	59905.1	82285.6	41212.16	105995.6	0
P29597	Non-receç	TYK2	18416.27	18058.32	17419.93	624058.2	420228.9	221371.3
P29692	Elongation	EEF1D	42238.5	37988.91	32373.99	0	0	0
P29966	Myristoyla	MARCKS	585363.9	817655.5	855201.3	145674.5	218640.9	173402
P30041	Peroxi-redc	PRDX6	330974.2	346297.6	325798.3	259275.2	386791.8	203849.8
P30044	Peroxi-redc	PRDX5	91115.11	90572.88	85953.5	18218.36	0	28496.21
P30046	D-dopachi	DDT	48175.3	50564.66	80489.84	0	0	0
P30050	60S riboso	RPL12	45886.82	43855.21	43431.68	65994.09	38388.59	59679.95
P30085	UMP-CMP	CMCK1	47799.12	50768.02	44973.64	0	66511.83	18704.8
P30086	Phosphatic	PEBP1	102572.2	89844.1	80956.58	864857.3	749178.4	378717.7
P30101	Protein dis	PDIA3	20344.7	21156.39	20954.79	117309.3	106873.5	101523
P30260	Cell divisio	CDC27	3836.85	3330.99	3222.542	0	0	0
P30530	Tyrosine-ç	AXL	36530.15	33484.78	86457.89	0	0	0
P30566	Adenylosu	ADSL	15836.91	16228.97	14415.16	0	0	0
P30613	Pyruvate k	PKLR	12472.59	14388.37	13292.7	0	0	0
P30626	Sorcina	SRI	174439.5	160505.6	158114.5	53859.1	0	121597.1
P30825	High affini	SLC7A1	317088.3	273609.4	288341	0	0	0
P30876	DNA-direc	POLR2B	9069.708	5233.447	6327.32	0	0	0
P31146	Coronin-1	CORO1A	14867.01	19086.17	19274.7	46749.95	0	73769.52
P31150	Rab GDP c	GDI1	39428.62	40732.27	38662.2	0	0	0
P31151	Protein S1	S100A7	0	6571.135	68214.88	69399.45	0	377961.9
P31323	cAMP-deç	PRKAR2B	13864.87	22949.46	22746.01	0	0	0
P31350	Ribonuclec	RRM2	29652.97	31828.51	21205.64	0	0	0
P31431	Syndecan-	SDC4	932008.1	887749.9	765806	278091	341028.8	188536.7
P31641	Sodium- a	SLC6A6	208750.4	225182.6	193144.2	0	0	0
P31689	DnaJ hom	DNAJA1	137367.2	132480	142788	0	0	0
P31749	RAC-alpha	AKT1	11623.66	10728.7	9195.713	0	0	0
P31939	Bifunction	ATIC	136393.5	137801.7	133328.4	66230.28	0	78304.53
P31946	14-3-3 pr	YWHAB	1487788	1302901	1420271	457719.9	665098	334443.9
P31948	Stress-ind	STIP1	47251.4	47934.93	41455.84	0	53418.32	39852.93
P31949	Protein S1	S100A11	92609.4	90579.77	74448.42	0	0	0
P32119	Peroxi-redc	PRDX2	124896.9	37985.19	56066.01	874579.1	2926373	696385.6
P32121	Beta-arres	ARRB2	14030.74	14347.3	11473.9	0	0	0
P32754	4-hydroxy	HPD	10108.37	16269.61	20645.22	82480.48	0	29991.63
P32856	Syntaxin-2	STX2	25070.3	25514.55	25689.71	0	0	0
P32929	Cystathion	CTH	3031.116	3120.146	1964.149	0	0	0
P32969	60S riboso	RPL9	14992.88	9667.371	13989.59	0	0	0
P32970	CD70 antiç	CD70	87878.7	85822.01	87573.87	0	0	0
P33121	Long-chai	ACSL1	6131.029	10545.73	6222.228	0	0	0
P33151	Cadherin-	CDH5	21131.63	16795.39	25167.44	0	0	0
P33176	Kinesin-1	KIF5B	41789.19	38997.11	33950.85	20263.89	0	97795.73
P33316	Deoxyuridi	DUT	68390.14	58249.77	70173.48	0	0	0
P33527	Multidrug	ABCC1	27046.61	35977.91	26107.52	0	0	0
P33908	Mannosyl-	MAN1A1	13268.09	16263.67	8548.771	0	0	0
P33991	DNA replic	MCM4	13203.59	35296.54	26697.95	0	0	0

P33993	DNA replic MCM7	7480.018	8401.94	8283.792	0	0	0
P34096	Ribonuclea RNASE4	25916.49	55479.34	78799.86	394484.2	899940.6	176979
P34810	Macrosialin CD68	26623.2	23829.88	24259.97	0	0	0
P34896	Serine hyd SHMT1	2795.367	8057.241	7389.356	0	0	0
P34897	Serine hyd SHMT2	18903.75	16770.21	15097.12	0	0	0
P34913	Bifunctional EPHX2	19730.54	18096.55	23392.5	0	0	0
P35052	Glypican-1GPC1	464633.8	470309.6	388622.2	374183.1	449793.3	346271.7
P35080	Profilin-2 PFN2	177153.5	165108	156367.4	0	0	0
P35222	Catenin beta CTNNB1	218222.7	218113.8	193836.7	1837456	0	259060.6
P35237	Serpin B6 SERPINB6	23095.93	20239.37	23209.21	0	0	0
P35240	Merlin NF2	30589.43	29773.34	28554.66	0	0	0
P35241	Radixin RDX	11674039	12040106	10426629	590720.6	0	491819.5
P35249	Replicator RFC4	7639.227	8899.927	7883.316	0	0	0
P35250	Replicator RFC2	6876.766	7892.565	6676.007	0	0	0
P35268	60S riboso RPL22	54380	58881.79	43815.88	0	0	0
P35354	Prostaglandin PTGS2	7051.1	3198.456	2796.361	0	0	0
P35367	Histamine HRH1	19142.36	15659.81	22017.63	0	0	0
P35442	Thrombosin THBS2	312506.6	286563.8	361508.3	12761292	16182934	18263486
P35443	Thrombosin THBS4	244322.3	238632.8	500335.6	4121698	5082330	3146594
P35520	Cystathionin CBS	9155.757	9973.041	6954.328	0	0	0
P35527	Keratin, type KRT9	68079.08	138127.1	88918.57	1450968	1080219	952070.8
P35555	Fibrillin-1 FBN1	11472.07	10436.49	11454.57	736185.1	819462.9	334094.3
P35573	Glycogen alpha AGL	7669.777	7300.216	8509.054	31137.61	0	22176.75
P35579	Myosin-9 MYH9	105033.2	109749.8	101047.5	1586663	1109664	2097555
P35580	Myosin-10 MYH10	21396.45	20884.98	20917.27	25781.76	0	41446.24
P35590	Tyrosine-phosphatase TIE1	15019.71	20994.79	19143.96	75566.35	151418.4	75198.24
P35606	Coatomer COPB2	25992.44	26533.77	18938.63	199634.6	0	51834.25
P35609	Alpha-actinin ACTN2	6182.233	8751.242	6000.094	0	0	0
P35611	Alpha-actinin ADD1	18400.9	19508.09	17332.95	0	0	0
P35613	Basigin BSG	2796074	2601753	2574789	111841.6	370525.9	229997.5
P35637	RNA-binding FUS	656.3418	949.5368	982.4919	0	0	0
P35659	Protein DEK	3654.717	6412.455	6146.479	0	0	0
P35754	Glutaredoxin GLRX	38207.89	38279.6	34984.61	27107.58	0	21645.74
P35813	Protein phosphatase PPM1A	10862.02	15310.34	13317.37	0	0	0
P35858	Insulin-like IGFALS	14425.52	20172.28	27117.75	157362.4	0	137216
P35908	Keratin, type KRT2	300333.8	813002.1	612862.1	3921650	4317927	3845191
P35998	26S proteasome PSMC2	43676.42	62664.58	73020.03	130122.5	0	114981.1
P36383	Gap junction GJC1	64676.75	57073.8	60841.4	0	0	0
P36404	ADP-ribosylation ARL2	13668.66	13928.68	14882.96	0	0	0
P36507	Dual specific MAP2K2	19632.41	13360.1	18452.63	0	0	0
P36578	60S riboso RPL4	101175.2	111443.4	48389.89	439432.4	163174.8	164768.5
P36639	7,8-dihydroxy NUDT1	10641.45	12795.19	12732.64	0	0	0
P36871	Phosphoglucose PGM1	29650.13	35263.84	35628.2	70538.02	0	57453.18
P36894	Bone morphogen BMPR1A	20567.06	19248.63	15717.92	0	0	0
P36896	Activin receptor ACVR1B	10459.79	5626.749	9606.875	0	0	0
P36897	TGF-beta type I TGFBR1	38731.53	32284.74	32415.27	0	0	0
P36915	Guanine nucleotide GNL1	8255.161	6253.688	7698.381	0	0	0
P36941	Tumor necrosis LTBR	23655.72	41670.96	38283.34	0	0	0
P36955	Pigment epithelial SERPINF1	717322.6	681092	952768.6	6594453	9604032	5833403
P36969	Phosphogluconate GPX4	13526.63	12529.72	15661.9	0	0	0
P37173	TGF-beta type I TGFBR2	11767.33	10778.83	8961.181	0	0	0
P37235	Hippocalcin HPCAL1	23907.62	22974.07	18400.56	0	0	0
P37802	Transgelin TAGLN2	300879.8	300655	303936.3	535100.7	755208.1	510033.4
P37837	Transaldolase TALDO1	35393.66	34400.63	32940.98	36514.13	0	19887
P38606	V-type proton ATPase ATP6V1A	27692.71	26885.82	26002.32	0	0	0
P38646	Stress-70 protein HSPA9	9891.303	10238.11	7698.904	0	0	0
P38919	Eukaryotic EIF4A3	30407.4	31866.76	33019.71	0	0	0
P39023	60S riboso RPL3	43698.73	35385.48	26855.36	301901	0	143680.8

P39059	Collagen a COL15A1	13881.52	14064.61	21347.51	299284.7	425056.8	527137.8
P39060	Collagen a COL18A1	27190.72	38239.04	46983.71	152962.1	246012.4	199019.7
P39656	Dolichyl-d DDOST	8008.86	9256.522	5817.031	0	0	0
P39748	Flap endor FEN1	20970.69	10122.68	11027.96	0	0	0
P40121	Macrophag CAPG	11916.52	16661.21	10957.68	0	0	0
P40123	Adenylyl c CAP2	15076.79	13125.08	11673.48	0	0	0
P40189	Interleukin IL6ST	28596.85	26874.38	27437.05	0	0	0
P40227	T-complex CCT6A	61407.16	53409.42	62511.23	36129.03	0	26595.21
P40261	Nicotinami NNMT	901470.7	913259.6	700146.3	128469.6	0	19585.66
P40429	60S riboso RPL13A	78398.63	90048.03	54935.95	374509.3	125134.8	187870.9
P40616	ADP-ribos ARL1	29685.28	30293.18	27943.67	0	0	0
P40763	Signal tran STAT3	6819.661	6958.905	7424.647	0	0	0
P40818	Ubiquitin c USP8	17515.62	17116.28	15983.46	0	0	0
P40925	Malate dehyd MDH1	80397.47	94369.52	87551.37	83937.3	76213.53	46654.41
P40937	Replicator RFC5	1815.882	1696.585	1452.854	0	0	0
P40938	Replicator RFC3	5320.766	5134.731	5497.268	0	0	0
P41091	Eukaryotic EIF2S3	29328.53	19000.34	46474.12	0	0	0
P41221	Protein Wnt WNT5A	26922.45	8045.867	16174.58	200939.4	197744.2	462463.6
P41227	N-alpha-a NAA10	5500.567	6299.499	6567.567	0	0	0
P41240	Tyrosine-tyr CSK	13715.51	12226.19	14333.92	0	0	0
P41250	Glycine--t GARS	36000.23	38298.39	33183.24	86277.4	0	78438.21
P41252	Isoleucine- IARS	32089.05	30598.56	39959.36	73344.55	0	47734.98
P41440	Folate tran SLC19A1	100204.9	110274.1	111975.1	0	0	0
P41743	Protein kin PRKCI	52312.89	43059.55	39755.03	0	0	0
P42025	Beta-centr ACTR1B	31003.24	31672.98	32124.29	0	0	0
P42166	Lamina-as TMPO	2285.93	3229.697	33941.52	0	0	0
P42229	Signal tran STAT5A	7886.298	6149.54	6814.457	0	0	0
P42285	Superkiller SKIV2L2	1472.843	1253.255	1329.052	0	0	0
P42336	Phosphatic PIK3CA	3586.386	3992.896	3371.67	0	0	0
P42345	Serine/thr MTOR	29331.96	30336.91	28346.55	0	0	0
P42356	Phosphatic PI4KA	49124.78	40473.19	42308.54	0	0	0
P42704	Leucine-ric LRPPRC	12942.58	16760.35	1739.361	0	0	0
P42766	60S riboso RPL35	36111.62	33002.69	17717.81	83681.4	0	68882.77
P42858	Huntingtin HTT	5657.713	6256.326	6780.435	0	0	0
P42892	Endothelin ECE1	26451.55	32661.33	22450.95	0	0	0
P43007	Neutral an SLC1A4	208222.1	201141.8	197525.4	84354.33	69500.54	160293.5
P43034	Platelet-ac PAFAH1B1	62973.39	45593.6	47829.24	0	106988.5	140059.1
P43121	Cell surfac MCAM	56888.41	47324.07	44489.8	0	0	0
P43246	DNA mism MSH2	8075.029	6895.141	7530.083	0	0	0
P43250	G protein- GRK6	16665.66	16682.11	14869.37	0	0	0
P43487	Ran-specif RANBP1	48922.02	55432.18	35946.98	0	0	0
P43490	Nicotinami NAMPT	21398.85	25495.73	22012.1	0	0	0
P43652	Afamin AFM	356036.3	715567.3	1025683	5852610	8279819	3657650
P45877	Peptidyl-p PPIC	5784.928	5902.411	8440.591	22691.54	0	14425.15
P45880	Voltage-d VDAC2	1491.421	4066.146	4980.331	0	0	0
P46019	Phosphory PHKA2	2592.138	2023.873	2749.859	0	0	0
P46060	Ran GTPas RANGAP1	20882.15	19435.88	20783.25	0	0	0
P46063	ATP-depei RECQL	8610.291	6896.357	5134.626	0	0	0
P46108	Adapter m CRK	16537.1	17278.27	11891.01	0	0	0
P46109	Crk-like pr CRKL	42047	41878	38630.55	0	0	0
P46379	Large proli BAG6	7691.73	12096.14	17070.12	0	0	0
P46531	Neurogeni NOTCH1	6923.657	9320.405	8136.783	0	0	0
P46734	Dual speci MAP2K3	3206.673	10123.54	12675.79	0	0	0
P46776	60S riboso RPL27A	197672	170159	101234.2	363245.3	0	244713.4
P46778	60S riboso RPL21	16042.35	28580.33	20855.61	44947.46	0	25222.69
P46779	60S riboso RPL28	11398.94	8992.952	10432.35	0	0	0
P46781	40S riboso RPS9	194786.3	216093.4	170276.8	286528.7	0	212652.6
P46783	40S riboso RPS10	13641.02	3690.124	22122.71	0	0	0

P46926	Glucosami GNPDA1	25811.36	11431.51	38885.9	0	0	0
P46939	Utrophin UTRN	21771.42	23197.9	21068.11	0	0	0
P46940	Ras GTPas IQGAP1	339740.3	331100.7	353268	946158.3	3378706	751005.9
P46952	3-hydroxy HAAO	34636.03	0	36279.78	154607	233416.2	0
P47755	F-actin-ca CAPZA2	249074.7	262877.9	223947.7	257106.1	340079.7	255140.5
P47895	Aldehyde c ALDH1A3	29027.59	30395.67	26542.73	0	0	0
P47914	60S riboso RPL29	43234.61	38734.45	25113.9	226760.7	0	122028.7
P47929	Galectin-7 LGALS7	8256.094	16841.57	8812.322	82412.69	0	124450
P48029	Sodium- a SLC6A8	20296.44	17268.24	16977.81	0	0	0
P48059	LIM and se LIMS1	113672.2	129151	146090.4	267761.3	131554.8	389170.4
P48060	Glioma pai GLIPR1	19148.36	16876.49	16220.96	0	0	0
P48067	Sodium- a SLC6A9	10038.46	12966.45	13623.92	0	0	0
P48147	Prolyl endc PREP	22475.03	27829.35	23413.46	0	0	0
P48163	NADP-dec ME1	20316.46	16033.1	1663.74	0	0	0
P48449	Lanosterol LSS	82676.38	72946.42	7106.087	0	0	0
P48506	Glutamate GCLC	10485.36	11792.8	9587.11	0	54635.28	29257.06
P48507	Glutamate GCLM	28812.53	27455.9	27030.01	93683.2	25525.57	118412.3
P48509	CD151 ant CD151	1229945	680427.5	1312156	86873.29	0	162621.3
P48556	26S protea PSMD8	14619.35	20908.58	21860.07	0	0	0
P48643	T-complex CCT5	54803.85	40518.79	56937.8	68410.31	0	74324.78
P48723	Heat shock HSPA13	64361.91	18570.69	18523.8	112141.1	196403.3	101769.1
P48729	Casein kinc CSNK1A1	19828.92	21593.97	18131.48	0	0	0
P48730	Casein kinc CSNK1D	13996.88	19125.25	13546.95	0	0	0
P48735	Isocitrate c IDH2	1964.843	2608.079	2213.171	0	0	0
P48736	Phosphatic PIK3CG	8108.986	9185.395	10445.05	0	0	0
P48739	Phosphatic PITPNB	52083.38	48074.86	45004.8	0	0	0
P48740	Mannan-b MASP1	32180.23	16866.11	32581.33	544179.4	468809.7	546199.8
P48960	CD97 antiç CD97	60958.88	62855.26	56501.46	0	0	0
P49023	Paxillin PXN	8854.212	12107.32	8433.752	0	0	0
P49189	4-trimethy ALDH9A1	43871.32	39163.85	49037.48	52866.31	0	39805
P49257	Protein ER LMAN1	30434.08	29455.45	26438.24	0	0	0
P49327	Fatty acid c FASN	176310.2	169428.8	204065	341196.7	296635.1	22849.91
P49368	T-complex CCT3	153116.2	152563.3	169169.6	251895.5	307944.7	226285.9
P49419	Alpha-ami ALDH7A1	16786.64	13052.17	15800.4	0	0	0
P49458	Signal recc SRP9	19471.38	20162.71	19231.41	0	0	0
P49589	Cysteine-- CARS	23645.4	20110.19	17286.85	0	0	0
P49591	Serine-- tR SARS	93523.41	92865.55	93221.33	165330.3	0	69157.27
P49642	DNA primc PRIM1	2384.919	2828.288	3513.458	0	0	0
P49721	Proteasom PSMB2	106251.2	101033.9	121856.4	107652.7	153592.3	124003.8
P49736	DNA replic MCM2	6254.597	6361.117	7336.646	0	0	0
P49746	Thrombosj THBS3	306084.3	307646.4	420117.3	3353682	1933116	1242553
P49747	Cartilage c COMP	82534.63	78965.99	115334.2	474714.5	842766	542616.3
P49756	RNA-bindir RBM25	6722.559	7173.258	9961.418	0	0	0
P49757	Protein nu NUMB	57881.11	59186.73	43296.98	0	0	0
P49773	Histidine tr HINT1	35204.43	28767.38	28270.36	0	0	0
P49795	Regulator c RGS19	83890.52	79367.48	83866.33	0	0	0
P49840	Glycogen c GSK3A	5082.756	5696.216	2793.087	0	0	0
P49841	Glycogen c GSK3B	4202.666	4461.722	3136.881	0	0	0
P49902	Cytosolic p NT5C2	18062.09	16210.5	14984.78	0	0	0
P49915	GMP synth GMPS	63483.11	66488.95	62751.54	55682.5	28037.98	64366.95
P49959	Double-str MRE11A	2007.486	5883.25	5228.863	0	0	0
P50148	Guanine nç GNAQ	422929.5	455005.3	404573.1	0	0	0
P50150	Guanine nç GNG4	87441.73	62785.22	90010.98	0	0	0
P50151	Guanine nç GNG10	293203	286466.6	313646.3	0	0	0
P50281	Matrix met MMP14	159112.7	156209.2	138976.2	14407011	17113416	6649655
P50395	Rab GDP c GDI2	268706.1	270500.3	250087.4	201159.8	289885.8	165554.2
P50443	Sulfate tras SLC26A2	43137.51	45056.08	39097.89	0	0	0
P50454	Serpin H1 SERPINH1	12283.42	12881.87	13134.04	92115.6	0	58914.52

P50479	PDZ and L PDLIM4	20542.83	9707.508	18358.49	0	0	0
P50502	Hsc70-inte ST13	89489.25	92321.56	81601.88	174720	113459.3	144820.3
P50570	Dynamin-1 DNMT2	35119.41	33620.13	32563.08	42013.88	14185.54	80349.38
P50583	Bis(5-nucle NUDT2	7226.916	7080.926	7269.183	10972.29	0	12644.83
P50748	Kinetochore KNTC1	10174.54	6527.131	6931.543	0	0	0
P50897	Palmitoyl- PPT1	20354.17	18451.44	11438.85	0	0	0
P50914	60S ribosome RPL14	140533.3	147550	94273.45	535075.2	0	202625.1
P50990	T-complex CCT8	145260.4	141788.4	146112	67177.52	69977.49	176332.5
P50991	T-complex CCT4	169511.3	157933.6	173796.7	129441.5	52399.73	139428.4
P50995	Annexin A ANXA11	506660.9	483501.9	502869.3	111385.3	81562.49	167797.1
P51148	Ras-related RAB5C	702735.3	686781.4	683213.1	0	0	0
P51149	Ras-related RAB7A	1091709	1053675	986073.9	167883.9	150092	231399.6
P51151	Ras-related RAB9A	20135.46	19712.33	13365.32	0	0	0
P51159	Ras-related RAB27A	34726.34	31503.49	28697.03	0	0	0
P51178	1-phospho PLCD1	5178.86	4943.55	9051.53	0	0	0
P51570	Galactokinase GALK1	103881.2	108566	128865.6	216940	0	310678.4
P51572	B-cell receptor BCAP31	11267.15	7257.913	12055.49	0	0	0
P51580	Thiopurine TPMT	11201.4	10597.25	12338.28	0	0	0
P51668	Ubiquitin-1 UBE2D1	12096.6	12621.43	10760.16	0	0	0
P51674	Neuronal r GPM6A	61218.56	60704.75	58413.63	0	0	0
P51797	Chloride transporter CLCN6	9083.168	8760.947	8381.09	0	0	0
P51798	H(+)/Cl(-) CLCN7	6652.594	6596.673	5700.028	0	0	0
P51809	Vesicle-associated VAMP7	24992.21	27380.83	18070.37	0	0	0
P51812	Ribosomal RPS6KA3	18360.34	20540.01	9787.271	0	0	0
P51828	Adenylate ADCY7	10999.24	9545.063	10081.38	0	0	0
P51884	Lumican LUM	409843.3	412555.9	626848.3	5233277	7073753	2957281
P52209	6-phospho PGD	65995.03	70056.84	62347.21	0	60463.39	59889.23
P52272	Heterogeneous HNRNPM	17545.69	10537.85	9179.9	0	0	0
P52292	Importin alpha KPNA2	75173.29	74962.46	63842.36	0	0	0
P52294	Importin alpha KPNA1	8740.892	6548.583	6069.178	0	0	0
P52306	Rap1 GTPase RAP1GDS1	8746.048	7823.974	264324.6	0	0	0
P52569	Cationic anion SLC7A2	92405.88	104249.2	117677.1	0	0	0
P52594	Arf-GAP domain AGFG1	25128.07	27334.77	31441.32	0	0	0
P52655	Transcription factor GTF2A1	8711.167	11910	7074.404	0	0	0
P52701	DNA mismatch MSH6	15850.48	12020.85	11999.66	0	0	0
P52758	Ribonucleic acid HRSP12	10160.4	9671.941	16697.44	62007.31	80021.64	37036.96
P52789	Hexokinase HK2	11037.78	10863.3	7725.922	0	0	0
P52799	Ephrin-B2 EFNB2	14468.85	13653.49	14793.56	0	0	0
P52823	Stanniocalcin STC1	0	0	0	108828.1	111768	47332.22
P52888	Thimet oligopeptidase THOP1	11380.39	9589.72	9742.567	0	0	0
P52907	F-actin-capping CAPZA1	303901.6	296001.9	242199.8	78834.39	117225.8	123305.7
P53004	Biliverdin reductase BLVRA	30767.21	27189.34	30572.52	0	0	0
P53384	Cytosolic FNUBP1	7324.387	7044.364	10049.1	0	0	0
P53396	ATP-citrate lyase ACLY	79852.66	83301.63	89141.04	127618.5	70695.2	122859
P53621	Coatomer complex COPA	13756.92	13897.77	11355.79	51662.27	0	17481.03
P53634	Dipeptidyl peptidase CTSC	39932.71	40223.91	54466.84	291105.8	605369.6	322451.3
P53675	Clathrin heavy chain CLTCL1	47883.61	38406.57	50099.5	0	0	0
P53680	AP-2 complex AP2S1	63691.2	67629.27	66106.4	12192.28	0	14399.82
P53794	Sodium/magnesium SLC5A3	84414.74	90742.07	89560.56	0	0	0
P53801	Pituitary tumor PTTG1IP	755788.6	689983.2	644428.4	0	0	0
P54136	Arginine-- RARS	60911.13	58983.97	62471.68	0	0	0
P54252	Ataxin-3 ATXN3	8464.431	7076.626	9429.407	0	0	0
P54289	Voltage-dependent CACNA2D	60837.35	59918.35	68665.7	130190.4	168615.8	75846.95
P54577	Tyrosine-- YARS	4752309	33025.7	43107.62	0	25972.88	2.32E+08
P54578	Ubiquitin conjugase USP14	46671.21	48425.78	46052.98	0	0	0
P54619	5-AMP-activated PRKAG1	7673.13	9317.71	11823.03	0	0	0
P54652	Heat shock protein HSPA2	4028717	3896790	3455992	1022708	834494.4	1333530
P54687	Branched-chain BCAT1	22180.82	28241.44	18825.49	0	0	0

P54727	UV excision	RAD23B	36251.02	34183.25	26513.34	0	0	0
P54760	Ephrin type 2	EPHB4	215235.3	224945.2	209064.7	0	0	0
P54764	Ephrin type 2	EPHA4	12550.2	13137.86	8577.389	0	0	0
P54852	Epithelial cell	EMP3	95368.49	125755.7	87132.06	0	0	0
P55001	Microfibrillar	MFAP2	11511.91	11613.31	15206.2	57025.92	132073.6	59632.9
P55011	Solute carrier	SLC12A2	44207.81	41151.49	36658.7	0	0	0
P55039	Developmental	DRG2	7338.25	8114.146	7591.102	0	0	0
P55058	Phospholipase	PLTP	4515.894	17125.04	15596.48	0	0	0
P55072	Transition state	VCP	234438.7	219419.1	270544.4	601210.6	702868.1	434573.7
P55082	Microfibrillar	MFAP3	27961.71	33419.82	11897.84	0	0	0
P55085	Proteinase	F2RL1	41302.2	41041.79	41805.88	0	0	0
P55196	Afadin	MLLT4	145138.4	129714.2	123137.4	0	0	0
P55263	Adenosine	ADK	90343.61	87128.39	95820.41	81258.3	74845.74	107763.4
P55268	Laminin subunit	LAMB2	0	0	0	240018.3	299273.3	269564.7
P55285	Cadherin-1	CDH6	8974.295	9176.19	16025.94	263199.5	355019.1	180554.9
P55287	Cadherin-1	CDH11	13763.77	23572.3	28573.01	51290.77	137032.8	63581.63
P55290	Cadherin-1	CDH13	69006.82	65259.14	73271.69	313293	335220.8	271303.9
P55854	Small ubiquitin	SUMO3	118085.5	140055.2	132955.2	0	83022.21	36787.14
P55884	Eukaryotic	EIF3B	46325.28	49490.45	47352.94	49992.45	0	58704.16
P56192	Methionine	MARS	45412.5	30527.98	54982.08	0	0	0
P56537	Eukaryotic	EIF6	59415.63	58402.25	53838.92	0	0	0
P56545	C-terminal	CTBP2	6184.859	5764.435	6291.619	0	0	0
P56557	Transmembrane	TMEM50B	11004.83	9917.006	10656.79	0	0	0
P56559	ADP-ribosyl	ARL4C	2071.729	2752.304	2597.038	0	0	0
P56945	Breast cancer	BCAR1	5453.484	6618.924	7275.281	0	0	0
P57075	Ubiquitin-1	UBASH3A	190448.2	188122.2	186554.9	0	0	0
P57087	Junctional	JAM2	14615.16	11406.89	11165.04	0	0	0
P57088	Transmembrane	TMEM33	10089.5	5206.209	9235.5	0	0	0
P57737	Coronin-7	CORO7	18372.98	14379.39	13488.54	0	0	0
P57764	Gasdermin	GSDMD	44236.64	43978.59	25436.34	0	0	0
P58546	Myotrophin	MTPN	31687.86	30289.22	29328.36	0	0	0
P59768	Guanine nucleotide	GNG2	72627.31	72684.46	75343.32	0	0	0
P59998	Actin-related	ARPC4	546434.8	550923.9	429952.3	0	83282.08	79696.24
P60033	CD81 antigen	CD81	9180990	8083270	8601820	1900062	1581627	3493846
P60174	Triosephosphate	TPI1	873439.4	875483.8	890705.8	612185.1	791724.8	478278.5
P60228	Eukaryotic	EIF3E	22124.94	22061.78	20291.72	0	34705.58	46802.96
P60468	Protein translocator	SEC61B	7120.533	10247.23	6004.925	0	0	0
P60510	Serine/threonine	PPP4C	6144.028	5590.85	4779.335	0	0	0
P60520	Gamma-aminobutyric acid	GABARAP1	46389.82	37595.43	36205.27	0	0	0
P60660	Myosin light chain	MYL6	281194.1	278378.6	253769.2	710507.8	645990.9	834062.3
P60709	Actin, cytoplasmic	ACTB	14243921	15145455	14161980	6261976	7845540	5209281
P60763	Ras-related	RAC3	3050777	3000850	2935979	487732.5	501458.9	874617.4
P60842	Eukaryotic	EIF4A1	668411.2	663240.4	617589.4	274392.6	309223.2	259137.9
P60866	40S ribosome	RPS20	52559.8	39343.82	40132.35	43334.54	0	43740.13
P60900	Proteasome	PSMA6	77575.3	77354.95	89368.62	89078.78	82337.61	75443.92
P60903	Protein S100	S100A10	539297.3	509740.5	471190.2	0	0	0
P60953	Cell division	CDC42	531263.4	635027.7	538824.9	141234.6	55109.74	193880.1
P60981	Dextrin	DSTN	429548.7	440206.7	398469.8	240116	0	247415.7
P60983	Glia maturation	GMFB	67418.47	60795.49	54834.76	0	0	0
P61011	Signal receptor	SRP54	5156.412	5500.787	0	145157.8	0	217647.1
P61019	Ras-related	RAB2A	296640.4	272412.6	263321.6	87045.52	160335.3	91564.16
P61020	Ras-related	RAB5B	38847.45	37612.67	35828.55	0	0	0
P61026	Ras-related	RAB10	507322.5	464808.2	594733.6	103561.3	122831.8	244707.1
P61077	Ubiquitin-1	UBE2D3	147926.7	147275.3	174801.1	0	0	0
P61081	NEDD8-ubiquitin	UBE2M	109254.2	110481.5	117685.8	0	0	0
P61086	Ubiquitin-1	UBE2K	42111.9	26166.86	31883.46	0	0	0
P61088	Ubiquitin-1	UBE2N	135403.6	125248.4	85138.89	0	0	0
P61106	Ras-related	RAB14	90537.01	92180.95	80637.11	0	0	0

P61160	Actin-relat	ACTR2	216555.9	216722.7	183366.5	62835.01	0	45822.85
P61163	Alpha-cen	ACTR1A	36116.54	37448.34	62829.45	0	0	0
P61204	ADP-ribos	ARF3	1050299	1045676	1069877	417896.3	304944.6	432398.3
P61221	ATP-bindin	ABCE1	37301.73	37763.85	42494.39	0	0	0
P61224	Ras-relate	RAP1B	1045838	1617043	1320353	951262.6	1428546	480165.9
P61247	40S riboso	RPS3A	90407.03	104816.7	86737.74	145218.5	46896.07	115120.1
P61289	Proteasom	PSME3	10470.94	9097.298	9078.174	0	0	0
P61313	60S riboso	RPL15	109833.3	60277.35	130109.2	206750.1	0	139648.8
P61353	60S riboso	RPL27	18293.08	20620.24	8542.936	160842	0	185503.7
P61421	V-type prc	ATP6V0D1	14852.18	18211.41	13940.13	0	0	0
P61457	Pterin-4-a	PCBD1	6006.209	5179.166	7003.997	0	0	0
P61586	Transformi	RHOA	183585.8	178978.3	199630.5	0	0	0
P61587	Rho-relate	RND3	15134.39	15014.74	15043.41	0	0	0
P61758	Prefoldin s	VBP1	42169.45	36221.02	44521.74	0	0	0
P61764	Syntaxin-b	STXBP1	30417.3	30805.01	33281.04	0	0	0
P61769	Beta-2-mi	B2M	125055.9	102698	61280.75	876844.1	1359867	630079.4
P61923	Coatome	COPZ1	9037.488	9798.712	6611.071	0	0	0
P61960	Ubiquitin-	UFM1	9853.445	14937.61	11461.99	0	0	0
P61966	AP-1 comp	AP1S1	17270.79	18081.53	17013.43	0	0	0
P61970	Nuclear tra	NUTF2	44060.55	42301.69	47265.5	0	0	0
P61978	Heterogen	HNRNPK	54067.92	63271.64	61591.28	0	95889.98	23617.05
P61981	14-3-3 prc	YWHAG	434417.7	390502.4	389770.7	155837.7	175087.5	149514.7
P62070	Ras-relate	RRAS2	54905.03	58098.03	65837.03	0	0	0
P62079	Tetraspani	TSPAN5	75064.06	74266.53	132525.9	0	0	0
P62140	Serine/thre	PPP1CB	54444.11	51999.54	50453.96	40180.05	0	35705.42
P62158	Calmodulin	CALM1	2699979	2641173	2314734	782175.1	927278.9	665159.1
P62166	Neuronal c	NCS1	53323.02	54814.75	47200.98	0	0	0
P62191	26S protea	PSMC1	75097.64	77134.24	72785.37	45534.24	39560.24	69532.2
P62195	26S protea	PSMC5	16772.83	19972.85	20897.58	42887.3	0	39157.28
P62241	40S riboso	RPS8	230510.4	237089.1	122213.8	472493.3	241984.1	265366.6
P62249	40S riboso	RPS16	99307.05	91550.59	100391.3	234529.9	0	221601.8
P62256	Ubiquitin-	UBE2H	651.2461	17494.94	1099.573	0	0	0
P62258	14-3-3 prc	YWHAE	982014.2	931389.8	811181.6	211570.7	366755.4	138827.3
P62263	40S riboso	RPS14	49732.34	54325.73	45141.75	105136.9	93636.84	129242.1
P62266	40S riboso	RPS23	40842.17	45253.61	32684.03	45551.25	0	49588.64
P62269	40S riboso	RPS18	57583.52	58399.34	61814.75	140462.4	90347.64	163563.9
P62277	40S riboso	RPS13	31558.9	33353.04	26647.39	87283.6	61189.55	75518.88
P62280	40S riboso	RPS11	43247.3	55674.29	59930.99	93967.92	0	81768.91
P62306	Small nucl	SNRPF	8891.437	8473.638	8678.691	0	0	0
P62310	U6 snRNA	LSM3	20358.38	20578.78	16727.62	0	0	0
P62318	Small nucl	SNRPD3	17878.46	20340.5	19297.43	53257.95	0	39733.36
P62328	Thymosin I	TMSB4X	42426.6	41356.95	46743.44	0	411711.1	180083
P62330	ADP-ribos	ARF6	402994.8	383906.4	341634.4	68841.8	0	42646.13
P62333	26S protea	PSMC6	48036.09	46155.38	53453.44	172746	0	111203.6
P62424	60S riboso	RPL7A	85263.25	86920.47	71739.77	193385.7	110345.1	151183.5
P62633	Cellular nu	CNBP	72422.82	70945.67	68694.66	0	0	0
P62701	40S riboso	RPS4X	46274.2	52568.11	47222.36	172884.6	0	134552.5
P62736	Actin, aorti	ACTA2	1069810	1127318	977674.3	546390	757150.4	623295.3
P62745	Rho-relate	RHOB	16569.37	101265.1	66814.63	0	0	0
P62750	60S riboso	RPL23A	9765.542	2427.965	0	10187.77	0	14947.42
P62753	40S riboso	RPS6	105206.3	100675.7	67615	419110.5	0	225311.6
P62805	Histone H4	HIST1H4A	12646569	14402630	15429954	1319124	5238356	2664199
P62820	Ras-relate	RAB1A	1440589	1412406	1316655	1081687	1032340	1383776
P62826	GTP-bindin	RAN	462883.6	429987.9	462293.9	471053.1	268026.7	583597.5
P62829	60S riboso	RPL23	37224.36	25328.45	21352.37	0	0	0
P62834	Ras-relate	RAP1A	325459.9	326477.4	299998.9	73275.25	0	85352.38
P62841	40S riboso	RPS15	3077.422	2619.534	7029.281	0	0	0
P62847	40S riboso	RPS24	38983.51	40872.03	30875.99	0	0	0

P62851	40S riboso RPS25	17899.9	20247	12195.62	84136.37	26728.56	52238.82
P62854	40S riboso RPS26	157678.4	148477.2	105058.4	192189.6	0	243160.2
P62857	40S riboso RPS28	115905.9	111478.8	97150.36	83164.5	116205.3	56583.36
P62873	Guanine nıGNB1	900910.4	838073.6	805890	0	0	0
P62877	E3 ubiquiti RBX1	8452.905	11389.48	12106.42	0	0	0
P62879	Guanine nıGNB2	2250715	2273586	1477535	418117.8	285086.9	422605.3
P62899	60S riboso RPL31	17024.65	16836.69	23304.86	0	0	0
P62906	60S riboso RPL10A	57085.67	49524.57	47402.39	167471.6	0	140242.3
P62917	60S riboso RPL8	51250.99	57033.64	20446.21	244910.3	147052.3	161696.1
P62937	Peptidyl-p PPIA	2158438	2091197	1853758	679068.9	738548	484851.5
P62942	Peptidyl-p FKBP1A	205291.6	309503.4	213848.4	718601.1	951429	469706.2
P62979	Ubiquitin-ıRPS27A	8734137	8635324	8777780	5457158	5896259	4741509
P62993	Growth fac GRB2	55200.62	53912.91	49386.64	0	0	0
P62995	TransformıTRA2B	10403.72	11645.56	8647.525	530145.9	843934.4	670002.1
P63010	AP-2 comıAP2B1	73228.8	62587.03	60150.06	145662	0	64156.13
P63096	Guanine nıGNAI1	49945.08	69017.04	50474.87	0	0	0
P63098	Calcineurı PPP3R1	39874.96	49728.18	41359.32	0	0	0
P63104	14-3-3 prıYWHAZ	650263.2	542450.6	461486.9	217797.2	353191.5	247508.4
P63165	Small ubiq SUMO1	11461.38	12684.16	8408.303	0	0	0
P63167	Dynein ligıDYNLL1	13991.32	15893	15196.4	0	0	0
P63173	60S riboso RPL38	9914.51	8751.33	8472.256	0	0	0
P63208	S-phase ki SKP1	110588.8	105789	103404.8	0	0	0
P63218	Guanine nıGNG5	136372.5	138451.9	156881.9	0	0	0
P63244	Guanine nıGNB2L1	67391.63	67025.38	75133.67	67212.32	0	58400.58
P63261	Actin, cyto ACTG1	1708002	1191062	1442109	359404.6	364770.3	0
P63279	SUMO-corıUBE2I	28119.97	28397.7	28496.65	0	0	0
P67775	Serine/threıPPP2CA	206244.9	213219.1	178561.3	162806.2	142829.9	141568.3
P67809	Nuclease-ıYBX1	38459.79	30590.14	27701.62	0	0	0
P67870	Casein kinıCSNK2B	79187.59	84190.92	72595.71	134752.7	0	78242.53
P67936	TropomyoıTPM4	278973.3	263483.9	260093.4	664716.5	824317.3	424795.4
P68036	Ubiquitin-ıUBE2L3	40589.93	41494.47	37014.74	0	0	0
P68104	ElongationıEEF1A1	2980547	2924158	2649892	2665316	2023420	2707649
P68363	Tubulin alıTUBA1B	2036896	1956375	2059270	14435993	5758159	17968256
P68366	Tubulin alıTUBA4A	355450.4	315721.7	340827.6	4405745	4899424	10116559
P68371	Tubulin beıTUBB4B	1301613	1201666	1257260	3311132	1586903	4510178
P68400	Casein kinıCSNK2A1	66434.24	46325.83	43696.3	55528.15	35800.42	76615.82
P68402	Platelet-acıPAFAH1B2	24485.34	17996.34	16032.5	0	0	0
P68431	Histone HıHIST1H3A	5419.544	4500.853	3240.767	0	0	0
P69891	HemoglobıHBG1	21290046	22325190	29510474	1.62E+08	1.78E+08	1.57E+08
P69905	HemoglobıHBA1	6335963	5738111	7285479	44398616	40482928	43246024
P78310	CoxsackievıCXADR	44774.28	27064.35	49558.82	0	0	0
P78324	Tyrosine-pıSIRPA	2534.379	3050.114	3055.742	0	0	0
P78344	EukaryoticıEIF4G2	40562.71	36879.16	35315.05	0	0	0
P78356	PhosphaticıPIP4K2B	11127.5	11251.39	9985.688	0	0	0
P78371	T-complexıCCT2	119448.8	124766	139654.4	177742.1	0	187005.8
P78509	ReelinıRELN	4575.363	9204.396	9414.576	0	0	0
P78527	DNA-depeıPRKDC	45100.39	44179.64	51193.51	1202790	2386365	812444.3
P78536	DisintegrinıADAM17	13009.88	26066.11	16860.21	0	0	0
P78539	Sushi repeıSRPX	322248.9	318791.8	283035	389804.3	232763.3	283262.5
P78552	InterleukinıIL13RA1	14544.26	15305.67	9638.896	0	0	0
P80162	C-X-C moıCXCL6	0	0	0	3016109	2149925	1037208
P80723	Brain acidıBASP1	1047194	1834839	1843298	378723.9	700093.6	450837.5
P83731	60S riboso RPL24	20802.56	19773.67	20490.21	51250.79	0	32660.62
P84022	Mothers aıSMAD3	26380.3	37360.91	34332.88	0	0	0
P84085	ADP-ribosıARF5	19726.32	13828.78	23958.87	0	0	0
P84090	Enhancer cıERH	44798.67	43626	39598.39	0	0	0
P84095	Rho-relateıRHOG	457651.9	442307.4	487567.9	14677.78	0	33250.8
P84098	60S riboso RPL19	40038.22	44803.41	14701.82	613335.1	0	167605.1

P84103	Serine/arg SRSF3	53451.89	55138.33	41088.93	280170.1	250698.9	235834.3
P86790	Vacuolar f ₁ CCZ1B	5482.636	7347.539	9207.359	0	0	0
P98095	Fibulin-2 FBLN2	30712.96	33108.81	44534.77	0	0	0
P98155	Very low- α VLDLR	15913.5	15801.36	12787.12	0	0	0
P98160	Basement HSPG2	219168.9	248984.8	178548.2	403314.8	502427	701589.1
P98172	Ephrin-B1 EFNB1	349983.9	342810.7	268609.7	0	0	0
P98194	Calcium-tr ATP2C1	32999.45	33021.87	34066.22	0	0	0
P98196	Probable γ ATP11A	213049.6	206940.3	139779.5	8535011	11612708	4439523
P98198	Phospholip ATP8B2	11824.56	18765.09	14941.6	0	0	0
P99999	Cytochrome CYCS	2920.682	3854.759	3626.338	0	0	0
Q00013	55 kDa ery MPP1	21290.36	21068.63	7267.303	0	0	0
Q00169	Phosphatic PITPNA	18775.72	11043.29	8349.547	0	0	0
Q00266	S-adenosy MAT1A	22078.02	24858.65	24425.84	0	0	0
Q00341	Vigilin HDLBP	19071.64	16835.82	1654.017	0	0	0
Q00534	Cyclin-de γ CDK6	6057.43	14899.38	14154.94	0	0	0
Q00535	Cyclin-de γ CDK5	4953.514	17325.27	4685.543	0	0	0
Q00537	Cyclin-de γ CDK17	24299.43	23836.75	20722.32	0	0	0
Q00577	Transcripti PURA	11267.65	8941.1	9093.983	0	0	0
Q00610	Clathrin h ϵ CLTC	742904.2	708280.5	840289	470776.2	624443.8	568830.6
Q00688	Peptidyl-p FKBP3	2482.183	2956.27	2222.776	0	0	0
Q00796	Sorbitol de SORD	55925.72	56904.2	53353.53	0	0	0
Q01082	Spectrin b ϵ SPTBN1	87384.93	87798.87	57584.35	6173.706	0	32380.52
Q01105	Protein SE SET	25018.81	26440.63	24813.76	133960	0	74832.05
Q01130	Serine/arg SRSF2	31312.49	35507.8	43663.32	246599.6	0	162563
Q01433	AMP deamr AMPD2	31047.33	25144.48	25496.75	47425.62	0	46546.25
Q01469	Fatty acid- FABP5	198221.5	186869	219581.2	266190.1	151779.6	124789.8
Q01518	Adenylyl γ CAP1	322608.9	326478.3	289650.3	157799.9	137914.4	166223.9
Q01581	Hydroxym α HMGCS1	73968.66	77088.48	77790.57	0	0	0
Q01628	Interferon- IFITM3	77410.53	73526.37	70650.82	27576.04	0	46307.61
Q01629	Interferon- IFITM2	70251.63	67708.8	66889.65	0	0	0
Q01650	Large neut SLC7A5	704307.9	713232	687927.6	0	0	0
Q01813	ATP-depe γ PFKP	69471.39	73030.27	66446.45	63212.09	0	74323.12
Q01970	1-phosph α PLCB3	32658.24	28884.6	27519.64	0	0	0
Q01974	Tyrosine- γ ROR2	16985.28	15962.26	15605.98	0	0	0
Q02241	Kinesin-lik KIF23	129557.4	111666.1	118955.8	0	0	0
Q02790	Peptidyl-p FKBP4	23621.24	22156.92	25283.57	0	0	0
Q02809	Procollage PLOD1	5940.784	5526.483	8395.998	138342.7	165899.1	140330.6
Q02818	Nucleobin α NUCB1	8178.85	5976.336	10034.65	134929.5	173293.9	115882
Q02878	60S riboso RPL6	21665.35	21676.16	15300.06	123840.5	24586.78	26101.67
Q02880	DNA topoi TOP2B	4315.163	5364.06	7651.334	0	0	0
Q02952	A-kinase α AKAP12	110973.7	102306.8	98238.21	0	0	0
Q03113	Guanine n α GNA12	28385.79	36480.36	27618.8	0	0	0
Q03135	Caveolin-1 CAV1	22960.76	42718.13	18425.09	0	0	0
Q03169	Tumor nec TNFAIP2	4299.382	6758.688	5870.63	0	0	0
Q03181	Peroxisom PPARD	1382024	1412161	1520314	95690448	1.2E+08	55573584
Q03405	Urokinase PLAUR	100382.8	135165.8	136371.9	0	0	0
Q03426	Mevalonat MVK	6463.75	6539.639	6188.786	0	0	0
Q04206	Transcripti RELA	41549.05	16043.44	16426.07	0	0	0
Q04446	1,4-alpha- GBE1	12930.96	12883.88	15311.29	0	0	0
Q04637	Eukaryotic EIF4G1	10376.41	10340.55	11456.06	0	0	0
Q04756	Hepatocyt α HGFAC	194989.4	211279.7	263617.8	572580.1	1077806	727438.1
Q04771	Activin rec ACVR1	47789.55	45670.77	44040.74	0	0	0
Q04917	14-3-3 pr α YWHAH	137669.1	112800.5	124005.8	41405.19	0	52227.13
Q05193	Dynamin-1 DNMT1	9666.969	7845.513	6539.436	0	0	0
Q05397	Focal adhe PTK2	19297.88	35176.93	30832.17	0	0	0
Q05519	Serine/arg SRSF11	23777.55	26331.98	57984.04	133929	128881.6	91454.57
Q05639	Elongation EEF1A2	36309.28	45262.17	40749.14	0	0	0
Q05655	Protein kin PRKCD	16993.75	19657.53	17626.26	0	0	0

Q06033	Inter-alpha; ITIH3	798618.1	730263.6	1043166	5470790	6167389	3656485
Q06124	Tyrosine- γ PTPN11	18855.7	16682.28	20538.71	0	0	0
Q06203	Amidopho PPAT	40803	35690.18	78344.38	2732075	3298194	1831235
Q06210	Glutamine GFPT1	20805.78	24691.53	24052.68	77428.16	286029.8	26590.38
Q06265	Exosome c EXOSC9	1578.692	1491.53	1899.39	0	0	0
Q06323	Proteasom PSME1	52867.49	47184.03	48040.46	15101.39	0	6016.05
Q06418	Tyrosine- γ TYRO3	9206.602	6149.745	7114.884	0	0	0
Q06481	Amyloid-li APLP2	9787.177	16119.1	14397.96	0	0	0
Q06828	Fibromodu FMOD	53181.96	65445.42	76135.14	472282	639771.8	355573.4
Q06830	Peroxiredc PRDX1	451835.6	427795.7	389257.4	861762.8	1150091	615647
Q07020	60S riboso RPL18	146768.2	141249.2	87121.98	295541.5	0	165165.9
Q07021	Compleme C1QBP	28818.52	26719.15	22144.97	0	0	0
Q07065	Cytoskeleton CKAP4	6851.082	6140.705	5097.701	0	0	0
Q07157	Tight junct TJP1	30779.71	26809.79	26682.71	0	0	0
Q07352	Zinc finger ZFP36L1	9490.103	10209.95	8905.653	0	0	0
Q07617	Sperm-ass SPAG1	13571.55	12623.04	12452.77	0	0	0
Q07812	Apoptosis BAX	19404.77	15295.06	17901.61	0	0	0
Q07954	Prolow-de LRP1	244118	215861.6	243186.1	206711	227710.2	205834.2
Q07955	Serine/arg SRSF1	31794.45	33904.33	32514.42	0	0	0
Q07960	Rho GTPas ARHGAP1	27042.61	29377.86	26374.72	0	0	0
Q08170	Serine/arg SRSF4	23439.42	19641.67	56587.17	0	0	0
Q08209	Serine/thre PPP3CA	168638.4	166016.3	160152.8	0	0	0
Q08257	Quinone o CRYZ	6050.297	7349.273	7677.097	0	0	0
Q08357	Sodium-d SLC20A2	25876.7	26350.62	47225.72	0	0	0
Q08380	Galectin-3 LGALS3BP	61241.78	83436.55	72899.27	902531.9	560760.2	1261738
Q08431	Lactadheri MFGE8	612598.1	720747.5	759273.6	1901814	1495151	3789209
Q08629	Testican-1 SPOCK1	74565.45	68742.36	64183.66	370466.2	697844.5	330086.3
Q08722	Leukocyte CD47	861895.1	796076.8	791722.6	0	0	0
Q08752	Peptidyl-p PPID	24261.47	24278.48	21314.8	0	0	0
Q08AM6	Protein VA VAC14	1751.354	4017.062	2824.938	0	0	0
Q08J23	tRNA (cytc NSUN2	11244.01	11756.63	13874.6	0	0	0
Q09666	Neuroblas AHNAK	913184.3	926263.4	847314.8	0	165102.5	56424.61
Q0VAQ4	Small cell s SMAGP	25516.76	27652.48	23204.69	0	0	0
Q10469	Alpha-1,6- MGAT2	10411.62	10267.07	17210.07	0	866996.6	322290.1
Q10471	Polypeptid GALNT2	6797.078	14882.33	0	54223.19	0	57685.2
Q10567	AP-1 com AP1B1	35515.19	31212.05	33432.81	0	30350.18	56866.69
Q10588	ADP-ribos BST1	26784.28	32293.73	27050.69	51451.12	0	41807.05
Q12765	Secernin-1 SCRNI	35207.45	31928.7	29598.78	0	0	0
Q12768	WASH con KIAA0196	4499.863	4019.654	3662.131	0	0	0
Q12788	Transducir TBL3	7549.285	8032.701	7679.236	0	0	0
Q12791	Calcium-a KCNMA1	25195.47	27192.13	24963.74	0	0	0
Q12792	Twinfilin-1 TWF1	38434.35	39757.19	32530.59	0	0	0
Q12805	EGF-conta EFEMP1	32742.71	46141.29	67704.9	555236.3	873508.7	402843.4
Q12841	Follistatin- FSTL1	47788.4	49379.16	68141.23	864688.6	1442083	576107.3
Q12846	Syntaxin-4 STX4	77215.47	79593.03	66398.38	0	0	0
Q12860	Contactin- CNTN1	25540.25	26905.02	35432.76	289396.3	354674.5	136727.6
Q12874	Splicing fa SF3A3	2881.852	3068.698	3067.576	0	0	0
Q12884	Prolyl endc FAP	43329.22	41670.77	53203.57	232141.7	228566.4	229654.2
Q12904	Aminoacyl AIMP1	16807.39	15466.84	18087.59	0	0	0
Q12905	Interleukin ILF2	12510.74	13539.39	11895.76	0	0	0
Q12906	Interleukin ILF3	22817.48	39103.9	7364.316	0	0	0
Q12907	Vesicular ir LMAN2	26262.62	25915.81	26275.65	175740	104373	145558.8
Q12913	Receptor-1 PTPRJ	34313.85	28726.25	32032.31	0	0	0
Q12923	Tyrosine- γ PTPN13	6420.339	6740.942	8199.23	0	0	0
Q12929	Epidermal EPS8	42939.29	40211.89	43654.5	0	0	0
Q12931	Heat shock TRAP1	2902899	2885581	2750584	1655165	1377226	1700805
Q12959	Disks large DLG1	172393.2	152596.7	157642.6	0	0	0
Q12965	Unconvent MYO1E	32904.73	32021.55	25362.95	0	0	0

Q12974	Protein tyr PTP4A2	45490.09	53094.52	46234.51	0	0	0
Q12979	Active bre:ABR	23805.86	24240.72	22144.03	0	0	0
Q13042	Cell divisio CDC16	4070.445	3567.729	4355.643	0	0	0
Q13043	Serine/thr:STK4	25886.96	23670.48	26965.94	0	0	0
Q13045	Protein flic FLII	9616.006	10638.53	6396	0	0	0
Q13085	Acetyl-Co:ACACA	5492.997	5706.652	10487.81	0	0	0
Q13093	Platelet-ac PLA2G7	5642.156	4764.579	9582.001	36724.54	58812.06	30298.66
Q13103	Secreted p SPP2	25596.22	25273.67	28894.85	384678.6	352302.3	443168.6
Q13107	Ubiquitin c USP4	7257.822	4854.266	6745.376	0	0	0
Q13131	5-AMP-ac PRKAA1	20008.84	21239.41	20457	0	0	0
Q13136	Liprin-alph:PPFIA1	25793.43	17403.3	26338.62	0	0	0
Q13148	TAR DNA- TARDBP	9830.063	14271.66	13864.83	0	0	0
Q13155	Aminoacyl AIMP2	27704.95	27049	18143.32	0	0	0
Q13162	Peroxiredc PRDX4	3861.994	4370.248	5505.465	0	0	0
Q13163	Dual speci MAP2K5	4087441	3641516	5486425	27340140	38997316	18936590
Q13177	Serine/thr:PAK2	24224.63	21724.19	22433.8	0	0	0
Q13200	26S protea PSMD2	100826.8	101249.2	101294.3	94136.73	49600.45	109541.2
Q13247	Serine/arg SRSF6	14275.94	15685.48	10618.53	0	0	0
Q13253	Noggin NOG	11927.35	10324.41	11476.01	0	0	0
Q13257	Mitotic spi MAD2L1	29948.5	27564.91	31180.33	0	0	0
Q13263	Transcripti TRIM28	8611.814	7720.773	10034.67	0	0	0
Q13277	Syntaxin-3 STX3	36510.52	37248.35	39067.34	0	0	0
Q13283	Ras GTPas:G3BP1	12170.98	11709.13	8722.356	0	0	0
Q13308	Inactive ty:PTK7	226106.6	245072.1	196680.3	213580	294510.3	145318.2
Q13322	Growth fac GRB10	12131.43	8069.064	12480.67	0	0	0
Q13325	Interferon- IFIT5	1810.013	11607.6	11392.71	0	0	0
Q13347	Eukaryotic EIF3I	26814.55	20076.77	21488.85	33469.04	0	40554.53
Q13409	Cytoplasm DYNC1I2	7739.724	5358.744	8308.866	0	0	0
Q13418	Integrin-lir ILK	128889.2	150355	159019.8	268917.5	116830.2	371684.4
Q13433	Zinc trans:SLC39A6	19492.77	37008.28	19992.98	0	0	0
Q13442	28 kDa he:PDAP1	31568.11	47403.43	30139.09	0	0	0
Q13443	Disintegrin ADAM9	68093.59	80540.16	81170.71	0	0	0
Q13459	Unconvent MYO9B	4370.762	3804.22	2648.804	0	0	0
Q13464	Rho-assoc ROCK1	18981.72	11925.18	2891.356	0	0	0
Q13492	Phosphatic PICALM	4090.637	4309.445	10686.18	0	0	0
Q13496	Myotubula MTM1	2448.893	2334.89	2392.259	0	0	0
Q13501	Sequestos:SQSTM1	17626.83	12736.35	15008.03	0	0	0
Q13509	Tubulin be TUBB3	58188.05	68498.4	79703.3	719906	0	1048418
Q13526	Peptidyl-p PIN1	4727.691	5466.894	4352	0	0	0
Q13535	Serine/thr:ATR	995.1937	1904.299	1728.355	0	0	0
Q13547	Histone de HDAC1	178283.7	71869.55	522098.1	0	0	0
Q13557	Calcium/c:CAMK2D	3144.137	6097.837	6663.453	0	0	0
Q13561	Dynactin s DCTN2	16803.99	20130.19	21756.6	0	0	0
Q13576	Ras GTPas:IQGAP2	43974.58	57483.11	17759.69	0	0	0
Q13614	Myotubula MTMR2	12318.41	20731.95	16020.1	0	0	0
Q13616	Cullin-1 CUL1	12706.38	12516.94	10194.56	0	0	0
Q13617	Cullin-2 CUL2	11844.42	15145.36	14885.1	0	0	0
Q13618	Cullin-3 CUL3	19313.37	25615.85	24094.2	0	0	0
Q13620	Cullin-4B CUL4B	7234.46	5975.685	4195.355	0	0	0
Q13625	Apoptosis- TP53BP2	47461.17	60644.56	40897.86	0	0	0
Q13630	GDP-L-fuc TSTA3	13411.58	11072.59	11156.74	0	0	0
Q13636	Ras-relate:RAB31	54088.73	54368.48	50040.99	0	0	0
Q13637	Ras-relate:RAB32	44092.98	45438.08	38481.97	65917.03	0	64449.97
Q13641	Trophobla:TPBG	150858	156856.5	139014.6	0	0	0
Q13642	Four and a FHL1	192974.6	207297.6	182500.8	545492.3	0	757147.1
Q13671	Ras and R:RIN1	44659.93	33466.76	24372.99	0	0	0
Q13685	Angio-ass: AAMP	16706.28	10263.91	10507.45	0	0	0
Q13740	CD166 ant ALCAM	66965.49	69189.92	64054.54	0	149907.5	66167.41

Q13748	Tubulin alç TUBA3C	612371.8	581482.3	563122.9	1258749	0	1384352
Q13822	Ectonuclec ENPP2	26072.61	18342.66	23298.73	174375.2	226232	231670.7
Q13838	Spliceoson DDX39B	18352.49	13661.84	11284.51	0	0	0
Q13867	Bleomycin BLMH	25345.29	31333.03	57954.92	0	0	0
Q13873	Bone morç BMPR2	16231.61	14231.7	13551.61	0	0	0
Q13884	Beta-1-syr SNTB1	10358.74	10676.77	13395.1	0	0	0
Q13895	Bystin BYSL	3151.673	2388.024	2353.277	0	0	0
Q14008	Cytoskelet CKAP5	8681.51	9233.457	12842.37	0	0	0
Q14019	Coactosin- COTL1	119363	150839.7	265454.3	177453.7	0	203258.5
Q14103	Heterogen HNRNPD	17817.5	19471.69	19881.22	43171.5	0	32162.7
Q14108	Lysosome SCARB2	60031.01	65199.8	61114.66	0	0	0
Q14112	Nidogen-2 NID2	51437.14	53907.41	43483.89	272059	382887.5	446308
Q14118	Dystroglyc DAG1	85631.26	84328.49	77828.28	0	0	0
Q14126	Desmoglei DSG2	361514.4	372242.7	339083	0	0	0
Q14141	Septin-6 6-Sep	21550.71	26706.09	24686.67	0	0	0
Q14145	Kelch-like KEAP1	9506.967	10640.43	8636.943	0	0	0
Q14152	Eukaryotic EIF3A	24463.14	21319.22	29036.12	3388728	0	1656833
Q14155	Rho guanin ARHGEF7	16393.56	12384.18	22141.66	0	0	0
Q14157	Ubiquitin- UBAP2L	3476.364	3199.709	3289.941	0	0	0
Q14160	Protein scr SCRIB	185433.5	195314	175783.2	0	0	0
Q14166	Tubulin--t TTLL12	29458.12	28256.82	29013.35	0	0	0
Q14168	MAGUK p5 MPP2	29887.48	27103.03	21264.52	0	0	0
Q14185	Dedicator DOCK1	12911.18	14662.43	63032.34	0	0	0
Q14192	Four and a FHL2	22710.19	25884.14	24400.74	0	0	0
Q14195	Dihydropy DPYSL3	31922.11	33005.63	32544.22	0	0	0
Q14203	Dynactin s DCTN1	9061.535	4775.824	8888.541	0	0	0
Q14204	Cytoplasm DYNC1H1	112817.8	114223.9	126208.1	141071.6	87666.41	197685.1
Q14240	Eukaryotic EIF4A2	25717.97	28392.22	32182.17	0	0	0
Q14247	Src substrè CTTN	542688.5	497354.2	443037.1	0	0	0
Q14254	Flotillin-2 FLOT2	137272.4	131410.3	132285.7	35988.51	0	63282.87
Q14258	E3 ubiquiti TRIM25	2537.875	2701.924	4352.725	0	0	0
Q14289	Protein-tyl PTK2B	59747.73	62201.38	93437.91	61265.67	105555.6	0
Q14315	Filamin-C FLNC	58450.32	56851.64	48641.71	0	0	0
Q14344	Guanine ni GNA13	2273103	2191041	2090379	2337526	0	389962.7
Q14376	UDP-glucç GALE	13509.57	13513.29	15612.42	0	0	0
Q14393	Growth arr GAS6	8789.074	9480.752	7765.577	0	0	0
Q14439	Probable C GPR176	20006.66	17287.86	15042.36	0	0	0
Q14444	Caprin-1 CAPRIN1	10033.66	7803.999	5683.656	0	0	0
Q14515	SPARC-like SPARCL1	53476.12	48511.52	53985.2	0	102401	55028.52
Q14517	Protocadh FAT1	9792.629	9201.183	20037.04	0	0	0
Q14520	Hyaluronai HABP2	108710.3	104257.8	103399.2	56901.07	56525.19	55130.77
Q14566	DNA replic MCM6	6154.124	7258.399	6403.049	0	0	0
Q14624	Inter-alphaç ITIH4	32037.14	49722.22	42147.91	210113.4	258568	202851.2
Q14627	Interleukin IL13RA2	23744.07	9351.157	7402.68	0	0	0
Q14642	Type I inos INPP5A	38614.09	40935.15	35492.57	0	0	0
Q14644	Ras GTPasç RASA3	54172.08	54797.39	49059.34	439620.3	0	44306.38
Q14651	Plastin-1 PLS1	13843.89	14950.47	13134.43	0	0	0
Q14676	Mediator c MDC1	19267.14	14723.72	18420.12	0	0	0
Q14677	Clathrin ini CLINT1	6155.07	10766.59	2318.639	0	0	0
Q14683	Structural i SMC1A	3444.142	3952.088	29840.8	0	0	0
Q14697	Neutral alç GANAB	20547.72	22342.55	25099.66	112382.4	128031.8	87484.97
Q14699	Raftlin RFTN1	240639.8	240124.6	227870.3	0	0	0
Q14703	Membrane MBTPS1	12541.82	12478.79	16686.02	0	0	0
Q14714	Sarcospan SSPN	9325.172	10430.53	7496.992	0	0	0
Q14738	Serine/thrè PPP2R5D	5372.16	7018.874	4005.371	0	0	0
Q14764	Major vault MVP	154333.6	157417.9	108385.8	765741.1	804876	841241
Q14766	Latent-trar LTBP1	0	0	0	380742.7	551262.3	152547.7
Q14847	LIM and St LASP1	98105.32	83749.19	83551.7	0	0	0

