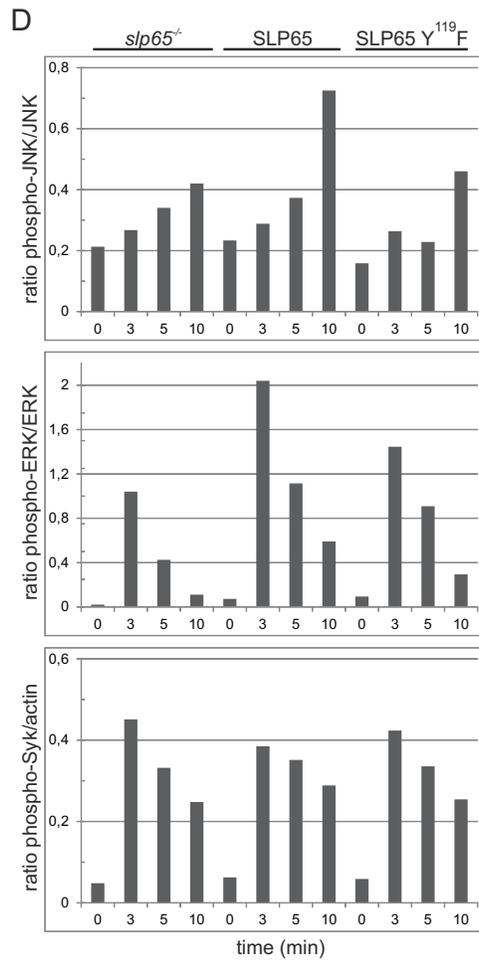
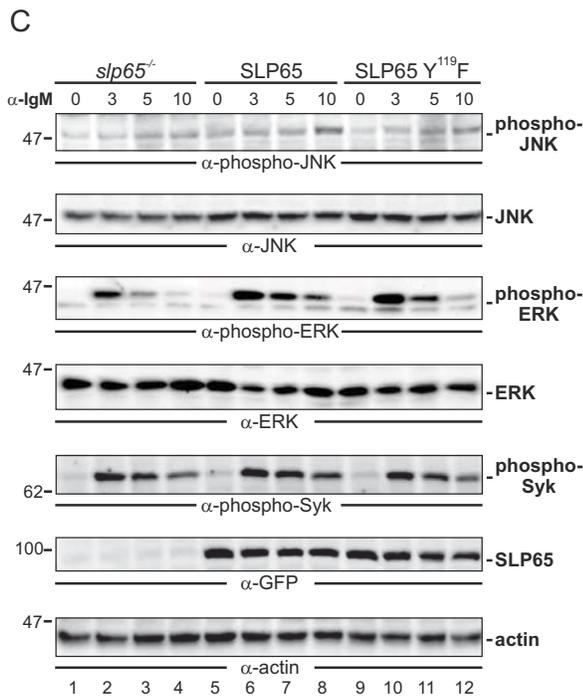
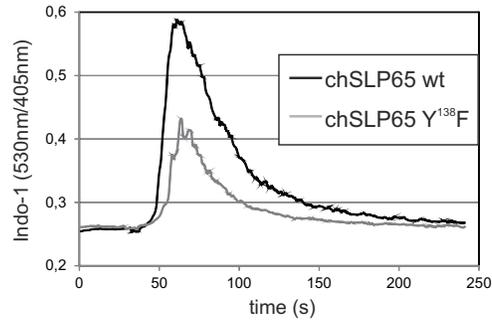
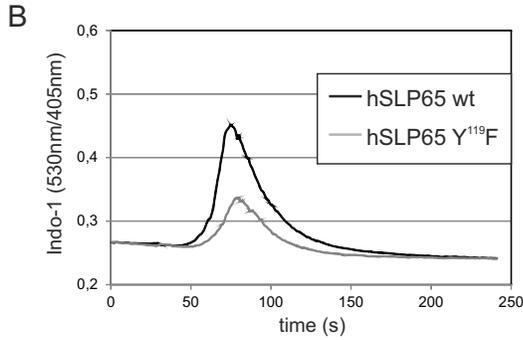


SUPPLEMENTAL FIGURE 1

A

<i>human SLP65</i>	113 PF--ARGE Y IDNRSSQR 127
<i>mouse SLP65</i>	113 PF--TRGE Y VDNRSSQR 127
<i>chicken SLP65</i>	132 PI--SRGE Y ADNRTSHH 146
<i>human SLP76</i>	165 PFPNSNSM Y IDRPPSGK 181



Legend to Supplemental Figure S1

The phosphorylation of EYΦDN in a Btk-independent manner controls BCR signaling to Ca²⁺ flux and MAPK activation. A) Amino acid sequence alignment of the EYΦDN phosphorylation motif of SLP adaptor proteins. B) BCR-induced flow cytometric Ca²⁺ profiles of SLP65-deficient DT40 B cells expressing citrine-tagged versions of either human wild-type SLP65 or human SLP65 Y¹¹⁹F (hSLP65 wt or hSLP65 Y¹¹⁹F, respectively; left panel), or of the corresponding avian orthologs (chSLP65 wt, chSLP65 Y¹³⁸F; right panel). C) To analyze the role of Y¹¹⁹ phosphorylation for protein kinase activation, DT40 transfectants expressing wild-type hSLP65 or hSLP65 Y¹¹⁹F were left untreated or stimulated via their BCR for the indicated time points (min), lysed and subjected to immunoblot analysis using antibodies that recognized either phospho-JNK or JNK (upper two panels), phospho-ERK or ERK (3rd-4th panels), or the activatory phospho-Y³⁵² site of Syk (5th panel). Blots were reprobed with antibodies against citrine/GFP (to detect the SLP65 fusion protein, 6th panel) or actin (to confirm equal loading, lower two panel). Antibodies against JNK, phospho-JNK (G9), phospho-ERK (D.13.14.4E) (all Cell Signaling), ERK (BD Bioscience), actin (Sigma), phospho-Tyr³⁵² of Syk (Santa Cruz), and GFP (Roche) were used for at 1:1000. D) Western Blot signals shown in C) were quantified using the Gel quantification plugin of the ImageJ software and ratios of signal intensities of phospho-Jnk to pan Jnk (upper panel), phospho-Erk to pan Erk (middle panel), and phospho-Syk to actin (lower panel) were plotted.

768;1300;4224;43 51;472	294;295	121;218	94;134	IP100018146;PI01 13;10;10	10;9;8	8;7;6	14-3-3 protein the YWHAQ	14-3-3 protein the P27348;B4DMT8; 1433T_HUMAN;B	ENST0000023808;OTTHUMP000000 NP_006817	PF00244	3/3;2014		
211;1579;1711;20 744;745;746		141;448;517		IP100030275;PI00 8;8	8;8	8;8	Heat shock protei TRAP1;HSP75	Heat shock protei Q12931;B4DR68; TRAP1_HUMAN;C	ENST0000024695;OTTHUMP000001 NP_057376	PF02518;PF00183	HATPase_c,HSP90		
2532;4741;4752;5	953		74	IP1000477313;PI01 6;6;6;6;4;4;4;3;3	6;6;6;6;4;4;4;3;3	6;6;6;6;4;4;4;3;3	Heterogeneous nu HNRNP;C,HNRNP;C	Importin subunit C of Het: P07910;1;P07910; HNRNP_HUMAN;E	ENST0000021629;OTTHUMP000000 NP_001070910;I	PF00706	RRM_1		
2368;6223				IP100002214	2	2	2 Importin subunit	Importin subunit: P52920;A8K709;IMA2_HUMAN	ENST00000330459;ENST000004087 NP_002577	PF00514;PF01749	IRM;IIB		
47;215;481;2980; 71;72;73	53;54	193;361;498	91;119	IP100002520;PI00 15;15;14;14;13;12	15;15;14;14;13;12	15;15;14;14;13;12	Serine hydroxyme SHMT2;KGC_4123	Serine hydroxyme P34897;B4DQ3;G103;M2_HUMAN;B	ENST00000328923;ENST0000039382 NP_005403;NP_0	PF00464	SHMT		
444;927;1242;301 1204;1205;1206;1207		698;869;1048;1110		IP1000299254	12	12	12 Eukaryotic transla EIF58;IF2;K1AA074	Eukaryotic transla Q60841;A0LIR8;B; IF2P_HUMAN;B	ENST0000028937;OTTHUMP000002 NP_056988	PF00009;PF03144	SHT_EFTU;GTP_EI		
3022;6137				IP100028520;PI00 2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	NADH dehydrogen NDUFU1;UQOR1	isoform 1 of NADH P49821;1;P49821; NDUFU1_HUMAN;A	ENST0000032277;OTTHUMP000002 NP_009034;NP_0	PF01512;PF10589	Complex1_S1K;NF		
1703;3881;14949;6 726;727		329;499		IP100029079;PI01 7;7;7	7;7;7	7;7;7	GMP synthase [gli] GMP5	GMP synthase [gli] P49915;A8K639;Q GUAA_HUMAN;B	ENST0000029592;OTTHUMP000002 NP_003866	PF06508;PF00117	ExsB;GATase;GMF		
533;723;1490;164 1449;1450;1451;1		882 51;95;105;479	244	IP1000440493;PI00 31;30;27	31;30;27	31;30;27	ATP synthase subu ATP5A1;ATP5A;AT	ATP synthase subu P25705;A8K092;B ATPA_HUMAN;A	ENST0000028205;OTTHUMP000001 NP_001001937;N	PF00006;PF03006	ATP_synt_ab;ATP-		
1292;3503;4865;5798;5910				IP100017303;PI01 5;5;4;4;3;2;1;1;1	5;5;4;4;3;2;1;1;1	5;5;4;4;3;2;1;1;1	DNA mismatch req MSH2	DNA mismatch req P43246;B4DL39;B MSH2_HUMAN;B	ENST0000023314;OTTHUMP000001 NP_000242	PF01624;PF05188	MutS_1;MutS_II;W		
4821;4883				IP1000299524;PI01 2;2;2;1	2;2;2;1	2;2;2;1	Condensin comple NCAPD2;CAPD2;C	Condensin comple Q15021;B3KMS0;I CND1_HUMAN;Q	ENST0000031557;OTTHUMP000002 NP_055680				
125;1609;1878;23 390;391	232;233	116;229	380;410	IP100013447;PI00 11;2	11;2	10;2	Cytochrome b-c1 UOQCRI	Cytochrome b-c1 P13930;B4DUL5;B QCR1_HUMAN;C	ENST0000020340;OTTHUMP000001 NP_003356	PF00675;PF05193	Peptidase_M16;P		
1446;2406;8336	241		3	IP100012442;PI00 3;2;2;1	3;2;2;1	2;1;1;1	Ras GTPase-activa G3BP1;G3BP	Ras GTPase-activa Q13283;B72K8;Q G3BP1_HUMAN;C	ENST00000335624;OTTHUMP000001 NP_005745;NP_9	PF02136;PF00076	NTF2;RRM_1		
4152;8476	1041	94		IP100219604;PI00 2;2;1;1;1	2;2;1;1;1	2;2;1;1;1	Dual specificity m MAP2K1;MEK1;PR	isoform 1 of Dual Q02750;1;Q02750 MP2K1_HUMAN;F	ENST0000030710;OTTHUMP000001 NP_002746;NP_3	PF00069	Kinase		
483;675;1365;142 1667;1668		548;569	556;657;665	IP1000925046;PI00 19;18;13;4;4;4;4;3	19;18;13;4;4;4;4;3	19;18;13;4;4;4;4;3	Glutaminyl-tRNA : QARS;hCG_9627	Glutaminyl-tRNA : P47897;A8K3A8;Q SYQ_HUMAN;B	ENST0000030612;OTTHUMP000002 NP_005042	PF00749;PF03950	tRNA-synt_1c;TRN		
14;611;1139;1602 613;614;615;616	370;371	573;817;820;920	344;387	IP100022744;PI00 16;15;12;12;8	16;15;12;12;8	16;15;12;12;8	Exportin-2;Import CSE1L;CAS;XPO2	isoform 1 of Expoi P55060;1;P55060; XPO2_HUMAN;B	ENST0000026298;OTTHUMP000000 NP_001307	PF03378;PF08506	CAS_CSE1;IB		
832;899;940;2562;7651		874;875;876;877;878;879;880;881	54;67;74;77;119;1	IP1000430812;PI00 5;5;4;4;4;4;4;4	5;5;4;4;4;4;4;4	5;5;4;4;4;4;4;4	Cellular nucleic ac CNBP;RNF163;ZNI	isoform 1 of Cellu P62633;1;P62633; CNBP_HUMAN;A	ENST0000030743;OTTHUMP000002 NP_003409;NP_0	PF00098	ZF_CCHC		
405;420;644;730; 805;806;807;808;809;810;811	156;206;212;369;515;723;889			IP100072534;PI00 18;18;7;5;1	18;18;7;5;1	18;18;7;5;1	Protein unc-45 ho UNC5A;SMAP1	isoform 1 of Prote Q9H3U1;1;Q9H3U1; UN45A_HUMAN	ENST0000026815;OTTHUMP000001 NP_061141;NP_0	PF00515;PF07719	tPR_2		
26;69;1300;1424; 50;51;52	36;37	33;160;221	97;98	IP100000816;PI00 13;12;4;4;3;2;1;1	13;12;4;4;3;2;1;1	10;10;4;3;0;0;2;0;1	14-3-3 protein exp YWHAE	isoform 1 of 14-3 P62258;1;P62258; 1433E_HUMAN	ENST0000026433;OTTHUMP000001 NP_006752	PF00244	3/3;2014		
2048;3974;4136;5	910		378	IP1001185374;PI00 5;4	5;4	5;4	26S proteasome n PSMHD12	26S proteasome n Q00232;A6N1P5 PSD12_HUMAN;A	ENST00000335612;OTTHUMP000001 NP_002807;NP_7	PF01399	PCI		
728;3161;6962;80 851;852		28;76		IP100419249;PI00 4;4	4;4	4;4	Proteasome subur PSM3A3;P3CB	isoform 1 of Prote P25788;1;P25788; P3A3_HUMAN	ENST0000021645;OTTHUMP000001 NP_002779;NP_6	PF00227;PF10584	Proteasome;Prote		
2387;2657;4410;6	630		184	IP100023860;PI01 5;5;5;5;5;5;5;5;5;5;5	5;5;5;5;5;5;5;5;5;5;5	4;4;4;4;4;4;4;4;4	Nucleosome asser NAP111;NRP;hCG	Nucleosome asser P55209;B3KNT8;B NP111_HUMAN;B	ENST00000261182;ENST0000039326 NP_004528;NP_6	PF00956	NEAT		
1567;2160;2364;2 1630;1631;1632;1	984;985;986;987	292;376;468;553	128;284;578;990	IP1000939304;PI00 17;17;16;15;6;5;4	17;17;16;15;6;5;4	17;17;16;15;6;5;4	Importin-5;import IPO5;KPNB3;RAN	isoform 3 of impo Q00410;3;Q000410 IPO5_HUMAN	ENST0000026157;OTTHUMP000000 NP_002262	PF02985	HAP		
2905;2906;3444;4	952		90	IP100216461;PI00 6;4;4	6;4;4	6;4;4	Acylphosphatase- ACYP2;ACYP	Acylphosphatase- P14621;Q4ZFV7;Q ACYP2_HUMAN;C	ENST0000030353;OTTHUMP000001 NP_612457	PF00708	Acylphosphatase		
56;1056;1136;148 235;236;237;238		143 151;376;551;636		IP100008982;PI00 24;24	24;24	24;24	Delta-1-pyrrolone- ALDH18A1;GSA5;F	isoform long of D P48886;1;P48886; P5CS_HUMAN;C	ENST0000037122;OTTHUMP000000 NP_061141;NP_0	PF00515;PF07719	AA_kinase		
172;1716;3883;8248				IP1000925052;PI00 4;4;4;3;3;3;2	4;4;4;3;3;3;2	4;4;4;3;3;3;2	Actin-related pro ARPc4;ARCO2	actin-related pro: C9JWM7;P59998; ARPc4_HUMAN;C	ENST0000028761;OTTHUMP000002 NP_001835709;N	PF05856	ARPC4		
375;2349				IP100000309;PI00 2;2;2;2;2	2;2;2;2;2	2;2;2;2;2	Serine/threonine- PPP2R5D	isoform Delta-1 of Q14738;1;Q14738 2A5D_HUMAN;B	ENST0000023040;OTTHUMP000000 NP_006236;NP_8	PF00656	BSP6		
135;1388;3955;42	783	470	340	IP1000941534;PI00 11;11;11;11;10;10	11;11;11;11;10;10	11;11;11;11;10;10	Septin-7;CDC10 pr SEPT7;CDC10	isoform 1 of Septi Q16181;1;Q16181 SEPT7_HUMAN;B	ENST0000035032;OTTHUMP000002 NP_001779;NP_0	PF00735	Septin		
1704;2806;2994;6945;7286;7716				IP100029267	6	5	U2 small nuclear r SNRPB2	U2 small nuclear r P08579;B5BTZ8;Q RU2B_HUMAN	ENST0000024607;OTTHUMP000000 NP_003083;NP_6	PF00076	RRM_1		
2072;2087;4987;5	712	440	34	IP100002804	5	5	Proteasome subur PSMB3	Proteasome subur P49720	PSB3_HUMAN	ENST0000022542;OTTHUMP000001 NP_002786	PF00027	Proteasome	
116;2397;2574;27	221	131	552	IP100008240;PI00 11;8;8;4;4;3;1;1;1	11;8;8;4;4;3;1;1;1	11;8;8;4;4;3;1;1;1	Methionyl-tRNA s MARS	Methionyl-tRNA s P56192;A8K492;A SYMC_HUMAN;A	ENST00000262027;ENST0000031547 NP_004981	PF00043;PF09334	GST_C;trNA-synt,		
412;790;2756;3921				IP100025366;PI00 4;4;4;2;2;2;2;1	4;4;4;2;2;2;2;1	4;4;4;2;2;2;2;1	Citrate synthase, r CS	isoform 1 of Citrate P075390;B3KTN4;B C1SY_HUMAN;B	ENST00000351328;ENST0000039399 NP_004068	PF00285	Citrate_synt		
1811;2608;2944;3917;3929;4696;62 711;712		236;434		IP100297982;PI00 10;9;6;2	10;9;6;2	10;9;6;2	Eukaryotic transla EIF2S3;EIF2G	Eukaryotic transla P41091;A8K278;B IF2G_HUMAN;F	ENST0000025303;OTTHUMP000000 NP_001406	PF00917;PF00009	eIF2_C;GTP_EFTU		
1857;6663				IP100299024;PI00 2;2	2;2	2;2	Brain acid soluble BASP1;NAP22	isoform 1 of Brain P08723;1;P08723; BASP_HUMAN	ENST0000032261;OTTHUMP000001 NP_006308	PF05466	BASP1		
6005;7548;8171	731	44		IP100029557;PI00 3;1	3;1	3;1	GrpE protein hom GRPEL1;GREP11	GrpE protein hom Q9HAV7	GRPE1_HUMAN	ENST0000026495;OTTHUMP000001 NP_079472	PF01025	GrpE	
714;8108	638	75		IP100024821	2	2	26S proteasome n PSMHD14;POH1	26S proteasome n Q00487;Q4ZG77;C PSDE_HUMAN	ENST0000040968;OTTHUMP000002 NP_005796	PF01398	MsV4		
820;1193;1194;31 27;33;34;78		45;48;191;356		IP100003269	12	1	Beta-actin-like prr ACTBL2	Beta-actin-like prr Q562R1	ACTBL_HUMAN	ENST0000030675;OTTHUMP000002 NP_0011017992	PF00022	Actin	
1059;5695;5785;8 800;801;802	317;842	13;17;29	24;56	IP100062037	6	4	4 Dynein light chain DYLL2;DL2C	Dynein light chain Q96F12	DYLL2_HUMAN	ENST00000240343	NP_524208	Dynein_light	
220;716;733;793; 188;189;190;191; 114;115;116;117; 302;313;377;398; 295;315;316;347;				IP100007750;PI00 16;16;3;3;3;3	4;4;1;1;1;1	2;2;1;1;1;1	Tubulin alpha-4A ;TUBA4A;TUBA1	Tubulin alpha-4A ; P68366;A8MU81;B TBA4A_HUMAN;A	ENST0000024843;OTTHUMP000001 NP_005991	PF00091;PF03953	Tubulin;Tubulin_C		
1974;3484;5379;7	1581		336	IP100746777;PI00 4;2;1	4;2;1	4;2;1	Alcohol dehydrog ADH5;ADHX;FDH	Alcohol dehydrog P11766;Q2VM17;C ADHX_HUMAN	ENST0000029641;OTTHUMP000002 NP_000662	PF08240;PF00107	ADH_N;ADH_zinc		
298;6050				IP100788907;PI00 2;2;2	2;2;2	2;2;2	Phosphoglycerate PGAM5	isoform 1 of Serin Q96HS1;1;Q96HS1; PGAM5_HUMAN	ENST0000031755;OTTHUMP000002 NP_002906;NP_8	PF10424	PAGM		
3087;4499;7941 1249;1250;1251;1252		61;72;112;352		IP100304417;PI00 3;3;2;1;1	3;3;2;1;1	3;3;2;1;1	Isoictrate dehydr IDH3B	Isoictrate dehydr Q43837;1;Q43837 IDH3B_HUMAN;B	ENST00000338084;OTTHUMP000000 NP_008830;NP_7	PF00180	Iso_dh		
1422;1952;4423;6	1369	273		IP1000396435;PI01 6;6	6;6	6;6	ATP-dependent R DDX1	Putative pre-mRN Q43143;B4E055;B DDX15_HUMAN	ENST0000033681;OTTHUMP000002 NP_001349	PF00717;PF04408	DUF1605;HA2;Hel		
1475;1715;2167;2197;7369;8407		686		IP1000293655;PI01 6;4	6;4	6;4	ATP-dependent R DDX1	Putative pre-mRN Q92499;A3RJH1;B DDX1_HUMAN;B	ENST0000023308;OTTHUMP000001 NP_004930	PF00270;PF00271	DEAD;Helicase_C;		
162;739;983;1069	1125	675	750	IP1000291646;PI01 18;6;5;4;4;3;3;2	18;6;5;4;4;3;3;2	18;6;5;4;4;3;3;2	Monofunctional C MTHFD1L;FTHF5D	Methylenetetrahy Q6U835;1;Q6U835 CITM_HUMAN	ENST0000036732;OTTHUMP000000 NP_056255	PF01268;PF00763	FTHF5;FTHF_DHG_1		
625;3040;4964;60	256 149;150;151	236 11;15;152		IP100010105;PI00 5;3;3;1;1	5;3;3;1;1	5;3;3;1;1	Eukaryotic transla EIF6;EIF3A;ITGB4E	Eukaryotic transla P56537;B7Z6G9;B IF6_HUMAN;B	ENST0000037443;OTTHUMP000000 NP_002203;NP_8	PF01912	eIF-6		
1391;2017;3260;3340;4239;4449;718	484			IP1000926925;PI00 8;8;8;8;7;3;2;2;1	8;8;8;8;7;3;2;2;1	8;8;8;8;7;3;2;2;1	OGDH protein;2-o OGDH	Uncharacterized p A2V2C3;A5XE11;E1 A2V2C3_HUMAN;	ENST0000022267;OTTHUMP000002 NP_002532;NP_0	PF00676;PF02779	R1_C;Transket_p		
7707;8607				IP100031521;PI00 2;2	2;2	2;2	Replication factor RFC3	Replication factor Q40938;B4DK6;Q RFC3_HUMAN;B	ENST00000318007;OTTHUMP000000 NP_002906;NP_8	PF10424	REC-C_C		
2043;2598				IP100014825;PI00 2;2	2;2	2;2	BTB/POZ domain- KCTD9	BTB/POZ domain- Q7L273;B4DPW0 KCTD9_HUMAN;B	ENST0000022120K;OTTHUMP000001 NP_060104	PF02214;PF00805	K_tetra;Pentapep		
220;716;734;793; 188;189;190;191; 114;115;117;118; 154;302;313;377; 129;295;315;316; 317				IP1000180675;PI01 20;20;16;15;14;13	20;20;16;15;14;13	11;1;1;1;1;1;0;1;1	Tubulin alpha-1A ;TUBA1A;TUBA3;T1	Tubulin alpha-1A ; Q171U36;B4BDQ04; TBA1A_HUMAN;B	ENST0000030107;OTTHUMP000000 NP_006000;NP_0	PF00091;PF03953	Tubulin;Tubulin_C		
421;3412				REV_IP100185146	2	2	2 Importin-9;Ran-bi IPO9;IMP9;KIAA11	Importin-9;Ran-bi IPO9;IMP9;KIAA11;H;PI;REV_IP100185	Q96P70	IPO9_HUMAN	ENST0000036156;OTTHUMP000000 NP_006055	PF03810	IBN_N
262;7030;7211;8433				IP100025202;PI00 4;4;2	4;4;2	4;4;2	Formin-like protei FMNL1;C17orf1;C	isoform 2 of Form Q95466;2;Q95466 FMNL1_HUMAN	ENST00000328118;ENST0000033149 NP_005883	PF06367;PF06371	Drf_FH3;Drf_GBD;		
264;470;1177;259	307 180;181;182</												

1170;2959;3609;4 130;131	83	61;119	226	IP000470573;PI00 6;6;5;1	6;6;5;5;1	6;6;5;5;1	cDNA FLJ51656, hi	ACTR2;ARP2	actin-related pro	B4DHK9;E9PF41;P	B4DHK9_HUMAN	ENST0000037798;OTTHUMP000002	NP_001005386;NP	PF00022	Actin
172;200;3801;463 815;816	25;31			IP000100160;PI00 6;5	6;5	6;5	Collin-associated I	CAND1;KIAA0829;	isoform 1 of	Cullir Q86VP6;1;Q86VP1	CAND1_HUMAN	ENST0000029921;OTTHUMP000002	NP_060918	PF02985;PF08623	HEAT;TIP120
3629;9053				IP000104149;PI00 2;1	2;1	2;1	Tetra-acyl peptide	TTC35;KIAA0103;T	tetra-acyl peptide	Q15006;A8K4R;T	TTC35_HUMAN	ENST0000022085;OTTHUMP000002	NP_055488	PF07129	TPR_2
2218;3093;4279;5351;5911;6528;697;943;944		130;138		IP000796462;PI00 9;9;9;6;4;3	9;9;9;6;4;3	9;9;9;6;4;3	Puative uncharac	RAN;ARA24;OKJ51	27 kDa protein;Un	BSMDF5;P62826;B	BSMDF5_HUMAN	ENST0000039236;OTTHUMP000001	NP_006316	PF00701	Ras
1;113;972;1285;2 609;610;611		432;436;635		IP00022462;PI00 21;19;5;2	21;19;5;2	21;19;5;2	Transferin recep	TFRC	Transferin recep	PO2786;B8KQ08;B	TFR1_HUMAN;B7	ENST0000036011;OTTHUMP000002	NP_00111620;NP	PF02225;PF04253	PAI_TFR_dimer
1172;1757;2037;2 989;990	586	43;143		IP000218493;PI00 12;10	12;10	12;10	Hypoxanthine-gua	HPRT1;HPRT	Hypoxanthine-gua	Q00492;Q6LE73	HPRT_HUMAN	ENST0000029855;OTTHUMP000000	NP_000182	PF00156	PhyT_anticond
164;551;604;1734 1590;1591;1592;1 968;969;970		55;202;239;281;54 461;466;471		IP000783097;PI00 24;1;1	24;1;1	24;1;1	Glycyl-tRNA synth	GARS	Glycyl-tRNA synth	P41250;Q75MN1	SYG_HUMAN	ENST0000038926;OTTHUMP000002	NP_002038	PF03129;PF00587	HGTP;anticond
45;5085;8567				IP000022240;PI00 3;3;2;2;2	3;3;2;2;2	3;3;2;2;2	Iron-sulfur cluster	ISCU;NIFUN	Iron-sulfur cluster	Q9H1K1-1;Q9H1K	ISCU_HUMAN;B3	ENST0000031189;OTTHUMP000002	NP_987670;NP_01	PF01592	NIFU_N
75;1308;2431;429 60;61;62		555;564;647		IP00001639;PI00 13;9;8	13;9;8	13;9;8	Importin subunit I	KPNB1;NTF97	Importin subunit I	Q14974;B2RR89;E	IMB1_HUMAN;B7	ENST0000029015;OTTHUMP000000	NP_002256	PF00514;PF02985	Arm;HEAT;IBN_N
367;1994;2665;34 325;326	189	29;33		IP000012007;PI00 9;8	9;8	9;8	Adenosylhomocys	AHCY;SAHH	Adenosylhomocys	P23526;B3KUN3;F	SAHH_HUMAN;Q	ENST0000021742;OTTHUMP000000	NP_000678;NP_01	PF05221;PF00670	AdoHC;AdoHC
694;6215;8314		1665		IP000914566;PI00 3;3;2;2	3;3;2;2	3;3;2;2	Farnesyl pyrophos	FPP5;KIAA129	Farnesyl pyrophos	P14324;E9PC19;Q	FPP5_HUMAN;Q1	ENST0000035665;OTTHUMP000000	NP_00112929;NP	PF003048	polyprenyl_synt
4158;4311;6103;8494		99		IP000220299;PI00 4;4;4;2;2	4;4;4;2;2	4;4;4;2;2	FAD synthetase;F	FLAD1;PP591;RP1	isoform 1 of FAD	Q8NF51-1;Q8NF1	FAD1_HUMAN;Q5	ENST0000029218;OTTHUMP000000	NP_079483;NP_91	PF00994;PF01507	MoCF_biosynth;P
1029;1601;2672;3 1470;1371;1372;1 824;825;826		102;155;276;335;1 111;234;411		IP000396485;PI00 20;19;17;16;11;10	20;19;17;16;11;10	20;19;17;16;11;10	Elongation factor	EEF1A1;EEF1A;EF1	Elongation factor	P68104;A8K9C4;B	EF1A1_HUMAN;E	ENST0000030926;OTTHUMP000000	NP_001393;NP_01	PF00009;PF03144	GTP_EFTU;GTP_EI
769;1300;1657;33 51;472		564 123;220		IP000216318;PI00 13;13;4;4	8;8;1;1	7;7;1;1	14-3-3 protein bet	YWHAH	isoform Long of 1-	P31946-1;P31946; 1433B	HUMAN	ENST0000035370;OTTHUMP000000	NP_003395;NP_61	PF00244	3/3;2014
1061;1300;2675;3	51	351	226	IP000982101;PI00 11;11;8;6;5;5;5;4; 7;7;6;4;3;3;3;2;2;1	7;7;6;4;3;3;3;2;2;1	7;7;6;4;3;3;3;2;2;1	14-3-3 protein zet	YWHAZ	Uncharacterized p	E7EX29;P63104;D	1433Z_HUMAN;B1	ENST0000035324;OTTHUMP000002	NP_00112917;NP	PF02745	3/3;2014
704;1826;2186;2258;6417;9019				IP00024364;PI00 6;6;5;2;2;2;2;1;1 6;6;5;2;2;2;2;1;1	6;6;5;2;2;2;2;1;1	6;6;5;2;2;2;2;1;1	Transportin-1;imp	TNPO1;KPNB2;MI	isoform 1 of Trans	Q92973-1;Q92973	TNPO1_HUMAN	ENST0000033727;OTTHUMP000001	NP_002261;NP_61	PF02985;PF03810	HEAT;IBN_N
699;1020;1021;14 786;787;788;789;791		471 25;40;57;73;74;83		IP000033494;PI00 12;10;6;4;3;3;1;1;1 0;0;0;0;0;0;0;0;0;0	0;0;0;0;0;0;0;0;0;0	0;0;0;0;0;0;0;0;0;0	Miosin regulatory	MYL12B;MYL2C;M	Yosin regulatory	Q14950;P24844;M	ML12B_HUMAN;N	ENST0000023750;OTTHUMP000001	NP_001138416;NP	PF000036	efhand
2011;5739;6648;7 1539		937	345	IP000604664;PI00 6;6;6;6;6;6	6;6;6;6;6;6	6;6;6;6;6;6	NADH-ubiquinone	NDFU51;hcG_172	NADH-ubiquinone	BDADJA0;P28331;E	BDADJA0_HUMAN;N	ENST0000023319;OTTHUMP000001	NP_001186913;NP	PF09326;PF00111	DUF1982;Fer2;Mo
802;1300;4039;59		51	223	IP000220642;PI01 8;7;7	4;4;3	4;4;3	14-3-3 protein gar	YWHAQ	14-3-3 protein gar	P61981;B3KNB84	1433G_HUMAN;B	ENST0000030763;OTTHUMP000001	NP_036611	PF00244	3/3;2014
3185;5760;6883;5 513;514		89;200		IP000550119;PI00 6;6;6;6;6;5;4	6;6;6;6;6;5;4	2;2;2;2;2;2;1	cDNA FLJ58821, hi	SEPT6;KIAA0128;S	cDNA FLJ58821, hi	BD42W0;E7ETH8;B	BD42W0_HUMAN;B	ENST0000036015;OTTHUMP000000	NP_059446;NP_61	PF00735	Septin
232;233;259;507;1 1413;1414		838;839;840;841 218;268		IP000639957;PI00 17;17;10	17;17;10	17;17;10	Histone-arginine	CARM1;PRMT4	isoform 3 of Histo	Q8X65;3;Q8X65	CARM1_HUMAN	ENST00000327064;ENST0000034415	NP_954592	PF06325	PpmA
1962;2323;2360;6965;8535;8794				IP000292499;PI00 6;3;1;1	6;3;1;1	6;3;1;1	Heat shock 70 kDa	HSPA1A;HSPA60;HS	Heat shock 70 kDa	Q0VDF9;B4DY15	HSP7E_HUMAN	ENST0000037837;OTTHUMP000000	NP_057383	PF00012	HSP70
4351;4478;6793;8		1659	72	IP000871174	5	5	C-Myc-binding prc	MYCBP;AMY1	C-Myc-binding prc	Q99417;BQ6168	MYCBP_HUMAN	ENST0000037299;OTTHUMP000000	NP_036465		
576;4285				IP000844000;PI00 2;2	2;2	2;2	UPF0555 protein I	KIAA0776	isoform 1 of E3	UQ94874-1;Q94874	K0776_HUMAN	ENST0000036927;OTTHUMP000000	NP_056138	PF09743	DUF2042
118;817;1275;152 1091;1092;1093 645;646		40;84;461 157;493		IP000220834;PI00 19;3;1	19;3;1	19;3;1	ATP-dependent D	XRC5;G22P2	X-ray repair cross-	P13010;Q15209;F	KU8E_HUMAN	ENST0000032806;OTTHUMP000001	NP_066964	PF00275;PF03730	Ku;Ku_C;Ku_N;Ku
200;719;1868;263 254;255		118;647		IP00009960;PI01 12;12;12;12;12	12;12;12;12;12	12;12;12;12;12	Mitochondrial inn	IMMT;HMP;PIG4	isoform 1 of Mitoc	Q16891-1;Q16891	IMMT_HUMAN;B	ENST0000025463;OTTHUMP000002	NP_050830;NP_01	PF09731	Mitofilin
4171;5385;6629;6 570;571		66;94		IP00020495;PI00 4;2	4;2	4;2	28S ribosomal pr	MRP536;DC47	28S ribosomal pr	PR2809;D6R941	RT36_HUMAN	ENST0000025644;OTTHUMP000002	NP_106597		
745;2315;2316;59		798	170	IP00061245	4	4	28S ribosomal pr	MRP510;MSTP04C	28S ribosomal pr	P82664;B4DP77;Q	RT10_HUMAN	ENST0000005346;OTTHUMP000000	NP_060611	PF00338	Ribosomal_S10
5009;6058;6066;8 247;248		495;672		IP00009790;PI00 4;4;2;2;1;1	4;4;2;2;1;1	4;4;2;2;1;1	6-phosphofructoc	PFKFB;PFKFB;R	11-2 6-phosphofructoc	Q01813;B3K515;Q	K6PP_HUMAN;B3	ENST0000038112;OTTHUMP000000	NP_002618	PF00365	PFK
936;3186;3612;46 936;937;938		22;110;134		IP000215914;PI00 7;7;5;5;4;3;3;2	7;7;5;5;4;3;3;2	5;5;3;3;4;2;1;1;1;0	ADP-ribosylation	ARF1;ARF3	ADP-ribosylation	F184077;P61204;F	ARF1_HUMAN;AR	ENST0000027210;OTTHUMP000000	NP_00103937;NP	PF00205	Arf
666;657;1052;182 168;169;170		39;75;93		IP000006579	7	7	Cytochrome c oxi	COX4I1;COX4	Cytochrome c oxi	P13073;Q86WV2	COX4I1_HUMAN	ENST0000025345;OTTHUMP000001	NP_001852	PF02936	COX4
1407;2142;3907;3920				IP000300371;PI00 4;3	4;3	4;3	Splicing factor 3B	SF3B3;KIAA0017	isoform 1 of Spli	Q15393-1;Q15393	SF3B3_HUMAN	ENST0000030251;OTTHUMP000001	NP_036558	PF03178	CPF5_A
5079;5198				IP000867714;PI00 2;2;1;1	2;2;1;1	2;2;1;1	Protein LSM12 h	LSM12	isoform 2 of Prote	Q3MH02-2;Q3MH1	LSM12_HUMAN;B	ENST00000293406	NP_689557	PF09793	AAA
4182;7895		485	373	IP00018398;PI00 2;2;1	2;2;1	2;2;1	26S protease regu	PSMC3;TBP1	26S protease regu	P17980;A8K781;E	PRSG6_HUMAN	ENST0000029885;OTTHUMP000002	NP_002795	PF00004	AD
566;613;2786;8466				IP000217104	4	4	Melanoma-associ	NDNL2;HCA4;MAC	Melanoma-associ	Q06G67	MAGG1_HUMAN	ENST0000033230;OTTHUMP000001	NP_619649	PF01454	MAGE
197;1462;5264;5362				IP000397904;PI00 4;4	4;4	4;4	Nuclear pore com	NUP93;KIAA0095	Nuclear pore com	Q8N1F7;A8K897;E	NUP93_HUMAN;E	ENST0000030815;OTTHUMP000001	NP_055484	PF04097	Nic96
2286;4998;5428;25 368;369		222 49;81	129	IP00013468;PI00 9;9;9;6;5	9;9;9;6;5	9;9;9;6;5	Mitotic checkpoi	BUB3	isoform 1 of Mitot	Q143684-1;Q43684	BUB3_HUMAN;B4	ENST0000034038;OTTHUMP000000	NP_005540;NP_01	PF04009	W40
160;251;623;815;1 1070;1071;1072;1 639;640;641;642;1 138;143;223;313;1 223;226;400;432;1				IP01018161;PI01 41;41;41;27;26;24 2;2;2;0;0;0;0;0;0	2;2;2;0;0;0;0;0;0	2;2;2;0;0;0;0;0;0	Pyruvate kinase	PKM2;PK2;PK3;PK	pyruvate kinase	I14618-2;P14618;K	KPYM_HUMAN;Q	ENST00000319622;ENST0000033518	NP_001193725;NP	PF00287	PK;PK_C
1319;1353;1460;1 1400;1401;1402;1403;1404;1405		83;237;238;486;681;751		IP000411559;PI00 31;30;27;9;4;3;3;3 31;30;27;9;4;3;3;3	31;30;27;9;4;3;3;3	31;30;27;9;4;3;3;3	Structural mainte	SMMC4;CAPCS;SMC4	isoform 1 of Struc	Q9NTJ3-1;Q109TJ3	SMMC4_HUMAN;B3	ENST0000034472;OTTHUMP000002	NP_001002800;NP	PF06470;PF02463	SMC_hinge;SMC_I
5166;8269;8593				IP000383581;PI00 3;3;2;2;2	3;3;2;2;2	3;3;2;2;2	Neutral alpha-lig	GANAB;G2AN;KIA	cDNA FLJ61290, hi	Q14697-1;Q14697	GANAB_HUMAN;J	ENST0000034617;OTTHUMP000002	NP_938148;NP_91	PF01055;PF04901	Glyc_hydro_31;F
362;7067				IP000410554;PI00 2;1	2;1	2;1	Actin-related prot	ARPC5L	Actin-related prot	Q9BPK5;B3KPC7	ARPC5L_HUMAN	ENST0000025947;OTTHUMP000000	NP_112240	PF04699	P16C
3551;3569;5205		82	520	IP000005158;PI00 3;3;3	3;3;3	3;3;3	Lon protease hom	LONP1;PRSS15	Lon protease hom	P36776;E5KMH8;F	LONM1_HUMAN;B	ENST00000360614;ENST0000035840	NP_004784	PF00004;PF02190	AAA;LON;Lon_C
647;1606;6022;7765				IP000005160;PI00 4;4;2;2;2;2;2;1	4;4;2;2;2;2;2;1	4;4;2;2;2;2;2;1	Actin-related prot	ARPC1B;ARCA1	Actin-related prot	Q15143;A4D275;E	ARPC1B_HUMAN	ENST0000025272;OTTHUMP000002	NP_005711;XP_94	PF00400	W40
465;756;1438;222 193;194;195;196;1 119;120;121		73;147;164;233;21 127;129;239		IP00007752;PI00 19;15;14;13;9;8;7; 3;2;3;2;0;0;0;1;0;1	3;2;3;2;0;0;0;1;0;1	3;2;3;2;0;0;0;1;0;1	Tubulin beta-2C	cl TUBB2C;TUBB4;T	Tubulin beta-2C	cl P68371;Q8IWP6;E	TBB2C_HUMAN;T	ENST0000034038;OTTHUMP000001	NP_006709;NP_01	PF00093;PF03953	Tubulin;Tubulin_C
6129;7112				IP000017376;PI00 2;2;2	2;2;2	2;2;2	Protein transport	SEC23B;RP11-379	Protein transport	Q15437;B4DJW8;C	SEC23B_HUMAN;B	ENST0000026254;OTTHUMP000000	NP_001162616;NP	PF00626;PF08033	Gelsolin;Sec23_B5
449;565;589;1030 708;709;710		46;67;143		IP000027626;PI01 19;17;17;11;5;4;3; 19;17;17;11;5;4;3; 19;17;17;11;5;4;3;	19;17;17;11;5;4;3; 19;17;17;11;5;4;3;	19;17;17;11;5;4;3; 19;17;17;11;5;4;3;	T-complex protein	CCT6A;CCT6;CCT2	T-complex protein	P40227;B2R9K8;Q	TCP2_HUMAN;A1	ENST0000027560;OTTHUMP000001	NP_0011753;NP_01	PF00118	Ntln0_TCP1
247;423;612;799;1 912;913;914;915;1 537;538;539;540;1 22;156;157;231;3 41;131;136;290;3				IP000186290;PI01 45;28;28;8	45;28;28;8	45;28;28;8	Elongation factor	EEF2;EF2	Elongation factor	P13639;Q6PK56;C	EF2_HUMAN;B4D	ENST00000309311	NP_001952	PF00679;PF03764	EF2_C;EF14;