Q14974	Importin α KPNB1	162822.5	189652.5	189538.3	39158.12	57689.78	46835.98
Q14997	Proteasom PSME4	4900.575	5339.742	4992.947	0	0	0
Q14999	Cullin-7 CUL7	15960.89	14774.4	12897.56	0	0	0
Q14C86	GTPase-ac GAPVD1	9139.57	13002.32	16687.69	0	0	0
Q14CN4	Keratin, type I KRT72	1253.022	18837.77	11150.39	0	0	0
Q15003	Condensin NCAPH	8429.953	6567.806	1935.686	0	0	0
Q15008	26S proteasome PSMD6	35416.98	38307.23	36889.72	61890.34	42058.74	51917.22
Q15012	Lysosomal LAPTM4A	40613.43	43433.43	38317.22	0	0	0
Q15021	Condensin NCAPD2	3612.006	3356.54	3178.739	0	0	0
Q15025	TNFAIP3-interacting TNIP1	15538.59	15424.28	12868.95	0	0	0
Q15029	116 kDa U-EIFTUD2	20334.92	18038.13	14813.79	0	0	0
Q15036	Sorting nexin-1 SNX17	16447.87	21029.83	27214.79	0	0	0
Q15052	Rho guanine nucleotide exchange factor ARHGEF6	24032.69	26017.46	21090.63	0	0	0
Q15056	Eukaryotic translation initiation factor 4H	56102.05	55611.32	56458.57	0	0	0
Q15057	Arf-GAP with ACAP2	9377.39	8919.769	9231.923	0	0	0
Q15063	Periostin POSTN	148781.5	140961	164623.5	1602861	2226877	1816469
Q15084	Protein disulfide isomerase PDIA6	10488.72	11398.51	10245.32	0	0	0
Q15102	Platelet-activating factor acyltransferase 1B3	20652.28	23096.06	21091.2	0	38401.33	29813.59
Q15113	Procollagen type I alpha1(C) PCOLCE	17403.11	16542.78	50534.54	4340181	5408422	4506807
Q15121	Astrocytic secretory phospholipase A2-15	6581.635	9305.422	2220.712	0	0	0
Q15124	Phosphoglucomutase 5 PGM5	9702.516	9914.223	16057.42	0	0	0
Q15172	Serine/threonine protein kinase PPP2R5A	8802.427	15167.34	6359.018	0	0	0
Q15181	Inorganic pyrophosphatase 1 PPA1	61952.73	60444.28	60075.94	0	0	0
Q15185	Prostaglandin synthase PTGES3	105114.9	99750.87	97078.46	0	0	0
Q15208	Serine/threonine kinase STK38	15965.88	17720.76	14296.73	0	0	0
Q15233	Non-polyoma virus-induced NONO	20505.3	22646.02	20112.09	0	0	0
Q15257	Serine/threonine protein kinase PPP2R4	38026.49	33523.71	28673.48	0	0	0
Q15262	Receptor-type tyrosine phosphatase ITPRK	34955.51	34267.93	29222.65	0	0	0
Q15283	Ras GTPase RASA2	23768.61	29343.14	26933.98	0	0	0
Q15286	Ras-related RAB35	1483694	1442558	1370325	1079379	660415.8	1388577
Q15293	Reticulocalcin RCN1	3048.666	3105.975	3171.936	0	0	0
Q15334	Lethal(2) giant larvae 1 LLGL1	136976.1	139574.6	119718.6	0	0	0
Q15349	Ribosomal protein S6KA2	12846.45	12810.04	15680.72	0	0	0
Q15365	Poly(rC)-binding protein 1 PCBP1	250085.5	270778.2	250799.1	186053.2	118090.2	167179.7
Q15366	Poly(rC)-binding protein 2 PCBP2	183204	191992.1	180878.3	345370.9	181962	339339.1
Q15369	Transcription factor 1 TCEB1	17098.97	13369.93	13843.31	0	0	0
Q15382	GTP-binding protein RHEB	132430.9	146855.5	123573.1	0	0	0
Q15392	Delta(24)-domain-containing DHCR24	20402.28	23645.09	28918.73	175281.1	0	129490.3
Q15393	Splicing factor SF3B3	20070	35197.15	15338.52	0	0	0
Q15404	Ras suppressor protein 1 RSU1	199730.4	152969.2	196829.9	101374.4	126301.4	109636.1
Q15417	Calponin-3 CNN3	29933.24	21865.8	21512.92	0	0	0
Q15418	Ribosomal protein S6KA1	12951.37	10801.27	21337.77	0	0	0
Q15427	Splicing factor SF3B4	22407.86	21677.09	21992.75	0	0	0
Q15435	Protein phosphatase 1R7	7034.77	6429.899	7033.54	0	0	0
Q15436	Protein translocator SEC23A	7352.077	9429.697	9319.452	0	0	0
Q15437	Protein translocator SEC23B	15025.08	11304	13790.86	0	0	0
Q15493	Regucalcin RGN	24918.83	19006.85	27056.25	175878.1	294994	258608.3
Q15555	Microtubule-associated protein 2 MAPRE2	23152.04	19206.25	22193.29	78771.14	77669.15	111437.9
Q15582	Transforming growth factor beta 1 TGFBI	269255.8	254313.9	342088.9	3156945	4577377	4117508
Q15599	Sodium/hydrogen exchanger SLC9A3R2	160136.3	156260.4	140432.8	0	0	0
Q15631	Translin TSN	54558.07	49091.53	34853.21	0	0	0
Q15642	Cdc42-interacting TRIP10	13767.64	16324.21	8627.617	0	0	0
Q15648	Mediator complex subunit MED1	35878.2	36318.85	41887.52	0	0	0
Q15654	Thyroid receptor TRIP6	10764.47	16880.15	11384.05	0	0	0
Q15678	Tyrosine phosphatase PTPN14	14283.59	16323.75	14876.17	0	0	0
Q15691	Microtubule-associated protein 1 MAPRE1	21185.62	40978.02	22808.72	0	0	0
Q15717	ELAV-like 1 ELAVL1	6580.167	6073.05	9043.709	0	0	0
Q15751	Probable E3 ubiquitin ligase HERC1	4911.732	3365.896	5091.338	0	0	0

Q15758	Neutral an	SLC1A5	3330772	3107550	3312355	488744.4	489888.5	781771.8
Q15785	Mitochond	TOMM34	85168.38	80747.31	72553.32	0	0	0
Q15797	Mothers a	SMAD1	47522.56	45405.66	42792.82	0	0	0
Q15813	Tubulin-s	TBCE	4398.528	4531.48	5038.469	0	0	0
Q15819	Ubiquitin-	UBE2V2	146290.3	124084	182693.9	0	0	0
Q15836	Vesicle-as	VAMP3	12201.24	41417.78	13590.71	0	0	0
Q15907	Ras-relate	RAB11B	1103947	1096471	1026268	73445.16	207065.8	366701.8
Q15942	Zyxin	ZYX	32778.16	36231.04	33470.41	0	0	0
Q16186	Proteasom	ADRM1	33385.15	19451	21869.28	0	0	0
Q16222	UDP-N-ac	UAP1	56651.09	56567.91	58788.11	0	0	0
Q16270	Insulin-li	IGFBP7	24884.1	22870.54	34722.39	1170431	1688007	859752.2
Q16363	Laminin su	LAMA4	3654.372	4246.252	4045.913	413254.1	400325.9	458215.7
Q16394	Exostosin-	EXT1	17769.4	18319.84	21433.2	64458.87	57028.74	56867.5
Q16401	26S protea	PSMD5	9170.339	8482.613	10609.78	80363.08	23702.31	33219.02
Q16512	Serine/thr	PKN1	4563.196	4310.443	2756.427	0	0	0
Q16513	Serine/thr	PKN2	20561.5	21120.58	20614.25	0	0	0
Q16537	Serine/thr	PPP2R5E	15701.85	16127.67	14808.88	0	0	0
Q16539	Mitogen-a	MAPK14	29480.09	24818.59	21889.13	0	0	0
Q16543	Hsp90 co-	CDC37	30385.58	39444.85	30477.62	0	0	0
Q16555	Dihydropy	DPYSL2	48099.3	49799.51	53954	94712.34	68673.52	77048.34
Q16563	Synaptoph	SYPL1	63134.88	57489.04	53164.43	0	0	0
Q16576	Histone-bi	RBBP7	13817.9	13014.99	12557.9	0	0	0
Q16610	Extracellul	ECM1	22471.54	15318.93	20253.48	209460.7	256405.7	324061.6
Q16625	Occludin	OCLN	28479.95	28686.49	38398.69	0	0	0
Q16637	Survival m	SMN1	25322.17	10442.28	20537.32	0	0	0
Q16643	Drebrin	DBN1	243764.5	146987.3	203479.4	0	0	0
Q16658	Fascin	FSCN1	369283.3	321269.7	357751	79565.14	53311.13	56508.36
Q16674	Melanoma	MIA	9855.498	8513.603	12160.12	89204.71	140415.5	80642.96
Q16719	Kynurenin	KYNU	4796.014	5188.229	6148.14	0	0	0
Q16739	Ceramide	UGCG	8342.184	9943.415	9427.756	0	0	0
Q16774	Guanylate	GUK1	6571.833	7030.688	5256.028	0	0	0
Q16775	Hydroxyac	HAGH	7517.462	8914.319	8960.565	0	0	0
Q16832	Discoidin c	DDR2	25967.89	41758.9	35872.52	0	0	0
Q16851	UTP--gluc	UGP2	24579.15	24993.88	29723.74	0	0	0
Q16853	Membrane	AOC3	152216.1	139337.4	161207.9	1155179	1155577	600363.4
Q16881	Thioredoxi	TXNRD1	25017.17	40878.44	34257.8	0	0	0
Q29980	MHC class	MICB	30856.98	28077.73	33158.33	0	0	0
Q29983	MHC class	MICA	33665.38	41778.95	33497.91	0	0	0
Q29RF7	Sister chro	PDS5A	8914.115	5764.592	7749.595	0	0	0
Q2M2H8	Probable r	MGAM2	3248.131	4435.173	4884.795	0	0	0
Q2M2I8	AP2-assoc	AAK1	7752.802	11765.31	5771.75	0	0	0
Q31612	HLA class I	HLA-B	599799.6	601416.3	544420.6	638216.1	901350.4	427994.2
Q32P28	Prolyl 3-hy	P3H1	8638.754	9347.077	6724.162	58860.05	0	42562.89
Q32P44	Echinoderr	EML3	2287.429	3823.884	26632.09	0	0	0
Q3SY69	Mitochond	ALDH1L2	147155.4	167662.3	114766	504748.3	1442816	1403507
Q3ZCW2	Galectin-r	LGALSL	20462.28	18765.22	24753	0	0	0
Q460N5	Poly [ADP-	PARP14	26203.28	23369.86	19496.99	0	0	0
Q4J6C6	Prolyl end	PREPL	9809.483	7790.578	9015.791	0	0	0
Q4KMP7	TBC1 dom	TBC1D10B	45383.93	39932.29	32335.28	0	0	0
Q4KMQ1	Taperin	TPRN	10905.25	6330.121	13322.33	0	0	0
Q4KMQ2	Anoctamir	ANO6	39852.55	43891.84	28909.81	0	0	0
Q52LJ0	Protein FA	FAM98B	6159.364	5213.557	6900.21	0	0	0
Q53EZ4	Centrosom	CEP55	39260.45	45408.93	44010.82	0	0	0
Q53GA4	Pleckstrin	PHLDA2	111003.8	109071.4	151325.3	0	0	0
Q53GL0	Pleckstrin	PLEKHO1	23187.11	13069.98	20615.47	0	0	0
Q53H76	Phospholip	PLA1A	30699.28	31660.44	44473.43	0	99442.86	74261.45
Q53H96	Pyrroline-	PYCRL	3382.893	4273.728	2840.203	0	0	0
Q562R1	Beta-actin	ACTBL2	3835528	6864551	3162676	539130.9	3083245	1032835

Q58FF6	Putative hεHSP90AB4	107953.3	131090.5	109082.6	0	0	0
Q58FF8	Putative hεHSP90AB2	177113	160181.9	177430.7	83086.01	73887.04	78047.16
Q5GLZ8	Probable EHERC4	7171.396	2847.247	5159.829	0	0	0
Q5H9R7	Serine/thrεPPP6R3	101819.9	104428.1	96113.06	0	0	0
Q5HYA8	Meckelin TMEM67	2917.022	2117.621	2583.819	0	0	0
Q5HYW2	NHS-like ρNHSL2	72988.77	64749.29	57790.71	0	0	0
Q5JSL3	Dedicator DOCK11	15346.24	13236.57	10603.63	0	0	0
Q5KU26	Collectin-1COLEC12	11182.92	14489.89	7457.54	0	0	0
Q5M775	Cytospin-εSPECC1	7508.437	7821.016	8400.76	0	0	0
Q5SR56	Hippocam HIATL1	14514.4	12960.31	13070.1	0	0	0
Q5SSJ5	HeterochrεHP1BP3	13464.38	20266.09	9423.014	0	0	0
Q5SYE7	NHS-like ρNHSL1	11044.84	10369.91	8473.705	0	0	0
Q5T0F9	Coiled-coi CC2D1B	10260.82	6231.636	9331.173	0	0	0
Q5T1M5	FK506-bin FKBP15	0	3554.406	5726.692	260015.3	341091.1	0
Q5T2T1	MAGUK pεMPP7	8360.761	4348.292	8042.355	0	0	0
Q5T447	E3 ubiquiti HECTD3	13613.67	3964.342	5880.235	0	0	0
Q5T4S7	E3 ubiquiti UBR4	23872.59	26272.05	32136.26	69927.66	15165.43	67587.99
Q5T5C0	Syntaxin-εSTXBP5	11540.71	13617.56	10986.87	0	0	0
Q5T9L3	Protein wnWLS	45781.99	47822.19	42187.61	0	0	0
Q5TAT6	Collagen αCOL13A1	79535.42	74532.34	73741.41	0	0	0
Q5TBA9	Protein fur FRY	37507.09	22273.9	22206.32	0	61508.5	418833.3
Q5TEC6	Histone HεHIST2H3Pε	9228294	9214771	9237425	2510084	2961339	3398035
Q5VSL9	Striatin-int STRIP1	5498.135	5394.349	5833.797	0	0	0
Q5VST6	Alpha/betεABHD17B	31477.39	17714.01	27966.42	0	0	0
Q5VU43	Myomegal PDE4DIP	26127.56	0	40109.39	1001814	1436005	595991.9
Q5VU97	VWFA and CACHD1	6572.452	7125.992	6277.56	0	0	0
Q5VVQ6	Ubiquitin tYOD1	11312.85	11590.86	11099.12	0	0	0
Q5VW32	BRO1 domεBROX	137462.2	136361.1	276733.4	0	0	0
Q5VW38	Protein GP GPR107	20012.51	17991.16	18754.98	0	0	0
Q5VWZ2	Lysophosp LYPLAL1	5697.698	6427.048	18844.97	0	0	0
Q5VZE5	N-α-a NAA35	1896.074	2292.516	2052.835	0	0	0
Q5W0Z9	Probable ρZDHHC20	46244.89	30915.57	34175.45	0	0	0
Q5W111	SPRY domεSPRYD7	17487.56	16211.04	15884.48	0	0	0
Q5ZPR3	CD276 ant CD276	86718.61	58960.72	85368.47	0	0	0
Q658P3	MetalloreεSTEAP3	333423.6	329629.3	288301.5	0	0	0
Q66K14	TBC1 domεTBC1D9B	5097	4380.699	5270.892	0	0	0
Q68CZ2	Tensin-3 TNS3	134360	122811.6	100796.3	0	0	0
Q68D85	Natural cyiNCR3LG1	40236.56	37998.1	38346.36	0	0	0
Q68D91	Metallo-βεMBLAC2	24862.12	25203.73	23145.93	0	0	0
Q68EM7	Rho GTPase ARHGAP1ε	36893.02	33494.53	34406.9	0	0	0
Q6DD88	Atlastin-3 ATL3	7177.754	6384.243	6522.832	56015	0	46711.82
Q6F5E8	Leucine-ricεRLTPR	7593.539	7117.796	7771.946	0	0	0
Q6FI81	Anamorsin CIAPIN1	1597.318	7272.537	1757.953	0	0	0
Q6GQQ9	OTU domεOTUD7B	19502.52	18314.02	16089.56	0	0	0
Q6IAA8	Ragulator εLAMTOR1	41310.05	39368.67	35830.52	0	0	0
Q6IBS0	Twinfilin-2 TWF2	70705.94	65513.48	34381.18	0	0	0
Q6IQ22	Ras-relateεRAB12	53136.05	53298.52	47138.75	0	0	0
Q6L8Q7	2,5-phosp PDE12	17943.62	19999.79	15353.98	0	0	0
Q6NYC8	Phostensin PPP1R18	53718.22	51299.33	51191.45	0	0	0
Q6P1N0	Coiled-coi CC2D1A	5810.28	9302.636	3321.809	0	0	0
Q6P2E9	Enhancer εEDC4	11409.48	4173.149	3570.202	0	0	0
Q6P2Q9	Pre-mRNA PRPF8	8842.534	8351.028	8056.503	0	0	0
Q6P4E1	Protein CA CASC4	6490.721	5540.1	4815.886	0	0	0
Q6P4Q7	Metal tranεCNNM4	10535.12	11442.2	8904.598	0	0	0
Q6P5Z2	Serine/thrεPKN3	1674.668	1436.317	1255.357	0	0	0
Q6P9B6	TLD doma TLDC1	137977.3	147474.7	122660.2	0	0	0
Q6P9B9	Integrator INTS5	2215.942	1547.632	14262.26	464583.6	674871.1	286240.6
Q6P9H4	Connector CNKSR3	12936.49	11990.8	10732.63	0	0	0

Q6PCB8	Embigin EMB	99135.72	93450.1	85625.52	0	0	0
Q6R327	Rapamycin RICTOR	36918.64	36932.84	35448.31	0	0	0
Q6RW13	Type-1 anti-AGTRAP	10060.84	9493.719	9420.163	0	0	0
Q6UWE0	E3 ubiquitin LRSAM1	10403.23	7377.051	10504.64	0	0	0
Q6UX71	Plexin domain PLXDC2	5731.179	5534.981	9638.06	0	0	0
Q6V1X1	Dipeptidyl DPP8	32776.91	39012.5	32281.43	0	0	0
Q6XZF7	Dynamin-1DNMBP	12994.7	10839.19	13540.63	0	0	0
Q6YHK3	CD109 anti-CD109	83712.88	84214.41	97910.44	443494.6	511132.1	318346.5
Q6ZNJ1	Neurobeatin NBEAL2	3176.714	3422.447	3687.619	0	0	0
Q6ZS17	Protein FA FAM65A	59770.76	63025.22	53408.98	0	0	0
Q6ZUX7	Lipoma HMLHFPL2	119462.3	105246	105478.1	0	0	0
Q6ZVL6	UPF0606 protein KIAA1549L	11785.41	12245.1	14000.27	0	0	0
Q70E73	Ras-associated RAPH1	9565.23	8513.322	8407.877	0	0	0
Q70IA6	MOB kinase MOB2	6492.048	8275.594	6906.896	0	0	0
Q75QN2	Integrator INTS8	3733.224	2183.175	2104.932	0	0	0
Q76LX8	A disintegrin ADAMTS1	33601.52	34261.28	48475.44	333701	390530.8	298895.4
Q7KYR7	Butyrophilin BTN2A1	44855.83	43053.37	39475.95	0	0	0
Q7KZ85	Transcriptin SUPT6H	10712351	11044703	6325591	1.03E+08	1.32E+08	80323176
Q7KZF4	Staphylococcal SND1	24030.49	18856.19	21489.13	0	0	0
Q7KZI7	Serine/threonine MARK2	73652.91	65131.27	71346.52	0	0	0
Q7L0J3	Synaptic vesicle SV2A	25179.77	25139.33	28158.82	0	0	0
Q7L0Q8	Rho-related RHOU	10454.01	11256.9	9073.689	0	0	0
Q7L1Q6	Basic leucine BZW1	55481.19	45803.59	46676.05	0	0	0
Q7L273	BTB/POZ class KCTD9	30094.36	30096.52	27662.95	0	0	0
Q7L2E3	Putative A' DHX30	9699.125	6668.414	3680.376	0	0	0
Q7L2H7	Eukaryotic EIF3M	18052.23	16954.9	17801.68	0	0	0
Q7L576	Cytoplasmic CYFIP1	217875.9	235676.1	180044.7	22524.39	21223.2	30570.35
Q7L7X3	Serine/threonine TAOK1	25025.55	20933.5	20955.32	0	0	0
Q7LBR1	Charged residue CHMP1B	295690.8	292869.8	280795.9	0	0	0
Q7LDG7	RAS guanine RASGRP2	47705.06	18108.11	5743.131	54803.99	0	63936.05
Q7RTV0	PHD finger PHF5A	4274.005	3869.318	4625.354	0	0	0
Q7Z2H8	Proton-coupled SLC36A1	5454.231	4567.335	8476.94	0	0	0
Q7Z2K8	G protein-coupled GPRIN1	30010.74	32761.03	28530.38	0	0	0
Q7Z2W4	Zinc finger ZC3HAV1	29331.8	33720.57	26185.96	0	0	0
Q7Z304	MAM domain MAMDC2	550522.2	22854.43	20786.71	43753.21	0	349404.8
Q7Z3C6	Autophagy ATG9A	6250.536	7602.928	6208.366	0	0	0
Q7Z3U7	Protein MCMON2	17583.39	17753.38	29904.57	4238394	4733293	2830150
Q7Z406	Myosin-14 MYH14	93929.33	94331.67	91325.9	1153926	730364.6	1417264
Q7Z460	CLIP-associated CLASP1	6335.898	13892.58	17435.18	0	0	0
Q7Z4F1	Low-density LRP10	31227.58	28775.18	26501.18	0	0	0
Q7Z4W1	L-xylulose DCXR	43048.44	43805.99	54267.08	0	0	0
Q7Z5N4	Protein side SDK1	33371.9	36292.18	32469.74	0	0	0
Q7Z698	Sprouty-related SPRED2	36695.52	47361.84	34618.52	0	0	0
Q7Z6B7	SLIT-ROBO SLRGAP1	19306.37	19686.34	17737.05	0	0	0
Q7Z6M1	Rab9 effector RABEPK	8974.256	7784.954	9746.842	0	0	0
Q7Z6Z7	E3 ubiquitin HUWE1	32145.53	34503.19	33454.63	15995571	20045522	4963382
Q7Z7A1	Centriolin CNTRL	168459.1	168196.8	129269.8	0	0	0
Q7Z7K6	Centromere CENPV	6608.472	7185.314	5988.179	0	0	0
Q86SF2	N-acetylglucosamine GALNT7	6931.566	6320.565	11190.88	0	0	0
Q86SJ2	Amphotericin AMIGO2	15695.44	19316.25	17300.67	0	0	0
Q86SQ4	G-protein GPR126	2567.114	3817.743	3678.225	0	0	0
Q86T03	Type 1 phosphatase TMEM55B	41113.75	36784.83	29145.36	0	0	0
Q86TI2	Dipeptidyl DPP9	17894.68	17566.2	15457.99	0	0	0
Q86TV6	Tetratricopeptide TTC7B	15003.08	14072.82	12433.65	0	0	0
Q86UD1	Out at first OAF	30438.72	32818.33	44863.54	168282.2	209887.3	114285.3
Q86UP2	Kinectin KTN1	44883.36	37377.55	56018.37	148453.7	0	87126.7
Q86UU1	Pleckstrin PHLDB1	4230.585	5024.806	4377.861	0	0	0
Q86UX7	Fermitin family FERMT3	120689.4	56933.38	92726.31	165117.6	152384.8	175049.1

Q86VE9	Serine incc	SERINC5	290935.9	178141.9	282791.9	0	0	0
Q86VI3	Ras GTPas	IQGAP3	19770.37	19551.79	11361.44	0	0	0
Q86VI4	Lysosomal	LAPTM4B	527767.9	546820.6	527836.8	0	0	0
Q86VN1	Vacuolar p	VPS36	8419.467	9679.582	6080.678	0	0	0
Q86VP6	Cullin-assc	CAND1	27065.79	26700.6	32565.17	66374.02	0	80426.06
Q86W42	THO comp	THOC6	3743.827	1343.155	2553.704	0	0	0
Q86W92	Liprin-bet	PPFIBP1	48786.98	51026.23	49989.79	0	0	0
Q86WI1	Fibrocystin	PKHD1L1	16172.07	15290.04	35085.83	0	0	0
Q86WR7	Proline anc	PROSER2	28012.95	31261.44	37900.81	0	0	0
Q86X55	Histone-ar	CARM1	20511.05	11909.3	16509.13	0	0	0
Q86XS8	E3 ubiquiti	RNF130	21688.04	20908.34	18908.98	0	0	0
Q86Y82	Syntaxin-1	STX12	50474.18	35237.11	72522.51	0	0	0
Q86YD5	Low-densi	LDLRAD3	11953.98	11901.42	9369.655	0	0	0
Q86YQ8	Copine-8	CPNE8	354830.1	333812.8	334843.8	66077.84	48093.49	86873.32
Q8IUC4	Rhopilin-	RHPN2	4767.081	4312.058	2389.073	0	0	0
Q8IUL8	Cartilage ir	CILP2	35772.81	35557.9	44440.3	212758	166226.9	168581.3
Q8IUR7	Armadillo	ARMC8	6437.25	4227.655	8589.728	0	0	0
Q8IUW5	RELT-like	RELL1	43830.29	47159.71	43190.9	0	0	0
Q8IUX7	Adipocyte	AEBP1	13697.11	12787.21	20695.71	177514.9	237493.7	176406.4
Q8IV08	Phospholip	PLD3	28567.39	29046.63	26586.6	0	0	0
Q8IVB5	LIX1-like	pLIX1L	11558.1	9662.39	11671.76	0	0	0
Q8IVF2	Protein AH	AHNAK2	29269.1	20337.91	20989.74	0	0	0
Q8IVF7	Formin-lik	FMNL3	33762.82	29747.86	33664.09	0	0	0
Q8IVM0	Coiled-coi	CCDC50	90860.79	91604.48	80136.79	0	0	0
Q8IWA0	WD repeat	WDR75	6046.27	4097.114	6003.846	0	0	0
Q8IWB7	WD repeat	WDFY1	6294.445	8647.307	7289.188	0	0	0
Q8IWE4	DCN1-like	DCUN1D3	31146.84	29812.04	27707.98	0	0	0
Q8IWT6	Volume-re	LRR8A	11930.65	11601.77	11358.94	0	0	0
Q8IWW6	Rho GTPas	ARHGAP13	5858.728	5359.231	4487.825	0	0	0
Q8IXI1	Mitochondr	RHOT2	533925.7	607868.4	522902.9	0	0	0
Q8IXS8	Protein FA	FAM126B	3504.967	2985.017	2564.834	0	0	0
Q8IXU6	Solute carr	SLC35F2	26355.76	21683.77	16758.78	0	0	0
Q8IY95	Transmem	TMEM192	22774.93	27672.97	48706.41	0	0	0
Q8IYB3	Serine/arg	SRRM1	3116.952	1586.457	3481.269	0	0	0
Q8IYI6	Exocyst co	EXOC8	39159.4	41032.12	30445.14	0	0	0
Q8IYJ1	Copine-9	CPNE9	156983.6	147703.7	158409.8	0	0	0
Q8IYT4	Katanin p6	KATNAL2	99584.11	100722.2	99624.45	0	0	0
Q8IZ07	Ankyrin re	ANKRD13A	13014.66	13522.37	12709.7	0	0	0
Q8IZZ1	Phosphata	PHACTR4	4697.133	6600.136	4722.886	0	0	0
Q8IZ83	Aldehyde	ALDH16A1	17776.19	10700.24	15873.61	41232.11	0	42253.07
Q8IZA0	Dyslexia-a	KIAA0319L	2795.68	2586.743	2749.023	0	0	0
Q8IZL8	Proline-, g	PELP1	7742.77	13675.21	13666.42	0	0	0
Q8IZP0	Abl interac	ABI1	115807.5	106971.3	99668.89	0	0	0
Q8N0X7	Spartin	SPG20	4827.226	5798.991	6218.386	0	0	0
Q8N0Y7	Probable	PGAM4	0	13303.74	17142.59	0	153991.7	309154.7
Q8N1F7	Nuclear pc	NUP93	21295.23	18461.67	22544.17	0	0	0
Q8N1G4	Leucine-ric	LRR47	24387.29	16870.03	21444.46	0	0	0
Q8N1N4	Keratin, ty	KRT78	7528.635	10987.26	13815.72	100808.7	71649.63	60882.41
Q8N392	Rho GTPas	ARHGAP18	93587.23	90261.28	75932.28	0	0	0
Q8N3C0	Activating	ASCC3	2118.179	3696.69	6401.993	0	0	0
Q8N3D4	EH domain	EHBP1L1	12540.9	13589.49	11931.6	0	0	0
Q8N3F8	MICAL-like	MICALL1	21415.69	19553.85	18599.58	0	0	0
Q8N3R9	MAGUK p5	MPP5	17279.57	25393.16	24874.26	0	0	0
Q8N3T6	Transmem	TMEM132C	3696.503	3872.768	5413.827	0	0	0
Q8N474	Secreted fr	SFRP1	38077.05	56585.94	47710.43	0	0	0
Q8N4C8	Misshapen	MINK1	93502.6	92228.73	87918.34	0	0	0
Q8N5I2	Arrestin dc	ARRDC1	107403.8	102985.9	81089.86	0	0	0
Q8N653	Leucine-zi	LZTR1	10135.26	7785.778	9487.822	0	0	0

Q8N7R7	Cyclin-Y-li CCNYL1	20626.5	23026.3	16892.08	0	0	0
Q8N884	Cyclic GMF MB21D1	26252.32	18480.34	34791.26	514410.3	727557.6	332782.3
Q8N8S7	Protein en: ENAH	14975.38	10520.45	15155.79	0	0	0
Q8N9N7	Leucine-ric LRR C57	104384.2	105451.8	90900.59	0	0	0
Q8NB49	Phospholip ATP11C	25463.42	26478.75	24112.99	0	0	0
Q8NB90	Spermatoç SPATA5	39087.32	56818.27	57787.05	0	0	0
Q8NBF2	NHL repea NHLRC2	30425.96	30523.94	33497.09	0	0	0
Q8NBJ4	Golgi meri GOLM1	28001.2	25255.7	29774.76	317513.1	487378.2	232587.2
Q8NBM8	Prenylcyste PCYOX1L	17901.54	19115.41	21702.63	0	0	0
Q8NBN3	Transmem TMEM87A	18878.67	21484.83	23256.95	0	0	0
Q8NBS9	Thioredoxi TXNDC5	6912.962	4633.802	9291.59	59496.86	79353.56	49275.71
Q8NBW4	Sodium-co SLC38A9	32996.48	40488.7	39675.39	0	0	0
Q8NC42	E3 ubiquiti RNF149	83115.27	81571.67	79596.1	0	0	0
Q8NC51	Plasminog SERBP1	12241.24	9973.752	11879.53	0	0	0
Q8NC54	Keratinocy KCT2	13222.33	14290.24	10828.43	0	0	0
Q8NCH0	Carbohydr CHST14	9230.646	10750.69	10815.94	0	0	0
Q8ND76	Cyclin-Y CCNY	28881.06	29124.48	26256.17	0	0	0
Q8NDI1	EH domain EHBP1	7262.23	8531.905	9907.51	0	0	0
Q8NDZ4	Deleted in C3orf58	4051.522	3999.53	5271.883	0	0	0
Q8NE01	Metal tran: CNM3	14659.36	16345.72	12434.76	0	0	0
Q8NE71	ATP-bindin ABCF1	4572.204	7354.465	4994.542	0	0	0
Q8NEM2	SHC SH2 c SHCBP1	15583.59	13053.49	34204.09	0	0	0
Q8NEW0	Zinc trans SLC30A7	6668.546	4056.631	7252.297	0	0	0
Q8NFA0	Ubiquitin c USP32	12487.5	13904.6	11347.4	0	0	0
Q8NFH3	Nucleopor NUP43	7704.96	6068.69	7407.505	0	0	0
Q8NFH5	Nucleopor NUP35	19260.9	20432.15	20672.68	0	0	0
Q8NFJ5	Retinoic ac GPRC5A	75365.1	73715.63	61545.98	0	0	0
Q8NFT2	Metallorec STEAP2	26069.52	28234.96	21687.4	0	0	0
Q8NG11	Tetraspani TSPAN14	468670.6	407565.9	358265.3	83921.62	0	106427.6
Q8NHP8	Putative pl PLBD2	7640.084	9984.08	11841.77	46761.61	49197.2	33544.15
Q8NI27	THO comp THOC2	2394.719	1584.426	2061.042	0	0	0
Q8NI35	InaD-like r INADL	17523262	19570016	12474945	2.11E+08	3.29E+08	1.42E+08
Q8TAA9	Vang-like VANG1	49399.23	56590.89	47390.59	0	0	0
Q8TAF3	WD repeat WDR48	20846.37	30055.71	33567.27	0	0	0
Q8TAG9	Exocyst co EXOC6	27227.08	23640.84	22610.58	0	0	0
Q8TAT6	Nuclear pr NPLOC4	8406.63	10357.91	7597.711	0	0	0
Q8TAV4	Stomatin-l STOML3	321057.7	186527.1	252755.1	0	377093.6	1059369
Q8TB03	Uncharact CXorf38	2189.489	1955.23	2051.495	0	0	0
Q8TB61	Adenosine SLC35B2	23690.21	21319.21	22191.43	44509.49	30410.88	32111.28
Q8TB68	Proline-ric PRR7	6907.346	7087.095	4462.879	0	0	0
Q8TB73	Protein NC NDNF	73209.55	80219.93	65036.23	96410.66	0	231979.5
Q8TB96	T-cell imm ITFG1	4061.157	4036.958	2805.109	0	0	0
Q8TBC3	SH3KBP1-l SHKBP1	9428.342	10288.53	10291.19	0	0	0
Q8TBC4	NEDD8-ac UBA3	13809.84	12446.5	19836.44	0	0	0
Q8TBF2	Prostamid FAM213B	15349.2	5303.695	9853.314	0	0	0
Q8TBX8	Phosphatic PIP4K2C	34496.44	33935.89	30462.84	0	0	0
Q8TBZ3	WD repeat WDR20	19190.09	24698.22	21308.04	0	0	0
Q8TC12	Retinol del RDH11	14481.07	14961.19	12677.34	0	0	0
Q8TCG1	Protein Clf KIAA1524	11982.86	7048.749	2923.995	0	0	0
Q8TCT8	Signal pep SPPL2A	35033.64	32884.09	26921.18	0	0	0
Q8TCT9	Minor hist HM13	38804.29	42821.11	28284.34	0	0	0
Q8TCU6	Phosphatic PREX1	5527.305	7624.571	7458.917	0	0	0
Q8TCZ2	CD99 antiç CD99L2	34685.09	32734.3	32231.17	0	0	0
Q8TD19	Serine/thre NEK9	9958.363	9855.197	9798.432	0	0	0
Q8TD55	Pleckstrin l PLEKHO2	35204.77	35255.75	31686.57	0	0	0
Q8TDM6	Disks large DLG5	7720.04	9184.438	7910.026	0	0	0
Q8TDN6	Ribosome BRX1	5865.197	5783.36	6217.377	0	0	0
Q8TDW0	Volume-re LRR C8C	18219.04	17906.93	16718.66	0	0	0

Q8TDZ2	Protein-m:MICAL1	4504.524	4215.168	6127.405	0	0	0
Q8TEQ6	Gem-asso:GEMIN5	10824.94	10323.94	11893.58	0	0	0
Q8TEW0	Partitionin:PARD3	17656.36	18425.83	21830.5	0	0	0
Q8TEX9	Importin-4:IPO4	15263.55	11707.75	9485.095	0	0	0
Q8TF42	Ubiquitin-:UBASH3B	130265.3	127151.9	124387.8	0	0	0
Q8WTT2	Nucleolar :NOC3L	3442.615	3448.682	7827.148	0	0	0
Q8WTV0	Scavenger SCARB1	186958.6	182766.5	183845.7	0	0	0
Q8WU20	Fibroblast FRS2	6415.71	5768.185	1295.974	0	0	0
Q8WUJ3	Cell migrat:CEMIP	11076.44	12133.23	12767.49	146531.9	116685.5	141083.8
Q8WUM4	Programm:PCDC6IP	634061.8	572903	613106.7	88995.02	59865.63	160786.5
Q8WUM9	Sodium-d:SLC20A1	119369.9	110622.8	106290.8	0	0	0
Q8WUW1	Protein BR BRK1	154187.5	137633.1	132421.6	0	0	0
Q8WUY9	DEP doma:DEPDC1B	26525.84	25966.89	26113.77	0	0	0
Q8WV24	Pleckstrin I:PHLDA1	102326.6	77694.72	85370.16	0	0	0
Q8WV41	Sorting ne:SNX33	13341.65	30759.48	24574.92	0	0	0
Q8WV99	AN1-type ZFAND2B	46601.39	46089.25	43123.73	0	0	0
Q8WVJ2	NudC dom:NUDCD2	19623.35	21122.72	18142.46	0	0	0
Q8WVM8	Sec1 family:SCFD1	14411.48	16548.52	15557.01	0	0	0
Q8WVY7	Ubiquitin-:UBLCP1	9726.165	15597.75	11667.99	0	0	0
Q8WWA0	Intellectin-:ITLN1	389680.2	341933.6	331559.3	287552.2	253904.9	260935.5
Q8WWI1	LIM domai:IMO7	12408.3	14623.45	11426.13	0	0	0
Q8WWI5	Choline tra:SLC44A1	193251.9	190316.2	217874.8	519212.8	0	161801.5
Q8WWN8	Arf-GAP w:ARAP3	8991.941	7506.612	6681.761	0	0	0
Q8WWU7	Intellectin-:ITLN2	826604.8	734785.9	742833.9	313265.5	289193	540924.7
Q8WWZ4	ATP-bindin:ABCA10	248608.2	216342.4	352554.6	1579875	2874770	1343837
Q8WWZ8	Oncoprote:OIT3	65153.9	66187.59	69892.95	197604.7	277849.5	190872.4
Q8WXE1	ATR-inter:ATRIP	12465.95	11848.33	15354.8	0	0	0
Q8WXE9	Stonin-2 STON2	4845.172	5506.961	4908.904	549122.7	585295.3	794003.8
Q8WYA6	Beta-cater:CTNBL1	7396.037	23246.02	6724.355	0	0	0
Q8WYP5	Protein EL:AHCTF1	484.8956	646.1437	436.0402	0	0	0
Q8WZA0	Protein LZ:ILZIC	14478.55	20499.51	13878.4	0	0	0
Q92499	ATP-deper:DDX1	14058.4	12774.95	12252.02	61581.58	0	46923.38
Q92520	Protein FA:FAM3C	12883.31	16362.14	14244.39	0	119390.1	58729.86
Q92530	Proteasom:PSMF1	32300.28	29932.48	29647.07	0	0	0
Q92536	Y+L aminc:SLC7A6	200348	198275.8	182499.6	0	0	0
Q92537	Sushi dom:SUSD6	13036.54	12576.45	11513.18	0	0	0
Q92538	Golgi-spec:GBF1	15710.65	5676.862	7653.734	0	0	0
Q92544	Transmem:TM9SF4	14212.82	13328.78	12996.93	23876.97	0	36278.88
Q92558	Wiskott-AI:WASF1	9963.431	10713.38	9169.637	0	0	0
Q92597	Protein NC:NDRG1	32802.95	35348.55	31166.17	0	0	0
Q92598	Heat shock:HSPH1	32620.36	34171.53	31204.95	0	0	0
Q92599	Septin-8 8-Sep	27953.88	27315.05	24217.38	0	0	0
Q92600	Cell differe:RQCD1	63481.78	9184.982	97207.8	0	0	0
Q92614	Unconvent:MYO18A	36614.96	31720.08	59277.77	631656.5	889543.4	285507.7
Q92616	Translatior:GCN1L1	260939.2	255263.2	353688	13711688	21284766	3531866
Q92626	Peroxidasin:PXDN	35444.11	44808.73	37690.18	874253.5	959492.4	1894679
Q92688	Acidic leuc:ANP32B	6952.751	8085.102	8912.4	0	0	0
Q92692	Nectin-2 PVRL2	316502.1	324842.1	285751.9	0	0	0
Q92696	Geranylger:RABGGTA	14532.64	12493.6	45022.13	0	0	0
Q92729	Receptor-i:PTPRU	3889.991	5582.064	4030.501	0	0	0
Q92734	Protein TF:TFG	58139.37	60905.2	57300.78	0	0	0
Q92738	USP6 N-te:USP6NL	12455.92	10672.07	11542.88	0	0	0
Q92743	Serine pro:HTRA1	20761.67	15646.81	19082.82	5173575	2761369	8269728
Q92747	Actin-relat:ARPC1A	36499.74	38986.38	33349.59	0	0	0
Q92769	Histone de:HDAC2	14766	36727.55	18227.34	0	0	0
Q92783	Signal tran:STAM	44365.3	41012.57	35639.52	0	0	0
Q92796	Disks large:DLG3	11303.48	11659.7	15405.39	0	0	0
Q92820	Gamma-g:GGH	22243.63	24150.68	24728.68	19831.76	0	23583.55

Q92841	Probable ADDX17	5347.089	4088.737	5011.25	0	0	0
Q92882	Osteoclast OSTF1	36117.3	28163.97	33837.67	0	0	0
Q92888	Rho guanine ARHGEF1	36537.03	39009.49	29124.72	0	0	0
Q92890	Ubiquitin f UFD1L	4467.002	4757.069	7038.358	0	0	0
Q92896	Golgi appa GLG1	18052.15	16957.69	17633.52	53510.26	0	34039.91
Q92905	COP9 sign COPS5	3221.082	3665.508	3083.323	0	0	0
Q92930	Ras-relate RAB8B	178081.5	188431.3	130620.8	42334.47	0	62894.6
Q92945	Far upstre KHSRP	6947.648	6611.358	5398.351	0	0	0
Q92954	Proteoglyc PRG4	22551.47	26924.04	34496.59	142148.6	195878	91801.29
Q93008	Probable c USP9X	7569.145	7863.054	8634.109	85802.86	33276.18	78836.37
Q93009	Ubiquitin c USP7	11623.51	14147.51	8131.401	0	0	0
Q93034	Cullin-5 CUL5	14595.04	11695.77	4858.045	0	0	0
Q93052	Lipoma-pr LPP	11804.49	17453.48	11478.16	0	0	0
Q93063	Exostosin- EXT2	21341.07	22358.08	27775.38	70040.61	0	37517.64
Q93088	Betaine- r BHMT	22608.24	28535.22	37111.95	216999.3	266992.1	143047.1
Q93096	Protein tyr PTP4A1	1909.984	1906.271	8260.496	0	0	0
Q969E2	Secretory c SCAMP4	25434.6	50517.39	54261.57	0	0	0
Q969P0	Immunogl IGSF8	360120.2	325066.1	336909.7	119654.4	85423.12	160093.8
Q969Q5	Ras-relate RAB24	24850.2	21771.89	13456.33	0	0	0
Q969W9	Protein TM PMEPA1	27319.04	31334.83	20121.81	0	0	0
Q969Z4	Tumor nec RELT	16894.07	16055.86	15681.78	0	0	0
Q96A54	Adiponect ADIPOR1	11234.72	12146.23	12662.18	0	0	0
Q96A57	Transmem TMEM230	11087.83	8975.771	6169.063	0	0	0
Q96A65	Exocyst co EXOC4	63072.56	64805.57	55502.29	0	0	0
Q96AC1	Fermitin fa FERMT2	248472.3	239032.8	224256.4	0	0	0
Q96AE4	Far upstre FUBP1	3418.791	3135.536	2749.921	0	0	0
Q96AG4	Leucine-ric LRRRC59	29233.41	14931.05	25913.29	0	0	0
Q96B97	SH3 doma SH3KBP1	7801.587	4039.11	10284.12	0	0	0
Q96BD0	Solute carr SLCO4A1	142476.8	138380.3	131029.9	0	0	0
Q96BJ3	Axin intera AIDA	83878.16	90740.8	75876.3	0	0	0
Q96BM9	ADP-ribos ARL8A	56320.09	68046.41	62797.14	0	0	0
Q96BN8	Ubiquitin t OTULIN	13156.71	11741.55	11703.29	0	0	0
Q96BY6	Dedicator DOCK10	33109.95	35482.48	30929.3	0	0	0
Q96CC6	Inactive rh RHBDF1	3600.882	3862.051	3132.114	0	0	0
Q96CG8	Collagen ti CTHRC1	5455.661	5766.625	12569.42	76020.31	64791.75	88464.18
Q96CN7	Isochorism ISOC1	19060.51	18641.14	16326.02	0	0	0
Q96CS7	Pleckstrin I PLEKHB2	79461.73	78190.95	68958.72	0	0	0
Q96CW5	Gamma-tu TUBGCP3	16134.33	15930.14	11087.81	0	0	0
Q96CX2	BTB/POZ c KCTD12	37823.79	39208.83	39143.39	114435	111293.4	69247.63
Q96D15	Reticulocal RCN3	54101.43	42751.39	84333.61	436612.4	604471.3	194022.6
Q96D31	Calcium re ORAI1	48765.95	54088.01	53622.88	0	0	0
Q96D71	RalBP1-as: REPS1	3712.46	3127.955	3585.978	0	0	0
Q96DG6	Carboxymr CMBL	37325.88	21335.69	7285.385	0	0	0
Q96DM3	Uncharact C18orf8	3336.323	4552.377	3491.099	0	0	0
Q96DX4	RING finger RSPRY1	39284.29	22621.86	25893.65	0	0	0
Q96EC8	Protein YIF YIPF6	24330.67	26950.11	31138.23	0	0	0
Q96EG1	Arylsulfata ARSG	16054.15	15023.16	15568.95	47078.93	48014.05	25521.71
Q96EK5	KIF1-bindr KIF1BP	4489.449	4955.668	5041.353	0	0	0
Q96EY5	Multivesicr MVB12A	109767.3	94952.79	114003.3	0	0	0
Q96F85	CB1 canna CNRIP1	103915.9	99102.61	108475.1	0	0	0
Q96FN4	Copine-2 CPNE2	13741.14	13581.91	15235.9	0	0	0
Q96FQ6	Protein S1(S100A16	212940.9	207687	193694.4	0	0	0
Q96FS4	Signal-ind SIPA1	12910.11	12482.96	12664.83	0	0	0
Q96FX8	p53 apopt PERP	53624.5	64112.86	48703.59	0	0	0
Q96FZ7	Charged r CHMP6	111114.8	95130.88	111440.1	0	0	0
Q96G03	Phosphogl PGM2	23188.94	22461.4	22398.5	0	0	0
Q96GD4	Aurora kin AURKB	18641.47	19038.81	16122.43	0	0	0
Q96GK7	Fumarylac FAHD2A	9294.835	6792.713	8678.108	0	0	0

Q96GQ7	Probable A	DDX27	3339.922	6736.204	5520.507	0	0	0
Q96GR4	Probable p	ZDHC12	5298.413	6571.111	5748.183	0	0	0
Q96HC4	PDZ and L	PDLIM5	70161.55	73440.97	73076.8	0	13015.1	19338.67
Q96HR9	Receptor e	REEP6	2968.467	7031.807	3175.076	0	0	0
Q96I24	Far upstre	FUBP3	47681.92	6826.471	6670.16	423461.2	0	619744.4
Q96I18	Leucine-ric	LRCH3	3181.988	3626.493	3268.702	0	0	0
Q96IJ6	Mannose-	GMPPA	6770.972	5290.899	4534.254	0	0	0
Q96IU4	Alpha/bet	ABHD14B	34578.09	31739.63	29569.77	0	0	0
Q96IY4	Carboxype	CPB2	119973.2	120028.8	144980.6	0	0	0
Q96J84	Kin of IRRE	KIRREL	68280.84	60552.09	63552.55	0	0	0
Q96J92	Serine/thr	WNK4	5134.127	5484.546	5095.969	0	0	0
Q96JA1	Leucine-ric	LRIG1	7214.342	7652.213	5443.468	0	0	0
Q96JB6	Lysyl oxida	LOXL4	0	0	0	31368.49	19492.06	32217.52
Q96JD6	1,5-anhyd	AKR1E2	35063.44	35622.3	41341.8	0	0	0
Q96KB5	Lymphokir	PBK	28867.23	24434.82	22570.12	0	0	0
Q96KG7	Multiple e	MEGF10	7895.114	15615.98	13577.16	0	0	0
Q96KP4	Cytosolic r	CNDP2	64130.89	45664.83	57195.74	0	0	0
Q96LD4	Tripartite r	TRIM47	4318.716	3441.152	3235.518	0	0	0
Q96ME1	F-box/LRR	FBXL18	9267.122	8657.162	3130.325	0	0	0
Q96N06	Spermato	SPATA33	6525.047	7731.021	7295.076	0	0	0
Q96N67	Dedicator	DOCK7	10369.12	12775.36	11384.14	0	0	0
Q96NE9	FERM dom	FRMD6	27391.87	27721.29	28532.4	0	0	0
Q96NT5	Proton-co	SLC46A1	9044.01	9742.818	8110.051	0	0	0
Q96NY7	Chloride ir	CLIC6	1249604	1307805	1090402	0	0	0
Q96P48	Arf-GAP w	ARAP1	13449.27	13359.73	12685.98	0	0	0
Q96P70	Importin-	εIPO9	5936.6	6087.417	1471.426	0	0	0
Q96PD2	Discoidin,	DCBLD2	24958.04	36521.18	15264.78	0	0	0
Q96PD5	N-acetyl	PGLYRP2	48308.66	49318.72	67120.68	217558.9	382687	0
Q96PK6	RNA-bind	RBM14	1951.19	3069.251	2748.677	0	0	0
Q96PU5	E3 ubiquiti	NEDD4L	99695.24	99978.46	91429.11	0	0	0
Q96PY5	Formin-lik	FMNL2	190047.1	188152.8	173153	0	0	0
Q96Q11	CCA tRNA	TRNT1	10599.52	13475.45	13285.55	0	0	0
Q96Q45	Transmem	TMEM237	64727.83	36787.95	38528.73	0	0	0
Q96QD8	Sodium-cc	SLC38A2	673942	786017.8	586850.8	0	0	0
Q96QE2	Proton my	SLC2A13	9608.821	9675.554	10451.14	0	0	0
Q96RF0	Sorting ne	SNX18	30391.9	31690.45	29373.46	0	0	0
Q96RI0	Proteinase	F2RL3	3942.285	2796.209	4764.685	49568.36	0	105924.1
Q96RS6	NudC dom	NUDCD1	19399.51	17619.83	12981.26	0	0	0
Q96RT1	Protein LA	ERBB2IP	114600.3	113449	107889.3	0	0	0
Q96RT8	Gamma-tu	TUBGCP5	1710.415	2674.235	3242.667	0	0	0
Q96RW7	Hemicentir	HMCN1	1366210	1581811	706604.1	47601024	65044392	31404530
Q96S59	Ran-bind	RANBP9	3869.88	3413.381	2673.258	0	0	0
Q96S86	Hyalurona	HAPLN3	2493.505	3057.867	4122.193	142351.1	0	184007.1
Q96S97	Myeloid-a	MYADM	235439.5	325991.3	228357.2	0	0	0
Q96S99	Pleckstrin	PLEKHF1	8293.021	5711.919	8830.189	0	0	0
Q96SB3	Neurabin-	PPP1R9B	11334.13	12633.91	11522.82	0	0	0
Q96SL1	Disrupted	DIRC2	24654.59	26584.95	22690.46	0	0	0
Q96SU4	Oxysterol-	OSBPL9	11150.47	13594.02	20729.11	0	0	0
Q96SZ5	2-aminoet	ADO	13021.38	9689.097	11932.37	0	0	0
Q96T76	MMS19 nu	MMS19	11847.64	11194.68	8497.676	0	0	0
Q96TA1	Niban-like	FAM129B	148273.7	151374.1	133829.5	1247459	0	671176.1
Q99417	C-Myc-bir	MYCBP	15152.36	15141.94	17608.93	0	0	0
Q99426	Tubulin-fo	TBCB	12447.45	14441.68	22406.48	0	0	0
Q99436	Proteasom	PSMB7	127927.2	126299.3	155551.5	126185.6	98506.67	112890.4
Q99447	Ethanolam	PCYT2	18466.79	16417.04	18921.29	0	0	0
Q99460	26S protea	PSMD1	42721.35	32348.42	42592.18	0	0	0
Q99497	Protein de	PARK7	159766.6	149498.5	142258.6	158832.8	163500.6	132105.1
Q99523	Sortilin	SORT1	35760.59	28704.83	28612.25	0	0	0

Q99536	Synaptic vesicle	VAT1	400805.2	418409.6	347790.3	73252.43	58272.39	64052.93
Q99569	Plakophilin	PKP4	21077.58	12536.51	10351.75	0	0	0
Q99570	Phosphoinositide	PIK3R4	8484.197	2369.439	3440.596	0	0	0
Q99584	Protein S100	S100A13	161976.2	159402.6	156454.8	0	0	0
Q99615	DnaJ homolog	DNAJC7	16010.93	14354.85	15643.01	0	0	0
Q99622	Protein C12orf57	C12orf57	20727.65	16811.27	18156.26	0	0	0
Q99627	COP9 signal	COPS8	21700.93	22250.66	23648.01	0	0	0
Q99650	Oncostatin	OSMR	31643.86	22519.35	34246.32	0	0	0
Q99653	Calcineurin	CHP1	59016.69	59082.5	50963.41	0	0	0
Q99661	Kinesin-like	KIF2C	10934.31	7404.416	6853.039	0	0	0
Q99685	Monoglycosyl	MGLL	41250.16	53955.99	39861.47	0	0	0
Q99715	Collagen alpha	COL12A1	2922520	2792096	2997279	9335523	8199789	12020047
Q99717	Mothers against	SMAD5	3020.275	4483.824	2585.594	0	0	0
Q99733	Nucleoson	NAP1L4	30638.62	28009.03	37439.86	0	0	0
Q99747	Gamma-secretase	NAPG	127877	119891.7	109260.3	0	0	0
Q99755	Phosphatidylinositol	PIP5K1A	123621.8	142165.9	132689.3	0	0	0
Q99805	Transmembrane	TM9SF2	101942.9	104640.2	101866.4	84320.18	32916.44	64334.05
Q99808	Equilibrative	SLC29A1	458354.4	532196.6	491910.5	47406.21	0	73315.46
Q99828	Calcium channel	CIB1	9768.196	10568.86	9045.471	0	0	0
Q99961	Endophilin	SH3GL1	80553.61	71142.33	71853.61	39432.07	0	30842.87
Q9BPX3	Condensin	NCAPG	15163.51	12099.51	11867.8	0	0	0
Q9BPX5	Actin-related	ARPC5L	176030.2	160027.3	145810.1	0	0	0
Q9BPZ7	Target of rapamycin	MAPKAP1	7955.141	9423.6	7905.598	0	0	0
Q9BQ04	RNA-binding	RBM4B	8948.372	6707.156	8899.47	0	0	0
Q9BQ24	Zinc finger	ZFYVE21	23736.55	23001.45	24076.37	0	0	0
Q9BQA1	Methyltransferase	WDR77	55234.9	55946.62	56765.5	0	0	0
Q9BQG0	Myb-binding	MYBBP1A	10630.74	10398.32	2291.89	0	0	0
Q9BQL6	Fermitin family	FERMT1	88363.13	90847.63	75151.88	0	0	0
Q9BR76	Coronin-1	CORO1B	74688.27	77827.91	70052.37	0	0	0
Q9BRA2	Thioredoxin	TXNDC17	87275.82	88351.53	83523.46	25577.71	121196.9	42447.66
Q9BRG1	Vacuolar protein	VPS25	55521.45	41600.27	48148.54	0	0	0
Q9BRP4	Proteasome	PAAF1	4578.001	9928.876	8620.063	0	0	0
Q9BRX2	Protein peptidase	PELO	5533.766	5765.06	5439.37	0	0	0
Q9BS26	Endoplasmic	ERP44	18870.19	16688.33	8500.584	0	0	0
Q9BSA4	Protein tyrosine	TTYH2	19622.46	18709.03	19411.35	0	0	0
Q9BSJ8	Extended synaptobrevin	ESYT1	15402.58	15805.77	6856.673	39546.98	0	82468.09
Q9BSQ5	Cerebral cortex	CCM2	19751.52	12516.63	16481.87	0	0	0
Q9BT09	Protein carrier	CNPY3	6648.5	13790.22	15179.51	0	0	0
Q9BT67	NEDD4 family	NDFIP1	75928.53	72117.86	55323.16	0	0	0
Q9BT78	COP9 signal	COPS4	13436.82	21189.62	21472.72	0	0	0
Q9BTE3	Mini-chromosome	MCMBP	9353.876	8807.186	11122.39	0	0	0
Q9BTM9	Ubiquitin-like	URM1	31992.59	29856.48	21151.51	0	0	0
Q9BTT0	Acidic leucine	ANP32E	32697.39	22374.79	14692.66	0	0	0
Q9BTT6	Leucine-rich	LRRC1	23835.25	27878.2	23541.61	0	0	0
Q9BTU6	Phosphatidylinositol	PI4K2A	30871.51	29126.15	28764.74	0	0	0
Q9BTW9	Tubulin-specific	TBCD	14318.77	11703.21	10798.91	0	0	0
Q9BTX1	Nucleoporin	NDC1	16499.71	18661.54	19164.77	0	0	0
Q9BUF5	Tubulin binding	TUBB6	160836.8	276092.9	337238.3	6209379	2288837	5673297
Q9BUJ2	Heterogeneous	HNRNPUL	4366.056	5572.911	5630.61	0	0	0
Q9BUL8	Programmed cell	PDCD10	210861.3	213442	205653.5	0	0	0
Q9BUN8	Derlin-1	DERL1	7970.88	9311.881	8684.131	0	0	0
Q9BV20	Methylthio	MRI1	3273.438	4017.172	2777.603	0	0	0
Q9BV57	1,2-dihydroxy	ADI1	13587.62	14500.21	12035.42	0	0	0
Q9BV68	E3 ubiquitin	RNF126	22400.91	21021.46	14499.44	0	0	0
Q9BV86	N-terminus	NTMT1	23710.25	22564.77	24559.39	0	0	0
Q9BVA1	Tubulin binding	TUBB2B	363484	380710.6	348144	1458404	1150398	3119961
Q9BVC4	Target of rapamycin	MLST8	12606.02	11270.46	9202.944	0	0	0
Q9BVC6	Transmembrane	TMEM109	149186	146071.1	139363	0	0	0

Q9BVG4	Protein PB PBDC1	14389.24	15632.3	13699.69	0	0	0
Q9BVG9	Phosphatic PTDSS2	14067.32	14838.9	11836.93	0	0	0
Q9BVK6	Transmem TMED9	10652.24	9093.951	13005.48	0	0	0
Q9BVL2	Nucleopor NUP58	4166.377	6713.87	4334.04	0	0	0
Q9BVQ7	Spermatoc SPATA5L1	5657.302	4163.413	8162.829	0	0	0
Q9BWS9	Chitinase c CHID1	6417.568	6550.017	8945.004	0	0	0
Q9BX67	Junctional JAM3	127174.4	117974.7	116424.2	0	0	0
Q9BX79	Stimulated STRA6	2252.665	2022.287	1624.19	0	0	0
Q9BX97	Plasmalemm PLVAP	31245.83	30643.11	39923.76	65092.79	0	56856.02
Q9BXB5	Oxysterol- OSBPL10	9619.296	10344.58	8629.391	0	0	0
Q9BXF6	Rab11 fam RAB11FIP5	12807.44	11370.7	14485.24	0	0	0
Q9BXI6	TBC1 dom TBC1D10A	56877.69	55146.13	50475.41	0	0	0
Q9BXJ9	N-alpha-a NAA15	18798.69	19278.12	18746.79	0	0	0
Q9BXP2	Solute carr SLC12A9	4002.359	4163.806	3014.037	0	0	0
Q9BXS4	Transmem TMEM59	23202.94	29225.49	21902.11	0	0	0
Q9BXX0	EMILIN-2 EMILIN2	44978.25	37165.32	42246.54	0	0	0
Q9BY32	Inosine triph ITPA	13047.46	13336.46	16555.51	0	0	0
Q9BY44	Eukaryotic EIF2A	13825.53	12667.18	13923.15	0	0	0
Q9BY67	Cell adhesi CADM1	55915.63	53854.32	52710.48	0	0	0
Q9BY76	Angiopoie ANGPTL4	0	0	0	119535.9	91896.05	168165.9
Q9BYG5	Partitioning PARD6B	9907.035	8371.726	8728.489	0	0	0
Q9BYI3	Hyccin FAM126A	20493.99	13324.72	18514.07	0	0	0
Q9BYN0	Sulfiredoxi SRXN1	2789.305	4188.848	2810.005	0	0	0
Q9BZ29	Dedicator DOCK9	23637.86	20185.34	18942.86	0	0	0
Q9BZ67	FERM dom FRMD8	13321.46	22273.5	19161.32	0	0	0
Q9BZE4	Nucleolar GTPBP4	5379.319	7271.304	4081.139	0	0	0
Q9BZE9	Tether con ASPSCR1	9674.993	9897.467	6618.756	0	0	0
Q9BZF9	Uveal auto UACA	4702.824	7453.68	5251.977	0	0	0
Q9BZG1	Ras-relate RAB34	164951.1	162685.1	149617.7	0	0	0
Q9BZG8	Diphthami DPH1	4648.462	5783.692	4111.265	0	0	0
Q9BZH6	WD repeat WDR11	5451.198	5650.534	6217.646	0	0	0
Q9BZK7	F-box-like TBL1XR1	5363.937	6680.294	7988.036	0	0	0
Q9BZL6	Serine/thr PRKD2	18318.67	18687.92	16798.58	17198.17	0	25297.49
Q9BZM6	NKG2D lig ULBP1	4777.597	4181.789	3512.154	0	0	0
Q9BZQ8	Protein Nil FAM129A	72811.75	72898.6	64429.36	0	0	0
Q9BZX2	Uridine-cy UCK2	14286.14	14289.07	13609.96	0	0	0
Q9C004	Protein spr SPRY4	111042.4	88646.48	70945.92	0	0	0
Q9C0B5	Palmitoyl tr ZDHHC5	67865.07	68296.95	52120.37	0	0	0
Q9C0C4	Semaphori SEMA4C	24333.07	27397.37	26432.46	0	0	0
Q9C0D5	Protein TA TANC1	14214.19	13586.43	11584.09	0	0	0
Q9C0D9	Ethanolam EPT1	25081.9	24678	24401.4	0	0	0
Q9C0H5	Rho GTPas ARHGAP35	10089.43	8840.366	9257.251	0	0	0
Q9C0I1	Myotubula MTMR12	2306.051	1775.648	1897.398	0	0	0
Q9GZM5	Protein YIF YIPF3	20877.52	24945.56	21781.2	0	0	0
Q9GZM7	Tubulointe TINAGL1	171326.1	187408.4	173897.7	0	0	0
Q9GZN8	UPF0687 p C20orf27	1507.387	2459.902	1055.402	0	0	0
Q9GZP1	Neurensin NRSN2	49621.76	71867.9	70463.7	0	0	0
Q9GZS3	WD repeat WDR61	9955.389	44022.16	47475.5	0	0	0
Q9GZU7	Carboxy-tr CTDSP1	32944.63	35356.15	29612.66	0	0	0
Q9GZX5	Zinc finger ZNF350	597641.6	627661.6	1091737	0	50420504	27278870
Q9GZZ9	Ubiquitin-UBA5	9673.714	10476.06	8555.549	0	0	0
Q9H013	Disintegrin ADAM19	13209.17	18058.78	11785.95	0	0	0
Q9H074	Polyadeny PAIP1	13852.63	14079.96	14086.83	0	0	0
Q9H0D6	5-3 exorib XRN2	1622.242	9207.782	1668.064	0	0	0
Q9H0N0	Ras-relate RAB6C	151331.7	115251.1	104308	0	0	0
Q9H0R3	Transmem TMEM222	7707.659	9120.064	7522.031	0	0	0
Q9H0U4	Ras-relate RAB1B	68939.6	77317.06	77937.07	0	0	0
Q9H0W9	Ester hydr C11orf54	23455.68	18257.93	17945.7	0	0	0

Q9H1A4	Anaphase-ANAPC1	8371.67	9245.748	12185.54	0	0	0
Q9H1C7	Cysteine-r CYSTM1	196600.8	167866.3	173940.9	0	0	0
Q9H1Y0	AutophagyATG5	2086.021	2383.824	2102.025	0	0	0
Q9H201	Epsin-3 EPN3	7735.877	6383.168	4807.047	0	0	0
Q9H228	Sphingosir S1PR5	7754.019	8247.444	7759.005	0	0	0
Q9H246	UncharactC1orf21	16228.69	17550.04	11359.89	0	0	0
Q9H267	Vacuolar pVPS33B	7734.353	7340.648	5021.919	0	0	0
Q9H299	SH3 doma SH3BGRL3	404385.7	186522.2	373690.7	470359	690882.8	355954
Q9H2C0	Gigaxonin GAN	7417.804	13098.56	7733.58	0	0	0
Q9H2G2	STE20-like SLK	68055.61	61659.73	80260.45	0	0	0
Q9H2H9	Sodium-co SLC38A1	235756.1	239856.5	233266.8	0	0	0
Q9H2K8	Serine/threTAOK3	23208.98	22067.71	22061.19	0	0	0
Q9H2U1	ATP-depeDHX36	3711.719	3063.425	2775.379	0	0	0
Q9H2U2	Inorganic pPPA2	105767.2	105652.5	104089.7	0	0	0
Q9H3K6	BolA-like pBOLA2	16331.5	23377.75	21559.58	0	0	0
Q9H3S7	Tyrosine-pPTPN23	18339.45	22176.06	22417.02	0	0	0
Q9H3U1	Protein un UNC45A	19391.9	18196.17	16209.91	0	0	0
Q9H3Z4	DnaJ homcDNAJC5	29321.59	26172.11	37778.14	0	0	0
Q9H425	UncharactC1orf198	4318.255	4644.426	3580.934	0	0	0
Q9H444	Charged rCHMP4B	363344.4	207329	253529.2	0	0	0
Q9H4A4	Aminopep RNPEP	26409.92	27649.13	25251.95	0	0	0
Q9H4B7	Tubulin beTUBB1	114478.5	70297.26	93422.71	3927363	1112367	5073463
Q9H4F8	SPARC-rel SMOC1	10241.63	9399.056	11480.86	154725.4	0	79816.55
Q9H4G0	Band 4.1-l EPB41L1	27946.81	28713.49	32113.13	0	0	0
Q9H4G4	Golgi-assc GLIPR2	132880.2	108049	109716.6	121954.1	179785.7	145865.8
Q9H583	HEAT repe HEATR1	59737.82	76904.23	3865.161	460353.1	0	492470
Q9H5V8	CUB doma CDCP1	290352.2	291369.1	295797.9	0	0	0
Q9H6B4	CXADR-lik CLMP	46041.66	1203838	48738.96	4471939	0	3086545
Q9H6X2	Anthrax to ANTXR1	27597.35	34224.99	32715.45	0	0	0
Q9H773	dCTP pyro DCTPP1	25704.07	18475.88	19413.31	0	0	0
Q9H7B4	Histone-ly SMYD3	4084.333	3658.66	3504.022	0	0	0
Q9H7D0	Dedicator DOCK5	7030.371	4434.81	6104.261	0	0	0
Q9H7D7	WD repeatWDR26	9934.765	9813.409	8214.436	0	0	0
Q9H7F0	Probable cATP13A3	21684.38	21662.49	21705.09	0	0	0
Q9H7F4	Transmem TMEM185I	10795.86	10215.82	8234.552	0	0	0
Q9H7P6	Multivesic MVB12B	8701.325	8668.724	7179.134	0	0	0
Q9H813	Transmem TMEM206	21593.28	19533.53	20213.55	0	0	0
Q9H832	Ubiquitin-iUBE2Z	35245.97	37222.83	32395.39	0	0	0
Q9H853	Putative tuTUBA4B	657242	656404.6	625444.1	4566328	1709119	5628501
Q9H8M9	Protein evEVA1A	498806.9	489682.1	479027.2	0	0	0
Q9H8S9	MOB kinasMOB1A	48989.75	45929.56	45983.79	0	0	0
Q9H8W4	Pleckstrin lPLEKHF2	9355.224	4705.364	6129.582	0	0	0
Q9H944	Mediator cMED20	2332.829	2645.923	1919.423	0	0	0
Q9H9A6	Leucine-ricLRRC40	9356.379	8944.264	9391.009	0	0	0
Q9H9H4	Vacuolar pVPS37B	134880.1	122529	129408	0	0	0
Q9H9Q2	COP9 sign COPS7B	7562.411	7677.614	7962.987	0	0	0
Q9H9T3	Elongator cELP3	8087.753	8807.787	9274.582	0	0	0
Q9H9Y6	DNA-direct POLR1B	1702.935	711.8166	1800.153	0	0	0
Q9HAB3	Solute carr SLC52A2	152880.4	181717.6	191482.4	0	0	0
Q9HAB8	PhosphopPPCS	8685.248	13206.3	11813.38	0	0	0
Q9HAC8	Ubiquitin cUBTD1	123424.3	124150.2	117309.5	0	0	0
Q9HAT8	E3 ubiquiti PELI2	20326.13	18767.05	18938.36	0	0	0
Q9HAU0	Pleckstrin lPLEKHA5	11527.89	8750.279	7839.19	0	0	0
Q9HAU4	E3 ubiquiti SMURF2	13403.8	19310.53	16997.8	0	0	0
Q9HAV0	Guanine nGNB4	51117.84	119724.7	43109.38	43964.9	0	72563.13
Q9HAV4	Exportin-5XPO5	3563.321	2955.407	2739.44	0	0	0
Q9HB07	UPF0160 pC12orf10	19323.53	23149.32	18110.38	0	0	0
Q9HB09	Bcl-2-like BCL2L12	44469.8	34259.17	25514.67	0	0	0

Q9HB71	Calcyclin-t CACYBP	40676.83	38701.6	44341.71	0	0	0
Q9HBA0	Transient r TRPV4	6974.054	8317.037	4868.224	0	0	0
Q9HBH0	Rho-relate RHOF	11973.3	12800.13	12349.22	0	0	0
Q9HBI1	Beta-parvi PARVB	55491.35	71050.05	88868.74	0	84116.48	156210.9
Q9HC07	Transmem TMEM165	9266.703	12357.1	9256.536	0	0	0
Q9HCE1	Putative h MOV10	2135.128	3167.771	1472.074	0	0	0
Q9HCE7	E3 ubiquiti SMURF1	2817.489	2830.686	3383.221	0	0	0
Q9HCJ6	Synaptic v VAT1L	4509.686	6543.694	5556.031	0	0	0
Q9HCM4	Band 4.1-l EPB41L5	29762.34	18898.43	37149.32	0	0	0
Q9HCN3	Transmem TMEM8A	30135.22	31731.22	26534.84	0	0	0
Q9HCP0	Casein kin CSNK1G1	24498.75	29348.14	23973.45	0	0	0
Q9HD45	Transmem TM9SF3	11224.86	30086.54	27120.08	0	0	0
Q9HD67	Unconvent MYO10	68772.76	68358.59	54172.98	0	0	0
Q9HDC5	Junctophil JPH1	19603.11	19810.88	21047.23	0	0	0
Q9HDC9	Adipocyte APMAP	65033.13	69158.13	69844.88	5043623	4710812	3572824
Q9NP58	ATP-bindin ABCB6	10779.44	9542.345	9261.832	0	0	0
Q9NP72	Ras-relate RAB18	23967.49	24379.87	17629.37	0	0	0
Q9NP79	Vacuolar p VTA1	127945.8	95069.14	98919.41	0	72524.54	61220.77
Q9NPF0	CD320 ant CD320	25540.57	52869.42	50551.92	0	0	0
Q9NPG4	Protocadh PCDH12	29728.85	30027.84	37515.59	0	215536.9	24885
Q9NPH2	Inositol-3- ISYNA1	8104.136	8765.729	9762.459	0	0	0
Q9NPH3	Interleukin IL1RAP	96826.47	93084.66	113005.4	534726.8	630523.4	404219
Q9NPI0	Transmem TMEM138	15193.17	19991.04	19017.86	0	0	0
Q9NPQ8	Synembryr RIC8A	22690.11	21539.15	19247.97	0	0	0
Q9NPR2	Semaphori SEMA4B	6131.955	5172.496	4748.667	0	0	0
Q9NQ79	Cartilage a CRTAC1	12345.3	7878.31	14768.35	0	0	0
Q9NQ84	G-protein GPRC5C	14066.97	15722.25	14705.08	0	0	0
Q9NQC3	Reticulon- RTN4	207621.7	215354.1	179082.5	990735.6	831440.5	818230.7
Q9NQH7	Probable X XPNPEP3	1384944	1355922	1348009	277034.8	278955.9	274383.6
Q9NQR4	Omega-ar NIT2	5582.064	7585.811	9304.943	0	0	0
Q9NQS3	Nectin-3 PVRL3	7469.054	8773.051	9755.804	0	0	0
Q9NQW7	Xaa-Pro ar XPNPEP1	22291.64	19393.56	23048.36	0	30603.16	24009.25
Q9NQX7	Integral m ITM2C	139623.8	139812.4	104976.8	0	0	0
Q9NR09	Baculoviral BIRC6	4720.087	5432.396	8102.783	0	0	0
Q9NR12	PDZ and L PDLIM7	141357	133910.9	121536.8	0	0	0
Q9NR19	Acetyl-coe ACSS2	10446.4	12217.89	10633.42	0	0	0
Q9NR30	Nucleolar I DDX21	16666.8	17611.76	15412.69	59828184	63204688	35631700
Q9NR31	GTP-bindin SAR1A	96875.98	70510.24	70320.36	94917.96	95572.46	164484.4
Q9NRA2	Sialin SLC17A5	7997.062	7393.208	7112.539	0	0	0
Q9NRG9	Aladin AAAS	265494.7	138165.4	461122.1	0	0	0
Q9NRN5	Olfactome OLFML3	16307.52	18371.35	24753.99	246114.2	344209.4	317987
Q9NRN7	L-aminoac AASDHPP	11750.46	8816.823	11591.21	0	0	0
Q9NRR3	CDC42 sm CDC42SE2	47532.98	42805.38	40632.63	0	0	0
Q9NRR8	CDC42 sm CDC42SE1	33058.52	43831.14	33725.6	0	0	0
Q9NRV9	Heme-bin HEBP1	60563.38	57665.58	44522.94	0	0	0
Q9NRW1	Ras-relate RAB6B	1114089	1263665	1188279	0	0	0
Q9NRW7	Vacuolar p VPS45	20701.84	18421.71	19580.54	0	0	0
Q9NRY6	Phospholip PLSCR3	154578.3	183628	200811.6	1263432	0	474169.8
Q9NS86	LanC-like L LANCL2	23027.6	19165.29	25146.86	0	0	0
Q9NS93	Transmem TM7SF3	4548.664	3181.507	1291.872	0	0	0
Q9NSD9	Phenylalan FARSB	11063.33	11505.27	11330.59	0	0	0
Q9NT62	Ubiquitin-l ATG3	18229.96	17924.3	16669.01	0	0	0
Q9NTJ3	Structural l SMC4	7909.427	6214.17	9389.512	0	0	0
Q9NTK5	Obg-like AOLA1	50714.38	57020.14	55545.51	0	0	0
Q9NUE0	Palmitoyltr ZDHHC18	18517.49	16707.8	17336.56	0	0	0
Q9NUM4	Transmem TMEM106I	91381.61	73376.33	122531.1	0	0	0
Q9NUP9	Protein lin LIN7C	271349.5	256924.3	240886	0	0	0
Q9NUQ8	ATP-bindin ABCF3	8216.902	7411.34	4437.373	0	0	0

Q9NUQ9	Protein FA FAM49B	298086	288672.3	261044	0	0	0
Q9NUS5	AP-5 comp AP5S1	76883.02	63728.13	58447.04	0	0	0
Q9NUU7	ATP-depe DDX19A	13424.04	16159.22	18627.13	0	0	0
Q9NV58	E3 ubiquiti RNF19A	10921.57	7118.723	10878.1	0	0	0
Q9NV70	Exocyst co EXOC1	17498.51	20574.93	17307.5	0	0	0
Q9NV96	Cell cycle c TMEM30A	67741.91	71035.11	62315.95	0	0	0
Q9NVE7	Pantothen. PANK4	11767.33	10101.99	12359.73	0	0	0
Q9NVJ2	ADP-ribos ARL8B	35812.73	38575.21	40427.83	0	0	0
Q9NVM1	Protein ev: EVA1B	40993.21	33369.1	33469.75	0	0	0
Q9NVP1	ATP-depe DDX18	8318.988	7767.488	7637.623	0	0	0
Q9NVQ4	Fas apoptc FAIM	21522.3	5622.451	20694.48	0	0	0
Q9NVS9	Pyridoxine PNPO	7916.906	7210.108	6712.774	0	0	0
Q9NWD8	Transmem TMEM248	16050.2	13733.85	14024.36	0	0	0
Q9NWX6	Probable t THG1L	14836.03	11616.57	15831.64	0	0	0
Q9NX47	E3 ubiquiti 5-Mar	3208.969	2067.339	3328.463	0	0	0
Q9NX57	Ras-relate RAB20	19374.04	21479.21	20224.78	0	0	0
Q9NX62	Inositol mc IMPAD1	18665.67	19556.4	20443.17	0	0	0
Q9NXH9	tRNA (gua TRMT1	1064.51	1054.183	1339.014	0	0	0
Q9NXU5	ADP-ribos ARL15	26836.28	32597.21	30630.4	0	0	0
Q9NY26	Zinc trans SLC39A1	1656.717	1225.554	1378.869	0	0	0
Q9NY33	Dipeptidyl DPP3	24088.18	24425.82	24803.95	0	0	0
Q9NY35	Claudin dc CLDND1	175999.4	185907.9	173766.2	0	0	0
Q9NY97	N-acetyl B3GNT2	3627.655	3936.165	4631.216	0	0	0
Q9NYB9	Abl interac ABI2	189701.5	184087.3	147148.7	0	0	0
Q9NYL2	Mitogen-a ZAK	8833.772	9831.66	9614.377	0	0	0
Q9NYL9	Tropomod TMOD3	29892.83	26408.71	27540.84	0	0	0
Q9NYM9	BET1-like t BET1L	18752.78	20183.56	16227.1	0	0	0
Q9NYT0	Pleckstrin- PLEK2	55905.66	50976.28	49186.22	0	0	0
Q9NZD2	Glycolipid GLTP	55044.65	32240.35	28409.61	0	0	0
Q9NZD8	Maspardin SPG21	19986.03	27472.36	17018.21	0	0	0
Q9NZJ4	Sacsin SACS	3256.53	6473.505	6201.248	0	0	0
Q9NZL4	Hsp70-bin HSPBP1	36580.07	35484.01	31844.96	0	0	0
Q9NZL9	Methionine MAT2B	12915.26	14229.97	11298.93	0	0	0
Q9NZN3	EH domain EHD3	531990.3	607679.7	547493	157525	161339	250372.8
Q9NZP8	Compleme C1RL	0	0	0	56888.91	66546.84	50780.08
Q9NZQ3	NCK-inter: NCKIPSD	15472.74	17112.02	13132.51	0	0	0
Q9NZQ7	Programm CD274	15711.9	13758.85	14743.51	0	0	0
Q9NZR2	Low-densi LRP1B	167663.5	154967.6	164071.5	0	0	0
Q9NZT1	Calmodulin CALML5	0	3064.045	1726.188	735275.8	0	546168.8
Q9NZT2	Opioid grc OGFR	7154.746	10924.11	9045.84	0	0	0
Q9NZV1	Cysteine-r CRIM1	27745.41	35664.19	38718.44	0	0	0
Q9NZW5	MAGUK p: MPP6	409900.6	421694.8	376775.1	0	0	0
Q9NZZ3	Charged n CHMP5	429032.3	308008.8	406834.7	0	0	0
Q9P0K7	Ankyorbir RAI14	6730.761	7026.801	5012.517	0	0	0
Q9P0M6	Core histor H2AFY2	60496.52	73967.4	39623.72	0	0	0
Q9P0T7	Transmem TMEM9	28789.66	18043.64	14738.54	0	0	0
Q9P0V3	SH3 doma SH3BP4	74827.25	68895.36	66752.02	0	0	0
Q9P0V9	Septin-10 10-Sep	28787.41	29552.9	27104.1	0	0	0
Q9P1F3	Costars far ABRACL	131810.2	70955.53	68881.56	0	0	0
Q9P1T7	MyoD fam MDFIC	2997.048	3721.059	3553.544	0	0	0
Q9P206	Uncharact KIAA1522	8182.695	15384.49	9411.014	0	0	0
Q9P258	Protein RC RCC2	10918.52	10001.92	8561.179	0	0	0
Q9P265	Disco-inte DIP2B	129780.8	175020.8	139801.5	0	109252.7	417751.8
Q9P270	SLAIN mot SLAIN2	17348.25	13164.61	13907.42	0	0	0
Q9P273	Teneurin-3 TENM3	14505.41	9903.511	12208.69	0	0	0
Q9P287	BRCA2 anc BCCIP	7704.938	6454.152	13674.11	0	0	0
Q9P289	Serine/thre STK26	189886.5	182321.7	167269.8	0	0	0
Q9P2B2	Prostaglan PTGFRN	2984692	2955263	2754783	429118	349189.3	619980.5

Q9P2D3	HEAT repe HEATR5B	27965	16789.19	31341.85	1624527	2242156	2293727
Q9P2I0	Cleavage ε CPSF2	784210.6	30885.85	35353.25	0	0	0
Q9P2J5	Leucine--t LARS	12258.93	13616.11	13634.1	0	0	0
Q9UBB4	Ataxin-10 ATXN10	12687.46	11343.1	12080.17	0	0	0
Q9UBB6	Neurochor NCDN	7234.018	5664.056	4316.177	0	0	0
Q9UBC2	Epidermal EPS15L1	8817.226	9318.151	10518.34	0	0	0
Q9UBF2	Coatomer COPG2	5024.568	4527.727	10919.85	40402.85	85860.48	28727.37
Q9UBF8	Phosphatic PI4KB	2405.984	3517.357	2867.935	0	0	0
Q9UBG0	C-type ma MRC2	20570.91	21968.99	25609.44	98426.73	154751.3	156549.5
Q9UBH6	Xenotropic XPR1	6217.9	6060.094	6475.825	0	0	0
Q9UBQ0	Vacuolar p VPS29	28126.19	20701.6	24125.66	0	0	0
Q9UBQ5	Eukaryotic EIF3K	9824.192	8118.224	13656.6	0	0	0
Q9UBQ7	Glyoxylate GRHPR	12497.22	13220.8	10936.16	0	0	0
Q9UBR2	Cathepsin CTSZ	61214.93	34322.88	50471.74	533875.4	626240.5	226822.2
Q9UBS4	DnaJ homc DNAJB11	26927.05	15745.1	16029.63	0	0	0
Q9UBV8	Peflin PEF1	76598.27	91966.58	92337.45	21869.42	0	57074.88
Q9UBX5	Fibulin-5 FBLN5	8424.685	0	11306.15	0	85261.71	59463.8
Q9UDY2	Tight junct TJP2	54485.28	54302.1	46668.63	32899.14	0	46084.13
Q9UDY4	DnaJ homc DNAJB4	4331.076	3824.681	4575.538	0	0	0
Q9UEY8	Gamma-ac ADD3	19393.23	18124.46	18374.04	0	0	0
Q9UGH3	Solute carr SLC23A2	68408.64	71177.44	55656.73	0	0	0
Q9UGJ0	5-AMP-ac PRKAG2	20178.36	14587.74	19207.79	0	0	0
Q9UGM3	Deleted in DMBT1	75712.56	82140.17	101509.2	1620548	1058128	1228339
Q9UGQ3	Solute carr SLC2A6	16802.01	16929.56	14068.71	0	0	0
Q9UHA4	Ragulator LAMTOR3	18132.11	20684.14	16571.97	0	0	0
Q9UHB6	LIM domai LIMA1	37875.28	39906.68	34876.21	0	0	0
Q9UHB9	Signal recc SRP68	6947.381	5449.29	6108.767	0	0	0
Q9UHD1	Cysteine ai CHORDC1	77619.83	62452.48	87515.43	0	0	0
Q9UHD2	Serine/thrε TBK1	2285.395	1815.07	982.4697	0	0	0
Q9UHD8	Septin-9 9-Sep	75673.2	80240.32	77122.4	69914.99	25911.91	65536.16
Q9UHE8	Metallored STEAP1	42146.21	42997.06	38935.78	0	0	0
Q9UHI6	Probable A DDX20	8812.599	10212.52	9762.775	0	0	0
Q9UHI8	A disintegr ADAMTS1	4737.664	4118.776	0	211929.6	79440.09	195730
Q9UHR4	Brain-spec BAIAP2L1	14034.38	22925.71	22638.62	0	0	0
Q9UHV9	Prefoldin s PFDN2	28689.35	34654.26	34322.24	0	0	0
Q9UHY7	Enolase-pl ENOPH1	11631.13	11883.54	10793.1	0	0	0
Q9UI10	Translator EIF2B4	6909.791	1335.778	2080.397	0	0	0
Q9UI12	V-type prc ATP6V1H	9015.301	14375.46	20130.79	0	0	0
Q9UI26	Importin-1 IPO11	9028.803	9666.316	6966.214	0	0	0
Q9UIA9	Exportin-7 XPO7	6578.74	7450.894	6512.186	0	0	0
Q9UID3	Vacuolar p VPS51	5859.301	888.6252	4183.605	0	103561.2	74403.73
Q9UIK4	Death-assr DAPK2	10888.18	10675.95	15423.12	0	0	0
Q9UIQ6	Leucyl-cys LNPEP	31112.39	32072.73	27657.17	0	0	0
Q9UIW2	Plexin-A1 PLXNA1	67289.13	73893.81	56829.33	0	0	0
Q9UJ68	Mitochonc MSRA	6025.712	7688.434	5709.044	0	0	0
Q9UJF2	Ras GTPasr RASAL2	2242.798	1737.952	1626.561	0	0	0
Q9UJU6	Drebrin-lik DBNL	39962.01	52407.53	44499.96	0	0	0
Q9UK41	Vacuolar p VPS28	193114.7	172089.5	182380.9	0	0	0
Q9UK55	Protein Z-ι SERPINA1C	16923.55	33367.94	51155.66	349665.4	471716.7	349283.9
Q9UK76	Hematolog HN1	26492.37	27843.43	31604.04	0	0	0
Q9UKD2	mRNA turr MRTO4	5597.471	2951.217	3875.341	0	0	0
Q9UKE5	TRAF2 and TNIK	54029.14	47953.04	47946.16	0	0	0
Q9UKF6	Cleavage ε CPSF3	18757.78	11368.31	4102.616	0	0	0
Q9UKJ5	Cysteine-r CHIC2	57188.89	50172.67	50342.92	0	0	0
Q9UKK9	ADP-suga NUDT5	38975.79	35394.41	26814.92	0	0	0
Q9UKN8	General trε GTF3C4	793973.1	427433.8	422944.1	0	0	0
Q9UKS6	Protein kin PACSIN3	168216.3	159485.2	150438.5	0	0	0
Q9UKZ9	Procollage PCOLCE2	19373.82	22200.09	4440.23	0	0	0

Q9UL15	BAG family BAG5	42277.29	58220.28	50640.79	0	0	0
Q9UL26	Ras-relate RAB22A	150743.2	158383.6	131187.6	0	0	0
Q9UL46	Proteasom PSME2	22706.54	22654.85	14701.95	0	0	0
Q9ULC4	Malignant MCTS1	3456.758	4351.976	3678.854	0	0	0
Q9ULC8	Probable p ZDHC8	5872.277	5954.503	7294.636	0	0	0
Q9ULF5	Zinc trans SLC39A10	111377.6	109318.1	82683.16	0	0	0
Q9ULH1	Arf-GAP w ASAP1	17697.17	3989.121	6753.726	0	0	0
Q9ULK4	Mediator c MED23	728.098	918.3856	614.769	0	0	0
Q9ULP9	TBC1 dom TBC1D24	5225.778	4872.148	5289.689	0	0	0
Q9ULT8	E3 ubiquiti HECTD1	10831.06	9776.334	9413.826	0	0	0
Q9ULV4	Coronin-1 CORO1C	97184.11	125423.3	101552	0	0	0
Q9UM47	Neurogeni NOTCH3	18425.17	18508.47	22724.52	0	120623.2	54712.08
Q9UM54	Unconvent MYO6	18149.23	16785.25	19305	0	0	0
Q9UMS4	Pre-mRNA PRPF19	25278.67	48736.36	132598	0	0	0
Q9UMX0	Ubiquilin-1 UBQLN1	12951.86	12477.68	13349.07	0	0	0
Q9UMY4	Sorting ne: SNX12	19749.77	18896.79	15603.46	0	0	0
Q9UN37	Vacuolar p VPS4A	121270.2	111676.5	123559.1	50112.12	35106.15	57587.57
Q9UN42	Protein AT ATP1B4	306962.4	362588.1	355112.1	0	0	0
Q9UN70	Protocadherin PCDHGC3	19537.91	19251.86	17944.68	0	0	0
Q9UN86	Ras GTPase G3BP2	1492.419	1726.258	1644.353	0	0	0
Q9UNF0	Protein kinase PACSIN2	62686.77	55919.01	53164.92	0	0	0
Q9UNH7	Sorting ne: SNX6	15770.43	16730.31	15076.15	0	0	0
Q9UNK0	Syntaxin-8 STX8	15789.77	21541.11	11015.63	0	0	0
Q9UNK4	Group IID : PLA2G2D	40678.41	38151.14	48105.55	0	0	0
Q9UNM6	26S proteasome PSMD13	27052.79	25834.55	32188.86	56780.98	0	61337.15
Q9UNN5	FAS-associat FAF1	14352.19	14114.96	10947.3	0	0	0
Q9UNN8	Endothelial PROCRA	151868.3	149418.5	129700.6	0	0	0
Q9UNP9	Peptidyl-p PPIE	71793.24	71800.04	1159747	318547.6	381440.6	282898.7
Q9UNQ0	ATP-binding ABCG2	41820.4	43459.96	39796.6	0	0	0
Q9UNS2	COP9 sign COP9	5674.709	18263.49	13506.49	0	0	0
Q9UNX4	WD repeat WDR3	3177.037	3555.513	3089.684	0	0	0
Q9UNY4	Transcript TTF2	3054.73	4170.855	4053.024	0	0	0
Q9UNZ2	NSFL1 cofactor NSFL1C	11245.33	11215.88	9864.317	0	0	0
Q9UPN3	Microtubule MACF1	21554.36	21896.34	19652.49	0	0	0
Q9UPT5	Exocyst co EXOC7	34325.5	37286.85	25951.09	0	0	0
Q9UPU5	Ubiquitin c USP24	5893.811	6458.474	6142.94	0	0	0
Q9UPY3	Endoribon DICER1	1403.439	2231.783	1067.398	0	0	0
Q9UPY5	Cystine/glutamate SLC7A11	16772.17	20470.56	15507.75	0	0	0
Q9UQ13	Leucine-rich SHOC2	22735.5	19920.55	25843.82	0	0	0
Q9UQ16	Dynamin-1 DNMT3	62087.58	61190.67	54781.97	97435.65	63464.75	119591.4
Q9UQ49	Sialidase-3 NEU3	35645.04	33855.11	32522.43	0	0	0
Q9UQ80	Proliferat PA2G4	39428.64	37004.57	46826.18	13828.51	0	30537.7
Q9UQB8	Brain-spec BAIAP2	58627.85	46795.13	51413.58	0	0	0
Q9UQE7	Structural SMC3	29309.87	28572.91	107414.5	0	0	0
Q9UQN3	Charged n CHMP2B	7042.969	2123.947	7249.437	0	0	0
Q9Y223	Bifunctional GNE	13372.38	18205.91	13356.14	0	0	0
Q9Y224	UPF0568 p C14orf166	8198.011	7384.636	7564.194	0	0	0
Q9Y225	RING finger RNF24	4140.067	10866.65	19871.06	0	0	0
Q9Y230	RuvB-like 1 RUVBL2	61335.84	62000.15	62552.71	15991016	32627920	83068.62
Q9Y262	Eukaryotic EIF3L	19864.49	19248.71	18186.88	21255.54	0	20137.19
Q9Y265	RuvB-like 1 RUVBL1	65073.77	66758.95	38958.36	91734.94	0	177367.7
Q9Y266	Nuclear membrane NUDC	74011.95	91471.92	80440.25	0	0	0
Q9Y281	Cofilin-2 CFL2	1308003	1250869	1160666	682974.3	457304.1	446995.5
Q9Y287	Integral membrane ITM2B	116935.7	112503.2	99554.02	0	0	0
Q9Y295	Developm DRG1	9673.732	12157.06	9523.27	0	0	0
Q9Y2A7	Nck-associat NCKAP1	187196.1	189738.9	164152.9	18227.92	0	16128.25
Q9Y2D4	Exocyst co EXOC6B	38880.92	33106.21	31311.06	0	0	0
Q9Y2D5	A-kinase associated AKAP2	211813.2	210551.4	185917	0	0	0

Q9Y2E4	Disco-inte DIP2C	7810.111	7033.623	7561.206	0	0	0
Q9Y2H0	Disks large DLGAP4	28198.42	25033.06	24723.05	0	0	0
Q9Y2H1	Serine/thrē STK38L	4290.479	6342.069	3604.601	0	0	0
Q9Y2I8	WD repeat WDR37	9880.698	9587.925	6201.439	0	0	0
Q9Y2J2	Band 4.1-l EPB41L3	172318.5	225004.6	210063.6	0	1999146	902620.4
Q9Y2L1	Exosome c DIS3	3151.746	6448.787	2532.948	0	0	0
Q9Y2P8	RNA 3-terē RCL1	11109.51	12664.5	11673.81	0	0	0
Q9Y2U9	Kelch dom KLHDC2	4489.575	3147.14	3012.248	0	0	0
Q9Y2V2	Calcium-rē CARHSP1	18649.69	19876.49	17491.28	0	0	0
Q9Y2X3	Nucleolar j NOP58	3898.712	3975.41	2252.344	0	0	0
Q9Y2X7	ARF GTPas GIT1	5652.251	6162.986	4173.238	832881.3	749694.8	1166966
Q9Y2Z0	Protein SG SUGT1	11933.48	12238.54	12617.23	0	0	0
Q9Y303	Putative N AMDHD2	10712.02	10723.18	12617.44	0	0	0
Q9Y316	Protein ME MEMO1	20631.39	18281.6	21471.11	0	0	0
Q9Y333	U6 snRNA LSM2	22698.84	15186.64	20464.56	0	0	0
Q9Y371	Endophilin SH3GLB1	2721.558	2325.222	1988.787	0	0	0
Q9Y383	Putative RI LUC7L2	2646.071	2421.966	2995.806	0	0	0
Q9Y3A5	Ribosome SBDS	20445.36	19983.41	15662.31	0	0	0
Q9Y3A6	Transmem TMED5	5439.915	5404.594	3003.657	0	0	0
Q9Y3B8	Oligoribon REXO2	57626.79	34309.37	22895.72	0	0	0
Q9Y3D0	Mitotic spi FAM96B	10999.51	10864.45	11976.33	0	0	0
Q9Y3D6	Mitochonc FIS1	11207.39	3863.112	11142.66	0	0	0
Q9Y3E7	Charged rē CHMP3	52568.02	49834	53582.82	0	0	0
Q9Y3F4	Serine-thrē STRAP	16684.82	10298.76	9512.531	0	0	0
Q9Y3I0	tRNA-splic RTCB	20109.95	19887.6	19721.48	0	0	0
Q9Y3L3	SH3 doma SH3BP1	6852.385	9639.76	4664.596	0	0	0
Q9Y3T9	Nucleolar rē NOC2L	3292.553	3719.122	9601.362	0	0	0
Q9Y3U8	60S riboso RPL36	34651.91	33821.23	24151.44	88326.1	0	59096.22
Q9Y446	Plakophilin PKP3	44678.56	43778.04	40967.29	0	0	0
Q9Y450	HBS1-like HBS1L	9808.274	17775.22	22362.99	0	0	0
Q9Y487	V-type prc ATP6V0A2	8450.901	8870.377	8116.367	0	0	0
Q9Y490	Talin-1 TLN1	292570.2	326805.2	291183.5	683451.7	546153.9	838229.5
Q9Y4C2	TRPM8 chē TCAF1	9674.198	14148.83	9882.302	0	0	0
Q9Y4D1	Dishevelec DAAM1	12560.97	9260.736	11682.98	0	0	0
Q9Y4D7	Plexin-D1 PLXND1	4440.812	4982.938	5672.821	0	0	0
Q9Y4E8	Ubiquitin c USP15	2408.191	1995.287	2141.506	0	0	0
Q9Y4G6	Talin-2 TLN2	15488.14	17269.26	14336.44	0	0	0
Q9Y4I1	Unconvent MYO5A	8288.72	15261.19	32790.64	0	0	0
Q9Y4K0	Lysyl oxida LOXL2	79924.15	74891.3	72203.17	642683.1	872959.6	732888.2
Q9Y4L1	Hypoxia uē HYOU1	5180.128	5315.193	5108.686	0	0	0
Q9Y4R8	Telomere lē TELO2	2836.051	5044.457	1038.199	0	0	0
Q9Y4X5	E3 ubiquiti ARIH1	2040.233	2151.856	2929.436	0	0	0
Q9Y547	Intraflagell HSPB11	17297.87	17543.46	15732.42	0	0	0
Q9Y570	Protein ph PPME1	11483.03	11344.71	11180.64	0	0	0
Q9Y597	BTB/POZ c KCTD3	5071.105	4685.59	7048.612	0	0	0
Q9Y5B8	Nucleosidē NME7	6456.507	6388.816	5226.852	0	0	0
Q9Y5C1	Angiopoie ANGPTL3	15162.97	15592.07	24271.66	113178.1	0	92974.05
Q9Y5K5	Ubiquitin c UCHL5	29716.04	30918.59	42403.12	0	0	0
Q9Y5K6	CD2-assoc CD2AP	26104.73	27338.95	25096.88	0	0	0
Q9Y5K8	V-type prc ATP6V1D	6562.016	3707.664	3465.495	0	0	0
Q9Y5L0	Transportin TNPO3	11150.42	5722.03	9417.571	0	0	0
Q9Y5M8	Signal recc SRPRB	10649.68	10347.63	11052.92	0	0	0
Q9Y5R8	Trafficking TRAPPC1	3555.572	2602.676	1846.575	0	0	0
Q9Y5S2	Serine/thrē CDC42BPE	13977.6	13814.61	13040.41	0	0	0
Q9Y5S9	RNA-bindin RBM8A	8322.004	12356.17	14655.54	0	0	0
Q9Y5X1	Sorting ne: SNX9	36077.16	37023.86	32110.13	49476.39	0	45505.39
Q9Y5X3	Sorting ne: SNX5	19729.58	14299.31	17338.75	0	0	0
Q9Y5X9	Endothelia LIPG	10001.36	18510.92	11884.73	0	0	0

Q9Y5Y0	Feline leuk FLVCR1	36063.94	28725.61	30177.14	0	0	0
Q9Y5Y2	Cytosolic FNUBP2	10796.62	21705.78	22851.84	0	0	0
Q9Y613	FH1/FH2 dFHOD1	8174.381	9149.942	7409.558	0	0	0
Q9Y617	Phosphoserine PSAT1	157250.2	166425.2	164755.9	0	0	0
Q9Y624	Junctional F11R	15641.67	17610	13809.22	0	0	0
Q9Y625	Glypican-6 GPC6	57598.46	53811.64	44875.04	0	39932.67	69858.97
Q9Y639	Neuropilin NPTN	245761.6	235711.3	209231	0	0	0
Q9Y653	G-protein GPR56	5993.801	8278.187	6321.939	0	0	0
Q9Y666	Solute carrier SLC12A7	10081.84	7226.621	6738.814	0	0	0
Q9Y678	Coatomer COPG1	15688.21	16472.22	20761.89	0	0	0
Q9Y696	Chloride channel CLIC4	605602.5	579022.1	507515.5	28295.85	0	84226.45
Q9Y6C2	EMILIN-1 EMILIN1	47080.34	55774.7	69798.81	256856.4	238170.1	430163.6
Q9Y6D5	Brefeldin A ARFGEF2	14377.14	15571.7	11001.12	0	0	0
Q9Y6D6	Brefeldin A ARFGEF1	4292.07	5417.717	2728.328	0	0	0
Q9Y6E0	Serine/threonine STK24	60120.32	59652.49	51782.94	0	0	0
Q9Y6E2	Basic leucine BZW2	45059.73	48503.27	40073.91	1457851	3367015	0
Q9Y6G9	Cytoplasmic DYNC1L1	17337.1	20878.32	22337.28	127102.4	0	36341.48
Q9Y6M4	Casein kinase CSNK1G3	97558.98	99907.52	88124.56	0	0	0
Q9Y6M5	Zinc transporter SLC30A1	79364.88	82078.95	71273.23	0	0	0
Q9Y6M7	Sodium bicarbonate SLC4A7	152475.8	152139.9	128322.1	0	0	0
Q9Y6N7	Roundabout ROBO1	30006.11	17299.61	34087.06	0	0	0
Q9Y6W5	Wiskott-Aldrich WASF2	47017.61	23206.83	23995.63	0	0	0
Q9Y6X5	Bis(5-adenosine) ENPP4	19726.01	20930.35	21873.19	0	0	0

h_143B.vs.h_143B	vs.h_143B	vs.h_143B	vs.h_143B	vs.h_143B	vs.GO_NUM	GO_Descri	KEGG_Des	KEGG_EC
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	--	--	CCR4-NO	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		4	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.103085	0.48299	-3.27809	Nonsignifi	None	--	--	small nucle	--
Inf	0	Inf	Significant up		2	Biological	A-kinase a	--
Inf	0	Inf	Significant up	--	--	integrin al	--	--
0.083754	0.094723	-3.5777	Nonsignifi	None	2	Molecular	componen	3.4.21.47
0.48841	0.117272	-1.03383	Nonsignifi	None	5	Molecular	translation	--
0.061936	0.025659	-4.01307	Significant down	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	eukaryotic	--	--
Inf	0	Inf	Significant up		1	Molecular	kinesin lig	--
Inf	0	Inf	Significant up		2	Biological	transmemt	--
Inf	0	Inf	Significant up	--	--	V-type H+	--	--
Inf	0	Inf	Significant up		2	Biological	vacuolar p	--
Inf	0	Inf	Significant up		1	Cellular Cc	syntaxin 1f	--
4.816613	4.29E-06	2.268019	Significant up	--	--	transmemt	--	--
Inf	0	Inf	Significant up	--	--	gamma-gl	4.3.2.9	--
Inf	0	Inf	Significant up		4	Molecular	seryl-tRNA	6.1.1.11
Inf	0	Inf	Significant up		4	Molecular	kinesin far	--
1.016465	0.954876	0.02356	Nonsignifi	None	2	Molecular	--	--
Inf	0	Inf	Significant up	--	--	acyl-coenz	3.1.2.2	--
4.252847	0.005995	2.088429	Significant up		4	Molecular	myosin I	--
Inf	0	Inf	Significant up	--	--	synaptoso	--	--
Inf	0	Inf	Significant up	--	--	AH recept	--	--
Inf	0	Inf	Significant up		2	Biological	syntaxin-b	--
0.006143	0.327974	-7.34684	Nonsignifi	None	3	Biological	AP-3 com	--
Inf	0	Inf	Significant up		1	Molecular	galectin-8	--
Inf	0	Inf	Significant up		2	Molecular	tumor nec	--
0.263965	0.001627	-1.92158	Nonsignifi	None	1	Molecular	26S protea	--
Inf	0	Inf	Significant up		1	Molecular	26S protea	--
Inf	0	Inf	Significant up		2	Biological	copper ch	--
19.03565	0.002911	4.250632	Significant up		1	Molecular	chloride in	--
0.368651	0.000999	-1.43967	Nonsignifi	None	1	Molecular	translation	--
Inf	0	Inf	Significant up		2	Molecular	NEDD4-lik	2.3.2.26
Inf	0	Inf	Significant up		1	Molecular	phosphatic	2.7.1.153
0.11021	0.031944	-3.18168	Significant down		3	Molecular	thiol oxida	1.8.3.2
Inf	0	Inf	Significant up		1	Molecular	Wiskott-AI	--
1.084947	0.638655	0.117624	Nonsignifi	None	1	Molecular	importin-5	--
Inf	0	Inf	Significant up	--	--	RNA 3'-ter	6.5.1.4	--
Inf	0	Inf	Significant up		3	Molecular	phosphatic	2.7.1.154
0.743724	0.046093	-0.42716	Nonsignifi	None	4	Molecular	agrin	--
0.044104	0.006241	-4.50296	Significant down		2	Molecular	procollage	1.14.11.4
Inf	0	Inf	Significant up		3	Cellular Cc	exocyst co	--
0.311196	0.000916	-1.6841	Nonsignifi	None	1	Molecular	26S protea	--
Inf	0	Inf	Significant up		2	Molecular	amphiphys	--
Inf	0	Inf	Significant up		5	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	serine/thre	2.7.11.1
Inf	0	Inf	Significant up	--	--	Krev intera	--	--
Inf	0	Inf	Significant up		2	Cellular Cc	pescadillo	--
5.056309	0.000451	2.338085	Significant up		1	Molecular	syntenin-1	--
Inf	0	Inf	Significant up	--	--	nucleolar p	--	--

Inf		0	Inf	Significant up	--	--	podocalyxi	--
0.045651	0.023136	-4.4532	Inf	Significant down		4	Biological	cysteine ric
Inf		0	Inf	Significant up		5	Molecular	--
0.211507	0.043265	-2.24122	Inf	Significant down		5	Molecular	lysosomal
Inf		0	Inf	Significant up	--	--	ubiquitin- κ	3.2.1.24
Inf		0	Inf	Significant up	--	--	pyridoxine	2.3.2.23
Inf		0	Inf	Significant up		1	Cellular	Cc claudin
Inf		0	Inf	Significant up		1	Biological	--
Inf		0	Inf	Significant up		3	Molecular	citron Rho
Inf		0	Inf	Significant up	--	--	coatome	2.7.11.1
4.725815	6.66E-05	2.240563	Inf	Significant up	--	--	disintegrin	3.4.24.81
Inf		0	Inf	Significant up		1	Molecular	programm
Inf		0	Inf	Significant up		2	Biological	type II pro
Inf		0	Inf	Significant up		1	Molecular	Na(+)/H(+)
Inf		0	Inf	Significant up		2	Molecular	tumor nec
0.927114	0.578519	-0.10918	Inf	Nonsignifi		1	Cellular	Cc neuropilin
Inf		0	Inf	Significant up		2	Biological	transportir
5.876467	0.000782	2.554949	Inf	Significant up		1	Cellular	Cc tetraspanir
1.710395	0.002277	0.77433	Inf	Nonsignifi		5	Molecular	20S protea
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		4	Molecular	inhibitor o
Inf		0	Inf	Significant up		1	Biological	histone ac
Inf		0	Inf	Significant up		4	Molecular	calcium/ca
Inf		0	Inf	Significant up		2	Molecular	phospholi
0.200003	0.018008	-2.32191	Inf	Significant down		1	Molecular	myosin re
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		2	Biological	hepatocyte
Inf		0	Inf	Significant up		3	Molecular	cyclin G- α
Inf		0	Inf	Significant up		1	Molecular	heterogen
Inf		0	Inf	Significant up		2	Biological	exportin-1
Inf		0	Inf	Significant up		2	Molecular	Rho guan
Inf		0	Inf	Significant up		1	Molecular	spectrin b
0.005302	0.306436	-7.55927	Inf	Nonsignifi	--	--	COPII coat	--
0.476345	0.142717	-1.06992	Inf	Nonsignifi		2	Molecular	plexin B
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	phosphoril	6.3.5.3
Inf		0	Inf	Significant up		3	Molecular	a disintegr
Inf		0	Inf	Significant up		1	Molecular	serine/thre
Inf		0	Inf	Significant up		1	Cellular	Cc Niemann-
1.014571	0.986856	0.02087	Inf	Nonsignifi		4	Cellular	Cc actin relat
6.137922	0.001511	2.61775	Inf	Significant up		4	Cellular	Cc actin relat
Inf		0	Inf	Significant up		2	Molecular	DNA-direc
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	carboxy-te	3.1.3.16
Inf		0	Inf	Significant up		3	Biological	prefoldin t
0.720828	0.26479	-0.47227	Inf	Nonsignifi		5	Molecular	laminin, al
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		1	Cellular	Cc --
0.079779	0.06551	-3.64784	Inf	Nonsignifi		1	Cellular	Cc ER-derivec
Inf		0	Inf	Significant up		3	Molecular	phosphom
Inf		0	Inf	Significant up	--	--	high mobil	5.4.2.8
Inf		0	Inf	Significant up		1	Molecular	neural cell
Inf		0	Inf	Significant up		2	Biological	importin- ϵ
0.866413	0.759964	-0.20687	Inf	Nonsignifi		1	Molecular	syntaxin 7
Inf		0	Inf	Significant up		2	Cellular	Cc MFS trans
0.656375	0.030664	-0.60741	Inf	Nonsignifi		2	Cellular	Cc MFS trans

Inf		0	Inf	Significant up		3	Molecular	solute carr	--
Inf		0	Inf	Significant up		2	Cellular	Cc synaptobro	--
Inf		0	Inf	Significant up		4	Cellular	Cc actin relat	--
Inf		0	Inf	Significant up		5	Molecular	potassium	--
Inf		0	Inf	Significant up		2	Molecular	Arf-GAP w	--
9.307748	9.68E-07	3.218432		Significant up		3	Biological	--	--
Inf		0	Inf	Significant up	--	--	--	dynein lig	--
0.349551	0.329239	-1.51643		Nonsignifi	None	4	Cellular	Cc 26S protea	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		2	Cellular	Cc protein tra	--
0.232713	0.023842	-2.10338		Significant down	--	--	--	beta-1,4-c	2.4.1.-
0.062722	0.299677	-3.99487		Nonsignifi	None	1	Molecular	--	--
0.382381	0.000213	-1.38692		Nonsignifi	None	1	Molecular	heterogen	--
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	5.2.1.8
Inf		0	Inf	Significant up	--	--	--	aflatoxin B	--
Inf		0	Inf	Significant up		5	Molecular	erythrocyt	--
0.20537	0.025646	-2.2837		Significant down	--	--	--	beta-1,4-c	2.4.1.-
Inf		0	Inf	Significant up		2	Biological	exportin-T	--
Inf		0	Inf	Significant up		3	Biological	protein sp	--
Inf		0	Inf	Significant up	--	--	--	trafficking	--
Inf		0	Inf	Significant up		1	Biological	charged m	--
Inf		0	Inf	Significant up		1	Cellular	Cc tetraspanir	--
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	--
0.007142	0.495626	-7.12942		Nonsignifi	None	4	Biological	AP-1 com	--
Inf		0	Inf	Significant up		3	Molecular	syntaxin 6	--
Inf		0	Inf	Significant up		1	Molecular	small gluta	--
Inf		0	Inf	Significant up		4	Molecular	myosin I	--
Inf		0	Inf	Significant up		3	Molecular	cleavage a	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	nardilysin	3.4.24.61
0.020725	0.014086	-5.59247		Significant down		1	Molecular	--	--
0.118762	0.082891	-3.07386		Nonsignifi	None	1	Molecular	--	--
0.876506	0.231509	-0.19016		Nonsignifi	None	3	Molecular	adenosylh	3.3.1.1
Inf		0	Inf	Significant up		3	Cellular	Cc origin recc	--
Inf		0	Inf	Significant up	--	--	--	retinal rod	--
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	--
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	--
0.511016	0.087215	-0.96856		Nonsignifi	None	1	Cellular	Cc neuropilin	--
Inf		0	Inf	Significant up		2	Molecular	long-chair	6.2.1.3
1.890087	0.00188	0.918453		Nonsignifi	None	1	Molecular	sorting ne	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		3	Biological	adenylate	4.6.1.1

Inf		0	Inf	Significant up		1	Molecular	heterogen	--
0.21006	0.004814	-2.25113		Significant down		2	Molecular	--	--
Inf		0	Inf	Significant up		4	Molecular	diaphanou	--
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	--
Inf		0	Inf	Significant up		1	Cellular	Cc cell cycle c3.1.11.2	
Inf		0	Inf	Significant up	--	--	--	type I prot 2.1.1.319	
Inf		0	Inf	Significant up		5	Molecular	--	--
0.048895	0.039393	-4.35418		Significant down	--	--	--	sushi repe	--
Inf		0	Inf	Significant up		1	Molecular	--	--
10.41382	0.000927	3.380428		Significant up		1	Molecular	catenin (ca	--
Inf		0	Inf	Significant up		2	Molecular	translation	--
Inf		0	Inf	Significant up		2	Biological	sorting ne	--
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	--
1.327906	0.533502	0.409153		Nonsignifi	None	1	Molecular	histone H2	--
0.260062	0.014739	-1.94307		Nonsignifi	None	2	Molecular	H/ACA rib	5.4.99.-
0.09493	0.156057	-3.39699		Nonsignifi	None	1	Molecular	translation	--
Inf		0	Inf	Significant up		1	Molecular	putative tr	--
Inf		0	Inf	Significant up		2	Molecular	DnaJ hom	--
0.124923	0.023009	-3.00088		Significant down		1	Biological	periplasmi	--
Inf		0	Inf	Significant up		3	Biological	prefoldin s	--
Inf		0	Inf	Significant up		2	Molecular	SLIT-ROBC	--
Inf		0	Inf	Significant up		2	Molecular	plexin A	--
Inf		0	Inf	Significant up	--	--	--	immunogl	--
1.986992	0.054998	0.990586		Nonsignifi	None	1	Molecular	--	--
Inf		0	Inf	Significant up		3	Molecular	frizzled 1/	--
Inf		0	Inf	Significant up		2	Molecular	phospholiq	3.6.3.1
0.246515	0.38792	-2.02025		Nonsignifi	None	4	Molecular	Rho-assoc	2.7.11.1
Inf		0	Inf	Significant up	--	--	--	CLIP-assoc	--
0.101268	0.041059	-3.30375		Significant down	--	--	--	inducible T	--
Inf		0	Inf	Significant up	--	--	--	obscurin-li	--
Inf		0	Inf	Significant up	--	--	--	protein TIF	--
0.407743	0.006039	-1.29427		Nonsignifi	None	--	--	DnaJ hom	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		2	Biological	ubiquitin c3.4.19.12	
Inf		0	Inf	Significant up		2	Molecular	semaphori	--
4.125283	5.28E-05	2.044493		Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		3	Biological	tubulin-sp	--
Inf		0	Inf	Significant up		1	Molecular	vacuolar p	--
Inf		0	Inf	Significant up	--	--	--	mannose-	--
0.554152	0.174782	-0.85165		Nonsignifi	None	1	Molecular	histone H2	--
0.895495	0.709157	-0.15924		Nonsignifi	None	1	Molecular	filamin	--
Inf		0	Inf	Significant up		3	Molecular	tripartite n	--
Inf		0	Inf	Significant up		2	Cellular	Cc MFS transp	--
Inf		0	Inf	Significant up		1	Molecular	pre-mRNA	--
Inf		0	Inf	Significant up	--	--	--	vacuolar p	--
Inf		0	Inf	Significant up		3	Cellular	Cc glypican 4	--
Inf		0	Inf	Significant up		1	Molecular	heat shock	--
Inf		0	Inf	Significant up		1	Cellular	Cc claudin	--
0.814361	0.578131	-0.29626		Nonsignifi	None	1	Molecular	barrier-to-	--
Inf		0	Inf	Significant up	--	--	--	splicing fac	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		1	Molecular	lysophospl	3.1.1.5
Inf		0	Inf	Significant up		2	Molecular	pre-mRNA	3.6.4.13
0.135496	0.029083	-2.88367		Significant down	--	--	--	type 2A p	--

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		3	Molecular	translation	--
Inf	0	Inf	Significant up		1	Molecular	26S protea	--
Inf	0	Inf	Significant up		2	Molecular	STE24 end	3.4.24.84
0.768057	0.628914	-0.38071	Nonsignifi	None	1	Biological	isocitrate c	1.1.1.42
0.386107	0.18644	-1.37293	Nonsignifi	None	4	Biological	formyltetr	1.5.1.6
0.077381	0.082742	-3.69187	Nonsignifi	None	--	--	PRA1 fami	--
1.99439	0.013303	0.995947	Nonsignifi	None	1	Cellular Cc	tetraspanir	--
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	--	--
0.016507	0.011749	-5.92076	Significant down		2	Molecular	--	--
0.036441	0.204025	-4.7783	Nonsignifi	None	4	Biological	--	--
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
0.108883	0.091618	-3.19915	Nonsignifi	None	1	Molecular	slit 2	--
0.005923	0.012934	-7.3994	Significant down		2	Molecular	phospholip	3.6.3.1
Inf	0	Inf	Significant up		2	Molecular	FERM, Rho	--
Inf	0	Inf	Significant up		2	Molecular	pre-mRNA	--
0.64551	0.189872	-0.63149	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		4	Biological	AP-2 com	--
0.262666	0.27228	-1.9287	Nonsignifi	None	3	Molecular	--	--
0.094487	0.059479	-3.40374	Nonsignifi	None	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	--
0.25501	0.009692	-1.97138	Nonsignifi	None	--	--	reticulon-	--
Inf	0	Inf	Significant up	--	--	--	--	--
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	--	--	--	myelin pro	--
Inf	0	Inf	Significant up		1	Biological	6-phospho	3.1.1.31
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		4	Molecular	structural r	--
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-l	--
Inf	0	Inf	Significant up		1	Molecular	lysophosph	3.1.1.5
Inf	0	Inf	Significant up	--	--	--	ariadne-2	2.3.2.27
Inf	0	Inf	Significant up		2	Biological	phosphoar	5.4.2.3
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.298252	0.039162	-1.7454	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		2	Cellular Cc	proteasom	--
Inf	0	Inf	Significant up		4	Molecular	--	--
Inf	0	Inf	Significant up		4	Biological	protein tra	--
Inf	0	Inf	Significant up		5	Molecular	latrophilin	--

0.160906	0.022119	-2.63571	Significant down		1 Biological	pantethein	3.5.1.92	
0.09901	0.07504	-3.33628	Nonsignifi	None	1 Biological	pantethein	3.5.1.92	
Inf	0	Inf	Significant up		2 Molecular	DNA-direc	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	
Inf	0	Inf	Significant up	--	--	synaptoso	--	
1.457705	0.068505	0.543699	Nonsignifi	None	4 Molecular	serine/thre	2.7.11.1	
Inf	0	Inf	Significant up	--	--	--	--	
Inf	0	Inf	Significant up	--	--	--	--	
Inf	0	Inf	Significant up	--	--	BCL2-asso	--	
Inf	0	Inf	Significant up		2 Molecular	BCL2-asso	--	
1.913115	5.11E-05	0.935924	Nonsignifi	None	3 Molecular	mitogen-a	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 tetraspanir	--	
Inf	0	Inf	Significant up		1 Cellular	Cc tetraspanir	--	
0.345929	0.118675	-1.53145	Nonsignifi	None	--	--	dimethylar	3.5.3.18
Inf	0	Inf	Significant up	--	--	--	protein-di	1.8.4.2
0.01919	0.013725	-5.70353	Significant down	--	--	--	--	--
Inf	0	Inf	Significant up		3 Molecular	p21-activa	2.7.11.1	
Inf	0	Inf	Significant up	--	--	actin-like	--	--
1.141975	0.122186	0.191532	Nonsignifi	None	2 Molecular	L-lactate c	1.1.1.27	
0.188428	0.001251	-2.40791	Significant down		3 Biological	retinal deh	1.2.1.36	
Inf	0	Inf	Significant up		4 Molecular	dihydrofol	1.5.1.3	
0.2272	0.084501	-2.13797	Nonsignifi	None	2 Molecular	cytochrom	1.6.2.2	
0.36773	0.020848	-1.44328	Nonsignifi	None	3 Molecular	glutathion	1.8.1.7	
0.297197	0.047719	-1.75051	Nonsignifi	None	3 Biological	superoxide	1.15.1.1	
0.174949	0.020963	-2.51499	Significant down		3 Molecular	ceruloplas	1.16.3.1	
0.067727	0.023497	-3.88412	Significant down		2 Molecular	coagulatio	2.3.2.13	
0.455822	0.036999	-1.13346	Nonsignifi	None	2 Molecular	purine-nur	2.4.2.1	
Inf	0	Inf	Significant up		1 Biological	hypoxanth	2.4.2.8	
4.662602	5.17E-05	2.221135	Significant up		6 Molecular	epidermal	2.7.10.1	
2.410179	0.00374	1.26914	Nonsignifi	None	2 Molecular	phosphogl	2.7.2.3	
Inf	0	Inf	Significant up	--	--	adenylate	2.7.4.3	
0.385102	0.027108	-1.37669	Nonsignifi	None	5 Molecular	coagulatio	3.4.21.5	
0.049177	0.251821	-4.34588	Nonsignifi	None	2 Molecular	haptoglob	--	
0.326649	0.074472	-1.61419	Nonsignifi	None	5 Molecular	coagulatio	3.4.21.22	
0.240215	0.038312	-2.0576	Significant down		5 Molecular	coagulatio	3.4.21.6	
0.016125	0.03797	-5.95455	Significant down		2 Molecular	plasminog	3.4.21.7	
Inf	0	Inf	Significant up		2 Molecular	urokinase	3.4.21.73	
Inf	0	Inf	Significant up		4 Molecular	tissue plasi	3.4.21.68	
0.126634	0.039461	-2.98127	Significant down	--	--	antithromk	--	
0.766313	0.079461	-0.38399	Nonsignifi	None	3 Molecular	alpha-2-r	--	
0.102087	0.042223	-3.29213	Significant down		3 Molecular	compleme	--	
0.035529	0.110771	-4.81485	Nonsignifi	None	3 Molecular	compleme	--	
0.00903	0.061402	-6.79099	Nonsignifi	None	1 Molecular	metallope	--	
0.062639	0.004884	-3.9968	Significant down		1 Molecular	cystatin-C	--	
0.083408	0.050125	-3.58368	Nonsignifi	None	1 Molecular	kininogen	--	
Inf	0	Inf	Significant up		2 Molecular	GTPase HF	--	
Inf	0	Inf	Significant up		2 Molecular	low-densit	--	
Inf	0	Inf	Significant up	--	--	thyroglob	--	
0.125952	0.040913	-2.98905	Significant down		2 Molecular	insulin-like	--	
Inf	0	Inf	Significant up		5 Molecular	interleukin	--	
0.016624	0.01116	-5.91057	Significant down	--	--	--	--	
0.147917	0.00531	-2.75714	Significant down	--	--	--	--	
1.191444	0.038233	0.252711	Nonsignifi	None	2 Biological	major histo	--	
1.498403	0.208958	0.583426	Nonsignifi	None	2 Biological	major histo	--	

0.22952	2.06E-05	-2.12331	Significant down		2 Molecular hemoglob	--
0.034762	0.018021	-4.84636	Significant down		2 Molecular hemoglob	--
0.008988	0.009981	-6.79771	Significant down		2 Molecular collagen, t	--
0.006592	0.041388	-7.24512	Significant down		2 Molecular collagen, t	--
0.073798	0.02433	-3.76027	Significant down		2 Molecular collagen, t	--
0.098788	0.082928	-3.33952	Nonsignifi	None	2 Molecular collagen, t	--
0.159295	0.075372	-2.65023	Nonsignifi	None	2 Molecular type I kera	--
0.14387	0.059174	-2.79716	Nonsignifi	None	2 Molecular type II ker	--
0.158541	0.045379	-2.65707	Significant down		4 Cellular Cc apolipoprc	--
0.022894	0.041248	-5.44886	Significant down		4 Cellular Cc apolipoprc	--
0.040428	0.00964	-4.6285	Significant down		4 Cellular Cc apolipoprc	--
0.092432	0.151096	-3.43547	Nonsignifi	None	5 Molecular fibrinogen	--
0.055704	0.039208	-4.16607	Significant down		5 Molecular fibrinogen	--
0.219719	0.144232	-2.18627	Nonsignifi	None	--	beta-2-gly --
0.004662	0.00997	-7.74474	Significant down		2 Molecular fibronectin	--
0.10565	0.005886	-3.24263	Significant down	--	--	retinol-bin --
0.008108	0.046938	-6.94651	Significant down		1 Molecular --	--
0.016969	0.010791	-5.88094	Significant down		1 Cellular Cc serum albu	--
0.113942	0.088644	-3.13363	Nonsignifi	None	1 Cellular Cc alpha-feto	--
0.1413	0.044131	-2.82317	Significant down		1 Cellular Cc vitamin D-	--
0.006596	0.476888	-7.24412	Nonsignifi	None	--	transferrin --
0.141134	0.055071	-2.82486	Nonsignifi	None	--	lactotransf 3.4.21.-
0.09638	0.104333	-3.37512	Nonsignifi	None	--	hemopexir --
0.104285	0.17749	-3.2614	Nonsignifi	None	2 Biological ferritin ligh	--
0.177148	0.133643	-2.49698	Nonsignifi	None	2 Biological ferritin hea	1.16.3.2
0.159754	0.155233	-2.64608	Nonsignifi	None	2 Molecular plasma kal	3.4.21.34
9.124617	0.001613	3.189764	Significant up		4 Molecular matrix met	3.4.24.7
0.153812	0.0351	-2.70076	Significant down	--	--	compleme --
0.165663	0.186626	-2.59367	Nonsignifi	None	3 Molecular vitronectin	--
0.053534	0.15625	-4.2234	Nonsignifi	None	3 Molecular catalase	1.11.1.6
Inf	0	Inf	Significant up		4 Molecular RAF proto	2.7.11.1
Inf	0	Inf	Significant up		2 Molecular alpha-L-fu	3.2.1.51
1.330267	0.06772	0.411716	Nonsignifi	None	2 Molecular fructose-b	4.1.2.13
Inf	0	Inf	Significant up		1 Molecular cystatin-A	--
0.773535	0.149304	-0.37046	Nonsignifi	None	2 Molecular annexin A1	--
0.032693	0.007176	-4.93489	Significant down		2 Molecular apolipoprc	--
Inf	0	Inf	Significant up		2 Biological lecithin-ch	2.3.1.43
#NAME?	0	#NAME?	Significant down	--	--	Thy-1 cell --
0.097712	0.227975	-3.35532	Nonsignifi	None	2 Molecular type II ker	--
0.064612	0.055341	-3.95206	Nonsignifi	None	2 Molecular type II ker	--
0.016239	0.0093	-5.94441	Significant down		1 Molecular von Willeb	--
0.185221	0.042963	-2.43268	Significant down	--	--	--
Inf	0	Inf	Significant up		1 Molecular tubulin bet	--
0.707012	0.098037	-0.50019	Nonsignifi	None	1 Biological glyceraldel	1.2.1.12
Inf	0	Inf	Significant up	--	--	argininosu 4.3.2.1
0.157938	0.04779	-2.66257	Significant down		3 Molecular alpha-amy	3.2.1.1
0.389043	0.014342	-1.362	Nonsignifi	None	--	heat shock --
Inf	0	Inf	Significant up	--	--	thymidylat 2.1.1.45
0.085484	0.135174	-3.5482	Nonsignifi	None	4 Molecular oligosacch	--
9.578544	2.17E-06	3.259806	Significant up		5 Molecular guanine nu	--
11.78436	5.26E-06	3.558801	Significant up		2 Molecular sodium/pc	3.6.3.9
Inf	0	Inf	Significant up		3 Cellular Cc sodium/pc	--
Inf	0	Inf	Significant up		2 Molecular fructose-b	4.1.2.13
0.09842	0.036172	-3.34491	Significant down	--	--	apolipoprc --
0.109299	0.066624	-3.19365	Nonsignifi	None	--	integrin be --
Inf	0	Inf	Significant up	--	--	integrin be --
0.053105	0.021749	-4.23502	Significant down	--	--	plasminog --
0.164543	0.061039	-2.60346	Nonsignifi	None	--	C1 inhibitc --

0.072289	0.065441	-3.79008	Nonsignifi	None		5	Molecular	compleme	3.4.21.45
0.166285	0.036477	-2.58827	Significant	down	--	--	--	coagulatio	--
#NAME?	0	#NAME?	Significant	down		3	Molecular	interleukin	--
Inf	0	Inf	Significant	up	--	--	--	intercellula	--
0.16045	0.221281	-2.6398	Nonsignifi	None	--	--	--	large subu	--
0.266947	0.096706	-1.90537	Nonsignifi	None	--	--	--	large subu	--
0.614389	0.213138	-0.70278	Nonsignifi	None		2	Cellular Cc	large subu	--
0.129645	0.000399	-2.94737	Significant	down	--	--	--	C-type lec	--
Inf	0	Inf	Significant	up		2	Molecular	lupus La pi	--
0.173715	0.036765	-2.5252	Significant	down	--	--	--	thyroxine-	--
0.161563	0.098623	-2.62983	Nonsignifi	None	--	--	--	heparin co	--
4.611572	3.19E-06	2.205259	Significant	up	--	--	--	integrin be	--
Inf	0	Inf	Significant	up		6	Molecular	classical pr	2.7.11.13
Inf	0	Inf	Significant	up		2	Molecular	type I kera	--
0.292323	0.015458	-1.77437	Nonsignifi	None		1	Molecular	myosin ligl	--
0.043151	0.056746	-4.53445	Nonsignifi	None		2	Molecular	collagen, t	--
Inf	0	Inf	Significant	up		2	Molecular	uroporphy	4.1.1.37
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
0.537192	0.037892	-0.89649	Nonsignifi	None	--	--	--	cholinester	3.1.1.8
0.221981	0.055374	-2.17149	Nonsignifi	None	--	--	--	gelsolin	--
Inf	0	Inf	Significant	up		3	Molecular	--	--
0.156	0.108586	-2.68038	Nonsignifi	None		4	Cellular Cc	apolipoprc	--
Inf	0	Inf	Significant	up		4	Molecular	translation	--
Inf	0	Inf	Significant	up		1	Molecular	creatine kin	2.7.3.2
2.499561	4.09E-05	1.321675	Nonsignifi	None	--	--	--	enolase	4.2.1.11
0.330061	0.236058	-1.5992	Nonsignifi	None		2	Biological	glycogen p	2.4.1.1
0.630858	0.004958	-0.66461	Nonsignifi	None		3	Molecular	glucose-6-	5.3.1.9
0.43431	0.017886	-1.2032	Nonsignifi	None		1	Molecular	nucleopho	--
3.67656	0.000721	1.878356	Nonsignifi	None	--	--	--	tropomyos	--
3.04663	2.28E-05	1.607214	Nonsignifi	None	--	--	--	integrin al	--
Inf	0	Inf	Significant	up		1	Molecular	lipoproteir	3.1.1.34
0.154371	0.001265	-2.69553	Significant	down		1	Biological	hexosamin	3.2.1.52
3.277615	0.001835	1.712646	Nonsignifi	None		1	Molecular	histone H2	--
0.034546	0.000996	-4.85533	Significant	down	--	--	--	glia-derive	--
Inf	0	Inf	Significant	up		1	Molecular	diazepam-	--
0.054634	0.235058	-4.19405	Nonsignifi	None	--	--	--	fatty acid-	--
1.80213	0.001567	0.849703	Nonsignifi	None		2	Molecular	L-lactate c	1.1.1.27
Inf	0	Inf	Significant	up		3	Molecular	glutathion	1.11.1.9
Inf	0	Inf	Significant	up		3	Molecular	thrombom	--
0.086367	0.034386	-3.53337	Significant	down		3	Molecular	protein S	--
0.196175	0.015241	-2.34979	Significant	down		1	Biological	protein dis	5.3.4.1
0.21144	0.039749	-2.24168	Significant	down		2	Molecular	cathepsin I	3.4.23.5
8.671814	2.35E-06	3.116334	Significant	up		2	Molecular	annexin A2	--
0.531369	0.317835	-0.91221	Nonsignifi	None		1	Molecular	tubulin bet	--
Inf	0	Inf	Significant	up	--	--	--	carbonic a	4.2.1.1
#NAME?	0	#NAME?	Significant	down		1	Molecular	decorin	--
0.207856	0.035151	-2.26635	Significant	down		1	Biological	saposin	--
0.176824	0.000922	-2.49962	Significant	down		1	Biological	hexosamin	3.2.1.52
7.077345	0.000103	2.823208	Significant	up	--	--	--	profilin	--
0.045982	0.073502	-4.44277	Nonsignifi	None	--	--	--	--	--
0.699491	0.679432	-0.51562	Nonsignifi	None		8	Molecular	--	--
0.099798	0.034988	-3.32485	Significant	down		4	Molecular	cathepsin I	3.4.22.1
2.426494	5.13E-05	1.278873	Nonsignifi	None		4	Molecular	molecular	--
0.070365	0.006492	-3.82899	Significant	down		1	Molecular	heterogen	--
0.311192	0.056618	-1.68412	Nonsignifi	None	--	--	--	laminin, be	--
16.14104	8.25E-05	4.012662	Significant	up		3	Molecular	tyrosine-p	2.7.10.2
Inf	0	Inf	Significant	up		3	Molecular	tyrosine-p	2.7.10.2