193;2099;2139;35	1212	734	121	195	IP000470502;IP009;9;9;8;6;4;4;2	8;8;8;8;6;3;4;1	8;8;8;8;6;3;4;1	Inorganic pyrophosphatase PPA2;HSPC124	Isoform 2 of Inorg	Q9H2U2-2;Q9H2L	IPYR2_HUMAN	ENST0000031026;OTTHUMP000001	NP_789845;NP_01	PF00719	Pyrophosphatase Cpn60_TCP1		
38;930;1461;1484	1175;1176;1177;1	707;708;709;710	62;87;160;244;411	289;371;395;412	IP000297779;IP000	31;30;26;26;23	31;30;26;26;23	T-complex protein CCT2;9908L1;CCT2	T-complex protein	P78371;A8K402L	TCPB_HUMAN;B7	ENST00000299300	NP_006422;NP_01	PF00118	Cpn60_TCP1		
151;695;800;1188	602;603;604	362;363;364	119;199;229	81;135;162	IP000021700	10	10	Proliferating cell n PCNA	Proliferating cell n	P12004;B4DU42	PCNA_HUMAN	ENST0000037914;OTTHUMP000000	NP_002583;NP_01	PF02747;PF00705	PCNA_CPCNA_N		
188;166;1624;127	29	986;987	1;152		IP000218374;IP000	11;10;9;9;8;7;3;1	11;10;9;9;8;7;3;1	Voltage-gated pot KCNA2B;KCNA2B	Isom of Volta	Q13303;KCA82	KCA82_HUMAN	ENST0000016624;OTTHUMP000000	NP_010228;NP_01	PF00248	Alpha_ket_red		
569;1282;1970;26	1368		823	496	515	IP000719752;IP000	10;10;10;10;3	10;10;10;3	Eukaryotic transla EIF3B;EIF3S9	Isom of Euka	P55884;P55884	EIF3B_HUMAN;B4	ENST0000031480;OTTHUMP000000	NP_00102386;NP_01	PF08662;PF00076	eIF2A;RRM_1	
175;1660;1939;55	1253;1254;1255;1		748	132;384;387;389;1	145	IP000304596;IP000	7;6;5;3;2;1;1;1	6;5;4;3;3;1;1;1;1	Non-POU domain	Q15233;AK8525	B_NONO_HUMAN	ENST0000027607;OTTHUMP000000	NP_00113880;NP_01	PF08675;PF00076	NOFS;RRM_1		
1508;1509;3895;4	1338;1339	797;798	109;171	103;159	IP000376005;IP000	13;13;10;6;6;6;6	13;13;10;6;6;6;6	Eukaryotic transla EIF5A;EIF5AL1	Isoform 2 of Euka	P63241;P63241	IF5A1_HUMAN;JF1	ENST0000033645;OTTHUMP000001	NP_00113732;NP_01	PF01287	eIF-5A		
6835;6981;7078	886		155		IP000178440;IP000	3;1;1;1	3;1;1;1	Elongation factor	EEF1B2;EEF1B;EF1	P24534;A4D1M6	EF1B_HUMAN	ENST0000023695;OTTHUMP000001	NP_00103275;NP_01	PF10587;PF00736	EF-1_beta_acid;EF		
662;1055;2584;32	774		464	15	142	IP00001836;IP000	8;2	8;2	Developmentally-	Q9Y295;Q9UFAS	DRG1_HUMAN	ENST0000033145;OTTHUMP000000	NP_004138	PF01926;PF02824	MMR_HSR1;TGS		
325;326;424;1105	636		211		IP000024175;IP000	13;9;8;5;5;5;5;3	13;9;8;5;5;5;5;3	Proteasome subu	PSMA7;RPS-100Sf	Isoform 1 of Prote	O14818;1;O14818	PSA7_HUMAN;Q5	ENST0000037087;OTTHUMP000000	NP_002783	PF00227;PF10584	Proteasome;Prote	
6;661;916;2019;2	98;1548;1664	1008;1009	87;463;494	17;251	IP000911039;IP000	15;14;14;12;12;12	11;10;10;8;8;8;8;8	cDNA FLJ54303, hi	HSPA1A;HSPA1L;h	cDNA FLJ54408, hi	B4DFN9;B4E386;F	B4DFN9_HUMAN	ENST0000037565;OTTHUMP000000	NP_005336;NP_01	PF00012	HSP70	
369;2528;2839;2867	5;883;6027;7374				IP000299571;IP01	7;7;7;7;7	7;7;7;7;7	Protein disulfide-	PDIAG6;TXNDC7	Isoform 2 of Prote	Q15084-2;Q15084	PDIAG6_HUMAN;B	ENST0000027222;OTTHUMP000002	NP_005733	PF00085	Thioredoxin	
5721;7735;7905					IP000021370;IP000	3;2;2;2	3;2;2;2	Ubiquitin-conjuga	UBE2K;HIP2;LIG	Isoform 1 of Ubiq	P10618;P10618	UBE2K_HUMAN;B	ENST0000026142;OTTHUMP000002	NP_005330;NP_01	PF00627;PF00179	UBA1;Ubi_con	
492;563;1932;329	175		104		IP000007074	13	13	Tyrosyl-tRNA synt	YARS	Tyrosyl-tRNA synt	P54577	SYYC_HUMAN	ENST0000037347;OTTHUMP000000	NP_003671	PF00579;PF01588	tRNA-synt_1b;tRN	
2678;2731					IP000007052	2	2	Mitochondrial fiss	FIS1;TTC11;CGI-13	Mitochondrial fiss	Q9Y3D6	FIS1_HUMAN	ENST0000022313;OTTHUMP000002	NP_0051752			
3805;440;493;653;1	216;217;218;219;1		130	146;156;164;988;1	132	IP000007927;IP000	42;40;8	42;40;8	Structural mainter	SMC2;CAPE_SMC2	Isoform 1 of Struc	Q9Y347-1;Q9Y347	SMC2_HUMAN	ENST0000028639;OTTHUMP000000	NP_001036015;NP	PF06470;PF02463	SMC_hinge;SMC_1
990;1379;2691;3614	3;650;5259;5728;7856				IP000641829;IP000	8;8;7;6;5;5;4;4;4	8;8;7;6;5;5;4;4;4	Spliceosome RNA	BAT1;UAP56;hCG	Isoform 2 of Splic	Q13838-2;Q13838	UAP56_HUMAN;B	ENST0000037617;OTTHUMP000000	NP_004633;NP_01	PF00270;PF00271	DEAD;Helicase_C	
3379;3763;3764;4	1042;1043;1044	615;616;617;618	205;222;294	91;165;226;230	IP000219616;IP000	10;8;5;3;3;3	10;8;5;3;3;3	Ribose-phosphate	PPR51;RPI1-540N	Ribose-phosphate	PPR51;RPI1-540N	PPR51_HUMAN;B	ENST0000037243;OTTHUMP000000	NP_002755;NP_01	PF00156	Phosphorylat	
1466;3235;5495;5	1337		1		IP000375527;IP000	4;4;4;3;3;3;3;1	3;3;3;3;2;2;2;1	IMP (Inosine mon	IMPDH1;hCG_181	inosine-5'-monop	A4D026;Q5H9Q6	A4D026_HUMAN	ENST0000033879;OTTHUMP000002	NP_000874;NP_01	PF00571;PF00478	CBS;IMPDH	
345;812;1492;157	889;890	516;517;518;519;1	1;132	112;126;144;145;1	IP000179330;IP000	19;17;17;17;17;17	19;17;17;17;17;17	40S ribosomal pro	RPS27A;UBA80;Ubl	Ubiquitin-40S	hCG_181;B2RDW11	R527A_HUMAN	ENST0000027231;OTTHUMP000002	NP_001129064;NP	PF01599;PF00240	Ribosomal_S27;ut	
1590;8669					IP00099871;IP000	2;2	2;2	39S ribosomal pro	MRP40;NLVCF;UI	39S ribosomal pro	Q9NQ50	MRM40_HUMAN	ENST0000033313;OTTHUMP000001	NP_003767	PF09812	MRP-L28	
2559;3302			588		83	IP000218699;IP000	2;2	2;2	Adenine phospho	APRT	Adenine phospho	P07741	APT_HUMAN	ENST00000378364	NP_000476;NP_01	PF00156	Phosphorylat
16;2661;4168;4366	4367;4368;4462;5333;8790				IP000910712	9	1	cDNA FLJ57036, highly similar to	Hrc	cDNA FLJ57036, hi	B4E3P1	B4E3P1_HUMAN	ENST00000378364	NP_000476;NP_01	PF00156	Tropomyosin	
1777;2115;3639;3	1330		172		IP000337772;IP000	6;6;6;6;6;5;3;1	6;6;6;6;6;5;3;1	Hyaluronan media	HMMR;IHABP;RH	Isoform 3 of Hyal.	O75330-3;O75330	HMMR_HUMAN;E	ENST00000353861;OTTHUMP000001	NP_001136028;NP	036616;NP_036617;NP	001136029	
648;1741;3779;47	233		142	509	415	IP000883896;IP000	10;10;10;10;10;10	10;10;10;10;10;10	LM domain and a	LMA1;EPLIN;SRE	Isoform 4 of LIM	Q09UH6-6;Q9UHI	LMA1_HUMAN;B	ENST00000341247;ENST00000349494	NP_001107180;NP	0100412	LIM
700;5055;7304;82	565		341	108	47	IP000199977;IP000	1;1;1;1;1;1;1;1;1	4;4;1;1;1;1;1;1;1	Lin-7 homolog C	UN7;CMALS3;VEL	Isoform 7 hom	Q9NUP9;Q53F5X	LIN7C_HUMAN	ENST0000027819;OTTHUMP000002	NP_060832	PF02828;PF00595	L2;PDZ
97;1323;1879;204	836		493	601	440	IP000140420;IP01	13;13;13;12	13;13;13;12	Staphylococcal nu	SND1;TORR11	Staphylococcal nu	Q7KZFA;B3KU67C	SND1_HUMAN;B2	ENST0000035472;OTTHUMP000002	NP_005205	PF00565;PF00567	SNase;TUDOR
1678;4161					IP00030919;IP000	2;2	2;2	Mitogen-activate	MAPKSP1;MAP2K3	Regulator comple	Q9UHA4;Q53FH6	MPKS1_HUMAN	ENST0000022652;OTTHUMP000001	NP_068805	PF08923	MAPKK1_int	
410;411;1264;281	694;695		427	93;130	89	IP000027255;IP000	11;10;9	8;7;6	Myosin light chain	MYL6B;MLC15A	Myosin light chain	P14649;B4E368	MYL6B_HUMAN;E	ENST00000207437	NP_001186588;NP	002466	
610;702;865;914;1	94;95;96;97;98;99	64;65;66	61;87;93;122;127;17	15;74;603	IP00003865;IP000	43;42;33;31;24;23	43;42;33;31;24;23	Heat shock cognat	HSPAB;HSC70;HSP	Isoform 1 of Heat	P11142-1;P11142	HSP7C_HUMAN;A	ENST0000022737;OTTHUMP000002	NP_005888;NP_01	PF00412	HSP70	
4401;4992;6740;7	1603		117		IP000783872;IP000	4;4;4;3;3;3	4;4;4;3;3;3	Caprin-1;Cytoplas	CAPRN1;GPIAP1;I	Isoform 1 of Capri	Q14444-1;Q14444	CAPR1_HUMAN;B	ENST0000034139;OTTHUMP000002	NP_005889;NP	0976240		
16;156;159;187;4	297;298;299		176	99;105;110	154	IP00010779;IP000	13;12;14;14;14;14	13;10;0;0;0;0;0;1	Tropomyosin alph	TPMA	Isoform 1 of Tro	P67936-1;P67936	TPMA_HUMAN	ENST00000309933;OTTHUMP000000	NP_003281;NP_01	PF00261	Tropomyosin
2481;5181			151;247		IP000219229;Rev_	2;1	2;1	U6 snRNA-associa	LSM3;MDS017;S	U6 snRNA-associa	P62310;B2R5H5C	LSM3_HUMAN;S	ENST0000030602;OTTHUMP000001	NP_052728;NP_01	PF02143;PF06294	LSM;DUF1042	
3870;4703;4817;5	742;743				IP000219445;IP000	8;8;6;2	8;8;6;2	Proteasome active	PSME3	Isoform 2 of Prote	P61289-2;P61289	PSME3_HUMAN;E	ENST00000293362	NP_789839;NP_01	PF02251;PF02252	PA28_alpha;PA28	
8444;8911					IP00027014;IP000	2;2;2;2;2	2;2;2;2;2	Dynactin subunit	1;DCTN3;DCTN2;R	Isoform 1 of Dyna	O75935-1;O75935	DCTN3_HUMAN;C	ENST0000025963;OTTHUMP000000	NP_009165;NP_01	PF07426	Dynactin_p22	
585;4791;4982;5202	5833;7799				IP00018931;IP01	6;4;1	6;4;1	Vacuolar protein	s VPS35;MEM3;TCC	Vacuolar protein	s Q96Q11;Q53FR4	VPS35_HUMAN;Q	ENST0000029913;OTTHUMP000001	NP_006076	PF03635	Vps35	
1280;1281;1643;2	328;329;330;331;1		192	66;93;101;115;208	134	IP000640590;IP000	13;13;10;9;6;5;4	13;13;10;9;6;5;4	Nucleoside diphos	NME1-NME2;hCG	Nucleoside diphos	Q32Q12;Q32Q12	NME1_HUMAN	ENST0000033913;OTTHUMP000001	NP_001018146;NP	0100334	Ndk
30;90;900;900					IP000292020	3	3	Spermidine synth	SRM5;SPS1;SRM1	Spermidine synth	P19623	SPEE_HUMAN	ENST0000037695;OTTHUMP000000	NP_003123	PF01564	Spermidine_synth	
1620;1621;3582					IP00020008;IP000	3;2;2;2	3;2;2;2	NEDD8;Ubiquitin-	NEDD8	NEDD8;NEDD8-MI	Q15843;E9PL57E	NEED8_HUMAN	ENST0000025049;OTTHUMP000001	NP_006147;NP_01	PF00240	ubiquitin	
122;530;854;855;1	1342;1343	804;805;806	596;732	542;719;720	IP000382470;IP000	34;34;23;8;7;6;4;4	19;19;13;1;3;0;2;3	Heat shock protei	HSP90AA1;HSP90	Isoform 2 of Heat	P07900-2;P07900	HSP90A_HUMAN;C	ENST00000216281;ENST0000033470	NP_001017963;NP	PF02518;PF00183	HATPase_c;HSP90	
186;1088;1737;2145	3937;4868;6482				IP000916503;IP000	7;7;6;3;3;2;2;1	7;7;6;3;3;2;2;1	cDNA FLJ55789, hi	BZAP45;KIA_C	cDNA FLJ55789, hi	B4DLZL;Q53FN7;B	B4DLZL_HUMAN	ENST00000410111;OTTHUMP000002	NP_055485	PF02020	W2	
2785;3333;3336;3	181;182		111	151;177	174	IP000007346;IP000	6;5;5;5;1	6;5;5;5;1	Peptidyl-prolyl	cis PPH;CYP20;CYPH	Peptidyl-prolyl cis	Q43447;Q6FH36C	PPH_HUMAN;A6I	ENST0000030497;OTTHUMP000000	NP_006338	PF00160	Pro_isomerase
1280;2204;2476;2	328;329;330;331		192	66;93;101;115	134	IP000375531;IP000	10;10;10	1;1	Nucleoside diphos	NME1;NDPKA;NM	Isoform 2 of Nucle	P15531-2;P15531	NDKA_HUMAN	ENST0000013037;OTTHUMP000001	NP_937818;NP_01	PF00334	NDK
474;480;1162;125	1134;1135;1136;1	679;680;681;682;1	64;276;291;581;8	87;128;173;179;31	IP000293464;IP000	39;34;34;30;27;16	39;34;34;30;27;16	DNA damage-bind	DBP1;XAP1	DNA damage-bind	Q16531;B722A1;F	DBP1_HUMAN;B4	ENST0000030176;OTTHUMP000002	NP_001914;XP_01	PF03178	CPSF_A	
320;737;1748;230	1530;1531;1532	933;934;935	489;521;528	148;154;390	IP000554737;IP000	16;16;15;11;6;5;5	16;16;15;11;6;5;5	Serine/threonine-	PP2R1A	Serine/threonine-	P30153;A8K3H8A	2AAA_HUMAN;B4	ENST0000032208;OTTHUMP000001	NP_005040	PF02985	HEAT	
138;1053;2248;38	1445;1446;1447;1448		297;303;423;482		IP000438229;IP000	10;10;10	10;10;10	Transcription inte	TRIM28;KAP1;RNF	Isoform 1 of Trans	Q13263-1;Q13263	TIF1B_HUMAN	ENST00000253024;ENST0000034175	NP_005753	PF00628;PF00643	PHD;zf-f_box;zf-C	
3081;4064			317;323		IP000910513;IP000	2;2;2;2;2	2;2;2;2;2	cDNA FLJ78119, hi	GSP1T;GSP2T;ERF	eukaryotic peptid	AK82W7;B2RC76	AK82W7_HUMAN	ENST0000021962;OTTHUMP000000	NP_006285;NP_01	PF00009;PF03144	CTP_EFTU;GTP_EI</	

2861;3886;6285;7059

3769;3910;6963;7

361;3166;4915

741;742;839;840; 327;1478;1479;14 901;902;903;904; 18;74;100;115

959;5420;6628;7118;8305

2149;4200;4546;6

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1358;4265;4266;4

897;1642;2620;26

764;1901;2806;40 339;340;341;342

5199;5708;5917

83;2436;2968;351

5;123;1022;2016;

252;1893;2919;29 1046;1047;1048 620;621

2655;3467;3575;3

332;1174;1922;2127;542;6275;6295;8658;8935

7220

2345;2451;3062;3 260;261

17;21;3458

6149;6211;7480;8 262;263

277;284;506;531; 1218;1219;1220;1 739;740;741

35;5971

7830;8463

1779;2292;2939;4 1503;1504

403;603;753;1429 581;582;583

693;2165;2784;35

522;2627;3105;40 305 177;178

173;180;995;2141 159;160;161

537;1396;5581;70 457;458

4842;8332

1589;3292;6944;8684

486;2138 1129;1130

696;1263;1680;25 654;655;656;657; 400;401

497;1351;1393;15 645;646;647

1859;4163;4482;8220

175;4118;1818;4932;5899

3554;5297;5622;7 405;406;407;408

163;567;3305;644

479;2957;7388

1032;2042;4350

1184;4688;5100

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60;2047;2775;312 903;904

893;1548;2455;26

202;3413;3695;5072;6112;8414

1463;5089;7892

1118;1348;1466;1 1124 673;674

740;3604;3913

609

3421;8345;8420

147;148;3571;357 965;966;967

1449;4661;6354

1397;2580;2835;2 943;944 945 554;555;556;557 42;283;321

928;1420;2220;23 605;606 365;366 187;204

223;435;1890;3153;3689;4045;4148; 132;133;134

3462;5057;5713

147;148;3571;357 965;966;967

2280;3763;3764;4 1042;1043;1044 616;617;618 208;225;297 91;229;233

665;1570;2710;4037;4038;4146;4574 431;432

2627;2802;5381;6024;9044

279;285;1587;219 1237;1238;1239;1240;1241;1242;12 113;145;217;250;272;339;342;408;4

1849;4698;6122;6130

960;5015;6556;8734;8783

558;580;3426

122

975

348

234

306

1476

403 241;242;243;244;

211

72,82;144;147

338

601

480

223;237;273

70,218

82

7220

158;159

64;189

86;108

14;55;221;249;266 187;244;430

218;340;573

332;335

654

191;196

121;127;149;165;1 131;134

111;119;186

251 374;378;380;382

124

187 283;318

51,124

83;227;228;326;3

187 283;318

1124 673;674

325 331;339

117

157 100 59;250

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78 78

70;172

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208;225;297

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2353;4848;5451;8 887;888	515 113;136	114	IP000645446;PI00 4,4,4	4,4,4	4,4,4	Malignant T cell a MCTS1;MCT1	Isoform 3 of Malig Q9JULC-3;Q9JULC-MCTS1_HUMAN	ENST00000037131;1	OTTHUMP000000 NP_001131026;NI PF01472	PUA	
2955;6524 1417;1418	844 67;104	60	IP000413778;PI00 2,2	2,2	2,2	Peptidyl-prolyl cis FKBP1A;FKBP1;FKI	FKBP1A protein;U P62942;Q0VDC6;C FKBP1A_HUMAN;C	ENST00000038171;1	OTTHUMP000000 NP_00100792;NP_01 PF00254	FKBP_C	
1382;1561;3016;4 357;358;359;360	112;164;249;316		IP00013122	9	9	Hsp90 co-chaperone CDC37;CDC37A	Hsp90 co-chaperone P16543;A1L0W4; CDC37_HUMAN	ENST00000222005	NP_008996	PF08564;PF08565	CDC37_C;CDC37_1
	4946 1634		IP000816555	1	1	V1-4 protein V1-4	V1-4 protein Q5NV63 Q5NV63_HUMAN	ENST0000039031;1	OTTHUMP000000199438	PF07686	V-Set5
1639;8510 1360	64		IP000395462;PI00 2,1	2,1	2,1	Huntingtin-interacti HYPK;HSPC136	Form 2 of Hunt Q9NXX5;2-Q9NXX5 HYPK_HUMAN	ENST0000033786;1	OTTHUMP000000 NP_057484;NP_001186814	PF06210	
1699;3376;5522;6	159		IP01013418;PI00 6;6,5;4;3;3;2;1;1;1	6,6,5;4;3;3;2;1;1;1	6,6,5;4;3;3;2;1;1;1	Ferritin;Ferritin he FTH1;FTH;FTHL6;C	Ferritin;Ferritin he FTH3;C;Q6N336;F B3KXC3_HUMAN;	ENST0000023755;1	OTTHUMP000002 NP_002023	PF0118214	Ferritin
2117;2854;4027;5268	873	84	IP000427330;PI00 4;1,1	4,1,1	4,1,1	Ribosome matura SBDS;CGI-97	Ribosome matura Q9Y3A5 SBDS_HUMAN	ENST0000024686;1	OTTHUMP000001 NP_057122	PF01172;PF09377	SBDS;SBDS_C
512;778;1354;135 1185;1186;1187;1	718 61;68;343;471	307	IP000298423;PI00 33;33;12;12;12;11	33;33;12;12;12;11	33;33;12;12;12;11	Pyruvate dehydro PDXH;PDX1	Pyruvate dehydro; Q00330;B2R673;E ODPX_HUMAN	ENST0000022786;1	OTTHUMP000002 NP_003468;NP_01 PF00198;PF00364	2-oxoacid_dh;Biot	
32;33;127;977;161 1623;1624;1625;1 978;979;980;981;1	203;210;245;306;3 313;335;376;445;4	IP000419237;PI00 29;29;17;10;5	29;29;17;10;5	29;29;17;10;5	29;29;17;10;5	Cytosol aminopep LAP3;LAPEP;PEPS	Isoform 1 of Cytos P2838;1;P28838; AMPL_HUMAN;B	ENST0000022629;1	OTTHUMP000001 NP_056991	PF00883;PF02789	P5514;M17;P
2402;3499;4098;4 1284	765 171	78	IP000328748;PI00 4;4,1	4,4,1	4,4,1	cDNA FLJ71717; hi ARMET;ARP	cDNA FLJ71717; hi ARK878;P55145 ARK878_HUMAN;	ENST0000027362;1	OTTHUMP000002 NP_006001	PF10208	Armet
65;267;687;688;5292;7204;8735 496;497	158;217		IP00744476;PI00 7;7;7;6;6;6;5;3	7;7;7;6;6;6;5;3	1;1;1;1;1;1;0;0;0;0;0	V1-2 protein;V1-3 V1-2;GLV2-11;V1-1	IGL on protein;IGL A2MYD6;Q61PQ0; A2MYD6_HUMAN	ENST00000039031;1	OTTHUMP00000199442;OTTHUMPO	PF07686;PF07654	V-set;C1-set
1185;4792;5081;5845;7157			IP000938079;PI00 5,5	5,5	5,5	cDNA FLJ55458; hi DRIP4;PDCDC6;AI	programmed cell l B4DH02;B7Z5C1;E B4DH02_HUMAN	ENST0000030729;1	OTTHUMP000001 NP_00115590;NI PF03907	PF07397	BR01
7229;9087			IP000237288;PI00 2,1	2,1	2,1	Gamma-glutamyl GGH	Gamma-glutamyl Q2R820;A8K335;B GGH_HUMAN	ENST0000026011;1	OTTHUMP000002 NP_003869	PF07202	Peptidase_C26
655;6644;6645;7784			IP000152692	4	4	D-tyrosyl-tRNA(Ty TDT1;C20orf88;H	D-tyrosyl-tRNA(Ty Q8TE48;Q496C9 DTD1_HUMAN	ENST0000037745;1	OTTHUMP000000 NP_543010	PF02580	Tyr_Deacylase
2734;5801			IP000924816;PI00 2,2	2,2	2,2	Myotrophin;Prote MTPN	Myotrophin;Unch. P58546;Q69YG1;C MTPN_HUMAN	ENST0000035670;1	OTTHUMP000002 NP_665807	PF00023	Ank
498;556;754;1658 931;932;933;934;5	551 53;78;110;115;16;6	92	IP000215901;PI00 13;13;13;13;11;11;11	13;13;13;13;11;11;11	13;13;13;13;11;11;11	G-rich sequence f GRSF1;hCG_1700K	G-rich sequence f GRSF1;hCG_1700K G-rich sequence f Q12849;B3KW50; GRSF1_HUMAN;B	ENST0000025479;1	OTTHUMP000002 NP_002083;NP_01 PF00076	PF00023	RRM_1
408;5507;6187 968;969;970	12;18;29		IP000217253	3	3	ATP cyclohydrolas GCFHR;GFRP	Isoform 1 of Aden P54819;1-P54819; KAD2_HUMAN	ENST0000035485;1	OTTHUMP000000 NP_001616;NP_01 PF00406;PF05191	ADK;ADK_lid	GRFP
942;1681;2053;31 1462 888;889;890;891;1	120 79;104;124;164;2		IP000465028;PI00 15;15;12;11	15;15;12;11	15;15;12;11	Trisphosphate i TP11;TP1	triphosphate i D3DUS5;Q53HE2; Q53HE2_HUMAN	ENST0000022927;1	OTTHUMP000001 NP_00115275;NI PF00121	PF00121	TIM
2256;4216;4596;4 481;482;483;484	303;304;305		IP00018352;PI00 14;13;13;10;2;1	13;13;13;10;2;1	14;13;13;10;2;1	Ubiquitin carboxyl UCHL1	Ubiquitin carboxyl Q09936;A6N1U7; UCHL1_HUMAN	ENST0000028444;1	OTTHUMP000001 NP_004172	PF01088	Peptidase_C12
2010;2477;3419;5 850	128		IP01021500;PI01 6;6;6;6;2	6;6;6;6;2	6;6;6;6;2	Vacuolar protein s VPS29;DC7;DC15;1	24 kDa protein;Prn Q9UBQ0;2-Q9UBC VPS29_HUMAN	ENST00000360579;1	ENST0000039767	NP_476528;NP_01 PF00149	Metallophos
963;1423;1948;25 671;672;673	58;91;151		IP00026328	8	8	Thioredoxin doma TXNDC12;TLP19;U	Thioredoxin doma Q95881 TXD12_HUMAN	ENST0000037162;1	OTTHUMP000000 NP_056997		
359;1131;1549;1933;2038;2354;2355	506;507;508;509;510		IP00017438;PI01 16;16;16	16;16;16	16;16;16	Thioredoxin doma TXNDC5;TLP46;UN	Thioredoxin doma Q8NB89;Q65859; TXND5_HUMAN;C	ENST0000037975;1	OTTHUMP000000 NP_110437;NP_01 PF00085	PF00085	Thioredoxin
2151;4198;5539;7 309;310;311	87;111;129		IP000112750;PI00 7,6	7,6	7,6	Ubiquitin carboxyl UCHL3;RP11-173B	Ubiquitin carboxyl P15374;E9PBF1;C UCHL3_HUMAN;C	ENST0000037758;1	OTTHUMP000000 NP_005993	PF01088	Peptidase_C12
1524;2699;4068			IP000212853	3	3	Cytochrome c oxid COX5B	Cytochrome c oxid P10606;Q5Y87;C COX5B_HUMAN	ENST0000025842;1	OTTHUMP000001 NP_001853	PF01215	COX5B
2831;3010;4965;5 560	337 115	192	IP00019755;PI00 6,5,5	6,5,5	6,5,5	Glutathione S-tran GSTO1;GSTTLP28;	Glutathione S-tran P78417;B2R983;C GSTO1_HUMAN;C	ENST0000036971;1	OTTHUMP000000 NP_004823;NP_01 PF00403;PF02798	GST_C;GST_N	Transaldolase
1936;3561;3969;4 1577;1578;1579	11;118;234		IP00744692;PI00 14;13;11	14;13;11	14;13;11	Transaldolase;DN TALD01;TAL	Transaldolase;Trai P78373;Q9UMF8;TALD0_HUMAN;B	ENST0000031900;1	OTTHUMP000001 NP_006746	PF09923	Transaldolase
134;560;1101;684 1457	288		IP000784614;PI00 7;7;7;7;7;7;4	7;7;7;7;7;7;4	7;7;7;7;7;7;4	cDNA FLJ55422; hi Ov/B septin;SEPT	septin-9 isoform a B4D7L7;Q96GF2;C B4D7L7_HUMAN;	ENST00000329047;1	ENST0000040779	NP_001106963;NI PF000735	Septin
4514;4866;6402			IP00003438	3	3	Dnaj homolog sub DNAI8;SPF31;HS	Dnaj homolog sub Q57997 DNJCB_HUMAN	ENST0000026369;1	OTTHUMP000000 NP_055095	PF00226	Dnaj
931;1847;4407;6423;7190;8025			IP00030706;PI01 6,4	6,4	6,4	Activator of 90 kD AHSA1;C14orf3;H	Activator of 90 kD Q95433;B4DUR9; AHSA1_HUMAN;B	ENST00000216479	NP_306243	PF09229;PF08327	Aha1_N;AHSA1
464;525;594;597; 1036;1037;1038;1039	200;305;433;451		IP000219365;PI01 12;8,5	12,0;3	12,0;3	Moesin;Membran MSN	Moesin P26038;Q6JPT4 MOESN_HUMAN	ENST0000036027;1	OTTHUMP000000 NP_002435	PF00769;PF09380	ERM;FERM_C;FER
194;323;1828;323 332;333	193;194;195		IP000796337;PI00 7;7;7;7;7;7;7;4	4;4;4;4;4;4;4;4	4;4;4;4;4;4;4;4	Myo(RC)-binding f PCBP2;hCG_2017;	poly(RC)-binding p Q59HD4;Q61PF4; Q59HD4_HUMAN	ENST00000359282;1	ENST0000035946	NP_059007;NP_01 PF00013	KH_1
806;849;3068;347 1101;1102	648;649		IP000239077;PI00 8;4;4;4;2,1	8;4;4;4;2,1	8;4;4;4;2,1	Histidine triad nuc HINT1;HINT	PKC11 Histidine triad nuc P49773;D6R6D0;E	ENST0000030404;1	OTTHUMP000001 NP_005331	PF01230	HIT
747;748;885;1511 327 190;191	153 77;177		IP000984795;PI00 16;16;16;15;12;7,2	16;16;16;15;12;7,2	14;14;14;13;10;7,2	Coflin;I;Coflin, n CFL1;CFL	Uncharacterized p E9P255;P23528;E	ENST0000030816;1	OTTHUMP000002 NP_005498	PF00241	Cofilin_ADF
4282;7638	473		IP00034319;PI00 2,2,2,2,1	2,2,2,2,1	2,2,2,2,1	Protein Cuta;Brain CUTA;ACHAP;C6o	Isoform A of Protc Q60888;2-Q60888	ENST0000037448;1	OTTHUMP000000 NP_001014433;NI PF03091	PF03091	CutA1
430;4566;7036			IP000328243;PI01 3,1	3,1	3,1	Phospholipase D3 PLD3	Phospholipase D3 Q8V108 PLD3_HUMAN	ENST0000035650;1	OTTHUMP000002 NP_001026866;NI PF08371;PF00614	PLD_envelope;PLI	
4302;5122			IP000008418;PI00 2,2,2,2,1	2,2,2,2,1	2,2,2,2,1	Diablo homolog, n DIABLO;SMAC	Diablo homolog, n Q9NR28;1-Q9NR28;1	ENST0000026716;1	OTTHUMP000002 NP_063940;NP_01 PF09057	PF09057	Smac_Diablo
4331;4662;4976;6091;6850			IP00019178;PI00 5,5	5,5	5,5	Phosphoserine ph PSPH	Phosphoserine ph P78330;Q53EY1;C	ENST0000027560;1	OTTHUMP000001 NP_004568	PF00702	Hydrolase
273;1436;2076;26 814	419		IP000909305;PI00 6,3	6,3	6,3	Coproporphyrinog CPOX;CPO;CPX	Coproporphyrinog P36551 HEMG_HUMAN	ENST0000026419;1	OTTHUMP000002 NP_000088	PF01218	Coprogen_oxidase
511;691;1115;113 1344;1345;1346	807;808;809;810;1 104;319;337		IP01014546;PI00 20;20;20;13;12	20;20;20;13;12	20;20;20;13;12	Protein arginine N PRMT1;HMT2;HRI	protein arginine N Q98873;1-Q99873	ENST0000035185;1	OTTHUMP000002 NP_001527;NP_938074	PF01257	Complex1_24kDa
2597;4929;7610			IP000035637	3,3,3	3,3,3	26S proteasome n PSMD10;RPS	26S proteasome n Q75832;Q5U0B2;I	ENST0000021795;1	OTTHUMP000000 NP_002805	PF00023	Ank
445;621;1270;154 1049;1050	622 20;92	48	IP000129757;PI00 11,8;1	11,8;1	11,8;1	Glutathione S-tran GSTP1;FAEES3;GS'	Glutathione S-tran P09211;C7JD51;C7	ENST0000019696;1	OTTHUMP000001 NP_000843	PF00043;PF02798	GST_C;GST_N
12;1068;1324;6003			IP000646556;PI00 4,4	4,4	4,4	NADH dehydroger NDUUF2	Uncharacterized p E7EPT4;P19404;A	ENST0000031838;1	OTTHUMP000001 NP_066552	PF01257	Complex1_24kDa
2415;7303	795	121	IP00056357	2	2	UPF0556 protein (C19orf10);IL25	UPF0556 protein (C19orf10);IL25	ENST00000262947	NP_061980	PF10572	UPF0556
2432;5395;6561;6 892	47		IP000180386;PI00 4,4;4,4;4,4;1,1	4,4;4,4;4,4;1,1	4,4;4,4;4,4;1,1	Glycogenin-1;CDN GYG1;GYG	Isoform GN-1L of P46976;1;P46976;	ENST0000029604;1	OTTHUMP000002 NP_004412;NP_01 PF01501	PF01501	Glyco_transf_8
1127;1350;3303;7 1416	194		IP000420084;PI00 4,4;4	4,4;3	4,4;3	BH3-interactin di BID	Isoform 2 of BH3-1; P59597;2-P59597;	ENST0000031736;1	OTTHUMP000001 NP_93270;NP_01 PF06393	PF06393	BID
1331;4223;5692;5733	790	271	IP00033215;PI00 4;3;2;2;1;1;1;1;1	4;3;2;2;1;1;1;1;1	4;3;2;2;1;1;1;1;1	Transcription elon TCEA1;TFIIH	Isoform 1 of Trans P23191;1-P23193;	ENST0000036038;1	OTTHUMP000002 NP_006747;NP_01 PF08711;PF01096	TFIIH;TFIIH_C;TFIIH	TFIIH;TFIIH_C;TFIIH
15;146;398;804;8 270;271;272;273;3	167;168;169;170;1 11;12;58;146;166;42	101;164;206;2	IP00010471;PI00 50;17;14;7;7;4;3	50;17;14;7;7;4;3	50;17;14;7;7;4;3	Plastin-2;L-plastin LCP1;PLS2	Plastin-2 P13796;B3KUI1;E;P	ENST0000032307;1	OTTHUMP000000 NP_002289	PF00307;PF00306	CH1;eFhand
872;875;1850;370 67;68;69	48;49;50		IP000514424;PI00 9;9,8;5;3;3;2,1	9;9,8;5;3;3;2,1	9;9,8;5;3;3;2,1	Palmitoyl-protein PPT1;RP11-115D7	Uncharacterized p E9PES1;E9PMG2;I	ENST0000037277;1	OTTHUMP000000 NP_000301;NP_01 PF02089	PF00589	Palm_thioest
4909;7052;7637;8501			IP00001663;PI00 4;4;4;2,1,1	4,4;4;2,1,1	4,4;4;2,1,1	Serine protease H HTRA2;OMI;PRSS	Isoform 1 of Serin Q43464;1-Q43464	ENST0000025808;1	OTTHUMP000001 NP_037379;NP_01 PF00595	PF00089	PH00819
396;641;954;1714 63;64;65	46;47		IP00001734;PI00 14;12;18	14;12;8	14;12;8	Phosphoserine ar PSAT1;PSA	Phosphoserine ar Q9Y611;1-Q9Y611;	ENST0000034715;1	OTTHUMP000000 NP_478059;NP_01 PF00266	PF00266	Aminotran_5
2222;4761;7070;773;8256			IP00009946;PI00 5,2	5,2	5,2	Mitochondrial imp; TOMM34;URCC3	Mitochondrial imp; Q15785;B4DXU3	ENST0000037281;1	OTTHUMP000000 NP_006800	PF00515	TPR_1
78;368;459;482;9 393;394;395;396;1	237;238;239;240		IP000479946;PI00 26;26;23;10;8;6	26;26;23;10;8;6	26;26;23;10;8;6	cDNA FLJ76863; hi ST1P1	ST1P1 protein;Stx ARK690;Q3ZCVR;E	ENST0000030521;1	OTTHUMP000002 NP_006810	PF00515;PF07719	TPR_1;TPR_2
358;1431;3107;33 300;301	324;425		IP00010796;PI00 14;13;12;7;3	14;13;12;7;3	14;13;12;7;3	Protein disulfide-i P4HB;ERBA2L;PDI	Protein disulfide-i P07237;B4DJS0;E	ENST0000033148;1	OTTHUMP000001 NP_000909	PF00085	Thioredoxin
234;1520;2412;37 772	267		IP00031801;PI00 7;6;6;5;4;1,1	3;2,2;1;0;0;1	3;2;2;1;						

3631;6872	2271	911	595		IP00185219;PI00 2,2;1	2,2;1	2,2;1	GAS2-like protein GAS2L3	GAS2-like protein Q86X1;B3KTH9	GA2L3_HUMAN	ENST00000266754	NP_777602	PF00307;PF02187	CH;GAS2
					IP00185919;PI00 1;1,1;1	1,1;1,1	1,1;1,1	La-related protein LARP1;K1AA0731;1	Isoform 1 of La-re Q6PKG;1,Q6PKG	LARP1_HUMAN	ENST0000028589;OTTHUMP000002	NP_056130	PF05383	La
3186;3612;4621	936		22		IP000215918;PI00 3,2;1	1,1	1,1	ADP-ribosylation f ARF4;ARF2	ADP-ribosylation f P18005;C9JAK5	ARF4_HUMAN	ENST0000030343;OTTHUMP000002	NP_001651	PF00025	Arf
	1315			559	IP000216099;PI00 1,1	1,1	1,1	Desmocollin-1;De DSC1;CDHF1	Isoform 1A of Des Q08554-1;Q08554	DSC1_HUMAN	ENST0000025719;OTTHUMP000001	NP_070028;NP_070028;NP_070028	PF00878;PF00878	Cadherin;Cadherin
5072;5548;6112		947	1		IP000216105;PI01 3,1	1,1	1,1	Obg-like ATPase 1 OLA1;GTPBP9;PTE	Isoform 2 of Obg-I Q9NTK5-2;Q9NTK	OLA1_HUMAN	ENST0000028471;OTTHUMP000002	NP_00101708	PF01926;PF06071	MMR_HSR1;YchF
	2126				IP000216873;PI00 1,1	1,1	1,1	3'-5' exoribonucle ERI1;3'EXO;THEX1	3'-5' exoribonucle Q81V48;B4DW4F4;1	ERI1_HUMAN;B4E	ENST0000025026;OTTHUMP000001	NP_699163	PF00929;PF02037	Exonuc_X-T_SAP
	6887				IP000217049;PI00 1;1,1;1	1,1;1,1	1,1;1,1	2'-5'-oligoadenylat OAS2	Isoform p71 of 2'- P29728-1;P29728;	OAS2_HUMAN;QE	ENST00000342315;ENST0000039258	NP_058197;NP_058197	PF01909;PF10421	NTP_transf_2;OAI
572;2525		961	3644		IP000329784;PI00 2,2;2,2	2,2;2,2	2,2;2,2	Ryanodine recept RYR3;HBRR	Isoform 1 of Ryan Q15413-1;Q15413	RYR3_HUMAN	ENST00000389232	NP_001027	PF00036;PF08709	ehfand;Ins145_P3
	7129				IP000376756;PI00 1,1,1,1;1,1;1	1,1,1,1;1,1;1	1,1,1,1;1,1;1	High mobility grou HMGB3;HMGB2;H	High mobility grou U15347;E7EQU1;E	HMGB3_HUMAN	ENST0000032530;OTTHUMP000000	XP_935058;XP_94	PF00505	HMG_box
	6749				IP000217661;PI00 1,1,1	1,1,1	1,1,1	Ribonucleoprotein RAVER1;K1AA197E	ribonucleoprotein Q81Y67-2;Q81Y67;	RAVR1_HUMAN	ENST00000293677;ENST0000033113	NP_597709	PF00076	RRM_1
	4598				IP000293425;PI00 1,1,1;1,1	1,1,1;1,1	1,1,1;1,1	Frataxin, mitochor FXN;FRDA;X25	Isoform 1 of Frata Q16595-1;Q16595	FRDA_HUMAN;A8	ENST0000037727;OTTHUMP000000	NP_000135;NP_8	PF01491	Frataxin_Cyay
50;2695		974	342		IP000217920;PI00 2,2;2,2	2,2;2,2	2,2;2,2	Aldehyde dehydr ALDH16A1	Isoform 1 of Aldeh Q81Z83-1;Q81Z83;	A16A1_HUMAN;B	ENST00000293350	NP_699160;NP_01	PF00171	Aldehyd
	3625				IP000396630;PI00 1,1;1	1,1,1	1,1;1	cAMP-dependent PRKACA;PKACA	Isoform 1 of cAMF P17612-1;P17612;	KAPCA_HUMAN;B	ENST00000308677;ENST0000035035	NP_000271;NP_9	PF00069	Pkinase
	3983				IP000218054	1	1	Selenoprotein H SELH;C11orf31	Selenoprotein H Q8IZQ5	SELH_HUMAN	ENST0000038885;OTTHUMP000002	NP_734467		
	6148				IP000796062;PI00 1,1	1,1	1,1	Cytochrome c oxid COX17	Uncharacterized p C9J8T6;Q14061	COX17_HUMAN	ENST0000026107;OTTHUMP000002	NP_005685	PF05051	COX17
	3394				IP000218465;PI00 1,1,1	1,1,1	1,1,1	Phospholipase A-2 PLAA;PLAP	Phospholipase A-2 Q9Y263;E5RIM3	PLAP_HUMAN	ENST0000038008;OTTHUMP000000	NP_001026859	PF09070;PF08324	PFU;PUL;WD40
	165		587		IP01021882;PI00 1,1	1,1	1,1	Gametocyte-speci GTSF1;FAM112B	20 kDa protein;Ga Q8WVV3	GTSF1_HUMAN	ENST00000305879	NP_653195	PF05253	UFPO224
	5515	1002	792		IP000218823	1	1	Histone-lysine N-r WBP7;HRX2;K1AA1	Isoform 1 of Histo Q9UIM6-1;Q9UIM	MLL4_HUMAN	ENST0000022227;OTTHUMP000000	NP_055542	PF02178;PF05965	Atf_hoock;FYRC;FYI
	4589	1032	26		IP000926491;PI00 1,1;1,1;1,1,1	1,1,1;1,1;1,1	1,1,1;1,1;1,1	cDNA FLJ56092, hi ATP5J2;ATP5JL	cDNA FLJ56092, hi B4DJ38;C9IJU2;P	B4DJ38_HUMAN;J	ENST0000029247;OTTHUMP000002	NP_004880;NP_01	PF01535;PF10206	PPR;WRW
	3598				IP010209222;PI00 1,1,1;1,1	1,1,1;1,1	1,1,1;1,1	ADP-ribosylation f ARL1	20 kDa protein;AC P40616;B4DWV1	ARL1_HUMAN;B4	ENST00000261636	NP_0001168	PF00025	Arf
	3428				IP000219575;PI00 1,1	1,1	1,1	Bleomycin hydrol BLMH	Bleomycin hydrol; Q13867;B4DXF3;E	BLMH_HUMAN;B	ENST00000261714;ENST0000039481	NP_000377	PF03051	Peptidase_C1_2
	2674		619		IP000219677;PI00 1,1,1;1,1,1	1,1,1;1,1,1	1,1,1;1,1,1	Putative deoxyribi DERA;CGI-26	Putative deoxyribi Q9Y315;E9PPM8;1	DEOC_HUMAN;B4	ENST00000002542;OTTHUMP000002	NP_057038	PF01791	Deoc
2857;5922;7510					IP000791893;PI00 3,3;3,2;2,2;2,2;1	3,3;3,2;2,2;2,2;1	3,3;3,2;2,2;2,2;1	Casein kinase I iso CSNK1G1;CSNK1G	HCG204507, isofo Q9HCPD-1;Q9HCP	KC1G1_HUMAN;B	ENST0000030303;OTTHUMP000001	NP_071331;NP_0	PF00069	Pkinase
	2720				IP000220059;PI00 1,1	1,1	1,1	NADH dehydrogen NDUFB4	NADH dehydrogen Q95168;B2RUY3	NDUB4_HUMAN;J	ENST0000018426;OTTHUMP000002	NP_006438;NP_0	PF07225	NDUF_B4
	7663	1061	25		IP000220402;PI00 1,1;1,1	1,1;1,1	1,1;1,1	Protein phosphat: PPP1R2;PPP2;PPP1	Protein phosphat: P41236;Q6NXS1;E	PPP2_HUMAN;JPP	ENST0000032843;OTTHUMP000002	NP_006232	PF04979	IPP-2
	8443	1090	168		IP000220770	1	1	Dynactin subunit C DCTN6;WS3	Dynactin subunit C Q00399	DCTN6_HUMAN	ENST0000022111;OTTHUMP000002	NP_006562	PF00132	Huxap62
	8044				IP000221106;PI00 1,1,1;1,1,1,1	1,1,1;1,1,1,1	1,1,1;1,1,1,1	Splicing factor 3B Q13435;SAP15;DKI	Splicing factor 3B Q13435;E9PP10;Q	SF3B2_HUMAN;Q	ENST0000032253;OTTHUMP000002	NP_006833	PF04037;PF04046	Hexap82;PSP;SAP
	2904				IP000221117	1	1	Acylphosphatase- ACYP1;ACYPE	Acylphosphatase- P07311	ACYP1_HUMAN	ENST00000238618	NP_0010198	PF00708	Acylphosphatase
	552				IP000221394;PI00 1,1	1,1	1,1	H/ACA ribonucleo DKC1;NOLA4	H/ACA ribonucleo Q60832;A8MUT5;	DKC1_HUMAN	ENST0000036955;OTTHUMP000000	NP_001354;NP_0	PF08068;PF01472	DKCLD;PUA;TruB
377;5228;5763;5767					IP000239406;PI00 4,4;4	4,4;4	4,4;4	Nesprin-2;Nuclear SYNE2;K1AA1011;1	Isoform 2 of Nesp Q8WXH0-2;Q8WX	SYNE2_HUMAN	ENST00000261678;ENST0000034147	NP_878918;NP_0	PF00307;PF10541	CH;KASH;Spectrin
	4735				IP000247871;PI00 1,1	1,1	1,1	Transcription elon TCERG1;CA150;TA	Isoform 1 of Trans Q14776-1;Q14776	TCRG1_HUMAN	ENST0000029670;OTTHUMP000001	NP_006697;NP_0	PF01846;PF00397	FF_WW
	5592	1111	1		IP000879123;PI00 1,1	1,1	1,1	Transmembrane p TMPRSS6;UNQ354	Isoform 1 of Trans Q8UIU0-4;Q8UIU0	TMPSS6_HUMAN	ENST0000025197;OTTHUMP000001	NP_705837	PF00057;PF00458	Ldl_recept_a;Tyrp
	3114				IP000250297	1	1	L-aminoadipate-se AASDHPPT;CGI-80	L-aminoadipate-se Q9NRN7	ADPPT_HUMAN	ENST0000027861;OTTHUMP000002	NP_056238	PF01648	ACPS
	5705				IP000289776;PI01 1,1	1,1	1,1	Probable E3 ubiqu MYCBP2;K1AA0911	probable E3 ubiqi Q75592-2;Q75592	MYCB2_HUMAN	ENST0000035733;OTTHUMP000000	NP_055872	PF08005;PF00415	PHR;RCC1
	3488				IP000290928	1	1	Guanine nucleotic GNA13	Guanine nucleotic Q14344	GNA13_HUMAN	ENST00000239138	NP_006563	PF00503	G-alpha
	4784				IP000291016	1	1	NADH dehydrogen NDUFV3	Isoform 2 of NADH P56181-2;P56181;	NDUV3_HUMAN	ENST0000034034;OTTHUMP000001	NP_006553		
	668				IP000643250;PI00 1,1,1;1	1,1,1,1	1,1,1,1	Rho/rac guanine r ARHGFE2;RP11-33	Rho/rac guanine r Q3DVAS;Q5V993;	Q5V993_HUMAN	ENST0000036831;OTTHUMP000000	NP_00115855;NP	PF00130;PF00169	C1_1;P;RhoGEF
984;1792;2458;4877;7249;8820					IP000291467;PI00 6,5	1,1	1,1	ADP/ATP transloc SLC25A6;ANT3;CD	ADP/ATP transloc P12236;Q75961;Q	ADT3_HUMAN	ENST0000038140;OTTHUMP000000	NP_001627	PF00153	Mito_carr
2103;5316;6896			676		IP000291783	3	3	Gem-associated p GEMIN5	Gem-associated p Q8TEQ6;B7ZLC9;C	GEM15_HUMAN	ENST0000028587;OTTHUMP000001	NP_056280	PF00400	WD40
	3063				IP000975549;PI00 1,1,1	1,1,1	1,1,1	cDNA FLJ1629, hi CLINT1;ENTH;EPN	clathrin interactor B7Z6F8;Q14677-1	B7Z6F8_HUMAN;J	ENST0000029695;OTTHUMP000002	NP_00184284;NP	PF01417	ENTH
	6788				IP000292140;PI00 1,1,1	1,1,1	1,1,1	Caspase-3;Apopai CASP3;CPP32;DKF	Caspase-3;Unchar P42574;ABMVM1;	CASP3_HUMAN;A	ENST0000030839;OTTHUMP000001	NP_004437;NP_1	PF00656	Peptidase_C14
	568				IP000293126;PI00 1,1	1,1	1,1	Tubulin folding co TBCB;CG22;CKAP1	Tubulin-folding co Q99426;Q6FGY5;E	TBCB_HUMAN;A8	ENST0000022185;OTTHUMP000000	NP_0010272	PF01302	CAP_GLY
	8882				IP000293331;PI00 1,1	1,1	1,1	Ribonucleases P/h POP1;K1AA0061	Ribonucleases P/h Q95755;Q96F88;E	POP1_HUMAN	ENST0000034969;OTTHUMP000002	NP_001139332;NP	PF06978;PF08170	POP1;POPLD
	7177				IP000293735;PI00 1,1	1,1	1,1	Elongator comple: IKBKAP;ELP1;IKAP	Elongator comple: Q95163;B3KXE7;B	ELP1_HUMAN;B3I	ENST0000037464;OTTHUMP000000	NP_003631	PF04762	IKI3
	4321				IP000294084;PI00 1,1	1,1	1,1	Endothelial PAS di EPAS1;HF2A;MOF	Endothelial PAS di Q98814;B3KW07;	EPAS1_HUMAN	ENST0000026373;OTTHUMP000001	NP_001421	PF08778;PF00010	HF1-NA_CTAD;HLH
	3338				IP000294242	1	1	28S ribosomal pro MRPS31;IMOGN31	28S ribosomal pro Q92665	RT31_HUMAN	ENST0000032356;OTTHUMP000000	NP_005821		
	7382				IP000295889;PI00 1,1	1,1	1,1	Signal recognition SRP19	Signal recognition P09132	SRP19_HUMAN	ENST0000028299;OTTHUMP000001	NP_003128;NP_0	PF01922	SRP19
	8162	1172	69		IP000296840;PI00 1,1	1,1	1,1	DNA polymerase i POLI;RAD30B	DNA polymerase i Q9UN44;B7Z780	POLI_HUMAN;B7I	ENST00000221780;OTTHUMP000001	NP_009126	PF00817	IMS
	6036				IP000297084;PI00 1,1	1,1	1,1	Dolichyl-diphosph DDOST;K1AA0115;	Dolichyl-diphosph P39656;B4DLU2;B4	OST48_HUMAN;B	ENST0000037504;OTTHUMP000000	NP_005207	PF03345	DDOST_48kD
101;5028					IP000297212	2	2	Paladin	PALD;K1AA1274	PALD_HUMAN	ENST0000026356;OTTHUMP000000	NP_055246		
61;938;979;1237;1192;1193;1194;1722;723			322;355;380;453 381;419		IP000298625;PI00 20;6;4,4;4,4;1,1;1	1,1;0,0;0,0;0,0;0,0	1,1;0,0;0,0;0,0;0,0	Tyrosine-protein k LYN	TYROSINE-PROTEIN K LYN	LYN_HUMAN	ENST0000027649;OTTHUMP000002	NP_002341	PF07714;PF00017	Pkinase_Tyr;SH2;S
	7729				IP000299214	1	1	Thymidine kinase, TK1	Thymidine kinase, P04183;B5BU32;B	KITH_HUMAN	ENST0000030163;OTTHUMP000001	NP_003249	PF00265	TK
	6399				IP000300127;PI00 1,1	1,1	1,1	N-acetyltransfer: NAT10;ALP;K1AA1	N-acetyltransfer: Q9H0A0;B4DFD5;	NAT10_HUMAN	ENST0000025782;OTTHUMP000002	NP_078938;NP_0	PF08351;PF05127	DUF1726;DUF699
	523				IP000301204;PI00 1,1,1	1,1,1	1,1,1	Retinol dehydroge RDH13;PSEC0082;	Isoform 1 of Retin Q8NB77-1;Q8NB1	RDH13_HUMAN	ENST00000291892	NP_001139443;NP	PF00106	adh_short
3222;8926					IP000301517;PI00 2,1;1	2,1;1	2,1;1	Uncharacterized p CxorF57;RP11-647	Isoform 1 of Unch Q6NSI4-1;Q6NSI4;	CXO57_HUMAN;B	ENST0000037254;OTTHUMP000000	NP_001171711		
111;3245;4691;47 162;164;165;166			106 154;605;724;939		IP000788782;PI00 10;10;10;10;7,1	1,1,1,1;1,1	1,1,1,1;1,1	cDNA FLJ78968, h ATP1A3	Uncharacterized p B7ZV94;E9PCS1;F;	B7ZV94_HUMAN;J	ENST0000030210;OTTHUMP000001	NP_689509	PF00689;PF00690	Cation_ATPase_C,
	784				IP000303318;PI00 1,1,1;1,1,1	1,1,1;1,1,1	1,1,1;1,1,1	Protein FAM49B;L FAM49B;BM-009;	Protein FAM49B;F Q9NUQ9;Q68D08	FA49B_HUMAN;Q	ENST0000035801;OTTHUMP000002	NP_057707	PF07159	DUF1394
	19	1248	463		IP000304187;PI00 1,1,1	1,1,1	1,1,1	RNA-binding proti RBM28	RNA-binding proti Q9NW13;B4DU52	RBM28_HUMAN;J	ENST0000022307;OTTHUMP000002	NP_006547;NP_0	PF00076	RRM_1
3009;5061														

7068					IP00307200;IP00 1,1	1,1	1,1	Switch-associated SWAP70;KIAA0641 Switch-associated Q9UH65;B4E245;E SWP70_HUMAN;E ENST0000031895; OTTHUMP000002 NP_055870	PF00169	PH
858	1282	566			IP00747362;IP00 1,1,1	1,1,1	1,1,1	PAB-dependent p PAN2;KIAA0710;U Isoform 1 of PAB- Q504Q3-1;Q504Q PAN2_HUMAN ENST00000257931;ENST0000037949 NP_001120932;NI PF00929;PF00443 Exonuc_X-T,UCH		
1680;2628;2680; 655;656;657		167;180;189			IP00409717;IP00 10;10;10;7,5	1,1,1;1,1	1,1,1;1,1	Eukaryotic initiator EIF4A2;DXX2B;EIF Isoform 2 of Eukai Q14240-2;Q14242 EIF4A2_HUMAN;Q ENST0000032396; OTTHUMP000002 NP_001958	PF00270;PF00271	DEAD;Helicase_C
7718					IP000328715;IP00 1,1,1	1,1,1	1,1,1	Protein LYRIC;Lysyl MTDH;AEG1;LYRIC Protein LYRIC;Unc Q86UEA;ESRJU9 LYRIC_HUMAN ENST0000033627; OTTHUMP000002 NP_848927		
7132					IP00515115;IP00 1,1,1,1,1,1,1,1,1,1	1,1,1,1,1,1,1,1,1,1	1,1,1,1,1,1,1,1,1,1	Putative uncharac ABUM1;ABUM1;Klu Uncharacterized p A6NCDF;Q5TG64; ANCDN9_HUMAN ENST0000036926; OTTHUMP000000 NP_002304;NP_O	PF00412;PF02209	LIM;VHP
2176					IP000329679;IP00 1,1	1,1	1,1	Protein zwilch hcr ZWILCH Isoform 1 of Prote Q9RH90-1;Q9RH90 ZWILCH_HUMAN ENST00000330789; OTTHUMP000001 NP_060445	PF09817	DUF2352
6705					IP000329801;IP00 1,1,1	1,1,1	1,1,1	Annexin A5;Annex ANXA5;ANX5;ENX Annexin A5;Uncha P08758;D6RBL5;D ANXA5_HUMAN ENST0000029651; OTTHUMP000001 NP_001145	PF00191	Annexin
3660	1323	236			IP000925520;IP00 1,1	1,1	1,1	6-phosphofructok PFKL Similar to Phosphr P17858-2;P17858; K6PL_HUMAN ENST0000031235; OTTHUMP000001 NP_002617	PF00365	PFK
3915;6903					IP000465457;IP00 2,2,2,2,1,1,1,1,1,1	2,2,2,2,1,1,1,1,1,1	2,2,2,2,1,1,1,1,1,1	Cyclin-Y;Cyclin foik CCNY;C10orf9;CB Isoform 1 of Cyciir Q8ND76-1;Q8ND7 CCNY_HUMAN;CC ENST0000026537; OTTHUMP000000 NP_659449;NP_8	PF00134	Cyclin_N
866;1515;1997;4031;4050;4310;5725 325;336;793		142;196;759			IP000941217;IP01 12;12;12;12;10;10	1,1,1,1,1,1,1,1,1	1,1,1,1,1,1,1,1,1	Myosin-14;Myosin MYH14;KIAA2034; Isoform 2 of Myos Q72406-2;Q72406 MYH14_HUMAN;ENST00000301415;ENST0000037696 NP_001139281;NI PF00612;PF00603	IQ;Myosin_head;I	
373					IP000926648;IP00 1,1,1,1,1	1,1,1,1,1	1,1,1,1,1	Acylamino-acid-re APEH;D3F1552;D3 Uncharacterized p CJ9JF;P13798;C9 ACPH_HUMAN ENST0000029645; OTTHUMP000002 NP_001631	PF00326	Peptidase_S9
5735					IP01008731;IP00 1,1,1,1,1	1,1,1,1,1	1,1,1,1,1	G patch domain-c GPATCH4;GPATCH4 Isoform 3 of G pat Q5T310-3;Q5T310; GPATCH_HUMAN ENST0000033458; OTTHUMP000002 NP_056405;NP_8	PF01585	G-patch
36;611;776;2777; 371;372		224;225;794	24;61	3;78;134	IP000375015	16	1	1 Deoxyuridine 5'-tr DUT Isoform 2 of Deox P33316-2;P33316 DUT_HUMAN ENST00000249783;ENST0000033120 NP_001939	PF00692	duITPase
327;2592					IP000375358;IP00 2,2,1	2,2,1	2,2,1	Replication factor RFC1;RFC140 Isoform 1 of Repli P35251-1;P35251; RFC1_HUMAN ENST0000034970; OTTHUMP000001 NP_001191676;NI PF00004;PF00533	AAA;BRCT;RFC1	
5472	1347			8	IP000383295	1	1	1 HCG1987117;Putu hCG_1987117 HCG1987117 Q8WZ41 Q8WZ41_HUMAN		
4672		813			IP000383656	1	1	1 KIAA0232 protein; KIAA0232 Putative uncharac Q9Y349 Q9Y349_HUMAN		
4228	1356			39	IP000384313	1	1	1 Leucine-rich repez LRRC7;KIAA1365;I cDNA FLJ54846; hi Q96NW7-3;Q96N LRRC7_HUMAN ENST0000033538; OTTHUMP0000065338	PF00560;PF00595	LRR_1;PDZ
8576	1357			220	IP000384708;IP00 1,1	1,1	1,1	1 Decaprenyl-dipho PDSS2;G6orf210;D Isoform 1 of Deca Q86YH6-1;Q86YH DLP1_HUMAN;B4 ENST0000036903; OTTHUMP000000 NP_065114		
8337	1358			375	IP000385267;IP00 1,1	1,1	1,1	1 Signal recognition SRPR Signal recognition P08240;B4E0H;D SRPR_HUMAN;ENST0000033211; OTTHUMP000002 NP_003130;NP_O	PF04086;PF00448	SRP-alpha_N;SRP1
5120;5256;8792					IP000386271;IP01 3,3	1,1	1,1	1 Calcium-binding n SLC25A12;ARALAF Calcium-binding n Q75746;B3KMV6; CMC1_HUMAN;B; ENST0000026381; OTTHUMP000001 NP_003696	PF00153	Mito_carr
4860					IP000387116	1	1	1 Ig kappa chain V-lII region NG9 Ig kappa chain V-I P01621 KV303_HUMAN ENST00000390255	PF07686	V-set
2614;4945;5001;7		1283			IP00046512;IP00 6,6,6;4,4,3;3,2;1	1,1,1,1,1,0;0,0,0,0	1,1,1,1,1,0;0,0,0,0	1 cDNA FLJ77317; hi RBBP7;RP11-716A histone-binding p1 A8K6A2;Q5J0;Q0 A8K6A2_HUMAN; ENST0000033073; OTTHUMP000000 NP_001185648;NI PF00400	WD40	
8981 1396;1397		86;98			IP000413518;IP00 1,1,1,1	1,1,1,1	1,1,1,1	1 Mirror-image poly MIPO1;hCG_201 Isoform 1 of Mirrc Q8TD10-1;Q8TD1 MIPO1_HUMAN;C ENST0000032744; OTTHUMP000001 NP_001182225;NP_001182226;NP_6	2;60059	
7349		835		459	IP000402014	1	1	1 Zinc finger protein ZNF837 Zinc finger protein Q96F63 ZN837_HUMAN ENST00000282333	NP_001123202;NI PF00096	zf-C2H2
638;667;4835;7833					IP000410067;IP00 4,3,3,3,1	4,3,3,3,1	4,3,3,3,1	1 Zinc finger CCCH-1 ZC3HAV1;ZC3HDC Isoform 1 of Zinc Q722W4-1;Q722V ZCCHV_HUMAN;C ENST0000024235; OTTHUMP000002 NP_064504;NP_O	PF00644;PF00642	PARP;zf-CCCH
4820					IP000414717;IP00 1,1,1	1,1,1	1,1,1	1 Golgi apparatus p1 GLG1;CFR1;ESL1;A Isoform 2 of Golgi Q92896-2;Q9289E GSLG1_HUMAN;B ENST00000205061	NP_003633;NP_O	PF00839
5392		14380		84	IP000418366;IP01 1,1,1,1	1,1,1,1	1,1,1,1	1 Uncharacterized a ADCK5 Uncharacterized a Q3MXK5;B3KS46;E ADCK5_HUMAN ENST0000030886; OTTHUMP000002 NP_777582	PF00319	ABC1
4048					IP000419626;IP00 1,1,1	1,1,1	1,1,1	1 39S ribosomal pro MRPL55;UNQ583; Isoform 2 of 39S r Q727F7-2;Q727F7 RM55_HUMAN ENST0000029500; OTTHUMP000000 NP_852127;NP_8	PF09776	Mitoc_L55
5327					IP000440688;IP00 1,1,1	1,1,1	1,1,1	1 Polymerase delta- POLDP3;KIAA164; cDNA FLJ54030; hi Q9BY77-1;Q9BY7; PDIP3_HUMAN;B ENST0000025211; OTTHUMP000001 NP_115687;NP_8	PF00076	RRM_1
2554					IP000641579;IP00 1,1,1,1	1,1,1,1	1,1,1,1	1 Cold-inducible RN CIRBP;A18HNRNP Cold inducible RN. Q14011;D6W5Y5; CIRBP_HUMAN;B ENST00000320936	NP_00101271	PF00076
3295					IP01021966;IP00 1,1,1,1,1	1,1,1,1,1	1,1,1,1,1	1 Protein canopy ho CNPY2;MSAP;TME 29 kDa protein;isc Q9Y2B0-1;Q9Y2B CNPY2_HUMAN ENST00000273308	NP_055070	
6124					IP000452731	1	1	1 NADH dehydrogen NDUFA7 NADH dehydrogen Q95182;Q3Q214;C NDUAF7_HUMAN ENST00000301457	NP_004992	PF07347
4357;7616					IP000477330;IP01 2,2,1	2,2,1	2,2,1	1 Rho GTPase-activ; ARHGAP11A;KIAA Rho GTPase-activ; Q6P4F7;B4DZN9 RHGBA_HUMAN;J ENST00000336162; OTTHUMP000001 NP_005598;NP_9	PF00620	RhoGAP
7540					IP000480022;IP00 1,1	1,1	1,1	1 Golgin subfamily / GOLGA7;GCP16;H Golgin subfamily / QZ7564 GOGA7_HUMAN ENST0000027653; OTTHUMP000002 NP_0010022596;NI PF101265	Erf4	
2189					IP000549540	1	1	1 p21-activated pro PAK1P1;PIP1;WD p21-activated pro Q9NWT1 PK1IP_HUMAN ENST0000037956; OTTHUMP000000 NP_060376	PF00400	WD40
8646		926			IP000909649;IP00 1,1,1,1,1,1,1,1,1	1,1,1,1,1,1,1,1,1	1,1,1,1,1,1,1,1,1	1 Ig kappa chain V-I IGKC;IGK@ Ig kappa chain C n P06310;Q8TCD0;P KV206_HUMAN;C ENST0000039026; OTTHUMP0000020369; OTTHUMPO PF07686;PF07654	V-set;C1-set	
58;4881;5002;537		1527 930;931;932		164 372;511;609	IP000554711;IP00 7,2,2,1	7,2,2,1	5,2,2,1	1 Junction plakoglobin JUP;CTNNG;DP3 Junction plakoglobin P14923;Q7K286 PLAK_HUMAN ENST0000031070; OTTHUMP000001 NP_002221;NP_O	PF00514;PF02985	ARM;HEAT
8584					IP000983068;IP00 1,1,1,1,1,1,1,1,1,1	1,1,1,1,1,1,1,1,1,1	1,1,1,1,1,1,1,1,1,1	1 Thioredoxin reduc TXNRD1;KDRF Isoform 1 of Thior Q16881-1;Q16881 TRXR1_HUMAN;C ENST0000035494; OTTHUMP000002 NP_001087240;NI PF00462;PF00070	Glutaredoxin;Pyr_	
7827					IP000559902	1	1	1 OCIA domain-cont OCIA2 Isoform 1 of OCIA Q56VL3-1;Q56VL3 OCAD2_HUMAN ENST0000027386; OTTHUMP000002 NP_001014446	PF07051	OCIA
2815					IP000888868;IP00 1,1,1	1,1,1	1,1,1	1 MAM and LDL-rec C10orf112 MAM and LDL-rec Q5VYV5 CI112_HUMAN ENST0000037726; OTTHUMP000002 NP_295865;XP_94	PF00057;PF00629	Ldl_recept_a;MAM
2215					IP000642584;IP00 1,1,1,1	1,1,1,1	1,1,1,1	1 Uncharacterized p KIAA0090;P5E02; Isoform 1 of Unch Q8N766-1;Q8N76 K0090_HUMAN ENST0000037519; OTTHUMP000000 NP_055862	PF07774	DUF1620
661;916;3495;385 1548;1549		127;615			IP000643152;IP00 9,9,9;9,7,7;5	1,1,1,1,1,1,0	1,1,1,1,1,1,0	1 cDNA FLJ56386; hi HSPAL1;DAAP-2IF cDNA FLJ56386; hi B4D154;P34931;B; B4D154_HUMAN;J ENST0000038318; OTTHUMP000000 NP_005518	PF00012	HSP70
990;1379;2691;3614;3650;5259;8490					IP000644431;IP00 7,7,4,3	1,1,1,1	1,1,1,1	1 cDNA FLJ55484; hi DDX39;hCG_1776; cDNA FLJ55484; hi B4DX78;O00148;C B4DX78_HUMAN; ENST00000242776;ENST0000032434 NP_005795	PF00128;PF00271	DEAD;Helicase_C
IP000644775					1	1	1	1 Exosome complex EXOSC5;CML28;Rf Exosome complex Q9NQ74;B2RC05 EXOS5_HUMAN ENST00000221233	NP_064543	
2677;4466		1570		538	IP000647217;IP01 2,2,1,1,1,1,1,1,1,1	2,2,1,1,1,1,1,1,1,1	1,1,0,0,0,0,0,0,0,0	1 Superkiller viralici SKIV2L2;KIAA0052 Superkiller viralici P42285;A8K614;B4 SK2L2_HUMAN;S ENST0000023064; OTTHUMP000001 NP_056175;NP_O	PF00270;PF01814	DEAD;SHCT;Helic
4734					IP000654820	1	1	1 ATP synthase subu MT-ATP6;ATP6;A1 ATP synthase subu P00846;A0S070;A1 ATP6_HUMAN ENST00000361899;ENST0000040900 NP_003024031	PF00119	ATP_synth_A
8631					IP000877726;IP00 1,1,1,1,1,1,1	1,1,1,1,1,1,1	1,1,1,1,1,1,1	1 Creatine kinase, u CKMT1A;CKMT;CK Isoform 2 of Creat P12532-2;P12532; KCRU_HUMAN;B4 ENST0000030028; OTTHUMP000000 NP_001015001;NI PF00217;PF02807	ATP_gua_Vtrans;A	
65;267;687;688;5294;7204;8735 496;497		158;217			IP000887169;IP00 7,7,1	1,1,1	1,1,1	1 Putative uncharac IGLV1-40;V1-13 Putative uncharac Q8NE11;Q5NV69;I Q8NE11_HUMAN; ENST0000039029; OTTHUMP0000019960	PF07654;PF07686	C1-set;V-set
7937	1575			35	IP00719622	1	1	1 40S ribosomal pro RPS28 40S ribosomal pro P62857;B2R4R9 R528_HUMAN	NP_001022	PF01200
1334	1576			1052	IP000739565	1	1	1 Protein unc-13 ho UNC13C Protein unc-13 ho Q8N866 UN13C_HUMAN ENST00000260323	NP_001074003	PF00130;PF00168
5342					IP01014660;IP00 1,1,1	1,1,1	1,1,1	1 MRPS17 protein;2 MRPS17;RPM517; 28S ribosomal pro Q8IY71;Q9Y2R5;E Q8IY71_HUMAN;J ENST0000028529; OTTHUMP000002 NP_057053	PF03666	Ribosomal_S17
5642 1584;1585		961 224;238		241	IP000749406	1	1	1 SPRY domain-cont SPSB1;SSB1 SPRY domain-cont Q96BDE SPSB1_HUMAN ENST0000032808; OTTHUMP000000 NP_079382	PF07525;PF00622	SOCS_box;SPRY
7365	1604			201	IP000784044;IP00 1,1,1,1	1,1,1,1	1,1,1,1	1 Methylocrotonoyl-C MCCB2;MCCB Isoform 1 of Meth Q9HCC0-1;Q9HCC MCCB_HUMAN;B; ENST0000032337; OTTHUMP000002 NP_071415	PF01039	Carboxyl_trans
5635 1650;1651		344;349			IP000844508;IP00 1,1	1,1	1,1	1 Cingulin CGN;KIAA1319 cingulin;isoform 2 Q9P2M7-1;Q9P2A CING_HUMAN ENST0000027163; OTTHUMP000000 NP_065821	PF01576	Myosin_tail_1
6875		1001;1002;1003;1004		37;40;51;54	IP000924727;IP00 1,1,1	1,1,1	1,1,1	1 Tensin 3 variant; TNS3;TEM6;TENS1 Uncharacterized p E9PCX8;Q596W4;Q Q596W4_HUMAN ENST0000031161; OTTHUMP0000020218; OTTHUMPO	PF00130;PF10409	C1_1;PTEN_C2;PT
7815					IP000873586	1	1	1 Serine/threonine- SAPS1;KIAA1115;F Serine/threonine- Q9UPN7;Q96ID3 SAPS1_HUMAN ENST00000327021	NP_055746	PF04499
4785					IP000885036	1	1	1 Endonuclease/exc EEPD1;KIAA1706 Endonuclease/exc; Q7L9B9 EEPD1_HUMAN ENST0000024210; OTTHUMP000002 NP_085139	PF03372;PF00633	Exo_endo_phos;H
1014;4336;6685;8853					IP000893541	4	1	1 14 kDa protein OTTHUMP00000199630		
654;1039;1140;1903;2895		138			IP000909039	5	1	1 cDNA FLJ53671; highly similar to Inte cDNA FLJ53671; hi B4DW82;E7ESS4 B4DW82_HUMAN ENST00000264832	PF03921	ICAM_N
3624					IP000910967	1	1	1 cDNA FLJ53093; moderately similar t cDNA FLJ53093; m B4DSH6 B4DSH6_HUMAN	PF00153	Mito_carr
3565					IP000942269;IP00 1,1,1	1,1,1	1,1,1	1 TBC1 domain fami TBC1D4;AS160;K1J TBC1 domain fami Q60343-1;Q60343 TBCD4_HUMAN ENST0000037763; OTTHUMP000000 NP_055647	PF00640;PF00566	PI0;TBC
1890;3153;3689;4045;4148;6007;667; 133;134		333;385			IP000939159	8	1	1 Adenyllyl cyclase-a CAP1;RP11-11507 Adenyllyl cyclase-a B4DNA3;B4DUZ8; B4DNA3_HUMAN ENST0000034045; OTTHUMP00000004831	PF08603;PF01213	CAP_C;CAP_N
1408;3029;3108;3 222;223		21;46			IP000978180;IP00 6,1	1,1	1,1	1 RPS10-NUDT3 protein RPS10-NUDT3 protein	NP_001189399	
260		1023			IP000983620	115	1	1 peptidyl-lyl cys-trans Isomerase A-like XP_001129774		
6633		1029			IP00100010194; 1,1,1,1,1	1,1,1,1,1	1,1,1,1,1	1 Probable protein -PORCN;MG61		