0.018946	0.00412	-5.72198	Significant down		4 Molecular thrombos	--
Inf	0	Inf	Significant up		6 Molecular insulin-like	2.7.10.1
0.00718	0.010209	-7.12177	Significant down		1 Molecular collagen, t	--
1.379438	0.054682	0.464081	Nonsignifi	None	2 Molecular annexin A	--
Inf	0	Inf	Significant up	--	--	decay acc
Inf	0	Inf	Significant up		5 Molecular ATP-bind	3.6.3.44
5.676396	4.91E-06	2.504975	Significant up		2 Molecular solute carr	--
Inf	0	Inf	Significant up		2 Molecular 6-phosph	2.7.1.11
2.297674	0.000179	1.200174	Nonsignifi	None	4 Molecular molecular	--
Inf	0	Inf	Significant up		2 Molecular asparagin	6.3.5.4
0.00522	0.025248	-7.58175	Significant down		4 Molecular matrix met	3.4.24.24
Inf	0	Inf	Significant up		2 Molecular neprilysin	3.4.24.11
0.021308	0.010008	-5.55245	Significant down		2 Molecular inhibin, be	--
0.057854	0.055826	-4.11145	Nonsignifi	None	1 Biological pleckstrin	--
0.390136	0.124518	-1.35795	Nonsignifi	None	2 Molecular collagen, t	--
Inf	0	Inf	Significant up		4 Molecular proto-onc	2.7.10.1
Inf	0	Inf	Significant up	--	--	melanoma
4.304779	0.00133	2.105939	Significant up	--	--	integrin al
0.188018	5.06E-06	-2.41106	Significant down		2 Molecular vimentin	--
0.156533	0.131046	-2.67546	Nonsignifi	None	--	alpha-2-a
0.430475	0.362093	-1.216	Nonsignifi	None	2 Molecular type I kera	--
1.504566	0.007404	0.589348	Nonsignifi	None	2 Molecular annexin A	--
0.185187	0.388023	-2.43295	Nonsignifi	None	2 Molecular type I kera	--
0.218293	0.272287	-2.19566	Nonsignifi	None	4 Molecular small subu	--
0.811591	0.51464	-0.30118	Nonsignifi	None	1 Cellular Cc CD63 anti	--
Inf	0	Inf	Significant up		1 Biological acetyl-Co	2.3.1.16
0.796056	0.438548	-0.32906	Nonsignifi	None	1 Molecular glutathioni	2.5.1.18
0.003482	0.071141	-8.16597	Nonsignifi	None	3 Cellular Cc C-X-C mo	--
1.336442	0.263949	0.418397	Nonsignifi	None	1 Molecular galectin-1	--
0.063253	7.14E-05	-3.98272	Significant down	--	--	high mobil
Inf	0	Inf	Significant up	--	--	--
Inf	0	Inf	Significant up		5 Molecular guanine n	--
0.030148	0.054253	-5.05178	Nonsignifi	None	4 Molecular	--
4.575559	1.32E-05	2.193948	Significant up	--	--	tropomyos
Inf	0	Inf	Significant up		5 Molecular clathrin lig	--
Inf	0	Inf	Significant up		5 Molecular clathrin lig	--
Inf	0	Inf	Significant up		2 Molecular annexin A	--
#NAME?	0	#NAME?	Significant down		2 Molecular platelet-d	2.7.10.1
0.199624	9.26E-05	-2.32464	Significant down		1 Molecular heterogen	--
0.095941	0.029996	-3.38171	Significant down		2 Molecular compleme	3.4.21.42
Inf	0	Inf	Significant up		4 Molecular poly [ADP-	2.4.2.30
Inf	0	Inf	Significant up		2 Molecular leukotrien	3.3.2.6
0.88014	0.106963	-0.1842	Nonsignifi	None	2 Molecular fructose-b	4.1.2.13
0.083729	0.012975	-3.57813	Significant down		3 Molecular compleme	--
5.667496	0.092565	2.502711	Nonsignifi	None	1 Molecular histone H2	--
Inf	0	Inf	Significant up		1 Molecular F-box prot	--
0.061883	0.000811	-4.01431	Significant down		1 Molecular protein ph	--
0.399573	0.066055	-1.32347	Nonsignifi	None	--	heat shock
Inf	0	Inf	Significant up	--	2 Molecular Ras-relate	--
0.250119	0.016639	-1.99931	Nonsignifi	None	--	proteoglyc
0.025563	0.064678	-5.28979	Nonsignifi	None	3 Cellular Cc interleukin	--
Inf	0	Inf	Significant up		1 Molecular 60 kDa SS-	--
3.100167	0.015169	1.632346	Nonsignifi	None	2 Molecular Ras-relate	--
Inf	0	Inf	Significant up		4 Molecular A-Raf prot	2.7.11.1
Inf	0	Inf	Significant up		3 Molecular receptor-t	3.1.3.48
0.450749	0.026246	-1.1496	Nonsignifi	None	1 Biological thioredoxi	--
Inf	0	Inf	Significant up		2 Molecular cathepsin	3.4.16.5
0.133134	0.011435	-2.90905	Significant down		1 Molecular compleme	--

0.078855	0.00564	-3.66465	Significant down		1 Molecular tissue factor	--
Inf	0	Inf	Significant up	--	-- S-formylgl	3.1.2.12
Inf	0	Inf	Significant up		1 Molecular chaperonin	--
0.010976	0.118783	-6.50952	Nonsignificant		2 Molecular hyaluronan	--
0.250937	0.094834	-1.9946	Nonsignificant	--	-- heat shock	--
0.298005	0.050853	-1.74659	Nonsignificant	--	-- laminin, gamma	--
Inf	0	Inf	Significant up		1 Molecular lysosomal	3.1.3.2
4.736433	6.89E-05	2.243801	Significant up	--	-- heat shock	--
3.798382	0.000973	1.925385	Nonsignificant		3 Cellular Cc MFS transporter	--
0.573871	0.258221	-0.8012	Nonsignificant		3 Cellular Cc MFS transporter	--
Inf	0	Inf	Significant up		5 Molecular erythrocyte	--
Inf	0	Inf	Significant up		3 Molecular --	--
0.239777	0.059267	-2.06023	Nonsignificant	--	-- pyruvate dehydrogenase	1.2.4.1
0.291693	0.309702	-1.77748	Nonsignificant		2 Biological glycogen phosphorylase	2.4.1.1
Inf	0	Inf	Significant up		2 Molecular Ras-related	--
Inf	0	Inf	Significant up		1 Cellular Cc lysosomal	--
0.189112	0.057462	-2.40268	Nonsignificant		2 Molecular fibroblast collagen	2.7.10.1
Inf	0	Inf	Significant up		4 Molecular DNA topoisomerase	5.9.9.1.2
Inf	0	Inf	Significant up		5 Molecular DNA topoisomerase	5.9.9.1.3
0.181784	0.394103	-2.45971	Nonsignificant		4 Molecular --	--
0.393964	0.009077	-1.34386	Nonsignificant		4 Molecular insulin-like	--
1.010689	0.928456	0.015339	Nonsignificant		1 Biological --	--
Inf	0	Inf	Significant up		3 Molecular cyclin-dependent	2.7.11.22
Inf	0	Inf	Significant up		3 Molecular ribose-phosphate	2.7.6.1
1.305123	0.409425	0.384186	Nonsignificant		2 Molecular polyadenylation	--
Inf	0	Inf	Significant up		2 Molecular proliferation	--
Inf	0	Inf	Significant up		3 Molecular histidyl-tRNA	6.1.1.21
0.031202	0.047447	-5.00224	Significant down		1 Molecular collagen, type I	--
0.017549	0.035766	-5.83243	Significant down	--	-- collagen, type I	--
0.064403	0.02844	-3.95673	Significant down	--	-- collagen, type I	--
0.063685	0.034823	-3.97291	Significant down		1 Molecular collagen, type I	--
0.247536	9.29E-06	-2.01429	Significant down		1 Molecular coagulation	--
1.642469	0.320127	0.715866	Nonsignificant		2 Molecular IMP dehydrogenase	1.1.1.205
Inf	0	Inf	Significant up		1 Molecular creatine kinase	2.7.3.2
Inf	0	Inf	Significant up		1 Molecular creatine kinase	2.7.3.2
4.340083	0.00127	2.117723	Significant up		1 Molecular actinin alpha	--
Inf	0	Inf	Significant up		3 Molecular tyrosine-phosphatase	2.7.10.2
0.490331	0.032034	-1.02817	Nonsignificant		2 Molecular Xaa-Pro dipeptidase	3.4.13.9
Inf	0	Inf	Significant up		3 Molecular ATP-dependent	--
Inf	0	Inf	Significant up		3 Molecular ATP-dependent	--
0.537142	0.188371	-0.89662	Nonsignificant		1 Cellular Cc lysosomal	--
0.165953	0.541108	-2.59115	Nonsignificant		1 Molecular ribonucleic acid	--
0.261483	0.068884	-1.93521	Nonsignificant		3 Molecular bone morphogenetic	3.4.24.19
Inf	0	Inf	Significant up		3 Molecular myosin heavy chain	--
0.298137	0.059656	-1.74595	Nonsignificant		1 Molecular neural cell	--
0.031136	0.006584	-5.00527	Significant down		3 Molecular versican core	--
22.64576	2.94E-05	4.501169	Significant up	--	-- integrin alpha	--
2.17325	0.002022	1.119854	Nonsignificant		1 Molecular elongation	--
0.126596	0.106122	-2.98169	Nonsignificant		2 Molecular type I keratin	--
0.114358	0.181299	-3.12837	Nonsignificant		2 Molecular type II keratin	--
Inf	0	Inf	Significant up		1 Biological protein disulfide	5.3.4.1
Inf	0	Inf	Significant up	--	-- --	--
Inf	0	Inf	Significant up		3 Molecular porphobilinogen	4.2.1.24
0.265164	0.025301	-1.91504	Nonsignificant		2 Molecular plastin-2	--
0.568426	0.153416	-0.81496	Nonsignificant		2 Molecular plastin-3	--
0.145036	0.043128	-2.78552	Significant down		2 Biological acylamino acid	3.4.19.1
Inf	0	Inf	Significant up		2 Molecular glycogen synthase	2.4.1.11
Inf	0	Inf	Significant up	--	-- cAMP-dependent	--

0.800292	0.208619	-0.3214	Nonsignifi	None	--	--	enolase	4.2.1.11
Inf	0	Inf	Significant	up		3	Cellular Cc	transcripti
1.142817	0.629767	0.192595	Nonsignifi	None	--	--	phenylpyr	5.3.2.1
Inf	0	Inf	Significant	up		1	Molecular	protein kin
Inf	0	Inf	Significant	up		1	Biological	--
Inf	0	Inf	Significant	up		3	Molecular	carboxype
0.469424	0.108253	-1.09104	Nonsignifi	None		2	Molecular	nidogen (e
Inf	0	Inf	Significant	up	--	--	alcohol de	1.1.1.2
1.531348	0.00565	0.614802	Nonsignifi	None		4	Molecular	pyruvate k
0.327606	0.003005	-1.60997	Nonsignifi	None		4	Molecular	heat shock
Inf	0	Inf	Significant	up	--	--	small nucle	--
Inf	0	Inf	Significant	up		4	Molecular	matrix met
Inf	0	Inf	Significant	up		1	Molecular	heterogen
Inf	0	Inf	Significant	up		1	Molecular	junction pl
Inf	0	Inf	Significant	up		3	Molecular	glutamine
1.049116	0.763378	0.069174	Nonsignifi	None	--	--	aldehyde r	1.1.1.21
8.27436	1.02E-05	3.048648	Significant	up		2	Molecular	aminopept
Inf	0	Inf	Significant	up	--	--	poliovirus	--
0.359066	0.003208	-1.47768	Nonsignifi	None		3	Molecular	carboxype
Inf	0	Inf	Significant	up		3	Molecular	interferon
Inf	0	Inf	Significant	up		3	Molecular	ubiquitin c
Inf	0	Inf	Significant	up	--	--	membrane	--
Inf	0	Inf	Significant	up	--	5	Molecular	nucleoside
0.734016	0.093566	-0.44612	Nonsignifi	None		4	Molecular	small subu
0.022613	0.035938	-5.46668	Significant	down		1	Molecular	Function:metalloendo
1.487012	0.07652	0.572416	Nonsignifi	None		2	Molecular	CD44 antiç
0.053904	0.009012	-4.21345	Significant	down		2	Molecular	aggrecan
Inf	0	Inf	Significant	up		1	Molecular	NCK adapt
0.014303	0.042563	-6.12753	Significant	down		4	Cellular Cc	histone H1
0.06038	8.58E-05	-4.04979	Significant	down		4	Cellular Cc	histone H1
Inf	0	Inf	Significant	up		5	Molecular	phosphatic
0.278686	0.044458	-1.84329	Nonsignifi	None		4	Molecular	fumarylac
Inf	0	Inf	Significant	up		1	Biological	stathmin
Inf	0	Inf	Significant	up		1	Molecular	cold shock
2.742723	0.000227	1.455609	Nonsignifi	None	--	--	heat shock	--
Inf	0	Inf	Significant	up		2	Molecular	Ras homol
Inf	0	Inf	Significant	up	--	--	high mobil	--
Inf	0	Inf	Significant	up		2	Biological	aspartate ε
19.49805	0.001758	4.285258	Significant	up	--	--	integrin alç	--
Inf	0	Inf	Significant	up	--	--	gap junctio	--
Inf	0	Inf	Significant	up	--	--	--	--
6.084756	5.01E-05	2.605199	Significant	up		4	Molecular	calpain-2
Inf	0	Inf	Significant	up		2	Molecular	CTP synthz
0.502085	0.039128	-0.994	Nonsignifi	None		2	Molecular	ATP-depei
0.410811	0.000221	-1.28345	Nonsignifi	None		2	Molecular	6-phospho
0.006346	0.018441	-7.29986	Significant	down		3	Biological	insulin-like
Inf	0	Inf	Significant	up		2	Molecular	FMS-like t
Inf	0	Inf	Significant	up		1	Molecular	26S protea
0.874749	0.043422	-0.19306	Nonsignifi	None		1	Molecular	T-complex
Inf	0	Inf	Significant	up		2	Molecular	tyrosine-p
0.028664	0.041277	-5.12463	Significant	down		3	Biological	--
Inf	0	Inf	Significant	up		4	Molecular	large subu
5.928937	0.000511	2.567773	Significant	up		1	Molecular	ADP-ribos
0.402519	0.601653	-1.31287	Nonsignifi	None	--	--	large subu	--
0.425905	0.175291	-1.2314	Nonsignifi	None		2	Biological	vinculin
Inf	0	Inf	Significant	up		2	Molecular	receptor-t
0.452693	0.332079	-1.14339	Nonsignifi	None		3	Molecular	large subu

Inf	0	Inf	Significant up	--	--	2,3-bisphosphoglycerate 5.4.2.11
Inf	0	Inf	Significant up	--	--	regulator c --
Inf	0	Inf	Significant up		5 Molecular	-- --
Inf	0	Inf	Significant up		4 Molecular	peptidylglycyl 1.14.17.3
Inf	0	Inf	Significant up		3 Molecular	cadherin 2 --
0.233242	0.044096	-2.1001	Significant down		1 Molecular	nucleolin --
Inf	0	Inf	Significant up		2 Molecular	hexokinase 2.7.1.1
Inf	0	Inf	Significant up		2 Molecular	DNA-directed --
Inf	0	Inf	Significant up		2 Molecular	tumor necrosis --
Inf	0	Inf	Significant up		3 Molecular	eukaryotic 2.7.11.1
Inf	0	Inf	Significant up	--	--	spermidine 2.5.1.16
Inf	0	Inf	Significant up		4 Biological	solute carrier --
Inf	0	Inf	Significant up		3 Molecular	casein kinase 2.7.11.1
0.176234	0.025262	-2.50444	Significant down		2 Molecular	inter-alpha 2 --
0.236433	0.012035	-2.0805	Significant down		2 Molecular	inter-alpha 2 --
0.017427	0.404971	-5.84255	Nonsignificant		2 Molecular	translation --
Inf	0	Inf	Significant up		2 Molecular	Ras-related --
Inf	0	Inf	Significant up		2 Molecular	Ras-related --
Inf	0	Inf	Significant up		2 Molecular	Ras-related --
Inf	0	Inf	Significant up		5 Molecular	atrial natriuretic 4.6.1.2
1.006529	0.957308	0.009389	Nonsignificant		3 Molecular	20S proteasome 3.4.25.1
Inf	0	Inf	Significant up		2 Molecular	lamin B --
0.827287	0.202954	-0.27354	Nonsignificant		3 Molecular	-- --
0.127108	0.058975	-2.97587	Nonsignificant		1 Molecular	osteoglycin --
0.167963	0.038358	-2.57378	Significant down	--	--	collagen, type I --
0.037511	0.018837	-4.73654	Significant down		1 Molecular	collagen, type I --
Inf	0	Inf	Significant up		2 Molecular	Ras GTPase --
Inf	0	Inf	Significant up	--	--	-- --
Inf	0	Inf	Significant up		3 Molecular	cell division 2.7.11.22
Inf	0	Inf	Significant up		1 Molecular	glutathione 2.5.1.18
Inf	0	Inf	Significant up		3 Molecular	V-type H+ --
Inf	0	Inf	Significant up		2 Molecular	V-type H+ --
Inf	0	Inf	Significant up		1 Molecular	cysteine aryl --
0.261463	6.52E-05	-1.93532	Nonsignificant		1 Molecular	filamin --
Inf	0	Inf	Significant up		1 Biological	neurofibromin --
0.72937	0.028998	-0.45528	Nonsignificant		1 Biological	aconitate hydratase 4.2.1.3
0.003298	0.04281	-8.24421	Significant down		3 Molecular	sphingosine --
0.663526	0.01111	-0.59177	Nonsignificant		2 Biological	5'-nucleotidase 3.1.3.5
0.007206	0.022204	-7.11662	Significant down		1 Molecular	biglycan --
3.088419	0.000338	1.626868	Nonsignificant		1 Cellular	Cc CD9 antigen --
Inf	0	Inf	Significant up		1 Molecular	catechol O-methyltransferase 2.1.1.6
0.01445	0.119912	-6.11279	Nonsignificant		2 Molecular	transglutaminase 2.3.2.13
Inf	0	Inf	Significant up	--	--	oxysterol-ligand --
Inf	0	Inf	Significant up		3 Molecular	-- --
0.020471	0.007345	-5.61031	Significant down		1 Molecular	tenascin --
Inf	0	Inf	Significant up		1 Biological	-- --
Inf	0	Inf	Significant up	--	--	acetylcholinesterase 3.1.1.7
0.501068	0.447877	-0.99692	Nonsignificant		1 Molecular	ubiquitin-conjugating enzyme 6.2.1.45
0.215006	0.158134	-2.21755	Nonsignificant		3 Molecular	glutathione S-transferase 1.11.1.9
4.046978	0.000111	2.016845	Significant up		5 Molecular	nucleoside 2.7.4.6
Inf	0	Inf	Significant up		7 Molecular	-- --
0.084795	0.010367	-3.55989	Significant down		1 Molecular	heterogeneous --
0.033569	0.08892	-4.89671	Nonsignificant		3 Biological	-- --
Inf	0	Inf	Significant up		3 Molecular	protein kinase 2.7.11.11
0.050921	0.022734	-4.2956	Significant down		1 Molecular	fibulin 1/2 --
2.694421	0.045594	1.429975	Nonsignificant	--	--	integrin alpha 5 --
0.494825	0.053822	-1.01501	Nonsignificant		1 Molecular	splicing factor --
Inf	0	Inf	Significant up		1 Molecular	tubulin gamma --

0.546861	0.131619	-0.87076	Nonsignifi	None	3 Biological	peptidyl-p	5.2.1.8
Inf	0	Inf	Significant	up	1 Molecular	--	--
0.591688	0.227674	-0.75709	Nonsignifi	None	1 Molecular	small subu	--
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
Inf	0	Inf	Significant	up	3 Molecular	receptor-t	3.1.3.48
0.211334	0.151126	-2.2424	Nonsignifi	None	3 Molecular	receptor-t	3.1.3.48
1.429634	0.007934	0.515646	Nonsignifi	None	3 Molecular	adenosylh	3.3.1.1
9.962797	0.00049	3.316551	Significant	up	2 Molecular	cofilin	--
Inf	0	Inf	Significant	up	1 Molecular	translation	--
Inf	0	Inf	Significant	up	1 Molecular	1D-myo-ir	2.7.1.127
Inf	0	Inf	Significant	up	--	dTMP kina	2.7.4.9
1.859958	0.021254	0.89527	Nonsignifi	None	3 Molecular	ribonucleo	1.17.4.1
0.937161	0.856137	-0.09363	Nonsignifi	None	5 Molecular	laminin, al	--
Inf	0	Inf	Significant	up	2 Molecular	--	--
Inf	0	Inf	Significant	up	3 Biological	interleukin	--
Inf	0	Inf	Significant	up	2 Molecular	elongation	--
Inf	0	Inf	Significant	up	--	--	--
0.090808	0.035532	-3.46103	Significant	down	1 Molecular	tenascin	--
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	--
Inf	0	Inf	Significant	up	3 Molecular	DNA replic	3.6.4.12
Inf	0	Inf	Significant	up	--	--	--
2.292414	0.121037	1.196868	Nonsignifi	None	5 Molecular	laminin, al	--
0.597729	0.011018	-0.74244	Nonsignifi	None	--	small subu	--
Inf	0	Inf	Significant	up	--	DnaJ hom	--
0.594729	0.175529	-0.7497	Nonsignifi	None	5 Molecular	20S protea	3.4.25.1
0.603601	0.131318	-0.72833	Nonsignifi	None	5 Molecular	20S protea	3.4.25.1
0.802597	0.386545	-0.31725	Nonsignifi	None	5 Molecular	20S protea	3.4.25.1
1.433796	0.043687	0.51984	Nonsignifi	None	5 Molecular	20S protea	3.4.25.1
6.023475	5.9E-05	2.590596	Significant	up	--	integrin al	--
0.035543	0.011956	-4.8143	Significant	down	--	--	--
20.84368	0.000443	4.381538	Significant	up	3 Cellular	Cc moesin	--
Inf	0	Inf	Significant	up	2 Biological	catenin al	--
Inf	0	Inf	Significant	up	3 Molecular	DNA (cyto	2.1.1.37
0.192308	0.255624	-2.37851	Nonsignifi	None	1 Molecular	splicing fac	--
0.519617	0.005958	-0.94448	Nonsignifi	None	4 Molecular	large subu	--
0.029655	0.09121	-5.07556	Nonsignifi	None	--	high mobil	--
Inf	0	Inf	Significant	up	5 Molecular	threonyl-tl	6.1.1.3
0.020297	0.499323	-5.62259	Nonsignifi	None	4 Molecular	valyl-tRNA	6.1.1.9
1.152692	0.309495	0.205008	Nonsignifi	None	3 Molecular	elongation	--
0.128165	0.040721	-2.96393	Significant	down	2 Molecular	--	--
0.471695	0.307549	-1.08407	Nonsignifi	None	--	erythrocyt	--
2.237674	0.028593	1.162	Nonsignifi	None	--	14-3-3 pr	--
Inf	0	Inf	Significant	up	3 Molecular	mitogen-a	2.7.11.24
Inf	0	Inf	Significant	up	3 Molecular	MAP/micr	2.7.11.1
0.064794	0.093946	-3.948	Nonsignifi	None	3 Molecular	large subu	--
0.025229	0.001516	-5.30876	Significant	down	--	--	--
Inf	0	Inf	Significant	up	4 Molecular	replication	--
Inf	0	Inf	Significant	up	--	AP endont	4.2.99.18
1.432869	0.021954	0.518907	Nonsignifi	None	1 Cellular	Cc CD82 anti	--
1.580858	0.145027	0.660708	Nonsignifi	None	5 Molecular	--	--
Inf	0	Inf	Significant	up	1 Molecular	microtubu	--
Inf	0	Inf	Significant	up	1 Biological	phosphoin	--
0.07856	0.006653	-3.67005	Significant	down	3 Molecular	20S protea	3.4.25.1
1.714478	0.035783	0.77777	Nonsignifi	None	5 Molecular	20S protea	3.4.25.1

Inf		0	Inf	Significant up		3	Molecular	20S protea	3.4.25.1
Inf		0	Inf	Significant up		3	Molecular	20S protea	3.4.25.1
1.222993	0.294246	0.290416	Nonsignifi	None		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
Inf		0	Inf	Significant up		3	Molecular	--	--
Inf		0	Inf	Significant up		1	Biological	myo-inosit	3.1.3.25
0.510917	0.193036	-0.96884	Nonsignifi	None		4	Biological	connective	--
1.034953	0.923296	0.049565	Nonsignifi	None		3	Molecular	Eph recept	2.7.10.1
Inf		0	Inf	Significant up		3	Molecular	Eph recept	2.7.10.1
Inf		0	Inf	Significant up		1	Molecular	SHC-trans	--
Inf		0	Inf	Significant up	--	--	--	cellular ret	--
0.992422	0.984027	-0.01097	Nonsignifi	None	--	--	--	transketol	2.2.1.1
0.042582	0.073778	-4.55361	Nonsignifi	None		2	Molecular	non-recep	2.7.10.2
Inf		0	Inf	Significant up		2	Molecular	elongation	--
4.199643	0.002746	2.070267	Significant	up		1	Molecular	myristoylat	--
1.180198	0.445708	0.239029	Nonsignifi	None		4	Molecular	--	--
3.819529	0.000636	1.933395	Nonsignifi	None		1	Molecular	peroxiredc	1.11.1.15
Inf		0	Inf	Significant up	--	--	--	D-dopach	4.1.1.84
0.811725	0.342655	-0.30094	Nonsignifi	None		3	Molecular	large subu	--
1.122948	0.862709	0.167291	Nonsignifi	None	--	--	--	--	--
0.137183	0.059399	-2.86582	Nonsignifi	None	--	--	--	--	--
0.191755	0.002717	-2.38266	Significant	down		1	Biological	protein dis	5.3.4.1
Inf		0	Inf	Significant up		1	Molecular	anaphase-	--
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
1.873438	0.060636	0.905688	Nonsignifi	None		1	Molecular	--	--
Inf		0	Inf	Significant up		3	Biological	solute carr	--
Inf		0	Inf	Significant up		2	Molecular	DNA-direc	2.7.7.6
0.294436	0.192428	-1.76397	Nonsignifi	None		1	Molecular	coronin-1	--
Inf		0	Inf	Significant up		2	Molecular	Rab GDP c	--
0.167171	0.358043	-2.5806	Nonsignifi	None	--	--	--	protein S1	--
Inf		0	Inf	Significant up	--	--	--	cAMP-dep	--
Inf		0	Inf	Significant up		1	Biological	ribonucleo	1.17.4.1
3.201317	0.000878	1.678665	Nonsignifi	None	--	--	--	syndecan	--
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
1.879702	0.000937	0.910504	Nonsignifi	None		3	Molecular	--	--
2.889639	0.00115	1.530889	Nonsignifi	None	--	--	--	14-3-3 pr	--
0.976665	0.861008	-0.03406	Nonsignifi	None		1	Molecular	stress-ind	--
Inf		0	Inf	Significant up		1	Molecular	--	--
0.048684	0.184265	-4.36041	Nonsignifi	None		4	Molecular	peroxiredc	1.11.1.15
Inf		0	Inf	Significant up	--	--	--	beta-arres	--
0.278725	0.362859	-1.84309	Nonsignifi	None	--	--	--	4-hydroxy	1.13.11.27
Inf		0	Inf	Significant up		2	Molecular	syntaxin 1	--
Inf		0	Inf	Significant up		1	Molecular	cystathioni	4.4.1.1
Inf		0	Inf	Significant up		4	Molecular	large subu	--
Inf		0	Inf	Significant up		3	Molecular	tumor nec	--
Inf		0	Inf	Significant up		2	Molecular	long-chair	6.2.1.3
Inf		0	Inf	Significant up		3	Molecular	cadherin 5	--
0.647905	0.686657	-0.62615	Nonsignifi	None		4	Molecular	kinesin far	--
Inf		0	Inf	Significant up		2	Molecular	dUTP pyro	3.6.1.23
Inf		0	Inf	Significant up		5	Molecular	ATP-bind	--
Inf		0	Inf	Significant up		3	Molecular	mannosyl-	3.2.1.113
Inf		0	Inf	Significant up		3	Molecular	DNA replic	3.6.4.12

Inf	0	Inf	Significant up		3	Molecular	DNA replic	3.6.4.12
0.108873	0.17743	-3.19929	Nonsignifi	None	--	--	ribonuclea	3.1.27.-
Inf	0	Inf	Significant up		1	Cellular	Cc CD68 antiç	--
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	--	--	--	--	--
1.131013	0.276744	0.177615	Nonsignifi	None	3	Cellular	Cc glypican 1	--
Inf	0	Inf	Significant up	--	--	--	profilin	--
0.200387	0.480824	-2.31914	Nonsignifi	None	1	Molecular	catenin be	--
Inf	0	Inf	Significant up	--	--	--	serpin B	--
Inf	0	Inf	Significant up		3	Cellular	Cc merlin	--
21.0251	0.000431	4.394041	Significant up		3	Cellular	Cc radixin	--
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		1	Molecular	prostaglan	1.14.99.1
Inf	0	Inf	Significant up		3	Molecular	histamine i	--
0.020348	0.010643	-5.61897	Significant down		4	Molecular	thrombosç	--
0.079615	0.019093	-3.65082	Significant down		3	Molecular	thrombosç	--
Inf	0	Inf	Significant up	--	--	--	cystathioni	4.2.1.22
0.084727	0.01771	-3.56104	Significant down		2	Molecular	type I kera	--
0.017655	0.053942	-5.82379	Nonsignifi	None	1	Molecular	fibrillin 1	--
0.293593	0.146754	-1.76811	Nonsignifi	None	--	--	--	--
0.065882	0.034621	-3.92397	Significant down		3	Molecular	myosin hei	--
0.62671	0.35515	-0.67413	Nonsignifi	None	4	Molecular	myosin hei	--
0.182533	0.082403	-2.45377	Nonsignifi	None	3	Molecular	tyrosine ki	2.7.10.1
0.18946	0.399213	-2.40004	Nonsignifi	None	5	Molecular	coatomer	--
Inf	0	Inf	Significant up		1	Molecular	actinin alpl	--
Inf	0	Inf	Significant up	--	--	--	adducin	--
11.19176	1.89E-05	3.484364	Significant up	--	--	--	basigin	--
Inf	0	Inf	Significant up		2	Molecular	RNA-bindin	--
Inf	0	Inf	Significant up	--	--	--	protein DE	--
1.524301	0.01404	0.608148	Nonsignifi	None	3	Molecular	glutaredox	--
Inf	0	Inf	Significant up		4	Molecular	protein ph	3.1.3.16
0.13967	0.000745	-2.83991	Significant down		1	Molecular	insulin-like	--
0.142841	7.87E-05	-2.80752	Significant down		2	Molecular	type II ker	--
0.487851	0.015033	-1.03549	Nonsignifi	None	1	Molecular	26S protea	--
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
0.340131	0.146579	-1.55584	Nonsignifi	None	3	Molecular	large subu	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.523693	0.011458	-0.93321	Nonsignifi	None	2	Biological	phosphogl	5.4.2.2
Inf	0	Inf	Significant up		5	Molecular	bone morç	2.7.11.30
Inf	0	Inf	Significant up		5	Molecular	activin rec	2.7.11.30
Inf	0	Inf	Significant up		5	Molecular	TGF-beta i	2.7.11.30
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	lymphotox	--
0.106717	0.028872	-3.22813	Significant down	--	--	--	pigment ej	--
Inf	0	Inf	Significant up		3	Molecular	phospholiç	1.11.1.12
Inf	0	Inf	Significant up		5	Molecular	TGF-beta i	2.7.11.30
Inf	0	Inf	Significant up		1	Molecular	--	--
0.502944	0.061884	-0.99153	Nonsignifi	None	1	Molecular	transgelin	--
1.214341	0.599459	0.280173	Nonsignifi	None	1	Biological	transaldol	2.2.1.2
Inf	0	Inf	Significant up		3	Molecular	V-type H+	3.6.3.14
Inf	0	Inf	Significant up	--	--	--	molecular	--
Inf	0	Inf	Significant up		2	Molecular	ATP-depei	3.6.4.13
0.158504	0.253133	-2.65741	Nonsignifi	None	4	Molecular	large subu	--

0.039388	0.025852	-4.66609	Significant down		3 Molecular collagen, t --
0.187984	0.004146	-2.41132	Significant down		4 Molecular collagen, t --
Inf	0	Inf	Significant up		2 Cellular Cc oligosacch --
Inf	0	Inf	Significant up		2 Molecular flap endon3.-.-.-
Inf	0	Inf	Significant up	--	-- capping pr --
Inf	0	Inf	Significant up		2 Molecular adenylyl cy --
Inf	0	Inf	Significant up		1 Molecular interleukin --
1.884735	0.012401	0.914361	Nonsignifi	None	1 Molecular T-complex --
11.32404	0.004397	3.501317	Significant up		1 Molecular nicotinami 2.1.1.1
0.324913	0.17264	-1.62187	Nonsignifi	None	3 Molecular large subu --
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 c3.4.19.12
1.268432	0.199611	0.343046	Nonsignifi	None	2 Molecular malate del 1.1.1.37
Inf	0	Inf	Significant up		1 Molecular replication --
Inf	0	Inf	Significant up	--	-- replication --
Inf	0	Inf	Significant up		1 Molecular translation --
0.059389	0.090741	-4.07365	Nonsignifi	None	4 Molecular wingless-t --
Inf	0	Inf	Significant up		1 Molecular N-alpha-a 2.3.1.255
Inf	0	Inf	Significant up		3 Molecular c-src tyros 2.7.10.2
0.43502	0.000912	-1.20085	Nonsignifi	None	4 Molecular glycyl-tRN 6.1.1.14
0.565177	0.082694	-0.82323	Nonsignifi	None	4 Molecular isoleucyl-t 6.1.1.5
Inf	0	Inf	Significant up		2 Biological solute carr --
Inf	0	Inf	Significant up		6 Molecular atypical pr 2.7.11.13
Inf	0	Inf	Significant up	--	-- centractin --
Inf	0	Inf	Significant up		1 Molecular -- --
Inf	0	Inf	Significant up		2 Molecular signal tran --
Inf	0	Inf	Significant up		2 Molecular ATP-depei 3.6.4.13
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
Inf	0	Inf	Significant up		1 Molecular phosphatic 2.7.1.67
Inf	0	Inf	Significant up	--	-- leucine-ric --
0.379434	0.014141	-1.39808	Nonsignifi	None	4 Molecular large subu --
Inf	0	Inf	Significant up	--	-- -- --
Inf	0	Inf	Significant up		2 Molecular endothelin 3.4.24.71
1.931856	0.072189	0.949988	Nonsignifi	None	2 Molecular solute carr --
0.422041	0.015154	-1.24455	Nonsignifi	None	1 Molecular platelet-ac --
Inf	0	Inf	Significant up	--	-- melanoma --
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
0.117891	0.05663	-3.08448	Nonsignifi	None	1 Cellular Cc -- --
0.361525	0.036366	-1.46783	Nonsignifi	None	3 Biological peptidyl-p 5.2.1.8
Inf	0	Inf	Significant up		2 Cellular Cc voltage-de --
Inf	0	Inf	Significant up	--	-- phosphory --
Inf	0	Inf	Significant up		3 Molecular Ran GTPas --
Inf	0	Inf	Significant up		2 Molecular ATP-depei 3.6.4.12
Inf	0	Inf	Significant up		1 Molecular proto-onc --
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 --
Inf	0	Inf	Significant up		3 Molecular mitogen-a 2.7.12.2
0.514361	0.083134	-0.95915	Nonsignifi	None	-- -- large subu --
0.622091	0.22624	-0.6848	Nonsignifi	None	4 Molecular large subu --
Inf	0	Inf	Significant up	--	-- large subu --
0.776146	0.183137	-0.3656	Nonsignifi	None	3 Molecular small subu --
Inf	0	Inf	Significant up	--	-- small subu --

Inf		0	Inf	Significant up	1	Biological	glucosamin	3.5.99.6
Inf		0	Inf	Significant up	2	Molecular	--	--
0.20176	0.251169	-2.30929	Nonsignifi	None	2	Molecular	Ras GTPas	--
0.182762	0.154939	-2.45196	Nonsignifi	None	3	Molecular	3-hydroxy	1.13.11.6
0.863402	0.268431	-0.2119	Nonsignifi	None	2	Cellular	Cc capping pr	--
Inf		0	Inf	Significant up	3	Biological	aldehyde c	1.2.1.5
0.204675	0.226662	-2.28859	Nonsignifi	None	4	Molecular	large subu	--
0.109283	0.010538	-3.19385	Significant	down	1	Molecular	galectin-7	--
Inf		0	Inf	Significant up	3	Molecular	solute carr	--
0.493241	0.213845	-1.01964	Nonsignifi	None	1	Molecular	--	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	3	Molecular	solute carr	--
Inf		0	Inf	Significant up	4	Molecular	prolyl oligo	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
0.253224	0.244289	-1.98152	Nonsignifi	None	2	Molecular	glutamate-	6.3.2.2
0.350552	0.205162	-1.5123	Nonsignifi	None	--	--	glutamate-	--
8.610816	0.034605	3.10615	Significant	up	1	Cellular	Cc CD151 ant	--
Inf		0	Inf	Significant up	--	--	26S protea	--
0.711156	0.060472	-0.49176	Nonsignifi	None	1	Molecular	T-complex	--
0.247266	0.03762	-2.01587	Significant	down	--	--	stress 70 p	--
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
Inf		0	Inf	Significant up	1	Molecular	phosphatic	2.7.1.153
Inf		0	Inf	Significant up	2	Cellular	Cc --	--
0.052353	4.57E-05	-4.25559	Significant	down	2	Molecular	mannan-b	3.4.21.-
Inf		0	Inf	Significant up	5	Molecular	CD97 anti	--
Inf		0	Inf	Significant up	1	Molecular	paxillin	--
0.950115	0.730088	-0.07383	Nonsignifi	None	3	Biological	--	--
Inf		0	Inf	Significant up	1	Cellular	Cc lectin, mar	--
0.832177	0.746657	-0.26504	Nonsignifi	None	2	Biological	fatty acid s	2.3.1.85
0.604037	0.013725	-0.72729	Nonsignifi	None	1	Molecular	T-complex	--
Inf		0	Inf	Significant up	3	Biological	--	--
Inf		0	Inf	Significant up	--	--	signal recc	--
Inf		0	Inf	Significant up	--	--	cysteinyl-t	6.1.1.16
0.794954	0.704864	-0.33106	Nonsignifi	None	4	Molecular	seryl-tRNA	6.1.1.11
Inf		0	Inf	Significant up	1	Molecular	DNA prim	2.7.7.-
0.854361	0.275747	-0.22708	Nonsignifi	None	3	Molecular	20S protea	3.4.25.1
Inf		0	Inf	Significant up	7	Molecular	DNA replic	3.6.4.12
0.158339	0.097858	-2.65892	Nonsignifi	None	3	Molecular	thrombos	--
0.148828	0.041705	-2.74828	Significant	down	3	Molecular	thrombos	--
Inf		0	Inf	Significant up	2	Molecular	RNA-bindi	--
Inf		0	Inf	Significant up	1	Molecular	numb	--
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	3	Molecular	glycogen s	2.7.11.26
Inf		0	Inf	Significant up	--	--	5'-nucleot	3.1.3.5
1.301418	0.306807	0.380084	Nonsignifi	None	4	Molecular	GMP synth	6.3.5.2
Inf		0	Inf	Significant up	5	Molecular	double-str	--
Inf		0	Inf	Significant up	5	Molecular	guanine nt	--
Inf		0	Inf	Significant up	3	Molecular	guanine nt	--
Inf		0	Inf	Significant up	3	Molecular	guanine nt	--
0.011902	0.056949	-6.39266	Nonsignifi	None	4	Molecular	matrix met	3.4.24.80
1.202093	0.303994	0.265548	Nonsignifi	None	2	Molecular	Rab GDP c	--
Inf		0	Inf	Significant up	3	Biological	solute carr	--
0.169058	0.164578	-2.56441	Nonsignifi	None	--	--	serpin pep	--

Inf	0	Inf	Significant up		2	Molecular	--	--
0.608344	0.034682	-0.71704	Nonsignifi	None	1	Molecular	suppressor	--
0.741879	0.60263	-0.43075	Nonsignifi	None	2	Molecular	dynamins	3.6.5.5
0.609079	0.112731	-0.7153	Nonsignifi	None	1	Molecular	bis(5'-nucl	3.6.1.17
Inf	0	Inf	Significant up	--	--	--	kinetochor	--
Inf	0	Inf	Significant up		1	Molecular	palmitoyl-	3.1.2.22
0.345539	0.381987	-1.53308	Nonsignifi	None	4	Molecular	large subu	--
1.381748	0.382461	0.466495	Nonsignifi	None	1	Molecular	T-complex	--
1.56019	0.097975	0.641721	Nonsignifi	None	1	Molecular	T-complex	--
4.138748	0.000137	2.049194	Significant up		2	Molecular	annexin A	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
5.70003	2.63E-05	2.51097	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		5	Molecular	phosphatic	3.1.4.11
0.431262	0.025715	-1.21336	Nonsignifi	None	1	Molecular	galactokin	2.7.1.6
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	--	--	--	ubiquitin-	2.3.2.23
Inf	0	Inf	Significant up		1	Cellular	Cc	--
Inf	0	Inf	Significant up		4	Molecular	chloride ct	--
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		6	Molecular	adenylate	4.6.1.1
0.094944	0.060304	-3.39679	Nonsignifi	None	1	Molecular	lumican	--
1.098988	0.130682	0.136175	Nonsignifi	None	3	Molecular	--	--
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	--
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		2	Cellular	Cc transcriptic	--
Inf	0	Inf	Significant up		3	Molecular	DNA mism	--
0.204002	0.019931	-2.29335	Significant down	--	--	--	2-iminobu	3.5.99.10
Inf	0	Inf	Significant up		2	Molecular	hexokinase	2.7.1.1
Inf	0	Inf	Significant up		1	Cellular	Cc ephrin-B	--
#NAME?	0	#NAME?	Significant down		2	Molecular	--	--
Inf	0	Inf	Significant up		2	Molecular	thimet olig	3.4.24.15
2.636797	0.001871	1.398787	Nonsignifi	None	2	Cellular	Cc capping pr	--
Inf	0	Inf	Significant up		5	Molecular	biliverdin r	1.3.1.24
Inf	0	Inf	Significant up	--	--	--	--	--
0.785544	0.334508	-0.34824	Nonsignifi	None	3	Molecular	ATP citrate	2.3.3.8
0.376132	0.426222	-1.41069	Nonsignifi	None	6	Molecular	coatomer	--
0.110444	0.068349	-3.17861	Nonsignifi	None	2	Biological	cathepsin	3.4.14.1
Inf	0	Inf	Significant up		5	Molecular	clathrin he	--
4.949512	7.37E-05	2.307286	Significant up	--	--	--	AP-2 comj	--
Inf	0	Inf	Significant up		4	Molecular	solute carr	--
Inf	0	Inf	Significant up	--	--	--	--	--
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.-
0.505591	0.147329	-0.98396	Nonsignifi	None	--	--	voltage-de	--
0.013871	0.504356	-6.17176	Nonsignifi	None	5	Molecular	tyrosyl-tR	6.1.1.1
Inf	0	Inf	Significant up		2	Biological	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up	--	--	--	5'-AMP-ac	--
3.567048	0.00027	1.834731	Nonsignifi	None	--	--	heat shock	--
Inf	0	Inf	Significant up		2	Molecular	branched-	2.6.1.42

Inf	0	Inf	Significant up		4	Molecular	UV excision	--
Inf	0	Inf	Significant up		3	Molecular	Eph receptor	2.7.10.1
Inf	0	Inf	Significant up		3	Molecular	Eph receptor	2.7.10.1
Inf	0	Inf	Significant up		1	Cellular Cc	--	--
0.154107	0.103753	-2.69799	Nonsignificant	None	1	Cellular Cc	--	--
Inf	0	Inf	Significant up		5	Molecular	solute carrier	--
Inf	0	Inf	Significant up		1	Molecular	uncharacterized	--
Inf	0	Inf	Significant up		1	Molecular	phospholipase	--
0.416646	0.013221	-1.26311	Nonsignificant	None	1	Molecular	transition	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	coagulation	--
Inf	0	Inf	Significant up		2	Molecular	afadin	--
1.035719	0.777436	0.050632	Nonsignificant	None	--	--	adenosine	2.7.1.20
#NAME?	0	#NAME?	Significant down	--	--	--	laminin, beta	--
0.042786	0.036687	-4.54671	Significant down		3	Molecular	cadherin 6	--
0.261642	0.084215	-1.93433	Nonsignificant	None	3	Molecular	cadherin 1	--
0.225629	0.005595	-2.14797	Significant down		3	Molecular	cadherin 1	--
2.176212	0.034773	1.121819	Nonsignificant	None	--	--	small ubiquitin	--
0.878093	0.151611	-0.18755	Nonsignificant	None	1	Molecular	translation	--
Inf	0	Inf	Significant up		4	Molecular	methionyl	6.1.1.10
Inf	0	Inf	Significant up		2	Biological	translation	--
Inf	0	Inf	Significant up		3	Biological	C-terminal	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	ADP-ribosyl	--
Inf	0	Inf	Significant up		1	Molecular	breast cancer	--
Inf	0	Inf	Significant up		1	Molecular	ubiquitin	3.1.3.48
Inf	0	Inf	Significant up	--	--	--	junctional	--
Inf	0	Inf	Significant up		1	Cellular Cc	transmembrane	--
Inf	0	Inf	Significant up		1	Molecular	coronin-7	--
Inf	0	Inf	Significant up	--	--	--	gasdermin	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	guanine nucleotide	--
6.247502	0.003586	2.643279	Significant up		4	Cellular Cc	actin related	--
3.708114	0.000719	1.890686	Nonsignificant	None	1	Cellular Cc	CD81 antigen	--
1.402425	0.108142	0.487924	Nonsignificant	None	2	Molecular	triosephosphate	5.3.1.1
0.527376	0.190711	-0.9231	Nonsignificant	None	1	Molecular	translation	--
Inf	0	Inf	Significant up	--	--	--	protein transport	--
Inf	0	Inf	Significant up		1	Molecular	serine/threonine	3.1.3.16
Inf	0	Inf	Significant up	--	--	--	GABA(A) receptor	--
0.371294	0.012522	-1.42937	Nonsignificant	None	1	Molecular	myosin light chain	--
2.254585	0.000619	1.172862	Nonsignificant	None	--	--	actin beta	--
4.822172	5.45E-05	2.269683	Significant up		2	Molecular	Ras-related	--
2.312943	7.31E-05	1.20973	Nonsignificant	None	2	Molecular	translation	--
1.010902	0.936978	0.015644	Nonsignificant	None	--	--	small subunit	--
0.989624	0.885985	-0.01505	Nonsignificant	None	5	Molecular	20S proteasome	3.4.25.1
Inf	0	Inf	Significant up	--	--	--	calpactin	--
4.369577	0.001122	2.127494	Significant up		2	Molecular	cell division	--
1.734212	0.001644	0.794281	Nonsignificant	None	2	Molecular	destrin (acidic)	--
Inf	0	Inf	Significant up		2	Molecular	--	--
0.029374	0.129236	-5.08929	Nonsignificant	None	4	Molecular	signal receptor	3.6.5.4
2.455781	0.003067	1.296182	Nonsignificant	None	2	Molecular	Ras-related	--
Inf	0	Inf	Significant up		2	Molecular	Ras-related	--
3.325968	0.003341	1.733774	Nonsignificant	None	2	Molecular	Ras-related	--
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-related	--

3.783405	0.002357	1.919685	Nonsignifi	None	--	--	actin-relat	--
Inf	0	Inf	Significant	up	--	--	centractin	--
2.740429	8.17E-05	1.454402	Nonsignifi	None		1 Molecular	ADP-ribos	--
Inf	0	Inf	Significant	up		2 Molecular	ATP-bindii	--
1.392751	0.306434	0.477938	Nonsignifi	None		2 Molecular	Ras-relate	--
0.91774	0.790102	-0.12384	Nonsignifi	None		3 Molecular	small subu	--
Inf	0	Inf	Significant	up		1 Cellular Cc	proteasom	--
0.577792	0.139879	-0.79138	Nonsignifi	None		3 Molecular	large subu	--
0.091347	0.000619	-3.4525	Significant	down		4 Molecular	large subu	--
Inf	0	Inf	Significant	up	--	--	V-type H+	--
Inf	0	Inf	Significant	up		2 Biological	4a-hydrox	4.2.1.96
Inf	0	Inf	Significant	up		2 Molecular	Ras homol	--
Inf	0	Inf	Significant	up		2 Molecular	Rho family	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up		2 Biological	syntaxin-b	--
0.100822	0.055933	-3.31012	Nonsignifi	None	--	--	beta-2-mi	--
Inf	0	Inf	Significant	up	--	--	coatomer	--
Inf	0	Inf	Significant	up	--	--	ubiquitin-f	--
Inf	0	Inf	Significant	up	--	--	AP-1 com	--
Inf	0	Inf	Significant	up		2 Cellular Cc	--	--
0.998161	0.998065	-0.00266	Nonsignifi	None		1 Molecular	heterogen	--
2.528289	0.000124	1.338161	Nonsignifi	None	--	--	14-3-3 pr	--
Inf	0	Inf	Significant	up		2 Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		1 Cellular Cc	tetraspanir	--
1.378372	0.007722	0.462965	Nonsignifi	None		1 Molecular	serine/thre	3.1.3.16
3.224056	0.000242	1.688877	Nonsignifi	None		1 Molecular	calmodulir	--
Inf	0	Inf	Significant	up		1 Molecular	neuronal c	--
1.455229	0.121973	0.541246	Nonsignifi	None		1 Molecular	26S protea	--
0.46839	0.001985	-1.09422	Nonsignifi	None		1 Molecular	26S protea	--
0.601946	0.188788	-0.73229	Nonsignifi	None	--	--	small subu	--
0.42568	0.000212	-1.23216	Nonsignifi	None		3 Molecular	small subu	--
Inf	0	Inf	Significant	up	--	--	ubiquitin-(	2.3.2.23
3.799167	0.001356	1.925683	Nonsignifi	None	--	--	14-3-3 pr	--
0.454856	0.005299	-1.13652	Nonsignifi	None		3 Molecular	small subu	--
0.832317	0.207926	-0.2648	Nonsignifi	None		4 Molecular	small subu	--
0.450835	0.078596	-1.14933	Nonsignifi	None		5 Molecular	small subu	--
0.408762	0.004819	-1.29067	Nonsignifi	None		4 Molecular	small subu	--
0.602615	0.021505	-0.73069	Nonsignifi	None		4 Molecular	small subu	--
Inf	0	Inf	Significant	up	--	--	small nucle	--
Inf	0	Inf	Significant	up	--	--	U6 snRNA	--
0.412342	0.151059	-1.27808	Nonsignifi	None	--	--	small nucle	--
0.147041	0.273824	-2.76571	Nonsignifi	None		2 Molecular	thymosin,	--
6.748328	0.001069	2.75453	Significant	up		1 Molecular	ADP-ribos	--
0.346646	0.202378	-1.52847	Nonsignifi	None		1 Molecular	26S protea	--
0.536197	0.045173	-0.89917	Nonsignifi	None	--	--	large subu	--
Inf	0	Inf	Significant	up		2 Molecular	cellular nu	--
0.316736	0.111873	-1.65865	Nonsignifi	None		1 Molecular	small subu	--
1.647676	0.005279	0.720433	Nonsignifi	None	--	--	actin, aorti	--
Inf	0	Inf	Significant	up		2 Molecular	Ras homol	--
0.485117	0.277075	-1.0436	Nonsignifi	None		3 Molecular	large subu	--
0.282938	0.248642	-1.82144	Nonsignifi	None		4 Molecular	small subu	--
4.606445	0.001406	2.203654	Significant	up	--	--	histone H4	--
1.192077	0.125911	0.253477	Nonsignifi	None		2 Molecular	Ras-relate	--
1.024562	0.917662	0.035008	Nonsignifi	None		2 Molecular	GTP-bindii	--
Inf	0	Inf	Significant	up		3 Molecular	large subu	--
4.000717	0.000284	2.000258	Significant	up		2 Molecular	Ras-relate	--
Inf	0	Inf	Significant	up		3 Molecular	small subu	--
Inf	0	Inf	Significant	up		4 Molecular	small subu	--

0.308653	0.149327	-1.69594	Nonsignifi	None	--	--	small subu	--
0.629707	0.065084	-0.66725	Nonsignifi	None		4 Molecular	small subu	--
1.267947	0.276323	0.342494	Nonsignifi	None		4 Molecular	small subu	--
Inf	0	Inf	Significan	up		1 Molecular	guanine n	--
Inf	0	Inf	Significan	up		1 Molecular	RING-box	--
5.331127	0.003605	2.414441	Significan	up		1 Molecular	guanine n	--
Inf	0	Inf	Significan	up		3 Molecular	large subu	--
0.333671	0.002501	-1.5835	Nonsignifi	None	--	--	large subu	--
0.232509	0.012105	-2.10464	Significan	down		4 Molecular	large subu	--
3.208144	0.000309	1.681739	Nonsignifi	None		3 Biological	peptidyl-p	5.2.1.8
0.34053	0.030264	-1.55415	Nonsignifi	None	--	--	FK506-bin	5.2.1.8
1.624564	0.009101	0.700053	Nonsignifi	None		4 Molecular	small subu	--
Inf	0	Inf	Significan	up		1 Molecular	growth fac	--
0.015017	0.017794	-6.05722	Significan	down		1 Molecular	transforme	--
0.622653	0.508304	-0.6835	Nonsignifi	None		4 Biological	AP-2 com	--
Inf	0	Inf	Significan	up		5 Molecular	guanine n	--
Inf	0	Inf	Significan	up		1 Molecular	serine/thre	--
2.021022	0.015185	1.015085	Nonsignifi	None	--	--	14-3-3 pr	--
Inf	0	Inf	Significan	up	--	--	small ubiq	--
Inf	0	Inf	Significan	up		2 Biological	dynein lig	--
Inf	0	Inf	Significan	up		4 Molecular	large subu	--
Inf	0	Inf	Significan	up		1 Biological	S-phase ki	--
Inf	0	Inf	Significan	up		3 Molecular	guanine n	--
1.112151	0.233694	0.153352	Nonsignifi	None		1 Molecular	guanine n	--
3.996431	0.018376	1.998712	Nonsignifi	None	--	--	actin beta/	--
Inf	0	Inf	Significan	up	--	--	ubiquitin- α	--
1.337253	0.016362	0.419272	Nonsignifi	None		1 Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significan	up		1 Molecular	Y-box-bin	--
0.73859	0.503336	-0.43715	Nonsignifi	None		2 Cellular Cc	casein kin	--
0.419343	0.085424	-1.2538	Nonsignifi	None	--	--	tropomyos	--
Inf	0	Inf	Significan	up	--	--	ubiquitin- α	2.3.2.23
1.156592	0.188439	0.20988	Nonsignifi	None		1 Molecular	elongation	--
0.1586	0.098223	-2.65654	Nonsignifi	None		1 Molecular	tubulin alp	--
0.052107	0.078348	-4.26239	Nonsignifi	None		1 Molecular	tubulin alp	--
0.399708	0.156558	-1.32298	Nonsignifi	None		1 Molecular	tubulin bet	--
0.931596	0.79516	-0.10222	Nonsignifi	None		3 Molecular	casein kin	2.7.11.1
Inf	0	Inf	Significan	up	--	--	platelet-ac	3.1.1.47
Inf	0	Inf	Significan	up		1 Molecular	histone H3	--
0.147139	3.57E-05	-2.76475	Significan	down		2 Molecular	hemoglob	--
0.151096	8.31E-06	-2.72646	Significan	down		2 Molecular	hemoglob	--
Inf	0	Inf	Significan	up	--	--	coxsackiev	--
Inf	0	Inf	Significan	up	--	--	signal-reg	--
Inf	0	Inf	Significan	up		2 Molecular	translation	--
Inf	0	Inf	Significan	up		2 Molecular	1-phosph	2.7.1.149
0.701615	0.007813	-0.51125	Nonsignifi	None		1 Molecular	T-complex	--
Inf	0	Inf	Significan	up	--	--	reelin	3.4.21.-
0.031914	0.095371	-4.96966	Nonsignifi	None		7 Molecular	DNA-depe	2.7.11.1
Inf	0	Inf	Significan	up	--	--	disintegrin	3.4.24.86
1.020142	0.905196	0.028771	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significan	up	--	--	interleukin	--
#NAME?	0	#NAME?	Significan	down		3 Cellular Cc	C-X-C mo	--
3.089148	0.019334	1.627209	Nonsignifi	None	--	--	brain acid	--
0.485166	0.258401	-1.04345	Nonsignifi	None	--	--	large subu	--
Inf	0	Inf	Significan	up		1 Cellular Cc	mothers a	--
Inf	0	Inf	Significan	up		1 Molecular	ADP-ribos	--
Inf	0	Inf	Significan	up		3 Biological	--	--
19.29993	0.000165	4.270524	Significan	up		2 Molecular	Ras homol	--
0.084977	0.354672	-3.55678	Nonsignifi	None		4 Molecular	large subu	--

0.195224	0.000117	-2.3568	Significant down		1 Molecular splicing fac --
Inf	0	Inf	Significant up	--	-- --
Inf	0	Inf	Significant up		2 Molecular fibulin 1/2 --
Inf	0	Inf	Significant up		2 Molecular very low-d --
0.402345	0.023671	-1.31349	Nonsignifi		1 Molecular heparan su --
Inf	0	Inf	Significant up		1 Cellular Cc ephrin-B --
Inf	0	Inf	Significant up		2 Molecular Ca2+-tran 3.6.3.8
0.022767	0.061165	-5.45693	Nonsignifi		2 Molecular phospholi 3.6.3.1
Inf	0	Inf	Significant up		2 Molecular phospholi 3.6.3.1
Inf	0	Inf	Significant up		2 Molecular cytochrom --
Inf	0	Inf	Significant up		1 Molecular 55 kDa ery --
Inf	0	Inf	Significant up		2 Cellular Cc -- --
Inf	0	Inf	Significant up		2 Molecular S-adenosy 2.5.1.6
Inf	0	Inf	Significant up		1 Molecular -- --
Inf	0	Inf	Significant up		3 Molecular cyclin-dep 2.7.11.22
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
Inf	0	Inf	Significant up	--	-- transcriptic --
1.377046	0.024994	0.461576	Nonsignifi		5 Molecular clathrin he --
Inf	0	Inf	Significant up	--	-- FK506-bin 5.2.1.8
Inf	0	Inf	Significant up		1 Biological L-itol 2- 1.1.1.14
4.024948	0.036725	2.00897	Significant up		1 Molecular spectrin be --
0.243538	0.227955	-2.03778	Nonsignifi		2 Cellular Cc template- 1 --
0.180016	0.153957	-2.4738	Nonsignifi		1 Molecular splicing fac --
0.579525	0.004173	-0.78706	Nonsignifi		1 Molecular AMP dearr 3.5.4.6
1.114069	0.666171	0.155839	Nonsignifi	--	-- fatty acid- --
2.032171	0.000382	1.023022	Nonsignifi		2 Molecular adenylyl cy --
Inf	0	Inf	Significant up		2 Molecular hydroxyme 2.3.3.10
1.999429	0.015625	0.999588	Nonsignifi		2 Biological interferon --
Inf	0	Inf	Significant up		2 Biological interferon --
Inf	0	Inf	Significant up		3 Biological solute carr --
1.012822	0.866363	0.018381	Nonsignifi		2 Molecular 6-phosphoc 2.7.1.11
Inf	0	Inf	Significant up		7 Molecular phosphatic 3.1.4.11
Inf	0	Inf	Significant up		3 Molecular receptor ty 2.7.10.1
Inf	0	Inf	Significant up		4 Molecular kinesin fan --
Inf	0	Inf	Significant up		1 Molecular FK506-bin 5.2.1.8
0.044679	0.003619	-4.48424	Significant down		2 Molecular procollage 1.14.11.4
0.057037	0.015309	-4.13195	Significant down		1 Molecular nucleobinc --
0.335999	0.360409	-1.57347	Nonsignifi		4 Molecular large subu --
Inf	0	Inf	Significant up		5 Molecular DNA topoi 5.99.1.3
Inf	0	Inf	Significant up		2 Biological A-kinase a --
Inf	0	Inf	Significant up		5 Molecular guanine nt --
Inf	0	Inf	Significant up		1 Biological caveolin 1 --
Inf	0	Inf	Significant up		2 Cellular Cc tumor necr --
0.015902	0.041826	-5.97462	Significant down		4 Cellular Cc peroxisom --
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 transcriptic --
Inf	0	Inf	Significant up		3 Molecular 1,4-alpha- 2.4.1.18
Inf	0	Inf	Significant up		2 Molecular translation --
0.281723	0.059956	-1.82765	Nonsignifi		4 Molecular hepatocyte 3.4.21.-
Inf	0	Inf	Significant up		5 Molecular activin rec 2.7.11.30
2.666283	0.00454	1.41483	Nonsignifi	--	-- 14-3-3 prc --
Inf	0	Inf	Significant up		2 Molecular dynamin G 3.6.5.5
Inf	0	Inf	Significant up		6 Molecular focal adhe 2.7.10.2
0.305121	0.009079	-1.71255	Nonsignifi		1 Molecular splicing fac --
Inf	0	Inf	Significant up		1 Molecular elongation --
Inf	0	Inf	Significant up		5 Molecular novel prot 2.7.11.13

0.168166	0.028126	-2.57204	Significant down		2 Molecular	--	--
Inf	0	Inf	Significant up		2 Molecular	tyrosine-p	3.1.3.48
0.019696	0.026451	-5.66598	Significant down		1 Biological	amidopho	2.4.2.14
0.178311	0.31059	-2.48753	Nonsignifi	None	2 Biological	glucosami	2.6.1.16
Inf	0	Inf	Significant up	--	--	exosome c	--
4.675188	0.002472	2.225024	Significant up		1 Cellular	Cc proteasom	--
Inf	0	Inf	Significant up		3 Molecular	TYRO3 prc	2.7.10.1
Inf	0	Inf	Significant up		3 Molecular	amyloid-lil	--
0.132706	0.035039	-2.9137	Significant down		1 Molecular	fibromodu	--
0.482926	0.097298	-1.05013	Nonsignifi	None	4 Molecular	peroxiredc	1.11.1.15
0.542846	0.148557	-0.88139	Nonsignifi	None	--	large subu	--
Inf	0	Inf	Significant up		1 Cellular	Cc compleme	--
Inf	0	Inf	Significant up	--	--	cytoskeletc	--
Inf	0	Inf	Significant up		1 Molecular	tight juncti	--
Inf	0	Inf	Significant up		1 Molecular	butyrate re	--
Inf	0	Inf	Significant up		1 Molecular	sperm-ass	--
Inf	0	Inf	Significant up		1 Biological	apoptosis	--
1.098258	0.147689	0.135217	Nonsignifi	None	2 Molecular	low-densit	--
Inf	0	Inf	Significant up		1 Molecular	splicing fac	--
Inf	0	Inf	Significant up		1 Biological	Rho GTPas	--
Inf	0	Inf	Significant up		1 Molecular	splicing fac	--
Inf	0	Inf	Significant up		1 Molecular	serine/thre	3.1.3.16
Inf	0	Inf	Significant up		1 Biological	NADPH2:q	1.6.5.5
Inf	0	Inf	Significant up		3 Molecular	solute carr	--
0.079844	0.053793	-3.64667	Nonsignifi	None	2 Molecular	galectin-3	--
0.291201	0.137695	-1.77991	Nonsignifi	None	1 Molecular	lactadherir	--
0.148378	0.076224	-2.75265	Nonsignifi	None	4 Molecular	sparc/oste	--
Inf	0	Inf	Significant up	--	--	CD47 antiç	--
Inf	0	Inf	Significant up		4 Biological	peptidyl-p	5.2.1.8
Inf	0	Inf	Significant up	--	--	vacuole m	--
Inf	0	Inf	Significant up		1 Molecular	tRNA (cytc	2.1.1.203
8.085578	0.000608	3.015351	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
0.021239	0.278617	-5.55715	Nonsignifi	None	4 Cellular	Cc alpha-1,6-	2.4.1.143
0.193725	0.009368	-2.36792	Significant down	--	--	polypeptid	2.4.1.41
0.765602	0.581413	-0.38533	Nonsignifi	None	4 Biological	AP-1 com	--
0.615701	0.02477	-0.6997	Nonsignifi	None	1 Molecular	--	--
Inf	0	Inf	Significant up		2 Biological	secernin	--
Inf	0	Inf	Significant up		1 Cellular	Cc WASH con	--
Inf	0	Inf	Significant up		3 Molecular	U3 small n	--
Inf	0	Inf	Significant up		5 Molecular	potassium	--
Inf	0	Inf	Significant up		2 Molecular	twinfilin	--
0.080034	0.055159	-3.64325	Nonsignifi	None	1 Molecular	EGF-conta	--
0.057342	0.070612	-4.12428	Nonsignifi	None	1 Molecular	--	--
Inf	0	Inf	Significant up		2 Molecular	syntaxin 4	--
0.112549	0.069732	-3.15138	Nonsignifi	None	1 Molecular	contactin 1	--
Inf	0	Inf	Significant up	--	--	splicing fac	--
0.20019	1.03E-06	-2.32056	Significant down		2 Biological	fibroblast	3.4.21.-
Inf	0	Inf	Significant up		1 Molecular	aminoacyl	--
Inf	0	Inf	Significant up	--	--	interleukin	--
Inf	0	Inf	Significant up	--	--	interleukin	--
0.184306	0.03048	-2.43982	Significant down		1 Cellular	Cc lectin, mar	--
Inf	0	Inf	Significant up		3 Molecular	receptor-t	3.1.3.48
Inf	0	Inf	Significant up		3 Molecular	tyrosine-p	--
Inf	0	Inf	Significant up		1 Molecular	epidermal	--
1.80408	0.000346	0.851263	Nonsignifi	None	4 Molecular	TNF recept	--
Inf	0	Inf	Significant up		1 Molecular	disks large	--
Inf	0	Inf	Significant up		4 Molecular	myosin I	--