6142		1030		1879	REV_IP1000873991;1;1;1;1	1;1;1;1	1;1;1;1	Dynein heavy chain DNAH8	>IP1:REV_IP100087:Q96JB1-1;Q96JB1_DYH8_HUMAN	ENST0000032747:OTTHUMP0000017872;OTTHUMPO	PF07728;PF08385,AAA_5,DHC_N1;D			
6563	1685;1686		914;917		REV_IP100030915;1;1	1;1	1;1	Ubiquitin carboxyl USP8;KIAA0055;U	>IP1:REV_IP100030:P40818;ABK8N5;CUBP8_HUMAN;B3	ENST0000030717:OTTHUMP000001	NP_001122082;NP_P08969;PF00581,DUF1873;Rhodan			
3685;5575	1687		972		REV_IP100065931;2;2;2;2;2;1;1	2;2;2;2;2;1;1	2;2;2;2;2;1;1	A-kinase anchor p AKAP13;BRX;HT31	>IP1:REV_IP100065:Q12802-2;Q12802_AKP13_HUMAN	ENST00000361243;ENST0000039451	NP_006729;NP_01_P00130;PF00169,C1_1,PH;RhoGEF;			
4178		1031		963	REV_IP100073196;1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Latent-transformer LTBP3;hCG_18126	>IP1:REV_IP100073:Q9NS15-1;Q9NS15_LTBP3_HUMAN;B	ENST0000030187:OTTHUMP000002	NP_001123616;NP_P00008;EGF;EGF_CA;TB			
6000	1688		191		REV_IP1000217052;1;1;1;1;1;1;1;1	1;1;1;1;1;1;1;1	1;1;1;1;1;1;1;1	Neuron navigator NAV2;HELAD1;KIA	>IP1:REV_IP100021:Q8IVL1-1;Q8IVL1_NAV2_HUMAN	ENST0000031104:OTTHUMP000002	NP_892009;NP_P000307	CH		
8486	1689		2007		REV_IP100164352;1;1	1;1	1;1	Zinc finger protein ZNF292;KIAA0530	>IP1:REV_IP100164:O60281-1;O60281_ZNF292_HUMAN	ENST0000033990:OTTHUMP000002	NP_055836	PF00096	zf-C2H2	
6643	1690		14		REV_IP100167913;1;1	1;1	1;1	Spermatid-associat SPERT;CBY2	>IP1:REV_IP100167:Q8NA61-1;Q8NA61_SPERT_HUMAN	ENST0000031052:OTTHUMP000000	NP_689932			
2428	1691	1032;1033	2695	2697;2702	REV_IP1000329784;1;1;1;1	1;1;1;1	1;1;1;1	Ryanodine receptor RYR3;HBRR	>IP1:REV_IP100032:Q15413-1;Q15413_RYR3_HUMAN	ENST00000389232	NP_001027	PF00036;PF08709	efhand;ins145_P3	
3332		1034		270	REV_IP1000217975;1;1;1	1;1;1	1;1;1	Lamin-B1;LMNB1 LMNB1;LMNB2;LMI	>IP1:REV_IP100021:P20700;B4DZT3;E:LMNB1_HUMAN;X	ENST0000026136:OTTHUMP000001	NP_005564;NP_01_P00038;PF00932	Filament;IF_tail		
6133		1035		32	REV_IP1000289243;1;1;1;1;1	1;1;1;1;1	1;1;1;1;1	Muscle, skeletal re MUSK	>IP1:REV_IP100028:O15146-1;O15146_MUSK_HUMAN	ENST0000037444:OTTHUMP000000	NP_005583;NP_01_P01392;PF07679	Fz1-set;Pkinase_T		
5882					REV_IP100298912;1;1	1;1	1;1	Coronin-2B;Coron COR02B;KIAA092	>IP1:REV_IP100298:Q9UQ03-1;Q9UQ03_COR2B_HUMAN	ENST0000026186:OTTHUMP000001	NP_006082;NP_01_P08953;PF08954	DUF1899;DUF1901		
6135	1692		63		REV_IP100382434	1	1	Ig lambda chain V-II region WIN	>IP1:REV_IP100382:P01712	LV209_HUMAN		PF07686	V-set	
8701	1693	1037	542	534	REV_IP100455518;1;1	1;1	1;1	MORC family CW-MORC2;KIAA0852	>IP1:REV_IP100455:Q9Y6X9;B2RNB1	MORC2_HUMAN;X	ENST0000039764:OTTHUMP000001	NP_055756	PF02518;PF07496	HATPase_czf-CW
3566					REV_IP100456737;1;1;1	1;1;1	1;1;1	DENN domain-cor DENN5A;KIAA10	>IP1:REV_IP100456:Q6IQ26;B4D115;B	DENSA_HUMAN;E	ENST0000032819:OTTHUMP000002	NP_056028	PF03455;PF02141	dDENN;DENN;PLA
1414	1695		570		REV_IP1000783017;1;1;1;1	1;1;1;1	1;1;1;1	Zinc finger E-box-1 ZEB2;KIAA0569;SI	>IP1:REV_IP100078:O60315;A0IP08;B	ZEB2_HUMAN;Q5	ENST0000030366:OTTHUMP000001	NP_055610;NP_01_P00096	zf-C2H2	
3201					REV_IP1000871834;1;1	1;1	1;1	Dystrophin-relatei DRP2	>IP1:REV_IP100087:Q13474;B4DIZ0;Q	DRP2_HUMAN;B4	ENST0000039520:OTTHUMP000000	NP_001930;NP_01_P09068;PF09069	efhand_1;efhand_	
4010					REV_IP1000917179	1	1		>IP1:REV_IP100091:C9JGH7		OTTHUMP00000204395			
4184	1696;1697		1038	19;26	REV_IP1000974301	1	1		>IP1:REV_IP100097:ESR12		OTTHUMP00000224385			
8137	1698		190		REV_IP100084112	1	1		>IP1:REV_IP100084112.1 REFSEQ_XP_003119890	Tax_Id=9606	Gene_Symbol=	putative ubiqi XP_003119890		

Pfam Description: GOCC	GOCC Names	GOMF	GOMF Names	GOBP	GOBP Names	KEGG	KEGG Pathways	KEGG Pathway No	KEGG Ortholog	Proteins	Peptides (seq)	Peptides (seq/mo	Peptides (seq/mo	Razor Peptides (si	Razor Peptides (si	Razor Peptides (si	Unique Peptides (
C2 domain;PH dor	GO:0005886;GO:0 plasma membrani	GO:0003824;GO:0 catalytic activity;1	GO:0006629;GO:0 lipid metabolic pn	hsa:5336	ko00562;ko04012	Inositol phosphat	K05859	1	50	53	54	50	53	54	49		
Protein tyrosine k	GO:0000242;GO:0 pericentriolar mat	GO:0000166;GO:0 nucleotide binding	GO:0001775;GO:0 cell activation;jm	hsa:3932	ko04650;ko04660	Natural killer cell i	K05856	8	7	7	5	5	5	5	5		
Protein tyrosine k	GO:0005794;GO:0 Golgi apparatus;p	GO:0000166;GO:0 nucleotide binding	GO:0002253;GO:0 activation of immu	hsa:4067	ko04662;ko04664	B cell receptor sig	K05854	2	20	21	22	20	21	22	1		
eIF3 subunit 6 N 1	GO:0005654;GO:0 nucleoplasm;cyto	GO:0003676;GO:0 nucleic acid bindir	GO:0000184;GO:0 nuclear-transcribe	hsa:3646			K03250	3	2	2	2	2	2	2	2		
Dnal domain;Dnal	GO:0005737;GO:0 cytoplasm;cytoske	GO:0005102;GO:0 receptor binding;1	GO:0006457;GO:0 protein folding;re	hsa:3301			K09502	12	8	8	10	8	8	10	8		
Eukaryotic transla	GO:0005829;GO:0 cytosol;eukaryotic	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:8664			K03251	6	2	2	2	2	2	2	2		
Ras family	GO:0000323;GO:0 lytic vacuole;lysos	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;endocyt	hsa:7879			K07897	7	5	5	6	5	5	6	5		
short chain dehyd	GO:0005739;GO:0 mitochondrion;pl	GO:0003824;GO:0 catalytic activity;3	GO:0006139;GO:0 nucleobase, nucle	hsa:3028	ko00280;ko05010	Valine, leucine ani	K08683	3	10	11	18	10	11	18	10		
RhoGAP domain;S	GO:0005942;GO:0 phosphoinositide	GO:0005102;GO:0 receptor binding;j	GO:0006629;GO:0 lipid metabolic pn	hsa:5295	ko04012;ko04370	ErbB signaling pat	K02649	18	20	23	19	19	21	19			
Diaphanous FH3 C	GO:0005737;GO:0 cytoplasm;intrace	GO:0003779;GO:0 actin binding;bind	GO:0006996;GO:0 organelle organiz	hsa:23002	ko04310	Wnt signaling pat	K04512	3	2	2	2	2	2	2	2		
Signal recognition	GO:0005785;GO:0 signal recognition	GO:0003676;GO:0 nucleic acid bindir	GO:0006417;GO:0 regulation of tran	hsa:653226	ko03060	Protein export	K03109	3	4	5	9	4	5	9	4		
GrpE	GO:0005759;GO:0 mitochondrial ma	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;im	hsa:134266			K03687	2	5	5	8	5	5	8	5		
K+ channel tetra	GO:0008076;GO:0 voltage-gated pot	GO:0005215;GO:0 transporter activit	GO:0006810;GO:0 transport;ion tran	hsa:200845				2	3	3	3	3	3	3	3		
Actin;Ankyrin rep	GO:0005737;GO:0 cytoplasm;cytoske	GO:0000166;GO:0 nucleotide binding;nucleoside binding;purine nucleosic	hsa:445582					22	7	8	16	1	1	2	1		
Anticodon-binding	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:51520	ko00290;ko00970	Valine, leucine ani	K01869	7	10	10	10	10	10	10	10		
Maf-like protein;c	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;n	GO:0006519;GO:0 cellular amino aci	hsa:8623				6	4	4	5	4	4	5	4		
		GO:0005814;GO:0 centriole;organel	GO:0005488;GO:0 binding;protein bi	hsa:116840				4	1	1	2	1	1	2	1		
Double stranded RNA binding protein (DUF2051)		GO:0005488;GO:0 binding;protein bi	GO:0007154;GO:0 cell communication;signal transduction;cell surface receptor linked signal transduction;cellul					6	5	5	5	5	5	5	4		
Proteasome A-ty	GO:0005634;GO:0 nucleus;cytosol;p	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5683	ko03050	Proteasome	K02726	5	7	7	9	7	7	9	7		
Histone deacetyla	GO:0000118;GO:0 histone deacetyla	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:3066;hsa:3061;ko04330;ko04110		Notch signaling ps	K06067	15	2	2	2	2	2	2	2		
DEAD/DEAH box F	GO:0005737;GO:0 cytoplasm;plasma	GO:0000166;GO:0 nucleotide binding	GO:0004419;GO:0 interspecies interi	hsa:1654;hsa:100130220;hsa:8653			K11594	13	11	11	13	11	11	13	10		
Ribosomal protein	GO:0005730;GO:0 nucleolus;cytosol;	GO:0003676;GO:0 nucleic acid bindir	GO:0006414;GO:0 translational elon	hsa:6133	ko03010	Ribosome	K02940	13	9	9	17	9	17	9	9		
Insulinase (Peptid	GO:0005743;GO:0 mitochondrial inn	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;metab	hsa:23203			K01412	3	3	3	3	3	3	3	3		
14-3-3 protein	GO:0005737;GO:0 cytoplasm;intrace	GO:0005102;GO:0 receptor binding;j	GO:0006629;GO:0 lipid metabolic pn	hsa:7533	ko04110	Cell cycle	K06630	2	6	7	13	2	2	3	2		
Dynamin family	GO:0005886;GO:0 plasma membrani	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;endocyt	hsa:10938;hsa:30845				12	6	6	6	6	6	6	6		
								4	9	9	10	1	1	2	1		
IQ calmodulin-bin	GO:0001725;GO:0 stress fiber;ruffl	GO:0000146;GO:0 microfilament mo	GO:0000910;GO:0 cytokinesis;angio	hsa:4627	ko04530	Tight junction	K10352	19	168	199	273	168	199	273	140		
Core histone H2A	GO:0000786;GO:0 nucleosome;nucle	GO:0003676;GO:0 nucleic acid bindir	GO:0006325;GO:0 chromatin organiz	hsa:121504;hsa:5	ko05322	Systemic lupus er	K11254	1	5	5	7	5	5	7	5		
EF hand	GO:0016459;GO:0 myosin complex;n	GO:0003774;GO:0 motor activity;catalytic activity;binding;calcium ion bin	hsa:10627		ko04810;ko04510	Regulation of acti	K10351	1	12	18	32	1	18	32	1		
Leucine Rich Repe	GO:0005604;GO:0 basement membr	GO:0005488;GO:0 binding;protein bi	GO:0006996;GO:0 organelle organiz	hsa:55914				10	5	5	5	5	5	5	5		
tRNA synthetases	GO:0000267;GO:0 cell fraction;solub	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:1615	ko00252;ko00970	Alanine and aspar	K01876	20	20	20	28	20	28	20	20		
PCI domain;Prote	GO:0000502;GO:0 proteasome comp	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5709	ko03050	Proteasome	K03033	3	5	5	5	5	5	5	5		
Cation transportin	GO:0000267;GO:0 cell fraction;meml	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucleoside, nucleotide and nucleic acid metabolic process;purine nucleotide me					17	5	5	5	5	5	5	5		
Elongation factor	GO:0009295;GO:0 nucleoid;mitochoi	GO:0000166;GO:0 nucleotide binding	GO:0006414;GO:0 translational elon	hsa:7284			K02358	1	20	20	36	20	20	36	20		
Elongation factor	GO:0005853;GO:0 eukaryotic transla	GO:0003676;GO:0 nucleic acid bindir	GO:0006414;GO:0 translational elon	hsa:1937			K03233	6	19	19	33	19	19	33	19		
Protein of unknown function (DUF1151)								6	2	2	3	2	2	3	2		
BAG domain		GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;ap	hsa:9532			K09556	3	5	5	9	5	5	9	5		
BRCA1 C Termin	GO:0005635;GO:0 nuclear envelope;	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:142	ko03410	Base excision repa	K10798	2	5	5	5	5	5	5	5		
B3/4 domain;TRN	GO:0000267;GO:0 cell fraction;solub	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:10056	ko00400;ko00970	Phenylalanine, tyr	K01890	6	11	11	13	11	11	13	11		
SPRY domain;B-bc	GO:0005737;GO:0 cytoplasm;intrace	GO:0005488;GO:0 binding;protein bi	GO:0006461;GO:0 protein complex a	hsa:89122			K11998	5	1	1	2	1	1	2	1		
SH2 domain;SH3 c	GO:0005794;GO:0 Golgi apparatus;c	GO:0004871;GO:0 signal transducer	GO:0007154;GO:0 cell communicati	hsa:2885	ko04010;ko04013	MAPK signaling ps	K04364	2	7	7	12	7	7	12	7		
		GO:0000796;GO:0 condensin comple	GO:0005488;GO:0 binding;protein bi	hsa:64151	ko04111	Cell cycle - yeast	K06678	3	8	8	8	8	8	8	8		
LSM domain	GO:0005654;GO:0 nucleoplasm;splic	GO:0003676;GO:0 nucleic acid bindir	GO:0000387;GO:0 spliceosomal snR	hsa:6628;hsa:6631;ko05322		Systemic lupus er	K11086;K11100	7	6	6	11	6	6	11	6		
Ras family	GO:0005622;GO:0 intracellular;mem	GO:0000166;GO:0 nucleotide binding	GO:0007154;GO:0 cell communicati	hsa:998	ko04010;ko04011	MAPK signaling ps	K04393	13	5	5	5	5	5	5	4		
Polyprenil synthetase		GO:0005488;GO:0 binding;protein bi	GO:0006629;GO:0 lipid metabolic pn	hsa:23590				7	4	4	6	4	4	6	4		
Ras family	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0007154;GO:0 cell communicati	hsa:5880;hsa:5871;ko04010;ko04310		MAPK signaling ps	K07860;K04392;K1	7	4	4	4	3	3	3	3		
Double-stranded I	GO:0005730;GO:0 nucleolus;mitoch	GO:0003676;GO:0 nucleic acid bindir	GO:0000279;GO:0 M phase;nucleob	hsa:3609				8	10	10	10	10	10	10	9		
RNA recognition n	GO:0005654;GO:0 nucleoplasm;cyto	GO:0000166;GO:0 nucleotide binding	GO:0000387;GO:0 spliceosomal snR	hsa:22916				5	2	2	2	2	2	2	2		
				hsa:90624				3	3	3	5	3	3	5	3		
	GO:0005737;GO:0 cytoplasm;integral to membrane;intrinsic to membrane	GO:0006810;GO:0 transport;cellular	hsa:29091				K08519	3	1	1	1	1	1	1	1		
MCM2/3/5 family	GO:0005654;GO:0 nucleoplasm;orga	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4174	ko03030;ko04110	DNA replication;C	K02209	7	5	5	5	5	5	5	5		
Casein kinase substrate phosphoprotein PP28		GO:0007154;GO:0 cell communicati	hsa:11333					2	5	5	9	5	5	9	5		
Ankyrin repeat	GO:0005737;GO:0 cytoplasm;intrace	GO:0004871;GO:0 signal transducer activity;binding;protein binding;mole	hsa:4659		ko04810;ko04510	Regulation of acti	K06270	16	25	25	31	25	25	31	24		
Cullin family;Cullin	GO:0005654;GO:0 nucleoplasm;cyto	GO:0005488;GO:0 binding;protein bi	GO:0000082;GO:0 G1/S transition of	hsa:8454	ko04120;ko04310	Ubiquitin mediate	K03347	3	17	17	18	17	17	18	17		
ATPase family ass	GO:0000502;GO:0 proteasome comp	GO:0000166;GO:0 nucleotide binding	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5700	ko03050	Proteasome	K03062	3	3	3	3	3	3	3	3		
CBS domain pair;P	GO:0005730;GO:0 nucleolus;cytosol;	GO:0003824;GO:0 catalytic activity;e	GO:0000096;GO:0 sulfur amino aci	hsa:875	ko00260;ko00271	Glycine, serine ani	K01697	7	7	7	8	7	7	8	7		
Tubulin/FtsZ fami	GO:0005874;GO:0 microtubule;orga	GO:0000166;GO:0 nucleotide binding	GO:0001906;GO:0 cell killing;leukocy	hsa:203068;hsa:7	ko04540	Gap junction	K07375	17	23	26	46	23	26	46	5		
	GO:0016592;GO:0 mediator complex	GO:0000166;GO:0 nucleotide binding	GO:0006352;GO:0 transcription initia	hsa:9967				2	2	2	2	2	2	2	2		
NUDIX domain	GO:0005813;GO:0 centrosome;micrc	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:11051				2	3	3	3	3	3	3	3		
Cullin family;Cullin	GO:0000151;GO:0 ubiquitin ligase cc	GO:0005488;GO:0 binding;protein bi	GO:0000082;GO:0 G1/S transition of	hsa:8452	ko04120	Ubiquitin mediate	K03869	4	6	6	6	6	6	6	6		
MCM2/3/5 family	GO:0000785;GO:0 chromatin;cytopl	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4176	ko03030;ko04110	DNA replication;C	K02210	3	13	13	13	13	13	13	13		
Insulinase (Peptid	GO:0005743;GO:0 mitochondrial inn	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;metab	hsa:9512			K01412	3	4	4	5	3	3	3	3		
Nuclear transport	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;cell com	hsa:9908				18	3	3	2	2	2	2	2		
2'-5'-oligoadenyla	GO:0000267;GO:0 cell fraction;meml	GO:0000166;GO:0 nucleotide binding	GO:0002376;GO:0 immune system process;immune response;response to stimulus;nucleobase, nucleoside, nuc					10	2	2	2	2	2	2	2		

14-3-3 protein	GO:0005634;GO:0 nucleus;centrosom	GO:0005488;GO:0 binding;protein bi	GO:0006355;GO:0 regulation of tran	hsa:10971	ko04110	Cell cycle	K06630	3	13	14	23	10	15	8
Histidine kinase	GO:0005739;GO:0 mitochondrion	GO:0001166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;re	hsa:10131			K09488	2	8	8	8	8	8	8
RNA recognition	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via t	hsa:343069				14	6	7	6	6	7	6
Armadillo/beta-ca	GO:0005643;GO:0 nuclear pore;nuclei	GO:0005048;GO:0 signal sequence b	GO:0000018;GO:0 regulation of DNA	hsa:3838;hsa:728860				1	2	2	2	2	2	2
Serine hydroxyme	GO:0009295;GO:0 nucleoid;mitochoi	GO:0003824;GO:0 catalytic activity;g	GO:0006082;GO:0 organic acid meta	hsa:6472	ko00680;ko00260	Methane metabol	K00600	13	15	15	20	15	15	20
Elongation factor	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006412;GO:0 translation;regula	hsa:9669				1	12	12	14	12	14	12
Respiratory-chain	GO:0005747;GO:0 mitochondrial res	GO:0000166;GO:0 nucleotide binding	GO:0006091;GO:0 generation of pre	hsa:4723	ko00190;ko05010	Oxidative phosph	K03942	5	2	2	2	2	2	2
Exs8;Glutamine ar	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:8833	ko00230;ko00251	Purine metabolis	K01951	3	7	7	9	7	9	7
ATP synthase alph	GO:0005753;GO:0 mitochondrial pro	GO:0000166;GO:0 nucleotide binding	GO:0001936;GO:0 regulation of end	hsa:498	ko00190;ko05010	Oxidative phosph	K02132	3	31	32	51	31	32	51
MutS domain 1;M	GO:0032300;GO:0 mismatch repair c	GO:0000166;GO:0 nucleotide binding	GO:0000018;GO:0 regulation of DNA	hsa:4436	ko03430;ko05200	Mismatch repair;P	K08735	11	5	5	6	5	6	5
GO:0000797;GO:0 condensin core he	GO:0005488;GO:0 binding;protein bi	GO:0006323;GO:0 DNA packaging;organelle organization;mitotic chromosome condensation;cellular process;ce						4	2	2	2	2	2	2
Insulinase (Peptid	GO:0005746;GO:0 mitochondrial res	GO:0003824;GO:0 catalytic activity;e	GO:0006091;GO:0 generation of pre	hsa:7384	ko00190;ko04260	Oxidative phosph	K00414	2	11	11	16	11	11	16
Nuclear transport	GO:0005634;GO:0 nucleus;cytosol;pl	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;cell com	hsa:10146				4	3	3	4	3	3	4
Protein kinase dor	GO:0005794;GO:0 Golgi apparatus;c	GO:0000166;GO:0 nucleotide binding	GO:0006928;GO:0 cell motion;chem	hsa:5604;hsa:5601;ko04010;ko04013	MAPK signaling pa	K04368;K04369		5	2	2	3	2	2	3
tRNA synthetases	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:5859	ko00251;ko00970	Glutamate metab	K01886	6	19	19	21	19	19	21
CAS/CSE protein,	GO:0005643;GO:0 nuclear pore;cyto	GO:0005049;GO:0 nuclear export sig	GO:0000059;GO:0 protein import int	hsa:1434				8	16	16	16	16	16	16
Zinc knuckle	GO:0005783;GO:0 endoplasmic retic	GO:0003676;GO:0 nucleic acid bindir	GO:0006066;GO:0 alcohol metabolic	hsa:7555			K09250	8	5	5	8	5	5	8
Tetrapeptide	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0007517;GO:0 muscle organ dev	hsa:55898				5	18	18	18	18	18	18
14-3-3 protein	GO:0016023;GO:0 cytoplasmic mem	GO:0005488;GO:0 binding;protein bi	GO:0007154;GO:0 cell communicati	hsa:7531	ko04110	Cell cycle	K06630	10	13	14	26	13	14	26
PCI domain	GO:0005829;GO:0 cytosol;proteasom	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5718	ko03050	Proteasome	K03035	2	5	6	5	5	6	5
Proteasome A-typ	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5684	ko03050	Proteasome	K02727	2	4	4	5	4	4	5
Nucleosome asser	GO:0005678;GO:0 chromatin assem	GO:0005488;GO:0 binding;protein bi	GO:0006139;GO:0 nucleobase, nucle	hsa:4673			K11279	5	5	6	5	5	6	5
HEAT repeat	GO:0005643;GO:0 nuclear pore;nuclei	GO:0004857;GO:0 enzyme inhibitor	GO:0000059;GO:0 protein import into nucleus, docking;protein complex assembly;protein targeting;protein imp					21	17	17	20	17	17	20
Acylphosphatase	GO:0003824;GO:0 catalytic activity;a	GO:0006793;GO:0 phosphorus metal	hsa:98		ko00620;ko00632	Pyruvate metabol	K01512	3	6	6	12	6	6	12
Amino acid kinase	GO:0005743;GO:0 mitochondrial inn	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:5832	ko00330	Arginine and proli	K00147;K00931	24	25	27	24	25	27	24
ARP2/3 complex 2	GO:0005737;GO:0 cytoplasm;Arp2/3	GO:0003779;GO:0 actin binding;bind	GO:0006461;GO:0 protein complex assembly;organelle organization;cytoskeleton organization;actin filament or					8	4	4	8	4	4	8
Protein phosphat	GO:0000159;GO:0 protein phosphat	GO:0005488;GO:0 binding;protein bi	GO:0007154;GO:0 cell communicati	hsa:5528	ko04310	Wnt signaling pat	K11584	5	2	2	2	2	2	2
Septin	GO:0000776;GO:0 kinetochore;cond	GO:0000166;GO:0 nucleotide binding	GO:0000280;GO:0 nuclear division;c	hsa:989				11	11	11	12	11	11	12
RNA recognition r	GO:0005686;GO:0 t2 snRNP;ribonuc	GO:0000166;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via t	hsa:6629			K11094	1	6	10	5	5	8	5
Proteasome A-typ	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5691	ko03050	Proteasome	K02735	1	5	5	5	5	8	5
Glutathione S-tran	GO:0005737;GO:0 cytoplasm;plasma	GO:0000049;GO:0 tRNA binding;nuclei	GO:0006082;GO:0 organic acid meta	hsa:4141	ko00271;ko00450	Methionine metal	K01874	15	11	11	11	11	11	11
Citrate synthase	GO:0005759;GO:0 mitochondrial ma	GO:0003824;GO:0 catalytic activity;g	GO:0005975;GO:0 carbohydrate met	hsa:1431	ko00020;ko00630	Citrate cycle (TCA	K01647	4	17	4	6	4	4	6
Initiation factor eI	GO:0005829;GO:0 cytosol;intracellul	GO:0000166;GO:0 nucleotide binding	GO:0006413;GO:0 translational initia	hsa:1968				4	10	10	13	10	10	13
Brain acid soluble	GO:0005856;GO:0 cytoskeleton;plasma membrane;membrane-bounded organelle;intracellu	hsa:10409						2	2	2	3	2	2	3
GrpE	GO:0005759;GO:0 mitochondrial ma	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;pn	hsa:80273			K03687	2	3	3	4	3	3	4
Mov34/MPN/PAD	GO:0000502;GO:0 proteasome comp	GO:0003824;GO:0 catalytic activity;g	GO:0006464;GO:0 protein modificati	hsa:10213	ko03050	Proteasome	K03030	1	2	2	2	2	2	2
Actin	GO:0005737;GO:0 cytoplasm;cytoske	GO:0000166;GO:0 nucleotide binding;nucleoside binding;purine nucleosic	hsa:345651					1	12	17	25	1	1	1
Dynein light chain	GO:0005829;GO:0 cytosol;microtubu	GO:0003774;GO:0 motor activity;mic	GO:0007017;GO:0 microtubule-base	hsa:140735			K10418	1	6	6	9	6	9	4
Tubulin/FtsZ fami	GO:0005874;GO:0 microtubule;macr	GO:0000166;GO:0 nucleotide binding	GO:0006461;GO:0 protein complex a	hsa:7277	ko04540	Gap junction	K07374	6	16	19	32	4	7	2
Alcohol dehydrog	GO:0005739;GO:0 mitochondrion;or	GO:0003824;GO:0 catalytic activity;a	GO:0006066;GO:0 alcohol metabolic	hsa:128	ko00010;ko00071	Glycolysis / Gluco	K00001;K00121	3	4	4	6	4	4	6
Phosphoglycerate	GO:0005634;GO:0 nucleus;cytoplasm;organelle;membrane-bounded organelle;intracellu	hsa:192111						3	2	2	2	2	2	2
Isocitrate/isoprop	GO:0005759;GO:0 mitochondrial ma	GO:0000166;GO:0 nucleotide binding	GO:0003008;GO:0 system process;or	hsa:3420	ko00020	Citrate cycle (TCA	K00030	5	3	3	3	3	3	3
Domain of unknow	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:1665				2	6	6	7	6	6	7
DEAD/DEAH box t	GO:0005029;GO:0 ribonucleoprotein	GO:0000166;GO:0 nucleotide binding	GO:0000245;GO:0 spliceosome asser	hsa:1653				2	6	6	6	6	6	6
Formate--tetrahy	GO:0005739;GO:0 mitochondrion;or	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:25902	ko00630;ko00670	Glyoxylate and dic	K00288;K01491;K1	11	18	18	26	18	18	26
eIF-6 family	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003676;GO:0 nucleic acid bindir	GO:0006412;GO:0 translation;metab	hsa:3692			K03264	6	5	5	9	5	5	9
Dehydrogenase E	GO:0005739;GO:0 mitochondrion;or	GO:0003824;GO:0 catalytic activity;g	GO:0005975;GO:0 carbohydrate met	hsa:4967	ko00020;ko00310	Citrate cycle (TCA	K00164	10	8	8	8	8	8	8
Clamp-loader com	GO:0005654;GO:0 nucleoplasm;DNA	GO:0000166;GO:0 nucleotide binding	GO:0000731;GO:0 DNA synthesis du	hsa:5983	ko03030;ko03420	DNA replication;N	K10756	2	2	2	2	2	2	2
K+ channel tetram	GO:0008076;GO:0 voltage-gated pot	GO:0005215;GO:0 transporter activit	GO:0006810;GO:0 transport;ion tran	hsa:54793				2	2	2	2	2	2	2
Tubulin/FtsZ fami	GO:0032991;GO:0 macromolecul c	GO:0000166;GO:0 nucleotide binding	GO:0006461;GO:0 protein complex a	hsa:7846;hsa:113;ko04540	Gap junction	K07374		3	20	23	36	20	23	36
Importin-beta N-t	GO:0005643;GO:0 nuclear pore;cyto	GO:0005215;GO:0 transporter activit	GO:0000059;GO:0 protein import int	hsa:55705				1	2	2	2	2	2	2
Diaphanous FH3 t	GO:0005737;GO:0 cytoplasm;intrace	GO:0003779;GO:0 actin binding;bind	GO:0006996;GO:0 organelle organiz	hsa:752				4	4	4	4	4	4	4
D-isomer specific 2-hydroxyacid dehydrogenase, cataly	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:26227		ko00260	Glycine, serine ani	K00058	4	11	11	18	11	11	18
Aminopeptidase 1	GO:0005773;GO:0 vacuole;organelle	GO:0003824;GO:0 catalytic activity;a	GO:0006508;GO:0 proteolysis;peptid	hsa:23549			K01267	12	23	26	38	23	26	38
Phosphatidylinosi	GO:0005942;GO:0 phospholinositide	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:5293	ko00562;ko04012	Inositol phosphat	K00922	4	7	7	7	7	7	7
WD domain, G-be	GO:0005829;GO:0 cytosol;eukaryotic	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:8668			K03246	2	7	7	10	7	7	10
TCP-1/cpn60 chap	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;gm	hsa:7203			K09495	10	14	14	25	14	14	25
HEAT repeat;Splic	GO:0005681;GO:0 spliceosomal com	GO:0003824;GO:0 catalytic activity;b	GO:0000375;GO:0 RNA splicing, via t	hsa:23451				4	4	4	4	4	4	4
Rieske [2Fe-2S] dc	GO:0005750;GO:0 mitochondrial res	GO:0003824;GO:0 catalytic activity;b	GO:0006091;GO:0 generation of pre	hsa:7386	ko00190;ko04260	Oxidative phosph	K00411	5	8	9	15	8	9	15
Coatomer WD ass	GO:0005829;GO:0 cytosol;membran	GO:0005198;GO:0 structural molecu	GO:0006810;GO:0 transport;intracell	hsa:9276				5	10	10	10	10	10	10
Mitochondrial rib	GO:0000314;GO:0 organellar small ri	GO:0003676;GO:0 nucleic acid binding;RNA binding;binding	hsa:28957					7	5	5	8	5	5	8
Eukaryotic transla	GO:0005852;GO:0 eukaryotic transla	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:8663			K03252	2	2	2	2	2	2	2
Glycosyl hydrolas	GO:0000323;GO:0 lytic vacuole;extra	GO:0003824;GO:0 catalytic activity;h	GO:0000272;GO:0 polysaccharide car	hsa:66005				13	5	5	5	5	5	5
TCP-1/cpn60 chap	GO:0005829;GO:0 cytosol;intracellul	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;protein complex assembly;tubulin complex assembly;metabolic process;cellu					11	17	17	22	17	17	22
Eukaryotic initiati	GO:0005737;GO:0 cytoplasm;intrace	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:253314	ko04150;ko04910	mTOR signaling pa	K03259	8	2	2	3	2	2	3