Inf		0	Inf	Significant up		2	Molecular	protein tyr	3.1.3.48
Inf		0	Inf	Significant up		4	Molecular	active bre	--
Inf		0	Inf	Significant up	--	--	--	anaphase-	--
Inf		0	Inf	Significant up		4	Molecular	serine/thre	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		3	Molecular	--	--
0.158848	0.015772	-2.65428		Significant down		2	Molecular	platelet-ac	3.1.1.47
0.067589	0.005146	-3.88707		Significant down		2	Cellular Cc	--	--
Inf		0	Inf	Significant up		3	Molecular	ubiquitin c	3.4.19.12
Inf		0	Inf	Significant up		3	Molecular	5'-AMP-ac	2.7.11.11
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up	--	--	--	aminoacyl	--
Inf		0	Inf	Significant up		4	Molecular	peroxiredc	1.11.1.15
0.154975	0.052739	-2.68989		Nonsignifi	None	4	Molecular	mitogen-a	2.7.12.2
Inf		0	Inf	Significant up		3	Molecular	p21-activa	2.7.11.1
1.197774	0.450927	0.260356		Nonsignifi	None	--	--	26S protea	--
Inf		0	Inf	Significant up		1	Molecular	splicing fac	--
Inf		0	Inf	Significant up	--	--	--	noggin	--
Inf		0	Inf	Significant up	--	--	--	mitotic spi	--
Inf		0	Inf	Significant up		3	Molecular	tripartite r	2.3.2.27
Inf		0	Inf	Significant up		2	Molecular	syntaxin 1f	--
Inf		0	Inf	Significant up		3	Molecular	--	--
1.022115	0.920543	0.031558		Nonsignifi	None	2	Molecular	PTK7 prote	2.7.10.1
Inf		0	Inf	Significant up		1	Biological	growth fac	--
Inf		0	Inf	Significant up		1	Molecular	--	--
0.615841	0.031966	-0.69937		Nonsignifi	None	1	Molecular	translation	--
Inf		0	Inf	Significant up		3	Molecular	dynein int	--
0.578618	0.286463	-0.78932		Nonsignifi	None	2	Molecular	integrin-lir	2.7.11.1
Inf		0	Inf	Significant up		4	Cellular Cc	solute carr	--
Inf		0	Inf	Significant up	--	--	--	--	--
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		1	Molecular	phosphatic	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		2	Molecular	sequestosc	--
0.07781	0.126122	-3.6839		Nonsignifi	None	1	Molecular	tubulin bet	--
Inf		0	Inf	Significant up		2	Molecular	peptidyl-p	5.2.1.8
Inf		0	Inf	Significant up		3	Molecular	serine/thre	2.7.11.1
Inf		0	Inf	Significant up	--	--	--	histone de	3.5.1.98
Inf		0	Inf	Significant up		5	Molecular	calcium/ca	2.7.11.17
Inf		0	Inf	Significant up	--	--	--	dynactin 2	--
Inf		0	Inf	Significant up		2	Molecular	Ras GTPas	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		2	Biological	cullin 1	--
Inf		0	Inf	Significant up		2	Biological	cullin 2	--
Inf		0	Inf	Significant up		2	Biological	cullin 3	--
Inf		0	Inf	Significant up		2	Biological	cullin 4	--
Inf		0	Inf	Significant up		1	Molecular	apoptosis-	--
Inf		0	Inf	Significant up		2	Molecular	GDP-L-fuc	1.1.1.271
Inf		0	Inf	Significant up		2	Molecular	Ras-relate	--
0.654629	0.004034	-0.61125		Nonsignifi	None	2	Molecular	Ras-relate	--
Inf		0	Inf	Significant up		1	Molecular	--	--
0.298252	0.143436	-1.74539		Nonsignifi	None	1	Molecular	four and a	--
Inf		0	Inf	Significant up		1	Biological	Ras and R	--
Inf		0	Inf	Significant up		1	Molecular	--	--
0.617718	0.504228	-0.69498		Nonsignifi	None	--	--	activated l	--

0.44316	0.000695	-1.1741	Nonsignifi	None		1 Molecular	tubulin alp	--
0.107095	0.008503	-3.22303	Significant	down		7 Molecular	ectonuclec	3.1.4.39
Inf	0	Inf	Significant	up		2 Molecular	ATP-depei	3.6.4.13
Inf	0	Inf	Significant	up		2 Molecular	bleomycin	3.4.22.40
Inf	0	Inf	Significant	up		5 Molecular	bone morp	2.7.11.30
Inf	0	Inf	Significant	up		1 Molecular	--	--
Inf	0	Inf	Significant	up	--	--	essential n	--
Inf	0	Inf	Significant	up	--	--	cytoskeletc	--
0.937991	0.852031	-0.09235	Nonsignifi	None		2 Molecular	--	--
0.505927	0.179081	-0.983	Nonsignifi	None		1 Molecular	heterogen	--
Inf	0	Inf	Significant	up		1 Cellular Cc	lysosome r	--
0.135144	0.024406	-2.88743	Significant	down		2 Molecular	nidogen (e	--
Inf	0	Inf	Significant	up		2 Biological	dystroglyc	--
Inf	0	Inf	Significant	up		3 Molecular	desmoglei	--
Inf	0	Inf	Significant	up		1 Molecular	septin 6/8/	--
Inf	0	Inf	Significant	up		1 Molecular	kelch-like	--
0.009886	0.212446	-6.66044	Nonsignifi	None		1 Molecular	translation	--
Inf	0	Inf	Significant	up		3 Molecular	Rho guanin	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up		1 Molecular	protein scr	--
Inf	0	Inf	Significant	up		1 Biological	tubulin--ty	--
Inf	0	Inf	Significant	up		1 Molecular	--	--
Inf	0	Inf	Significant	up		1 Molecular	dedicator c	--
Inf	0	Inf	Significant	up		1 Molecular	four and a	--
Inf	0	Inf	Significant	up		1 Molecular	--	--
Inf	0	Inf	Significant	up	--	--	dynactin 1	--
0.828402	0.523698	-0.2716	Nonsignifi	None		5 Molecular	dynein hec	--
Inf	0	Inf	Significant	up		2 Molecular	translation	--
Inf	0	Inf	Significant	up		1 Molecular	cortactin	--
2.692742	0.004008	1.429076	Nonsignifi	None	--	--	flotillin	--
Inf	0	Inf	Significant	up		1 Molecular	tripartite r	2.3.2.27
0.86075	0.628755	-0.21633	Nonsignifi	None		6 Molecular	focal adhe	2.7.10.2
Inf	0	Inf	Significant	up		1 Molecular	filamin	--
1.60209	0.55382	0.679955	Nonsignifi	None		5 Molecular	guanine nu	--
Inf	0	Inf	Significant	up	--	--	UDP-glucc	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	--
0.660498	0.460972	-0.59837	Nonsignifi	None		4 Molecular	--	--
Inf	0	Inf	Significant	up		4 Molecular	protocadh	--
1.876915	9.08E-06	0.908364	Nonsignifi	None		3 Molecular	hyaluronar	3.4.21.-
Inf	0	Inf	Significant	up		3 Molecular	DNA replic	3.6.4.12
0.184514	0.000558	-2.4382	Significant	down		2 Molecular	--	--
Inf	0	Inf	Significant	up	--	--	interleukin	--
Inf	0	Inf	Significant	up	--	--	inositol-1,3	3.1.3.56
0.217704	0.51376	-2.19956	Nonsignifi	None		3 Molecular	Ras GTPas	--
Inf	0	Inf	Significant	up		2 Molecular	plastin-1	--
Inf	0	Inf	Significant	up		1 Molecular	mediator c	--
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up		4 Molecular	structural r	--
0.20735	0.017084	-2.26986	Significant	down		1 Biological	alpha 1,3-	3.2.1.84
Inf	0	Inf	Significant	up	--	--	--	--
Inf	0	Inf	Significant	up		2 Molecular	membrane	3.4.21.112
Inf	0	Inf	Significant	up		1 Cellular Cc	sarcospan	--
Inf	0	Inf	Significant	up		3 Cellular Cc	serine/thre	--
0.174196	1.61E-05	-2.52121	Significant	down	--	--	major vaul	--
#NAME?	0	#NAME?	Significant	down		1 Molecular	latent tran	--
Inf	0	Inf	Significant	up		2 Molecular	--	--

3.772262	0.000218	1.91543	Nonsignifi	None		2 Biological	importin st	--
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 Molecular	type II ker	--
Inf	0	Inf	Significant up			2 Cellular Cc	condensin	--
0.709672	0.115993	-0.49478	Nonsignifi	None		1 Molecular	26S protea	--
Inf	0	Inf	Significant up			1 Cellular Cc	lysosomal-	--
Inf	0	Inf	Significant up	--		--	condensin	--
Inf	0	Inf	Significant up	--		--	--	--
Inf	0	Inf	Significant up			1 Molecular	116 kDa U	--
Inf	0	Inf	Significant up			1 Molecular	sorting ne	--
Inf	0	Inf	Significant up			3 Molecular	Rho guanin	--
Inf	0	Inf	Significant up			1 Molecular	--	--
Inf	0	Inf	Significant up			1 Molecular	Arf-GAP w	--
0.080473	0.010923	-3.63536	Significant down	--		--	--	--
Inf	0	Inf	Significant up			1 Biological	protein dis	5.3.4.1
0.633679	0.033443	-0.65818	Nonsignifi	None	--	--	platelet-ac	3.1.1.47
0.005926	0.004859	-7.39868	Significant down	--		--	--	--
Inf	0	Inf	Significant up			2 Molecular	--	--
Inf	0	Inf	Significant up			1 Biological	phosphogl	--
Inf	0	Inf	Significant up			3 Cellular Cc	serine/thre	--
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	--
1.373423	0.203875	0.457776	Nonsignifi	None		2 Molecular	Ras-relate	--
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
1.637227	0.0094	0.711254	Nonsignifi	None		1 Molecular	poly(rC)-b	--
0.64162	0.192129	-0.64021	Nonsignifi	None		1 Molecular	poly(rC)-b	--
Inf	0	Inf	Significant up			1 Biological	transcripti	--
Inf	0	Inf	Significant up			2 Molecular	Ras homol	--
0.159608	0.10924	-2.64739	Nonsignifi	None		3 Molecular	--	--
Inf	0	Inf	Significant up			2 Molecular	splicing fac	--
1.629143	0.013605	0.704114	Nonsignifi	None		1 Molecular	--	--
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	--
Inf	0	Inf	Significant up			4 Biological	protein tra	--
0.097305	0.024378	-3.36135	Significant down	--		--	gluconolac	3.1.1.17
0.240974	0.02459	-2.05305	Significant down			2 Molecular	microtubul	--
0.07304	0.012533	-3.77517	Significant down	--		--	transformii	--
Inf	0	Inf	Significant up			1 Molecular	Na(+)/H(+)	--
Inf	0	Inf	Significant up			1 Molecular	--	--
Inf	0	Inf	Significant up			1 Molecular	thyroid ho	--
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	tyrosine-p	3.1.3.48
Inf	0	Inf	Significant up			2 Molecular	microtubul	--
Inf	0	Inf	Significant up			1 Molecular	ELAV-like	--
Inf	0	Inf	Significant up			2 Molecular	E3 ubiquiti	2.3.2.26

5.538883	2.51E-05	2.469595	Significant up		2 Molecular solute carr --
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-c --
Inf		0 Inf	Significant up		2 Cellular Cc vesicle-ass --
4.98551	0.000623	2.317741	Significant up		2 Molecular Ras-relate --
Inf		0 Inf	Significant up		1 Molecular zyxin --
Inf		0 Inf	Significant up		2 Cellular Cc 26S protea --
Inf		0 Inf	Significant up		2 Biological -- --
0.022182	0.037484	-5.49446	Significant down		4 Biological -- --
0.009393	0.001739	-6.73413	Significant down		5 Molecular laminin, al --
0.322516	0.000127	-1.63256	Nonsignifi None		3 Biological -- --
0.20587	0.173572	-2.28019	Nonsignifi None		1 Biological 26S protea --
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 divisio --
0.631577	0.019907	-0.66297	Nonsignifi None		1 Molecular dihydropy --
Inf		0 Inf	Significant up		1 Cellular Cc -- --
Inf		0 Inf	Significant up		1 Molecular histone-bi --
0.07348	0.017761	-3.7665	Significant down		2 Cellular Cc -- --
Inf		0 Inf	Significant up		1 Cellular Cc occludin --
Inf		0 Inf	Significant up		4 Molecular survival m --
Inf		0 Inf	Significant up		2 Molecular -- --
5.535317	6.74E-05	2.468666	Significant up		1 Molecular fascin 1/2 --
0.098398	0.037417	-3.34523	Significant down	--	-- melanoma --
Inf		0 Inf	Significant up	--	-- kynurenine 3.7.1.3
Inf		0 Inf	Significant up	--	-- ceramide c 2.4.1.80
Inf		0 Inf	Significant up	--	-- guanylate 2.7.4.8
Inf		0 Inf	Significant up	--	-- hydroxyac 3.1.2.6
Inf		0 Inf	Significant up		2 Molecular discoidin c 2.7.10.1
Inf		0 Inf	Significant up		2 Biological UTP--gluc 2.7.7.9
0.155528	0.047226	-2.68475	Significant down		5 Molecular primary-ar 1.4.3.21
Inf		0 Inf	Significant up		5 Molecular thioredoxii 1.8.1.9
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		1 Biological -- --
Inf		0 Inf	Significant up		3 Molecular AP2-assoc 2.7.11.1
0.887208	0.64432	-0.17265	Nonsignifi None		2 Biological major histc --
0.162422	0.117945	-2.62218	Nonsignifi None		2 Molecular leucine prc --
Inf		0 Inf	Significant up		1 Molecular echinoderr --
0.128193	0.085968	-2.96361	Nonsignifi None		4 Biological formyltetr 1.5.1.6
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	--	-- protein FA --
Inf		0 Inf	Significant up	--	-- centrosom --
Inf		0 Inf	Significant up	--	-- -- --
Inf		0 Inf	Significant up	--	-- -- --
0.410019	0.01865	-1.28624	Nonsignifi None	--	-- phospholip 3.1.1.-
Inf		0 Inf	Significant up	--	-- pyrroline-1.5.1.2
2.9779	0.090117	1.574296	Nonsignifi None	--	-- -- --

Inf	0	Inf	Significant up		4	Molecular	molecular	--
2.190134	0.00012	1.131019	Nonsignifi	None	4	Molecular	molecular	--
Inf	0	Inf	Significant up		1	Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up	--	--	--	serine/thre	--
Inf	0	Inf	Significant up		3	Biological	meckelin	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	dedicator c	--
Inf	0	Inf	Significant up	--	--	--	collectin st	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		2	Cellular Cc	--	--
Inf	0	Inf	Significant up		4	Cellular Cc	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	coiled-coil	--
0.01544	0.086479	-6.01718	Nonsignifi	None	--	--	FK506-bin	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Molecular	E3 ubiquiti	2.3.2.26
0.538907	0.319086	-0.89189	Nonsignifi	None	1	Molecular	E3 ubiquiti	2.3.2.27
Inf	0	Inf	Significant up		1	Molecular	syntaxin-b	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	collagen, t	--
0.11379	0.444444	-3.13555	Nonsignifi	None	--	--	--	--
3.120877	0.001657	1.641952	Nonsignifi	None	1	Molecular	histone H3	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
0.032749	0.056223	-4.93239	Nonsignifi	None	1	Cellular Cc	myomegal	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	ubiquitin t	3.1.2.-
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Cellular Cc	--	--
Inf	0	Inf	Significant up		1	Molecular	phospholiç	--
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	--	--
Inf	0	Inf	Significant up	--	--	--	immune cc	--
Inf	0	Inf	Significant up	--	--	--	metallored	1.16.1.-
Inf	0	Inf	Significant up	--	--	--	TBC1 dom	--
Inf	0	Inf	Significant up		1	Molecular	tensin	--
Inf	0	Inf	Significant up		2	Molecular	natural cyt	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	Rho GTPas	--
0.130345	0.065392	-2.9396	Nonsignifi	None	2	Molecular	atlastin	3.6.5.-
Inf	0	Inf	Significant up		1	Molecular	leucine-ric	--
Inf	0	Inf	Significant up		5	Cellular Cc	--	--
Inf	0	Inf	Significant up		2	Molecular	OTU domz	3.4.19.12
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	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	phostensir	--
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	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	metal trans	--
Inf	0	Inf	Significant up		5	Molecular	protein kin	2.7.11.13
0.012644	0.052618	-6.30546	Nonsignifi	None	--	--	integrator	--
Inf	0	Inf	Significant up		4	Molecular	--	--

Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	rapamycin	--
Inf	0	Inf	Significant up		1 Biological	--	--
Inf	0	Inf	Significant up		1 Molecular	E3 ubiquiti	2.3.2.27
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	dynamins	--
0.208832	0.026475	-2.25958	Significant down		3 Molecular	CD109 ant	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	1 Biological	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	integrator	--
0.113708	0.00037	-3.13659	Significant down		2 Molecular	a disintegr	3.4.24.87
Inf	0	Inf	Significant up		1 Molecular	butyrophili	--
0.089019	0.022458	-3.48974	Significant down		2 Molecular	transcripti	--
Inf	0	Inf	Significant up	--	--	staphylocc	--
Inf	0	Inf	Significant up		3 Molecular	MAP/micr	2.7.11.1
Inf	0	Inf	Significant up		3 Cellular Cc	MFS transp	--
Inf	0	Inf	Significant up		2 Molecular	Ras homol	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		1 Biological	BTB/POZ c	--
Inf	0	Inf	Significant up		3 Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		1 Molecular	translation	--
8.525487	0.000363	3.091782	Significant up	--	--	cytoplasmic	--
Inf	0	Inf	Significant up		3 Molecular	thousand t	2.7.11.1
Inf	0	Inf	Significant up		1 Biological	charged m	--
0.401753	0.11935	-1.31562	Nonsignifi	None	4 Molecular	RAS guany	--
Inf	0	Inf	Significant up	--	--	PHD finger	--
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
1.007506	0.995737	0.010788	Nonsignifi	None	1 Cellular Cc	--	--
Inf	0	Inf	Significant up	--	--	autophagy	--
0.005528	0.020577	-7.49901	Significant down	--	--	--	--
0.084683	0.037259	-3.56178	Significant down		3 Molecular	myosin he	--
Inf	0	Inf	Significant up	--	--	CLIP-assoc	--
Inf	0	Inf	Significant up		1 Molecular	low-densit	--
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		1 Molecular	Rab9 effec	--
0.002441	0.094084	-8.67815	Nonsignifi	None	1 Molecular	E3 ubiquiti	2.3.2.26
Inf	0	Inf	Significant up	--	--	centriolin	--
Inf	0	Inf	Significant up		2 Biological	--	--
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	tetratricop	--
0.219554	0.010261	-2.18735	Significant down	--	--	--	--
0.391315	0.057677	-1.3536	Nonsignifi	None	--	kinectin	--
Inf	0	Inf	Significant up	--	--	--	--
0.548875	0.019396	-0.86545	Nonsignifi	None	--	kindlin 3	--

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	--	--
0.39206	0.004521	-1.35086		Nonsignifi	None	--	--	cullin-assc	--
Inf		0	Inf	Significant up		1	Molecular THO comp	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		2	Biological type I prot	2.1.1.319	
Inf		0	Inf	Significant up		2	Molecular E3 ubiquiti	2.3.2.27	
Inf		0	Inf	Significant up		1	Molecular syntaxin 1	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--
5.090843	3.11E-05	2.347904		Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		1	Biological	--	--
0.211428	0.000732	-2.24176		Significant down	--	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
0.079775	0.011217	-3.64792		Significant down		3	Molecular adipocyte	--	--
Inf		0	Inf	Significant up		1	Molecular phospholip	3.1.4.4	
Inf		0	Inf	Significant up	--	--	LIX1-like p	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
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 GTPas	--	--
Inf		0	Inf	Significant up		2	Molecular mitochondr	3.6.5.-	
Inf		0	Inf	Significant up	--	--	protein FA	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		1	Biological serine/argi	--	--
Inf		0	Inf	Significant up	--	--	exocyst co	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--
Inf		0	Inf	Significant up		2	Molecular katanin p6	3.6.4.3	
Inf		0	Inf	Significant up	--	--	ankyrin re	--	--
Inf		0	Inf	Significant up	--	--	phosphata	--	--
0.354155	0.00227	-1.49755		Nonsignifi	None	3	Biological	--	--
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up	--	--	proline-, g	--	--
Inf		0	Inf	Significant up		2	Molecular	--	--
Inf		0	Inf	Significant up	--	--	spartin	--	--
0.065738	0.21901	-3.92713		Nonsignifi	None	--	--	2,3-bisphc	5.4.2.11
Inf		0	Inf	Significant up		2	Cellular Cc nuclear po	--	--
Inf		0	Inf	Significant up		3	Molecular	--	--
0.13856	0.027925	-2.85142		Significant down		2	Molecular type II ker	--	--
Inf		0	Inf	Significant up		1	Biological Rho GTPas	--	--
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 p	--	--
Inf		0	Inf	Significant up	--	--	transmem	--	--
Inf		0	Inf	Significant up		1	Molecular secreted fr	--	--
Inf		0	Inf	Significant up		3	Molecular misshapen	2.7.11.1	
Inf		0	Inf	Significant up	--	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular	--	--

Inf		0	Inf	Significant up	--	--	--	--
0.050499	0.048384	-4.30759		Significant down	--	--	cyclic GMF	2.7.7.86
Inf		0	Inf	Significant up	--	--	enabled	--
Inf		0	Inf	Significant up		1	Molecular	--
Inf		0	Inf	Significant up		2	Molecular	phospholip
Inf		0	Inf	Significant up		1	Molecular	AAA family
Inf		0	Inf	Significant up		1	Molecular	--
0.080032	0.051166	-3.64328		Nonsignifi	--	--	--	--
Inf		0	Inf	Significant up		2	Biological	--
Inf		0	Inf	Significant up		1	Cellular Cc	--
0.110768	0.022098	-3.17439		Significant down		1	Biological	thioredoxin
Inf		0	Inf	Significant up	--	--	solute carr	--
Inf		0	Inf	Significant up		2	Molecular	E3 ubiquitin
Inf		0	Inf	Significant up	--	--	plasminog	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		2	Molecular	dermatan
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-binding
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		4	Biological	solute carr
Inf		0	Inf	Significant up		4	Molecular	ubiquitin c
Inf		0	Inf	Significant up		1	Molecular	nuclear po
Inf		0	Inf	Significant up	--	--	nuclear po	--
Inf		0	Inf	Significant up		3	Molecular	G protein-
Inf		0	Inf	Significant up	--	--	metallored	1.16.1.-
4.32364	0.004875	2.112246		Significant up		1	Cellular Cc	tetraspanin
0.227531	0.002651	-2.13587		Significant down	--	--	--	--
Inf		0	Inf	Significant up	--	--	THO comp	--
0.072673	0.060584	-3.78244		Nonsignifi		1	Molecular	InaD-like p
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 pro	--
0.352876	0.40084	-1.50277		Nonsignifi	--	--	erythrocyte	--
Inf		0	Inf	Significant up	--	--	--	--
0.62786	0.092758	-0.67149		Nonsignifi		1	Biological	solute carr
Inf		0	Inf	Significant up	--	--	--	--
0.443508	0.405599	-1.17297		Nonsignifi	--	--	--	--
Inf		0	Inf	Significant up	--	--	integrin al	--
Inf		0	Inf	Significant up		1	Biological	SH3KBP1-
Inf		0	Inf	Significant up		4	Molecular	ubiquitin-
Inf		0	Inf	Significant up	--	--	prostamid	1.11.1.20
Inf		0	Inf	Significant up		2	Molecular	1-phospho
Inf		0	Inf	Significant up		1	Molecular	--
Inf		0	Inf	Significant up	--	--	retinol deh	1.1.1.300
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		2	Molecular	signal pep
Inf		0	Inf	Significant up		2	Molecular	minor hist
Inf		0	Inf	Significant up		3	Molecular	phosphatic
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		3	Molecular	NIMA (nev
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	F-actin mc	1.14.13.22!
Inf	0	Inf	Significant up		1	Molecular	gem assoc	--
Inf	0	Inf	Significant up		1	Molecular	partitionin	--
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		1	Molecular	fibroblast c	--
0.088986	0.005432	-3.49028	Significant down	--	--	--	cell migrat	3.2.1.35
5.87789	0.000135	2.555298	Significant up		1	Molecular	programm	--
Inf	0	Inf	Significant up		3	Molecular	solute carr	--
Inf	0	Inf	Significant up	--	--	--	chromosom	--
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	--	--	--	--	--
Inf	0	Inf	Significant up		2	Biological	sec1 family	--
Inf	0	Inf	Significant up		1	Molecular	ubiquitin-l	3.1.3.16
1.325004	0.013531	0.405996	Nonsignifi	--	--	--	intelectin	--
Inf	0	Inf	Significant up		2	Molecular	F-box prot	--
0.588772	0.576744	-0.76422	Nonsignifi	--	--	--	solute carr	--
Inf	0	Inf	Significant up		3	Molecular	Arf-GAP w	--
2.015269	0.010571	1.010972	Nonsignifi	--	--	--	intelectin	--
0.140986	0.072181	-2.82638	Nonsignifi		2	Molecular	ATP-bindin	--
0.302006	0.03069	-1.72735	Nonsignifi	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	ATR intera	--
0.007914	0.01402	-6.98142	Significant down	--	--	--	stonin-1/2	--
Inf	0	Inf	Significant up	--	--	--	beta-cater	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.240145	0.110452	-2.05802	Nonsignifi		3	Molecular	ATP-depei	3.6.4.13
0.162774	0.245623	-2.61906	Nonsignifi	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	proteasom	--
Inf	0	Inf	Significant up		3	Biological	solute carr	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	golgi-spec	--
0.449261	0.227017	-1.15437	Nonsignifi		1	Cellular	Cc transmemt	--
Inf	0	Inf	Significant up		1	Molecular	WAS prote	--
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 ⁻	--
0.070633	0.085068	-3.82352	Nonsignifi		4	Molecular	myosin XV	--
0.022578	0.134753	-5.46894	Nonsignifi	--	--	--	--	--
0.031633	0.066481	-4.9824	Nonsignifi		1	Molecular	peroxidase	1.11.1.7
Inf	0	Inf	Significant up	--	--	--	acidic leuc	--
Inf	0	Inf	Significant up	--	--	--	poliovirus	--
Inf	0	Inf	Significant up		4	Molecular	geranylger	2.5.1.60
Inf	0	Inf	Significant up		4	Molecular	receptor-t	3.1.3.48
Inf	0	Inf	Significant up		1	Molecular	protein TF	--
Inf	0	Inf	Significant up	--	--	--	USP6 N-te	--
0.003424	0.077631	-8.18993	Nonsignifi		4	Biological	HtrA serinε	3.4.21.-
Inf	0	Inf	Significant up		1	Molecular	actin relate	--
Inf	0	Inf	Significant up	--	--	--	histone de	3.5.1.98
Inf	0	Inf	Significant up		2	Molecular	signal tran	--
Inf	0	Inf	Significant up		1	Molecular	discs large	--
1.092134	0.32457	0.12715	Nonsignifi		2	Biological	gamma-gl	3.4.19.9

Inf	0	Inf	Significant up		2	Molecular	ATP-depe	3.6.4.13
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		3	Molecular	Rho guan	--
Inf	0	Inf	Significant up		1	Biological	ubiquitin f	--
0.400862	0.225949	-1.31882	Nonsignifi	None	1	Cellular Cc	golgi appa	--
Inf	0	Inf	Significant up		1	Molecular	COP9 sign	3.4.-.-
3.149533	0.018546	1.655138	Nonsignifi	None	2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up		1	Molecular	far upstrea	--
0.195362	0.059902	-2.35578	Nonsignifi	None	3	Molecular	--	--
0.121599	0.072099	-3.0398	Nonsignifi	None	2	Biological	ubiquitin c	3.4.19.12
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	--
0.443013	0.313036	-1.17458	Nonsignifi	None	3	Biological	--	--
0.14075	0.036356	-2.8288	Significant down	--	--	--	betaine-hc	2.1.1.5
Inf	0	Inf	Significant up		2	Biological	protein tyr	3.1.3.48
Inf	0	Inf	Significant up		2	Biological	secretory c	--
2.79895	0.000789	1.484886	Nonsignifi	None	--	--	immunogl	--
Inf	0	Inf	Significant up		2	Molecular	Ras-relate	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	tumor nec	--
Inf	0	Inf	Significant up		1	Cellular Cc	adiponecti	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		3	Cellular Cc	exocyst co	--
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	--	--	--	dedicator c	--
Inf	0	Inf	Significant up		2	Molecular	--	--
0.103769	0.000689	-3.26856	Significant down	--	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		5	Biological	gamma-tu	--
0.393849	0.054739	-1.34429	Nonsignifi	None	1	Biological	BTB/POZ c	--
0.146697	0.09678	-2.76909	Nonsignifi	None	1	Molecular	--	--
Inf	0	Inf	Significant up	--	--	--	calcium rel	--
Inf	0	Inf	Significant up		1	Molecular	RaBP1-as	--
Inf	0	Inf	Significant up		1	Molecular	carboxyme	3.1.1.45
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	--	--
Inf	0	Inf	Significant up		1	Cellular Cc	--	--
0.386738	0.078234	-1.37057	Nonsignifi	None	2	Biological	arylsulfata	3.1.6.-
Inf	0	Inf	Significant up	--	--	--	--	--
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-ind	--
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
4.464793	0.000247	2.158593	Significant up		2	Molecular	--	--
Inf	0	Inf	Significant up	--	--		receptor e	--
0.039097	0.006896	-4.67682	Significant down		1	Molecular	far upstre	--
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	--	--		--	--
Inf	0	Inf	Significant up		4	Molecular	WNK lysin	2.7.11.1
Inf	0	Inf	Significant up		1	Molecular	--	--
#NAME?	0	#NAME?	Significant down		4	Molecular	lysyl oxida	1.4.3.-
Inf	0	Inf	Significant up	--	--		1,5-anhyd	1.1.1.263
Inf	0	Inf	Significant up		3	Molecular	PDZ-bindi	2.7.12.2
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		2	Biological	cytosolic n	3.4.13.18
Inf	0	Inf	Significant up		2	Cellular Cc	tripartite n	--
Inf	0	Inf	Significant up		1	Molecular	F-box and	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up	--	--		dedicator	--
Inf	0	Inf	Significant up	--	--		FERM dom	--
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	--	--		--	--
0.182978	0.205108	-2.45025	Nonsignifi		2	Molecular	peptidogly	--
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		3	Cellular Cc	MFS trans	--
Inf	0	Inf	Significant up		2	Molecular	sorting ne	--
0.049319	0.231753	-4.3417	Nonsignifi		3	Molecular	coagulatio	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		1	Molecular	erbb2-inte	--
Inf	0	Inf	Significant up		5	Biological	gamma-tu	--
0.025371	0.040392	-5.3007	Significant down		1	Molecular	hemicentir	--
Inf	0	Inf	Significant up		1	Molecular	--	--
0.019761	0.082292	-5.66123	Nonsignifi		2	Molecular	hyaluronar	--
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	--	--		MFS trans	--
Inf	0	Inf	Significant up	--	--		oxysterol-l	--
Inf	0	Inf	Significant up		1	Biological	cysteamine	1.13.11.19
Inf	0	Inf	Significant up	--	--		DNA repai	--
0.15062	0.21628	-2.73101	Nonsignifi	--	--		--	--
Inf	0	Inf	Significant up	--	--		--	--
Inf	0	Inf	Significant up		1	Molecular	tubulin-fol	--
1.21386	0.124449	0.279602	Nonsignifi		3	Molecular	20S protea	3.4.25.1
Inf	0	Inf	Significant up		2	Molecular	ethanolam	2.7.7.14
Inf	0	Inf	Significant up	--	--		26S protea	--
0.993586	0.933987	-0.00928	Nonsignifi	--	--		protein DJ	3.5.1.124
Inf	0	Inf	Significant up	--	--		sortilin	--

5.966963	0.000117	2.576997	Significant up		1 Biological	--	--
Inf		0 Inf	Significant up		1 Molecular	--	--
Inf		0 Inf	Significant up		4 Molecular	phosphoin	2.7.11.1
Inf		0 Inf	Significant up	--	--	--	--
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	--
Inf		0 Inf	Significant up	--	--	acylglycer	3.1.1.23
0.294765	0.025287	-1.76236	Nonsignifi	None	1 Molecular	collagen, t	--
Inf		0 Inf	Significant up		1 Cellular	Cc mothers a	--
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
1.698785	0.105126	0.764503	Nonsignifi	None	1 Cellular	Cc transmem	--
8.186663	0.000662	3.033276	Significant up		3 Molecular	solute carr	--
Inf		0 Inf	Significant up		1 Molecular	calcium an	--
2.120714	0.00439	1.08455	Nonsignifi	None	2 Molecular	endophilin	--
Inf		0 Inf	Significant up	--	--	condensin	--
Inf		0 Inf	Significant up		4 Cellular	Cc actin relat	--
Inf		0 Inf	Significant up	--	--	target of r	--
Inf		0 Inf	Significant up		2 Molecular	RNA-bindi	--
Inf		0 Inf	Significant up		1 Molecular	--	--
Inf		0 Inf	Significant up		1 Molecular	methyloso	--
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	--
1.369557	0.511931	0.45371	Nonsignifi	None	--	--	--
Inf		0 Inf	Significant up	--	--	ESCRT-II c	--
Inf		0 Inf	Significant up		1 Molecular	proteasom	--
Inf		0 Inf	Significant up	--	--	protein pe	--
Inf		0 Inf	Significant up		1 Biological	endoplasm	--
Inf		0 Inf	Significant up	--	--	--	--
0.20798	0.060495	-2.26548	Nonsignifi	None	2 Molecular	--	--
Inf		0 Inf	Significant up	--	--	--	--
Inf		0 Inf	Significant up	--	--	--	--
Inf		0 Inf	Significant up		2 Biological	--	--
Inf		0 Inf	Significant up		1 Molecular	COP9 sign	--
Inf		0 Inf	Significant up	--	--	--	--
Inf		0 Inf	Significant up		2 Cellular	Cc ubiquitin r	--
Inf		0 Inf	Significant up	--	--	acidic leuc	--
Inf		0 Inf	Significant up		1 Molecular	--	--
Inf		0 Inf	Significant up		1 Molecular	phosphatic	2.7.1.67
Inf		0 Inf	Significant up	--	--	tubulin-sp	--
Inf		0 Inf	Significant up	--	--	nucleopori	--
0.054628	0.067671	-4.1942	Nonsignifi	None	1 Molecular	tubulin bet	--
Inf		0 Inf	Significant up		1 Molecular	heterogen	--
Inf		0 Inf	Significant up	--	--	programm	--
Inf		0 Inf	Significant up	--	--	Derlin-1	--
Inf		0 Inf	Significant up		1 Biological	methylothio	5.3.1.23
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
0.190676	0.12736	-2.3908	Nonsignifi	None	1 Molecular	tubulin bet	--
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		2 Biological	p24 family	--
Inf	0	Inf	Significant up	--	--	nucleoporin	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		1 Biological	chitinase d	--
Inf	0	Inf	Significant up	--	--	junctional	--
Inf	0	Inf	Significant up	--	--	--	--
0.556587	0.011993	-0.84532	Nonsignificant	--	--	plasmalemma	--
Inf	0	Inf	Significant up	--	--	oxysterol-l	--
Inf	0	Inf	Significant up		1 Molecular	Rab11 fam	--
Inf	0	Inf	Significant up	--	--	TBC1 dom	--
Inf	0	Inf	Significant up		1 Molecular	N-alpha-a	--
Inf	0	Inf	Significant up		5 Molecular	solute carr	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Molecular	--	--
Inf	0	Inf	Significant up		1 Molecular	inosine triph	3.6.1.-
Inf	0	Inf	Significant up	--	--	translation	--
Inf	0	Inf	Significant up	--	--	cell adhesi	--
#NAME?	0	#NAME?	Significant down	--	--	angiopoiet	--
Inf	0	Inf	Significant up		1 Molecular	partitioning	--
Inf	0	Inf	Significant up	--	--	protein FA	--
Inf	0	Inf	Significant up	--	--	sulfiredoxin	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	--	--	--	--
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		1 Molecular	transducin	--
0.844089	0.364825	-0.24453	Nonsignificant		4 Molecular	protein kin	2.7.11.13
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 sp	--
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		3 Molecular	Rho GTPas	--
Inf	0	Inf	Significant up	--	--	myotubula	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		2 Biological	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1 Molecular	WD repeat	--
Inf	0	Inf	Significant up	--	--	carboxy-te	3.1.3.16
0.01988	0.18775	-5.65251	Nonsignificant		3 Molecular	KRAB dom	--
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		2 Molecular	5'-3' exoril	3.1.13.-
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	--
Inf		0	Inf	Significant up	--	--	epsin	--
Inf		0	Inf	Significant up		3	Molecular sphingosin	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		2	Biological	--
0.635777	0.198275	-0.65341	Nonsignifi	None	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular kelch-like	--
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	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	3.6.1.1
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		3	Molecular tyrosine-p	3.1.3.48
Inf		0	Inf	Significant up		1	Molecular protein un	--
Inf		0	Inf	Significant up	--	--	DnaJ hom	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		1	Biological charged m	--
Inf		0	Inf	Significant up		2	Molecular aminopept	3.4.11.6
0.027508	0.108303	-5.18398	Nonsignifi	None		1	Molecular tubulin bet	--
0.088461	0.214469	-3.49882	Nonsignifi	None		4	Molecular	--
Inf		0	Inf	Significant up		5	Molecular erythrocyt	--
0.783381	0.157157	-0.35221	Nonsignifi	None	--	--	--	--
0.098309	0.000804	-3.34653	Significant down	--	--	--	U3 small n	--
Inf		0	Inf	Significant up	--	--	CUB doma	--
0.11454	0.018577	-3.12608	Significant down			1	Molecular adipocyte-	--
Inf		0	Inf	Significant up		2	Molecular anthrax to	--
Inf		0	Inf	Significant up		1	Molecular dCTP diph	3.6.1.12
Inf		0	Inf	Significant up		1	Molecular SET and M	--
Inf		0	Inf	Significant up		1	Molecular dedicator	--
Inf		0	Inf	Significant up		1	Molecular Function:protein bindi	
Inf		0	Inf	Significant up		5	Molecular cation-trar	3.6.3.-
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		1	Cellular Cc ESCRT-I cc	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	ubiquitin-(	2.3.2.23
0.162895	0.104944	-2.61799	Nonsignifi	None		1	Molecular tubulin alp	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	MOB kinas	--
Inf		0	Inf	Significant up		1	Molecular	--
Inf		0	Inf	Significant up		3	Molecular mediator c	--
Inf		0	Inf	Significant up		1	Molecular	--
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	Molecular DNA-direc	2.7.7.6
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
1.224037	0.720066	0.291647	Nonsignifi	None		1	Molecular guanine nt	--
Inf		0	Inf	Significant up	--	--	exportin-5	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--

Inf		0	Inf	Significant up	--	--	calcyclin bi	--
Inf		0	Inf	Significant up		5	Molecular transient r	--
Inf		0	Inf	Significant up		2	Molecular Ras homol	--
0.597546	0.200945	-0.74288	Nonsignifi	None		1	Molecular parvin	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	helicase M	3.6.4.13
Inf		0	Inf	Significant up		2	Molecular E3 ubiquiti	2.3.2.26
Inf		0	Inf	Significant up		1	Biological	-- --
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 transmemt	--
Inf		0	Inf	Significant up		6	Molecular myosin X	--
Inf		0	Inf	Significant up	--	--	junctophili	--
0.01531	0.010203	-6.02941	Significant down			2	Biological adipocyte	--
Inf		0	Inf	Significant up		5	Molecular ATP-bindii	--
Inf		0	Inf	Significant up		2	Molecular Ras-relate	--
1.604714	0.06355	0.682316	Nonsignifi	None	--	--	vacuolar p	--
Inf		0	Inf	Significant up		1	Molecular CD320 ant	--
0.269727	0.526133	-1.89043	Nonsignifi	None		3	Molecular protocadh	--
Inf		0	Inf	Significant up		3	Molecular myo-inosit	5.5.1.4
0.193006	0.022499	-2.37328	Significant down			2	Molecular interleukin	--
Inf		0	Inf	Significant up	--	--	--	--
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-	--
0.228017	0.000274	-2.13279	Significant down	--	--	--	reticulon-4	--
4.924134	8.71E-05	2.29987	Significant up			2	Molecular Xaa-Pro ar	3.4.11.9
Inf		0	Inf	Significant up		1	Biological omega-an	3.5.1.3
Inf		0	Inf	Significant up	--	--	poliovirus	--
0.790218	0.137723	-0.33968	Nonsignifi	None		1	Molecular Xaa-Pro ar	3.4.11.9
Inf		0	Inf	Significant up	--	--	integral m	--
Inf		0	Inf	Significant up		3	Molecular baculoviral	2.3.2.23
Inf		0	Inf	Significant up		2	Molecular	-- --
Inf		0	Inf	Significant up		2	Molecular acetyl-CoA	6.2.1.1
0.000313	0.025927	-11.6407	Significant down			5	Molecular ATP-depe	3.6.4.13
0.669643	0.188807	-0.57853	Nonsignifi	None		1	Molecular GTP-bindii	3.6.5.-
Inf		0	Inf	Significant up		2	Cellular Cc MFS trans	--
Inf		0	Inf	Significant up		1	Molecular aladin	--
0.065432	0.01014	-3.93385	Significant down	--	--	--	--	--
Inf		0	Inf	Significant up		2	Molecular 4'-phosph	2.7.8.-
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		2	Molecular Ras-relate	--
Inf		0	Inf	Significant up		2	Biological vacuolar p	--
0.206805	0.330812	-2.27365	Nonsignifi	None	--	--	--	--
Inf		0	Inf	Significant up	--	--	--	--
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		4	Molecular structural r	--
Inf		0	Inf	Significant up		1	Molecular obg-like A	--
Inf		0	Inf	Significant up	--	--	palmitoyltr	2.3.1.225
Inf		0	Inf	Significant up	--	--	--	--
Inf		0	Inf	Significant up		1	Molecular protein lin	--
Inf		0	Inf	Significant up		2	Molecular ATP-bindii	--

Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		3	Biological	AP-5 comp --
Inf	0	Inf	Significant up		2	Molecular	ATP-depe 3.6.4.13
Inf	0	Inf	Significant up	--	--		E3 ubiquiti 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-depe 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	--	--	--	--
Inf	0	Inf	Significant up		3	Molecular	tRNA(His) 2.7.7.79
Inf	0	Inf	Significant up		1	Molecular	E3 ubiquiti 2.3.2.27
Inf	0	Inf	Significant up		2	Molecular	Ras-relate --
Inf	0	Inf	Significant up		1	Biological	-- --
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
Inf	0	Inf	Significant up		2	Molecular	abl interac --
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 eε --
Inf	0	Inf	Significant up		1	Biological	pleckstrin --
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
2.963903	0.000613	1.567498	Nonsignifi		1	Molecular	EH domain --
#NAME?	0	#NAME?	Significant down		2	Molecular	-- --
Inf	0	Inf	Significant up		1	Molecular	-- --
Inf	0	Inf	Significant up	--	--		programm --
Inf	0	Inf	Significant up		2	Molecular	low-densit --
0.003738	0.093606	-8.06346	Nonsignifi		1	Molecular	calmodulir --
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	Cellular	Cc -- --
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	--	--	--	--
0.562428	0.590976	-0.83026	Nonsignifi		2	Molecular	-- --
Inf	0	Inf	Significant up	--	--		SLAIN mot --
Inf	0	Inf	Significant up		2	Biological	-- --
Inf	0	Inf	Significant up	--	--		protein BC --
Inf	0	Inf	Significant up		3	Molecular	serine/thre 2.7.11.1
6.218132	2.3E-05	2.636481	Significant up	--	--		prostaglan --

0.012352	0.011026	-6.33906	Significant down	--	--	--	--
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	--	--	ataxin-10	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		1	Molecular	epidermal --
0.132086	0.121736	-2.92045	Nonsignifi	None	5	Molecular	coatome r --
Inf	0	Inf	Significant up		1	Molecular	phosphatic 2.7.1.67
0.166328	0.026341	-2.58789	Significant down	--	--	mannose r	--
Inf	0	Inf	Significant up		1	Cellular Cc	-- --
Inf	0	Inf	Significant up	--	--	vacuolar p	--
Inf	0	Inf	Significant up	--	--	translation	--
Inf	0	Inf	Significant up		3	Biological	-- --
0.105275	0.075042	-3.24777	Nonsignifi	None	2	Biological	cathepsin 3.4.18.1
Inf	0	Inf	Significant up	--	--	DnaJ hom	--
2.20326	0.048419	1.13964	Nonsignifi	None	1	Molecular	-- --
0.136333	0.040525	-2.8748	Significant down		1	Molecular	fibulin 5 --
1.312143	0.129287	0.391925	Nonsignifi	None	1	Molecular	tight juncti --
Inf	0	Inf	Significant up	--	--	DnaJ hom	--
Inf	0	Inf	Significant up	--	--	adducin	--
Inf	0	Inf	Significant up		4	Molecular	solute carr --
Inf	0	Inf	Significant up	--	--	5'-AMP-ac	--
0.066384	0.018068	-3.91303	Significant down		2	Molecular	deleted in --
Inf	0	Inf	Significant up		3	Cellular Cc	MFS transp --
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-bin 2.7.11.10
1.444171	0.229105	0.530242	Nonsignifi	None	1	Molecular	septin 3/9/ --
Inf	0	Inf	Significant up	--	--	metallored	1.16.1.-
Inf	0	Inf	Significant up		2	Molecular	ATP-depe 3.6.4.13
0.027273	0.06324	-5.19638	Nonsignifi	None	3	Molecular	a disintegr 3.4.24.-
Inf	0	Inf	Significant up		2	Molecular	BAI1-asso --
Inf	0	Inf	Significant up		3	Biological	prefoldin s --
Inf	0	Inf	Significant up	--	--	enolase-pl	3.1.3.77
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		2	Biological	exportin-7 --
0.04095	0.104853	-4.60999	Nonsignifi	None	--	--	vacuolar p --
Inf	0	Inf	Significant up		3	Molecular	death-ass 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		2	Molecular	RAS protei --
Inf	0	Inf	Significant up		3	Molecular	drebrin-lik --
Inf	0	Inf	Significant up	--	--	ESCRT-I cc	--
0.086658	0.00105	-3.52853	Significant down	--	--	serpin pep	--
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
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	--	--	general tra	2.3.1.48
Inf	0	Inf	Significant up		1	Molecular	protein kin --
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	--
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	--
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-1f	--
0.226835	0.287612	-2.14029	Nonsignifi	None	6	Molecular	Notch 3	--
Inf	0	Inf	Significant up		3	Molecular	myosin VI	--
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	--
2.496438	0.000702	1.319871	Nonsignifi	None	1	Molecular	vacuolar p	--
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	--
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 p	3.1.1.4
0.480176	0.002055	-1.05837	Nonsignifi	None	1	Molecular	26S protea	--
Inf	0	Inf	Significant up		1	Molecular	FAS-assoc	--
Inf	0	Inf	Significant up	--	--	--	protein C r	--
1.326033	0.796407	0.407117	Nonsignifi	None	4	Biological	peptidyl-p	5.2.1.8
Inf	0	Inf	Significant up		3	Molecular	ATP-bindin	--
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	transcripti	3.6.4.-
Inf	0	Inf	Significant up		1	Molecular	UBX doma	--
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	--
Inf	0	Inf	Significant up		1	Molecular	leucine-ric	--
0.634814	0.169225	-0.65559	Nonsignifi	None	2	Molecular	dynamamin	3.6.5.5
Inf	0	Inf	Significant up	--	--	--	sialidase-	2.3.2.1.18
1.852151	0.081161	0.889202	Nonsignifi	None	--	--	--	--
Inf	0	Inf	Significant up		2	Molecular	BAI1-assoc	--
Inf	0	Inf	Significant up		4	Molecular	structural r	--
Inf	0	Inf	Significant up		1	Biological	charged m	--
Inf	0	Inf	Significant up	--	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	RLL motif	--
Inf	0	Inf	Significant up		2	Molecular	--	--
0.003817	0.227351	-8.0334	Nonsignifi	None	2	Molecular	RuvB-like	3.6.4.12
0.922869	0.12568	-0.1158	Nonsignifi	None	3	Molecular	translation	--
0.423113	0.106396	-1.24089	Nonsignifi	None	2	Molecular	RuvB-like	--
Inf	0	Inf	Significant up	--	--	--	--	--
2.34335	0.001284	1.228573	Nonsignifi	None	2	Molecular	cofilin	--
Inf	0	Inf	Significant up	--	--	--	integral m	--
Inf	0	Inf	Significant up		1	Molecular	--	--
10.49958	0.000585	3.392259	Significant up	--	--	--	NCK-assoc	--
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	--	--
0.139544	0.263209	-2.84121	Nonsignifi	5	Molecular	erythrocyt	--
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	--	--	nucleolar p	--
0.005815	0.019023	-7.42602	Significant down	1	Molecular	G protein-	--
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	2	Molecular	endophilin	--
Inf	0	Inf	Significant up	3	Molecular	RNA-bindi	--
Inf	0	Inf	Significant up	1	Biological	ribosome r	--
Inf	0	Inf	Significant up	2	Biological	p24 family	--
Inf	0	Inf	Significant up	--	--	oligoribon	3.1.-.-
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	mitochonc	--
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	3	Molecular	SH3-dom	--
Inf	0	Inf	Significant up	--	--	nucleolar c	--
0.418863	0.035447	-1.25545	Nonsignifi	4	Molecular	large subu	--
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+	--
0.440344	0.042363	-1.1833	Nonsignifi	5	Cellular	Cc talin	--
Inf	0	Inf	Significant up	--	--	--	--
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 talin	--
Inf	0	Inf	Significant up	4	Molecular	myosin V	--
0.100963	0.009677	-3.3081	Significant down	4	Molecular	lysyl oxida	1.4.3.-
Inf	0	Inf	Significant up	--	--	hypoxia up	--
Inf	0	Inf	Significant up	--	--	telomere l	--
Inf	0	Inf	Significant up	--	--	ariadne-1	2.3.2.27
Inf	0	Inf	Significant up	--	--	heat shock	--
Inf	0	Inf	Significant up	--	--	protein ph	3.1.1.89
Inf	0	Inf	Significant up	1	Biological	BTB/POZ c	--
Inf	0	Inf	Significant up	5	Molecular	nucleoside	2.7.4.6
0.177948	0.00211	-2.49047	Significant down	--	--	angiopoiet	--
Inf	0	Inf	Significant up	3	Molecular	ubiquitin c	3.4.19.12
Inf	0	Inf	Significant up	1	Molecular	CD2-assoc	--
Inf	0	Inf	Significant up	--	--	V-type H+	--
Inf	0	Inf	Significant up	--	--	transportir	--
Inf	0	Inf	Significant up	--	--	signal recc	--
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	--
0.738465	0.014695	-0.4374	Nonsignifi	2	Molecular	sorting ne	--
Inf	0	Inf	Significant up	1	Molecular	sorting ne	--
Inf	0	Inf	Significant up	1	Molecular	endothelia	3.1.1.3

Inf	0	Inf	Significant up		2	Cellular Cc MFS transp	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up	--	--	phosphoserine	2.6.1.52
Inf	0	Inf	Significant up	--	--	junctional	--
0.94898	0.832779	-0.07555	Nonsignificant		3	Cellular Cc glypican 6	--
Inf	0	Inf	Significant up	--	--	--	--
Inf	0	Inf	Significant up		4	Molecular G protein-	--
Inf	0	Inf	Significant up		5	Molecular solute carr	--
Inf	0	Inf	Significant up		5	Molecular coatamer	--
10.02551	0.001321	3.325604	Significant up	--	--	chloride in	--
0.186614	0.053025	-2.42187	Nonsignificant		1	Molecular	--
Inf	0	Inf	Significant up		2	Molecular brefeldin A	--
Inf	0	Inf	Significant up		2	Molecular brefeldin A	--
Inf	0	Inf	Significant up		3	Molecular serine/threonine	2.7.11.1
0.018465	0.243955	-5.75906	Nonsignificant		1	Molecular	--
0.246987	0.404329	-2.01749	Nonsignificant	--	--	dynein light	--
Inf	0	Inf	Significant up		4	Molecular casein kinase	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 roundabout	--
Inf	0	Inf	Significant up		1	Molecular WAS protein	--
Inf	0	Inf	Significant up		1	Molecular ectonucleoside	3.6.1.29

KEGG_ko	COG_Func	COG_Func	COG_Class	IPR_Term
--	--	--	--	IPR009038 [GOLD domain]
--	Peptidyl-p O		Posttransla	IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans is
--	--	--	--	--
--	Predicted IR		General fu	IPR026937 [Strawberry notch, helicase C domain]
ko03018 R	--	--	--	IPR007196 [CCR4-Not complex component, Not1, C-t
--	--	--	--	IPR004241 [Autophagy protein Atg8 ubiquitin-like]
--	--	--	--	IPR010935 [SMCs flexible hinge]
--	--	--	--	IPR019359 [CCDC85 family]
--	--	--	--	--
ko03040 S	Small nucle	K	Transcripti	IPR001163 [LSM domain, eukaryotic/archaea-type]
--	--	--	--	IPR004965 [Paralemmmin]
--	--	--	--	--
ko04610 C	Secreted tr	O	Posttransla	IPR000436 [Sushi/SCR/CCP domain] ; IPR001254[Serine
ko03013 R	--	--	--	IPR000717 [Proteasome component (PCI) domain] ; IPR
--	--	--	--	IPR003597 [Immunoglobulin C1-set]
--	--	--	--	--
ko05132 S	Tfp pilus a	NW	Cell motilit	IPR011990 [Tetratricopeptide-like helical domain] ; IPR
--	--	--	--	IPR004240 [Nonaspanin (TM9SF)] ; IPR005024[Snf7 fan
ko00190 C	--	--	--	--
--	--	--	--	IPR001619 [Sec1-like protein]
ko04130 S	--	--	--	IPR006011 [Syntaxin, N-terminal domain]
--	Sterol des	I	Lipid trans	IPR000608 [Ubiquitin-conjugating enzyme E2] ; IPR019
ko00480 G	Cation trar	P	Inorganic i	--
ko00970 A	Seryl-tRNA	J	Translatior	IPR002314 [Aminoacyl-tRNA synthetase, class II (G/ P/
--	--	--	--	IPR001752 [Kinesin motor domain]
--	--	--	--	IPR001478 [PDZ domain] ; IPR001781[Zinc finger, LIM-
ko00062 F	Acyl-CoA II		Lipid trans	IPR006683 [Thioesterase domain]
--	--	--	--	IPR000048 [IQ motif, EF-hand binding site] ; IPR00160
ko04130 S	--	--	--	IPR000928 [SNAP-25]
--	--	--	--	IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
--	--	--	--	IPR001619 [Sec1-like protein]
ko04142 L	--	--	--	IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
--	--	--	--	IPR001079 [Galectin, carbohydrate recognition domain
ko04210 A	--	--	--	IPR000488 [Death domain] ; IPR001368[TNFR/NGFR cy
ko03050 P	--	--	--	IPR000717 [Proteasome component (PCI) domain]
--	Membrane	OK	Posttransla	IPR001478 [PDZ domain]
ko04978 M	--	--	--	IPR006121 [Heavy metal-associated domain, HMA]
--	Glutathion	O	Posttransla	IPR004045 [Glutathione S-transferase, N-terminal]
ko03013 R	--	--	--	IPR000555 [JAB1/MPN/MOV34 metalloenzyme domain
ko04120 U	--	--	--	IPR000569 [HECT domain] ; IPR001202[WW domain]
ko00562 Ir	--	--	--	IPR000341 [Phosphatidylinositol 3-kinase Ras-binding
--	--	--	--	IPR013766 [Thioredoxin domain] ; IPR017905[ERV/ALR
ko04062 C	Acyl transf	Q	Secondary	IPR000095 [CRIB domain] ; IPR000697[WH1/EVH1 dom
--	--	--	--	IPR000357 [HEAT repeat]
--	RNA 3'-ter	A	RNA proce	IPR013791 [RNA 3'-terminal phosphate cyclase, insert
ko00562 Ir	--	--	--	IPR000008 [C2 domain] ; IPR000341[Phosphatidylinosit
ko04512 E	--	--	--	IPR000082 [SEA domain] ; IPR000742[EGF-like domain]
ko00310 L	Glycosyltra	M	Cell wall/r	IPR005123 [Oxoglutarate/iron-dependent dioxygenase
--	--	--	--	IPR009976 [Exocyst complex component Sec10-like]
ko03050 P	Proteasom	O	Posttransla	IPR000555 [JAB1/MPN/MOV34 metalloenzyme domain
ko04144 E	--	--	--	IPR001452 [SH3 domain] ; IPR004148[BAR domain]
--	--	--	--	IPR000225 [Armadillo] ; IPR002652[Importin-alpha, imp
--	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain]
ko04015 R	Ankyrin re	T	Signal tran	IPR019748 [FERM central domain] ; IPR032022[KRIT, N-
--	--	--	--	IPR001357 [BRCT domain] ; IPR010613[Pescadillo]
--	--	--	--	IPR001478 [PDZ domain]
ko03008 R	RNA proce	J	Translatior	IPR002687 [Nop domain] ; IPR012974[NOP5, N-termin

--	--	--	--	IPR013836	[CD34/Podocalyxin]	
--	--	--	--	IPR000867	[Insulin-like growth factor-binding protein,	
--	--	--	--	IPR000225	[Armadillo] ; IPR002652[Importin-alpha, imp	
ko00511	C	Alpha-mar	G	Carbohydr	IPR000602	[Glycoside hydrolase family 38, N-terminal c
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608	[Ubiquitin-conjugating enzyme E2]
ko00750	V	Pyridoxal/	H	Coenzyme	IPR013749	[Pyridoxamine kinase/Phosphomethylpyrim
ko04514	C	--	--	--	IPR004031	[PMP-22/EMP/MP20/Claudin superfamily]
--		Negative r	O	Posttransla	IPR013766	[Thioredoxin domain]
--		Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001180[Citron
--	--	--	--	--	--	--
ko05010	A	--	--	--	IPR001762	[Disintegrin domain] ; IPR002870[Peptidase
--		DNA-bind	R	General fu	IPR002836	[PDCD5-related protein]
ko03013	R	Predicted	I	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
ko04360	A	Phage-rel	X	Mobilome	IPR000421	[Coagulation factor 5/8 C-terminal domain]
--	--	--	--	--	IPR001494	[Importin-beta, N-terminal domain]
--	--	--	--	--	IPR018499	[Tetraspanin/Peripherin]
ko03050	P	20S protea	O	Posttransla	IPR000426	[Proteasome alpha-subunit, N-terminal dor
--	--	--	--	--	IPR001478	[PDZ domain]
--	--	--	--	--	IPR001478	[PDZ domain]
--	--	--	--	--	IPR001478	[PDZ domain] ; IPR014775[L27 domain, C-ter
ko01523	A	PASTA	dor	Cell wall/r	IPR000719	[Protein kinase domain] ; IPR022007[I-kapp
ko05034	A	--	--	--	IPR019467	[Histone acetyl transferase HAT1 N-termina
--		Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001478[PDZ d
ko00564	G	Phosphatic	I	Lipid trans	IPR001683	[Phox homologous domain] ; IPR001736[Ph
ko04510	F	Ca2+ -binc	T	Signal tran	IPR002048	[EF-hand domain] ; IPR015070[DJBP, EF-ha
--		Murein	D	Cell wall/r	IPR016047	[Peptidase M23]
ko04144	E	--	--	--	IPR000306	[FYVE zinc finger] ; IPR002014[VHS domain]
--		Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR014020[Tensin
--		RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain]
ko03008	R	--	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
--	--	--	--	--	IPR000219	[Dbl homology (DH) domain]
--	--	--	--	--	IPR001715	[Calponin homology domain] ; IPR002017[S
--	--	--	--	--	IPR024298	[Ancestral coatomer element 1, Sec16/Sec3
ko04360	A	DNA-bind	R	General fu	IPR001627	[Sema domain] ; IPR002165[Plexin repeat] ;
--	--	--	--	--	IPR006624	[Beta-propeller repeat TECPR]
ko00230	P	Phosphoril	F	Nucleotide	IPR010918	[AIR synthase-related protein, C-terminal d
--	--	--	--	--	IPR000884	[Thrombospondin type-1 (TSP1) repeat] ; IF
--		Chromoso	D	Cell cycle c	IPR002110	[Ankyrin repeat] ; IPR020683[Ankyrin repeat
ko04142	L	Predicted	R	General fu	IPR000731	[Sterol-sensing domain] ; IPR003392[Protein
ko04144	E	--	--	--	IPR007188	[Actin-related protein 2/3 complex subunit
ko04144	E	--	--	--	IPR007204	[Actin-related protein 2/3 complex subunit
ko00230	P	DNA-direct	K	Transcripti	IPR011262	[DNA-directed RNA polymerase, insert dom
--		Uncharact	S	Function u	IPR005552	[Scramblase]
--		TFIIF-inter	K	Transcripti	IPR004274	[FCP1 homology domain]
--		Prefoldin,	O	Posttransla	IPR002777	[Prefoldin beta-like]
ko01100	N	Uncharact	S	Function u	IPR000034	[Laminin IV] ; IPR001791[Laminin G domain]
--	--	--	--	--	--	--
--	--	--	--	--	IPR004932	[Retrieval of early ER protein Rer1]
--		Uncharact	S	Function u	IPR002995	[Surfeit locus 4]
ko00051	F	Hydroxym	HR	Coenzyme	IPR005002	[Phosphomannomutase]
--	--	--	--	--	IPR009071	[High mobility group box domain]
ko04514	C	Outer men	M	Cell wall/r	IPR003961	[Fibronectin type III] ; IPR013098[Immunogl
--	--	--	--	--	IPR001494	[Importin-beta, N-terminal domain] ; IPR01
ko04130	S	--	--	--	IPR000727	[Target SNARE coiled-coil homology doma
--		Sugar pho	G	Carbohydr	IPR011701	[Major facilitator superfamily]
ko05230	C	Predicted	G	Carbohydr	IPR011701	[Major facilitator superfamily]

ko01524 P -- --	-- IPR007274 [Ctr copper transporter]
ko04130 S -- --	-- IPR001388 [Synaptobrevin] ; IPR010908[Longin domain]
ko04144 E -- --	-- IPR006789 [Actin-related protein 2/3 complex subunit]
ko04911 Ir Signal-tran T	Signal tran IPR004178 [Calmodulin-binding domain] ; IPR013099[
ko04144 E Ankyrin rej T	Signal tran IPR001164 [Arf GTPase activating protein] ; IPR001452[
ko00260 G Phosphogl HR	Coenzyme IPR006139 [D-isomer specific 2-hydroxyacid dehydrog
ko04145 P -- --	-- IPR022780 [Dynein family light intermediate chain]
ko03050 P -- --	-- IPR000717 [Proteasome component (PCI) domain] ; IPF
ko00230 P ATP sulfur P	Inorganic i IPR024951 [Sulphate adenylyltransferase catalytic domi
-- -- --	-- IPR009361 [RZZ complex, subunit Zw10]
ko00512 N Glycosyltra G	Carbohydr IPR027791 [Galactosyltransferase, C-terminal] ; IPR0279
-- -- --	-- IPR001781 [Zinc finger, LIM-type]
-- RNA recog J	Translatio IPR000504 [RNA recognition motif domain]
-- Thiol-disul O	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 is
ko00980 N Predicted c R	General fu IPR023210 [NADP-dependent oxidoreductase domain]
-- -- --	-- IPR007477 [SAB domain] ; IPR008379[Band 4.1, C-term
ko00515 N -- --	-- --
ko03013 R -- --	-- IPR001494 [Importin-beta, N-terminal domain] ; IPR01
ko05206 N -- --	-- IPR007875 [Sprouty]
-- -- --	-- IPR007194 [Transport protein particle (TRAPP) compon
ko04144 E -- --	-- IPR005024 [Snf7 family]
-- -- --	-- IPR018499 [Tetraspanin/Peripherin]
-- Anion-tran P	Inorganic i IPR025723 [Anion-transporting ATPase-like domain]
ko04110 C Predicted IT	Signal tran IPR001680 [WD40 repeat]
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
ko04142 L -- --	-- IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
ko04130 S -- --	-- IPR000727 [Target SNARE coiled-coil homology doma
-- Tetratricopep R	General fu IPR001440 [Tetratricopeptide repeat 1] ; IPR019734[Tet
-- -- --	-- IPR000048 [IQ motif, EF-hand binding site] ; IPR001609
ko03015 n -- --	-- IPR016706 [Cleavage/polyadenylation specificity factor
-- Lantibiotic V	Defense m IPR007822 [Lanthionine synthetase C-like]
-- Secreted/c O	Posttransla IPR007863 [Peptidase M16, C-terminal] ; IPR011765[Pe
-- Ca2+ -bind T	Signal tran IPR002048 [EF-hand domain]
-- -- --	-- IPR000421 [Coagulation factor 5/8 C-terminal domain]
ko00270 C S-adenosy H	Coenzyme IPR000043 [Adenosylhomocysteinase] ; IPR015878[S-a
ko04110 C -- --	-- IPR020796 [Origin recognition complex, subunit 5]
ko00230 P -- --	-- IPR008015 [GMP phosphodiesterase, delta subunit]
ko03040 S HrpA-like J	Translatio IPR001650 [Helicase, C-terminal] ; IPR007502[Helicase-
-- Large exo c U	Intracellular IPR002126 [Cadherin] ; IPR013164[Cadherin, N-termina
-- Phosphoril FE	Nucleotide IPR005946 [Ribose-phosphate diphosphokinase] ; IPRC
-- Uncharacter S	Function u IPR000330 [SNF2-related, N-terminal domain] ; IPR001
-- -- --	-- IPR019143 [JNK/Rab-associated protein-1, N-terminal]
ko04120 U -- --	-- --
-- Monoamin E	Amino acid IPR002937 [Amine oxidase] ; IPR007526[SWIRM domai
ko04919 T -- --	-- IPR000195 [Rab-GTPase-TBC domain] ; IPR006020[PTE
ko04150 n -- --	-- IPR000539 [Frizzled protein] ; IPR020067[Frizzled doma
ko00230 P Nucleoside F	Nucleotide IPR001564 [Nucleoside diphosphate kinase]
-- -- --	-- IPR007677 [Gasdermin]
-- Regulatory O	Posttransla IPR000421 [Coagulation factor 5/8 C-terminal domain]
ko00061 F Long-chain I	Lipid trans IPR000873 [AMP-dependent synthetase/ligase]
ko04144 E -- --	-- IPR001683 [Phox homologous domain]
ko04931 Ir N-acetyl-t G	Carbohydr IPR011496 [Beta-N-acetylglucosaminidase]
ko00230 P Adenylate T	Signal tran IPR001054 [Adenylyl cyclase class-3/4/guanylyl cyclase

--	RNA recog J	Translator	IPR000504	[RNA recognition motif domain]
ko00310	L Glycosyltra M	Cell wall/r	IPR005123	[Oxoglutarate/iron-dependent dioxygenase
ko04510	F Transcripti K	Transcripti	IPR009408	[Formin Homology 1] ; IPR010465[DRF auto
--	--	--	IPR010326	[Exocyst complex component EXOC3/Sec6]
--	--	--	IPR004279	[Perilipin]
--	Predicted z G	Carbohydr	IPR011701	[Major facilitator superfamily]
ko04218	C --	--	IPR003021	[Rad1/Rec1/Rad17]
--	Predicted IR	General fu	--	--
--	--	--	IPR000225	[Armadillo] ; IPR002652[Importin-alpha, imp
--	Outer men M	Cell wall/r	IPR000436	[Sushi/SCR/CCP domain] ; IPR003410[HYR c
--	--	--	IPR001781	[Zinc finger, LIM-type]
ko04015	R --	--	IPR000225	[Armadillo]
ko03013	R Translator J	Translator	IPR001950	[SUI1 domain]
ko04144	E --	--	IPR001683	[Phox homologous domain] ; IPR005329[So
--	--	--	IPR006953	[Vesicle tethering protein Uso1/P115-like , I
ko04977	V --	--	IPR002666	[Reduced folate carrier]
--	--	--	IPR002014	[VHS domain] ; IPR004152[GAT domain]
ko05034	A --	--	IPR007125	[Histone H2A/H2B/H3]
ko03008	R Glutamate E	Amino acid	IPR002478	[PUA domain] ; IPR002501[Pseudouridine sy
ko03013	R Translator J	Translator	IPR004161	[Translation elongation factor EFTu-like, do
--	Archaeal ri J	Translator	IPR001387	[Cro/C1-type helix-turn-helix domain] ; IPR
ko04141	P DnaJ-class O	Posttransla	IPR001305	[Heat shock protein DnaJ, cysteine-rich don
--	Uncharact P	Inorganic i	IPR004323	[Divalent ion tolerance protein, CutA]
--	--	--	IPR002777	[Prefoldin beta-like]
ko04360	A --	--	IPR000198	[Rho GTPase-activating protein domain] ; IF
ko04360	A Streptogra V	Defense m	IPR001627	[Sema domain] ; IPR002165[Plexin repeat] ;
--	--	--	IPR013106	[Immunoglobulin V-set domain]
--	Predicted IT	Signal tran	IPR001680	[WD40 repeat]
ko04150	r --	--	IPR000539	[Frizzled protein] ; IPR020067[Frizzled doma
--	Magnesiur P	Inorganic i	IPR008250	[P-type ATPase, A domain] ; IPR032630[P-i
ko04022	c Serine/thre T	Signal tran	IPR000719	[Protein kinase domain] ; IPR015008[Rho bi
--	--	--	IPR024395	[CLASP N-terminal domain]
ko04514	C --	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
--	Uncharact R	General fu	IPR013098	[Immunoglobulin I-set]
--	Tetratricop R	General fu	IPR025697	[CLU domain] ; IPR028275[Clustered mitoch
--	DnaJ-class O	Posttransla	IPR001623	[DnaJ domain] ; IPR025640[Domain of unkn
--	--	--	--	--
--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko04360	A --	--	IPR001627	[Sema domain] ; IPR002165[Plexin repeat] ;
--	Ca2+ -binc T	Signal tran	IPR002048	[EF-hand domain]
--	--	--	IPR004226	[Tubulin binding cofactor A]
ko04144	E AAA+ -typ MDT	Cell wall/r	IPR003959	[ATPase, AAA-type, core] ; IPR007330[MIT]
--	--	--	IPR006603	[PQ-loop repeat]
ko04217	N O-acetyl- /J	Translator	IPR002589	[Macro domain] ; IPR007125[Histone H2A/H
ko04010	N Uncharact S	Function u	IPR001715	[Calponin homology domain] ; IPR017868[F
--	DNA-bind R	General fu	IPR000315	[B-box-type zinc finger] ; IPR001258[NHL re
--	--	--	IPR011701	[Major facilitator superfamily]
ko03040	S --	--	IPR001202	[WW domain] ; IPR002713[FF domain]
ko04144	E --	--	IPR028934	[Vacuolar protein sorting protein 26 related
ko04310	V --	--	IPR001863	[Glypican]
--	--	--	IPR009643	[Heat shock factor binding 1]
ko04514	C --	--	IPR004031	[PMP-22/EMP/MP20/Claudin superfamily]
--	--	--	IPR004122	[Barrier- to-autointegration factor, BAF]
ko03040	S --	--	IPR015016	[Splicing factor 3B subunit 1]
--	--	--	IPR002059	[Cold-shock protein, DNA-binding] ; IPR02-
ko00564	G Predicted e R	General fu	IPR003140	[Phospholipase/carboxylesterase/thioestera
ko03040	S Replicative L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR004179[Sec63 dc
--	--	--	IPR007303	[TIP41-like protein]

--	--	--	--	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	--	--	--	IPR013906 [Eukaryotic translation initiation factor 3 sub
--	Ankyrin re	T		Signal tran IPR002110 [Ankyrin repeat] ; IPR020683[Ankyrin repeat
ko00900 T Zn-depen	c	O		Posttransla IPR001915 [Peptidase M48] ; IPR032456[CAAX prenyl p
ko00020 C Isocitrate c	C			Energy prc IPR024084 [Isopropylmalate dehydrogenase-like dom
ko00670 C Acyl-CoA	c	C		Energy prc IPR002376 [Formyl transferase, N-terminal] ; IPR00579
--	--	--	--	IPR004895 [Prenylated rab acceptor PRA1]
--	--	--	--	IPR018499 [Tetraspanin/Peripherin]
--	PASTA dom	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
--	--	--	--	IPR004978 [Stanniocalcin]
--	--	--	--	IPR000867 [Insulin-like growth factor-binding protein,
--	--	--	--	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)]
ko04360 A Leucine-rich	K			Transcripti IPR000372 [Leucine-rich repeat N-terminal domain] ; I
--	Magnesiur	P		Inorganic i IPR008250 [P-type ATPase, A domain] ; IPR032630[P-1
ko04015 R	--	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR001849[P
ko03040 S Tetratricop	R			General fu IPR010491 [PRP1 splicing factor, N-terminal] ; IPR0197
--	--	--	--	IPR025481 [Cell morphogenesis protein C-terminal] ; IF
ko04144 E	--	--	--	IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
--	--	--	--	IPR002126 [Cadherin]
--	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]
ko05010 A	--	--	--	IPR003388 [Reticulon]
--	--	--	--	IPR007262 [Vacuolar protein sorting 55]
ko04144 E	--	--	--	IPR001683 [Phox homologous domain]
--	--	--	--	IPR001752 [Kinesin motor domain]
--	--	--	--	IPR001194 [DENN domain] ; IPR001849[Pleckstrin hom
ko04130 S	--	--	--	--
ko04514 C	--	--	--	IPR013106 [Immunoglobulin V-set domain]
ko00030 P 6-phospho	c	G		Carbohydr IPR006148 [Glucosamine/galactosamine-6-phosphate
ko00230 P ATP sulfur	P			Inorganic i IPR024951 [Sulphate adenylyltransferase catalytic dom
--	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	c	R		General fu IPR003140 [Phospholipase/carboxylesterase/thioester
--	--	--	--	IPR002867 [IBR domain]
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
--	--	--	--	IPR022734 [Apolipoprotein M]
--	--	--	--	IPR016565 [Proteasome assembly chaperone 1]
--	--	--	--	IPR010472 [Formin, FH3 domain] ; IPR010473[Formin, (
ko04141 P	--	--	--	IPR006895 [Zinc finger, Sec23/Sec24-type] ; IPR006896
--	--	--	--	IPR000203 [GPS motif] ; IPR000832[GPCR, family 2, sec

ko00770 P Predicted ;R	General fu IPR003010 [Carbon-nitrogen hydrolase]
ko00770 P Predicted ;R	General fu IPR003010 [Carbon-nitrogen hydrolase]
ko00230 P DNA-direct K	Transcripti IPR000722 [RNA polymerase, alpha subunit] ; IPR00706
ko04144 E Proteasom O	Posttransla IPR000555 [JAB1/MPN/MOV34 metalloenzyme domain
ko04910 Ir -- --	-- IPR005036 [CBM21 (carbohydrate binding type-21) do
ko04120 U Alpha-tub DZ	Cell cycle c IPR000408 [Regulator of chromosome condensation, R
ko04130 S -- --	-- --
-- Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR024678[Serine/
-- -- --	-- IPR019498 [MENTAL domain]
-- -- --	-- IPR007919 [Uncharacterised protein family UPF0220]
ko04141 P -- --	-- --
-- -- --	-- IPR001202 [WW domain] ; IPR003103[BAG domain]
ko04010 M Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR001180[Citron
-- WD40 rep R	General fu IPR001680 [WD40 repeat] ; IPR005108[HELP]
ko04390 H PASTA dom M	Cell wall/r IPR000719 [Protein kinase domain] ; IPR015940[Ubiqui
-- -- --	-- IPR018499 [Tetraspanin/Peripherin]
-- -- --	-- IPR018499 [Tetraspanin/Peripherin]
-- N-Dimethy E	Amino acid --
ko00480 G Thiol:disulf O	Posttransla --
-- -- --	-- IPR013111 [EGF-like domain, extracellular]
ko04012 E Serine/thre T	Signal tran IPR000095 [CRIB domain] ; IPR000719[Protein kinase d
ko05225 H Actin-relat Z	Cytoskelet IPR004000 [Actin family]
ko00010 G Malate/lac C	Energy prc IPR001236 [Lactate/malate dehydrogenase, N-termina
ko00830 R Acyl-CoA C	Energy prc IPR015590 [Aldehyde dehydrogenase domain]
ko00670 C Dihydrofol H	Coenzyme IPR001796 [Dihydrofolate reductase domain]
ko00520 A Ferredoxin C	Energy prc IPR001433 [Oxidoreductase FAD/NAD(P)-binding] ; IP
ko00480 G Pyruvate/2 C	Energy prc IPR004099 [Pyridine nucleotide-disulphide oxidoreduc
ko04146 P Cu/Zn sup P	Inorganic i IPR001424 [Superoxide dismutase, copper/zinc binding
ko00860 P Multicopp DPM	Cell cycle c IPR001117 [Multicopper oxidase, type 1] ; IPR011706[M
ko04610 C -- --	-- IPR001102 [Transglutaminase, N-terminal] ; IPR002931
ko00230 P Purine nuc F	Nucleotide IPR000845 [Nucleoside phosphorylase domain]
ko00230 P Hypoxanth F	Nucleotide IPR000836 [Phosphoribosyltransferase domain]
ko01521 E Serine/thre T	Signal tran IPR000494 [Receptor L-domain] ; IPR001245[Serine-th
ko00010 G 3-phosph G	Carbohydr IPR001576 [Phosphoglycerate kinase]
ko00230 P Adenylate F	Nucleotide --
ko04080 N Secreted tr O	Posttransla IPR000001 [Kringle] ; IPR000294[Gamma-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
ko04080 N Secreted tr O	Posttransla IPR000001 [Kringle] ; IPR001254[Serine proteases, tryp
ko04064 N Secreted tr O	Posttransla IPR000001 [Kringle] ; IPR001254[Serine proteases, tryp
ko04371 A Secreted tr O	Posttransla IPR000001 [Kringle] ; IPR000083[Fibronectin, type I] ; IP
ko04610 C Serine pro: O	Posttransla IPR023796 [Serpin domain]
ko04610 C Uncharact R	General fu IPR001599 [Alpha-2-macroglobulin] ; IPR002890[Alph
ko04145 P Uncharact R	General fu IPR000020 [Anaphylatoxin/fibulin] ; IPR001599[Alpha-2
ko04610 C Uncharact R	General fu IPR000020 [Anaphylatoxin/fibulin] ; IPR001599[Alpha-2
ko04066 H -- --	-- IPR001820 [Protease inhibitor I35 (TIMP)]
ko04970 S -- --	-- IPR000010 [Cystatin domain]
ko04610 C ABC-type P	Inorganic i IPR000010 [Cystatin domain]
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
ko04918 T Carboxyles I	Lipid trans IPR000716 [Thyroglobulin type-1] ; IPR002018[Carboxy
ko04010 M -- --	-- IPR013576 [Insulin-like growth factor II E-peptide, C-te
ko04010 M -- --	-- IPR000975 [Interleukin-1 family] ; IPR003502[Interleukin
-- -- --	-- IPR024110 [Immunoglobulin J chain]
-- -- --	-- IPR013106 [Immunoglobulin V-set domain]
ko04144 E -- --	-- IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC
ko04144 E -- --	-- IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC

--	--	--	--	IPR000971	[Globin]
--	--	--	--	IPR000971	[Globin]
ko04151	P Autotransf	UW	Intracellular	IPR000885	[Fibrillar collagen, C-terminal] ; IPR001007[
ko04151	P Autotransf	UW	Intracellular	IPR000885	[Fibrillar collagen, C-terminal] ; IPR001007[
ko04611	P Autotransf	UW	Intracellular	IPR000885	[Fibrillar collagen, C-terminal] ; IPR001007[
ko04151	P Autotransf	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]
ko04979	C --	--	--	IPR000074	[Apolipoprotein A/E]
ko03320	P --	--	--	IPR008403	[Apolipoprotein CIII]
ko04610	C --	--	--	IPR002181	[Fibrinogen, alpha/beta/gamma chain, C-te
ko04610	C --	--	--	IPR002181	[Fibrinogen, alpha/beta/gamma chain, C-te
ko04979	C --	--	--	IPR000436	[Sushi/SCR/CCP domain] ; IPR015104[Beta-
ko04151	P Phage-rel	X	Mobilome	IPR000083	[Fibronectin, type I] ; IPR000562[Fibronectin
--	--	--	--	IPR000566	[Lipocalin/cytosolic fatty-acid binding dom
--	--	--	--	IPR000010	[Cystatin domain]
ko04918	T --	--	--	IPR014760	[Serum albumin, N-terminal]
ko04390	H --	--	--	IPR014760	[Serum albumin, N-terminal]
--	--	--	--	IPR014760	[Serum albumin, N-terminal] ; IPR015247[Vi
ko04066	H --	--	--	IPR001156	[Transferrin-like domain]
--	--	--	--	IPR001156	[Transferrin-like domain]
--	--	--	--	IPR018487	[Hemopexin-like repeats]
ko04216	F Ferritin	P	Inorganic i	IPR008331	[Ferritin/DPS protein domain]
ko04216	F Ferritin	P	Inorganic i	IPR008331	[Ferritin/DPS protein domain]
ko04610	C Secreted tr	O	Posttransla	IPR001254	[Serine proteases, trypsin domain] ; IPR0036
ko03320	P Predicted	O	Posttransla	IPR001818	[Peptidase M10, metallopeptidase] ; IPR002-
ko04610	C --	--	--	IPR000436	[Sushi/SCR/CCP domain]
ko04151	P --	--	--	IPR001212	[Somatomedin B domain] ; IPR018487[Hem
ko00380	T Catalase	P	Inorganic i	IPR010582	[Catalase immune-responsive domain] ; IPR
ko01521	E HEAT repe	R	General fu	IPR001245	[Serine-threonine/tyrosine-protein kinase c
ko00511	C Alpha-L-fu	G	Carbohydr	IPR000933	[Glycoside hydrolase, family 29] ; IPR031919
ko00010	G Fructose-k	G	Carbohydr	IPR000741	[Fructose-bisphosphate aldolase, class-I]
--	--	--	--	IPR000010	[Cystatin domain]
--	--	--	--	IPR018502	[Annexin repeat]
ko04975	F PPE-repea	S	Function u	IPR001747	[Lipid transport protein, N-terminal] ; IPR00
ko00564	G --	--	--	IPR003386	[Lecithin:cholesterol/phospholipid:diacylgly
ko04670	L --	--	--	IPR013151	[Immunoglobulin]
--	DNA repair	L	Replication	IPR001664	[Intermediate filament protein] ; IPR032444[
--	Uncharacter	S	Function u	IPR001664	[Intermediate filament protein] ; IPR032444[
ko04151	P Secreted p	R	General fu	IPR001007	[VWFC domain] ; IPR001846[von Willebranc
--	--	--	--	IPR001791	[Laminin G domain]
ko04145	P --	--	--	IPR003008	[Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko00010	G Glyceralde	G	Carbohydr	IPR020828	[Glyceraldehyde 3-phosphate dehydrogen
ko00220	A Argininosu	E	Amino acid	IPR022761	[Fumarate lyase, N-terminal] ; IPR029419[Ar
ko00500	S Glycosidas	G	Carbohydr	IPR006047	[Glycosyl hydrolase, family 13, catalytic dom
ko04010	N Molecular	O	Posttransla	IPR002068	[Alpha crystallin/Hsp20 domain]
ko00240	P Thymidylat	F	Nucleotide	IPR023451	[Thymidylate synthase/dCMP hydroxymethy
ko00510	N --	--	--	IPR007676	[Ribophorin I]
ko04015	R --	--	--	IPR001019	[Guanine nucleotide binding protein (G-prc
ko04022	c Magnesiur	P	Inorganic i	IPR004014	[Cation-transporting P-type ATPase, N-terr
ko04022	c --	--	--	IPR000402	[Sodium/potassium-transporting ATPase su
ko00010	G Fructose-k	G	Carbohydr	IPR000741	[Fructose-bisphosphate aldolase, class-I]
--	Bacterial li	M	Cell wall/r	IPR000566	[Lipocalin/cytosolic fatty-acid binding dom
ko04015	R Secreted p	R	General fu	IPR002369	[Integrin beta subunit, VWA domain] ; IPR0:
ko04015	R Secreted p	R	General fu	IPR002369	[Integrin beta subunit, VWA domain] ; IPR0:
ko04066	H Serine pro	O	Posttransla	IPR023796	[Serpine domain]
ko04610	C Serine pro	O	Posttransla	IPR023796	[Serpine domain]

ko04610 C Secreted tr O	Posttransla IPR001190 [SRCR domain] ; IPR001254[Serine protease
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain]
ko01521 E -- --	-- IPR003574 [Interleukin-6]
ko04064 N -- --	-- IPR013768 [Intercellular adhesion molecule, N-termina
ko03010 R -- --	-- --
ko03010 R -- --	-- --
ko03010 R Ribosomal J	Translatior IPR001790 [Ribosomal protein L10P]
-- Uncharact R	General fu IPR001304 [C-type lectin-like]
ko05322 S -- --	-- IPR000504 [RNA recognition motif domain] ; IPR00663
ko04918 T Serine pro O	Posttransla IPR023796 [Serp domain]
ko04610 C Serine pro O	Posttransla IPR023796 [Serp domain]
ko04015 R Secreted p R	General fu IPR002369 [Integrin beta subunit, VWA domain] ; IPR0
ko01521 E Serine/thre T	Signal tran IPR000008 [C2 domain] ; IPR000719[Protein kinase dor
-- -- --	-- IPR001664 [Intermediate filament protein]
-- Ca2+ -binc T	Signal tran IPR002048 [EF-hand domain]
ko04974 P Autotransp UW	Intracellula IPR000885 [Fibrillar collagen, C-terminal] ; IPR001007[
ko00860 P Uroporphyr H	Coenzyme IPR000257 [Uroporphyrinogen decarboxylase (URO-D)
ko04010 N Ankyrin rej T	Signal tran IPR000494 [Receptor L-domain] ; IPR001245[Serine-th
ko04071 S TolB aminc R	General fu IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
-- Carboxyles I	Lipid trans IPR002018 [Carboxylesterase, type B] ; IPR014788[Acet
ko04666 F -- --	-- IPR007123 [Gelsolin-like domain]
ko04110 C Predicted , R	General fu IPR000719 [Protein kinase domain]
ko04975 F Chromoso D	Cell cycle c IPR000074 [Apolipoprotein A/E]
ko01521 E -- --	-- IPR001040 [Translation Initiation factor eIF- 4e]
ko00330 A Protein-ari O	Posttransla IPR022413 [ATP:guanido phosphotransferase, N-termi
ko00010 G Enolase G	Carbohydr IPR020810 [Enolase, C-terminal TIM barrel domain] ; IF
ko00500 S Glucan phr 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, i U	Intracellula IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
ko00561 G Ca2+ -binc Q	Secondary IPR001024 [PLAT/LH2 domain] ; IPR013818[Lipase/vitel
ko00511 C N-acetyl-k G	Carbohydr IPR015883 [Glycoside hydrolase family 20, catalytic dor
ko05034 A -- --	-- IPR007125 [Histone H2A/H2B/H3]
-- Serine pro O	Posttransla IPR023796 [Serp domain]
ko03320 P Acyl-CoA-I	Lipid trans IPR000582 [Acyl-CoA-binding protein, ACBP]
ko03320 P -- --	-- --
ko00010 G Malate/lac C	Energy prc IPR001236 [Lactate/malate dehydrogenase, N-termina
ko00480 G Glutathion VI	Defense m IPR000889 [Glutathione peroxidase]
ko04610 C -- --	-- IPR001304 [C-type lectin-like] ; IPR001881[EGF-like cal
ko04610 C -- --	-- IPR000294 [Gamma-carboxyglutamic acid-rich (GLA) c
ko04141 P Negative r O	Posttransla IPR013766 [Thioredoxin domain]
ko04071 S -- --	-- IPR012848 [Aspartic peptidase, N-terminal] ; IPR03312:
-- -- --	-- IPR018502 [Annexin repeat]
ko04145 P -- --	-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko00910 N Carbonic a P	Inorganic i IPR001148 [Alpha carbonic anhydrase]
ko04350 T Leucine-ric K	Transcripti IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04142 L -- --	-- IPR003119 [Saposin A-type domain] ; IPR007856[Sapo:
ko00511 C N-acetyl-k G	Carbohydr IPR015883 [Glycoside hydrolase family 20, catalytic dor
ko04015 R -- --	-- IPR005455 [Profilin]
ko00010 G Phosphogl G	Carbohydr IPR013078 [Histidine phosphatase superfamily, clade-1
ko00860 P Prolyl-tRN J	Translatior IPR000738 [WHEP-TRS domain] ; IPR002314[Aminoacy
ko04140 A Cysteine p O	Posttransla IPR000668 [Peptidase C1A, papain C-terminal] ; IPR012
ko04141 P Molecular O	Posttransla IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
ko03040 S RNA recog J	Translatior IPR000504 [RNA recognition motif domain]
ko04151 P Uncharact S	Function u IPR002049 [Laminin EGF domain] ; IPR008211[Laminin,
ko04520 A Serine/thre T	Signal tran IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
ko04062 C Serine/thre T	Signal tran IPR000980 [SH2 domain] ; IPR001245[Serine-threonine

ko04015 R Alpha-tub DZ	Cell cycle c IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IPR000494 [Receptor L-domain] ; IPR001245 [Serine-threonine/tyrosine-protein kinase c]
ko01521 E Ankyrin rej T	Signal tran IPR000494 [Receptor L-domain] ; IPR001245 [Serine-threonine/tyrosine-protein kinase c]
ko04151 P Autotransport UW	Intracellular IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160 [Collagen IV, non-collagenous] ; IPR008160 [Collagen IV, non-collagenous] ; IPR008160 [Collagen IV, non-collagenous]
-- -- --	-- IPR018502 [Annexin repeat]
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain]
ko02010 A ABC-type V	Defense m IPR003439 [ABC transporter-like] ; IPR011527 [ABC transporter-like] ; IPR011527 [ABC transporter-like]
ko04150 n Glycosidase G	Carbohydr IPR006047 [Glycosyl hydrolase, family 13, catalytic domain] ; IPR006047 [Glycosyl hydrolase, family 13, catalytic domain] ; IPR006047 [Glycosyl hydrolase, family 13, catalytic domain]
ko00010 G 6-phosphatase G	Carbohydr IPR000023 [Phosphofructokinase domain]
ko04141 P Molecular O	Posttranslational IPR001404 [Heat shock protein Hsp90 family] ; IPR0035 [Heat shock protein Hsp90 family] ; IPR0035 [Heat shock protein Hsp90 family]
ko00250 A Asparagine E	Amino acid IPR001962 [Asparagine synthase] ; IPR017932 [Glutamine synthase] ; IPR017932 [Glutamine synthase]
ko01522 E Predicted iO	Posttranslational IPR000562 [Fibronectin, type II, collagen-binding] ; IPR000562 [Fibronectin, type II, collagen-binding] ; IPR000562 [Fibronectin, type II, collagen-binding]
ko04614 R Predicted iO	Posttranslational IPR008753 [Peptidase M13, N-terminal domain] ; IPR008753 [Peptidase M13, N-terminal domain] ; IPR008753 [Peptidase M13, N-terminal domain]
ko04350 T -- --	-- IPR001111 [Transforming growth factor-beta, N-terminal domain] ; IPR001111 [Transforming growth factor-beta, N-terminal domain] ; IPR001111 [Transforming growth factor-beta, N-terminal domain]
-- -- --	-- IPR000591 [DEP domain] ; IPR001849 [Pleckstrin homology domain] ; IPR001849 [Pleckstrin homology domain] ; IPR001849 [Pleckstrin homology domain]
ko04151 P Autotransport UW	Intracellular IPR001442 [Collagen IV, non-collagenous] ; IPR008160 [Collagen IV, non-collagenous] ; IPR008160 [Collagen IV, non-collagenous]
ko01521 E Ankyrin rej T	Signal tran IPR001245 [Serine-threonine/tyrosine-protein kinase c]
-- -- --	-- IPR001156 [Transferrin-like domain]
ko04145 P Cytolysin, iU	Intracellular IPR013517 [FG-GAP repeat] ; IPR013649 [Integrin alpha] ; IPR013649 [Integrin alpha] ; IPR013649 [Integrin alpha]
ko05169 E -- --	-- IPR001664 [Intermediate filament protein] ; IPR006821 [Intermediate filament protein] ; IPR006821 [Intermediate filament protein]
ko04610 C Serine protease O	Posttranslational IPR023796 [Serpine domain]
-- -- --	-- IPR001664 [Intermediate filament protein]
-- -- --	-- IPR018502 [Annexin repeat]
-- -- --	-- IPR001664 [Intermediate filament protein]
ko03010 R Ribosomal J	Translation IPR001865 [Ribosomal protein S2] ; IPR032281 [40S ribosomal protein S2] ; IPR032281 [40S ribosomal protein S2]
ko04142 L -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko00071 F Acetyl-CoA I	Lipid trans IPR020616 [Thiolase, N-terminal] ; IPR020617 [Thiolase, N-terminal] ; IPR020617 [Thiolase, N-terminal]
ko00480 G Glutathione O	Posttranslational IPR004045 [Glutathione S-transferase, N-terminal] ; IPR004045 [Glutathione S-transferase, N-terminal] ; IPR004045 [Glutathione S-transferase, N-terminal]
ko04062 C -- --	-- IPR001811 [Chemokine interleukin-8-like domain]
-- -- --	-- IPR001079 [Galectin, carbohydrate recognition domain]
ko03410 B -- --	-- IPR009071 [High mobility group box domain]
-- -- --	-- IPR000566 [Lipocalin/cytosolic fatty-acid binding domain]
ko04015 R -- --	-- IPR001019 [Guanine nucleotide binding protein (G-protein)] ; IPR001019 [Guanine nucleotide binding protein (G-protein)] ; IPR001019 [Guanine nucleotide binding protein (G-protein)]
-- -- --	-- IPR002350 [Kazal domain] ; IPR015369 [Follistatin/Osteonectin] ; IPR015369 [Follistatin/Osteonectin] ; IPR015369 [Follistatin/Osteonectin]
ko04260 C Cell division D	Cell cycle c IPR000533 [Tropomyosin]
ko04142 L -- --	-- IPR000996 [Clathrin light chain]
ko04142 L -- --	-- IPR000996 [Clathrin light chain]
-- -- Tfp pilus a: NW	Cell motility IPR018502 [Annexin repeat]
ko01521 E Serine/threonine T	Signal tran IPR001245 [Serine-threonine/tyrosine-protein kinase c]
ko03040 S RNA recognition J	Translation IPR000504 [RNA recognition motif domain] ; IPR02166 [RNA recognition motif domain] ; IPR02166 [RNA recognition motif domain]
ko04610 C Secreted transmembrane O	Posttranslational IPR000436 [Sushi/SCR/CCP domain] ; IPR000859 [CUB domain] ; IPR000859 [CUB domain]
ko03410 B WGR domain K	Transcript IPR001357 [BRCT domain] ; IPR001510 [Zinc finger, PAF] ; IPR001510 [Zinc finger, PAF]
ko00590 A Amino peptide E	Amino acid IPR014782 [Peptidase M1, membrane alanine aminopeptidase] ; IPR014782 [Peptidase M1, membrane alanine aminopeptidase] ; IPR014782 [Peptidase M1, membrane alanine aminopeptidase]
ko00010 G Fructose-1,6-bisphosphate G	Carbohydr IPR000741 [Fructose-bisphosphate aldolase, class-I]
ko04610 C Uncharacterized R	General function IPR000020 [Anaphylatoxin/fibulin] ; IPR001599 [Alpha-2-macroglobulin] ; IPR001599 [Alpha-2-macroglobulin]
ko04217 N -- --	-- IPR007125 [Histone H2A/H2B/H3] ; IPR032454 [Histone H2A/H2B/H3] ; IPR032454 [Histone H2A/H2B/H3]
-- -- --	-- IPR001810 [F-box domain] ; IPR003877 [SPRY domain]
-- -- Leucine-rich K	Transcript IPR001611 [Leucine-rich repeat]
ko03040 S Molecular O	Posttranslational IPR013126 [Heat shock protein 70 family]
-- -- GTPase SAR	General function IPR001806 [Small GTPase superfamily]
-- -- --	-- IPR007455 [Serglycin]
ko04060 C -- --	-- IPR001811 [Chemokine interleukin-8-like domain]
ko05322 S Secreted protein R	General function IPR008858 [TROVE domain]
ko04010 N GTPase SAR	General function IPR001806 [Small GTPase superfamily]
ko01521 E Ankyrin rej T	Signal tran IPR001245 [Serine-threonine/tyrosine-protein kinase c]
ko04514 C Protein tyrosine T	Signal tran IPR000242 [PTP type protein phosphatase] ; IPR003961 [PTP type protein phosphatase] ; IPR003961 [PTP type protein phosphatase]
ko04621 N Negative regulation O	Posttranslational IPR013766 [Thioredoxin domain]
ko04142 L Carboxypeptidase E	Amino acid IPR001563 [Peptidase S10, serine carboxypeptidase]
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain] ; IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IPR000884 [Thrombospondin type-1 (TSP1) repeat]

ko04610 C -- --	-- IPR002223 [Pancreatic trypsin inhibitor Kunitz domain]
ko01200 C S-formylgl V	Defense m IPR000801 [Putative esterase]
ko03018 R Chaperoni O	Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
-- -- --	-- IPR000538 [Link domain] ; IPR013106[Immunoglobulin
ko03060 P Molecular O	Posttransla IPR013126 [Heat shock protein 70 family]
ko04151 P Methyl-acNT	Cell motilit IPR000034 [Laminin IV] ; IPR002049[Laminin EGF doma
ko00740 R -- --	-- IPR000560 [Histidine phosphatase superfamily, clade-2
ko03040 S Molecular O	Posttransla IPR013126 [Heat shock protein 70 family]
ko04066 H Predicted ;G	Carbohydr IPR005828 [Major facilitator, sugar transporter-like]
-- Predicted ;G	Carbohydr IPR005828 [Major facilitator, sugar transporter-like]
-- -- --	-- IPR007477 [SAB domain] ; IPR008379[Band 4.1, C-term
ko00240 P Orotate ph F	Nucleotide IPR000836 [Phosphoribosyltransferase domain] ; IPR00
ko00010 G Pyruvate/2 C	Energy prc IPR005475 [Transketolase-like, pyrimidine-binding dor
ko00500 S Glucan phrG	Carbohydr IPR000811 [Glycosyl transferase, family 35]
ko04014 R GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko04140 A -- --	-- IPR002000 [Lysosome-associated membrane glycopro
ko04010 M PASTA dor M	Cell wall/r IPR001245 [Serine-threonine/tyrosine-protein kinase c
-- DNA topoi L	Replicatio IPR008336 [DNA topoisomerase I, DNA binding, eukan
ko01524 P DNA gyrase L	Replicatio IPR002205 [DNA topoisomerase, type IIA, subunit A/C-
ko00030 P Glucose-6 G	Carbohydr IPR022674 [Glucose-6-phosphate dehydrogenase, NA
ko04142 L -- --	-- IPR000479 [Cation-independent mannose-6-phosphat
ko00010 G Zn-depend R	General fu IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
ko01522 E Serine/thre T	Signal tran IPR000719 [Protein kinase domain]
ko00030 P Phosphoril FE	Nucleotide IPR005946 [Ribose-phosphate diphosphokinase] ; IPRC
ko03013 R RNA recog J	Translatio IPR000504 [RNA recognition motif domain] ; IPR00200-
ko03030 D DNA polyr L	Replicatio IPR022648 [Proliferating cell nuclear antigen, PCNA, N-
ko00970 A Histidyl-tR J	Translatio IPR000738 [WHEP-TRS domain] ; IPR004154[Anticodon
ko04974 P Autotransf UW	Intracellul IPR000885 [Fibrillar collagen, C-terminal] ; IPR001791[L
ko04151 P Autotransf UW	Intracellul IPR002035 [von Willebrand factor, type A] ; IPR008160[
ko04151 P Autotransf UW	Intracellul IPR002035 [von Willebrand factor, type A] ; IPR008160[
ko04151 P Transcripti K	Transcripti IPR002035 [von Willebrand factor, type A] ; IPR002223[
ko04610 C Multicopp DPM	Cell cycle c IPR000421 [Coagulation factor 5/8 C-terminal domain]
ko00230 P CBS doma T	Signal tran IPR000644 [CBS domain] ; IPR001093[IMP dehydrogen
ko00330 A Protein-ar O	Posttransla IPR022413 [ATP:guanido phosphotransferase, N-termi
ko00330 A Protein-ar O	Posttransla IPR022413 [ATP:guanido phosphotransferase, N-termi
ko04510 F -- --	-- IPR001715 [Calponin homology domain] ; IPR002017[S
ko01521 E Serine/thre T	Signal tran IPR000980 [SH2 domain] ; IPR001245[Serine-threonine
-- Xaa-Pro ar E	Amino acid IPR000994 [Peptidase M24] ; IPR007865[Aminopeptida
ko03450 N -- --	-- IPR003034 [SAP domain] ; IPR005160[Ku70/Ku80 C-ter
ko03450 N -- --	-- IPR005160 [Ku70/Ku80 C-terminal arm] ; IPR005161[Ku
ko04140 A -- --	-- IPR002000 [Lysosome-associated membrane glycopro
-- Leucine-rich K	Transcripti IPR001611 [Leucine-rich repeat]
-- Tfp pilus a NW	Cell motilit IPR000859 [CUB domain] ; IPR001506[Peptidase M12A]
ko04530 T Uncharact S	Function u IPR001609 [Myosin head, motor domain] ; IPR002928[F
ko04514 C Uncharact S	Function u IPR003961 [Fibronectin type III] ; IPR013098[Immunogl
ko04514 C Spore coat M	Cell wall/r IPR000436 [Sushi/SCR/CCP domain] ; IPR000538[Link c
ko04151 P Cytolysin, U	Intracellul IPR013517 [FG-GAP repeat] ; IPR013649[Integrin alpha
ko04152 A Translator J	Translatio IPR000640 [Translation elongation factor EFG, V domai
-- -- --	-- IPR001664 [Intermediate filament protein]
-- -- --	-- IPR001664 [Intermediate filament protein] ; IPR032444[
ko04141 P Negative r O	Posttransla IPR013766 [Thioredoxin domain]
-- -- --	-- IPR018105 [Translationally controlled tumour protein]
ko00860 P Delta-amir H	Coenzyme IPR001731 [Delta-aminolevulinic acid dehydratase]
-- -- --	-- IPR001715 [Calponin homology domain] ; IPR002048[E
-- -- --	-- IPR001715 [Calponin homology domain] ; IPR002048[E
-- Dipeptidyl E	Amino acid IPR001375 [Peptidase S9, prolyl oligopeptidase, catalyt
ko00500 S Glycosyltra M	Cell wall/r IPR008631 [Glycogen synthase]
ko04910 Ir cAMP-bin T	Signal tran IPR000595 [Cyclic nucleotide-binding domain] ; IPR00:

ko00010 G Enolase G	Carbohydr IPR020810 [Enolase, C-terminal TIM barrel domain] ; IF
ko03022 B -- --	-- IPR003196 [Transcription initiation factor IIF, beta subu
ko00350 T Phenylpyru Q	Secondary IPR001398 [Macrophage migration inhibitory factor]
ko04141 P Cell divisio D	Cell cycle c IPR002048 [EF-hand domain] ; IPR009011[Mannose-6-
ko00900 T Geranylger H	Coenzyme IPR000092 [Polyprenyl synthetase]
-- Murein trix M	Cell wall/r IPR000834 [Peptidase M14, carboxypeptidase A]
-- Glucose/ar G	Carbohydr IPR000033 [LDLR class B repeat] ; IPR000716[Thyroglob
ko00010 G Aldo/keto Q	Secondary IPR023210 [NADP-dependent oxidoreductase domain]
ko00010 G Phosphohi T	Signal tran IPR015793 [Pyruvate kinase, barrel] ; IPR015795[Pyruva
ko04141 P Molecular O	Posttransla IPR001404 [Heat shock protein Hsp90 family] ; IPR0035
ko03040 S -- --	-- IPR001163 [LSM domain, eukaryotic/archaea-type]
ko01522 E Predicted i O	Posttransla IPR000562 [Fibronectin, type II, collagen-binding] ; IPR
-- -- --	-- IPR000504 [RNA recognition motif domain]
ko05200 P -- --	-- IPR000225 [Armadillo]
ko00220 A Glutamine E	Amino acid IPR008146 [Glutamine synthetase, catalytic domain] ; IF
ko00040 P Aldo/keto Q	Secondary IPR023210 [NADP-dependent oxidoreductase domain]
ko00480 G Aminopep E	Amino acid IPR014782 [Peptidase M1, membrane alanine aminope
ko04514 C -- --	-- IPR013106 [Immunoglobulin V-set domain] ; IPR01316
-- Bacillopep O	Posttransla IPR000834 [Peptidase M14, carboxypeptidase A]
ko04060 C -- --	-- IPR003961 [Fibronectin type III] ; IPR021126[Interferon
-- -- --	-- IPR001578 [Peptidase C12, ubiquitin carboxyl-terminal
ko04610 C -- --	-- IPR000436 [Sushi/SCR/CCP domain]
ko00230 P Nucleoside F	Nucleotide IPR001564 [Nucleoside diphosphate kinase]
ko00130 U Putative N. R	General fu IPR003680 [Flavodoxin-like fold]
ko03010 R Ribosomal J	Translatio IPR005324 [Ribosomal protein S5, C-terminal] ; IPR013
peptidase i -- --	-- IPR001820 [Protease inhibitor I35 (TIMP)]
ko04512 E -- --	-- IPR000538 [Link domain]
-- Spore coat M	Cell wall/r IPR000436 [Sushi/SCR/CCP domain] ; IPR000538[Link c
ko04012 E -- --	-- IPR000980 [SH2 domain] ; IPR001452[SH3 domain]
-- -- --	-- IPR005818 [Linker histone H1/H5, domain H15]
-- -- --	-- IPR005818 [Linker histone H1/H5, domain H15]
ko00562 Ir -- --	-- IPR000008 [C2 domain] ; IPR000909[Phosphatidylinosit
ko00350 T 2-keto-4- Q	Secondary IPR011234 [Fumarylacetoacetase, C-terminal-related] ;
ko04010 N -- --	-- IPR000956 [Stathmin family]
ko04530 T Cold shock K	Transcripti IPR002059 [Cold-shock protein, DNA-binding]
ko03040 S Molecular O	Posttransla IPR013126 [Heat shock protein 70 family]
ko04910 Ir GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- -- --	-- --
ko00220 A Aspartate/ E	Amino acid IPR004839 [Aminotransferase, class I/classII]
ko04145 P Ca2+ -binc Q	Secondary IPR002035 [von Willebrand factor, type A] ; IPR013517[
ko04540 G -- --	-- IPR013092 [Connexin, N-terminal] ; IPR013124[Gap junc
ko00120 P Aldo/keto Q	Secondary IPR023210 [NADP-dependent oxidoreductase domain]
ko04141 P Serine pro: O	Posttransla IPR001300 [Peptidase C2, calpain, catalytic domain] ; IF
ko00240 P CTP synth: F	Nucleotide IPR017456 [CTP synthase, N-terminal] ; IPR017926[Glu
ko03040 S Superfamil L	Replicatio IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
ko00010 G 6-phospho G	Carbohydr IPR000023 [Phosphofructokinase domain]
ko04115 p -- --	-- IPR000716 [Thyroglobulin type-1] ; IPR000867[Insulin-
ko04010 N Periplasmic U	Intracellul IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko03050 P ATP-depe: O	Posttransla IPR003959 [ATPase, AAA-type, core]
-- Chaperoni O	Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
ko04520 A Protein tyr T	Signal tran IPR000242 [PTP type protein phosphatase]
-- -- --	-- IPR000716 [Thyroglobulin type-1] ; IPR000867[Insulin-
ko03010 R Ribosomal J	Translatio IPR001780 [Ribosomal protein L35A]
-- 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]
-- Protein tyr T	Signal tran IPR000242 [PTP type protein phosphatase]
ko03010 R Ribosomal J	Translatio IPR001063 [Ribosomal protein L22/L17]

ko00010 G Phosphoglucose	Carbohydr IPR013078 [Histidine phosphatase superfamily, clade-1
-- Alpha-tubulin DZ	Cell cycle c IPR000408 [Regulator of chromosome condensation, R
ko03030 D ATP-dependent L	Replication IPR012308 [DNA ligase, ATP-dependent, N-terminal] ;
-- DNA-binding R	General function IPR000323 [Copper type II, ascorbate-dependent mono
ko04514 C Large exon U	Intracellular IPR000233 [Cadherin, cytoplasmic domain] ; IPR002126
ko05130 P RNA recognition J	Translation IPR000504 [RNA recognition motif domain]
ko00010 G Hexokinase G	Carbohydr IPR022672 [Hexokinase, N-terminal] ; IPR022673 [Hexol
ko00230 P DNA-directed K	Transcription IPR011262 [DNA-directed RNA polymerase, insert dom
ko04010 N -- --	-- IPR000488 [Death domain] ; IPR001368 [TNFR/NGFR cy
ko04141 P Serine/threonine T	Signal transduction IPR000719 [Protein kinase domain] ; IPR014720 [Double
ko00270 C Spermidine E	Amino acids --
ko04024 c NhaP-type P	Inorganic i IPR006153 [Cation/H ⁺ exchanger] ; IPR032103 [Sodium
ko03008 R Serine/threonine T	Signal transduction IPR000719 [Protein kinase domain]
-- Secreted p R	General function IPR002035 [von Willebrand factor, type A] ; IPR010600 [
-- Secreted p R	General function IPR002035 [von Willebrand factor, type A] ; IPR010600 [
ko03013 R Translation J	Translation IPR002735 [Translation initiation factor IF2/IF5]
-- GTPase SAR	General function IPR001806 [Small GTPase superfamily]
ko04144 E GTPase SAR	General function IPR001806 [Small GTPase superfamily]
-- GTPase SAR	General function IPR001806 [Small GTPase superfamily]
ko00230 P Signal transduction T	Signal transduction IPR001054 [Adenylyl cyclase class-3/4/guanylyl cyclase
ko03050 P 20S proteasome O	Posttranslational IPR001353 [Proteasome, subunit alpha/beta]
ko04210 A -- --	-- IPR001322 [Lamin Tail Domain] ; IPR001664 [Intermediate
-- Uncharacterized R	General function IPR001599 [Alpha-2-macroglobulin] ; IPR002890 [Alpha
-- Leucine-rich K	Transcription IPR001611 [Leucine-rich repeat]
ko04151 P Autotransporter UW	Intracellular IPR008160 [Collagen triple helix repeat]
ko04974 P Autotransporter UW	Intracellular IPR000885 [Fibrillar collagen, C-terminal] ; IPR008160 [C
ko04010 N -- --	-- 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] ; IPR
ko00190 C Archaeal/v C	Energy processing IPR000194 [ATPase, F1/V1/A1 complex, alpha/beta sub
ko00190 C -- --	-- IPR004907 [ATPase, V1 complex, subunit C]
-- -- --	-- IPR001781 [Zinc finger, LIM-type]
ko04010 N Autotransporter U	Intracellular IPR001715 [Calponin homology domain] ; IPR017868 [F
ko01521 E -- --	-- IPR001251 [CRAL-TRIO lipid binding domain] ; IPR0019
ko00020 C Aconitase C	Energy processing IPR000573 [Aconitase A/isopropylmalate dehydratase s
ko04068 F -- --	-- IPR000276 [G protein-coupled receptor, rhodopsin-like
ko00230 P 2',3'-cyclic FV	Nucleotide IPR004843 [Calcineurin-like phosphoesterase domain,
-- Leucine-rich K	Transcription IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04640 H -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko00140 S Predicted (R	General function IPR002935 [O-methyltransferase, family 3]
ko05016 H -- --	-- IPR001102 [Transglutaminase, N-terminal] ; IPR002931
-- -- --	-- IPR000648 [Oxysterol-binding protein] ; IPR001849 [Ple
ko00230 P Phosphoryl F	Nucleotide IPR002376 [Formyl transferase, N-terminal] ; IPR010918
ko04151 P Phage-related X	Mobilome IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
ko00230 P Phosphoryl F	Nucleotide IPR000031 [PurE domain] ; IPR028923 [SAICAR synthetase
ko00564 G Carboxylesterase I	Lipid trans IPR002018 [Carboxylesterase, type B] ; IPR014788 [Acetyl
ko04120 U Ubiquitin O	Posttranslational IPR000594 [THIF-type NAD/FAD binding fold] ; IPR018
ko00480 G Glutathione VI	Defense mechanism IPR000889 [Glutathione peroxidase]
ko00230 P Nucleoside F	Nucleotide IPR001564 [Nucleoside diphosphate kinase]
ko00230 P Predicted (R	General function IPR001212 [Somatomedin B domain] ; IPR001604 [DNA
-- RNA recognition J	Translation IPR000504 [RNA recognition motif domain]
-- -- --	-- IPR000716 [Thyroglobulin type-1] ; IPR000867 [Insulin-
ko01522 E WD40 repeat R	General function IPR000719 [Protein kinase domain]
-- -- --	-- IPR001881 [EGF-like calcium-binding domain] ; IPR026
ko04151 P Cytolysin, (U	Intracellular IPR013517 [FG-GAP repeat] ; IPR013649 [Integrin alpha
-- RNA recognition J	Translation IPR000504 [RNA recognition motif domain] ; IPR01297
ko05165 H Cell division D	Cell cycle c IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316 [

--	Peptidyl-p O	Posttransla	IPR002130	[Cyclophilin-type peptidyl-prolyl cis-trans is
--	--	--	IPR002048	[EF-hand domain] ; IPR013787[S100/CaBP-
ko03010 R	Ribosomal J	Translatior	IPR004044	[K Homology domain, type 2]
ko01521 E	PASTA dor M	Cell wall/r	IPR001245	[Serine-threonine/tyrosine-protein kinase c
--	Protein tyr T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR003961
--	Protein tyr T	Signal tran	IPR000242	[PTP type protein phosphatase]
--	Protein tyr T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR001148
ko05120 E	Protein tyr T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR001148
ko00270 C	S-adenosy H	Coenzyme	IPR000043	[Adenosylhomocysteinase] ; IPR015878[S-a
ko04360 A	--	--	IPR002108	[Actin-depolymerising factor homology dor
ko03013 R	--	--	IPR000504	[RNA recognition motif domain]
ko00562 Ir	--	--	IPR005522	[Inositol polyphosphate kinase]
ko00240 P	Thymidylai F	Nucleotide	--	
ko00230 P	Ribonucleo F	Nucleotide	IPR000788	[Ribonucleotide reductase large subunit, C-
ko04151 P	DNA repai L	Replicatio	IPR000034	[Laminin IV] ; IPR001791[Laminin G domain]
--	--	--	IPR018203	[GDP dissociation inhibitor]
ko04060 C	--	--	IPR015319	[Interleukin-4 receptor alpha, N-terminal]
--	--	--	IPR014038	[Translation elongation factor EF1B, beta/de
ko00730 T	Protein-tyl T	Signal tran	IPR023485	[Phosphotyrosine protein phosphatase I sup
ko04151 P	Phage-rela X	Mobilome	IPR002181	[Fibrinogen, alpha/beta/gamma chain, C-te
ko04068 F	Serine/thre T	Signal tran	IPR000719	[Protein kinase domain]
ko04062 C	Serine/thre T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001849[Pleckst
ko04015 R	--	--	IPR000276	[G protein-coupled receptor, rhodopsin-lik
ko03030 D	DNA replic L	Replicatio	IPR001208	[MCM domain] ; IPR027925[MCM N-termin
ko00270 C	3-mercapt P	Inorganic i	IPR001763	[Rhodanese-like domain]
ko04151 P	Chromoso D	Cell cycle c	IPR000034	[Laminin IV] ; IPR001791[Laminin G domain]
ko03010 R	Ribosomal J	Translatior	IPR004038	[Ribosomal protein L7Ae/L30e/S12e/Gadd4
ko04141 P	DnaJ-class O	Posttransla	IPR001623	[DnaJ domain] ; IPR002939[Chaperone Dna
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
ko04151 P	Cytolysin, ;U	Intracellula	IPR013517	[FG-GAP repeat] ; IPR013649[Integrin alpha
--	Autotransf U	Intracellula	IPR001759	[Pentraxin-related]
ko04530 T	--	--	IPR011259	[Ezrin/radixin/moesin, C-terminal] ; IPR0189
ko04390 H	--	--	IPR006077	[Vinculin/alpha-catenin]
ko00270 C	Site-specif L	Replicatio	IPR001025	[Bromo adjacent homology (BAH) domain]
ko03040 S	RNA recog J	Translatior	IPR000504	[RNA recognition motif domain]
ko03010 R	Ribosomal J	Translatior	IPR001380	[Ribosomal protein L13e]
--	--	--	IPR009071	[High mobility group box domain]
ko00970 A	Threonyl-t J	Translatior	IPR002314	[Aminoacyl-tRNA synthetase, class II (G/ P/
ko00970 A	Tfp pilus a: NW	Cell motilit	IPR002300	[Aminoacyl-tRNA synthetase, class Ia] ; IPRC
ko05134 L	Glutathion O	Posttransla	IPR001662	[Translation elongation factor EF1B, gamma
--	Secreted tr O	Posttransla	IPR000001	[Kringle] ; IPR001254[Serine proteases, tryps
--	Regulator : O	Posttransla	IPR001107	[Band 7 domain]
ko04110 C	--	--	IPR023410	[14-3-3 domain]
ko01521 E	Serine/thre T	Signal tran	IPR000719	[Protein kinase domain]
--	PASTA dor M	Cell wall/r	IPR000719	[Protein kinase domain] ; IPR001772[Kinase
ko03010 R	Ribosomal J	Translatior	IPR016180	[Ribosomal protein L10e/L16]
--	Autotransf UW	Intracellula	IPR001073	[C1q domain] ; IPR008160[Collagen triple h
ko03030 D	ssDNA-bir L	Replicatio	IPR004365	[OB-fold nucleic acid binding domain, AA-t
ko03410 B	Exonuclea: L	Replicatio	IPR005135	[Endonuclease/exonuclease/phosphatase]
ko04115 p	--	--	IPR018499	[Tetraspanin/Peripherin]
ko00240 P	Carbamoyl EF	Amino acid	IPR002474	[Carbamoyl-phosphate synthase, small subu
--	--	--	IPR001084	[Microtubule associated protein, tubulin-bi
ko01521 E	--	--	IPR000198	[Rho GTPase-activating protein domain] ; IF
ko03050 P	20S protea O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]
ko03050 P	20S protea O	Posttransla	IPR000426	[Proteasome alpha-subunit, N-terminal dor

ko03050 P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]	
ko03050 P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]	
ko03050 P 20S protea	O	Posttransla	IPR001353	[Proteasome, subunit alpha/beta]	
ko00230 P DNA polyr	L	Replicatio	IPR006133	[DNA-directed DNA polymerase, family B, e	
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	
ko00330 A Leucyl ami	E	Amino acic	IPR000819	[Peptidase M17, leucyl aminopeptidase, C-t	
ko00562 Ir Archaeal fr	G	Carbohydr	IPR000760	[Inositol monophosphatase-like]	
ko04371 A --	--	--	IPR000867	[Insulin-like growth factor-binding protein,	
ko04010 N Ankyrin rej	T	Signal tran	IPR001090	[Ephrin receptor ligand binding domain] ; IF	
ko04360 A Ankyrin rej	T	Signal tran	IPR001090	[Ephrin receptor ligand binding domain] ; IF	
ko01521 E --	--	--	IPR000980	[SH2 domain] ; IPR006020[PTB/PI domain]	
--	--	--	IPR000566	[Lipocalin/cytosolic fatty-acid binding dom	
ko00030 P Transketol	G	Carbohydr	IPR005474	[Transketolase, N-terminal] ; IPR005475[Tra	
ko04217 N Serine/thre	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c	
ko05168 H --	--	--	IPR014038	[Translation elongation factor EF1B, beta/de	
ko04666 F --	--	--	IPR002101	[Myristoylated alanine-rich C-kinase substr	
ko01100 N Alkyl hydr	V	Defense m	IPR000866	[Alkyl hydroperoxide reductase subunit C/ 1	
ko04146 P Peroxiredc	O	Posttransla	IPR013740	[Redoxin]	
--	Phenylpyr	Q	Secondary	IPR001398	[Macrophage migration inhibitory factor]
ko03010 R Ribosomal	J	Translatio	IPR020783	[Ribosomal protein L11, C-terminal] ; IPR02	
ko00240 P Adenylate	F	Nucleotide	--	--	
--	Uncharact	R	General fu	IPR008914	[Phosphatidylethanolamine-binding proteir
ko04141 P Negative r	O	Posttransla	IPR013766	[Thioredoxin domain]	
ko04110 C Tetratricop	R	General fu	IPR001440	[Tetratricopeptide repeat 1] ; IPR019734[Tet	
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	
--	--	--	IPR002048	[EF-hand domain]	
ko05206 N 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,	
ko04145 P Membrane	M	Cell wall/r	IPR001680	[WD40 repeat] ; IPR015048[Domain of unkn	
--	--	--	IPR018203	[GDP dissociation inhibitor]	
ko04657 IL --	--	--	IPR013787	[S100/CaBP-9k-type, calcium binding, subc	
ko04910 Ir cAMP-bin	T	Signal tran	IPR000595	[Cyclic nucleotide-binding domain] ; IPR00	
ko00230 P Ribonucle	F	Nucleotide	IPR000358	[Ribonucleotide reductase small subunit fan	
ko04512 E --	--	--	IPR027789	[Syndecan/Neurexin domain]	
--	Na+ -depe	R	General fu	IPR000175	[Sodium:neurotransmitter symporter]
ko04141 P DnaJ-class	O	Posttransla	IPR001305	[Heat shock protein DnaJ, cysteine-rich don	
ko01521 E Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001849[Pleckst	
ko00230 P AICAR trar	F	Nucleotide	IPR002695	[AICARFT/IMPCHase bienzyme] ; IPR011607	
ko04110 C --	--	--	IPR023410	[14-3-3 domain]	
ko05020 P Uncharact	S	Function u	IPR011990	[Tetratricopeptide-like helical domain] ; IPR	
--	--	--	IPR002048	[EF-hand domain] ; IPR013787[S100/CaBP-	
--	Alkyl hydr	V	Defense m	IPR000866	[Alkyl hydroperoxide reductase subunit C/ 1
ko04010 N --	--	--	IPR011021	[Arrestin-like, N-terminal] ; IPR011022[Arre	
ko00130 U 4-hydroxy	ER	Amino acic	IPR004360	[Glyoxalase/fosfomycin resistance/dioxygen	
ko04130 S --	--	--	IPR000727	[Target SNARE coiled-coil homology doma	
ko00260 G Cystathion	E	Amino acic	IPR000277	[Cys/Met metabolism, pyridoxal phosphate-	
ko03010 R Ribosomal	J	Translatio	IPR020040	[Ribosomal protein L6, alpha-beta domain]	
ko04060 C --	--	--	IPR006052	[Tumour necrosis factor domain]	
ko00061 F Long-chai	I	Lipid trans	IPR000873	[AMP-dependent synthetase/ligase]	
ko04514 C Large exo	U	Intracellul	IPR000233	[Cadherin, cytoplasmic domain] ; IPR00212	
ko04144 E --	--	--	IPR001752	[Kinesin motor domain]	
ko00240 P dUTPase	FV	Nucleotide	IPR008180	[Deoxyuridine triphosphate nucleotidohydr	
ko01523 A ABC-type	V	Defense m	IPR003439	[ABC transporter-like] ; IPR011527[ABC tran	
ko00510 N --	--	--	IPR001382	[Glycoside hydrolase family 47]	
ko03030 D DNA replic	L	Replicatio	IPR001208	[MCM domain] ; IPR027925[MCM N-termin	

ko03030 D DNA replic L	Replicatio	IPR001208 [MCM domain] ; IPR027925[MCM N-termin
-- -- --	--	IPR023412 [Ribonuclease A-domain]
ko04142 L -- --	--	IPR002000 [Lysosome-associated membrane glycopro
ko00260 G Glycine/ser E	Amino acid	IPR001085 [Serine hydroxymethyltransferase]
ko00260 G Glycine/ser E	Amino acid	IPR001085 [Serine hydroxymethyltransferase]
ko00590 A Lysophosphol	Lipid trans	IPR000073 [Alpha/beta hydrolase fold-1] ; IPR023214[
ko05205 P -- --	--	IPR001863 [Glypican]
ko04015 R -- --	--	IPR005455 [Profilin]
ko04015 R -- --	--	IPR000225 [Armadillo]
ko05146 A Serine pro:O	Posttransla	IPR023796 [Serpine domain]
ko04390 H -- --	--	IPR011259 [Ezrin/radixin/moesin, C-terminal] ; IPR0189
ko04530 T -- --	--	IPR011259 [Ezrin/radixin/moesin, C-terminal] ; IPR0189
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]
ko00590 A Cytochrome QV	Secondary	IPR000742 [EGF-like domain] ; IPR019791[Haem perox
ko04020 C -- --	--	IPR000276 [G protein-coupled receptor, rhodopsin-lik
ko04145 P Alpha-tub DZ	Cell cycle c	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IP
ko04145 P Alpha-tub DZ	Cell cycle c	IPR001881 [EGF-like calcium-binding domain] ; IPR003
ko00260 G CBS doma T	Signal tran	IPR000644 [CBS domain] ; IPR001926[Tryptophan synt
-- -- --	--	IPR001664 [Intermediate filament protein]
-- -- --	--	IPR001881 [EGF-like calcium-binding domain] ; IPR017
ko00500 S Glycogen c G	Carbohydr	IPR029436 [Eukaryotic glycogen debranching enzyme,
ko04530 T Chromoso D	Cell cycle c	IPR001609 [Myosin head, motor domain] ; IPR002928[
ko04530 T Chromoso D	Cell cycle c	IPR000048 [IQ motif, EF-hand binding site] ; IPR001609
-- Serine/thr c T	Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
-- WD40 rep c R	General fu	IPR001680 [WD40 repeat] ; IPR006692[Coatomer, WD c
ko05412 A -- --	--	IPR001715 [Calponin homology domain] ; IPR002017[S
-- Ribulose-5 G	Carbohydr	IPR001303 [Class II aldolase/adducin N-terminal]
-- -- --	--	--
ko05202 T RNA recog J	Translatio	IPR000504 [RNA recognition motif domain] ; IPR00187
-- -- --	--	IPR014876 [DEK, C-terminal]
-- Glutaredox O	Posttransla	IPR002109 [Glutaredoxin]
ko04010 N Serine/thr c T	Signal tran	IPR001932 [PPM-type phosphatase domain] ; IPR0129
-- Leucine-rich K	Transcripti	IPR000372 [Leucine-rich repeat N-terminal domain] ; I
-- Uncharacter S	Function u	IPR001664 [Intermediate filament protein] ; IPR032444[
ko03050 P ATP-depe c O	Posttransla	IPR003959 [ATPase, AAA-type, core]
-- -- --	--	IPR013092 [Connexin, N-terminal]
-- GTPase SAR	General fu	IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko01521 E Serine/thr c T	Signal tran	IPR000719 [Protein kinase domain]
ko03010 R Ribosomal J	Translatio	IPR002136 [Ribosomal protein L4/L1e] ; IPR025755[60S
-- ADP-ribos F	Nucleotide	IPR000086 [NUDIX hydrolase domain]
ko00010 G Phosphogl G	Carbohydr	IPR005843 [Alpha-D-phosphohexomutase, C-terminal
ko04060 C Serine/thr c T	Signal tran	IPR000472 [Activin types I and II receptor domain] ; IPR
ko04060 C Serine/thr c T	Signal tran	IPR000472 [Activin types I and II receptor domain] ; IPR
ko04010 N Serine/thr c T	Signal tran	IPR000472 [Activin types I and II receptor domain] ; IPR
-- Ribosome J	Translatio	IPR006073 [GTP binding domain]
ko04060 C -- --	--	IPR001368 [TNFR/NGFR cysteine-rich region]
ko04310 V Serine pro:O	Posttransla	IPR023796 [Serpine domain]
ko00480 G Glutathion VI	Defense m	IPR000889 [Glutathione peroxidase]
ko04010 N Serine/thr c T	Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
-- Ca2+ -binc T	Signal tran	IPR002048 [EF-hand domain]
-- -- --	--	IPR000557 [Calponin repeat] ; IPR001715[Calponin hor
ko00030 P Transaldol. G	Carbohydr	IPR001585 [Transaldolase/Fructose-6-phosphate aldol
ko00190 C Archaeal/v C	Energy prc	IPR000194 [ATPase, F1/V1/A1 complex, alpha/beta sub
ko03018 R Molecular O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko03013 R Superfamil L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/D
ko03010 R Ribosomal J	Translatio	IPR000597 [Ribosomal protein L3]

ko04974	P Autotransf	UW	Intracellular	IPR008160	[Collagen triple helix repeat] ; IPR010515[Co
ko04974	P Autotransf	UW	Intracellular	IPR008160	[Collagen triple helix repeat] ; IPR010363[Do
ko00510	N --	--	--	IPR005013	[Dolichyl-diphosphooligosaccharide--prote
ko03030	D 5'-3' exon	L	Replicatio	IPR006085	[XPG N-terminal] ; IPR006086[XPG-I domain
--	--	--	--	IPR007123	[Gelsolin-like domain]
--	--	--	--	IPR013912	[Adenylate cyclase-associated CAP, C-term
ko04060	C --	--	--	IPR003961	[Fibronectin type III] ; IPR010457[Immunogl
--	Chaperon	O	Posttransl	IPR002423	[Chaperonin Cpn60/TCP-1 family]
ko00760	N --	--	--	IPR000940	[Methyltransferase, NNMT/PNMT/TEMT]
ko03010	R Ribosomal	J	Translator	IPR005822	[Ribosomal protein L13]
--	GTPase	SAR	General fu	IPR006689	[Small GTPase superfamily, ARF/SAR type]
ko01521	E --	--	--	IPR000980	[SH2 domain] ; IPR013799[STAT transcrip
ko04137	N --	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko00020	C Malate/lac	C	Energy prc	IPR001236	[Lactate/malate dehydrogenase, N-termina
ko03030	D DNA polyr	L	Replicatio	IPR003959	[ATPase, AAA-type, core] ; IPR013748[Repli
ko03030	D DNA polyr	L	Replicatio	--	--
ko03013	R Translator	J	Translator	IPR004161	[Translation elongation factor EFTu-like, do
ko04150	n --	--	--	IPR005817	[Wnt]
--	Ribosomal	J	Translator	IPR000182	[GNAT domain]
ko05120	E PASTA	dor M	Cell wall/r	IPR000980	[SH2 domain] ; IPR001245[Serine-threonine
ko00970	A Glycyl-tRN	J	Translator	IPR000738	[WHEP-TRS domain] ; IPR002314[Aminoacy
ko00970	A Isoleucyl-t	J	Translator	IPR002300	[Aminoacyl-tRNA synthetase, class Ia] ; IPRC
ko01523	A --	--	--	IPR002666	[Reduced folate carrier]
ko04015	R Serine/thre	T	Signal tran	IPR000270	[PB1 domain] ; IPR000719[Protein kinase dc
--	Actin-relat	Z	Cytoskelet	IPR004000	[Actin family]
--	--	--	--	IPR003887	[LEM domain] ; IPR013146[LEM-like domain
ko04012	E --	--	--	IPR000980	[SH2 domain] ; IPR013799[STAT transcrip
ko03018	R Superfamil	L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/D
ko00562	Ir --	--	--	IPR000341	[Phosphatidylinositol 3-kinase Ras-binding
ko01521	E --	--	--	IPR000403	[Phosphatidylinositol 3-/4-kinase, catalytic
ko00562	Ir --	--	--	IPR000403	[Phosphatidylinositol 3-/4-kinase, catalytic
--	--	--	--	IPR002885	[Pentatricopeptide repeat] ; IPR033443[Pent
ko03010	R Ribosomal	J	Translator	IPR001854	[Ribosomal protein L29]
--	--	--	--	IPR024613	[Huntingtin, middle-repeat]
--	Predicted	O	Posttransl	IPR008753	[Peptidase M13, N-terminal domain] ; IPR0
--	Na+/H+-c	C	Energy prc	IPR001991	[Sodium:dicarboxylate symporter]
ko00565	E WD40 rep	R	General fu	IPR001680	[WD40 repeat] ; IPR006594[LIS1 homology
--	--	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01315
ko01524	P DNA mism	L	Replicatio	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
--	--	--	--	IPR014760	[Serum albumin, N-terminal]
--	Peptidyl-p	O	Posttransl	IPR002130	[Cyclophilin-type peptidyl-prolyl cis-trans i
ko04020	C --	--	--	IPR027246	[Eukaryotic porin/Tom40]
ko04020	C Glucoamyl	G	Carbohydr	IPR011613	[Glycoside hydrolase family 15/Phosphoryla
ko03013	R Leucine-rich	K	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR009109[Ran-GTP
--	Superfamil	L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/D
ko04010	N --	--	--	IPR000980	[SH2 domain] ; IPR001452[SH3 domain] ; IP
ko04010	N --	--	--	IPR000980	[SH2 domain] ; IPR001452[SH3 domain] ; IP
--	Ubiquitin	O	Posttransl	IPR000626	[Ubiquitin domain] ; IPR021925[Protein of u
ko01522	E Ankyrin re	T	Signal tran	IPR000742	[EGF-like domain] ; IPR000800[Notch doma
ko04010	N Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
ko03010	R Ribosomal	J	Translator	IPR021131	[Ribosomal protein L18e/L15P]
ko03010	R Ribosomal	J	Translator	IPR001147	[Ribosomal protein L21e]
ko03010	R --	--	--	IPR029004	[Ribosomal L28e/Mak16]
ko03010	R Ribosomal	J	Translator	IPR001912	[Ribosomal protein S4/S9, N-terminal] ; IPR
ko03010	R --	--	--	IPR005326	[Plectin/S10, N-terminal]

ko00520 A 6-phospho G	Carbohydr IPR006148 [Glucosamine/galactosamine-6-phosphate
-- -- --	-- IPR000433 [Zinc finger, ZZ-type] ; IPR001715[Calponin
ko04520 A -- --	-- IPR000048 [IQ motif, EF-hand binding site] ; IPR000595
ko00380 T Mannose- G	Carbohydr IPR010329 [3-hydroxyanthranilic acid dioxygenase]
ko04144 E -- --	-- IPR002189 [F-actin-capping protein subunit alpha]
ko00010 G Acyl-CoA :C	Energy prc IPR015590 [Aldehyde dehydrogenase domain]
ko03010 R -- --	-- IPR002673 [Ribosomal protein L29e]
-- WGR dom.K	Transcripti IPR001079 [Galectin, carbohydrate recognition domain
-- Na+ -depe R	General fu IPR000175 [Sodium:neurotransmitter symporter]
-- -- --	-- IPR001781 [Zinc finger, LIM-type]
-- Uncharact.S	Function u IPR014044 [CAP domain]
-- Na+ -depe R	General fu IPR000175 [Sodium:neurotransmitter symporter]
ko04614 R Prolyl oligo E	Amino aci IPR001375 [Peptidase S9, prolyl oligopeptidase, catalyt
ko00620 P Malic enzy C	Energy prc IPR012301 [Malic enzyme, N-terminal domain] ; IPR012
ko00100 S Squalene c l	Lipid trans IPR032696 [Squalene cyclase, C-terminal] ; IPR032697[
ko00270 C -- --	-- IPR004308 [Glutamate-cysteine ligase catalytic subunit
ko00270 C Aldo/keto Q	Secondary IPR023210 [NADP-dependent oxidoreductase domain]
-- -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko03050 P -- --	-- IPR033464 [CSN8/PSMD8/EIF3K]
-- Chaperoni O	Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
-- Molecular O	Posttransla IPR013126 [Heat shock protein 70 family]
ko04310 V Serine/thre T	Signal tran IPR000719 [Protein kinase domain]
ko04340 H Serine/thre T	Signal tran IPR000719 [Protein kinase domain]
ko00020 C Isocitrate c C	Energy prc IPR024084 [Isopropylmalate dehydrogenase-like doma
ko00562 Ir -- --	-- IPR000341 [Phosphatidylinositol 3-kinase Ras-binding
-- -- --	-- IPR001666 [Phosphatidylinositol transfer protein]
ko04610 C Secreted tr O	Posttransla IPR000436 [Sushi/SCR/CCP domain] ; IPR000859[CUB c
-- -- --	-- IPR000203 [GPS motif] ; IPR000832[GPCR, family 2, sec
ko04062 C -- --	-- IPR001781 [Zinc finger, LIM-type]
ko00010 G Acyl-CoA :C	Energy prc IPR015590 [Aldehyde dehydrogenase domain]
ko04141 P -- --	-- IPR005052 [Legume-like lectin]
ko00061 F NADP-dep C	Energy prc IPR001031 [Thioesterase] ; IPR009081[Phosphopanteth
-- Chaperoni O	Posttransla IPR002423 [Chaperonin Cpn60/TCP-1 family]
ko00010 G Acyl-CoA :C	Energy prc IPR015590 [Aldehyde dehydrogenase domain]
ko03060 P -- --	-- --
ko00970 A Cysteiny-l t J	Translatio IPR032678 [tRNA synthetases class I, catalytic domain]
ko00970 A Seryl-tRN/J	Translatio IPR002314 [Aminoacyl-tRNA synthetase, class II (G/ P/
ko00230 P Eukaryotic L	Replicatio IPR002755 [DNA primase, small subunit]
ko03050 P 20S protea O	Posttransla IPR001353 [Proteasome, subunit alpha/beta]
ko03030 D DNA replic L	Replicatio IPR001208 [MCM domain] ; IPR008045[DNA replicatio
ko04145 P DNA-bind R	General fu IPR001881 [EGF-like calcium-binding domain] ; IPR003
ko04145 P Alpha-tub DZ	Cell cycle c IPR001881 [EGF-like calcium-binding domain] ; IPR003
ko03040 S ABC-type . P	Inorganic i IPR000504 [RNA recognition motif domain] ; IPR00248
ko04330 N -- --	-- IPR006020 [PTB/PI domain] ; IPR010449[NUMB domain
-- Diadenosir FGR	Nucleotide IPR001310 [Histidine triad (HIT) protein]
-- -- --	-- IPR016137 [RGS domain]
ko04062 C Formylglyc O	Posttransla IPR000719 [Protein kinase domain]
ko01521 E Serine/thre T	Signal tran IPR000719 [Protein kinase domain]
ko00230 P Chromoso D	Cell cycle c IPR008380 [HAD-superfamily hydrolase, subfamily IG, t
ko00230 P GMP synth F	Nucleotide IPR001674 [GMP synthase, C-terminal] ; IPR017926[Glu
ko03440 H DNA repai L	Replicatio IPR004843 [Calcineurin-like phosphoesterase domain,
ko04015 R -- --	-- IPR001019 [Guanine nucleotide binding protein (G-prc
ko04014 R -- --	-- IPR015898 [G-protein gamma-like domain]
ko04014 R -- --	-- IPR015898 [G-protein gamma-like domain]
ko04668 T Predicted i O	Posttransla IPR001818 [Peptidase M10, metallopeptidase] ; IPR002
-- -- --	-- IPR018203 [GDP dissociation inhibitor]
-- Sulfate per P	Inorganic i IPR002645 [STAS domain] ; IPR011547[SLC26A/SulP tra
-- Serine pro: O	Posttransla IPR023796 [Serpine domain]