Actin	GO:0005737;GO:0 cytoplasm;Arp2/3	GO:0005488;GO:0 binding;protein bi	GO:0006928;GO:0 cell motion;cellular process	5	6	6	6	6	6	6	6
HEAT repeat;TAT	GO:0000151;GO:0 ubiquitin ligase cc	GO:0005488;GO:0 binding;protein bi	GO:0006139;GO:0 nucleobase, nucle	2	6	6	6	6	6	6	6
Tetrahelicopeptide	GO:0005634;GO:0 nucleus;endoplasi	GO:0005488 binding	hsa:9694	2	2	2	2	2	2	2	2
Ras family	GO:0005643;GO:0 nuclear pore;nuclei	GO:0001666;GO:0 nucleotide binding	GO:0006810;GO:0 transport;intracell	7	9	9	15	9	9	15	9
PA domain;Transf	GO:0005576;GO:0 extracellular regio	GO:0004871;GO:0 signal transducer	GO:0006810;GO:0 transport;cellular	4	21	21	26	21	21	26	21
Phosphoribosyl tr	GO:0005829;GO:0 cytosol;intracellu	GO:0000287;GO:0 magnesium ion bi	GO:0006139;GO:0 nucleobase, nucle	2	12	15	27	12	15	27	12
Anticodon binding	GO:0000267;GO:0 cell fraction;solub	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	3	24	24	36	24	24	36	24
NiFu-like N termin	GO:0005634;GO:0 nucleus;mitochon	GO:0005198;GO:0 structural molecu	GO:0006807;GO:0 nitrogen compou	6	3	3	6	3	3	6	3
Armadillo/beta-ca	GO:0005643;GO:0 nuclear pore;nuclei	GO:0005048;GO:0 signal sequence b	GO:0000059;GO:0 protein import int	3	13	13	17	13	13	17	13
S-adenosyl-L-hom	GO:0016023;GO:0 cytoplasmic meml	GO:0003824;GO:0 catalytic activity;a	GO:0006730;GO:0 one-carbon meta	2	9	9	15	9	9	15	9
Polyprenyl synthe	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;d	GO:0006066;GO:0 alcohol metabolic	4	3	3	4	3	3	4	3
Probable myoblc	GO:0005829;GO:0 cytosol;intracellu	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	6	4	4	4	4	4	4	4
Elongation factor	GO:0005829;GO:0 cytosol;eukaryotic	GO:0000166;GO:0 nucleotide binding	GO:0006414;GO:0 translational elon	11	20	22	38	20	22	38	20
14-3-3 protein	GO:0005634;GO:0 nucleus;centrosor	GO:0005488;GO:0 binding;protein bi	GO:0007154;GO:0 cell communicati	4	13	14	23	8	8	12	7
14-3-3 protein	GO:0016023;GO:0 cytoplasmic meml	GO:0005488;GO:0 binding;protein bi	GO:0006916;GO:0 anti-apoptosis;cel	4	11	12	21	7	7	11	7
HEAT repeat;Impc	GO:0005643;GO:0 nuclear pore;cyto	GO:0005048;GO:0 signal sequence b	GO:0000059;GO:0 protein import int	12	6	6	6	6	6	6	6
EF hand	GO:0016459;GO:0 myosin complex;n	GO:0003774;GO:0 motor activity;cat	GO:0006937;GO:0 regulation of mus	15	12	17	31	1	2	3	1
Domain of unkno	GO:0005739;GO:0 mitochondrion;mi	GO:0003824;GO:0 catalytic activity;n	GO:0006091;GO:0 generation of pre	6	6	6	6	6	6	7	6
14-3-3 protein	GO:0005737;GO:0 cytoplasm;intrace	GO:0004857;GO:0 enzyme inhibitor	GO:0006469;GO:0 negative regulati	3	8	9	17	4	4	7	4
Septin	GO:001105;GO:0 septin complex;n	GO:0000166;GO:0 nucleotide binding	GO:0007049;GO:0 cell cycle;cellular	7	6	6	6	6	6	6	2
Ribosomal protein	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003712;GO:0 transcription cofa	GO:0006139;GO:0 nucleobase, nucle	3	17	17	26	17	17	26	17
Hsp70 protein	GO:0000166;GO:0 nucleotide binding	GO:0006950;GO:0 response to stress	hsa:51182	4	6	6	7	6	6	7	6
	GO:0005634;GO:0 nucleus;mitochon	GO:0003712;GO:0 transcription cofa	GO:0006139;GO:0 nucleobase, nucle	1	5	5	8	5	5	8	5
Uncharacterized conserved protein (DUF2042)	GO:0005488;GO:0 binding;protein binding	hsa:23376		2	2	2	2	2	2	2	2
Ku70/Ku80 beta-b	GO:0000782;GO:0 telomere cap com	GO:0000166;GO:0 nucleotide binding	GO:0000723;GO:0 telomere mainten	3	19	19	20	19	19	20	19
Mitochondrial inn	GO:0016021;GO:0 integral to membr	GO:0005488;GO:0 binding;protein binding	hsa:10989	11	12	12	12	12	12	12	12
	GO:0000314;GO:0 organellar small ri	GO:0003735;GO:0 structural constitu	GO:0006412;GO:0 translation;metab	2	4	4	5	4	4	5	4
Ribosomal protein	GO:0005739;GO:0 mitochondrion;rlt	GO:0003735;GO:0 structural constitu	GO:0006412;GO:0 translation;metab	1	4	4	8	4	4	8	4
Phosphofruktokin	GO:0005945;GO:0 6-phosphofruktok	GO:0000166;GO:0 nucleotide binding	GO:0005975;GO:0 carbohydrate met	6	4	4	4	4	4	4	4
ADP-ribosylation	GO:0000139;GO:0 Golgi membrane;c	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;retro	15	7	8	13	7	8	13	5
Cytochrome c oxid	GO:0005634;GO:0 nucleus;mitochon	GO:0003824;GO:0 catalytic activity;c	GO:0006091;GO:0 generation of pre	1	7	8	14	7	8	14	7
CPSE A subunit rej	GO:0005681;GO:0 spliceosomal com	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via	2	4	5	4	4	5	4	4
Anticodon-binding domain	GO:0005488;GO:0 binding;protein binding	hsa:124801		4	2	2	4	2	2	4	2
ATPase family ass	GO:0000502;GO:0 proteasome comp	GO:0000166;GO:0 nucleotide binding	GO:0006508;GO:0 proteolysis;ubiqui	3	2	2	3	2	2	3	2
MAGE family	GO:0005634;GO:0 nucleus;cytoplasm;organelle;membrane-bounded orga	GO:0004008;GO:0 regulation of grow	hsa:56160	1	4	4	6	4	4	6	4
Nup93/Nic96	GO:0005643;GO:0 nuclear pore;macr	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;intracell	4	2	4	4	4	4	4	4
WD domain, G-be	GO:0000776;GO:0 kinetochore;nucle	GO:0005488;GO:0 binding;protein bi	GO:0000075;GO:0 cell cycle checkpoin	5	9	9	11	9	9	11	9
Pyruvate kinase, b	GO:0005829;GO:0 cytosol;intracellu	GO:0000166;GO:0 nucleotide binding	GO:0005975;GO:0 carbohydrate met	12	12	43	74	2	2	2	2
SMC proteins Flex	GO:0000796;GO:0 condensin comple	GO:0000166;GO:0 nucleotide binding	GO:0006323;GO:0 DNA packaging;or	10	41	31	38	31	31	38	31
Glycosyl hydrolasi	GO:0005783;GO:0 endoplasmic retic	GO:0003824;GO:0 catalytic activity;h	GO:0005975;GO:0 carbohydrate met	5	3	3	3	3	3	3	3
ARP2/3 complex 1	GO:0005737;GO:0 cytoplasm;cytoske	GO:0003779;GO:0 actin binding;bind	GO:0008064;GO:0 regulation of actin	2	2	2	3	2	2	3	2
ATPase family ass	GO:0009295;GO:0 nucleoid;mitochon	GO:0000166;GO:0 nucleotide binding	GO:0001666;GO:0 response to hypo	3	3	3	4	3	3	4	3
WD domain, G-be	GO:0005737;GO:0 cytoplasm;Arp2/3	GO:0003779;GO:0 actin binding;stru	GO:0006928;GO:0 cell motion;regula	4	4	4	5	4	4	5	4
Tubulin/FtsZ famil	GO:0005874;GO:0 microtubule;macr	GO:0000166;GO:0 nucleotide binding	GO:0001906;GO:0 cell killing;leukocy	20	19	22	38	3	3	5	3
Gelsolin/Repeat;Se	GO:0005789;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;intracell	3	2	2	2	2	2	2	2
TCP-1/cpn60 chap	GO:0005832;GO:0 chaperonin-conta	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;mi	9	19	19	30	19	19	30	19
Elongation factor	GO:0005737;GO:0 cytoplasm;ribonou	GO:0000166;GO:0 nucleotide binding	GO:0006414;GO:0 translational elon	4	45	45	75	45	45	75	45
Protein of unknown function (DUF1014)	hsa:115098			1	3	3	4	3	3	4	3
AIR synthase relat	GO:0005634;GO:0 nucleus;mitochon	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	11	7	7	8	7	7	8	7
RNA recognition n	GO:0005654;GO:0 nucleoplasm;splic	GO:0000166;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via	3	5	5	8	5	5	8	5
	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0006464;GO:0 protein modificali	1	9	11	18	3	3	5	3
Ribosomal protein	GO:0005634;GO:0 nucleus;plasma m	GO:0003735;GO:0 structural constitu	GO:0006414;GO:0 translational elon	9	6	6	10	6	6	10	6
Aldehyde dehydr	GO:0005759;GO:0 mitochondrial ma	GO:0003824;GO:0 catalytic activity;a	GO:0005975;GO:0 carbohydrate met	5	8	8	11	8	8	11	8
Rad50 zinc hook	GO:0000781;GO:0 chromosome, telc	GO:0000166;GO:0 nucleotide binding	GO:0000018;GO:0 regulation of DNA	7	6	6	6	6	6	6	6
Adaptin N termin	GO:0005829;GO:0 cytosol;membran	GO:0005198;GO:0 structural molecu	GO:0006810;GO:0 transport;intracell	4	18	18	25	18	18	25	18
Nucleoplasmnin	GO:0005654;GO:0 nucleoplasm;nucle	GO:0003676;GO:0 nucleic acid bindir	GO:0006325;GO:0 chromatin organiz	6	9	9	15	9	9	15	9
Ubiquitin famil	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;h	GO:0006464;GO:0 protein modificali	3	7	7	13	7	7	13	7
ATPase family ass	GO:0000123;GO:0 histone acetyltran	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	3	14	14	16	14	14	16	14
Pyridine nucleotid	GO:0005634;GO:0 nucleus;mitochon	GO:0000166;GO:0 nucleotide binding	GO:0000737;GO:0 DNA catabolic pro	6	4	4	4	4	4	4	4
Phosphoglucoxi	GO:0005615;GO:0 extracellular spac	GO:0003824;GO:0 catalytic activity;c	GO:0005975;GO:0 carbohydrate met	6	20	21	37	20	21	35	20
Calponin homolog	GO:0005730;GO:0 nucleolus;pseudoj	GO:0001882;GO:0 nucleoside binding	GO:00010941;GO:0 regulation of cell	22	52	52	87	52	52	87	52
Ribosomal protein	GO:0005829;GO:0 cytosol;ribosome;	GO:0003676;GO:0 nucleic acid bindir	GO:0006414;GO:0 translational elon	2	12	12	21	12	12	21	12
UTP-glucose-1-pf	GO:0005829;GO:0 cytosol;intracellu	GO:0003824;GO:0 catalytic activity;n	GO:0008152;GO:0 metabolic process	9	5	5	7	5	5	7	5
Poly-adenylate bi	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	6	8	8	12	2	2	12	2

Glyoxalase/Bleom	GO:0005739;GO:0 mitochondrion;or	GO:0003824;GO:0 catalytic activity;n	GO:0006732;GO:0 coenzyme metab	hsa:84693	ko00640;ko00280	Propanoate metal	K05606	3	3	3	5	3	3	5	3
ATP synthase D c	GO:0000276;GO:0 mitochondrial pro	GO:0005215;GO:0 transporter activi	GO:0006139;GO:0 nucleobase, nucle	hsa:10476	ko00190;ko05010	Oxidative phosph	K02138	5	11	11	13	11	11	13	11
PPR repeat	GO:0000228;GO:0 nuclear chromoso	GO:0003676;GO:0 nucleic acid bindi	GO:0006139;GO:0 nucleobase, nucle	hsa:10128				10	10	30	30	30	30	32	30
lactate/malate de	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;l	GO:0005975;GO:0 carbohydrate met	hsa:3945	ko00010;ko00620	Glycolysis / Gluco	K00016	11	23	23	47	21	24	43	21
CRM1 C terminal	GO:0005642;GO:0 annulate lamella	GO:0003676;GO:0 nucleic acid bindi	GO:0000059;GO:0 protein import int	hsa:7514				7	6	6	6	6	6	6	6
Phosphoribulokin	GO:0005828;GO:0 cytoplasm;intracell	GO:0000166;GO:0 nucleotide binding	GO:0008152	hsa:7371	ko00240;ko00983	Pyrimidine metab	K00876	3	2	2	3	2	2	3	2
Thif family;Ubiqu	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:55236	ko04120	Ubiquitin mediate	K10699	5	6	6	6	6	6	6	6
Ubiquitin-conjuga	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0000724;GO:0 double-strand bre	hsa:7334;hsa:389	ko04120	Ubiquitin mediate	K10580	6	7	7	11	7	7	11	7
WD domain, G-be	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0006139;GO:0 nucleobase, nucleoside,	nucleotide and nucleic acid metabolic process;DNA metabolic proce				7	9	9	13	9	9	13	4
Adaptin N termin	GO:0005829;GO:0 cytosol;membran	GO:0005198;GO:0 structural molecu	GO:0006810;GO:0 transport;intracell	hsa:22820				1	6	6	6	6	6	6	5
Pyruvate kinase, b	GO:0005829;GO:0 cytosol;intracellu	GO:0000166;GO:0 nucleotide binding	GO:0005975;GO:0 carbohydrate met	hsa:5315	ko00010;ko00620	Glycolysis / Gluco	K00873	3	43	45	80	43	45	80	4
Peptidase family I	GO:0005634;GO:0 nucleus;cytosol;or	GO:0003824;GO:0 catalytic activity;a	GO:0006508;GO:0 proteolysis;metab	hsa:9520				10	4	4	4	4	4	4	4
Ribosomal protein	GO:0015935;GO:0 small ribosomal s	GO:0003735;GO:0 structural constitu	GO:0006414;GO:0 translational elong	hsa:6227	ko03010	Ribosome	K02971	3	2	2	3	2	3	2	2
Importin-beta N-t	GO:0000267;GO:0 cell fraction;solub	GO:0005083;GO:0 small GTPase reg.	GO:0000059;GO:0 protein import int	hsa:10527				1	4	4	4	4	4	4	4
MCM2/3/5 family	GO:0005654;GO:0 nucleoplasm;alph	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4172	ko03030;ko04110	DNA replication;C	K02541	13	4	4	4	4	4	4	4
Cation transporti	GO:0000267;GO:0 cell fraction;meml	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:476	ko04260	Cardiac muscle co	K01539	15	18	19	18	18	18	19	9
Formate--tetrahy	GO:0005739;GO:0 mitochondrion;or	GO:0000166;GO:0 nucleotide binding	GO:0000096;GO:0 sulfur amino acid	hsa:4522	ko00630;ko00670	Glyoxylate and dic	K00288;K00295;K1	2	3	9	9	9	9	9	9
ATPase family ass	GO:0000502;GO:0 proteasome com	GO:0000166;GO:0 nucleotide binding	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5706	ko03050	Proteasome	K03064	2	3	3	3	3	3	3	3
Proteasome/cyclo	GO:0005829;GO:0 cytosol;proteaso	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5708	ko03050	Proteasome	K03028	7	21	21	28	21	21	28	21
WD domain, G-be	GO:0005737;GO:0 cytoplasm;cytosk	GO:0003779;GO:0 actin binding;bind	GO:0003008;GO:0 system process;se	hsa:9948				3	3	3	3	3	3	3	3
Ankyrin repeat;Gh	GO:0005759;GO:0 mitochondrion;ma	GO:0003824;GO:0 catalytic activity;g	GO:0006082;GO:0 organic acid meta	hsa:2744	ko00910;ko00251	Nitrogen metabol	K01425	7	4	4	5	4	4	5	4
Cytoplasmic Fragl	GO:0005576;GO:0 extracellular regio	GO:0001664;GO:0 G-protein-couple	GO:0002376;GO:0 immune system p	hsa:26999;hsa:23	ko04810	Regulation of acti	K05749	8	2	2	2	2	2	2	2
Subtilase family	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;metab	hsa:7174				18	18	20	18	18	20	18	18
Dynein light chain	GO:0005829;GO:0 cytosol;cytoplasm	GO:0003774;GO:0 motor activity;mic	GO:0006996;GO:0 organelle organiz	hsa:8655				4	5	5	9	3	3	5	3
Phosphoglycerate	GO:0005829;GO:0 cytosol;intracellu	GO:0003824;GO:0 catalytic activity;b	GO:0005975;GO:0 carbohydrate met	hsa:5223	ko00010	Glycolysis / Gluco	K01834	11	11	11	20	11	11	20	11
KH domain	GO:0005634;GO:0 nucleus;membran	GO:0003676;GO:0 nucleic acid bindi	GO:0000086;GO:0 G2/M transition o	hsa:10657				10	3	3	5	3	3	5	3
tRNA synthetases	GO:0000267;GO:0 cell fraction;solub	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid metabolic process;nucleobase,	nucleoside, nucleotide and nucleic acid metaboli				4	17	17	26	17	17	26	17
Leucine Rich Repe	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein binding	hsa:10541					7	3	3	3	3	3	3	3
EF hand	GO:0016459;GO:0 myosin complex;u	GO:0003774;GO:0 motor activity;cat	GO:0006810;GO:0 transport;skeletal	hsa:4637				15	11	14	27	11	14	27	8
SAP domain	GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindi	GO:0006139;GO:0 nucleobase, nucle	hsa:84324				5	5	5	5	5	5	5	5
ATP-grasp domain	GO:0005759;GO:0 mitochondrion;ma	GO:0000166;GO:0 nucleotide binding	GO:0006084;GO:0 acetyl-CoA metab	hsa:8801	ko00020;ko00640	Citrate cycle (TCA	K01900	4	2	2	2	2	2	2	2
Domain of unkno	GO:0005737;GO:0 cytoplasm;intrace	GO:0004857;GO:0 enzyme inhibitor	GO:0006915;GO:0 apoptosis;anti-ap	hsa:25816				5	1	1	2	1	1	2	1
AIR synthase relat	GO:0005829;GO:0 cytosol;intracellu	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid metabolic process;nucleobase,	nucleoside, nucleotide and nucleic acid metaboli				2	1	2	2	2	2	2	2
Roadblock/LC7 do	GO:0005737;GO:0 cytoplasm;cytopla	GO:0003774;GO:0 motor activity;mic	GO:0007017;GO:0 microtubule-base	hsa:83658;hsa:83657				4	2	2	4	2	2	4	2
Peptidase family I	GO:0005758;GO:0 mitochondrion;intr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;metab	hsa:57486	ko04614	Renin-angiotensin	K01393	6	4	4	5	4	4	5	4
Cullin family;Cull	GO:0000151;GO:0 ubiquitin ligase cc	GO:0005488;GO:0 binding;protein bi	GO:0000082;GO:0 G1/S transition of	hsa:8451;hsa:845	ko04120;ko03420	Ubiquitin mediate	K10609	7	6	6	6	6	6	6	6
LEM domain;Thyn	GO:0000785;GO:0 chromatin;nuclea	GO:0003676;GO:0 nucleic acid binding;DNA	binding;binding;protein bindi	hsa:7112				4	12	12	12	12	12	12	12
Cullin family;Cull	GO:0000151;GO:0 ubiquitin ligase cc	GO:0004871;GO:0 signal transducer	GO:0000082;GO:0 G1/S transition of	hsa:8065	ko04120	Ubiquitin mediate	K10612	2	4	4	4	4	4	4	4
Immunoglobulin V-set domain								27	4	4	8	4	4	8	4
LSM domain	GO:0005681;GO:0 spliceosomal com	GO:0003676;GO:0 nucleic acid bindi	GO:0006139;GO:0 nucleobase, nucle	hsa:6637				6	2	2	4	2	2	4	2
Mago nashi protei	GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindi	GO:0006139;GO:0 nucleobase, nucle	hsa:55110;hsa:4116				6	5	5	9	5	5	9	5
RNA recognition n	GO:0005737;GO:0 cytoplasm;ribonuc	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:9987				3	6	6	7	6	6	7	6
Immunoglobulin C	GO:0000267;GO:0 cell fraction;extra	GO:0003823;GO:0 antigen binding;bi	GO:0002376;GO:0 immune system process;immune response;response to stimulus					1	13	14	27	13	14	27	2
F-actin capping pr	GO:0008290;GO:0 F-actin capping pr	GO:0003779;GO:0 actin binding;bind	GO:0006996;GO:0 organelle organiz	hsa:832				4	19	20	37	19	20	37	19
Alanine dehydrog	GO:0005746;GO:0 mitochondrion;res	GO:0000166;GO:0 nucleotide binding	GO:0006084;GO:0 acetyl-CoA metab	hsa:23530	ko00760	Nicotinate and nic	K00324;K00325	6	3	3	3	3	3	3	3
C-terminal domain	GO:0005739;GO:0 mitochondrion;zen	GO:0003824;GO:0 catalytic activity;g	GO:0000302;GO:0 response to reacti	hsa:10935				2	11	12	22	11	12	22	11
Immunoglobulin C	GO:0000267;GO:0 cell fraction;extra	GO:0003823;GO:0 antigen binding;bi	GO:0002376;GO:0 immune system process;immune response;response to stimulus					2	13	14	25	2	2	25	2
MCM2/3/5 family	GO:0005654;GO:0 nucleoplasm;orga	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4173	ko03030;ko04110	DNA replication;C	K02212	4	5	5	6	5	5	6	5
RanGAP1 C-termin	GO:0000267;GO:0 cell fraction;kinet	GO:0005083;GO:0 small GTPase reg.	GO:0007154;GO:0 cell communicati	hsa:5905				5	6	6	6	6	6	6	6
Transketolase, pyr	GO:0005829;GO:0 cytosol;intracellu	GO:0003824;GO:0 catalytic activity;f	GO:0008152;GO:0 metabolic process	hsa:7086	ko00030;ko00710	Pentose phosphat	K00615	5	24	25	45	24	25	45	24
Alpha amylase, ca	GO:0009986;GO:0 cell surface;integ	GO:0003824;GO:0 catalytic activity;t	GO:0005975;GO:0 carbohydrate met	hsa:6520				11	5	5	6	5	5	6	5
GO:0005739;GO:0 mitochondrion;sr	GO:0003735;GO:0 structural constitu	GO:0006412;GO:0 translation;metab	hsa:64968					1	5	5	6	5	5	6	5
DHHA1 domain;tR	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0001101;GO:0 response to acid;f	hsa:16	ko00252;ko00970	Alanine and aspar	K01872	2	3	3	3	3	3	3	3
Eukaryotic elonga	GO:0005853;GO:0 eukaryotic transla	GO:0003676;GO:0 nucleic acid bindi	GO:0006414;GO:0 translational elongation;metabolic process;biosynthetic process;macromolecule biosynthetic					3	8	8	13	8	8	13	1
Histidine kinase-	GO:0016023;GO:0 cytoplasmic meml	GO:0000166;GO:0 nucleotide binding	GO:0001959;GO:0 regulation of cyto	hsa:3326	ko04914;ko04612	Progesterone-met	K04079	10	39	40	71	39	40	71	22
EF hand	GO:0000922;GO:0 spindle pole;centr	GO:0005488;GO:0 binding;calcium ie	GO:0007154;GO:0 cell communicati	hsa:801;hsa:805;h	ko04020;ko04070	Calcium signaling	K02183	6	3	3	6	3	3	6	3
AICARFT/MPCHase	bienszyme;MGS-like domain	GO:0003824;GO:0 catalytic activity;f	GO:0006139;GO:0 nucleobase, nucle	hsa:471	ko00230;ko00670	Purine metabolis	K00602	7	15	15	15	15	15	15	15
GTF2l-like repeat	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003676;GO:0 nucleic acid bindi	GO:0006352;GO:0 transcription initi	hsa:2969	ko03022	Basal transcriptior	K03121	11	6	6	7	6	6	7	6
2-oxoacid dehydr	GO:0005967;GO:0 mitochondrion;pyr	GO:0003824;GO:0 catalytic activity;d	GO:0005975;GO:0 carbohydrate met	hsa:1737	ko00010;ko00020	Glycolysis / Gluco	K00627	2	35	43	79	35	43	79	7
Adaptin N termin	GO:0005794;GO:0 Golgi apparatus;c	GO:0005215;GO:0 transporter activi	GO:0006810;GO:0 transport;intracell	hsa:162;hsa:163	ko04142;ko05016	Huntington's dise	K12392;K11825	10	2	2	2	2	2	2	2
lactate/malate de	GO:0005829;GO:0 cytosol;intracellu	GO:0003824;GO:0 catalytic activity;n	GO:0005975;GO:0 carbohydrate met	hsa:4190	ko00020;ko00620	Citrate cycle (TCA	K00026	6	9	15	9	9	15	9	9
RNA recognition n	GO:0005654;GO:0 nucleoplasm;splic	GO:0000166;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via t	hsa:3178;hsa:14983				19	14	15	26	14	15	26	14
Enoyl-CoA hydrat	GO:0005759;GO:0 mitochondrion;ma	GO:0003824;GO:0 catalytic activity;e	GO:0006082;GO:0 organic acid meta	hsa:1892	ko00640;ko00650	Propanoate metal	K07511	1	9	9	15	9	9	15	9
Proteasome A-ty	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5695	ko03050	Proteasome	K02739	1	2	2	3	2	2	3	2

Tetrahydrofolate	GO:0005739;GO:0 mitochondrion;or	GO:0000287;GO:0 magnesium ion bi	GO:0006082;GO:0 organic acid meta	hsa:10797	ko00630;ko00670	Glyoxylate and dic	K00295;K01491	5	4	4	7	4	4	7	4
MCM2/3/5 family	GO:0000785;GO:0 cytosol;intracell	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4171	ko03030;ko04110	DNA replication;C	K02540	3	3	3	3	3	3	3	3
Aminotransferase	GO:0005759;GO:0 mitochondrion;ma	GO:00003824;GO:0 catalytic activity;t	GO:0006082;GO:0 organic acid meta	hsa:2806	ko00710;ko00251	Carbon fixation in	K00813	3	18	18	26	18	18	26	18
Low molecular wt	GO:0000267;GO:0 cell fraction;solub	GO:00003824;GO:0 catalytic activity;a	GO:0006464;GO:0 protein modification process;protein	hsa:9188				7	2	2	2	2	2	2	2
RF-1 domain	GO:0003676;GO:0 nucleic acid bindir	GO:0006415;GO:0 translational term	hsa:3396					1	2	2	3	2	2	3	2
Protein kinase dor	GO:0005737;GO:0 cytoplasm;intrac	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:8428				19	3	3	3	3	3	3	3
Inositol monopho	GO:0005829;GO:0 cytosol;intracellu	GO:0000287;GO:0 magnesium ion bi	GO:0006139;GO:0 nucleobase, nucle	hsa:10380	ko00920	Sulfur metabolism	K01082	9	2	2	2	2	2	2	2
Elongation factor	GO:0005739;GO:0 mitochondrion;or	GO:0000166;GO:0 nucleotide binding	GO:0006414;GO:0 translational elon	hsa:85476				5	7	7	7	7	7	7	7
DEAD/DEAH box f	GO:0005730;GO:0 nucleolus;organel	GO:0000166;GO:0 nucleotide binding;nucleoside binding;purine nucleosid	hsa:9188					5	4	4	4	4	4	4	4
Trm112p-like protein	GO:0005488;GO:0 binding;protein binding	hsa:51504						4	3	3	4	3	3	4	3
NAD-dependent g	GO:0009331;GO:0 glycerol-3-phosph	GO:0000166;GO:0 nucleotide binding	GO:0005975;GO:0 carbohydrate met	hsa:23171	ko00564	Glycerophospholi	K00006	4	3	3	3	3	3	3	3
WD domain, G-be	GO:0005886;GO:0 plasma membrana	GO:0005102;GO:0 receptor binding;binding;protein binding;enzyme bindi	hsa:10399					25	15	15	27	15	15	27	15
Enhancer of nudin	GO:0005634;GO:0 nucleus;cytoplasm	GO:0005488;GO:0 binding;protein bi	GO:0006139;GO:0 nucleobase, nucle	hsa:2079				1	3	3	5	3	3	5	3
U-box domain	GO:0000151;GO:0 ubiquitin ligase cc	GO:0003824;GO:0 catalytic activity;u	GO:0006464;GO:0 protein modificati	hsa:51070				2	16	16	28	16	16	28	16
DZF	GO:0005730;GO:0 nucleolus;organel	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:3608				3	11	11	20	11	11	20	11
Pro-kumamolisin,	GO:0000267;GO:0 cell fraction;lytic	GO:0003824;GO:0 catalytic activity;e	GO:0001894;GO:0 tissue homeostasi	hsa:1200	ko04142		K01279	4	3	3	3	3	3	3	3
Stathmin family	GO:0005737;GO:0 cytoplasm;microt	GO:0004871;GO:0 signal transducer	GO:0000226;GO:0 microtubule cytos	hsa:3925	ko04010	MAPK signaling pa	K04381	9	6	6	9	6	6	9	6
Ankyrin repeat	GO:0005488;GO:0 binding;protein binding	hsa:91526						2	2	2	2	2	2	2	2
Hsp70 protein	GO:0009295;GO:0 nucleoid;cell surfa	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;an	hsa:3313				5	33	36	66	33	36	66	33
ATPase family ass	GO:0000267;GO:0 cell fraction;membr	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:7415				6	14	14	17	14	14	17	14
Nucleoside diphos	GO:0005829;GO:0 cytosol;intracellu	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4832				1	2	2	4	2	2	4	2
	GO:0005576	extracellular region	hsa:79879					2	5	5	8	5	5	8	5
Proteasome A-ty	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5686	ko03050	Proteasome	K02729	2	7	7	12	7	7	12	7
Spinocerebellar at	GO:00030425;GO:0 dendrite;cell proj	GO:0005488;GO:0 binding;protein bi	GO:0007399;GO:0 nervous system di	hsa:25814				5	2	3	6	2	3	6	2
Hsp70 protein	GO:0005737;GO:0 cytoplasm;intrac	GO:0000166;GO:0 nucleotide binding	GO:0006950;GO:0 response to stress	hsa:10808				7	7	7	9	7	9	7	7
GDP dissociation	GO:0005737;GO:0 cytoplasm;microt	GO:0005083;GO:0 small GTPase regu	GO:0006810;GO:0 transport;protein	hsa:2665				9	17	18	28	17	18	28	17
Septin	GO:0001725;GO:0 stress fiber;nucleu	GO:0000166;GO:0 nucleotide binding	GO:0006461;GO:0 protein complex a	hsa:55752				24	6	6	7	2	2	3	2
lactate/malate de	GO:0005759;GO:0 mitochondrion;ma	GO:0003824;GO:0 catalytic activity;b	GO:0005975;GO:0 carbohydrate met	hsa:4191	ko00020;ko00620	Citrate cycle (TCA	K00026	3	16	16	30	16	16	30	16
Histidine kinase,	GO:0000267;GO:0 cell fraction;membr	GO:0000166;GO:0 nucleotide binding	GO:0001666;GO:0 response to hypoo	hsa:7184				7	13	13	17	11	11	13	11
Hydroxymethylglu	GO:0000267;GO:0 cell fraction;solub	GO:0003824;GO:0 catalytic activity;h	GO:0006066;GO:0 alcohol metabolic	hsa:3157				8	8	8	13	8	8	13	8
Proteasome A-ty	GO:0005634;GO:0 nucleus;mitochon	GO:0003676;GO:0 nucleic acid bindir	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5687	ko03050	Proteasome	K02730	2	9	9	15	9	9	15	9
CAF1 family ribon	GO:0005667;GO:0 transcription fact	GO:0003676;GO:0 nucleic acid bindir	GO:0005975;GO:0 carbohydrate met	hsa:29883				4	3	3	4	3	3	4	3
CS domain;SGS do	GO:0005634;GO:0 nucleus;cytoplasm	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;metab	hsa:27101	ko04310	Wnt signaling pat	K04507	1	14	15	26	14	15	26	14
LSM domain	GO:0005654;GO:0 nucleoplasm;splic	GO:0003676;GO:0 nucleic acid bindir	GO:0000387;GO:0 spliceosomal snR	hsa:6636				9	2	2	4	2	2	4	2
C-terminal domain	GO:0005759;GO:0 mitochondrion;ma	GO:0003824;GO:0 catalytic activity;p	GO:0006464;GO:0 protein modificati	hsa:10549				4	12	12	21	8	8	13	8
WD domain, G-be	GO:0005634;GO:0 nucleus;cytoplasm;organelle;membrane-bounded orga	GO:0000387;GO:0 spliceosomal snR	hsa:79084					4	6	6	11	6	6	11	6
Thif family;Ubiqui	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:7317	ko04120;ko05012	Ubiquitin mediate	K03178	9	14	14	21	14	14	21	14
Mitochondrial gly	GO:0005759;GO:0 mitochondrion;ma	GO:0001846;GO:0 opsonin binding;c	GO:0002376;GO:0 immune system p	hsa:708				1	6	6	12	6	6	12	6
Tropomyosin								1	22	22	37	11	11	16	1
Poly-adenylate bir	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:26986;hsa:5042				30	20	20	36	20	20	36	13
Pyridine nucleotid	GO:0005759;GO:0 mitochondrion;ma	GO:0000166;GO:0 nucleotide binding	GO:0009987;GO:0 cellular process;cellular homeostasi;homeostatic process;cell redox homeostasi;regulation					7	19	21	40	19	21	40	19
F-actin capping pr	GO:0005737;GO:0 cytoplasm;F-actin	GO:0003779;GO:0 actin binding;bind	GO:0006461;GO:0 protein complex a	hsa:830				5	13	13	22	8	8	13	8
eIF4-gamma/eIF5/eIF2-epsilon	GO:0005488;GO:0 binding;protein bi	GO:0007399;GO:0 nervous system di	hsa:28969					10	6	6	8	4	4	5	4
Elongation factor	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via t	hsa:9343				4	3	3	3	3	3	3	3
SCP-2 sterol trans	GO:0005739;GO:0 mitochondrion;pe	GO:0003824;GO:0 catalytic activity;b	GO:0006629;GO:0 lipid metabolic process;steroid biosynthetic process;transport;lipid transport;metabolic proc					9	6	6	10	6	6	10	6
Aminotransferase class IV	GO:0003824;GO:0 catalytic activity;b	GO:0000082;GO:0 G1/S transition of	hsa:586		ko00280;ko00290	Valine, leucine ani	K00826	6	7	7	12	6	7	12	7
Proteasome A-ty	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5685	ko03050	Proteasome	K02728	2	5	5	10	5	5	10	5
								2	8	8	13	3	3	4	1
Tetrapeptide	GO:0005742;GO:0 mitochondrion;out	GO:0005215;GO:0 transporter activity;binding;protein binding;protein tra	hsa:9868					2	3	3	3	3	3	3	3
Glucosamine-6-phosphate isomerases/6-phosphogluco	GO:0003824;GO:0 catalytic activity;c	GO:0005975;GO:0 carbohydrate met	hsa:25796		ko00030	Pentose phosphat	K01057	1	2	2	2	2	2	2	2
TCP-1/cpn60 chap	GO:0005737;GO:0 cytoplasm;intrac	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;mi	hsa:10574				7	28	28	49	28	28	49	28
Proteasome/cyco	GO:0005829;GO:0 cytosol;proteasom	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5707	ko03050	Proteasome	K03032	5	6	6	7	6	6	7	6
Single-strand bind	GO:0009295;GO:0 nucleoid;mitochoi	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:6742	ko03030;ko03430	DNA replication;M	K03111	4	7	7	14	7	7	14	7
39S ribosomal pro	GO:0005739;GO:0 mitochondrion;ribosome;ribonucleoprotein complex;macromolecular complex;organelle;me	hsa:116540						1	3	3	5	3	3	5	3
Initiation factor 2	GO:0000267;GO:0 cell fraction;membr	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:1967				5	3	3	4	3	3	4	3
Prefoldin subunit	GO:0016272;GO:0 prefoldin complex	GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;mi	hsa:5202				1	5	5	8	5	5	8	5
AIR carboxylase;SAICAR synthetase	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:10606		ko00230	Purine metabolis	K01587	4	32	34	64	32	34	64	32
SAC3/GANP/Nin1	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5714	ko03050	Proteasome	K03031	2	2	2	3	2	2	3	2
Protein of unknown function (DUF1241)	GO:0005488;GO:0 binding;protein bi	GO:0006915;GO:0 apoptosis;cell dea	hsa:11235					7	7	7	11	7	7	11	7
DnaJ domain;Tetrapeptide repeat	GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;mi	hsa:7266					9	11	11	16	11	11	16	11
Calreticulin family	GO:0005578;GO:0 proteinaceous ext	GO:0001846;GO:0 opsonin binding;	GO:0000122;GO:0 negative regulatio	hsa:811	ko04612	Antigen processin	K08057	2	9	9	15	9	9	15	9
Aldo/keto reducta	GO:0005615;GO:0 extracellular spac	GO:0003824;GO:0 catalytic activity;a	GO:0005975;GO:0 carbohydrate met	hsa:231	ko00040;ko00051	Pentose and gluc	K00011	6	2	2	3	2	2	3	2
C-terminal domain	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;p	GO:0000302;GO:0 response to reacti	hsa:5052				3	23	26	45	23	26	45	18
MCM2/3/5 family	GO:0005654;GO:0 nucleoplasm;orga	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4175	ko03030;ko04110	DNA replication;C	K02542	1	4	4	4	4	4	4	4
Arp2/3 complex, z	GO:0005737;GO:0 cytoplasm;Arp2/3	GO:0003779;GO:0 actin binding;struc	GO:0006928;GO:0 cell motion;cellula	hsa:10109	ko04810	Regulation of actin	K05758	6	16	16	26	16	16	26	16

Inorganic pyrophosphatase	GO:0005739;GO:0 mitochondrion;or GO:0000287;GO:0 magnesium ion bi	GO:0006793;GO:0 phosphorus metal hsa:27068	ko00190	Oxidative phosph K01507	9	9	9	16	8	8	14	8
TCP-1/cpn60 chap	GO:0005634;GO:0 nucleus;organelle	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;hm	hsa:10576	5	31	31	55	31	31	55	31
Proliferating cell nuclear antigen	GO:0005654;GO:0 nucleoplasm;DNA	GO:0000700;GO:0 mismatch base pa	GO:0006139;GO:0 nucleobase, nucle	hsa:5111	1	10	11	17	10	11	17	10
Aldolase B	GO:0005737;GO:0 cytoplasm;integra	GO:0003824;GO:0 catalytic activity;tr	GO:0006810;GO:0 transport;ion tran	hsa:8514	18	11	11	18	11	18	11	18
Eukaryotic translation initiation factor 4E	GO:0005829;GO:0 cytosol;eukaryotic	GO:0000166;GO:0 nucleotide binding	GO:0006413;GO:0 translational initia	hsa:8662	4	10	10	13	10	10	13	10
Nucleoside diphosphate kinase 1	GO:0005634;GO:0 nucleus;organelle	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4841	12	7	7	11	6	6	10	6
Eukaryotic translation initiation factor 4E	GO:0005642;GO:0 annulate lamellae	GO:0003676;GO:0 nucleic acid bindir	GO:0006405;GO:0 RNA export from r	hsa:1984;hsa:143244	7	13	14	23	13	14	23	13
Eukaryotic elongation factor 1A	GO:0005829;GO:0 cytosol;eukaryotic	GO:0003676;GO:0 nucleic acid bindir	GO:0006414;GO:0 translational elon	hsa:1933	4	3	3	5	3	3	5	3
GTPase of unknown class	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4733	2	8	8	11	8	8	11	8
Proteasome A1-type	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5688	ko03050	Proteasome	K02731	9	13	14	26	13
Hsp70 protein	GO:0005634;GO:0 nucleus;mitochon	GO:0000166;GO:0 nucleotide binding	GO:0006950;GO:0 response to stress	hsa:3303;hsa:3304;ko04010;ko04612	MAPK signaling pa	K03283	11	15	15	25	11	17
Thioredoxin	GO:0005783;GO:0 endoplasmic retic	GO:0003756;GO:0 protein disulfide l	GO:0006457;GO:0 protein folding;hm	hsa:10130	K09584		5	7	7	12	7	12
UBA1/UBT1 domain	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modification process;proteolysis;ubiquitin-dependent	protein catabolic process;meti	4	3	3	5	3	3	5	3
tRNA synthetases	GO:0000267;GO:0 cell fraction;extra	GO:0000049;GO:0 tRNA binding;nucl	GO:0006082;GO:0 organic acid meta	hsa:8565	ko00400;ko00970	Phenylalanine, tyr	K01866	1	13	13	15	13
SMC proteins Flex	GO:0000228;GO:0 nuclear chromoso	GO:0000166;GO:0 nucleotide binding	GO:0006323;GO:0 DNA packaging;or	hsa:10592	ko04111	Cell cycle - yeast	K06674	1	2	2	3	2
DEAD/DEAH box 1	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via t	hsa:7919	30	8	8	14	8	8	14	2
Phosphoribosyl transferase	GO:0005829;GO:0 cytosol;intracellul	GO:0000166;GO:0 nucleotide binding	GO:0003008;GO:0 system process;or	hsa:5631;hsa:2211;ko00030;ko00230	Pentose phosphat	K00948	6	10	11	16	3	10
CBS domain pair1	GO:0005829;GO:0 cytosol;intracellul	GO:0003824;GO:0 catalytic activity;tr	GO:0006139;GO:0 nucleobase, nucle	hsa:3614	ko00230;ko00983	Purine metabolis	K00088	11	4	4	6	3
Ribosomal protein L16	GO:0015935;GO:0 small ribosomal s	GO:0003735;GO:0 structural consti	GO:0006414;GO:0 translational elon	hsa:6233;hsa:7311;ko03010;ko05012	Ribosome;Parkins	K02977;K04551;K0	26	19	21	35	19	21
Mitochondrial ribosome	GO:0000313;GO:0 organelle;ribosome;nucleus;mitochondrial	ribosome;ri	GO:0009653;GO:0 anatomical struct	hsa:64976	2	2	2	4	2	2	4	2
Phosphoribosyl transferase	GO:0005829;GO:0 cytosol;intracellul	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:353	ko00230	Purine metabolis	K00759	2	2	2	3	2
Tropomyosin	GO:0005737;GO:0 cytoplasm;cell sur	GO:0001871;GO:0 pattern binding;binding;glycosaminoglycan binding;hya	hsa:3161	ko04512	ECM-receptor inte	K06267	8	6	6	6	6	6
LIM domain	GO:0001725;GO:0 stress fiber;cytop	GO:0003779;GO:0 actin binding;actin	GO:0006996;GO:0 organelle organizi	hsa:51474	9	10	10	17	10	10	17	10
L27 domain;PDZ 1	GO:0000267;GO:0 cell fraction;meml	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;exocyto	hsa:55327	4	4	4	5	4	4	5	4
Staphylococcal nuclease	GO:0005634;GO:0 nucleus;Golgi app	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:27044	4	13	13	20	13	13	20	13
Mitogen-activated protein kinase 1	GO:0010008;GO:0 endosome membi	GO:0005488;GO:0 binding;protein bi	GO:0000186;GO:0 activation of MAP	hsa:8649	ko04010	MAPK signaling pa	K04370	2	2	2	2	2
Hsp70 protein	GO:0005859;GO:0 muscle myosin co	GO:0003774;GO:0 motor activity;cat	GO:0006810;GO:0 transport;skeletal	hsa:140465	K05738		3	11	12	22	8	14
Hsp70 protein	GO:0009986;GO:0 cell surface;cytop	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;re	hsa:3312	ko04010;ko04612	MAPK signaling pa	K03283	21	43	49	43	49
Tropomyosin	GO:0005829;GO:0 cytosol;integra	GO:0005488;GO:0 binding;protein binding	hsa:4076	6	4	4	5	4	4	5	4	4
Tropomyosin	GO:0005862;GO:0 muscle thin filam	GO:0003779;GO:0 actin binding;stru	GO:0006928;GO:0 cell motion;cellula	hsa:7171	ko04260	Cardiac muscle co	K10375	16	31	31	57	13
LSM domain;Dom	GO:0005681;GO:0 spliceosomal com	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:27258;hsa:25876	K04796		2	2	3	2	3	2
Proteasome activator complex 1	GO:0005829;GO:0 cytosol;proteaso	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:10197	ko03050;ko04612	Proteasome;Antig	K06698	4	8	13	8	8
Dynactin subunit 1	GO:0000776;GO:0 kinetochore;cond	GO:0005198;GO:0 structural molecu	GO:0000280;GO:0 nuclear division;c	hsa:11258	K10425		5	2	2	2	2	2
Vacuolar protein sorting 4	GO:0005768;GO:0 endosome;cytoso	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;cellular	hsa:55737	6	3	6	6	6	6	6	6
Nucleoside diphosphate kinase 1	GO:0001726;GO:0 ruffle;nucleus;cyt	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4831;hsa:654;ko00230;ko00240	Purine metabolis	K00940	13	16	29	13	16	29
Spermine/spermidine synthase	GO:0003824;GO:0 catalytic activity;s	GO:0006519;GO:0 cellular amino aci	hsa:6723	ko00271;ko00330	Methionine metal	K00797	1	3	3	3	3	3
Ubiquitin family	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0006464;GO:0 protein modificali	hsa:4738	K12158		4	3	3	6	3	3
Histidine kinase	GO:0005829;GO:0 cytosol;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;pn	hsa:3320	ko04914;ko04612	Progesterone-met	K04079	12	34	34	19	33
eIF4-gamma/eIF5	GO:0005737;GO:0 cytoplasm;intrace	GO:0005488 binding	GO:0006139;GO:0 nucleobase, nucle	hsa:9689	9	7	7	10	7	7	10	5
Cyclophilin type P	GO:0005681;GO:0 spliceosomal com	GO:0003755;GO:0 peptidyl-prolyl	GO:0006139;GO:0 nucleobase, nucle	hsa:10465	K09567		5	6	6	8	6	6
Nucleoside diphosphate kinase 1	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:4830	ko00230;ko00240	Purine metabolis	K00940	10	12	22	1	1
CP5F A subunit	GO:0005654;GO:0 nucleoplasm;cyto	GO:0003676;GO:0 nucleic acid bindir	GO:0000075;GO:0 cell cycle checkpo	hsa:1642	ko04120;ko03420	Ubiquitin mediate	K10610	19	39	43	71	39
HEAT repeat	GO:0000159;GO:0 protein phosphat	GO:0003823;GO:0 antigen binding;bi	GO:0000188;GO:0 inactivation of Mf	hsa:5518	ko04310;ko04350	Wnt signaling pat	K03456	17	16	16	24	16
PHD-finger;B-box	GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindir	GO:0000902;GO:0 cell morphogenes	hsa:10155	K08882		2	10	10	14	10	14
Elongation factor 1	GO:0005737;GO:0 cytoplasm;intrace	GO:0000166;GO:0 nucleotide binding	GO:0006412;GO:0 translation;cell cy	hsa:23708	5	2	2	2	2	2	2	2
CS domain	GO:0005634;GO:0 nucleus;cytoplasm	GO:0005488;GO:0 binding;protein bi	GO:0000280;GO:0 nuclear division;or	hsa:10726	3	6	6	10	6	6	10	6
PHF5-like protein	GO:0005686;GO:0 U2 snRNP;ribonuc	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:84844	1	3	3	5	3	3	5	3
TCP-1/cpn60 chap	GO:0016023;GO:0 cytoplasmic meml	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;hm	hsa:10575	K09496		5	28	28	52	28	28
CHCH domain	GO:0005747;GO:0 mitochondrial res	GO:0003824;GO:0 catalytic activity;tr	GO:0006091;GO:0 generation of pre	hsa:4702	ko00190;ko05010	Oxidative phosph	K03952	2	6	6	9	6
Proteasome A1-type	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5690	ko03050	Proteasome	K02734	6	6	11	6	6
CHCH domain	GO:0005758;GO:0 mitochondrial intermembrane space;organelle envelop	GO:0006810;GO:0 transport;intracell	hsa:11474	2	2	2	2	2	2	2	2	2
WD domain, G-be	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein binding	hsa:13091	1	3	4	4	3	4	4	3	4
TCP-1/cpn60 chap	GO:0005730;GO:0 nucleus;organel	GO:0000166;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;hm	hsa:22948	K09497		9	19	19	31	19	19
Erv1 / Air family	GO:0005739;GO:0 mitochondrion;or	GO:0003824;GO:0 catalytic activity;tr	GO:0007276;GO:0 gamete generation;spmatogenesis;metabolic process;cell proliferation;cellular process;rep	hsa:23294	2	4	4	4	4	4	4	4
Ankyrin repeat;Ph	GO:0005737;GO:0 cytoplasm;intrace	GO:0005488;GO:0 binding;protein binding	hsa:23294	5	3	3	3	3	3	3	3	3
Kinase binding pr	GO:0005634;GO:0 nucleus;cytosol;or	GO:0005488;GO:0 binding;protein bi	GO:0008152;GO:0 metabolic process	hsa:51002	5	2	2	2	2	2	2	2
Hsp70 protein	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 nucleotide binding	GO:0006461;GO:0 protein complex a	hsa:3308	ko04612	Antigen processin	K09489	3	10	11	10	10
Putative carnitine	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein binding;identical protein binding	hsa:51637	3	17	18	33	17	18	33	17	17
DEAD/DEAH box 1	GO:0000932;GO:0 cytoplasmic mRN	GO:0000166;GO:0 nucleotide binding;nucleoside binding;nucleoside binding;purine nucleosid	hsa:1656	2	5	5	7	5	5	7	5	5
ATPase family ass	GO:0005654;GO:0 nucleoplasm;DNA	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:5984	ko03030;ko03420	DNA replication;N	K10755	6	6	6	7	6
TCL1/MTCP1 fami	GO:0000267;GO:0 cell fraction;meml	GO:0005488;GO:0 binding;protein bi	GO:0007275;GO:0 multicellular orga	hsa:8115	K10167		1	3	3	3	4	3
Ion transport prot	GO:0008076;GO:0 voltage-gated pot	GO:0005215;GO:0 transporter activit	GO:0003008;GO:0 system process;m	hsa:3784	ko05110	Vibrio cholerae in	K04926	2	1	2	2	1

Amidohydrolase f	GO:0005739;GO:0 mitochondrion;ax	GO:0003824;GO:0 catalytic activity;h	GO:0006139;GO:0 nucleobase, nucle	hsa:1808;hsa:1401 ko04360	Axon guidance	K07528	12	4	4	5	2	2	2
Immunoglobulin C	GO:0000139;GO:0 Golgi membrane;x	GO:0005488;GO:0 binding;protein bi	GO:0002376;GO:0 immune system p	hsa:567 ko04612	Antigen processin	K08055	3	5	5	9	5	9	5
Ubiquitin-conjugating enzyme		GO:0001666;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:2738 ko04120	Ubiquitin mediate	K10583	2	3	3	3	3	3	3
Cofilin/Tropomyos	GO:0005856;GO:0 cytoskeleton;corti	GO:0003779;GO:0 actin binding;bind	GO:0006996;GO:0 organelle organizi	hsa:11034 K10363			6	6	20	32	14	17	28
ATP cone domain;	GO:0005829;GO:0 cytosol;ribonucleo	GO:0001666;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:6240 ko00230;ko00240	Purine metabolisn	K10807	8	5	5	5	5	5	5
EF hand	GO:000267;GO:0 cell fraction;meme	GO:0005215;GO:0 transporter activ	GO:0006810;GO:0 transport;ion tran	hsa:1192 K05021			1	4	4	6	4	4	6
Hyaluronan / mR	NA GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:26135			4	17	17	31	17	17	31
Ribosomal protein	GO:0015935;GO:0 small ribosomal s	GO:0003735;GO:0 structural constitu	GO:0006414;GO:0 translational elongation;metabolic process;biosynthetic process;macromolecule biosynthetic				1	7	7	13	7	7	13
Glycosyl hydrolase	GO:0000323;GO:0 lytic vacuole;lysos	GO:0003824;GO:0 catalytic activity;h	GO:0001501;GO:0 skeletal system de	hsa:3074 ko00530;ko00603	Aminosugars met;	K12373	14	12	12	20	12	12	20
RNA recognition n	GO:0005681;GO:0 spliceosomal com	GO:0001666;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via t	hsa:6626 K11091			2	6	6	10	6	6	10
Catalase;Catalase	GO:0005778;GO:0 peroxisomal mem	GO:0001666;GO:0 nucleotide binding	GO:0000302;GO:0 response to reacti	hsa:847 ko00680;ko00380	Methane metabol	K03781	1	3	3	4	3	4	3
Fibronectin type II	GO:0005737;GO:0 cytoplasm;macror	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:3054			5	9	9	11	9	9	11
EF hand		GO:0005488;GO:0 binding;calcium ion binding;ion binding;cation binding;	hsa:79180				6	8	8	11	8	8	11
Eukaryotic transla	GO:0005829;GO:0 cytosol;polysome;	GO:0003676;GO:0 nucleic acid bindir	GO:0006412;GO:0 translation;metab	hsa:1965 K03237			2	9	9	13	9	9	13
Cytochrome c oxid	GO:0005743;GO:0 mitochondrion;inn	GO:0003824;GO:0 catalytic activity;c	GO:0008152;GO:0 metabolic process;oxidation reduction				1	8	8	13	8	8	13
Glutathione S-tran	GO:0005634;GO:0 nucleus;cytoplasm;organelle;membrane-bounded organ	GO:0006412;GO:0 translation;metabolic process;negative regulation of cell proliferation;biosynthetic process;n					7	9	9	17	9	9	17
PA domain	GO:0005576	extracellular region	hsa:84279				1	1	1	2	1	1	2
S-adenosylmethionine synthetase, C-terminal domain;S	GO:0001666;GO:0 nucleotide binding	GO:0006730;GO:0 one-carbon metal	hsa:4144 ko00271;ko00450	Methionine metal	K00789		5	11	11	19	11	11	19
NUDIX domain	GO:0005777;GO:0 peroxisome;cytos	GO:000287;GO:0 magnesium ion bi	GO:0006066;GO:0 alcohol metabolic process;lipid metabolic process;steroid biosynthetic process;cholesterol bi				4	2	2	3	2	3	2
Acyl CoA binding protein		GO:0000062;GO:0 acyl-CoA binding;r	GO:0006810;GO:0 transport;establis	hsa:1622 ko03320	PPAR signaling pa	K08762	6	4	4	6	4	4	6
TCP-1/cpn60 chap	GO:0005829;GO:0 cytosol;intracellu	GO:0001666;GO:0 nucleotide binding	GO:0006457;GO:0 protein folding;mi	hsa:10694 K09500			5	31	31	57	31	31	57
Pterin 4 alpha carbinolamine dehydratase		GO:0003824;GO:0 catalytic activity;b	GO:0006355;GO:0 regulation of tran	hsa:84105 K01724			2	2	2	2	2	2	2
ATPase family ass	GO:0005743;GO:0 mitochondrion;inn	GO:0001666;GO:0 nucleotide binding	GO:0006508;GO:0 proteolysis;ense	hsa:10939 K08956			8	2	2	2	2	2	2
Adaptor complex	GO:000119;GO:0 AP-type membr	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;intracell	hsa:372			5	10	10	18	10	10	18
ATPase family ass	GO:000123;GO:0 histone acetyltran	GO:0001666;GO:0 nucleotide binding	GO:0000280;GO:0 nuclear division;n	hsa:8607 ko04310	Wnt signaling patl	K04499	5	15	15	30	15	15	30
'Cold-shock' DNA	GO:0005737;GO:0 cytoplasm;intrace	GO:0003676;GO:0 nucleic acid bindir	GO:0006355;GO:0 regulation of tran	hsa:7812			5	8	8	10	8	8	10
ATPase family ass	GO:0005634;GO:0 nucleus;cytosol;pi	GO:0003712;GO:0 transcription cofa	GO:0002791;GO:0 regulation of pept	hsa:5715 K06693			9	9	9	15	9	9	15
DEAD/DEAH box f	GO:0005634;GO:0 nucleus;organelle	GO:0001666;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:10521 K06027			4	20	20	27	20	20	27
SH2 domain;STAT	GO:0005730;GO:0 nucleolus;cytopla	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:6772 ko04630;ko04620	Jak-STAT signaling	K11220	8	6	6	7	4	4	4
Caldesmon	GO:0005856;GO:0 cytoskeleton;plasi	GO:0004871;GO:0 signal transducer	GO:0007154;GO:0 cell communicati	hsa:4046			11	4	4	6	4	4	6
MIR domain	GO:0005615;GO:0 extracellular spac	GO:0000030;GO:0 mannosyltransfer	GO:0005975;GO:0 carbohydrate met	hsa:6388			1	2	2	2	2	2	2
DEAD/DEAH box f	GO:0005829;GO:0 cytosol;eukaryotic	GO:0001666;GO:0 nucleotide binding	GO:0006412;GO:0 translation;metab	hsa:1973 K03257			6	15	15	26	15	15	26
Proteasome A-type	GO:0005634;GO:0 nucleus;cytosol;pi	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5689 ko03050	Proteasome	K02732	2	8	8	14	8	8	14
PDZ domain [Also	GO:000164;GO:0 protein phosphat	GO:0003779;GO:0 actin binding;enzy	GO:0001558;GO:0 regulation of cell	hsa:84687			6	4	4	4	4	4	4
Septin	GO:0005634;GO:0 nucleus;spindle;se	GO:0001666;GO:0 nucleotide binding	GO:0000280;GO:0 nuclear division;o	hsa:4735			10	5	5	6	5	5	6
ATP synthase, Del	GO:0000275;GO:0 mitochondrion pro	GO:0003824;GO:0 catalytic activity;ti	GO:0006139;GO:0 nucleobase, nucle	hsa:513 ko00190;ko05010	Oxidative phosph	K02134	1	5	5	8	5	5	8
Ankyrin repeat;SH	GO:0005737;GO:0 cytoplasm;intrace	GO:0005488;GO:0 binding;protein bi	GO:0001503;GO:0 ossification;cell cc	hsa:26578			1	3	3	6	3	3	6
Exportin 1-like pr	GO:0005654;GO:0 nucleoplasm;cyto	GO:0000049;GO:0 tRNA binding;nucl	GO:0006405;GO:0 RNA export from i	hsa:11260			3	3	3	3	3	3	3
Myosin-like coiled	GO:0005576;GO:0 extracellular regio	GO:0005102;GO:0 receptor binding;x	GO:0006810;GO:0 transport;exocyto	hsa:200081			1	3	3	3	3	3	3
ARP2/3 complex 1	GO:0005737;GO:0 cytoplasm;Arp2/3	GO:0003779;GO:0 actin binding;stru	GO:0006928;GO:0 cell motion;organ	hsa:10092 ko04810	Regulation of acti	K05754	3	3	3	4	3	3	4
F-box domain;FIS	GO:0003824;GO:0 catalytic activity;y	GO:0006464;GO:0 protein modificati	hsa:26263 K10302				12	13	13	18	13	13	18
WD domain, G-be	GO:0005681;GO:0 spliceosomal com	GO:0003824;GO:0 catalytic activity;s	GO:0006139;GO:0 nucleobase, nucle	hsa:11171			4	13	13	17	13	13	17
GTPase of unknow	GO:0005737;GO:0 cytoplasm;intrace	GO:0001666;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:29789 K06942			4	6	6	10	6	6	10
RNA recognition n	GO:0005829;GO:0 cytosol;eukaryotic	GO:0001666;GO:0 nucleotide binding	GO:0006412;GO:0 translation;regula	hsa:7458			2	3	3	4	3	3	4
CBS domain pair;j	GO:0005829;GO:0 cytosol;intracellu	GO:0003824;GO:0 catalytic activity;ll	GO:0006139;GO:0 nucleobase, nucle	hsa:3615 ko00230;ko00983	Purine metabolisn	K00088	3	18	18	29	18	18	29
Cyclophilin type p	GO:0005737;GO:0 cytoplasm;intrace	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0006457;GO:0 protein folding;mi	hsa:5481 ko04020;ko05012	Cell signaling	K05864	1	3	3	5	3	3	5
ATP synthase (E/3	GO:0032991;GO:0 macromolecula	GO:0003824;GO:0 catalytic activity;ti	GO:0006139;GO:0 nucleobase, nucle	hsa:529 ko00190;ko05110	Oxidative phosph	K02150	3	1	1	1	1	1	1
Surp module;Ubiq	GO:0005681;GO:0 spliceosomal com	GO:0003676;GO:0 nucleic acid bindir	GO:0000389;GO:0 nuclear mRNA 3'-	hsa:10291			4	3	3	4	3	3	4
Calponin homolog	GO:0005856;GO:0 cytoskeleton;corti	GO:0005488;GO:0 binding;protein bi	GO:0000280;GO:0 nuclear division;o	hsa:22919 K10436			2	1	1	1	1	1	1
F-actin capping pr	GO:0008290;GO:0 F-actin capping pr	GO:0003779;GO:0 actin binding;bind	GO:0006461;GO:0 protein complex a	hsa:829 K10364			1	13	13	23	13	13	23
XPG I-region;XPG	GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:2237 ko03030;ko03410	DNA replication;B	K04799	2	3	3	4	3	3	4
KH domain;ROK/N	GO:0005654;GO:0 nucleoplasm;splic	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:3190			7	15	15	25	15	15	25
Domain found in I	GO:0005829;GO:0 cytosol;eukaryotic	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:8894 K03238			2	11	11	19	11	11	19
DE Adenylate cy	GO:0005886;GO:0 plasma membran	GO:0003779;GO:0 actin binding;bind	GO:0006140;GO:0 regulation of nucl	hsa:10487			14	10	10	14	10	10	14
Ubiquitin interact	GO:0000502;GO:0 proteasome comf	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5710 ko03050	Proteasome	K03029	5	3	3	6	3	3	6
Tubulin binding cc	GO:0005737;GO:0 cytoplasm;microt	GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;pn	hsa:6902			6	9	9	14	9	9	14
Phosphoribosyl transferase domain		GO:0001666;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:5634 ko00030;ko00230	Pentose phosphat	K00948	4	9	10	14	2	2	2
C-terminal domain	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;p	GO:0006916;GO:0 anti-apoptosis;res	hsa:7001 K03386			4	13	13	23	12	12	21
Cathepsin propep	GO:0000323;GO:0 lytic vacuole;extra	GO:0003824;GO:0 catalytic activity;e	GO:0002376;GO:0 immune system p	hsa:1520 ko04142;ko04612	Antigen processin	K01368	2	5	5	8	5	5	8
ATP synthase alph	GO:0005754;GO:0 mitochondrion;inn	GO:0001666;GO:0 nucleotide binding	GO:0001525;GO:0 angiogenesis;nucl	hsa:506 ko00190;ko05010	Oxidative phosph	K02133	7	27	27	38	27	27	38
GO:0005622;GO:0 intracellular;cell p	GO:0005488;GO:0 binding;zinc ion bi	GO:0006355;GO:0 regulation of tran	hsa:7756				6	4	4	8	4	4	8
Ubiquinol-coctchr	GO:0005746;GO:0 mitochondrion res	GO:0003824;GO:0 catalytic activity;h	GO:0006091;GO:0 generation of prex	hsa:7381 ko00190;ko04260	Oxidative phosph	K00417	5	5	5	5	5	5	5
Replication protei	GO:0005654;GO:0 nucleoplasm;DNA	GO:0003676;GO:0 nucleic acid bindir	GO:0000718;GO:0 nucleotide-excisio	hsa:6118 ko03030;ko03420	DNA replication;N	K10739	4	3	3	4	3	3	4

eRF1 domain 1;eR	GO:0005737;GO:0 cytoplasm;intrac	GO:0003676;GO:0 nucleic acid bindir	GO:0006415;GO:0 translational term	hsa:2107	K03265	5	6	6	11	6	6	11	6
Dynein light inter	GO:0005874;GO:0 microtubule;micrc	GO:0001166;GO:0 nucleotide binding;nucleoside binding;purine nucleosic	hsa:51143	K10416	4	8	8	12	8	8	12	8	8
Anticodon binding	GO:0005737;GO:0 cytoplasm;intrac	GO:0001166;GO:0 nucleotide binding;GO:0006082;GO:0 organic acid meta	hsa:6897	ko00260;ko00970	Glycine, serine ani	K01868	4	2	2	2	2	2	2
Tetrapeptide repeat;Tetrapeptide repeat	GO:0005488 binding	GO:0006873;GO:0 cellular ion home	hsa:57217		7	2	2	2	2	2	2	2	2
IQ, calmodulin-bin	GO:0001725;GO:0 stress fiber;cell	GO:0000146;GO:0 microfilament mo	GO:0000281;GO:0 cytokinesis after n	hsa:4628	ko04530	Tight junction	K10352	5	100	104	119	79	79
C-terminal domain	GO:0003232;GO:0 lytic vacuole;nucle	GO:0003824;GO:0 catalytic activity;e	GO:0006629;GO:0 lipid metabolic pri	hsa:9588	ko00360;ko00623	Phenylalanine me	K00430;K01066;K	2	14	14	23	14	23
Intermediate filan	GO:0005882;GO:0 intermediate filan	GO:0005198;GO:0 structural molecu	GO:0007398;GO:0 ectoderm develop	hsa:3854			K07605	1	32	33	33	3	3
Proteasome activ	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0005338;GO:0 proteasome activ	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5720	ko03050;ko04612	Proteasome;Antig	K06696	2	16	17	30	16	17
	GO:0005783;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;protein bi	GO:0006461;GO:0 protein complex a	hsa:8624			K11875	4	2	2	3	2	3
Electron transfer I	GO:0005759;GO:0 mitochondrial ma	GO:0009055 electron carrier ac	GO:0006091;GO:0 generation of precursor metabolites and energy;transport;metabolic process;cellular proces					2	5	5	6	5	5
SRP40, C-terminal	GO:0005730;GO:0 nucleolus;cytopla	GO:0000166;GO:0 nucleotide binding;GO:0000280;GO:0 nuclear division;n	hsa:9221		3	4	4	4	4	4	4	4	4
ETC complex I sub	GO:0005747;GO:0 mitochondrial res	GO:0003824;GO:0 catalytic activity;N	GO:0006091;GO:0 generation of pre	hsa:4698	ko00190;ko05010	Oxidative phosph	K03949	5	4	4	5	4	4
BoJA-like protein					2	4	4	7	4	4	7	4	4
Hsp70 protein	GO:0005634;GO:0 nucleus;endoplasm	GO:0001166;GO:0 nucleotide binding;GO:0006916;GO:0 anti-apoptosis;res	hsa:3309		5	41	46	82	39	44	78	39	39
Cyclophilin type p	GO:0005681;GO:0 spliceosomal com	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0006139;GO:0 nucleobase, nucle	hsa:53938			K01802	6	2	2	2	2	2
Cofilin/tropomyos	GO:0005634;GO:0 nucleus;mitochon	GO:0003779;GO:0 actin binding;rece	GO:0006464;GO:0 protein modificati	hsa:2764	3	5	5	5	5	5	5	4	4
RNB domain	GO:0000178;GO:0 exosome (RNase	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:22894			K01149	4	4	4	4	4	4
Inorganic pyropho	GO:0005829;GO:0 cytosol;intracellul	GO:0000287;GO:0 magnesium ion bi	GO:0006793;GO:0 phosphorus metal	hsa:5464	ko00190	Oxidative phosph	K03507	3	35	40	69	35	40
Tetrapeptide	GO:0005737;GO:0 cytoplasm;intrac	GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;mi	hsa:6767			K09560	7	6	6	11	6	6
Coatomer epsilon	GO:0005829;GO:0 cytosol;membran	GO:0005198;GO:0 structural molecu	GO:0006810;GO:0 transport;retrogra	hsa:11316	4	4	4	6	4	4	6	4	4
Kinesin motor dor	GO:0005813;GO:0 centrosome;micrc	GO:0001166;GO:0 nucleotide binding;GO:0007017;GO:0 microtubule-base	hsa:3796;hsa:11004;hsa:84643		11	2	2	2	2	2	2	2	2
WD domain, G-beta repeat		GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;intracellular protein transport;ER to Golgi vesicle-mediated transport;cellular proci		5	3	3	4	3	3	4	3	3
PCI domain	GO:0005829;GO:0 cytosol;proteasom	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5719	ko03050	Proteasome	K03039	8	4	4	5	4	4
ATPase family ass	GO:0005794;GO:0 Golgi apparatus;c	GO:0001166;GO:0 nucleotide binding;GO:0000226;GO:0 microtubule cytos	hsa:1778		1	20	20	20	20	20	20	20	20
Proteasome A-type	GO:0005634;GO:0 nucleus;centrosor	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5692	ko03050	Proteasome	K02736	1	2	2	3	2	2
NAC domain	GO:0005634;GO:0 nucleus;organelle	GO:0003702;GO:0 RNA polymerase I	GO:0006139;GO:0 nucleobase, nucle	hsa:689			K01527	2	2	4	2	2	4
DNA polymerase	GO:0005654;GO:0 nucleoplasm;orga	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:23649	ko03030	DNA replication	K02321	2	2	2	3	2	2
Cna protein B-type	GO:0005789;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;protein binding;carbohydrate binding	hsa:283820;hsa:408050;hsa:23420		9	8	8	14	8	8	8	14	8
FKBP-type peptid	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0006457;GO:0 protein folding;mi	hsa:2289			K09571	6	19	20	30	19	20
RNA recognition n	GO:0005654;GO:0 nucleoplasm;cyto	GO:0001166;GO:0 nucleotide binding;GO:0000375;GO:0 RNA splicing, via t	hsa:8106		3	2	2	2	2	2	2	2	2
Phosphorylase su	GO:0005829;GO:0 cytosol;intracellul	GO:0001882;GO:0 nucleoside binding;GO:0002376;GO:0 immune system p	hsa:4860		1	8	10	13	8	10	13	8	8
Copper/zinc super	GO:0005615;GO:0 extracellular spac	GO:0003824;GO:0 catalytic activity;e	GO:0000187;GO:0 activation of MAP	hsa:6647	ko05014;ko05016	Amyotrophic later	K04565	6	6	6	9	6	6
FKBP-type peptid	GO:0000267;GO:0 cell fraction;meml	GO:0003712;GO:0 transcription cofa	GO:0006457;GO:0 protein folding;xenobiotic metabolic process;metabolic process;cellular process;protein met		2	2	2	2	2	2	2	2	2
Clathrin light chain	GO:0030117;GO:0 membrane coat;c	GO:0005198;GO:0 structural molecu	GO:0006810;GO:0 transport;intracell	hsa:1211	ko04142;ko05016	Huntington's dise	K04644	7	2	2	2	2	2
Cathepsin C excl	GO:0003323;GO:0 lytic vacuole;lysos	GO:0003824;GO:0 catalytic activity;e	GO:0002376;GO:0 immune system process;proteolysis;immune response;metabolic process;catabolic process;n		5	6	6	9	6	6	9	6	9
	GO:0005686;GO:0 u2 snRNP;ribonuc	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:6627			K11092	5	8	8	9	8	8
Thioredoxin	GO:0005730;GO:0 nucleolus;mitoch	GO:0003824;GO:0 catalytic activity;e	GO:0006091;GO:0 generation of pre	hsa:25828				7	7	10	7	10	7
Tumour protein D52 family	GO:0005488;GO:0 binding;protein binding	hsa:7165			2	2	2	2	2	2	2	2	2
FKBP-type peptid	GO:0005789;GO:0 endoplasmic retic	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0006457;GO:0 protein folding;mi	hsa:2286			K09569	7	9	10	18	9	10
Mov34/MPN/PAD	GO:0005829;GO:0 cytosol;eukaryotic	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:8667			K03247	6	5	5	6	5	6
HMG (high mobil)	GO:0000228;GO:0 nuclear chromoso	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:3148			K11295	2	4	4	7	3	6
Prefoldin subunit	GO:0005634;GO:0 nucleus;prefoldin	GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;mi	hsa:7411				2	4	4	4	4	4
F5/8 type C domain		GO:0006950;GO:0 response to stress	hsa:51668		1	2	2	2	2	2	2	2	2
Chaperone for wingless signalling and trafficking of LDL receptor		GO:0007498;GO:0 mesoderm develo	hsa:23184		1	5	5	6	5	5	6	5	5
RNA recognition n	GO:0005634;GO:0 nucleus;organelle	GO:0001166;GO:0 nucleotide binding;GO:0006139;GO:0 nucleobase, nucle	hsa:5725		18	7	12	7	7	7	12	7	7
Ubiquitin carboxyl	GO:0005737;GO:0 cytoplasm;intrac	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:9097			K11843	4	5	5	7	5	7
2-oxoacid dehydr	GO:0005947;GO:0 mitochondrial alpi	GO:0003824;GO:0 catalytic activity;e	GO:0006082;GO:0 organic acid meta	hsa:1629	ko00280	Valine, leucine ani	K09699	3	16	16	26	16	16
Cytochrome c	GO:0000159;GO:0 protein phosphati	GO:0005488;GO:0 binding;iron ion b	GO:0000737;GO:0 DNA catabolic pro	hsa:54205	ko04210;ko04115	Apoptosis;p53 sig	K08738	3	4	4	7	4	4
Chaperonin 10 kD	GO:0005759;GO:0 mitochondrial ma	GO:0000166;GO:0 nucleotide binding;GO:0006457;GO:0 protein folding;ac	hsa:3336		6		K04078	6	17	30	17	17	30
2-oxoacid dehydr	GO:0005634;GO:0 nucleus;mitochon	GO:0003824;GO:0 catalytic activity;d	GO:0006084;GO:0 acetyl-CoA metabolic process;tricarboxylic acid cycle;coenzyme metabolic process;metabolic		4	12	13	24	12	13	24	12	13
Cofilin/tropomyos	GO:0005737;GO:0 cytoplasm;cytosk	GO:0003779;GO:0 actin binding;binding;protein binding;cytoskeletal prot	hsa:23406		1	3	3	4	3	3	4	3	4
SH3-binding, glut	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;e	GO:0009987;GO:0 cellular process;cc	hsa:83442				2	2	2	2	2	2
MIR domain;Amid	GO:0005783;GO:0 endoplasmic retic	GO:0003824;GO:0 catalytic activity;hydrolase activity;hydrolase activity, a	hsa:23753		1	7	7	10	7	7	10	5	7
Phosphoglycerate	GO:0005737;GO:0 cytoplasm;intrac	GO:0001166;GO:0 nucleotide binding;GO:0005975;GO:0 carbohydrate met	hsa:5230		6	19	19	31	19	19	31	19	19
NAD dependent e	GO:0005737;GO:0 cytoplasm;intrac	GO:0003824;GO:0 catalytic activity;b	GO:0005975;GO:0 carbohydrate met	hsa:2762	ko00051	Fructose and man	K01711	2	9	9	13	9	9
RNA recognition n	GO:0000267;GO:0 cell fraction;meml	GO:0001166;GO:0 nucleotide binding;GO:0006139;GO:0 nucleobase, nucle	hsa:10492		12	8	8	12	8	8	12	8	8
Proteasome A-type	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5694	ko03050	Proteasome	K02738	2	1	2	2	2	2
PCI domain	GO:0000502;GO:0 proteasome comp	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5717	ko03050	Proteasome	K03036	2	15	15	24	15	24
Thioredoxin	GO:0005829;GO:0 cytosol;intracellul	GO:0005488;GO:0 binding;protein bi	GO:0006091;GO:0 generation of pre	hsa:7295			K03671	2	6	6	8	12	6
DJ-1/Pfp1 family	GO:0005739;GO:0 mitochondrial;organelle;membrane-bounded organelle;intracellular organelle;intracellular r	hsa:8209			7	7	7	10	7	7	10	7	7
Lipocalin / cytosol	GO:0005737;GO:0 cytoplasm;intrac	GO:0005215;GO:0 transporter activit	GO:0006629;GO:0 lipid metabolic pri	hsa:2171;hsa:728	ko03320	PPAR signaling pa	K08754	3	14	16	25	14	16
Fumarase C C-ter	GO:0005759;GO:0 mitochondrial ma	GO:0003824;GO:0 catalytic activity;f	GO:0006082;GO:0 organic acid meta	hsa:2271	ko00020;ko00720	Citrate cycle (TCA	K01679	2	9	9	15	9	9
Prefoldin subunit	GO:0005886;GO:0 plasma membran	GO:0003676;GO:0 nucleic acid bindir	GO:0006457;GO:0 protein folding;cc	hsa:5201			K09548	2	2	2	2	2	2
Microtubule assor	GO:0000139;GO:0 Golgi membrane;x	GO:0000149;GO:0 SNARE binding;ret	GO:0006810;GO:0 transport;intra-G	hsa:11345	ko04140	Regulation of aut	K08341	1	6	6	10	6	10
Immunoglobulin e	GO:0005576;GO:0 extracellular regio	GO:0004871;GO:0 signal transducer	GO:0009987;GO:0 cellular process;cc	hsa:84824				9	3	3	5	3	3