--	--	--	--	IPR001478	[PDZ domain] ; IPR001781[Zinc finger, LIM-
--	Tetratricop	R	General fu	IPR019734	[Tetratricopeptide repeat]
ko04072	P	--	--	IPR000375	[Dynamin central domain] ; IPR001849[Plect
ko00230	P	8-oxo-dG	V	Defense m	IPR000086 [NUDIX hydrolase domain]
--	--	--	--	IPR019527	[RZZ complex, subunit KNTC1/ROD, C-term
ko00062	F	--	--	IPR002472	[Palmitoyl protein thioesterase]
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	GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
ko04137	M	GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
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
ko00052	G	Galactokin	G	Carbohydr	IPR006204 [GHMP kinase N-terminal domain] ; IPR013
ko04141	P	--	--	IPR008417	[B-cell receptor-associated protein 29/31]
ko00983	D	SAM-depe	QR	Secondary	IPR008854 [TPMT family]
ko04120	U	Ubiquitin-	O	Posttransla	IPR000608 [Ubiquitin-conjugating enzyme E2]
--	--	--	--	IPR001614	[Myelin proteolipid protein PLP]
--	Nucleotide	T	Signal tran	IPR000644	[CBS domain] ; IPR001807[Chloride channel
--	Nucleotide	T	Signal tran	IPR000644	[CBS domain] ; IPR001807[Chloride channel
ko04130	S	--	--	IPR001388	[Synaptobrevin] ; IPR010908[Longin domain
ko04010	M	Cell divisio	D	Cell cycle c	IPR000719 [Protein kinase domain] ; IPR017892[Protein
ko00230	P	Adenylate	T	Signal tran	IPR001054 [Adenylyl cyclase class-3/4/guanylyl cyclase
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
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
--	--	--	--	IPR000225	[Armadillo]
--	Amino acid	E	Amino acid	IPR002293	[Amino acid/polyamine transporter I] ; IPR0
ko05164	Ir	--	--	IPR001164	[Arf GTPase activating protein]
ko03022	B	--	--	IPR004855	[Transcription factor IIA, alpha/beta subunit
ko01524	P	DNA mism	L	Replicatio	IPR000313 [PWWP domain] ; IPR000432[DNA mismatch
--	Enamine d	V	Defense m	IPR006175	[YjgF/YER057c/UK114 family]
ko00010	G	Hexokinase	G	Carbohydr	IPR022672 [Hexokinase, N-terminal] ; IPR022673[Hexol
ko04360	A	--	--	IPR001799	[Ephrin receptor-binding domain]
--	--	--	--	IPR004978	[Stanniocalcin]
ko04614	R	Zn-depende	E	Amino acid	IPR001567 [Peptidase M3A/M3B catalytic domain]
ko04144	E	--	--	IPR002189	[F-actin-capping protein subunit alpha]
ko00860	P	Predicted c	R	General fu	IPR000683 [Oxidoreductase, N-terminal] ; IPR015249[B
--	Chromoso	D	Cell cycle c	IPR033756	[Flagellum site-determining protein YlxH/ F
ko00020	C	Citrate syn	C	Energy pro	IPR002020 [Citrate synthase] ; IPR003781[CoA-binding
--	Predicted	IT	Signal tran	IPR001680	[WD40 repeat] ; IPR006692[Coatomer, WD
ko04142	L	Cysteine p	O	Posttransla	IPR000668 [Peptidase C1A, papain C-terminal] ; IPR014
ko04142	L	--	--	IPR000547	[Clathrin, heavy chain/VPS, 7-fold repeat] ; I
ko04144	E	--	--	IPR022775	[AP complex, mu/sigma subunit]
--	Uncharacter	R	General fu	IPR001734	[Sodium/solute symporter]
--	--	--	--	--	--
ko00970	A	Arginyl-tR	J	Translatior	IPR001278 [Arginine-tRNA ligase] ; IPR005148[Arginyl
ko04141	P	--	--	IPR003903	[Ubiquitin interacting motif] ; IPR006155[Jos
ko04010	M	Secreted p	R	General fu	IPR002035 [von Willebrand factor, type A] ; IPR013608[
ko00970	A	Tryptophan	J	Translatior	IPR002305 [Aminoacyl-tRNA synthetase, class Ic] ; IPRC
--	--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko04068	F	CBS doma	T	Signal tran	IPR000644 [CBS domain]
ko03040	S	Molecular	O	Posttransla	IPR013126 [Heat shock protein 70 family]
ko00270	C	Branched-	EH	Amino acid	IPR001544 [Aminotransferase class IV]

ko03420 N Ubiquitin O	Posttransla IPR000626 [Ubiquitin domain] ; IPR015360[XPC-bindin
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
-- -- --	-- IPR004031 [PMP-22/EMP/MP20/Claudin superfamily]
-- -- --	-- IPR003582 [ShKT domain] ; IPR008673[Microfibril-asso
ko04970 S Amino acicE	Amino acic IPR004841 [Amino acid permease/ SLC12A domain] ; IF
-- Ribosome-J	Translatior IPR004095 [TGS] ; IPR006073[GTP binding domain] ; IP
ko03320 P -- --	-- IPR001124 [Lipid-binding serum glycoprotein, C-termi
ko04141 P ATP-depeiO	Posttransla IPR003338 [CDC48, N-terminal subdomain] ; IPR00395
-- -- --	-- IPR013151 [Immunoglobulin]
ko04080 N -- --	-- IPR000276 [G protein-coupled receptor, rhodopsin-lik
ko04014 R -- --	-- IPR000159 [Ras-associating (RA) domain] ; IPR000253[I
ko00230 P Sugar or n G	Carbohydr IPR011611 [Carbohydrate kinase PfkB]
ko04151 P Methyl-acNT	Cell motilit IPR002049 [Laminin EGF domain] ; IPR008211[Laminin,
-- Large exoçU	Intracellul IPR000233 [Cadherin, cytoplasmic domain] ; IPR002126
-- Large exoçU	Intracellul IPR000233 [Cadherin, cytoplasmic domain] ; IPR002126
-- Large exoçU	Intracellul IPR002126 [Cadherin] ; IPR014868[Cadherin prodomair
ko03013 R -- --	-- IPR022617 [Rad60/SUMO-like domain]
ko03013 R -- --	-- IPR000504 [RNA recognition motif domain] ; IPR01397
ko00450 S Methionyl-J	Translatior IPR000738 [WHEP-TRS domain] ; IPR004046[Glutathior
ko03008 R Translatior J	Translatior IPR002769 [Translation initiation factor IF6]
ko04310 V Lactate de CHR	Energy prc IPR006139 [D-isomer specific 2-hydroxyacid dehydrog
-- -- --	-- IPR007919 [Uncharacterised protein family UPF0220]
-- GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko04015 R -- --	-- IPR001452 [SH3 domain] ; IPR014928[Serine rich protei
-- Broad specG	Carbohydr IPR001452 [SH3 domain] ; IPR013078[Histidine phosph
ko04514 C -- --	-- IPR013106 [Immunoglobulin V-set domain]
-- -- --	-- IPR005344 [Per33/Pom33 family]
-- WD40 repçR	General fu IPR001680 [WD40 repeat] ; IPR015048[Domain of unkn
ko04621 N -- --	-- IPR007677 [Gasdermin]
-- Predicted IT	Signal tran IPR020683 [Ankyrin repeat-containing domain]
ko04014 R -- --	-- IPR015898 [G-protein gamma-like domain]
ko04144 E -- --	-- IPR008384 [Actin-related protein 2/3 complex subunit
ko04662 B -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko00010 G TriosephosçG	Carbohydr IPR000652 [Triosephosphate isomerase]
ko03013 R -- --	-- IPR000717 [Proteasome component (PCI) domain] ; IPF
ko03060 P -- --	-- IPR016482 [Protein transport protein SecE/Sec61-beta
ko04922 G Diadenosir T	Signal tran IPR004843 [Calcineurin-like phosphoesterase domain,
ko04068 F -- --	-- IPR004241 [Autophagy protein Atg8 ubiquitin-like]
ko04270 V Ca2+ -bincT	Signal tran IPR002048 [EF-hand domain]
ko04015 R Actin-relat Z	Cytoskelet IPR004000 [Actin family]
ko04010 N GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03013 R Superfamil L	Replicatior IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DI
ko03010 R Ribosomal J	Translatior IPR027486 [Ribosomal protein S10 domain]
ko03050 P 20S proteaO	Posttransla IPR000426 [Proteasome alpha-subunit, N-terminal dor
-- -- --	-- IPR013787 [S100/CaBP-9k-type, calcium binding, subc
ko04010 N GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- -- --	-- IPR002108 [Actin-depolymerising factor homology doi
-- -- --	-- IPR002108 [Actin-depolymerising factor homology doi
ko03060 P Signal reccU	Intracellul IPR000897 [Signal recognition particle, SRP54 subunit,
ko04152 A GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko04014 R GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko04144 E GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko04120 U Ubiquitin-O	Posttransla IPR000608 [Ubiquitin-conjugating enzyme E2]
ko04120 U Ubiquitin-O	Posttransla IPR000608 [Ubiquitin-conjugating enzyme E2]
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]

ko04530 T Actin-relat Z	Cytoskelet IPR004000 [Actin family]
-- Actin-relat Z	Cytoskelet IPR004000 [Actin family]
ko04144 E GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
-- Translatior J	Translatior IPR003439 [ABC transporter-like] ; IPR007209[RNase L
ko04010 M GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03010 R Ribosomal J	Translatior IPR001593 [Ribosomal protein S3Ae]
ko03050 P -- --	-- IPR003185 [Proteasome activator pa28, N-terminal dor
ko03010 R Ribosomal J	Translatior IPR000439 [Ribosomal protein L15e]
ko03010 R -- --	-- IPR001141 [Ribosomal protein L27e] ; IPR005824[KOW
ko00190 C -- --	-- IPR002843 [ATPase, V0 complex, c/d subunit]
ko00790 F Pterin-4a- H	Coenzyme IPR001533 [Transcriptional coactivator/pterin dehydrat
ko04014 R GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- -- --	-- IPR004127 [Prefoldin alpha-like]
ko04721 S -- --	-- IPR001619 [Sec1-like protein]
ko04612 A -- --	-- IPR003597 [Immunoglobulin C1-set]
-- -- --	-- IPR022775 [AP complex, mu/sigma subunit]
-- -- --	-- IPR005375 [Ubiquitin-fold modifier 1]
ko04142 L -- --	-- IPR022775 [AP complex, mu/sigma subunit]
-- -- --	-- IPR002075 [Nuclear transport factor 2]
ko03040 S -- --	-- IPR004088 [K Homology domain, type 1] ; IPR012987[F
ko04110 C -- --	-- IPR023410 [14-3-3 domain]
ko04010 M GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
-- -- --	-- IPR018499 [Tetraspanin/Peripherin]
ko03015 n Diadenosir T	Signal tran IPR004843 [Calcineurin-like phosphoesterase domain,
ko04014 R Ca2+ -binc T	Signal tran IPR002048 [EF-hand domain]
-- Ca2+ -binc T	Signal tran IPR002048 [EF-hand domain]
ko03050 P ATP-depei O	Posttransla IPR003959 [ATPase, AAA-type, core]
ko03050 P ATP-depei O	Posttransla IPR003959 [ATPase, AAA-type, core]
ko03010 R Ribosomal J	Translatior IPR022309 [Ribosomal protein S8e/ribosomal biogenes
ko03010 R Ribosomal J	Translatior IPR000754 [Ribosomal protein S9]
ko04120 U Ubiquitin- O	Posttransla IPR000608 [Ubiquitin-conjugating enzyme E2]
ko04110 C -- --	-- IPR023410 [14-3-3 domain]
ko03010 R Ribosomal J	Translatior IPR001971 [Ribosomal protein S11]
ko03010 R Ribosomal J	Translatior IPR006032 [Ribosomal protein S12/S23]
ko03010 R Ribosomal J	Translatior IPR001892 [Ribosomal protein S13]
ko03010 R Ribosomal J	Translatior IPR000589 [Ribosomal protein S15] ; IPR012606[Ribosc
ko03010 R Ribosomal J	Translatior IPR000266 [Ribosomal protein S17/S11] ; IPR032440[4C
ko03040 S Small nucl K	Transcripti IPR001163 [LSM domain, eukaryotic/archaea-type]
ko03018 R Small nucl K	Transcripti IPR001163 [LSM domain, eukaryotic/archaea-type]
ko03040 S -- --	-- IPR001163 [LSM domain, eukaryotic/archaea-type]
ko04810 R -- --	-- IPR001152 [Beta-thymosin]
ko04014 R GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko03050 P ATP-depei O	Posttransla IPR003959 [ATPase, AAA-type, core]
ko03010 R Ribosomal J	Translatior IPR004038 [Ribosomal protein L7Ae/L30e/S12e/Gadd4
-- -- --	-- IPR001878 [Zinc finger, CCHC-type]
ko03010 R Ribosomal J	Translatior IPR002942 [RNA-binding S4 domain] ; IPR005824[KOV
ko04270 V Actin-relat Z	Cytoskelet IPR004000 [Actin family]
-- GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03010 R Ribosomal J	Translatior IPR005633 [Ribosomal protein L23/L25, N-terminal] ; IF
ko01521 E Ribosomal J	Translatior IPR001377 [Ribosomal protein S6e]
ko05034 A -- --	-- --
ko05134 L GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03008 R GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03010 R Ribosomal J	Translatior IPR000218 [Ribosomal protein L14P]
ko04010 M GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03010 R Ribosomal J	Translatior IPR002222 [Ribosomal protein S19/S15]
ko03010 R Ribosomal J	Translatior IPR001976 [Ribosomal protein S24e]

ko03010 R -- --	-- IPR004977 [Ribosomal protein S25]
ko03010 R Ribosomal J	Translatior IPR000892 [Ribosomal protein S26e]
ko03010 R Ribosomal J	Translatior IPR000289 [Ribosomal protein S28e]
ko04014 R WD40 rep R	General fu IPR001680 [WD40 repeat]
ko03420 N -- --	-- IPR024766 [Zinc finger, RING-H2-type]
ko04014 R WD40 rep R	General fu IPR001680 [WD40 repeat]
ko03010 R Ribosomal J	Translatior IPR000054 [Ribosomal protein L31e]
ko03010 R Ribosomal J	Translatior IPR028364 [Ribosomal protein L1/ribosomal biogenesis]
ko03010 R Ribosomal J	Translatior IPR022666 [Ribosomal Proteins L2, RNA binding domain]
ko04217 N Peptidyl-p O	Posttranslat IPR002130 [Cyclophilin-type peptidyl-prolyl cis-trans isomerase]
-- FKBP-type O	Posttranslat IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomerase]
ko03010 R Ubiquitin O	Posttranslat IPR000626 [Ubiquitin domain] ; IPR002906 [Ribosomal protein L16]
ko01521 E -- --	-- IPR000980 [SH2 domain] ; IPR001452 [SH3 domain]
ko03040 S RNA recog J	Translatior IPR000504 [RNA recognition motif domain]
ko04144 E Predicted IT	Signal tran IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N-terminal domain]
ko04015 R -- --	-- IPR001019 [Guanine nucleotide binding protein (G-protein) gamma subunit]
ko04010 N Ca2+ -bind T	Signal tran IPR002048 [EF-hand domain]
ko04110 C -- --	-- IPR023410 [14-3-3 domain]
ko03013 R -- --	-- IPR022617 [Rad60/SUMO-like domain]
ko04962 V -- --	-- IPR001372 [Dynein light chain, type 1/2]
ko03010 R -- --	-- IPR002675 [Ribosomal protein L38e]
ko04110 C -- --	-- IPR016072 [SKP1 component, dimerisation] ; IPR016073 [SKP1 component, dimerisation]
ko04014 R -- --	-- IPR015898 [G-protein gamma-like domain]
ko05162 N Uncharacter R	General fu IPR001680 [WD40 repeat]
ko04015 R Actin-relat Z	Cytoskeleton IPR004000 [Actin family]
ko03013 R Ubiquitin-O	Posttranslat IPR000608 [Ubiquitin-conjugating enzyme E2]
ko03015 n Diadenosin T	Signal tran IPR004843 [Calcineurin-like phosphoesterase domain]
-- Cold shock K	Transcripti IPR002059 [Cold-shock protein, DNA-binding]
ko03008 R -- --	-- IPR000704 [Casein kinase II, regulatory subunit]
ko04260 C Chromoso D	Cell cycle c IPR000533 [Tropomyosin]
ko04120 U Ubiquitin-O	Posttranslat IPR000608 [Ubiquitin-conjugating enzyme E2]
ko03013 R Translatior J	Translatior IPR004160 [Translation elongation factor EFTu/EF1A, C-terminal domain]
ko04145 P -- --	-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316 [Tubulin/FtsZ, GTPase domain]
ko04145 P -- --	-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316 [Tubulin/FtsZ, GTPase domain]
ko04145 P -- --	-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316 [Tubulin/FtsZ, GTPase domain]
ko03008 R PASTA dom M	Cell wall/nr IPR000719 [Protein kinase domain]
ko00565 E Lysophosp E	Amino acid IPR013830 [SGNH hydrolase-type esterase domain]
ko05034 A -- --	-- IPR007125 [Histone H2A/H2B/H3]
-- -- --	-- IPR000971 [Globin]
ko05143 A Hemoglob C	Energy prc IPR000971 [Globin]
ko05416 V -- --	-- IPR013106 [Immunoglobulin V-set domain] ; IPR01315 [Immunoglobulin V-set domain]
ko04380 C -- --	-- IPR003597 [Immunoglobulin C1-set] ; IPR013106 [Immunoglobulin C1-set]
ko03013 R -- --	-- IPR003307 [W2 domain] ; IPR003890 [MIF4G-like, type 1]
ko00562 Ir -- --	-- IPR002498 [Phosphatidylinositol-4-phosphate 5-kinase]
-- Chaperonin O	Posttranslat IPR002423 [Chaperonin Cpn60/TCP-1 family]
ko04151 P PKD repea S	Function u IPR002861 [Reeler domain]
ko03450 N -- --	-- IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic domain]
ko04330 N -- --	-- IPR001762 [Disintegrin domain] ; IPR002870 [Peptidase]
-- -- --	-- IPR000436 [Sushi/SCR/CCP domain] ; IPR003410 [HYR domain]
ko04060 C -- --	-- IPR015321 [Type I cytokine receptor, cytokine-binding domain]
ko04062 C -- --	-- IPR001811 [Chemokine interleukin-8-like domain]
-- -- --	-- IPR008408 [Brain acid soluble protein 1]
ko03010 R Ribosomal J	Translatior IPR000988 [Ribosomal protein L24e-related]
ko04068 F -- --	-- IPR001132 [SMAD domain, Dwarfina-type] ; IPR003619 [SMAD domain, Dwarfina-type]
ko04144 E GTPase SAR	General fu IPR006689 [Small GTPase superfamily, ARF/SAR type]
-- -- --	-- IPR000781 [Enhancer of rudimentary]
ko05100 B GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko03010 R Ribosomal J	Translatior IPR000196 [Ribosomal protein L19/L19e]

ko03040 S RNA recog J	Translator IPR000504 [RNA recognition motif domain]
-- -- --	-- IPR013176 [Protein of unknown function DUF1712, fun
-- -- --	-- IPR000020 [Anaphylatoxin/fibulin] ; IPR001881[EGF-like
-- Glucose/ar G	Carbohydr IPR000033 [LDLR class B repeat] ; IPR001881[EGF-like c
ko04512 E Outer men M	Cell wall/r IPR000034 [Laminin IV] ; IPR000742[EGF-like domain] ;
ko04360 A -- --	-- IPR001799 [Ephrin receptor-binding domain]
-- Magnesiur P	Inorganic i IPR004014 [Cation-transporting P-type ATPase, N-terr
-- Magnesiur P	Inorganic i IPR008250 [P-type ATPase, A domain] ; IPR032630[P-i
-- Magnesiur P	Inorganic i IPR008250 [P-type ATPase, A domain] ; IPR032630[P-i
ko00920 S Cytochrome C	Energy prc IPR009056 [Cytochrome c-like domain]
-- Guanylate F	Nucleotide IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
-- -- --	-- IPR001666 [Phosphatidylinositol transfer protein]
ko00270 C S-adenosy H	Coenzyme IPR022628 [S-adenosylmethionine synthetase, N-termi
-- -- --	-- IPR004088 [K Homology domain, type 1]
ko04110 C PASTA dom M	Cell wall/r IPR000719 [Protein kinase domain]
ko04360 A Predicted , R	General fu IPR000719 [Protein kinase domain]
-- Predicted , R	General fu IPR000719 [Protein kinase domain]
-- -- --	-- IPR006628 [Purine-rich element binding protein family
ko04142 L -- --	-- IPR000547 [Clathrin, heavy chain/VP5, 7-fold repeat] ; I
-- FKBP-type O	Posttransla IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
ko00040 P Threonine ER	Amino acic IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
-- -- --	-- IPR001715 [Calponin homology domain] ; IPR002017[S
-- -- --	-- IPR002164 [Nucleosome assembly protein (NAP)]
ko03040 S RNA recog J	Translator 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
ko00072 S 3-hydroxy I	Lipid trans IPR013528 [Hydroxymethylglutaryl-coenzyme A synth
-- -- --	-- IPR007593 [CD225/Dispanin family]
-- -- --	-- IPR007593 [CD225/Dispanin family]
ko04150 r Amino acic E	Amino acic IPR002293 [Amino acid/polyamine transporter I]
ko00010 G 6-phospho G	Carbohydr IPR000023 [Phosphofructokinase domain]
ko00562 I r -- --	-- IPR000008 [C2 domain] ; IPR000909[Phosphatidylinosit
-- Ankyrin rej T	Signal tran IPR000001 [Krigle] ; IPR001245[Serine-threonine/tyro
ko05206 I -- --	-- IPR001752 [Kinesin motor domain] ; IPR032384[Kinesin
ko04915 E FKBP-type O	Posttransla IPR001179 [FKBP-type peptidyl-prolyl cis-trans isomer
ko00310 L Glycosyltra M	Cell wall/r IPR005123 [Oxoglutarate/iron-dependent dioxygenase
-- -- --	-- IPR002048 [EF-hand domain]
ko03010 R -- --	-- IPR000915 [60S ribosomal protein L6E] ; IPR005568[Rib
ko01524 P DNA gyrase L	Replicatio IPR002205 [DNA topoisomerase, type IIA, subunit A/C-
-- -- --	-- IPR001573 [Protein kinase A anchoring, WSK motif] ; IP
ko04010 I -- --	-- IPR001019 [Guanine nucleotide binding protein (G-prc
ko04144 E -- --	-- IPR001612 [Caveolin]
-- -- --	-- IPR010326 [Exocyst complex component EXOC3/Sec6]
ko03320 P -- --	-- IPR000536 [Nuclear hormone receptor, ligand-binding
ko04610 C -- --	-- IPR016054 [Ly-6 antigen/uPA receptor-like]
ko00900 T Mevalonat 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	Carbohydr IPR004193 [Glycoside hydrolase, family 13, N-terminal]
ko03013 R -- --	-- IPR003307 [W2 domain] ; IPR003890[MIF4G-like, type :
-- Secreted tr O	Posttransla IPR000001 [Krigle] ; IPR000083[Fibronectin, type I] ; IP
ko04060 C Serine/thre T	Signal tran IPR000472 [Activin types I and II receptor domain] ; IP
ko04110 C -- --	-- IPR023410 [14-3-3 domain]
ko04072 P -- --	-- IPR000375 [Dynamin central domain] ; IPR001849[Plecl
ko01522 E Ankyrin rej T	Signal tran IPR001245 [Serine-threonine/tyrosine-protein kinase c
-- -- --	-- IPR000504 [RNA recognition motif domain]
ko03013 R Translator J	Translator IPR004160 [Translation elongation factor EFTu/EF1A, C
ko04062 C Serine/thre T	Signal tran IPR000719 [Protein kinase domain] ; IPR002219[Protein

--	Secreted p R	General fu IPR002035	[von Willebrand factor, type A] ; IPR010600]
ko04014 R	Protein tyr T	Signal tran IPR000242	[PTP type protein phosphatase] ; IPR00098C
ko00230 P	Glutamine F	Nucleotide IPR000836	[Phosphoribosyltransferase domain]
ko00250 A	Glucosami M	Cell wall/r IPR001347	[Sugar isomerase (SIS)]
ko03018 R	Exosome c J	Translatior IPR001247	[Exoribonuclease, phosphorolytic domain 1
ko03050 P	--	--	IPR003185 [Proteasome activator pa28, N-terminal dor
--	Ankyrin rej T	Signal tran IPR001245	[Serine-threonine/tyrosine-protein kinase c
--	--	--	IPR002223 [Pancreatic trypsin inhibitor Kunitz domain]
--	Leucine-rich K	Transcripti IPR000372	[Leucine-rich repeat N-terminal domain] ; I
ko04146 P	Alkyl hydr V	Defense m IPR000866	[Alkyl hydroperoxide reductase subunit C/ 1
ko03010 R	--	--	IPR021131 [Ribosomal protein L18e/L15P]
ko05168 H	--	--	IPR003428 [Mitochondrial glycoprotein]
ko04141 P	--	--	--
ko04520 A	--	--	IPR000906 [ZU5 domain] ; IPR001478[PDZ domain] ; IP
ko04218 C	--	--	IPR000571 [Zinc finger, CCCH-type] ; IPR007635[Tis11f
--	Tetratricop R	General fu IPR001440	[Tetratricopeptide repeat 1] ; IPR019734[Tet
ko01521 E	--	--	IPR026298 [Blc2 family]
ko04979 C	Glucose/ar G	Carbohydr IPR000033	[LDLR class B repeat] ; IPR001881[EGF-like c
ko03040 S	RNA recog J	Translatior IPR000504	[RNA recognition motif domain]
--	--	--	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]
--	--	--	IPR001190 [SRCR domain] ; IPR011705[BTB/Kelch-asso
--	--	--	IPR000421 [Coagulation factor 5/8 C-terminal domain]
--	--	--	IPR000716 [Thyroglobulin type-1] ; IPR002350[Kazal dc
ko04512 E	--	--	IPR013147 [CD47 transmembrane] ; IPR013270[CD47 ir
ko04217 N	Peptidyl-p O	Posttransla IPR002130	[Cyclophilin-type peptidyl-prolyl cis-trans is
ko05166 H	--	--	IPR021841 [Vacuolar protein 14 C-terminal Fig4-bindir
--	16S rRNA (J	Translatior IPR001678	[SAM-dependent methyltransferase RsmB/I
--	Ca2+-binc Q	Secondary --	--
--	--	--	--
ko00510 N	--	--	IPR007754 [N-acetylglucosaminyltransferase II]
ko00512 N	Glycosyltra G	Carbohydr IPR000772	[Ricin B, lectin domain] ; IPR001173[Glycosy
ko04142 L	Predicted IT	Signal tran IPR002553	[Clathrin/coatomer adaptor, adaptin-like, N
ko00760 N	--	--	IPR003193 [ADP-ribosyl cyclase (CD38/157)]
--	Dipeptidas E	Amino acic 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 dor
--	--	--	IPR001881 [EGF-like calcium-binding domain] ; IPR026
--	--	--	IPR002350 [Kazal domain] ; IPR015369[Follistatin/Ostec
ko04130 S	--	--	IPR000727 [Target SNARE coiled-coil homology doma
ko04514 C	Sugar lact G	Carbohydr IPR003961	[Fibronectin type III] ; IPR013098[Immunogl
ko03040 S	--	--	IPR021966 [Splicing factor SF3a60 binding domain] ; IP
--	Dipeptidyl E	Amino acic IPR001375	[Peptidase S9, prolyl oligopeptidase, catalyt
--	tRNA-binc J	Translatior IPR002547	[tRNA-binding domain]
--	--	--	IPR006561 [DZF domain]
--	--	--	IPR006561 [DZF domain] ; IPR014720[Double-strandec
ko04141 P	--	--	IPR005052 [Legume-like lectin]
ko04520 A	Protein tyr T	Signal tran IPR000242	[PTP type protein phosphatase] ; IPR003961
ko04210 A	Protein tyr T	Signal tran IPR000242	[PTP type protein phosphatase] ; IPR001478
--	--	--	IPR001452 [SH3 domain] ; IPR013625[Tensin/EPS8 pho
--	Molecular O	Posttransla IPR001404	[Heat shock protein Hsp90 family]
ko04390 H	Guanylate F	Nucleotide IPR001478	[PDZ domain] ; IPR008145[Guanylate kinase
--	--	--	IPR001452 [SH3 domain] ; IPR001609[Myosin head, mc

--	Protein-tyr	Signal tran	IPR000242 [PTP type protein phosphatase]
--	--	--	IPR000008 [C2 domain] ; IPR000198[Rho GTPase-activ
ko04110 C	Tetratricop	General fu	--
ko04010 M	Serine/thr	Signal tran	IPR000719 [Protein kinase domain] ; IPR024205[Mst1 S
--	Leucine-ric	Transcripti	IPR001611 [Leucine-rich repeat] ; IPR007123[Gelsolin-I
ko00061 F	Biotin carb	Lipid trans	IPR000022 [Carboxyl transferase] ; IPR000089[Biotin/lip
ko00565 E	Predicted	General fu	IPR005065 [Platelet-activating factor acetylhydrolase-li
--	--	--	IPR010892 [Secreted phosphoprotein 24]
--	Ubiquitin (O	Posttransla	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04068 F	Serine/thr	Signal tran	IPR000719 [Protein kinase domain] ; IPR032270[AMPK,
--	--	--	IPR001660 [Sterile alpha motif domain]
--	RNA recog	Translatior	IPR000504 [RNA recognition motif domain]
--	--	--	IPR004046 [Glutathione S-transferase, C-terminal] ; IPR
--	Alkyl hydr	Defense m	IPR000866 [Alkyl hydroperoxide reductase subunit C/ T
ko04010 M	Serine/thr	Signal tran	IPR000270 [PB1 domain] ; IPR000719[Protein kinase dc
ko04010 M	Serine/thr	Signal tran	IPR000095 [CRIB domain] ; IPR000719[Protein kinase d
ko03050 P	--	--	IPR002015 [Proteasome/cyclosome repeat]
ko03040 S	RNA recog	Translatior	IPR000504 [RNA recognition motif domain]
ko04350 T	--	--	--
ko04110 C	--	--	IPR003511 [HORMA domain]
--	--	--	IPR000315 [B-box-type zinc finger] ; IPR001841[Zinc fi
ko04130 S	--	--	IPR000727 [Target SNARE coiled-coil homology doma
--	RNA recog	Translatior	IPR000504 [RNA recognition motif domain] ; IPR00207
--	PASTA dom	Cell wall/r	IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko04150 r	--	--	IPR000159 [Ras-associating (RA) domain] ; IPR000980[
--	4-amino-4	Cell wall/r	IPR011990 [Tetratricopeptide-like helical domain] ; IPR
ko03013 R	WD40 rep	General fu	IPR001680 [WD40 repeat]
ko04145 P	Predicted	Signal tran	IPR001680 [WD40 repeat] ; IPR025956[Cytoplasmic dyr
ko03320 P	Ankyrin re	Signal tran	IPR001245 [Serine-threonine/tyrosine-protein kinase c
--	Zinc trans	Inorganic i	IPR003689 [Zinc/iron permease]
--	--	--	IPR019380 [Casein kinase substrate, phosphoprotein PI
--	--	--	IPR001590 [Peptidase M12B, ADAM/reprolysin] ; IPR00
--	--	--	IPR000048 [IQ motif, EF-hand binding site] ; IPR00015
ko04022 c	Serine/thr	Signal tran	IPR000719 [Protein kinase domain] ; IPR015008[Rho bi
--	--	--	IPR011417 [AP180 N-terminal homology (ANTH) dom
ko00562 l	--	--	IPR004182 [GRAM domain] ; IPR010569[Myotubularin-
ko04137 M	--	--	IPR000270 [PB1 domain] ; IPR000433[Zinc finger, ZZ-ty
ko04145 P	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko04622 R	Parvulin-lil	Posttransla	IPR000297 [Peptidyl-prolyl cis-trans isomerase, PpiC-t
ko03460 F	--	--	IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic
ko04110 C	Acetoin ut	Chromatin	IPR023801 [Histone deacetylase domain]
ko04012 E	Serine/thr	Signal tran	IPR000719 [Protein kinase domain] ; IPR013543[Calciur
ko04962 V	--	--	--
ko04810 R	--	--	IPR000048 [IQ motif, EF-hand binding site] ; IPR00059
ko00562 l	--	--	IPR004182 [GRAM domain] ; IPR010569[Myotubularin-
ko04110 C	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko04066 H	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko04120 U	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko03420 N	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
ko04390 H	Chromoso	Cell cycle	IPR001452 [SH3 domain] ; IPR020683[Ankyrin repeat-c
ko00051 F	Nucleoside	Cell wall/r	IPR001509 [NAD-dependent epimerase/dehydratase]
ko04144 E	GTPase SAR	General fu	IPR001806 [Small GTPase superfamily]
--	GTPase SAR	General fu	IPR001806 [Small GTPase superfamily]
--	Leucine-ric	Transcripti	IPR000372 [Leucine-rich repeat N-terminal domain] ; I
ko04630 J	--	--	IPR001781 [Zinc finger, LIM-type]
ko04014 R	--	--	IPR000159 [Ras-associating (RA) domain] ; IPR003123[
--	Uncharact	General fu	IPR001680 [WD40 repeat]
ko04514 C	--	--	IPR013162 [CD80-like, immunoglobulin C2-set]

ko04145 P -- --	-- IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko00565 E Predicted jR	General fu IPR001212 [Somatomedin B domain] ; IPR001604[DNA
ko03013 R Superfamil L	Replicatio IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DI
-- Aminopep E	Amino acid IPR004134 [Peptidase C1B, bleomycin hydrolase]
ko04060 C Serine/thre T	Signal tran IPR000472 [Activin types I and II receptor domain] ; IPR
-- -- --	-- IPR001478 [PDZ domain] ; IPR001849[Pleckstrin homol
-- -- --	-- IPR007955 [Bystin]
-- -- --	-- IPR024395 [CLASP N-terminal domain]
-- -- --	-- IPR002108 [Actin-depolymerising factor homology do
-- RNA recog J	Translatio IPR000504 [RNA recognition motif domain] ; IPR01295
ko04142 L -- --	-- IPR002159 [CD36 family]
-- Glucose/ar G	Carbohydr IPR000033 [LDLR class B repeat] ; IPR000716[Thyroglob
ko04512 E -- --	-- IPR008465 [Dystroglycan]
ko05412 A Large exo rU	Intracellul IPR002126 [Cadherin]
ko05100 B -- --	-- IPR030379 [Septin-type guanine nucleotide-binding (C
ko04120 UN-acetylne M	Cell wall/r IPR000210 [BTB/POZ domain] ; IPR006652[Kelch repea
ko03013 R 16S rRNA lJ	Translatio IPR000717 [Proteasome component (PCI) domain]
ko04810 R -- --	-- IPR000219 [Dbl homology (DH) domain] ; IPR001715[C
-- -- --	-- IPR022166 [Protein of unknown function DUF3697, ubi
ko04390 H Leucine-rich K	Transcripti IPR001478 [PDZ domain] ; IPR001611[Leucine-rich rep
-- -- --	-- IPR004344 [Tubulin-tyrosine ligase/Tubulin polyglutara
-- Guanylate F	Nucleotide IPR001478 [PDZ domain] ; IPR008145[Guanylate kinase
ko04510 F -- --	-- IPR001452 [SH3 domain] ; IPR010703[Deducator of cytc
ko04380 C -- --	-- IPR001781 [Zinc finger, LIM-type]
-- Dihydrooxo F	Nucleotide IPR006680 [Amidohydrolase-related]
ko04962 V Uncharact S	Function u IPR000938 [CAP Gly-rich domain] ; IPR022157[Dynein ;
ko04145 P -- --	-- IPR004273 [Dynein heavy chain domain] ; IPR011704[A
ko03013 R Superfamil L	Replicatio IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DI
ko04530 T -- --	-- IPR001452 [SH3 domain] ; IPR003134[Hs1/Cortactin]
ko04910 Ir Uncharact S	Function u IPR001107 [Band 7 domain] ; IPR031905[Flotillin, C-ter
ko04064 N -- --	-- IPR003877 [SPRY domain] ; IPR006574[SPRY-associated
ko04020 C Serine/thre T	Signal tran IPR001245 [Serine-threonine/tyrosine-protein kinase c
ko04010 N Uncharact S	Function u IPR001715 [Calponin homology domain] ; IPR017868[F
ko04022 c -- --	-- IPR001019 [Guanine nucleotide binding protein (G-prc
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-like
-- -- --	-- IPR022070 [Cytoplasmic activation/proliferation-associ
-- -- --	-- IPR002350 [Kazal domain] ; IPR015369[Follistatin/Ostec
-- Large exo rU	Intracellul IPR000742 [EGF-like domain] ; IPR001791[Laminin G d
-- Secreted tr O	Posttransl IPR000001 [Krigle] ; IPR000742[EGF-like domain] ; IPR
ko03030 D DNA replic L	Replicatio IPR001208 [MCM domain] ; IPR027925[MCM N-termin
-- Secreted p R	General fu IPR002035 [von Willebrand factor, type A] ; IPR010600[
ko04630 J -- --	-- IPR015321 [Type I cytokine receptor, cytokine-binding
ko00562 Ir -- --	-- --
ko04014 R -- --	-- IPR000008 [C2 domain] ; IPR001562[Zinc finger, Btk mc
-- -- --	-- IPR001715 [Calponin homology domain] ; IPR002048[E
-- -- --	-- IPR000253 [Forkhead-associated (FHA) domain] ; IPR0
-- -- --	-- IPR013809 [ENTH domain]
ko04110 C Chromoso D	Cell cycle c IPR003395 [RecF/RecN/SMC, N-terminal] ; IPR010935[
ko00510 N Alpha-gluc G	Carbohydr IPR000322 [Glycoside hydrolase family 31] ; IPR025887
-- -- --	-- IPR028169 [Raftlin family]
ko04141 P Serine proi O	Posttransl IPR000209 [Peptidase S8/S53 domain]
-- -- --	-- IPR007237 [CD20-like family]
ko03015 r -- --	-- IPR002554 [Protein phosphatase 2A, regulatory B subu
-- Uncharact S	Function u IPR002499 [Major vault protein, N-terminal] ; IPR02187
ko04350 T -- --	-- IPR001881 [EGF-like calcium-binding domain] ; IPR017
-- -- --	-- IPR000900 [Nebulin repeat] ; IPR001452[SH3 domain] ;

ko03013 R	--	--	--	IPR001494	[Importin-beta, N-terminal domain]
ko03050 P	--	--	--	IPR021843	[Protein of unknown function DUF3437] ; IP
ko04120 U	--	--	--	IPR001373	[Cullin, N-terminal] ; IPR004939[APC10/DO
--	--	--	--	IPR001936	[Ras GTPase-activating protein] ; IPR003123
--	Chromoso	D	Cell cycle c	IPR001664	[Intermediate filament protein] ; IPR032444[
--	--	--	--	IPR022816	[Condensin complex subunit 2/barren]
ko03050 P	--	--	--	IPR000717	[Proteasome component (PCI) domain] ; IPF
ko04142 L	--	--	--	IPR004687	[Lysosomal-associated transmembrane pro
--	--	--	--	IPR024324	[Condensin complex subunit 1, N-terminal]
--	--	--	--	--	--
ko03040 S	Translatio	J	Translatio	IPR000640	[Translation elongation factor EFG, V domai
--	--	--	--	IPR001683	[Phox homologous domain]
ko04810 R	--	--	--	IPR000219	[Dbl homology (DH) domain] ; IPR001452[S
--	RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain]
ko04144 E	SUMO liga	L	Replicatio	IPR001164	[Arf GTPase activating protein] ; IPR001849[
--	Uncaracter	R	General fu	IPR000782	[FAS1 domain]
ko04141 P	Negative r	O	Posttransla	IPR013766	[Thioredoxin domain]
ko00565 E	Lysosphosp	E	Amino acid	IPR013830	[SGNH hydrolase-type esterase domain]
--	--	--	--	IPR000859	[CUB domain] ; IPR018933[Netrin module, r
--	--	--	--	IPR001875	[Death effector domain]
--	Phosphogl	G	Carbohydr	IPR005844	[Alpha-D-phosphohexomutase, alpha/beta
ko03015 r	--	--	--	IPR002554	[Protein phosphatase 2A, regulatory B subu
ko00190 C	Inorganic p	CP	Energy prc	IPR008162	[Inorganic pyrophosphatase]
ko00590 A	--	--	--	IPR007052	[CS domain]
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR017892[Protein
--	RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain] ; IPR01297
ko04931 Ir	--	--	--	IPR004327	[Phosphotyrosyl phosphatase activator, PTP
--	Protein tyr	T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR000998
ko04010 M	--	--	--	IPR000008	[C2 domain] ; IPR001562[Zinc finger, Btk mc
ko04144 E	GTPase SAR		General fu	IPR001806	[Small GTPase superfamily]
--	--	--	--	IPR002048	[EF-hand domain]
ko04390 H	--	--	--	IPR001680	[WD40 repeat] ; IPR013577[Lethal giant larv
ko04010 M	Cell divisio	D	Cell cycle c	IPR000719	[Protein kinase domain] ; IPR017892[Protein
ko03040 S	--	--	--	IPR004088	[K Homology domain, type 1]
ko04216 F	--	--	--	IPR004088	[K Homology domain, type 1]
ko04066 H	--	--	--	IPR016073	[SKP1 component, POZ domain]
ko04072 P	GTPase SAR		General fu	IPR001806	[Small GTPase superfamily]
ko00100 S	FAD/FMN- C		Energy prc	IPR006094	[FAD linked oxidase, N-terminal]
ko03040 S	--	--	--	IPR004871	[Cleavage/polyadenylation specificity factor
--	Leucine-rich	K	Transcripti	IPR001611	[Leucine-rich repeat]
--	--	--	--	IPR000557	[Calponin repeat] ; IPR001715[Calponin hor
ko04010 M	Cell divisio	D	Cell cycle c	IPR000719	[Protein kinase domain] ; IPR017892[Protein
ko03040 S	RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain]
--	Leucine-rich	K	Transcripti	--	--
ko04141 P	--	--	--	IPR006895	[Zinc finger, Sec23/Sec24-type] ; IPR006896
ko04141 P	--	--	--	IPR006895	[Zinc finger, Sec23/Sec24-type] ; IPR006896
ko00030 P	Sugar lact	G	Carbohydr	IPR013658	[SMP-30/Gluconolactonase/LRE-like region
--	--	--	--	IPR001715	[Calponin homology domain] ; IPR004953[E
--	Uncaracter	R	General fu	IPR000782	[FAS1 domain]
ko04960 A	Periplasmic	O	Posttransla	IPR001478	[PDZ domain] ; IPR015098[EBP50, C-termin
--	--	--	--	IPR002848	[Translin family]
ko04910 Ir	--	--	--	IPR001060	[FCH domain] ; IPR001452[SH3 domain]
ko01522 E	--	--	--	IPR019680	[Mediator complex, subunit Med1]
ko04621 N	--	--	--	IPR001781	[Zinc finger, LIM-type]
--	Protein tyr	T	Signal tran	IPR000242	[PTP type protein phosphatase] ; IPR018979
--	--	--	--	IPR001715	[Calponin homology domain] ; IPR004953[E
ko04152 A	RNA recog	J	Translatio	IPR000504	[RNA recognition motif domain]
ko04120 U	Alpha-tub	DZ	Cell cycle c	IPR000408	[Regulator of chromosome condensation, R

ko04974 P Na ⁺ /H ⁺ -c C	Energy prc IPR001991 [Sodium:dicarboxylate symporter]
-- Serine/thrεT	Signal tran IPR001440 [Tetratricopeptide repeat 1]
ko04350 T -- --	-- IPR001132 [SMAD domain, Dwarfina-type] ; IPR003619[
-- Leucine-ricK	Transcripti IPR000626 [Ubiquitin domain] ; IPR000938[CAP Gly-ric
-- -- --	-- IPR000608 [Ubiquitin-conjugating enzyme E2]
ko04130 S -- --	-- IPR001388 [Synaptobrevin]
ko04144 E GTPase SAR	General fu IPR001806 [Small GTPase superfamily]
ko04510 F -- --	-- IPR001781 [Zinc finger, LIM-type]
ko03050 P -- --	-- IPR006773 [26S proteasome complex ubiquitin receptc
ko00520 A UDP-N-ac G	Carbohydr IPR002618 [UDPGP family]
-- -- --	-- IPR000867 [Insulin-like growth factor-binding protein,
ko04151 P Methyl-acNT	Cell motilit IPR001791 [Laminin G domain] ; IPR002049[Laminin EC
ko00534 G -- --	-- IPR004263 [Exostosin-like] ; IPR015338[Exostosin , C-te
-- -- --	-- IPR019538 [26S proteasome non-ATPase regulatory su
ko04151 P Serine/thrεT	Signal tran IPR000719 [Protein kinase domain] ; IPR011072[HR1 rh
ko04151 P Serine/thrεT	Signal tran IPR000719 [Protein kinase domain] ; IPR011072[HR1 rh
ko03015 r -- --	-- IPR002554 [Protein phosphatase 2A, regulatory B subu
ko01522 E Serine/thrεT	Signal tran IPR000719 [Protein kinase domain]
ko04151 P -- --	-- IPR013855 [Cdc37, N-terminal domain] ; IPR013873[Cc
ko04360 A DihydroorεF	Nucleotide IPR006680 [Amidohydrolase-related]
-- -- --	-- IPR008253 [Marvel domain]
-- WD40 repεR	General fu IPR001680 [WD40 repeat] ; IPR022052[Histone-binding
-- -- --	-- IPR008605 [Extracellular matrix protein 1]
ko04514 C -- --	-- IPR008253 [Marvel domain] ; IPR010844[Occludin hom
ko03013 R -- --	-- IPR010304 [Survival motor neuron]
-- -- --	-- IPR002108 [Actin-depolymerising factor homology do
-- -- --	-- IPR022768 [Fascin domain]
-- -- --	-- IPR011511 [Variant SH3 domain]
ko00380 T KynureninεE	Amino acid IPR000192 [Aminotransferase class V domain]
ko00600 S GlycosyltrεN	Cell motilit IPR025993 [Ceramide glucosyltransferase]
ko00230 P Guanylate F	Nucleotide IPR008145 [Guanylate kinase/L-type calcium channel b
ko00620 P Glyoxylase R	General fu IPR001279 [Metallo-beta-lactamase] ; IPR032282[Hydr
-- Ankyrin rejT	Signal tran IPR000421 [Coagulation factor 5/8 C-terminal domain]
ko00040 P UDP-N-ac G	Carbohydr IPR002618 [UDPGP family]
ko00260 G Cu ²⁺ -con Q	Secondary IPR015798 [Copper amine oxidase, C-terminal] ; IPR01
ko00450 S Pyruvate/2 C	Energy prc IPR002109 [Glutaredoxin] ; IPR004099[Pyridine nucleot
ko05167 K -- --	-- IPR003597 [Immunoglobulin C1-set] ; IPR011161[MHC
ko05167 K -- --	-- IPR003597 [Immunoglobulin C1-set] ; IPR011161[MHC
-- -- --	-- --
ko00052 G Alpha-glucG	Carbohydr IPR000322 [Glycoside hydrolase family 31] ; IPR000519
-- Serine/thrεT	Signal tran IPR000719 [Protein kinase domain]
ko04144 E -- --	-- IPR003597 [Immunoglobulin C1-set] ; IPR010579[MHC
-- -- --	-- IPR005123 [Oxoglutarate/iron-dependent dioxygenase
-- WD40 repεR	General fu IPR001680 [WD40 repeat] ; IPR005108[HELP]
ko00670 C Acyl-CoA εC	Energy prc IPR002376 [Formyl transferase, N-terminal] ; IPR00579
-- -- --	-- IPR001079 [Galectin, carbohydrate recognition domain
-- O-acetyl-εJ	Translatio 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] ; IPR
-- -- --	-- IPR007632 [Anoctamin] ; IPR032394[Anoctamin, dimeri
-- -- --	-- IPR018797 [Uncharacterised protein family FAM98]
-- -- --	-- IPR022008 [TSG101 and ALIX binding domain of CEP5
-- -- --	-- --
-- -- --	-- IPR001849 [Pleckstrin homology domain]
ko04014 R Ca ²⁺ -binc Q	Secondary IPR013818 [Lipase/vitellogenin]
ko00330 A Pyrroline-εE	Amino acid IPR028939 [Pyrroline-5-carboxylate reductase, catalyti
-- Actin-relat Z	Cytoskelet IPR004000 [Actin family]

ko04141 P Molecular O	Posttransla	IPR001404	[Heat shock protein Hsp90 family] ; IPR0035
ko04141 P Molecular O	Posttransla	IPR001404	[Heat shock protein Hsp90 family] ; IPR0035
ko04120 UAlpha-tub DZ	Cell cycle c	IPR000408	[Regulator of chromosome condensation, R
-- -- --	--	IPR007587	[SIT4 phosphatase-associated protein famil
-- -- --	--	IPR019170	[Meckelin]
-- -- --	--	IPR024845	[Nance-Horan syndrome protein family]
-- -- --	--	IPR001849	[Pleckstrin homology domain] ; IPR010703[I
ko04145 P Type V sec MU	Cell wall/r	IPR001304	[C-type lectin-like] ; IPR008160[Collagen tri
-- -- --	--	IPR001715	[Calponin homology domain]
-- Predicted ;G	Carbohydr	IPR011701	[Major facilitator superfamily]
-- -- --	--	IPR005818	[Linker histone H1/H5, domain H15]
-- -- --	--	IPR024845	[Nance-Horan syndrome protein family]
-- -- --	--	IPR000008	[C2 domain]
-- FKBP-type O	Posttransla	IPR001179	[FKBP-type peptidyl-prolyl cis-trans isomer
-- Guanylate F	Nucleotide	IPR001478	[PDZ domain] ; IPR008145[Guanylate kinase
-- -- --	--	IPR000569	[HECT domain] ; IPR004939[APC10/DOC dc
ko05165 H -- --	--	IPR003126	[Zinc finger, UBR-type] ; IPR025704[E3 ubiq
-- WD40 rep;R	General fu	IPR001680	[WD40 repeat] ; IPR013577[Lethal giant larv
-- -- --	--	--	--
ko04974 P Autotrans; UW	Intracellul	IPR008160	[Collagen triple helix repeat]
-- -- --	--	IPR025481	[Cell morphogenesis protein C-terminal] ; If
ko05034 A -- --	--	IPR007125	[Histone H2A/H2B/H3]
-- -- --	--	IPR012486	[N1221-like] ; IPR021819[Protein of unknow
-- Fermentati T	Signal tran	IPR022742	[Serine aminopeptidase, S33]
-- -- --	--	IPR010630	[Neuroblastoma breakpoint family (NBPF) d
-- Methyl-ac; NT	Cell motilit	IPR002035	[von Willebrand factor, type A] ; IPR013608[
ko04141 P -- --	--	IPR003323	[OTU domain]
-- -- --	--	IPR004328	[BRO1 domain]
-- -- --	--	IPR009637	[Lung seven transmembrane receptor-like]
-- Predicted ;R	General fu	IPR003140	[Phospholipase/carboxylesterase/thioestera
-- -- --	--	IPR007244	[NatC N(alpha)-terminal acetyltransferase, I
-- -- --	--	IPR001594	[Palmitoyltransferase, DHHC domain]
-- -- --	--	IPR003877	[SPRY domain]
ko04514 C -- --	--	IPR013106	[Immunoglobulin V-set domain]
ko04115 p Predicted ;R	General fu	IPR013130	[Ferric reductase transmembrane compone
-- -- --	--	IPR000195	[Rab-GTPase-TBC domain] ; IPR004182[GR,
-- -- --	--	IPR000980	[SH2 domain] ; IPR013625[Tensin/EPS8 pho
-- -- --	--	IPR000840	[Gamma-retroviral matrix protein] ; IPR0035
-- Glyoxylase R	General fu	IPR001279	[Metallo-beta-lactamase]
ko04530 T -- --	--	IPR000198	[Rho GTPase-activating protein domain] ; If
-- -- --	--	IPR003191	[Guanylate-binding protein, C-terminal] ; IP
-- Leucine-rich K	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR031943[CARMIL, (
-- -- --	--	IPR007785	[Anamorsin] ; IPR013216[Methyltransferase
-- -- --	--	IPR002653	[Zinc finger, A20-type] ; IPR003323[OTU do
ko04150 r -- --	--	IPR028209	[LAMTOR1/MEH1]
-- -- --	--	IPR002108	[Actin-depolymerising factor homology dor
-- GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
-- -- --	--	IPR005135	[Endonuclease/exonuclease/phosphatase]
-- -- --	--	IPR025903	[Phostensin/Taperin N-terminal domain] ; If
-- -- --	--	IPR000008	[C2 domain]
ko03018 R -- --	--	IPR032401	[Enhancer of mRNA-decapping protein 4, V
ko03040 S -- --	--	IPR000555	[JAB1/MPN/MOV34 metalloenzyme domair
-- -- --	--	--	--
-- Hemolysin R	General fu	IPR000644	[CBS domain] ; IPR002550[Domain of unknc
ko04151 P Serine/thr; T	Signal tran	IPR000719	[Protein kinase domain] ; IPR011072[HR1 rh
-- -- --	--	IPR006571	[TLDC domain]
-- -- --	--	IPR029444	[Integrator complex subunit 5, C-terminal] ;
-- -- --	--	IPR001478	[PDZ domain] ; IPR001660[Sterile alpha mot

--	--	--	--	IPR013098	[Immunoglobulin I-set] ; IPR013151[Immun
ko04150	r	--	--	--	IPR028267 [Rapamycin-insensitive companion of mTO
--	--	--	--	--	IPR009436 [Type-1 angiotensin II receptor-associated
--	Leucine-rich	K	Transcripti	IPR001611	[Leucine-rich repeat] ; IPR001660[Sterile alp
--	Serine pro	O	Posttransla	IPR002165	[Plexin repeat]
--	Dipeptidyl	E	Amino acid	IPR001375	[Peptidase S9, prolyl oligopeptidase, catalyt
--	--	--	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR001452[S
--	Uncharacter	R	General fu	IPR001599	[Alpha-2-macroglobulin] ; IPR002890[Alph
--	WD40 rep	R	General fu	IPR000409	[BEACH domain] ; IPR001680[WD40 repeat]
--	--	--	--	--	IPR031780 [FAM65, N-terminal]
--	--	--	--	--	IPR019372 [Lipoma HMGIC fusion partner-like protein]
--	--	--	--	--	IPR024606 [Protein of unknown function DUF3827]
--	--	--	--	--	IPR000159 [Ras-associating (RA) domain] ; IPR001849[
--	--	--	--	--	IPR005301 [MOB kinase activator family]
--	--	--	--	--	--
--	--	--	--	--	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IF
--	--	--	--	--	IPR003877 [SPRY domain] ; IPR006574[SPRY-associated
--	Transcripti	K	Transcripti	IPR000980	[SH2 domain] ; IPR003029[S1 domain] ; IPR
ko05169	E	Endonucle	Replicatio	IPR002999	[Tudor domain] ; IPR016071[Staphylococcal
--	PASTA do	M	Cell wall/r	IPR000719	[Protein kinase domain] ; IPR001772[Kinase
ko04512	E	Predicted	Carbohydr	IPR001646	[Pentapeptide repeat] ; IPR005828[Major fa
--	GTPase	SAR	General fu	IPR001806	[Small GTPase superfamily]
--	--	--	--	--	IPR003307 [W2 domain]
--	Uncharacter	S	Function u	IPR001646	[Pentapeptide repeat] ; IPR003131[Potassiu
--	HrpA-like	J	Translatio	IPR001650	[Helicase, C-terminal] ; IPR007502[Helicase-
--	--	--	--	--	IPR000717 [Proteasome component (PCI) domain]
ko03013	R	--	--	--	IPR008081 [Cytoplasmic FMR1-interacting] ; IPR00982
ko04010	M	Serine/thr	Signal tran	IPR000719	[Protein kinase domain]
ko04144	E	--	--	--	IPR005024 [Snf7 family]
ko04010	M	--	--	--	IPR000651 [Ras-like guanine nucleotide exchange fact
ko03040	S	--	--	--	IPR005345 [PHF5-like]
--	--	--	--	--	IPR013057 [Amino acid transporter, transmembrane dc
--	--	--	--	--	IPR032745 [G protein-regulated inducer of neurite out
--	--	--	--	--	IPR004170 [WWE domain] ; IPR012317[Poly(ADP-ribos
--	Phage-rel	X	Mobilome	IPR000998	[MAM domain]
ko04136	A	--	--	--	IPR007241 [Autophagy-related protein 9]
--	--	--	--	--	IPR015403 [Sec7, C-terminal] ; IPR032629[Mon2, dimer
ko04530	T	--	--	--	IPR001609 [Myosin head, motor domain] ; IPR002928[
--	--	--	--	--	IPR024395 [CLASP N-terminal domain]
--	--	--	--	--	IPR000859 [CUB domain] ; IPR002172[Low-density lipo
ko00040	P	NAD(P)-de	Lipid trans	--	--
--	Phage-rel	X	Mobilome	IPR003961	[Fibronectin type III] ; IPR013098[Immunogl
--	--	--	--	--	IPR000697 [WH1/EVH1 domain] ; IPR007875[Sprouty]
ko04360	A	--	--	--	IPR000198 [Rho GTPase-activating protein domain] ; IF
--	N-acetyl	M	Cell wall/r	IPR006652	[Kelch repeat type 1] ; IPR011498[Kelch rep
ko04120	U	--	--	--	IPR000569 [HECT domain] ; IPR004170[WWE domain] ;
--	Leucine-rich	K	Transcripti	--	--
--	Uncharacter	S	Function u	IPR006913	[Glutathione-dependent formaldehyde-acti
ko00512	M	Uncharacter	General fu	IPR000772	[Ricin B, lectin domain] ; IPR001173[Glycosy
ng (GO:00	Leucine-rich	K	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 acid	IPR001375	[Peptidase S9, prolyl oligopeptidase, catalyt
--	Tetratricop	R	General fu	IPR019734	[Tetratricopeptide repeat]
--	--	--	--	--	IPR026315 [Out at first protein]
--	--	--	--	--	--
--	--	--	--	--	IPR001849 [Pleckstrin homology domain]
ko04611	P	--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR019748[