ARP2/3 complex	GO:0005737;GO:0 cytoplasm;Arp2/3	GO:0003779;GO:0 actin binding;struc	GO:0006928;GO:0 cell motion;regula	hsa:10094	ko04810	Regulation of actin	K05756	4	7	8	10	7	8	10	7
Ubiquitin-conjug	GO:0001151;GO:0 ubiquitin ligase	GO:0003824;GO:0 catalytic activity;li	GO:0006464;GO:0 protein modificati	hsa:7332	ko04120;ko05012	Ubiquitin mediate	K04552	3	3	3	5	3	3	5	3
Endonuclease/Exc	GO:0005654;GO:0 nucleoplasm;endc	GO:0000287;GO:0 magnesium ion bi	GO:0006139;GO:0 nucleobase, nucle	hsa:328	ko03410	Base excision repa	K10771	3	7	7	9	7	7	9	7
Calponin homolog	GO:0008091;GO:0 spectrin;organelle	GO:0003779;GO:0 actin binding;struc	GO:0006810;GO:0 transport;regulati	hsa:6712		K06115		7	19	19	19	16	16	16	16
La domain;RNA re	GO:0005634;GO:0 nucleus;ribonucle	GO:0000049;GO:0 tRNA binding;nuc	GO:0006139;GO:0 nucleobase, nucle	hsa:6741	ko05322	Systemic lupus en	K11090	5	18	18	29	18	18	29	18
ADP-ribosylation	GO:0000139;GO:0 Golgi membrane;r	GO:0000166;GO:0 nucleotide bindin	GO:0007049;GO:0 cell cycle;cell com	hsa:4043		K07944		1	3	3	4	3	3	4	3
Proteasome activ	GO:0005829;GO:0 cytosol;proteasom	GO:0008538;GO:0 proteasome activ	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5721	ko03050;ko04612	Proteasome;Antig	K06697	1	12	13	20	12	13	20	12
Protein of unknow	GO:0016021;GO:0 integral to membr	GO:0005215;GO:0 transporter activit	GO:0006810;GO:0 transport;ion tran	hsa:63982				4	1	2	2	1	2	2	1
Redoxin;AhpC/Ts	GO:0005739;GO:0 mitochondrion;pe	GO:0003824;GO:0 catalytic activity;p	GO:0000302;GO:0 response to reacti	hsa:25824		K11187		4	9	9	14	9	14	9	9
Skp1 family, dime	GO:0005654;GO:0 nucleoplasm;cyto	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:6500	ko04120;ko04310	Ubiquitin mediate	K03094	12	9	9	13	9	9	13	9
Macrophage migr	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;d	GO:0006082;GO:0 organic acid meta	hsa:1652;hsa:100037417		K10028		9	7	7	13	7	13	7	7
Double-stranded	GO:0003676;GO:0 nucleic acid bindir	GO:0006915;GO:0 apoptosis;inductio	hsa:9141			K06875		2	2	2	2	2	2	2	2
RanBP1 domain	GO:0005634;GO:0 nucleus;organelle	GO:0005083;GO:0 small GTPase regu	GO:0006810;GO:0 transport;cell com	hsa:5902				13	8	8	13	8	8	13	8
Exonuclease	GO:0016604;GO:0 nuclear body;PML	GO:0000175;GO:0 3'-5'-exoribonucle	GO:0000738;GO:0 DNA catabolic pro	hsa:3669		K01147		3	6	6	8	6	6	8	6
HMG (high mobil	GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindir	GO:0000122;GO:0 negative regulatio	hsa:3146;hsa:103;ko03410		Base excision repa	K10802	15	7	7	11	7	7	11	6
EGF-like domain	GO:0016021;GO:0 integral to membr	GO:0005488;GO:0 binding;calcium io	GO:0006810;GO:0 transport;endocyt	hsa:53353				2	2	2	2	2	2	2	2
Endoplasmic retic	GO:0005783;GO:0 endoplasmic retic	GO:0003756;GO:0 protein disulfide I	GO:0006457;GO:0 protein folding;transport;intracellular protein transport;metabolic process;protein secretion;					4	11	11	11	11	11	11	11
Protein of unknow	GO:0005634;GO:0 nucleus;organelle;membrane-bounded organelle;intracellular organelle;intracellular membr	hsa:25915				K09008		2	6	6	6	6	6	6	6
Alcohol dehydrog	GO:0000267;GO:0 cell fraction;extra	GO:0000166;GO:0 nucleotide bindin	GO:0005975;GO:0 carbohydrate met	hsa:6652	ko00051	Fructose and man	K00008	2	5	5	8	5	5	8	5
short chain dehyd	GO:0005739;GO:0 mitochondrion;or	GO:0000166;GO:0 nucleotide bindin	GO:0006082;GO:0 organic acid meta	hsa:1666		K00219		7	8	8	12	8	8	12	8
DEAD/DEAH box f	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide bindin	GO:0000184;GO:0 nuclear-transcribe	hsa:9775		K03257		4	6	6	9	4	4	6	4
Dynamin	GO:0000776;GO:0 kinetochore;centr	GO:0003774;GO:0 motor activity;cat	GO:0000280;GO:0 nuclear division;o	hsa:10540	ko05016	Huntington's dise	K10424	12	10	17	10	17	10	17	10
Iron/manganese s	GO:0005759;GO:0 mitochondrial ma	GO:0003824;GO:0 catalytic activity;s	GO:0000302;GO:0 response to reacti	hsa:6648	ko05016	Huntington's dise	K04564	8	5	5	6	5	6	5	6
FKBP-type peptid	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0006457;GO:0 protein folding;m	hsa:2287		K09570		3	3	3	3	3	3	3	3
Transcriptional	GO:0005667;GO:0 transcription fact	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:10923				2	2	2	2	2	2	2	2
metallopeptidase	GO:0005730;GO:0 nucleus;cytoplasm	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:5036				8	18	18	30	18	18	30	18
Ubiquitin-conjug	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;b	GO:0000209;GO:0 protein polyubiqu	hsa:7336		K10704		8	5	5	9	5	5	9	1
SH3-binding, glut	GO:0005634;GO:0 nucleus;cytoplasm	GO:0004871;GO:0 signal transducer activity;SH3/SH2 adaptor activity;bins	hsa:6451					1	5	5	7	5	5	7	5
	GO:0005576	extracellular regio	GO:0003823;GO:0 antigen binding;bi	GO:0002376;GO:0 immune system process;immune response;response to stimulus				4	4	4	8	4	4	8	4
Ribosomal protein	GO:0000315;GO:0 organelle large r	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:65008				4	6	6	7	6	6	7	6
TCP-1/cpn60 chap	GO:0005615;GO:0 extracellular spac	GO:0000166;GO:0 nucleotide bindin	GO:0001775;GO:0 cell activation;cyt	hsa:3329	ko04940	Type I diabetes m	K04077	9	39	42	73	39	42	73	39
Mov34/MPN/PAD	GO:0005829;GO:0 cytosol;proteasom	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;ubiqui	hsa:5713	ko03050	Proteasome	K03038	2	10	18	10	18	10	18	10
RHO protein GDP	GO:0005737;GO:0 cytoplasm;cytosk	GO:0005083;GO:0 small GTPase regu	GO:0006916;GO:0 anti-apoptosis;cel	hsa:396				3	11	12	19	11	12	19	11
Protein of unknow	GO:0005730;GO:0 nucleus;cell cort	GO:0000166;GO:0 nucleotide bindin	GO:0001525;GO:0 angiogenesis;anat	hsa:4691		K11294		3	29	29	52	29	52	29	29
Double stranded	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucleoside, nucleotide and nucleic acid metabolic process;transcription;regulati					5	4	4	6	3	3	5	3
Thioredoxin	GO:0005783;GO:0 endoplasmic retic	GO:0003756;GO:0 protein disulfide I	GO:0006810;GO:0 transport;protein	hsa:9601	ko05110	Vibrio cholerae in	K09582	1	11	11	14	11	11	14	11
Proteasome A-ty	GO:0005634;GO:0 nucleus;cytosol;pr	GO:0003824;GO:0 catalytic activity;c	GO:0002376;GO:0 immune system p	hsa:5698	ko03050	Proteasome	K02741	7	3	3	4	3	3	4	3
Cofilin/tropomyos	GO:0005634;GO:0 nucleus;mitochon	GO:0003779;GO:0 actin binding;enz	GO:0006464;GO:0 protein modificati	hsa:9535				4	1	5	8	4	4	7	4
Thif family;Ubiqui	GO:0005634;GO:0 nucleus;organelle	GO:0000166;GO:0 nucleotide bindin	GO:0006464;GO:0 protein modificati	hsa:10054	ko04120	Ubiquitin mediate	K10685	3	5	5	5	5	5	6	5
Hsp70 protein	GO:0005783;GO:0 endoplasmic retic	GO:0000166;GO:0 nucleotide bindin	GO:0001666;GO:0 response to hypoo	hsa:10525		K09486		8	3	3	4	3	3	4	3
Prefoldin subunit	GO:0016272;GO:0 prefolddin complex	GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;pn	hsa:10471		K04798		2	2	2	4	2	2	2	2
Cyclophilin type	GO:0005576;GO:0 extracellular regio	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0006139;GO:0 nucleobase, nucle	hsa:5478		K03767		19	13	18	32	13	18	32	13
Protein-L-isoaspar	GO:0005783;GO:0 endoplasmic retic	GO:0003824;GO:0 catalytic activity;p	GO:0006464;GO:0 protein modificati	hsa:5110		K00573		8	13	15	25	13	15	25	13
Ribose 5-phospha	GO:0005829;GO:0 cytosol;intracellu	GO:0003824;GO:0 catalytic activity;r	GO:0005975;GO:0 carbohydrate met	hsa:22934	ko00030;ko00710	Pentose phosphat	K01807	2	13	13	21	13	13	21	13
Tetrapeptide	GO:0005737;GO:0 cytoplasm;intrace	GO:0005488;GO:0 binding;protein bi	GO:0044419;GO:0 interspecies interi	hsa:6449				2	7	7	10	7	7	10	7
Ezrin/radixin/moe	GO:0005829;GO:0 cytosol;cytoskelet	GO:0003779;GO:0 actin binding;bind	GO:0006996;GO:0 organelle organiz	hsa:7430	ko04810;ko04670	Regulation of actin	K08007	8	29	29	46	29	29	46	19
SPFH domain / Ba	GO:0005856;GO:0 cytoskeleton;orga	GO:0005102;GO:0 receptor binding;binding;protein binding	hsa:30968					3	2	2	3	2	2	3	2
	GO:0005576;GO:0 extracellular regio;cytoplasm;intracellular part;cell par	GO:0006915;GO:0 apoptosis;cell dea	hsa:51237					6	8	8	12	8	9	12	8
FAT domain;FATC	GO:0005654;GO:0 nucleoplasm;DNA	GO:0000166;GO:0 nucleotide bindin	GO:0000726;GO:0 non-recombinatio	hsa:5591	ko03450;ko04110	Non-homologous	K06642	3	43	43	43	43	43	43	43
Ubiquitin family	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0006508;GO:0 proteolysis;metab	hsa:6613;hsa:387082		K12160		8	2	2	4	2	2	4	2
GDSL-like Lipase/l	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;1	GO:0006629;GO:0 lipid metaboli	pn hsa:5049	ko00565	Ether lipid metab	K01062	5	3	3	5	3	3	5	3
CUB domain;Low	GO:0005887;GO:0 integral to plasma	GO:0003824;GO:0 catalytic activity;c	GO:0006508;GO:0 proteolysis;metab	hsa:6768		K08670		3	2	3	3	3	3	3	3
'chromo' (CHRrom	GO:0000775;GO:0 chromosome, cen	GO:0003682;GO:0 chromatin binding	GO:0006139;GO:0 nucleobase, nucle	hsa:11335;hsa:653972		K11586		5	6	6	8	6	6	8	6
	GO:0000323;GO:0 lytic vacuole;lysos	GO:0000847;GO:0 enzyme activator	GO:0001573;GO:0 ganglioside meta	hsa:2760	ko04142	K12383		4	6	6	6	6	6	6	6
P21-Rho-binding	GO:0005634;GO:0 nucleus;cytosol;m	GO:0000166;GO:0 nucleotide bindin	GO:0006464;GO:0 protein modificati	hsa:5062		K04010;ko04012	MAPK signaling p	11	3	3	5	3	3	5	3
Translationally co	GO:0005737;GO:0 cytoplasm;intrace	GO:0005488;GO:0 binding;calcium io	GO:0006810;GO:0 transport;ion tran	hsa:7178;hsa:392490				11	3	3	5	3	3	5	3
Endoplasmic Reti	GO:0000267;GO:0 cell fraction;memb	GO:0000166;GO:0 nucleotide bindin	GO:0006091;GO:0 generation of pre	hsa:30001;hsa:561	ko05110	Vibrio cholerae in	K10950;K10976	3	2	2	2	2	2	2	2
Eukaryotic protei	GO:0005829;GO:0 cytosol;intracellu	GO:0003824;GO:0 catalytic activity;p	GO:0007154;GO:0 cell communicati	hsa:84817				1	3	3	4	3	3	4	3
NAC domain;UBA	GO:0005634;GO:0 nucleus;nascent	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:4666		K03626		11	3	3	6	3	3	6	3
Tumour protein D	GO:0005783;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;calcium io	GO:0001775;GO:0 cell activation;jmr	hsa:7163				3	5	3	3	3	3	3	3
DnaI domain;DnaI	GO:0005783;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;protein bi	GO:0006457;GO:0 protein folding;m	hsa:51726		K09517		2	2	2	2	2	2	2	2
'Cold-shock' DNA	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:4904		K09276		11	11	11	17	11	11	17	11
Centromere/kinet	GO:0000776;GO:0 kinetochore;cond	GO:0003676;GO:0 nucleic acid bindir	GO:0000070;GO:0 mitotic sister chro	hsa:9183		K11578		2	2	2	2	2	2	2	2
Tau and MAP prot	GO:0005874;GO:0 microtubule;micro	GO:0005198;GO:0 structural molecul	GO:0007026;GO:0 negative regulatio	hsa:4134		K10431		7	7	7	11	7	7	11	7
Ubiquitin-conjug	GO:0000795;GO:0 synaptonemal cor	GO:0003824;GO:0 catalytic activity;li	GO:0006464;GO:0 protein modificati	hsa:7329	ko04120	Ubiquitin mediate	K10577	2	3	3	4	3	3	4	3

Adenylate kinase	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:51727	ko00240	Pyrimidine metab	K00945	5	4	4	4	4	4	4
Cytophilin type p	GO:0000267;GO:0 cell fraction;meml	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0006457;GO:0 protein folding;mi	hsa:10105			K09565	9	8	8	10	8	8	10
Domain of unkno	GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:8880				17	16	17	23	15	16	21
Ubiquitin carboxyl	GO:0005622;GO:0 intracellular;cell p	GO:0003824;GO:0 catalytic activity;u	GO:0006508;GO:0 proteolysis;ubiqui	hsa:51377			K05610	12	5	5	5	5	5	5
								2	1	1	1	1	1	1
								1	1	1	1	1	1	1
Intermediate filan	GO:0005882;GO:0 intermediate filan	GO:0005198;GO:0 structural molecul	GO:0008544;GO:0 epidermis development;tissue development;developmental process;anatomical structure de					5	2	2	2	2	2	2
								2	2	2	2	2	2	2
Intermediate filan	GO:0005882;GO:0 intermediate filan	GO:0005198 structural molecul activity						2	7	7	7	1	1	1
Intermediate filan	GO:0005882;GO:0 intermediate filan	GO:0005198 structural molecul activity	hsa:144501					4	1	1	1	1	1	1
Calponin homolog	GO:0016604;GO:0 nuclear body;PML	GO:0005488;GO:0 binding;protein bi	GO:0007399;GO:0 nervous system d	hsa:4034				2	4	4	4	4	4	4
HIT domain	GO:0005576;GO:0 extracellular regio	GO:0003824;GO:0 catalytic activity;hydrolase activity		hsa:84681				1	1	1	1	1	1	1
	GO:0005730;GO:0 nucleolus;cytoplasm	GO:0003676;GO:0 nucleic acid bindir	GO:0000226;GO:0 microtubule cytos	hsa:51203				5	1	1	1	1	1	1
UTP-glucose-1-ph	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;u	GO:0005975;GO:0 carbohydrate met	hsa:6675;hsa:913;ko00530		Aminosugars met;	K00972	5	1	1	1	1	1	1
WD domain, G-be	GO:0005739;GO:0 mitochondrion;organelle;membrane-bounded organelle;intracellular organelle;intracellular r			hsa:26608				2	1	1	1	1	1	1
LSM domain	GO:0005737;GO:0 cytoplasm;ribonu	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:11157			K04796	1	1	1	2	1	1	2
_001280	GO:0005737;GO:0 cytoplasm;plasma	GO:0005215;GO:0 transporter activi	GO:0006810;GO:0 transport;ion tran	hsa:54102;hsa:100131610;hsa:53405;hsa:25932;hsa:111	K05026;K05025;K1			10	1	1	1	1	1	1
ADP-ribosylation f	GO:0005794;GO:0 Golgi apparatus;o	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;intracell	hsa:56681;hsa:51128			K07953;K07954	6	1	1	1	1	1	1
	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0000079;GO:0 regulation of cyc	hsa:56647				5	1	1	1	1	1	1
Adaptin N termin	GO:0030117;GO:0 membrane coat;v	GO:0005198;GO:0 structural molecul	GO:0006810;GO:0 transport;intracell	hsa:26958				1	2	2	1	1	1	1
pinin/SDK/memA	GO:0005681;GO:0 spliceosomal com	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:5411				2	1	1	1	1	1	1
RNA polymerase F	GO:0005654;GO:0 nucleoplasm;nuclei	GO:0003824;GO:0 catalytic activity;D	GO:0000375;GO:0 RNA splicing, via t	hsa:5437	ko03020;ko05016	RNA polymerase;†	K03016	4	1	1	2	1	1	2
ADP-ribosylation f	GO:0005813;GO:0 centrosome;micrc	GO:0000166;GO:0 nucleotide binding	GO:0006461;GO:0 protein complex a	hsa:4042			K07943	1	1	1	1	1	1	1
Zinc finger, C3HC4	GO:0005634;GO:0 nucleus;cytosol	GO:0003824;GO:0 catalytic activity;†	GO:0006139;GO:0 nucleobase, nucle	hsa:9978	ko04120;ko03420	Ubiquitin mediate	K03868	1	1	1	2	1	1	2
ATPase family ass	GO:0005634;GO:0 nucleus;organelle	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:9319				1	1	1	1	1	1	1
Actin	GO:0000123;GO:0 histone acetyltran	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:86			K11340	2	1	1	1	1	1	1
NL3L/Grn1 putat	GO:0005730;GO:0 nucleus;organel	GO:0000166;GO:0 nucleotide binding	GO:0042127;GO:0 regulation of cell l	hsa:26354				1	1	1	1	1	1	1
Transport protein	GO:0005783;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;ER to Gr	hsa:27095				3	1	1	2	1	1	2
NUDIX domain	GO:0003824;GO:0 catalytic activity;G	GO:0006139;GO:0 nucleobase, nucle	hsa:4521				K03574	4	1	1	1	1	1	1
FRG1-like family	GO:0005681;GO:0 spliceosomal complex;nucleolus;Cajal body;nuclear boc	GO:0006139;GO:0 nucleobase, nucle	hsa:2483					2	1	1	1	1	1	1
Nucleotide-sensit	GO:0005634;GO:0 nucleus;cytoskeleton;plasma membrane;membrane;or	GO:0000387;GO:0 spliceosomal snR	hsa:1207				K05019	1	1	1	1	1	1	1
NIPSNAP	GO:0005829;GO:0 cytosol;intracellular part;cytoplasmic part;cell part			hsa:25934				4	1	1	1	1	1	1
Endoribonuclease	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;n	GO:0006417;GO:0 regulation of tran	hsa:10247				1	1	1	1	1	1	1
Sedlin, N-terminal	GO:0005783;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;protein bi	GO:0001501;GO:0 skeletal system de	hsa:6399				4	1	1	1	1	1	1
RNA recognition n	GO:0005634;GO:0 nucleus;organelle	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:10929;hsa:6427				8	1	1	1	1	1	1
Lipocalin / cytosol	GO:0005615;GO:0 extracellular spac	GO:0005215;GO:0 transporter activi	GO:0006629;GO:0 lipid metabolic pr	hsa:347				4	2	2	2	2	2	2
Synaptobrevin	GO:0000139;GO:0 Golgi membrane;x	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;ER to Gr	hsa:9554	ko04130	SNARE interaction	K08517	1	1	1	1	1	1	1
Complex 1 protein (LYR family)	hsa:57226							1	1	1	1	1	1	1
short chain dehyd	GO:0005789;GO:0 endoplasmic retic	GO:0003824;GO:0 catalytic activity;e	GO:0006629;GO:0 lipid metabolic pr	hsa:51144	ko00150;ko01040	Androgen and est	K00044;K10251	1	1	1	1	1	1	1
ATP synthase alph	GO:0005887;GO:0 integral to plasma	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:523	ko00190;ko05110	Oxidative phosph	K02145	3	1	1	1	1	1	1
Ras family	GO:0000139;GO:0 Golgi membrane;x	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;cell com	hsa:23011			K07890	1	1	1	1	1	1	1
ATP synthase alph	GO:0012505;GO:0 endomembrane s	GO:0003824;GO:0 catalytic activity;ti	GO:0006139;GO:0 nucleobase, nucle	hsa:526	ko00190;ko05110	Oxidative phosph	K02147	2	1	1	1	1	1	1
Nucleoside 2-deo	GO:0005634;GO:0 nucleus;organelle;membrane-bounded organelle;intrac	GO:0008283;GO:0 cell proliferation;x	hsa:10591					3	1	1	1	1	1	1
Mov34/MPN/PAD	GO:0005682;GO:0 US snRNP;nuclear	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:10594				1	1	1	2	1	1	2
Calcineurin-like pl	GO:0000159;GO:0 protein phosphat	GO:0003824;GO:0 catalytic activity;p	GO:0000188;GO:0 inactivation of Mf	hsa:5515;hsa:5511	ko04310;ko04350	Wnt signaling patl	K04382	1	1	1	1	1	1	1
60s Acidic ribosom	GO:0015934;GO:0 large ribosomal s	GO:0003676;GO:0 nucleic acid bindir	GO:0006414;GO:0 translational elon	hsa:6176	ko03010	Ribosome	K02942	1	1	1	2	1	1	2
Ferredoxin-fold ar	GO:0000267;GO:0 cell fraction;solub	GO:0000049;GO:0 tRNA binding;nuclei	GO:0006082;GO:0 organic acid meta	hsa:10667	ko00400;ko00970	Phenylalanine, tyr	K01889	1	2	2	2	2	2	2
Glucosamine-6-ph	GO:0005634;GO:0 nucleus;Golgi app	GO:0003824;GO:0 catalytic activity;g	GO:0005975;GO:0 carbohydrate met	hsa:10007	ko00530	Aminosugars met;	K02564	8	1	1	1	1	1	1
RNA recognition n	GO:0005622;GO:0 intracellular;cell p	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:2130				8	1	1	1	1	1	1
S-100/ICaBP type	GO:0005737;GO:0 cytoplasm;intrace	GO:0005488;GO:0 binding;calcium ion binding;ion binding;cation binding;	hsa:57402					1	1	1	1	1	1	1
4Fe-4S binding do	GO:0005747;GO:0 mitochondrial res	GO:0003824;GO:0 catalytic activity;N	GO:0006091;GO:0 generation of prex	hsa:4728	ko00190;ko05010	Oxidative phosph	K03941	5	2	2	2	2	2	2
Protein kinase dor	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:1454;hsa:145;ko04310;ko04340	Wnt signaling patl	K08960;K08959		9	1	1	1	1	1	1
ETC complex 1 sub	GO:0005747;GO:0 mitochondrial res	GO:0003824;GO:0 catalytic activity;N	GO:0001932;GO:0 regulation of prot	hsa:4724	ko00190;ko05010	Oxidative phosph	K03937	2	1	1	2	1	1	2
RNA recognition n	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:22913				6	1	1	1	1	1	1
Zinc knuckle	GO:0003676;GO:0 nucleic acid binding;binding;zinc ion binding;ion binding;hsa:85364							1	1	1	1	1	1	1
Bacterial transfer	GO:0005634;GO:0 nucleus;eukaryoti	GO:0003676;GO:0 nucleic acid bindir	GO:0001541;GO:0 ovarian follicle de	hsa:8893			K03240	2	1	1	1	1	1	1
PDZ domain of MCC-2 bdg protein for Usher syndrome	GO:0004871;GO:0 signal transducer	GO:0007049;GO:0 cell cycle;cell communication;signal transduction;cellular process;negative regulation of cell						3	1	1	1	1	1	1
RNA recognition n	GO:0005829;GO:0 cytosol;eukaryotic	GO:0000166;GO:0 nucleotide binding	GO:0006412;GO:0 translation;regula	hsa:1975	ko04150	mTOR signaling px	K03258	5	1	1	1	1	1	2
MazG nucleotide i	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;binding;protein binding;pyrophosphat	hsa:79077					1	1	1	1	1	1	1
D-isomer specific	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:1487	ko04310;ko04330	Wnt signaling patl	K04496	5	1	1	1	1	1	1
Ubiquitin-conjuga	GO:0005654;GO:0 nucleoplasm;cyto	GO:0000166;GO:0 nucleotide binding	GO:0000226;GO:0 microtubule cytos	hsa:11065	ko04120	Ubiquitin mediate	K06688	4	1	1	1	1	1	1
Anticodon binding	GO:0000267;GO:0 cell fraction;solub	GO:0000166;GO:0 nucleotide binding	GO:0006082;GO:0 organic acid meta	hsa:2058	ko00251;ko00860	Glutamate metab	K01881;K01885	1	2	2	2	2	2	2
Regulator of G protein signaling domain	GO:0004871;GO:0 signal transducer	GO:0009966;GO:0 regulation of sign	hsa:6001					3	1	1	2	1	1	2
PP1C-type PPIASE	GO:0005634;GO:0 nucleus;organelle	GO:0003755;GO:0 peptidyl-prolyl cis	GO:0001932;GO:0 regulation of prot	hsa:5300			K09578	2	1	1	1	1	1	1
Caspase domain	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;apopt	hsa:23581			K04401	1	3	3	3	3	3	3

PCI domain;26S pr	GO:000502;GO:0 proteasome comp;GO:0003824;GO:0 catalytic activity;b	GO:0006508;GO:0 proteolysis;ubiqui	hsa:9861	ko03050	Proteasome	K03037	4	1	1	1	1	1	1	1	1	1	1
Calponin homolog	GO:0005737;GO:0 cytoplasm;intrace	GO:0005083;GO:0 small GTPase regu	GO:0000165;GO:0 MAPKK cascade;	hsa:9459	ko04810;ko05212	Regulation of acti	K05729	1	1	1	1	1	1	1	1	1	1
Nse4	GO:0005634;GO:0 nucleus;cytoplasm;organelle;membrane-bounded orga	GO:0006139;GO:0 nucleobase, nucle	hsa:54780;hsa:493861					4	1	1	1	1	1	1	1	1	1
Translation initiat	GO:0005737;GO:0 cytoplasm;intrace	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:10289;hsa:10209				2	1	1	1	1	1	1	1	1	1
Cyclin-dependent	GO:0005654;GO:0 nucleoplasm;orga	GO:0005488;GO:0 binding;protein bi	GO:0000079;GO:0 regulation of cycli	hsa:1163	ko04111;ko05200	Cell cycle - yeast;F	K02219	3	1	1	1	1	1	1	1	1	1
Ras family	GO:0005829;GO:0 cytosol;plasma m	GO:0000166;GO:0 nucleotide binding	GO:0007154;GO:0 cell communicatic	hsa:5908;hsa:643	ko04010;ko04510	MAPK signaling pa	K07836	21	1	1	1	1	1	1	1	1	1
Calponin family re	GO:0005856;GO:0 cytoskeleton;cell-	GO:0003779;GO:0 actin binding;bind	GO:0006996;GO:0 organelle organiz	hsa:1265				3	1	1	1	1	1	1	1	1	1
HcaRG protein	GO:0005488;GO:0 binding;protein binding		hsa:23412					5	1	1	1	1	1	1	1	1	1
PH domain	GO:0005737;GO:0 cytoplasm;intracellular part;cell part	GO:0006810;GO:0 transport;intracell	hsa:26228					1	1	1	1	1	1	1	1	1	1
CD80-like C2-set i	GO:0005634;GO:0 nucleus;Golgi app	GO:0005488;GO:0 binding;protein bi	GO:0007155;GO:0 cell adhesion;anat	hsa:4162				1	1	1	1	1	1	1	1	1	1
emp24/gp25L/p2	GO:0000139;GO:0 Golgi membrane;x	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;cellular	hsa:10959				4	1	1	1	1	1	1	1	1	1
LisH;Ran binding i	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein binding		hsa:54994				2	1	1	1	1	1	1	1	1	1
Pyridine nucleotid	GO:0005739;GO:0 mitochondrion;cy	GO:0000166;GO:0 nucleotide binding	GO:0006518;GO:0 peptide metabolic	hsa:2936	ko00480	Glutathione meta	K00383	5	1	1	1	1	1	1	1	1	1
LETM1-like protei	GO:0005743;GO:0 mitochondrial inn	GO:0005488;GO:0 binding;calcium io	GO:0006996;GO:0 organelle organiz	hsa:3954				1	1	1	1	1	1	1	1	1	1
HMG (high mobil)	GO:0000228;GO:0 nuclear chromoso	GO:0003676;GO:0 nucleic acid bindir	GO:0006325;GO:0 chromatin organiz	hsa:6605				7	1	1	1	1	1	1	1	1	1
Nucleosome asse	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0006325;GO:0 chromatin organiz	hsa:4676				12	2	2	2	1	1	1	1	1	1
Hexokinase;Hexo	GO:0005741;GO:0 mitochondrial out	GO:0000166;GO:0 nucleotide binding	GO:0005975;GO:0 carbohydrate met	hsa:3098;hsa:309	ko00010;ko00051	Glycolysis / Gluco	K00844	9	1	1	1	1	1	1	1	1	1
ER lumen protein	GO:0005789;GO:0 endoplasmic retic	GO:0004871;GO:0 signal transducer	GO:0006621;GO:0 protein retention in ER lumen;transport;intracellular protein transport;cellular process;prote					1	1	1	1	1	1	1	1	1	1
Frizzled/Smoother	GO:0016021;GO:0 integral to membr	GO:0004871;GO:0 signal transducer	GO:0007154;GO:0 cell communicatic	hsa:6608	ko04340;ko05200	Hedgehog signalin	K06226	2	1	1	1	1	1	1	1	1	1
7 transmembrane	GO:0005886;GO:0 plasma membr	GO:0004871;GO:0 signal transducer	GO:0003008;GO:0 system process;ce	hsa:158131	ko04740	Olfactory transduc	K04257	1	1	1	1	1	1	1	1	1	1
Translin family	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:7247				4	1	1	1	1	1	1	1	1	1
Hamt family	GO:0005737;GO:0 cytoplasm;intrace	GO:0000287;GO:0 magnesium ion bi	GO:0006139;GO:0 nucleobase, nucle	hsa:3704	ko00230;ko00240	Purine metabolism	K01519	3	1	1	1	1	1	1	1	1	1
Calponin homolog	GO:0008091;GO:0 spectrin;axon;cell	GO:0003779;GO:0 actin binding;stru	GO:0003008;GO:0 system process;ax	hsa:57731				3	2	2	3	1	1	1	1	1	1
RNase P subunit p	GO:0005655;GO:0 nucleolar ribonuc	GO:0003824;GO:0 catalytic activity;n	GO:0006139;GO:0 nucleobase, nucle	hsa:10556				6	1	1	1	1	1	1	1	1	1
WD domain, G-beta repeat			hsa:80349					2	2	2	2	2	2	2	2	2	2
Tctex-1 family	GO:0005874;GO:0 microtubule;micr	GO:0003774;GO:0 motor activity;catalytic activity;binding;protein binding	hsa:6993					1	1	1	1	1	1	1	1	1	1
Kua-ubiquitin con	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;b	GO:0000209;GO:0 protein polyubiqu	hsa:387522				7	5	5	8	1	1	1	1	1	1
Immunoglobulin c	GO:0000139;GO:0 Golgi membrane;	GO:0005488;GO:0 binding;protein bi	GO:0007154;GO:0 cell communicatic	hsa:682				4	1	1	1	1	1	1	1	1	1
short chain dehyd	GO:0005788;GO:0 peroxisomal matri	GO:0003824;GO:0 catalytic activity;3	GO:0008152;GO:0 metabolic process	hsa:3295	ko00120	Bile acid biosynth	K12405	2	1	1	1	1	1	1	1	1	1
Ubiquitin-conjugating enzyme	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:7323;hsa:732	ko04120				9	1	1	1	1	1	1	1	1	1
Sec1 family	GO:0000149;GO:0 SNARE binding;bir	GO:0006904;GO:0 vesicle docking during exocytosis;cellular process;membrane docking;vesicle docking;transp						5	1	1	1	1	1	1	1	1	1
TFII beta subunit	GO:0005667;GO:0 transcription fact	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:2961	ko03022	Basal transcription	K03137	1	1	1	1	1	1	1	1	1	1
RNA recognition i	GO:0005634;GO:0 nucleus;organelle	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:8148;hsa:2521				8	1	1	1	1	1	1	1	1	1
Ras family	GO:0005622;GO:0 intracellular;plasm	GO:0000166;GO:0 nucleotide binding	GO:0007154;GO:0 cell communicatic	hsa:6237	ko04010;ko04810	MAPK signaling pa	K07829	1	2	2	2	1	1	1	1	1	1
Thioesterase superfamily	GO:0003824;GO:0 catalytic activity;C	GO:0006461;GO:0 protein complex a	hsa:55856					2	1	1	1	1	1	1	1	1	1
Serine-threonine j	GO:0000159;GO:0 protein phosphat	GO:0008601;GO:0 protein phosphat	GO:0007154;GO:0 cell communicatic	hsa:5521;hsa:55844;hsa:5520				10	1	1	1	1	1	1	1	1	1
C2 domain	GO:0016021;GO:0 integral to membrane;intrinsic to membrane;membrane part;cell part		hsa:23344					4	1	1	1	1	1	1	1	1	1
KH domain	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003676;GO:0 nucleic acid bindir	GO:0006066;GO:0 alcohol metabolic	hsa:3069				3	1	1	2	1	1	2	1	1	1
Eukaryotic family	GO:0005730;GO:0 nucleus;organelle;non-membrane-bounded organelle;intracellular organelle;intracellular n	hsa:26017						1	1	1	1	1	1	1	1	1	1
Translation initiat	GO:0005737;GO:0 cytoplasm;intrace	GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:9086;hsa:1964				4	1	1	2	1	1	2	1	1	1
Cell differentiation	GO:0005634;GO:0 nucleus;organelle	GO:0005488;GO:0 binding;protein bi	GO:0003006;GO:0 reproductive deve	hsa:9125				2	1	1	2	1	1	2	1	1	1
Su72-like protein	GO:0005634;GO:0 nucleus;cytoplasm	GO:0003824;GO:0 catalytic activity;p	GO:0006139;GO:0 nucleobase, nucle	hsa:29101				4	1	1	1	1	1	1	1	1	1
Region in Clathrin	GO:0016023;GO:0 cytoplasmic meml	GO:0005198;GO:0 structural molecu	GO:0006810;GO:0 transport;intracell	hsa:1213;hsa:8211	ko04142;ko05016	Huntington's dise	K04646	5	2	2	2	2	2	2	2	2	2
UBA/TS-N domain	GO:0005634;GO:0 nucleus;endoplasi	GO:0005488;GO:0 binding;protein bi	GO:0006464;GO:0 protein modificati	hsa:56893;hsa:29979				5	1	1	1	1	1	1	1	1	1
Transcription fact	GO:0000123;GO:0 histone acetyltran	GO:0003712;GO:0 transcription cofa	GO:0006139;GO:0 nucleobase, nucle	hsa:56943				3	2	2	3	2	2	3	2	2	2
Protein of unknow	GO:0016021;GO:0 integral to membr	GO:0005488;GO:0 binding;protein binding		hsa:57003				1	1	1	1	1	1	1	1	1	1
Respiratory-chain	GO:0005747;GO:0 mitochondrial res	GO:0000166;GO:0 nucleotide binding	GO:0006091;GO:0 generation of pre	hsa:4720	ko00190;ko05010	Oxidative phosph	K03935	3	1	1	1	1	1	1	1	1	1
PCI domain	GO:0005737;GO:0 cytoplasm;signal	GO:0005488;GO:0 binding;protein bi	GO:0007154;GO:0 cell communicatic	hsa:8533				2	1	1	1	1	1	1	1	1	1
BCL7, N-terminal conserved region	GO:0005783;GO:0 endoplasmic retic	GO:0005488;GO:0 binding;protein bi	GO:0006950;GO:0 response to stress	hsa:819				2	1	1	1	1	1	1	1	1	1
Eukaryotic protei	GO:0000139;GO:0 Golgi membrane;endoplasmic reticulum membrane;membrane;integral to membrane;organ	hsa:54499						3	1	1	1	1	1	1	1	1	1
CPF A subunit re	GO:0005847;GO:0 mRNA cleavage ar	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via t	hsa:29894				1	1	1	1	1	1	1	1	1	1
Asparaginase	GO:0000323;GO:0 lytic vacuole;lysos	GO:0003824;GO:0 catalytic activity;n	GO:0006464;GO:0 protein modificati	hsa:175	ko00511;ko04142	Other glycan degr	K01444	3	1	1	1	1	1	1	1	1	1
HECT-domain (ubi	GO:0000267;GO:0 cell fraction;solub	GO:0003676;GO:0 nucleic acid bindir	GO:0006464;GO:0 protein modificati	hsa:51366	ko04120	Ubiquitin mediate	K10593	4	1	1	1	1	1	1	1	1	1
Adenylylcinnate	GO:0005737;GO:0 cytoplasm;intrace	GO:0003824;GO:0 catalytic activity;y	GO:0006139;GO:0 nucleobase, nucle	hsa:158	ko00230;ko00252	Purine metabolism	K01756	3	1	1	1	1	1	1	1	1	1
metallopeptidase	GO:0005654;GO:0 nucleoplasm;chro	GO:0003711;GO:0 transcription elon	GO:0006139;GO:0 nucleobase, nucle	hsa:11198				2	1	1	1	1	1	1	1	1	1
Microtubule asso	GO:0005773;GO:0 vacuole;autophag	GO:0004871;GO:0 signal transducer	GO:0006605;GO:0 protein targeting;	hsa:23710;hsa:11	ko04140	Regulation of aut	K08341	4	2	2	3	1	1	1	1	1	1
Calcineurin-like p	GO:0005737;GO:0 cytoplasm;macror	GO:0003824;GO:0 catalytic activity;p	GO:0005975;GO:0 carbohydrate met	hsa:5499	ko04810;ko04510	Regulation of acti	K06269	4	8	8	9	1	1	1	1	1	1
RNA recognition n	GO:0005654;GO:0 nucleoplasm;ribor	GO:0000166;GO:0 nucleotide binding	GO:0000375;GO:0 RNA splicing, via t	hsa:3191				2	4	4	5	2	2	2	2	2	2
emp24/gp25L/p2	GO:0000139;GO:0 Golgi membrane;x	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;exocyto	hsa:10972				2	1	1	1	1	1	1	1	1	1
Regulator of G pr	GO:0000267;GO:0 cell fraction;meml	GO:0004871;GO:0 signal transducer	GO:0006914;GO:0 autophagy;cell coi	hsa:10287				1	1	1	1	1	1	1	1	1	1
Protein kinase do	GO:0005634;GO:0 nucleus;cytoplasm	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:8536				3	1	1	1	1	1	1	1	1	1
Ankyrin repeat;RP	GO:0005856;GO:0 cytoskeleton;cell	GO:0005488;GO:0 binding;protein binding;actin binding;enzyme inhibitor	hsa:26064;hsa:221692					9	1	1	2	1	1	2	1	2	1
F-box domain	GO:0000151;GO:0 ubiquitin ligase cc	GO:0005488;GO:0 binding;protein bi	GO:0000075;GO:0 cell cycle checkpo	hsa:79791				2	1	1	1	1	1	1	1	1	1
Ankyrin repeat	GO:0005737;GO:0 cytoplasm;intrace	GO:0008047;GO:0 enzyme activator	GO:0006937;GO:0 regulation of mus	hsa:4660	ko04270	Vascular smooth r	K12329	5	2	2	3	1	1	1	1	1	1