--	--	--	--	IPR005016	[Serine incorporator/TMS membrane protei
ko04810 R	--	--	--	IPR000048	[IQ motif, EF-hand binding site] ; IPR000593
ko04142 L	--	--	--	IPR004687	[Lysosomal-associated transmembrane pro
ko04144 E	--	--	--	IPR007286	[EAP30] ; IPR021648[Vacuolar protein sortin
--	--	--	--	IPR013932	[TATA-binding protein interacting (TIP20)]
ko03013 R	Uncharact	R	General fu	IPR001680	[WD40 repeat]
--	--	--	--	IPR001660	[Sterile alpha motif domain]
--	Plastocyan	C	Energy prc	IPR002909	[IPT domain] ; IPR011658[PA14 domain] ; IP
--	--	--	--	--	--
ko01522 E	Predicted IR		General fu	IPR020989	[Histone-arginine methyltransferase CARM
--	--	--	--	IPR001841	[Zinc finger, RING-type] ; IPR003137[PA do
ko04145 P	--	--	--	IPR000727	[Target SNARE coiled-coil homology doma
--	--	--	--	IPR002172	[Low-density lipoprotein (LDL) receptor clas
--	--	--	--	IPR000008	[C2 domain] ; IPR010734[Copine]
--	--	--	--	IPR004328	[BRO1 domain] ; IPR011072[HR1 rho-bindir
--	Uncharact	R	General fu	IPR000884	[Thrombospondin type-1 (TSP1) repeat] ; IF
--	--	--	--	IPR000225	[Armadillo]
--	--	--	--	IPR022248	[TNF receptor family, RELT]
--	Bacillopep	O	Posttransla	IPR000421	[Coagulation factor 5/8 C-terminal domain]
ko00564 G	Phosphatic I		Lipid trans	IPR001736	[Phospholipase D/Transphosphatidylase] ; II
--	--	--	--	IPR029270	[Limb expression 1]
--	--	--	--	--	--
--	--	--	--	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
ko04137 M	--	--	--	IPR001806	[Small GTPase superfamily] ; IPR013566[EF 1
--	--	--	--	IPR018619	[Hyccin]
--	Permease	GER	Carbohydr	IPR009262	[Solute carrier family 35 member SLC35F1/F
--	--	--	--	IPR029399	[TMEM192 family]
ko03013 R	--	--	--	IPR002483	[PWI domain]
--	--	--	--	IPR032403	[Exocyst component Exo84, C-terminal]
--	Ca ²⁺ -dep	R	General fu	IPR000008	[C2 domain] ; IPR010734[Copine]
--	AAA+-typ	MDT	Cell wall/r	IPR003959	[ATPase, AAA-type, core] ; IPR006594[LIS1 I
--	Ankyrin re	T	Signal tran	IPR021832	[Ankyrin repeat domain-containing protein
--	--	--	--	IPR004018	[RPEL repeat]
--	Acyl-CoA	C	Energy prc	IPR015590	[Aldehyde dehydrogenase domain]
--	Uncharact	S	Function u	--	--
--	--	--	--	IPR012583	[Pre-rRNA-processing protein RIX1, N-term
--	--	--	--	IPR001452	[SH3 domain] ; IPR012849[Abl-interactor, h
ko04144 E	--	--	--	IPR009686	[Senescence/spartin-associated]
ko00010 G	Phosphogl	G	Carbohydr	IPR013078	[Histidine phosphatase superfamily, clade-1
ko03013 R	--	--	--	IPR007231	[Nucleoporin interacting component Nup93
--	Phenylalan	J	Translatior	IPR001611	[Leucine-rich repeat] ; IPR005146[B3/B4 tRN
--	--	--	--	IPR001664	[Intermediate filament protein] ; IPR032444[
--	--	--	--	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/thr	T	Signal tran	IPR000719	[Protein kinase domain] ; IPR001180[Citron
--	--	--	--	IPR011021	[Arrestin-like, N-terminal] ; IPR011022[Arres
--	N-acetyl	M	Cell wall/r	IPR000210	[BTB/POZ domain] ; IPR006652[Kelch repea

--	--	--	--	IPR006671 [Cyclin, N-terminal]
ko04623 C	--	--	--	IPR024810 [Mab-21 domain]
ko04360 A	Membrane	M	--	Cell wall/r IPR000697 [WH1/EVH1 domain] ; IPR014885[VASP tetr
--	Leucine-rich	K	--	Transcripti IPR001611 [Leucine-rich repeat]
--	Magnesium	P	--	Inorganic i IPR008250 [P-type ATPase, A domain] ; IPR032630[P-t
ko03008 R	ATP-depen	O	--	Posttransla IPR003959 [ATPase, AAA-type, core]
--	DNA-bind	R	--	General fu IPR001258 [NHL repeat] ; IPR012336[Thioredoxin-like f
--	--	--	--	--
--	--	--	--	IPR010795 [Prenylcysteine lyase]
--	--	--	--	IPR009637 [Lung seven transmembrane receptor-like]
ko04141 P	Negative r	O	--	Posttransla IPR013766 [Thioredoxin domain]
ko04150 r	--	--	--	IPR013057 [Amino acid transporter, transmembrane dc
--	--	--	--	IPR001841 [Zinc finger, RING-type] ; IPR003137[PA do
--	--	--	--	IPR006861 [Hyaluronan/mRNA-binding protein] ; IPR0
--	--	--	--	--
ko00532 G	Putative Zr	R	--	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
--	--	--	--	--
--	Co/Zn/Cd	P	--	Inorganic i IPR002524 [Cation efflux protein]
--	--	--	--	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko03013 R	WD40 rep	R	--	General fu IPR001680 [WD40 repeat]
ko03013 R	--	--	--	IPR007846 [RNA-recognition motif (RRM) Nup35-type
--	--	--	--	IPR017978 [GPCR family 3, C-terminal]
ko04978 N	Predicted c	R	--	General fu IPR013130 [Ferric reductase transmembrane compone
--	--	--	--	IPR018499 [Tetraspanin/Peripherin]
--	--	--	--	IPR007000 [Phospholipase B-like]
ko03013 R	--	--	--	IPR021418 [THO complex, subunitTHOC2, C-terminal]
ko04390 H	--	--	--	IPR001478 [PDZ domain] ; IPR015132[L27-2]
ko04310 V	--	--	--	IPR009539 [Vang-like protein]
ko03460 F	WD40 rep	R	--	General fu IPR001680 [WD40 repeat] ; IPR021772[Protein of unknc
--	--	--	--	IPR007225 [Exocyst complex component EXOC6/Sec15
ko04141 P	--	--	--	IPR007716 [NPL4, zinc-binding putative] ; IPR007717[N
--	Regulator	O	--	Posttransla IPR001107 [Band 7 domain]
--	--	--	--	IPR027897 [Protein of unknown function DUF4559]
--	--	--	--	IPR013657 [UAA transporter]
--	--	--	--	--
--	--	--	--	IPR019326 [Protein of unknown function DUF2369]
--	Ca ²⁺ -bind	Q	--	Secondary --
--	--	--	--	IPR003131 [Potassium channel tetramerisation-type BT
ko04120 U	Ubiquitin	O	--	Posttransla IPR000594 [THIF-type NAD/FAD binding fold] ; IPR014
ko00590 A	Peroxi	O	--	Posttransla IPR032801 [Peroxi
ko00562 I	--	--	--	IPR002498 [Phosphatidylinositol-4-phosphate 5-kinas
--	WD40 rep	R	--	General fu IPR001680 [WD40 repeat]
ko00830 R	NAD(P)-de	IQR	--	Lipid trans IPR002347 [Short-chain dehydrogenase/reductase SDF
--	--	--	--	--
--	--	--	--	IPR003137 [PA domain] ; IPR007369[Peptidase A22B, si
--	--	--	--	IPR007369 [Peptidase A22B, signal peptide peptidase]
ko04062 C	Small-con	M	--	Cell wall/r IPR000219 [Dbl homology (DH) domain] ; IPR000591[C
--	--	--	--	IPR022078 [CD99 antigen-like protein 2]
--	Alpha-tub	DZ	--	Cell cycle c IPR000408 [Regulator of chromosome condensation, R
--	--	--	--	IPR001849 [Pleckstrin homology domain]
--	Uncharact	S	--	Function u IPR001478 [PDZ domain] ; IPR006907[Domain of unknc
--	--	--	--	IPR007109 [Brix domain]
--	Leucine-rich	K	--	Transcripti IPR001611 [Leucine-rich repeat] ; IPR021040[LRRC8, p

--	--	--	--	IPR001715 [Calponin homology domain] ; IPR001781[Z
ko03013 R	Predicted IT		Signal tran	IPR001680 [WD40 repeat] ; IPR024977[Anaphase-prom
ko04015 R	--	--	--	IPR001478 [PDZ domain] ; IPR021922[Domain of unkn
--	--	--	--	IPR000357 [HEAT repeat] ; IPR001494[Importin-beta, N
--	Broad spec	G	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]
--	Plastocyan C		Energy prc	IPR019316 [G8 domain] ; IPR025155[WxxW domain]
ko04144 E	--	--	--	IPR004328 [BRO1 domain] ; IPR025304[ALIX V-shaped
--	Phosphate P		Inorganic i	IPR001204 [Phosphate transporter]
ko04810 R	--	--	--	--
--	--	--	--	IPR000198 [Rho GTPase-activating protein domain] ; IF
--	Periplasmic	M	Cell wall/r	--
--	--	--	--	IPR001452 [SH3 domain] ; IPR001683[Phox homologou
--	--	--	--	IPR000058 [Zinc finger, AN1-type]
--	--	--	--	IPR007052 [CS domain]
--	--	--	--	IPR001619 [Sec1-like protein]
--	--	--	--	IPR000626 [Ubiquitin domain] ; IPR004274[FCP1 homo
--	--	--	--	--
ko04520 A	--	--	--	IPR001478 [PDZ domain] ; IPR001715[Calponin homol
ko05231 C	--	--	--	IPR007603 [Choline transporter-like]
ko04015 R	Predicted	/R	General fu	IPR000159 [Ras-associating (RA) domain] ; IPR000198[I
--	--	--	--	--
ko02010 A	ABC-type	V	Defense m	IPR003439 [ABC transporter-like]
--	--	--	--	IPR001507 [Zona pellucida domain]
ko03460 F	--	--	--	--
--	--	--	--	IPR022699 [Stonin-2, N-terminal] ; IPR028565[Mu hom
ko03040 S	--	--	--	IPR013180 [Beta-catenin-like protein 1, N-terminal]
--	--	--	--	IPR025151 [ELYS-like domain] ; IPR032040[ELYS, beta-
--	--	--	--	IPR009428 [Beta-catenin-interacting ICAT]
--	Superfamil	L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR003877[SPRY dor
--	--	--	--	--
ko03050 P	--	--	--	IPR013886 [PI31 proteasome regulator, C-terminal] ; IF
--	Amino acid	E	Amino acid	IPR002293 [Amino acid/polyamine transporter I]
--	--	--	--	IPR000436 [Sushi/SCR/CCP domain]
ko04144 E	Guanine-n	R	General fu	IPR000904 [Sec7 domain] ; IPR032691[Guanine nucleot
--	--	--	--	IPR004240 [Nonaspanin (TM9SF)]
ko04520 A	--	--	--	IPR003124 [WH2 domain]
--	Pimeloyl- <i>A</i>	HR	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	--	--	--	--
--	--	--	--	IPR001478 [PDZ domain] ; IPR001609[Myosin head, mc
--	Predicted IT		Signal tran	--
--	Ca ²⁺ -bind	Q	Secondary	IPR001007 [VWFC domain] ; IPR001611[Leucine-rich re
--	Leucine-rich	K	Transcripti	--
ko04514 C	--	--	--	IPR013106 [Immunoglobulin V-set domain] ; IPR01316
--	Leucine-rich	K	Transcripti	IPR002088 [Protein prenyltransferase, alpha subunit] ; I
--	Protein tyr	T	Signal tran	IPR000242 [PTP type protein phosphatase] ; IPR000998
ko05200 P	--	--	--	IPR000270 [PB1 domain]
--	--	--	--	IPR000195 [Rab-GTPase-TBC domain]
--	Periplasmic	O	Posttransla	IPR000867 [Insulin-like growth factor-binding protein,
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] ; IP
ko04390 H	Guanylate	F	Nucleotide	IPR001452 [SH3 domain] ; IPR001478[PDZ domain] ; IP
ko00790 F	Gamma-gl	E	Amino acid	IPR011697 [Peptidase C26]

--	Superfamily L	Replication IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/DIE
--	Ankyrin repeat	Signal transduction IPR001452	[SH3 domain] ; IPR020683[Ankyrin repeat-c
ko04270 V	--	--	IPR000219 [Dbl homology (DH) domain] ; IPR015212[R
ko04141 P	--	--	IPR004854 [Ubiquitin fusion degradation protein UFD1
ko04514 C	--	--	IPR001893 [Cysteine-rich Golgi apparatus protein 1 repeat
--	Proteasome O	Posttranslational IPR000555	[JAB1/MPN/MOV34 metalloenzyme domain
ko04530 T	GTPase SAR	General function IPR001806	[Small GTPase superfamily]
--	--	--	IPR004088 [K Homology domain, type 1] ; IPR015096[L
--	Leucine-rich K	Transcription IPR001212	[Somatomedin B domain] ; IPR018487[Hem
--	--	--	IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04068 F	Ubiquitin (O	Posttranslational IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko04120 U	--	--	IPR001373 [Cullin, N-terminal] ; IPR019559[Cullin prote
--	--	--	IPR001781 [Zinc finger, LIM-type]
ko00534 G	--	--	IPR004263 [Exostosin-like] ; IPR015338[Exostosin , C-te
ko00260 G	Methionine E	Amino acid IPR003726	[Homocysteine-binding domain]
--	Protein-tyrosine T	Signal transduction IPR000340	[Dual specificity phosphatase, catalytic dom
--	--	--	IPR007273 [SCAMP]
--	--	--	IPR013106 [Immunoglobulin V-set domain]
--	GTPase SAR	General function IPR001806	[Small GTPase superfamily]
--	--	--	--
ko04060 C	--	--	IPR022248 [TNF receptor family, RELT]
ko04152 A	Predicted intracellular U	Intracellular IPR004254	[AdipoR/Haemolysin-III-related]
--	--	--	IPR008590 [Protein of unknown function DUF872, trans
--	--	--	IPR007191 [Sec8 exocyst complex component specific
--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR019748[P
--	Uncharacterized S	Function unknown IPR004088	[K Homology domain, type 1] ; IPR015096[L
--	Leucine-rich K	Transcription IPR001611	[Leucine-rich repeat]
ko04144 E	--	--	IPR001452 [SH3 domain]
--	Sugar phosphate G	Carbohydrate IPR002350	[Kazal domain] ; IPR004156[Organic anion t
--	--	--	IPR023421 [Axin interactor, dorsalization-associated pr
--	GTPase SAR	General function IPR006689	[Small GTPase superfamily, ARF/SAR type]
--	--	--	IPR023235 [FAM105]
--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR010703[L
--	Membrane O	Posttranslational IPR022241	[Rhomboid serine protease] ; IPR022764[Pe
--	--	--	--
--	Nicotinamide HR	Coenzyme IPR000868	[Isochorismatase-like]
--	--	--	IPR001849 [Pleckstrin homology domain]
--	--	--	IPR007259 [Gamma-tubulin complex component prote
--	--	--	IPR003131 [Potassium channel tetramerisation-type BT
--	--	--	IPR002048 [EF-hand domain]
ko04020 C	--	--	IPR012446 [Calcium release-activated calcium channel
--	--	--	IPR000261 [EH domain]
ko01100 M	Dienelactone Q	Secondary IPR002925	[Dienelactone hydrolase]
--	--	--	IPR009755 [Colon cancer-associated Mic1-like]
--	--	--	IPR003877 [SPRY domain]
--	--	--	IPR006977 [Yip1 domain]
ko04142 L	Arylsulfatase P	Inorganic ion IPR000917	[Sulfatase, N-terminal]
--	--	--	IPR022083 [KIF-1 binding protein]
ko04144 E	--	--	IPR018798 [Multivesicular body subunit 12]
--	--	--	IPR029204 [CB1 cannabinoid receptor-interacting prot
--	Ca ²⁺ -dependent R	General function IPR000008	[C2 domain] ; IPR010734[Copine]
--	--	--	IPR002048 [EF-hand domain] ; IPR013787[S100/CaBP-
ko04015 R	--	--	IPR000331 [Rap GTPase activating protein domain] ; IP
ko04115 p	--	--	IPR004031 [PMP-22/EMP/MP20/Claudin superfamily]
ko04144 E	--	--	IPR005024 [Snf7 family]
ko00010 G	Phosphomannose G	Carbohydrate IPR005843	[Alpha-D-phosphohexomutase, C-terminal
--	PASTA domain M	Cell wall/membrane IPR000719	[Protein kinase domain]
--	2-keto-4-epimerase Q	Secondary IPR011234	[Fumarylacetoacetase, C-terminal-related]

--	Superfamil L	Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/DI
--	--	--	IPR001594 [Palmitoyltransferase, DHHC domain]
--	--	--	IPR001478 [PDZ domain] ; IPR001781[Zinc finger, LIM-
--	--	--	IPR004345 [TB2/DP1/HVA22-related protein]
--	--	--	IPR004088 [K Homology domain, type 1]
--	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 triç M	Cell wall/r	IPR000834 [Peptidase M14, carboxypeptidase A] ; IPR0
--	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] ;
--	--	--	IPR001190 [SRCR domain] ; IPR001695[Lysyl oxidase]
--	Aldo/keto Q	Secondary	IPR023210 [NADP-dependent oxidoreductase domain]
--	Serine/thrç T	Signal tran	IPR000719 [Protein kinase domain]
--	--	--	IPR002049 [Laminin EGF domain] ; IPR013032[EGF-like
ko00330 A	Acetylornit E	Amino acid	IPR002933 [Peptidase M20] ; IPR011650[Peptidase M20
--	--	--	IPR000315 [B-box-type zinc finger]
--	--	--	IPR001810 [F-box domain]
--	--	--	IPR027930 [Protein of unknown function DUF4609]
--	--	--	IPR010703 [Dedicator of cytokinesis, C-terminal] ; IPR0
ko04390 H	--	--	IPR018979 [FERM, N-terminal] ; IPR018980[FERM, C-te
ko01523 A	Predicted ç 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]
--	N-acetylm M	Cell wall/r	IPR002502 [N-acetylmuramoyl-L-alanine amidase don
--	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] ; IPR032ç
--	--	--	IPR029409 [Transmembrane protein 237]
ko04724 G	--	--	IPR013057 [Amino acid transporter, transmembrane dc
--	Predicted ç G	Carbohydr	IPR005828 [Major facilitator, sugar transporter-like]
--	--	--	IPR001452 [SH3 domain] ; IPR001683[Phox homologou
ko04015 R	--	--	IPR000276 [G protein-coupled receptor, rhodopsin-lik
--	--	--	IPR007052 [CS domain]
ko04621 N	Leucine-ric K	Transcripti	IPR001478 [PDZ domain] ; IPR001611[Leucine-rich rep
--	--	--	IPR007259 [Gamma-tubulin complex component prote
--	Outer men M	Cell wall/r	IPR000884 [Thrombospondin type-1 (TSP1) repeat] ; IF
--	--	--	IPR003877 [SPRY domain] ; IPR006594[LIS1 homology
--	--	--	IPR000538 [Link domain] ; IPR013106[Immunoglobulin
--	--	--	IPR008253 [Marvel domain]
--	--	--	IPR000306 [FYVE zinc finger] ; IPR001849[Pleckstrin ho
--	--	--	IPR001478 [PDZ domain]
--	Predicted ç G	Carbohydr	--
--	--	--	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
ko03050 P	20S protea O	Posttransla	IPR001353 [Proteasome, subunit alpha/beta] ; IPR0246ç
ko00440 P	Glycerol-3 M	Cell wall/r	IPR004821 [Cytidyltransferase-like domain]
ko03050 P	Predicted IT	Signal tran	IPR002015 [Proteasome/cyclosome repeat]
ko05012 P	Putative in R	General fu	IPR002818 [DJ-1/PfpI]
ko04142 L	Uncharactç R	General fu	IPR031777 [Sortilin, C-terminal] ; IPR031778[Sortilin, N-

--	NADPH:qu CR	Energy prc	IPR013149 [Alcohol dehydrogenase, C-terminal] ; IPR0
--	--	--	IPR000225 [Armadillo]
ko04136 A	WD40 repcR	General fu	IPR000719 [Protein kinase domain] ; IPR001680[WD40
--	--	--	IPR013787 [S100/CaBP-9k-type, calcium binding, subc
--	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]
ko00561 G	LysophospI	Lipid trans	IPR022742 [Serine aminopeptidase, S33]
ko04974 P	Cell divisioD	Cell cycle c	IPR002035 [von Willebrand factor, type A] ; IPR003961[
ko04350 T	--	--	IPR001132 [SMAD domain, Dwarfing-type] ; IPR003619[
--	--	--	IPR002164 [Nucleosome assembly protein (NAP)]
--	--	--	--
ko00562 Ir	--	--	IPR002498 [Phosphatidylinositol-4-phosphate 5-kinase
--	--	--	IPR004240 [Nonaspanin (TM9SF)]
--	--	--	IPR002259 [Equilibrative nucleoside transporter]
--	Ca ²⁺ -bincT	Signal tran	IPR002048 [EF-hand domain]
ko04144 E	--	--	IPR001452 [SH3 domain] ; IPR004148[BAR domain]
--	--	--	IPR025977 [Nuclear condensin complex subunit 3, C-te
ko04144 E	--	--	IPR006789 [Actin-related protein 2/3 complex subunit
ko04150 n	--	--	IPR031313 [SAPK-interacting protein 1, Pleckstrin-hom
--	RNA recogJ	Translatior	IPR000504 [RNA recognition motif domain] ; IPR00187
--	--	--	IPR000306 [FYVE zinc finger] ; IPR032031[Zinc finger F
--	Predicted ,R	General fu	IPR001680 [WD40 repeat]
--	--	--	IPR007015 [DNA polymerase V]
--	--	--	IPR001849 [Pleckstrin homology domain] ; IPR019748[
--	MembraneM	Cell wall/m	IPR001680 [WD40 repeat] ; IPR015048[Domain of unkn
--	--	--	IPR010357 [Protein of unknown function DUF953, thior
ko04144 E	--	--	IPR008570 [ESCRT-II complex, vps25 subunit]
--	WD40 repcR	General fu	IPR001680 [WD40 repeat]
ko03015 n	Stalled ribcJ	Translatior	IPR005140 [eRF1 domain 1/Pelota-like] ; IPR005141[eR
--	Negative rO	Posttransla	IPR013766 [Thioredoxin domain]
--	--	--	IPR006990 [Tweety]
--	--	--	IPR000008 [C2 domain] ; IPR031468[Synaptotagmin-lik
--	--	--	IPR032375 [Cerebral cavernous malformations 2, harm
--	--	--	IPR021852 [Domain of unknown function DUF3456]
--	--	--	IPR019325 [NEDD4/Bsd2]
--	--	--	IPR000717 [Proteasome component (PCI) domain]
--	--	--	IPR019140 [Mini-chromosome maintenance complex-l
ko04122 S	--	--	IPR015221 [Ubiquitin-related modifier 1]
--	--	--	--
--	Leucine-richK	Transcripti	IPR001611 [Leucine-rich repeat]
ko00562 Ir	--	--	IPR000403 [Phosphatidylinositol 3-/4-kinase, catalytic
--	--	--	IPR022577 [Tubulin-specific chaperone D, C-terminal]
ko03013 R	--	--	IPR019049 [Nucleoporin protein Ndc1-Nup]
ko04145 P	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko05164 Ir	--	--	IPR003034 [SAP domain] ; IPR003877[SPRY domain]
--	--	--	--
ko04141 P	--	--	--
ko00270 C	MethylthioE	Amino aci	IPR000649 [Initiation factor 2B-related]
ko00270 C	AcireductcE	Amino aci	IPR004313 [Acireductone dioxygenase ARD family]
--	--	--	IPR001841 [Zinc finger, RING-type]
--	Cycloprop.i	Lipid trans	IPR008576 [Alpha-N-methyltransferase NTM1]
ko04145 P	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
ko04136 A	Predicted ,R	General fu	IPR001680 [WD40 repeat]
--	--	--	--

--	--	--	--	IPR021148	[Polysaccharide biosynthesis domain]
ko00564	G	--	--	IPR004277	[Phosphatidyl serine synthase]
--	--	--	--	IPR009038	[GOLD domain]
ko03013	R	--	--	--	--
--	ATP-depe	O		Posttransla	IPR003959 [ATPase, AAA-type, core]
--	Spore gerr	D		Cell cycle c	IPR001223 [Glycoside hydrolase family 18, catalytic dor
ko04514	C	--	--	IPR013106	[Immunoglobulin V-set domain]
--	--	--	--	--	--
--	--	--	--	IPR009538	[PV-1]
--	--	--	--	IPR000648	[Oxysterol-binding protein]
ko04144	E	--	--	IPR000008	[C2 domain] ; IPR019018[Rab-binding dom
--	--	--	--	IPR000195	[Rab-GTPase-TBC domain]
--	Tetratricop	R		General fu	IPR019734 [Tetratricopeptide repeat] ; IPR021183[N-te
--	Amino aci	E		Amino aci	IPR004841 [Amino acid permease/ SLC12A domain] ; If
--	--	--	--	IPR022065	[Uncharacterised protein family, TMEM59]
--	--	--	--	IPR001073	[C1q domain] ; IPR011489[EMI domain]
ko00230	P	Inosine/xai	F	Nucleotide	IPR002637 [Ham1-like protein]
--	--	--	--	IPR013979	[Translation initiation factor, beta propellor-
ko04514	C	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
ko03320	P	--	--	IPR002181	[Fibrinogen, alpha/beta/gamma chain, C-te
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-bindin	R	General fu	IPR010674 [Nucleolar GTP-binding protein 1, Rossman
ko05202	T	--	--	IPR001012	[UBX domain] ; IPR021569[TUG ubiquitin-li
--	Ankyrin rej	T		Signal tran	IPR020683 [Ankyrin repeat-containing domain]
--	GTPase SAR			General fu	IPR001806 [Small GTPase superfamily]
--	Diphthami	J		Translatio	IPR016435 [Diphthamide synthesis DPH1/DPH2]
--	WD40 rep	R		General fu	--
ko04310	V	Predicted IT		Signal tran	IPR001680 [WD40 repeat] ; IPR006594[LIS1 homology
ko04015	R	Serine/thre	T	Signal tran	IPR000719 [Protein kinase domain] ; IPR002219[Protein
ko04650	N	--	--	IPR011161	[MHC class I-like antigen recognition-like]
--	--	--	--	--	--
ko00240	P	Uridine kin	F	Nucleotide	IPR006083 [Phosphoribulokinase/uridine kinase]
--	--	--	--	IPR007875	[Sprouty]
--	--	--	--	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]
--	--	--	--	IPR000198	[Rho GTPase-activating protein domain] ; If
--	--	--	--	IPR010569	[Myotubularin-like phosphatase domain] ; I
--	--	--	--	--	--
--	Cysteine p	O		Posttransla	IPR000668 [Peptidase C1A, papain C-terminal]
--	--	--	--	IPR026794	[Uncharacterised protein family UPF0687]
--	--	--	--	--	--
ko03018	R	WD40 rep	R	General fu	IPR001680 [WD40 repeat]
--	TFIIF-inter	K		Transcripti	IPR004274 [FCP1 homology domain]
--	FOG: Zn-fi	R		General fu	IPR001909 [Krueppel-associated box] ; IPR007087[Zinc
--	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
ko03008	R	--	--	IPR004859	[Putative 5-3 exonuclease]
--	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]
ko04144 E	--	--	--	IPR003903 [Ubiquitin interacting motif] ; IPR013809[EN
ko04071 S	--	--	--	IPR000276 [G protein-coupled receptor, rhodopsin-lik
--	--	--	--	IPR027967 [Protein of unknown function DUF4612]
--	--	--	--	IPR001619 [Sec1-like protein]
--	--	--	--	IPR006993 [SH3-binding, glutamic acid-rich protein]
--	N-acetylneM		Cell wall/r	IPR000210 [BTB/POZ domain] ; IPR006652[Kelch repea
ko04114 C	Serine/threT		Signal tran	IPR000719 [Protein kinase domain] ; IPR022165[Polo ki
ko04724 G	--	--	--	IPR013057 [Amino acid transporter, transmembrane dc
ko04010 M	Serine/threT		Signal tran	IPR000719 [Protein kinase domain]
ko03018 R	HrpA-like J		Translatio	IPR001650 [Helicase, C-terminal] ; IPR007502[Helicase-
ko00190 C	Inorganic pCP		Energy prc	IPR008162 [Inorganic pyrophosphatase]
--	Acid stressT		Signal tran	IPR002634 [BoIA protein]
--	Protein tyr T		Signal tran	IPR000242 [PTP type protein phosphatase] ; IPR004328
--	TetratricopeR		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]
--	Aminopep E		Amino acid	IPR014782 [Peptidase M1, membrane alanine aminope
ko04145 P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain] ; IPR018316[
--	--	--	--	IPR000716 [Thyroglobulin type-1] ; IPR002350[Kazal dc
--	--	--	--	IPR007477 [SAB domain] ; IPR008379[Band 4.1, C-term
--	UncharacterS		Function u	IPR014044 [CAP domain]
ko03008 R	--	--	--	IPR012954 [BP28, C-terminal domain] ; IPR022125[U3 s
--	--	--	--	--
--	--	--	--	IPR007110 [Immunoglobulin-like domain] ; IPR013106[
ko04621 N	--	--	--	IPR002035 [von Willebrand factor, type A] ; IPR008399[
ko00240 P	NTP pyropV		Defense m	IPR025984 [dCTP pyrophosphatase 1]
--	--	--	--	IPR001214 [SET domain] ; IPR002893[Zinc finger, MYNI
--	--	--	--	IPR001452 [SH3 domain] ; IPR010703[Dedicator of cytc
ng (GO:000	WD40 repR		General fu	IPR001680 [WD40 repeat]
--	Magnesiur P		Inorganic i	IPR004014 [Cation-transporting P-type ATPase, N-terr
--	--	--	--	IPR019396 [Transmembrane Fragile-X-F-associated pr
ko04144 E	--	--	--	IPR018798 [Multivesicular body subunit 12]
--	--	--	--	IPR029366 [TMEM206 protein]
ko04120 U	--	--	--	IPR000608 [Ubiquitin-conjugating enzyme E2]
ko04145 P	--	--	--	IPR003008 [Tubulin/FtsZ, GTPase domain]
--	--	--	--	--
ko04390 H	--	--	--	IPR005301 [MOB kinase activator family]
--	--	--	--	IPR000306 [FYVE zinc finger] ; IPR001849[Pleckstrin ho
--	--	--	--	IPR013921 [Mediator complex, subunit Med20]
--	Leucine-richK		Transcripti	IPR001611 [Leucine-rich repeat]
ko04144 E	--	--	--	IPR009851 [Modifier of rudimentary, Modr]
--	--	--	--	IPR000717 [Proteasome component (PCI) domain]
--	Histone acKB		Transcripti	IPR000182 [GNAT domain] ; IPR007197[Radical SAM] ;
ko00230 P	DNA-directed K		Transcripti	IPR007120 [DNA-directed RNA polymerase, subunit 2,
--	--	--	--	IPR009357 [Solute carrier family 52, riboflavin transport
ko00770 P	PhosphopH		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
ko04014 R	WD40 repR		General fu	IPR001680 [WD40 repeat]
ko03013 R	--	--	--	IPR013598 [Exportin-1/Importin-beta-like]
--	UncharacterS		Function u	IPR003226 [Metal-dependent protein hydrolase]
--	--	--	--	--

ko04310 V	--	--	--	IPR007052	[CS domain] ; IPR007699[SGS domain] ; IPR
ko04218 C	Ankyrin re	T		Signal tran	IPR002110 [Ankyrin repeat] ; IPR005821[Ion transport c
--	GTPase SAR			General fu	IPR001806 [Small GTPase superfamily]
ko04510 F	--	--	--	IPR001715	[Calponin homology domain]
--	Putative C	R		General fu	IPR001727 [Gdt1 family]
--	Superfamil	L		Replicatio	--
ko04120 U	--	--	--	IPR000008	[C2 domain] ; IPR000569[HECT domain] ; IP
--	NADPH:qu	CR		Energy prc	IPR013154 [Alcohol dehydrogenase, N-terminal]
--	--	--	--	IPR014847	[FERM adjacent (FA)] ; IPR018979[FERM, N-
--	--	--	--	IPR021910	[Protein of unknown function DUF3522]
ko04340 H	Periplasmic	U		Intracellular	IPR000719 [Protein kinase domain] ; IPR022247[Casein
--	--	--	--	IPR004240	[Nonaspanin (TM9SF)]
ko04666 F	HD super	JR		Translatio	IPR000048 [IQ motif, EF-hand binding site] ; IPR000155
--	Uncharact	S		Function u	IPR003409 [MORN motif]
--	Sugar lact	G		Carbohydr	IPR018119 [Strictosidine synthase, conserved region]
ko02010 A	ABC-type	O		Posttransla	IPR003439 [ABC transporter-like] ; IPR011527[ABC tran
--	GTPase SAR			General fu	IPR001806 [Small GTPase superfamily]
ko04144 E	--	--	--	--	--
--	--	--	--	IPR002172	[Low-density lipoprotein (LDL) receptor clas
--	Large exo	U		Intracellular	IPR002126 [Cadherin] ; IPR013164[Cadherin, N-termina
ko00562 I	Myo-inositol			Lipid trans	IPR002587 [Myo-inositol-1-phosphate synthase] ; IPR0
ko04010 N	--	--	--	IPR000157	[Toll/interleukin-1 receptor homology (TIR)
--	--	--	--	IPR024133	[Transmembrane protein 138]
--	--	--	--	IPR019318	[Guanine nucleotide exchange factor, Ric8]
ko04360 A	--	--	--	IPR001627	[Sema domain] ; IPR002165[Plexin repeat]
--	PKD repea	S		Function u	IPR001881 [EGF-like calcium-binding domain] ; IPR011
--	--	--	--	IPR017978	[GPCR family 3, C-terminal]
ko05010 A	--	--	--	IPR003388	[Reticulon]
--	Xaa-Pro ar	E		Amino acid	IPR000994 [Peptidase M24] ; IPR007865[Aminopeptida
ko00250 A	Predicted	R		General fu	IPR003010 [Carbon-nitrogen hydrolase]
ko04514 C	--	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
--	Xaa-Pro ar	E		Amino acid	IPR000587 [Creatinase, N-terminal] ; IPR000994[Peptid
--	--	--	--	IPR007084	[BRICHOS domain]
ko04120 U	--	--	--	IPR000608	[Ubiquitin-conjugating enzyme E2] ; IPR001
--	--	--	--	IPR001478	[PDZ domain] ; IPR001781[Zinc finger, LIM-
ko00010 G	Acyl-coen	I		Lipid trans	IPR000873 [AMP-dependent synthetase/ligase] ; IPR02
--	Superfamil	L		Replicatio	IPR001650 [Helicase, C-terminal] ; IPR011545[DEAD/Df
ko04141 P	GTPase SAR			General fu	IPR006689 [Small GTPase superfamily, ARF/SAR type]
ko04142 L	Sugar pho	G		Carbohydr	IPR011701 [Major facilitator superfamily]
ko03013 R	WD40 rep	R		General fu	IPR001680 [WD40 repeat]
--	--	--	--	IPR003112	[Olfactomedin-like domain]
ko00770 P	Phosphop	H		Coenzyme	IPR008278 [4'-phosphopantetheinyl transferase super
--	--	--	--	IPR000095	[CRIB domain]
--	--	--	--	--	--
--	DNA gyra	L		Replicatio	IPR006917 [SOUL haem-binding protein]
--	GTPase SAR			General fu	IPR001806 [Small GTPase superfamily]
ko04144 E	--	--	--	IPR001619	[Sec1-like protein]
--	Uncharact	S		Function u	IPR005552 [Scramblase]
--	Lantibiotic	V		Defense m	IPR007822 [Lanthionine synthetase C-like]
--	--	--	--	IPR025256	[Domain of unknown function DUF4203]
ko00970 A	Phenylalan	J		Translatio	IPR005146 [B3/B4 tRNA-binding domain] ; IPR005147[
ko04136 A	--	--	--	IPR007134	[Autophagy-related protein 3, N-terminal] ;
--	Chromoso	D		Cell cycle c	IPR003395 [RecF/RecN/SMC, N-terminal] ; IPR010935[
--	Ribosome	J		Translatio	IPR006073 [GTP binding domain] ; IPR013029[Domain
--	--	--	--	IPR001594	[Palmitoyltransferase, DHHC domain]
--	--	--	--	IPR009790	[Protein of unknown function DUF1356, TM
--	--	--	--	IPR001478	[PDZ domain] ; IPR014775[L27 domain, C-ter
--	ATPase co	R		General fu	IPR003439 [ABC transporter-like] ; IPR032781[ABC-tran

--	--	--	--	IPR009828	[Protein of unknown function DUF1394]
--	--	--	--	IPR029392	[AP-5 complex subunit sigma-1]
--	Superfamil	L	Replicatio	IPR001650	[Helicase, C-terminal] ; IPR011545[DEAD/D
--	--	--	--	IPR002867	[IBR domain]
--	--	--	--	IPR019160	[Exocyst complex component Sec3, C-termi
--	--	--	--	IPR005045	[CDC50/LEM3 family]
ko00770 P	Uncharact	S	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/D
--	--	--	--	IPR010695	[Fas apoptotic inhibitory molecule 1]
ko00750 V	Pyridoxine. H		Coenzyme	IPR011576	[Pyridoxamine 5'-phosphate oxidase-like, F
--	--	--	--	--	--
--	tRNA(His) J		Translatio	IPR024956	[tRNAHis guanylyltransferase catalytic dom
--	--	--	--	IPR011016	[Zinc finger, RING-CH-type]
--	GTPase SAR		General fu	IPR001806	[Small GTPase superfamily]
ko00562 Ir	3'-Phosph P		Inorganic i	IPR000760	[Inositol monophosphatase-like]
--	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]
ko04810 R	--	--	--	IPR001452	[SH3 domain] ; IPR012849[Abl-interactor, h
ko04010 N	Ankyrin rej	T	Signal tran	IPR001245	[Serine-threonine/tyrosine-protein kinase c
--	Leucine-ric	K	Transcripti	IPR004934	[Tropomodulin]
ko04130 S	--	--	--	--	--
--	--	--	--	IPR000591	[DEP domain] ; IPR001849[Pleckstrin homol
--	--	--	--	IPR014830	[Glycolipid transfer protein domain]
ko04144 E	Lysophosph	I	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-d	M	Cell wall/r	IPR029903	[RmlD-like substrate binding domain]
ko04144 E	Replicatio	L	Replicatio	IPR000261	[EH domain] ; IPR022812[Dynamin superfan
--	Secreted tr	O	Posttransla	IPR000859	[CUB domain] ; IPR001254[Serine proteases
--	--	--	--	IPR001452	[SH3 domain] ; IPR018556[Domain of unknc
ko04514 C	--	--	--	IPR013106	[Immunoglobulin V-set domain] ; IPR01316
--	Glucose/ar	G	Carbohydr	IPR000033	[LDLR class B repeat] ; IPR000742[EGF-like c
ko04014 R	Ca2+ -binc	T	Signal tran	IPR002048	[EF-hand domain]
--	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 rej	T	Signal tran	IPR002110	[Ankyrin repeat] ; IPR020683[Ankyrin repeat
ko04217 N	O-acetyl-/J		Translatio	IPR002589	[Macro domain] ; IPR007125[Histone H2A/H
--	--	--	--	IPR008853	[TMEM9]
--	--	--	--	IPR000906	[ZU5 domain] ; IPR001452[SH3 domain] ; IP
--	--	--	--	IPR030379	[Septin-type guanine nucleotide-binding (C
--	--	--	--	IPR027817	[Costars domain]
--	--	--	--	IPR026134	[MyoD family inhibitor/MyoD family inhibitc
--	--	--	--	--	--
--	Alpha-tub	DZ	Cell cycle c	IPR000408	[Regulator of chromosome condensation, R
--	Thioestera	Q	Secondary	IPR000873	[AMP-dependent synthetase/ligase] ; IPR01
--	--	--	--	IPR026179	[SLAIN motif-containing protein]
--	DNA-bind	R	General fu	IPR009471	[Teneurin intracellular, N-terminal] ; IPR028'
--	--	--	--	IPR025602	[BCP1 family]
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
--	--	--	--	IPR013106	[Immunoglobulin V-set domain]

ko03015	n	Predicted	r	R
ko00970	A	Leucyl-tRNA		J
--	--	--	--	--
--	--	--	--	--
ko04144	E	Uncharacter	s	S
--	--	--	--	--
ko00562	l	r	--	--
ko04145	P	Ca2+-bind	Q	Q
--	--	--	--	--
ko04144	E	Predicted	r	R
--	--	--	--	--
ko00260	G	Lactate de	CHR	CHR
ko04142	L	Cysteine p	O	O
ko04141	P	DnaJ-class	O	O
--	--	--	--	--
--	--	--	--	--
ko04530	T	--	--	--
--	--	DnaJ-class	O	O
--	--	Ribulose-5	G	G
--	--	Xanthine/	L	L
ko04068	F	CBS doma	T	T
ko04970	S	--	--	--
--	--	Predicted	s	G
ko04010	M	--	--	--
--	--	--	--	--
ko03060	P	--	--	--
--	--	--	--	--
ko04014	R	Serine/thr	e	T
ko05100	B	Predicted	(	R
ko04978	M	--	--	--
ko03013	R	Superfamil	L	L
--	--	--	--	--
--	--	--	--	--
--	--	Prefoldin,	(	O
ko00270	C	Enolase-pl	E	E
ko03013	R	Translator	J	J
ko00190	C	--	--	--
--	--	--	--	--
--	--	--	--	--
--	--	--	--	--
ko04140	A	Serine/thr	e	T
ko04614	R	Aminopep	E	E
ko04360	A	DNA-bind	R	R
--	--	Peptide m	(	O
ko04014	R	--	--	--
--	--	--	--	--
ko04144	E	--	--	--
--	--	Serine pro	(	O
--	--	--	--	--
--	--	Ribosomal	J	J
--	--	Serine/thr	e	T
ko03015	n	RNA proce	J	J
--	--	--	--	--
ko00230	P	8-oxo-dG	^	V
--	--	--	--	--
--	--	--	--	--
--	--	--	--	--

--	--	--	--	IPR003103	[BAG domain]
ko04144	E	GTPase SAR	General fu	IPR001806	[Small GTPase superfamily]
ko03050	P	--	--	IPR003185	[Proteasome activator pa28, N-terminal dor
--	--	Predicted rJ	Translatior	IPR002478	[PUA domain]
--	--	--	--	IPR001594	[Palmitoyltransferase, DHHC domain]
--	--	Zinc transP	Inorganic i	IPR003689	[Zinc/iron permease]
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
ko01522	E	Ankyrin rejT	Signal tran	IPR000742	[EGF-like domain] ; IPR000800[Notch doma
--	--	--	--	IPR001609	[Myosin head, motor domain] ; IPR032412[
ko03040	S	Predicted rR	General fu	IPR001680	[WD40 repeat] ; IPR003613[U box domain] ;
ko04141	P	--	--	IPR000626	[Ubiquitin domain] ; IPR015940[Ubiquitin-a
ko04144	E	--	--	IPR001683	[Phox homologous domain]
ko04144	E	AAA+-typ MDT	Cell wall/r	IPR003959	[ATPase, AAA-type, core] ; IPR007330[MIT]
ko04022	c	--	--	IPR000402	[Sodium/potassium-transporting ATPase su
--	--	Large exoU	Intracellular	IPR002126	[Cadherin] ; IPR013164[Cadherin, N-termina
--	--	RNA recoJ	Translatior	IPR000504	[RNA recognition motif domain] ; IPR00207
--	--	--	--	IPR001060	[FCH domain] ; IPR001452[SH3 domain]
ko04144	E	--	--	IPR001683	[Phox homologous domain] ; IPR015404[So
ko04130	S	--	--	IPR000727	[Target SNARE coiled-coil homology doma
ko00564	G	--	--	IPR016090	[Phospholipase A2 domain]
ko03050	P	--	--	IPR000717	[Proteasome component (PCI) domain]
ko04217	N	--	--	IPR001012	[UBX domain]
ko04610	C	--	--	IPR011161	[MHC class I-like antigen recognition-like]
ko03040	S	Peptidyl-p O	Posttransla	IPR000504	[RNA recognition motif domain] ; IPR00213
ko01523	A	Forkhead zT	Signal tran	IPR003439	[ABC transporter-like] ; IPR013525[ABC-2 ty
--	--	--	--	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]
--	--	--	--	IPR001101	[Plectin repeat] ; IPR001715[Calponin homo
ko04910	Ir	--	--	IPR004140	[Exocyst complex component Exo70]
--	--	--	--	IPR001394	[Peptidase C19, ubiquitin carboxyl-terminal
ko05206	N	dsRNA-spK	Transcripti	IPR000999	[Ribonuclease III domain] ; IPR001650[Helic
ko04216	F	Amino acidE	Amino acid	IPR002293	[Amino acid/polyamine transporter I]
ko04014	R	Leucine-richK	Transcripti	IPR001611	[Leucine-rich repeat]
ko04072	P	--	--	IPR000375	[Dynamin central domain] ; IPR001849[Plect
ko00511	C	Neuramini GM	Carbohydr	IPR011040	[Sialidases]
--	--	MethioninJ	Translatior	IPR000994	[Peptidase M24]
ko04520	A	--	--	IPR001452	[SH3 domain] ; IPR013606[IMD/I-BAR doma
ko04110	C	Chromoso D	Cell cycle c	IPR003395	[RecF/RecN/SMC, N-terminal] ; IPR010935[
ko04144	E	--	--	IPR005024	[Snf7 family]
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]
--	--	DNA helicK	Transcripti	IPR010339	[TIP49, C-terminal]
--	--	--	--	IPR019382	[Translation initiation factor 3 complex subu
ko04310	V	DNA helicK	Transcripti	IPR010339	[TIP49, C-terminal]
--	--	--	--	IPR007052	[CS domain] ; IPR025934[NudC N-terminal
ko04360	A	--	--	IPR002108	[Actin-depolymerising factor homology dor
--	--	--	--	IPR007084	[BRICHOS domain]
--	--	Ribosome-J	Translatior	IPR004095	[TGS] ; IPR006073[GTP binding domain] ; IP
ko04810	R	--	--	IPR019137	[Nck-associated protein 1]
--	--	--	--	IPR007225	[Exocyst complex component EXOC6/Sec15
--	--	--	--	IPR029304	[A-kinase anchor protein 2, C-terminal dor

--	Thioesterase Q	Secondary IPR000873 [AMP-dependent synthetase/ligase] ; IPR01
--	--	-- IPR005026 [SAPAP family]
--	Serine/threonine T	Signal transduction IPR000719 [Protein kinase domain] ; IPR017892[Protein
--	Uncharacterized S	Function unknown IPR001680 [WD40 repeat]
--	--	-- IPR007477 [SAB domain] ; IPR008379[Band 4.1, C-term
ko03018 R	Exoribonuclease K	Transcript processing IPR002716 [PIN domain] ; IPR033770[Exosome complex
ko03008 R	RNA 3'-terminal A	RNA processing IPR013791 [RNA 3'-terminal phosphate cyclase, insert
--	N-acetyltransferase M	Cell wall/membrane --
--	Cold shock protein K	Transcript processing IPR002059 [Cold-shock protein, DNA-binding]
ko03008 R	RNA processing J	Translation IPR002687 [Nop domain] ; IPR012974[NOP5, N-termin
ko04144 E	Ankyrin repeat T	Signal transduction IPR001164 [Arf GTPase activating protein] ; IPR013724[
ko04621 N	Serine/threonine T	Signal transduction IPR007052 [CS domain] ; IPR007699[SGS domain]
ko00520 A	N-acetylglucosyl G	Carbohydrate IPR006680 [Amidohydrolase-related]
--	Predicted cytosolic R	General function IPR002737 [MEMO1 family]
ko03018 R	--	-- IPR001163 [LSM domain, eukaryotic/archaea-type]
ko04140 A	--	-- IPR001452 [SH3 domain] ; IPR004148[BAR domain]
--	--	-- IPR004882 [Luc7-related]
ko03008 R	Ribosome J	Translation IPR018978 [Ribosome maturation protein SBDS, C-term
--	--	-- IPR009038 [GOLD domain]
ko03008 R	Oligoribonuclease A	RNA processing IPR013520 [Exonuclease, RNase T/DNA polymerase III]
--	Metal-sulfur O	Posttranslational IPR002744 [Domain of unknown function DUF59]
ko04137 N	--	-- IPR028058 [Fis1, N-terminal tetratricopeptide repeat] ;
ko04144 E	--	-- IPR005024 [Snf7 family]
ko03013 R	Predicted intracellular T	Signal transduction IPR001680 [WD40 repeat]
--	RNA-splicing J	Translation IPR001233 [tRNA-splicing ligase, RtcB]
--	Cell division D	Cell cycle control IPR000198 [Rho GTPase-activating protein domain] ; IF
--	--	-- IPR005343 [Nucleolar complex protein 2]
ko03010 R	--	-- IPR000509 [Ribosomal protein L36e]
--	--	-- IPR000225 [Armadillo]
ko03015 R	Translation J	Translation IPR004160 [Translation elongation factor EFTu/EF1A, C
ko00190 C	Archaeal/vacuolar C	Energy processing IPR002490 [V-type ATPase, V0 complex, 116kDa subu
ko04015 R	--	-- IPR002558 [I/LWEQ domain] ; IPR015009[Vinculin-binc
--	Membrane M	Cell wall/membrane IPR031161 [Peptidase family M60 domain]
ko04310 V	--	-- IPR010472 [Formin, FH3 domain] ; IPR010473[Formin, (
--	Type V secretion MU	Cell wall/membrane IPR001627 [Sema domain] ; IPR002165[Plexin repeat] ;
ko04137 N	Ubiquitin (O	Posttranslational IPR001394 [Peptidase C19, ubiquitin carboxyl-terminal
ko04015 R	--	-- IPR002558 [I/LWEQ domain] ; IPR015009[Vinculin-binc
--	Phosphoesterase G	Carbohydrate IPR000048 [IQ motif, EF-hand binding site] ; IPR001605
--	--	-- IPR001190 [SRCR domain] ; IPR001695[Lysyl oxidase]
ko04141 P	Molecular O	Posttranslational IPR013126 [Heat shock protein 70 family]
ko03460 F	--	-- IPR019337 [Telomere length regulation protein, conser
--	--	-- IPR002867 [IBR domain]
--	--	-- IPR000421 [Coagulation factor 5/8 C-terminal domain]
--	Lysophospholipid I	Lipid transport IPR000073 [Alpha/beta hydrolase fold-1]
--	--	-- IPR003131 [Potassium channel tetramerisation-type BT
ko00230 P	Nucleoside diphosphate F	Nucleotide IPR001564 [Nucleoside diphosphate kinase] ; IPR01055
ko04979 C	--	-- IPR002181 [Fibrinogen, alpha/beta/gamma chain, C-te
--	--	-- IPR001578 [Peptidase C12, ubiquitin carboxyl-terminal
ko05100 B	--	-- IPR001452 [SH3 domain]
ko00190 C	Archaeal/vacuolar C	Energy processing IPR002699 [ATPase, V1 complex, subunit D]
--	--	-- IPR013598 [Exportin-1/Importin-beta-like]
ko03060 P	--	-- IPR019009 [Signal recognition particle receptor, beta su
--	--	-- IPR007233 [Trafficking protein particle complex subuni
--	Serine/threonine T	Signal transduction IPR000719 [Protein kinase domain] ; IPR001180[Citron
ko03013 R	RNA recognition J	Translation IPR000504 [RNA recognition motif domain]
--	--	-- IPR001452 [SH3 domain] ; IPR001683[Phox homologou
ko04144 E	--	-- IPR001683 [Phox homologous domain] ; IPR015404[So
ko00561 G	Ca ²⁺ -binding Q	Secondary IPR001024 [PLAT/LH2 domain] ; IPR013818[Lipase/vitel

--	Sugar pho	G	Carbohydr	IPR011701	[Major facilitator superfamily]
--	Chromoso	D	Cell cycle c	IPR033756	[Flagellum site-determining protein YlxH/ F
--	--	--	--	IPR015425	[Formin, FH2 domain]
ko00260	G	Phosphose	HE	Coenzyme	IPR000192 [Aminotransferase class V domain]
ko04514	C	--	--	--	IPR013151 [Immunoglobulin]
--	--	--	--	--	IPR001863 [Glypican]
--	--	--	--	--	--
--	--	--	--	IPR000203	[GPS motif] ; IPR000832[GPCR, family 2, sec
ko04966	C	Amino acic	E	Amino acic	IPR004841 [Amino acid permease/ SLC12A domain] ; If
--	--	--	--	--	IPR002553 [Clathrin/coatomer adaptor, adaptin-like, N
--	Glutathion	O	Posttransla	--	--
--	Chromoso	D	Cell cycle c	IPR001073	[C1q domain] ; IPR008160[Collagen triple h
ko04144	E	Guanine-n	R	General fu	IPR000904 [Sec7 domain] ; IPR015403[Sec7, C-termina
ko04144	E	Guanine-n	R	General fu	IPR000904 [Sec7 domain] ; IPR015403[Sec7, C-termina
--	Serine/thre	T	Signal tran	IPR000719	[Protein kinase domain]
--	--	--	--	IPR003307	[W2 domain]
ko04145	P	--	--	--	IPR022780 [Dynein family light intermediate chain]
ko04340	H	Periplasmi	U	Intracellula	IPR000719 [Protein kinase domain] ; IPR022247[Casein
ko04978	N	Co/Zn/Cd	P	Inorganic i	IPR002524 [Cation efflux protein]
--	--	--	--	IPR011531	[Bicarbonate transporter, C-terminal] ; IPR0
ko04360	A	PKD repea	S	Function u	IPR003961 [Fibronectin type III] ; IPR013098[Immunogl
ko04520	A	--	--	--	IPR003124 [WH2 domain]
ko00230	P	Predicted	R	General fu	IPR002591 [Type I phosphodiesterase/nucleotide pyro

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

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

ol 3-kinase Ras-binding (PI3K RBD) domain] ; IPR000403[Phosphatidylinositol 3-/4-kinase, catalytic
] ; IPR001791[Laminin G domain] ; IPR002049[Laminin EGF domain] ; IPR002350[Kazal domain] ; IPR

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

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

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

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

PR001590[Peptidase M12B, ADAM/reprolysin] ; IPR002870[Peptidase M12B, propeptide] ; IPR010294

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

[SH3 domain] ; IPR001849[Pleckstrin homology domain] ; IPR020683[Ankyrin repeat-containing domain, catalytic domain] ; IPR006140[D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding

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

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

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

IPR01650[Helicase, C-terminal] ; IPR015194[ISWI, HAND domain] ; IPR015195[SLIDE domain] ; IPR02083[Helicase, C-terminal]

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

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

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

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
PR000483[Cysteine-rich flanking region, C-terminal] ; IPR000742[EGF-like domain] ; IPR001611[Leu
leckstrin homology domain] ; IPR014847[FERM adjacent (FA)] ; IPR018979[FERM, N-terminal] ; IPR0
PR025614[Cell morphogenesis protein N-terminal] ; IPR029473[Cell morphogenesis central region]
-terminal] ; IPR003164[Clathrin adaptor, alpha-adaptin, appendage, C-terminal subdomain] ; IPR00

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

i[Sec23/Sec24, trunk domain] ; IPR006900[Sec23/Sec24, helical domain] ; IPR007123[Gelsolin-like do
retin-like] ; IPR000922[D-galactoside/L-rhamnose binding SUEL lectin domain] ; IPR001879[GPCR, ·

06[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

reonine/tyrosine-protein kinase catalytic domain] ; IPR006211[Furin-like cysteine-rich domain] ; IPF
mic acid-rich (GLA) domain] ; IPR001254[Serine proteases, trypsin domain] ; IPR018992[Thrombin li

α -2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding] ; IPR011625[β -2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding] ; IPR011625[β -2-macroglobulin] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin, receptor-binding]

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

terminal globular domain] ; IPR012290[Fibrinogen, alpha/beta/gamma chain, coiled coil domain]
terminal globular domain] ; IPR012290[Fibrinogen, alpha/beta/gamma chain, coiled coil domain]

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

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

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

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

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

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

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

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

calcium-binding domain] ; IPR015149[Thrombomodulin-like, EGF-like] ; IPR026823[Complement C1r-like domain] ; IPR000742[EGF-like domain] ; IPR001791[Laminin G domain] ; IPR001881[EGF-like calcium-binding domain]

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

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

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

atalytic domain] ; IPR001627[Sema domain] ; IPR002165[Plexin repeat] ; IPR002909[IP3 domain]

IPR004102[Poly(ADP-ribose) polymerase, regulatory domain] ; IPR008893[WGR domain] ; IPR015211[Peptidase M1, leukotriene A4 hydrolase/aminopeptidase C-terminal] ; IPR002890[Alpha-2-macroglobulin, N-terminal] ; IPR009048[Alpha-macroglobulin]

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

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

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

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

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

domain] ; IPR000742[EGF-like domain] ; IPR001304[C-type lectin-like] ; IPR013106[Immunoglobulin domain] ; IPR004161[Translation elongation factor EFTu-like, domain 2] ; IPR005517[Translation elongation factor EFTu-like, domain 1]

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

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

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

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

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

'R002048[EF-hand domain] ; IPR022682[Peptidase C2, calpain, large subunit, domain III]

terminal] ; IPR005144[ATP-cone domain] ; IPR013509[Ribonucleotide reductase large subunit, N-terminal] ; IPR002049[Laminin EGF domain] ; IPR008211[Laminin, N-terminal] ; IPR009254[Laminin alpha, dc

elta subunit, guanine nucleotide exchange domain] ; IPR018940[Elongation factor 1 beta central acidic terminal globular domain] ; IPR003961[Fibronectin type III] ; IPR013111[EGF-like domain, extracellular

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

179[FERM, N-terminal] ; IPR018980[FERM, C-terminal PH-like domain] ; IPR019748[FERM central domain] ; IPR002857[Zinc finger, CXXC-type] ; IPR010506[DMAP1-binding domain] ; IPR022702[DNA (cytosine)

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

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

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

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

IGFBP] ; IPR000884[Thrombospondin type-1 (TSP1) repeat] ; IPR001007[VWFC domain] ; IPR006208
IPR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha motif
IPR001245[Serine-threonine/tyrosine-protein kinase catalytic domain] ; IPR001660[Sterile alpha motif]

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

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

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

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

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

obulin C2-set-like, ligand-binding] ; IPR015321[Type I cytokine receptor, cytokine-binding domain]

in factor, protein interaction] ; IPR013800[STAT transcription factor, all-alpha domain] ; IPR013801[
hydrolase] ; IPR001763[Rhodanese-like domain] ; IPR015063[USP8 dimerisation domain]

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

in factor, protein interaction] ; IPR013800[STAT transcription factor, all-alpha domain] ; IPR013801[
EAH box helicase domain] ; IPR012961[ATP-dependent RNA helicase Ski2, C-terminal] ; IPR025696[
(PI3K RBD) domain] ; IPR000403[Phosphatidylinositol 3-/4-kinase, catalytic domain] ; IPR001263[Pr
domain] ; IPR003151[PIK-related kinase, FAT] ; IPR003152[FATC domain] ; IPR009076[FKBP12-rapar

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

EAH box helicase domain] ; IPR032284[ATP-dependent DNA helicase RecQ, zinc-binding domain]

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

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

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

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

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

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

ol-specific phospholipase C, X domain] ; IPR001711[Phospholipase C, phosphatidylinositol-specific
750[GHMP kinase, C-terminal domain] ; IPR019539[Galactokinase galactose-binding domain]

] ; IPR009398[Adenylate cyclase, conserved domain] ; IPR032628[Adenylate cyclase, N-terminal]

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

] ; IPR005811[ATP-citrate lyase/succinyl-CoA ligase] ; IPR032263[ATP-citrate synthase, citrate-binding
associated region] ; IPR010714[Coatomer, alpha subunit, C-terminal] ; IPR024977[Anaphase-promo
IPR015348[Clathrin, heavy chain, linker, core motif] ; IPR022365[Clathrin, heavy chain, propeller repeat]

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

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]

IPR001245[ATPase, AAA-type, core] ; IPR004201[CDC48, domain 2] ; IPR015415[Vps4 oligomerisation, C-terminal]

IPR001245[Forkhead-associated (FHA) domain] ; IPR001478[PDZ domain] ; IPR002710[Dilute domain]

IPR001245[Dehydrogenase, catalytic domain] ; IPR006140[D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain]

IPR001245[GTPase domain] ; IPR004125[Signal recognition particle, SRP54 subunit, M-domain] ; IPR013822[Signal recognition particle, SRP54 subunit, M-domain]

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

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

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

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

calcium-binding domain] ; IPR002172[Low-density lipoprotein (LDL) receptor class A repeat]
IPR001791[Laminin G domain] ; IPR002049[Laminin EGF domain] ; IPR002172[Low-density lipoprotein
terminal] ; IPR006068[Cation-transporting P-type ATPase, C-terminal] ; IPR008250[P-type ATPase, A

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

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

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

phospholipase C, X domain] ; IPR001711[Phospholipase C, phosphatidylinositol-specific
sine-protein kinase catalytic domain] ; IPR013098[Immunoglobulin I-set] ; IPR020067[Frizzled domain]
ase domain] ; IPR001440[Tetratricopeptide repeat 1] ; IPR013105[Tetratricopeptide repeat 2]

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

] ; IPR006047[Glycosyl hydrolase, family 13, catalytic domain] ; IPR006048[Alpha-amylase/branching
IPR000562[Fibronectin, type II, collagen-binding] ; IPR000742[EGF-like domain] ; IPR001254[Serine p

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

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

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

IPR008145[Guanylate kinase/L-type calcium channel beta subunit] ; IPR011511[Variant SH3 domain]
:ratricopeptide repeat] ; IPR025986[RNA-polymerase II-associated protein 3-like, C-terminal domain]
calcium-binding domain] ; IPR002172[Low-density lipoprotein (LDL) receptor class A repeat] ; IPR02

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

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

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

: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]
oyl attachment] ; IPR005479[Carbamoyl-phosphate synthetase large subunit-like, ATP-binding domain]
hydrolase] ; IPR006615[Peptidase C19, ubiquitin-specific peptidase, DUSP domain] ; IPR028135[Ub

SH2 domain] ; IPR001849[Pleckstrin homology domain] ; IPR015042[BPS (Between PH and SH2) domain]

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

domain] ; IPR003151[PIK-related kinase, FAT] ; IPR003152[FATC domain] ; IPR012993[UME domain]

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

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

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

alponin homology domain] ; IPR001849[Pleckstrin homology domain] ; IPR011511[Variant SH3 domain]

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

.TPase, dynein-related, AAA domain] ; IPR013594[Dynein heavy chain, domain-1] ; IPR013602[Dynein heavy chain, domain-2]

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

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

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

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

n] ; IPR004161[Translation elongation factor EFTu-like, domain 2] ; IPR005517[Translation elongatic
H3 domain] ; IPR001715[Calponin homology domain] ; IPR001849[Pleckstrin homology domain] ; If

/alpha domain I] ; IPR005845[Alpha-D-phosphohexomutase, alpha/beta/alpha domain II] ; IPR0058

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

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

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

5800[Copper amine oxidase, N2-terminal] ; IPR015802[Copper amine oxidase, N3-terminal]
ide-disulphide oxidoreductase, dimerisation domain] ; IPR023753[FAD/NAD(P)-binding domain]

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

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

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

IPR025614[Cell morphogenesis protein N-terminal] ; IPR029473[Cell morphogenesis central region]

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

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

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

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

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

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

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

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

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

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

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

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

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

ogy domain] ; IPR001781[Zinc finger, LIM-type] ; IPR031865[Domain of unknown function DUF4757
Rho GTPase-activating protein domain] ; IPR001164[Arf GTPase activating protein] ; IPR001660[Ste

R008145[Guanylate kinase/L-type calcium channel beta subunit] ; IPR019583[PDZ-associated dom

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

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

'R001881[EGF-like calcium-binding domain] ; IPR006605[G2 nidogen/fibulin G2F] ; IPR013098[Imm

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

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

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

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

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

cytokinesis, C-terminal] ; IPR027007[DHR-1 domain] ; IPR032376[Dedicator of cytokinesis, N-terminal]

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

domain 6] ; IPR007641[RNA polymerase Rpb2, domain 7] ; IPR007642[RNA polymerase Rpb2, domain 8]

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

] [Ras-associating (RA) domain] ; IPR000857[MyTH4 domain] ; IPR001609[Myosin head, motor domain]

isporter type 1, transmembrane domain] ; IPR032410[Mitochondrial ABC-transporter, N-terminal five

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

; 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

er/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

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

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

'R001590[Peptidase M12B, ADAM/reprolysin] ; IPR002870[Peptidase M12B, propeptide] ; IPR010294

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

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

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

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

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

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

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

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

-terminal] ; IPR004161[Translation elongation factor EFTu-like, domain 2] ; IPR015033[HBS1-like pr
ding site-containing domain] ; IPR015224[Talin, central] ; IPR018979[FERM, N-terminal] ; IPR019748

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

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

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

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

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

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

IPR001849[Pleckstrin homology domain] ; IPR002017[Spectrin repeat] ; IPR013098[Immunoglobulin I-

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

ce, cysteine rich domain] ; IPR014853[Uncharacterised domain, cysteine-rich] ; IPR032361[von Wille]

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

phosphoinositide 3-kinase, accessory (PIK) domain] ; IPR002420[Phosphatidylinositol 3-kinase, C2 domain, rapamycin binding domain] ; IPR024585[Domain of unknown function DUF3385, target of rapamycin protein]

DNA mismatch repair protein MutS, core] ; IPR007860[DNA mismatch repair protein MutS, connector domain] ; IPR007861[DNA mismatch repair protein MutS, C-terminal domain]

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

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

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

; Y domain] ; IPR015359[Phosphoinositide-specific phospholipase C, EF-hand-like domain]

] ; 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]

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

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

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

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

26823[Complement C1r-like EGF domain] ; IPR032485[Domain of unknown function DUF5050]

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

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

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

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

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

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

site] ; IPR029451[Rapamycin-insensitive companion of mTOR, middle domain] ; IPR029452[Rapamycin-insensitive companion of mTOR, C-terminal domain]

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

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

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

se, domain of unknown function DUF913] ; IPR015940[Ubiquitin-associated domain] ; IPR025527[Domain of unknown function DUF1224]

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

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

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

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

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

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

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

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

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

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

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

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

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

domain 3] ; IPR007646[RNA polymerase Rpb2, domain 4] ; IPR007647[RNA polymerase Rpb2, domain 5]

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

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

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

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