Calponin homology (CH) domain;Growth-Arrest-Specific Protein 2 Domain	GO:0007050;GO:0 cell cycle arrest;cc	hsa:283431	3	2	2	2	2	2	2
La domain	GO:0003676;GO:0 nucleic acid binding;RNA binding;binding;protein bindir	hsa:23367	4	1	1	1	1	1	1
ADP-ribosylation f	GO:0005794;GO:0 Golgi apparatus;o	GO:0000166;GO:0 nucleotide binding	GO:0006810;GO:0 transport;cell com	hsa:378	K07939	2	3	4	6
Cadherin domain;	GO:0000267;GO:0 cell fraction;meml	GO:0005488;GO:0 binding;calcium io	GO:0007155;GO:0 cell adhesion;hom	hsa:1823	K07600	2	1	1	1
GTPase of unknown	GO:0005737;GO:0 cytoplasm;intrac	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:29789	K06942	2	3	3	4
Exonuclease;SAP I	GO:0005730;GO:0 nucleolus;cytopla	GO:0000287;GO:0 magnesium ion bi	GO:0006139;GO:0 nucleobase, nucle	hsa:90459	K01175	2	1	1	1
Nucleotidyltransf	GO:0000267;GO:0 cell fraction;meml	GO:0000166;GO:0 nucleotide binding	GO:0002376;GO:0 immune system p	hsa:4939	K00992	4	1	1	1
EF hand;inositol 1	GO:0016021;GO:0 integral to membr	GO:0004871;GO:0 signal transducer	GO:0006810;GO:0 transport;ion tran	hsa:6263	ko04020;ko05010 Calcium signaling	4	2	2	3
HMG (high mobil)	GO:0005634;GO:0 nucleus;chromosc	GO:0003676;GO:0 nucleic acid bindir	GO:0007275;GO:0 multicellular orga	hsa:3149	K11296	7	1	1	2
RNA recognition n	GO:0005634;GO:0 nucleus;cytoplasn	GO:0000166;GO:0 nucleotide binding;nucleic acid binding;RNA binding;bi	hsa:125950			3	1	1	1
Frataxin-like domi	GO:0005759;GO:0 mitochondrial ma	GO:0005488;GO:0 binding;iron ion b	GO:0001558;GO:0 regulation of cel	hsa:2395		5	1	1	1
Aldehyde dehydrogenase family		GO:0003824;GO:0 catalytic activity;b	GO:0008152	metabolic process	hsa:126133	4	2	2	2
Protein kinase dor	GO:0005634;GO:0 nucleus;CAMP-dej	GO:0000166;GO:0 nucleotide binding	GO:0007154;GO:0 cell communicat	hsa:5566	ko04010;ko04310 MAPK signaling pa	3	1	1	1
	GO:0005488;GO:0 binding;seleni	GO:0009987;GO:0 cellular process;cc	hsa:280636			1	1	1	1
Cytochrome C oxid	GO:0005758;GO:0 mitochondrial intr	GO:0005488;GO:0 binding;copper io	GO:0000041;GO:0 transition metal ic	hsa:10063	ko00190 Oxidative phosph	2	1	1	1
PFU (PLAA family ubiquitin binding);PUL domain;WD dc	GO:0008047;GO:0 enzyme activator	GO:0006629;GO:0 lipid metabolic pn	hsa:9373			3	1	1	1
Uncharacterised protein family (LUF0224)	GO:0005488;GO:0 binding;zinc ion binding;ion binding;cation binding;met	hsa:121355				2	1	1	2
AT hook motif;F/Y	GO:0005737;GO:0 cytoplasm;macror	GO:0003676;GO:0 nucleic acid bindir	GO:0006139;GO:0 nucleobase, nucle	hsa:9757	K09186	1	1	1	1
PPR repeat;Mitod	GO:0005753;GO:0 mitochondrial pro	GO:0005215;GO:0 transporter activit	GO:0006139;GO:0 nucleobase, nucle	hsa:9551	ko00190 Oxidative phosph	8	1	1	1
ADP-ribosylation f	GO:0000139;GO:0 Golgi membrane;r	GO:0000166;GO:0 nucleotide binding	GO:0007154;GO:0 cell communicat	hsa:400	K07942	5	1	1	1
Peptidase C1-like	GO:0005634;GO:0 nucleus;cytoplasn	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;metab	hsa:642	K01372	2	1	1	2
DeoC/LacC family	GO:0005737;GO:0 cytoplasm;intrac	GO:0003824;GO:0 catalytic activity;d	GO:0006139;GO:0 nucleobase, nucle	hsa:51071	ko00030 Pentose phosphat	1	1	1	1
Protein kinase dor	GO:0005737;GO:0 cytoplasm;intrac	GO:0000166;GO:0 nucleotide binding	GO:0006464;GO:0 protein modificati	hsa:53944;hsa:14	ko04340	12	3	3	3
NADH-ubiquinone	GO:0005747;GO:0 mitochondrial res;	GO:0003824;GO:0 catalytic activity;h	GO:0006091;GO:0 generation of pre	hsa:4710	ko00190;ko05010 Oxidative phosph	2	1	1	1
Protein phosphatase inhibitor 2 (PPP-2)		GO:0004857;GO:0 enzyme inhibitor	GO:0005975;GO:0 carbohydrate met	hsa:5504		4	1	1	1
Bacterial transfer	GO:0005737;GO:0 cytoplasm;intrac	GO:0003824;GO:0 catalytic activity;transferase activity	hsa:10671		K10428	1	1	1	1
Domain of unknown	GO:0005681;GO:0 spliceosomal com	GO:0003676;GO:0 nucleic acid bindir	GO:0000375;GO:0 RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions v			8	1	1	1
Acylphosphatase		GO:0003824;GO:0 catalytic activity;a	GO:0006793;GO:0 phosphorus metal	hsa:97	ko00620;ko00632 Pyruvate metabol	1	1	2	1
DKCLD (NUC011)	GO:0005697;GO:0 telomerase holoe	GO:0003676;GO:0 nucleic acid bindir	GO:0000723;GO:0 telomere mainten	hsa:1736	K11131	2	1	1	1
Calponin homolog	GO:0005640;GO:0 nuclear outer mer	GO:0003779;GO:0 actin binding;binding;protein binding;cytoskeletal prot	hsa:23224			4	4	4	4
FF domain;WW d	GO:0005634;GO:0 nucleus;organelle	GO:0003702;GO:0 RNA polymerase I	GO:0006139;GO:0 nucleobase, nucle	hsa:10915		1	1	1	1
Low-density lipop	GO:0005886;GO:0 plasma membranc	GO:0003824;GO:0 catalytic activity;e	GO:0001525;GO:0 angiogenesis;prot	hsa:164656	K09637	2	1	1	1
4'-phosphopantet	GO:0005829;GO:0 cytosol;intracellul	GO:0000287;GO:0 magnesium ion bi	GO:0008152;GO:0 metabolic process	hsa:60496	ko00300;ko00310 Lysine biosynthesi	1	1	1	1
PHR domain;Regu	GO:0000151;GO:0 ubiquitin ligase cc	GO:0003824;GO:0 catalytic activity;b	GO:0006139;GO:0 nucleobase, nucle	hsa:23077	K10693	2	1	1	1
G-protein alpha s	GO:0016020;GO:0 membrane;cytopl	GO:0000166;GO:0 nucleotide binding	GO:0006928;GO:0 cell motion;cell cc	hsa:10672	ko04810;ko04270 Regulation of acti	1	1	1	1
	GO:0005747;GO:0 mitochondrial res;	GO:0003824;GO:0 catalytic activity;h	GO:0006091;GO:0 generation of pre	hsa:4731	ko00190;ko05010 Oxidative phosph	1	1	1	1
Phorbol esters/di	GO:0005622;GO:0 intracellular;cell p	GO:0005083;GO:0 small GTPase regu	GO:0009966;GO:0 regulation of sign	hsa:9181		4	1	1	1
Mitochondrial car	GO:0005744;GO:0 mitochondrial inn	GO:0005215;GO:0 transporter activit	GO:0006810;GO:0 transport;apoptos	hsa:293	ko04020;ko05012 Calcium signaling	2	6	6	8
WD domain, G-be	GO:0005681;GO:0 spliceosomal com	GO:0003676;GO:0 nucleic acid bindir	GO:0000387;GO:0 spliceosomal snR	hsa:25929		1	3	3	3
ENTH domain	GO:0005794;GO:0 Golgi apparatus;r	GO:0005488;GO:0 binding;protein bi	GO:0006810;GO:0 transport;endocyt	hsa:9685		3	1	1	1
Caspase domain	GO:0005654;GO:0 nucleoplasm;mito	GO:0003824;GO:0 catalytic activity;e	GO:0006508;GO:0 proteolysis;cell str	hsa:836	ko04010;ko04210 MAPK signaling pa	3	1	2	1
CAP-Gly domain	GO:0005737;GO:0 cytoplasm;microtr	GO:0005488;GO:0 binding;protein bi	GO:0007399;GO:0 nervous system d	hsa:1155		2	1	1	2
Ribonucleases P/h	GO:0000172;GO:0 ribonuclease MRP	GO:0000171;GO:0 ribonuclease MRP	GO:0001682;GO:0 tRNA 5'-leader rer	hsa:10940	K01164	2	1	1	1
IKI3 family	GO:0005730;GO:0 nucleolus;cytopla	GO:0004871;GO:0 signal transducer	GO:0002376;GO:0 immune system p	hsa:8518	K11373	2	1	1	1
HIF-1 alpha C tern	GO:0005667;GO:0 transcription factc	GO:0003676;GO:0 nucleic acid bindir	GO:0001525;GO:0 angiogenesis;resp	hsa:2034	ko05200;ko05211 Pathways in cance	2	1	1	1
	GO:0005739;GO:0 mitochondrion;rit	GO:0005488;GO:0 binding;protein binding;protein domain specific binding	hsa:10240			1	1	1	2
SRP19 protein	GO:0005730;GO:0 nucleolus;signa	GO:0003676;GO:0 nucleic acid bindir	GO:0006605;GO:0 protein targeting;	hsa:6728	ko03060 Protein export	2	1	1	2
impB/mucB/samb	GO:0005654;GO:0 nucleoplasm;orga	GO:0000287;GO:0 magnesium ion bi	GO:0006139;GO:0 nucleobase, nucle	hsa:11201	K03510	2	1	1	1
Dolichyl-diphosph	GO:0000267;GO:0 cell fraction;meml	GO:0003824;GO:0 catalytic activity;o	GO:0001775;GO:0 cell activation;jimr	hsa:1650	ko00510 N-Glycan biosynth	2	1	1	1
				hsa:27143		1	2	2	2
Protein tyrosine k	GO:0005634;GO:0 nucleus;Golgi app	GO:0000166;GO:0 nucleotide binding	GO:0001932;GO:0 regulation of protein amino acid phosphorylation;positive regulation of protein amino acid p			69	20	21	22
Thymidine kinase	GO:0005829;GO:0 cytosol;intracellul	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:7083	ko00240;ko00983 Pyrimidine metab	1	1	1	1
Domain of unknown	GO:0005730;GO:0 nucleolus;organel	GO:0000166;GO:0 nucleotide binding	GO:0008152	metabolic process	hsa:55226	2	1	1	1
short chain dehydrogenase		GO:0003824;GO:0 catalytic activity;b	GO:0008152;GO:0 metabolic process	hsa:112724	K11161	3	1	1	1
				hsa:55086		3	2	2	2
Cation transportin	GO:0005634;GO:0 nucleus;cytoplasn	GO:0000166;GO:0 nucleotide binding	GO:0003008;GO:0 system process;ni	hsa:478	ko04260 Cardiac muscle co	6	10	10	11
Protein of unknown function (DUF1394)				hsa:51571		6	1	1	1
RNA recognition n	GO:0005681;GO:0 spliceosomal com	GO:0000166;GO:0 nucleotide binding	GO:0006139;GO:0 nucleobase, nucle	hsa:55131		2	1	1	1
'Cold-shock' DNA	GO:0005737;GO:0 cytoplasm;intrac	GO:0003676;GO:0 nucleic acid bindir	GO:0006355;GO:0 regulation of tran	hsa:23589		1	2	2	3
Calcineurin-like phosphoesterase		GO:0003824;GO:0 catalytic activity;binding;hydrolase activity;ion binding;	hsa:55313			3	1	1	1
PRP1 splicing fact	GO:0005681;GO:0 spliceosomal com	GO:0003712;GO:0 transcription cofa	GO:0000245;GO:0 spliceosome asser	hsa:24148		2	1	1	1
Kinesin motor dor	GO:0005737;GO:0 cytoplasm;spindle	GO:0000166;GO:0 nucleotide binding	GO:0000226;GO:0 microtubule cytos	hsa:3832	K10398	1	3	3	3
	GO:0005737;GO:0 cytoplasm;intracellular part;cell part					5	1	1	1
Translation initiation factor SUI1		GO:0003676;GO:0 nucleic acid bindir	GO:0006413;GO:0 translational initia	hsa:8562		2	1	1	1
CS domain		GO:0002376;GO:0 immune system p	hsa:84955			3	1	1	1

Unique Peptides	Unique Peptides (Sequence Coverage)	Unique + Razor Set	Unique Sequence	Mol. Weight [kDa]	Sequence Length	PEP	Mean Ratio H/L	Mean Ratio H/L	N Ratio H/L	Significance Ratio H/L	Variability Ratio H/L	Count	Intensity	Intensity L	Intensity H	Reverse	Contaminant
52	52	45.6	45.6	45.1	147.87	1265	0	39.506	19.967	0.00014984	14.788	46	237150000	4226400	232920000		
5	5	16.7	13.4	13.4	61.189	539	4.82E-35	7.988	7.963	0.05991	10.609	3	4104500	121050	3983400		
1	1	41.6	41.6	2.4	65.808	582	2.74E-148	4.103	5.6674	0.057329	21.355	39	62350000	3709700	58640000		
2	2	3.8	3.8	3.8	52.22	445	0.0036274	3.0664	2.9655	0.2704	1.9989	2	1194000	271950	922010		
8	10	25.9	25.9	25.9	44.868	397	3.02E-18	3.1092	2.9593	0.27096	22.996	8	10976000	2214700	8761500		
2	2	4.7	4.7	4.7	63.972	548	2.48E-09	3.2623	2.9545	0.2714	20.338	2	1537200	296720	1240500		
5	6	30.9	30.9	30.9	23.489	207	1.35E-31	2.6181	2.9318	0.2735	20.392	5	4983800	1386900	3596900		
11	18	65.1	65.1	261	26.923	261	1.26E-158	1.832	2.9067	0.27584	17.593	13	16830000	5598900	11231000		
19	21	30.6	29.6	29.6	84.473	732	1.98E-82	6.6969	2.8967	0.27679	23.365	18	17795000	2273100	15522000		
2	2	1.8	1.8	1.8	123.47	1078	3.82E-06	5.7189	2.8889	0.27752	12.23	2	764410	162570	601840		
5	9	44.2	44.2	44.2	10.112	86	4.72E-24	1.2085	2.8783	0.27853	20.116	8	21517000	9775700	11741000		
5	8	20.4	20.4	20.4	25.431	225	1.64E-11	1.6847	2.8471	0.28152	19.894	5	6557400	2338000	4219400		
3	3	16	16	16	27.61	237	0.0003825	1.6765	2.8469	0.28154	5.6574	3	1137100	352210	784910		
1	2	9.3	1.7	1.7	121.36	1075	3.84E-113	6.6785	2.8431	0.28191	14.619	5	67208000	8268800	58940000		
10	10	11.1	11.1	11.1	134.46	1176	2.73E-48	5.4317	2.842	0.28203	12.924	6	3525100	347990	3177100		
4	5	8.7	8.7	8.7	68.856	621	3.20E-08	2.0504	2.8299	0.2832	12.651	4	1964400	662610	1301800		
1	2	1.1	1.1	1.1	103.81	925	0.209	1.9157	2.828	0.28339	36.406	2	2843800	892880	1950900		
4	4	7.8	7.8	6.1	82.17	721	5.24E-31	3.9244	2.8252	0.28367	10.191	5	2881700	445970	2435700		
7	9	44	44	44	25.898	234	3.21E-24	1.8024	2.8225	0.28393	10.67	7	7131000	2498500	4632500		
2	2	4.1	4.1	4.1	65.537	582	2.26E-06	3.4205	2.8189	0.28428	8.6798	2	1380000	306180	1073800		
10	12	20.8	20.8	19.2	73.243	662	4.80E-51	2.9518	2.8174	0.28443	25.424	12	6996700	1589600	5407200		
9	17	60.9	60.9	60.9	21.863	192	6.84E-66	2.4134	2.8064	0.28551	26.335	19	45713000	12838000	32875000		
3	3	5.9	5.9	5.9	58.252	525	4.28E-06	4.2382	2.7831	0.28784	18.501	3	1368200	239190	1129000		
2	3	22.4	8.9	8.9	28.218	246	1.67E-27	1.511	2.7799	0.28816	57.245	2	2175600	834710	1340800		
6	6	12.5	12.5	12.5	60.626	534	5.65E-19	3.3952	2.7744	0.28871	25.177	5	2508100	469370	2038700		
1	2	12.8	2.1	2.1	32.548	289	1.31E-32	2.6076	2.7692	0.28923	36.92	2	2471700	661800	1809900		
166	224	71	71	59.4	226.53	1960	0	19.75	2.7632	0.28984	17.09	1148	34056000000	1392300000	32664000000		
5	7	42.7	42.7	42.7	11.367	103	1.40E-09	1.7664	2.7607	0.29009	34.001	7	11141000	3938600	7202000		
3	4	80.7	80.7	17.5	19.794	171	1.97E-170	1.8744	2.7604	0.29012	16.558	58	744630000	252250000	492380000		
5	5	4	4	4	159.02	1419	5.90E-08	6.9156	2.7431	0.29189	18.815	4	1852600	124340	1728300		
20	28	46.7	46.7	46.7	57.136	501	2.35E-125	3.3693	2.7061	0.29571	28.136	22	38918000	8159900	30758000		
5	5	10.1	10.1	10.1	60.977	534	1.11E-15	3.3099	2.7047	0.29585	35.779	5	2952200	418700	2533500		
5	5	5.7	5.7	5.7	114.76	1042	2.43E-29	4.8609	2.69	0.29739	18.146	5	2489600	249130	2240400		
20	36	51.9	51.9	51.9	49.874	455	1.05E-142	2.7259	2.6635	0.3002	10.422	24	63326000	16997000	46330000		
19	33	46.4	46.4	46.4	56.149	487	1.18E-99	2.8027	2.6383	0.30291	31.152	40	102580000	25521000	77054000		
2	3	6.9	6.9	6.9	34.759	306	9.65E-10	1.2793	2.634	0.30338	18.236	2	1156500	472300	684210		
5	9	24.2	24.2	24.2	23.772	211	1.73E-13	1.5795	2.63	0.30381	19.515	6	7352400	3294900	4057500		
5	5	6.1	6.1	6.1	113.08	1014	5.72E-48	5.1684	2.6108	0.30591	23.87	5	3275700	433080	2842600		
11	13	18.5	18.5	18.5	66.115	589	2.16E-47	3.4393	2.6044	0.30661	61.843	10	8036900	1677900	6359000		
1	2	2.2	2.2	2.2	57.46	500	0.33829	1.9777	2.6016	0.30692	17.742	4	27586000	9149200	18437000		
7	12	30.9	30.9	30.9	25.206	217	2.15E-09	1.5995	2.5914	0.30805	14.848	7	7655800	2776800	4879000		
8	8	9.6	9.6	9.6	114.33	1015	1.41E-54	5.1228	2.5878	0.30845	194.27	5	5325600	3678800	1646800		
6	11	20.4	20.4	20.4	30.032	289	1.92E-49	1.7477	2.5855	0.3087	24.86	10	28573000	10457000	18116000		
4	4	25	25	20.3	26.528	236	2.51E-17	2.2799	2.5763	0.30974	186.5	5	5395200	1385800	4009400		
4	6	11.8	11.8	11.8	46.261	415	3.60E-24	2.2603	2.5627	0.31127	9.913	5	2661100	782680	1878500		
3	3	22.4	16.7	16.7	21.429	192	1.04E-18	2.2855	2.5593	0.31164	53.505	3	3447900	947450	2500400		
9	9	13.9	13.9	12.7	95.807	898	1.85E-59	6.4406	2.5547	0.31217	54.129	9	5506400	533150	4973300		
2	2	11.5	11.5	11.5	18.001	156	0.0019728	1.3292	2.5513	0.31255	36.558	2	2006500	860420	1146100		
3	5	31.7	31.7	31.7	11.955	104	1.23E-17	1.1557	2.5429	0.31351	21.314	3	13985000	6503300	7482000		
1	1	3.8	3.8	3.8	23.554	210	0.04239	1.8521	2.5358	0.31432	7.3282	2	631790	168500	463290		
5	5	6.9	6.9	6.9	82.285	734	6.14E-16	6.3805	2.5308	0.31489	39.212	5	2072300	164760	1907600		
5	9	27.1	27.1	27.1	20.63	181	1.34E-25	1.3838	2.5307	0.3149	10.189	6	9000600	3726200	5274300		
24	29	27.7	27.7	26.7	115.28	1030	6.61E-107	4.6333	2.5179	0.31638	44.155	30	20525000	3444000	17081000		
17	18	23.6	23.6	23.6	89.677	776	2.52E-29	6.5948	2.4935	0.31922	67.953	16	7569000	723150	6845800		
3	3	7.7	7.7	7.7	49.184	440	8.34E-09	3.1999	2.4892	0.31971	45.117	3	1484400	325500	1158900		
7	8	15.2	15.2	15.2	61.862	565	2.74E-27	3.0002	2.4833	0.32041	19.294	7	8213900	2071800	6142100		
5	10	68	68	16.2	49.67	444	0	3.7144	2.4796	0.32085	43.26	36	229810000	46250000	183560000		
2	2	1.9	1.9	1.9	108.66	955	0.020504	5.3023	2.4779	0.32105	39.701	2	944650	89542	855110		
3	3	14.5	14.5	14.5	26.227	227	5.66E-05	1.3527	2.4639	0.32271	22.914	3	1981400	847720	1133700		
6	6	8.6	8.6	8.6	88.929	768	3.43E-10	5.6512	2.4601	0.32316	47.612	6	2003300	170380	1833000		
13	13	21.8	21.8	21.8	81.307	719	1.91E-54	5.5003	2.4443	0.32506	51.934	13	6336100	830170	5506000		
3	3	9.6	8.2	8.2	54.191	490	3.11E-31	2.5636	2.4441	0.32508	2.9133	3	3142500	770800	2371700		
2	2	7.5	5	5	54.12	482	2.46E-10	2.6447	2.4433	0.32517	30.108	2	1415500	303860	1111700		
2	2	8.3	8.3	8.3	52.065	459	0.00029362	6.2619	2.442	0.32533	27.287	2	905540	55201	850340		

8	12	44.1	33.9	27.8	27.764	245	7.90E-96	1.5043	2.4334	0.32636	25.507	14	37151000	14589000	22562000
8	8	15.3	15.3	15.3	80.109	704	2.20E-47	2.5189	2.4186	0.32817	18.31	8	18272000	12280000	5991700
6	7	19.3	19.3	19.3	33.67	306	5.59E-58	3.4037	2.4122	0.32896	91.601	8	11200000	2559200	8640400
2	2	5.5	5.5	5.5	57.861	529	0.006536	2.9135	2.4036	0.33001	8.4011	2	1015300	248760	766580
15	20	34.7	34.7	34.7	55.992	504	8.07E-128	4.1445	2.3804	0.33289	21.365	17	44854000	7853300	37001000
12	14	12.1	12.1	12.1	138.83	1220	3.05E-96	5.5702	2.3672	0.33454	26.611	12	11142000	1612000	9529700
2	2	1.9	1.9	1.9	50.817	464	0.015962	1.7083	2.3653	0.33478	169.36	2	1039000	454540	584450
7	9	13.7	13.7	13.7	76.715	693	3.23E-36	2.3564	2.3639	0.33496	15.507	7	12779000	7201500	5577400
32	51	56.8	56.8	56.8	59.75	553	1.10E-271	3.5197	2.3569	0.33584	40.708	55	245790000	52641000	193150000
5	6	5.5	5.5	5.5	104.74	934	4.04E-13	4.9177	2.3541	0.3362	184.47	6	2934900	776000	2159000
2	2	1.5	1.5	1.5	157.18	1401	0.0017826	5.6364	2.3497	0.33675	29.741	2	678680	52491	626190
10	14	27.9	27.9	26.5	52.645	480	1.78E-44	2.4484	2.3392	0.33809	42.291	14	22754000	6677700	16077000
2	3	6.9	6.9	4.3	52.164	466	3.39E-08	2.8246	2.3121	0.34158	0.11163	3	2338100	587750	1750300
2	3	6.1	6.1	6.1	43.439	393	0.0001918	2.0799	2.3083	0.34207	40.059	2	935470	274850	660620
19	21	28.9	28.9	28.9	87.798	775	1.42E-74	5.9405	2.3018	0.34293	45.566	19	13425000	1646400	11778000
16	16	19.8	19.8	19.8	110.42	971	2.91E-78	4.1364	2.2971	0.34353	33.729	17	12770000	1870600	10900000
5	8	35	35	35	19.463	177	8.49E-47	1.2516	2.2928	0.34409	35.855	9	18733000	8080000	10653000
18	18	24.8	24.8	24.8	103.08	944	5.58E-131	5.9978	2.2841	0.34524	35.045	16	17243000	1903700	15340000
10	18	58.4	58.4	58.4	29.174	255	1.30E-124	1.5633	2.2836	0.3453	13.053	20	72856000	27369000	45486000
5	6	12.9	12.9	12.9	52.904	456	1.70E-15	2.3365	2.2781	0.34603	24.485	4	2101700	657810	1443900
4	5	17.6	17.6	17.6	28.433	255	9.66E-20	1.4408	2.242	0.35086	10.752	4	3685000	1608400	2076700
4	5	17.1	17.1	14.6	45.374	391	9.24E-35	2.7564	2.2345	0.35188	33.092	12	10097000	2635200	7461500
17	20	20	20	20	125.54	1115	5.04E-102	4.2927	2.2108	0.35512	43.376	20	13620000	2544800	11075000
6	12	40.2	40.2	40.2	13.891	127	3.03E-10	0.94517	2.2101	0.35522	25.126	11	9776200	5075700	4700500
25	27	32.5	32.5	32.5	87.301	795	2.45E-93	5.753	2.209	0.35537	63.795	26	24494000	5047500	19447000
4	8	20.3	20.3	20.3	21.588	187	5.27E-15	1.3442	2.2075	0.35557	39.989	7	12075000	5078500	6996200
2	2	3.7	3.7	3.7	69.991	602	0.0062434	2.35	2.2063	0.35574	25.738	2	950990	0	950990
11	12	32	32	32	50.808	438	3.56E-100	3.0768	2.2018	0.35637	43.239	13	15339000	3700700	11638000
5	8	32.9	29.3	29.3	25.486	225	9.10E-22	1.418	2.1956	0.35723	13.911	6	6641300	2679200	3962200
5	8	31.2	31.2	31.2	22.949	205	3.37E-52	1.9785	2.1923	0.35769	79.639	5	4479300	1885200	2594100
11	11	17.3	17.3	17.3	101.11	900	1.43E-54	5.0555	2.1667	0.36127	45.605	13	10916000	1429300	9487000
4	6	10.1	10.1	10.1	51.712	466	5.87E-22	2.2351	2.1615	0.36201	2.2931	4	9870400	2948000	6922400
10	13	31.4	31.4	31.4	51.109	472	1.02E-33	2.7527	2.1495	0.36372	21.443	10	14555000	3475400	11080000
2	3	15.4	15.4	15.4	22.693	227	0.0018343	1.6447	2.1404	0.36502	34.302	2	583350	218970	364390
3	4	16.1	16.1	16.1	24.279	217	2.24E-26	1.2287	2.1401	0.36506	11.386	3	4181000	1822800	2358100
2	2	12.6	12.6	12.6	34.577	310	3.57E-15	1.6499	2.1266	0.36701	49.422	2	3516000	1077400	2438500
1	1	27.4	4.8	4.8	42.003	376	4.62E-82	3.8871	2.1263	0.36705	136.38	10	38490000	6425700	32064000
4	5	64	64	39.3	10.35	89	6.14E-09	0.89359	2.1162	0.36852	61.263	11	11665000	6170500	5494000
2	3	48.9	11.6	5.6	49.924	448	1.05E-199	3.2995	2.1061	0.36999	24.521	5	24112000	5578200	18534000
4	6	10.2	10.2	10.2	39.724	374	4.54E-07	1.6715	2.1034	0.37038	16.089	4	2727400	1001200	1726200
2	2	7.6	7.6	7.6	32.004	289	4.62E-07	1.6462	2.1016	0.37065	107.68	2	1057400	377060	680310
3	3	12.5	12.5	12.5	42.881	393	7.92E-15	5.0642	2.1005	0.37081	31.781	3	1578400	92670	1485800
6	7	9.1	9.1	9.1	90.932	795	1.10E-20	5.8862	2.1005	0.37081	70.448	5	2894800	296890	2597900
6	6	12.4	12.4	12.4	82.431	740	2.01E-32	5.1804	2.0994	0.37097	62.068	6	2793500	368910	2424600
18	26	21.6	21.6	21.6	105.89	979	2.51E-84	4.1137	2.0962	0.37145	26.359	19	24779000	4612900	20166000
5	9	33.1	33.1	33.1	26.599	245	4.87E-48	1.2817	2.0877	0.37271	14.037	5	5707100	2416900	3290200
8	8	8	8	8	117.66	1038	1.77E-22	4.9397	2.0877	0.37271	25.508	8	3528600	397000	3131600
2	2	6.5	6.5	6.5	40.556	356	5.57E-10	5.1904	2.0875	0.37273	6.1292	2	629880	45356	584520
2	2	6.9	6.9	6.9	42.566	389	1.71E-05	2.1465	2.0683	0.37559	28.7	2	764280	222720	541560
1	1	63.6	63.6	3.1	50.135	451	5.52E-252	3.1463	2.0681	0.37563	36.311	34	235740000	54931000	180810000
2	2	1.7	1.7	1.7	115.96	1041	0.050884	2.263	2.0652	0.37605	113.79	2	798750	324910	473840
4	4	4.3	4.3	4.3	122.41	1104	1.61E-07	4.9343	2.057	0.37729	8.4306	2	1137400	56231	1081200
11	18	24.4	24.4	24.4	56.65	533	1.88E-78	2.5278	2.0309	0.38127	17.376	12	22460000	6131900	16328000
26	38	61.1	61.1	61.1	54.53	493	1.24E-168	3.3526	2.0205	0.38287	48.086	35	158570000	34427000	124140000
7	7	8.3	8.3	8.3	119.48	1044	2.83E-53	3.9876	2.0143	0.38382	76.568	4	2879100	124730	2754400
7	10	24.3	24.3	24.3	36.501	325	2.38E-25	1.6064	2.0043	0.38538	21.711	7	8922500	3244300	5678200
14	25	28.1	28.1	28.1	60.533	545	1.78E-52	2.4237	2.0029	0.3856	104.16	32	47147000	14356000	32791000
4	4	4.1	4.1	4.1	145.83	1304	3.64E-19	5.0337	1.9946	0.38689	13.17	3	1852500	187210	1665300
9	15	31.8	31.8	31.8	29.668	274	4.52E-78	1.1501	1.9943	0.38695	28.636	15	28942000	13248000	15694000
10	10	14.8	14.8	14.8	102.49	906	1.01E-22	4.4921	1.9929	0.38716	29.284	10	7457400	1076300	6381100
3	5	36.9	36.9	23	20.843	187	1.84E-32	1.146	1.989	0.38778	23.28	5	13021000	6244600	6776700
2	2	3	3	3	105.47	914	1.21E-05	3.9064	1.9733	0.39026	2.2397	2	562750	150340	412410
5	5	13.9	13.9	13.9	51.05	454	5.54E-20	4.7549	1.9722	0.39043	19.308	5	4220900	418970	3802000
17	22	46.4	46.4	46.4	60.343	556	5.21E-181	2.417	1.9541	0.39333	36.21	36	41326000	11477000	29849000
2	3	7.3	7.3	7.3	28.777	248	5.95E-06	1.2504	1.9522	0.39364	8.2877	2	913250	413120	500140

6	6	18.8	18.8	18.8	45.376	399	1.08E-28	4.6895	1.9451	0.39479	106.92	7	16749000	9173500	7575500
6	6	6.1	6.1	6.1	136.37	1230	2.04E-18	3.5182	1.939	0.39577	12.357	5	1370100	210020	1160100
2	2	8.4	8.4	8.4	34.833	297	1.32E-10	1.7051	1.9331	0.39673	7.7669	2	1360800	496110	864740
9	15	37.2	37.2	37.2	26.816	234	3.26E-74	1.0365	1.9201	0.39886	18.598	12	41420000	21054000	20365000
21	26	34.1	34.1	34.1	84.87	760	4.53E-126	4.1108	1.9134	0.39996	44.54	28	42427000	7946600	34480000
15	27	56.9	56.9	56.9	24.579	218	5.44E-100	1.1896	1.9072	0.40098	23.021	21	69435000	31571000	37864000
24	36	41.9	41.9	41.9	83.165	739	9.02E-133	2.1442	1.9056	0.40125	42.584	38	57581000	18075000	39506000
3	6	14.4	14.4	14.4	17.999	167	0.0072052	0.94525	1.9048	0.40139	16.21	6	2476100	1265900	1210200
13	17	19.9	19.9	19.9	97.169	876	7.65E-58	3.24	1.887	0.40435	41.706	15	15197000	3372400	11825000
9	15	23.1	23.1	23.1	47.716	432	8.62E-57	2.0444	1.8783	0.40582	14.675	11	33464000	10919000	22545000
3	4	9.5	9.5	9.5	48.275	419	0.021888	1.6521	1.8731	0.40671	14.772	3	2638500	987880	1650600
4	4	10.1	10.1	10.1	65.265	587	4.06E-10	2.5301	1.8495	0.41074	38.972	4	2189600	516570	1673000
22	38	58	58	58	50.14	462	1.37E-116	1.9185	1.8442	0.41165	36.599	67	616590000	206180000	410410000
7	10	63	46.7	38.6	28.082	246	9.56E-106	1.1721	1.8404	0.4123	41.204	14	20037000	9490100	10547000
7	11	51.2	32.9	32.9	28.036	246	2.69E-99	1.2367	1.8371	0.41286	35.424	14	31907000	14342000	17565000
6	6	6.9	6.9	6.9	102.35	898	2.37E-23	3.2258	1.829	0.41427	36.941	6	3110200	629870	2480400
2	3	80.2	17.4	17.4	19.779	172	1.22E-167	1.6827	1.8246	0.41505	40.778	3	13304000	4868600	8435200
6	7	11.1	11.1	11.1	80.996	741	6.78E-50	1.8376	1.8124	0.41718	6.7725	6	5167800	1580900	3586900
4	7	34.8	21.5	21.5	28.302	247	4.50E-42	1.1646	1.8102	0.41756	21.574	8	25296000	12578000	12718000
2	2	14	14	6.6	52.183	457	1.15E-10	2.2181	1.8036	0.41874	29.652	6	4806800	1426900	3379900
17	26	32.6	32.6	32.6	65.853	608	1.84E-72	2.2036	1.8003	0.41931	29.105	30	39785000	11709000	28075000
6	7	14.1	14.1	14.1	54.794	509	2.54E-31	2.0429	1.7814	0.42269	7.4731	6	4917700	1630300	3287400
5	8	55.3	55.3	55.3	11.967	103	7.71E-14	0.85669	1.7741	0.42401	39.412	6	5079700	2752100	2327700
2	2	2	2	2	89.594	794	0.005695	4.4658	1.7713	0.42451	85.966	2	297840	41057	256780
19	20	30.7	30.7	30.7	82.704	732	7.37E-50	4.8047	1.7667	0.42535	21.388	19	15583000	2539200	13044000
12	12	16.2	16.2	16.2	83.677	758	1.26E-33	4.6651	1.7634	0.42595	50.05	12	6817500	1581900	5235500
4	5	45.6	45.6	45.6	11.466	103	5.41E-24	1.3416	1.7539	0.42768	38.884	5	3874000	1657100	2216900
4	8	19.4	19.4	19.4	22.999	201	1.21E-32	0.80235	1.7512	0.42817	24.268	4	7559600	4208500	3351200
4	4	5.9	5.9	5.9	85.595	784	4.15E-11	4.647	1.7483	0.4287	30.907	4	1627700	273370	1354300
5	8	45.9	45.9	29.8	20.697	181	1.11E-46	0.87069	1.7445	0.4294	42.533	9	14410000	7289700	7120200
8	14	34.9	34.9	34.9	19.576	169	4.94E-20	0.79512	1.7427	0.42974	81.616	16	20630000	10262000	10368000
4	5	3.7	3.7	3.7	135.58	1217	2.84E-23	3.3593	1.7371	0.43076	9.2127	4	2211100	511640	1699400
2	4	18.7	18.7	18.7	21.999	198	3.14E-54	0.9126	1.7358	0.43101	13.569	2	3698200	1919200	1779000
2	3	5.7	5.7	5.7	49.203	439	1.47E-05	2.4703	1.7288	0.43231	15.255	3	1590600	398480	1192100
4	6	16.4	16.4	16.4	34.308	304	6.90E-10	1.5226	1.7263	0.43278	11.721	4	1243400	470640	772760
4	4	4.5	4.5	4.5	93.487	819	0.00069202	4.3186	1.7129	0.43527	25.018	3	1103600	123540	980030
9	11	35.7	35.7	35.7	37.154	328	4.72E-95	4.3354	1.7105	0.43572	14.307	10	23024000	4994500	18030000
2	2	61.2	3.5	3.5	65.93	605	0	2.085	1.7037	0.437	20.335	2	1065800	385550	680230
31	38	26.6	26.6	26.6	147.18	1288	2.26E-183	3.8998	1.7021	0.43732	38.845	35	40380000	7993100	32386000
3	3	4.4	4.4	4.4	112.92	995	2.45E-12	2.9962	1.6988	0.43793	22.658	3	2023700	475720	1548000
2	3	16.3	16.3	16.3	16.941	153	2.77E-25	0.97738	1.6963	0.43842	4.4612	2	2450800	1249100	1201700
3	4	3.5	3.5	3.5	106.49	959	7.69E-12	3.5875	1.6921	0.43921	21.691	3	1662200	205590	1456600
4	5	15.6	15.6	15.6	40.949	372	5.72E-18	3.5575	1.6919	0.43924	101.88	5	6813400	1215900	5597400
3	5	59.6	12.1	49.83	445	1.34E-278	3.5488	1.6916	0.43932	49.276	3	16721000	3458000	13263000	
2	2	4.7	4.7	4.7	86.478	767	1.01E-12	4.2557	1.688	0.43999	25.539	2	691310	122750	568560
19	30	38.8	38.8	38.8	58.024	531	2.46E-114	2.0052	1.6873	0.44013	22.812	20	50226000	15327000	34899000
45	75	64.8	64.8	64.8	95.337	858	0	3.2061	1.6847	0.44062	43.049	55	203920000	47600000	156320000
3	4	20.2	20.2	20.2	25.835	223	1.89E-09	1.1689	1.6827	0.441	24.657	3	3166800	1418700	1748000
7	8	8.4	8.4	8.4	107.77	1010	1.51E-32	3.2665	1.6811	0.44132	28.493	8	3154300	815740	2338500
5	8	19.3	19.3	19.3	37.429	353	3.25E-34	2.1251	1.6784	0.44184	49.631	8	9053300	3367700	5685600
3	5	35.4	13.8	13.8	35.868	333	8.93E-145	1.3147	1.6749	0.4425	23.669	3	4720200	1847100	2873200
2	2	14.6	14.6	14.6	20.891	199	1.73E-05	0.97797	1.6726	0.44295	6.4607	2	721830	356620	365210
6	10	24.7	24.7	24.7	33.313	300	5.29E-81	1.4626	1.652	0.44696	72.424	9	19503000	7698400	11804000
8	11	18.6	18.6	18.6	56.381	517	6.48E-68	2.5561	1.6493	0.44748	17.483	9	8749900	2428500	6321400
6	6	4.6	4.6	4.6	154.59	1318	6.83E-19	4.1596	1.6482	0.44769	66.714	5	1810600	215280	1595300
18	25	22	22	22	107.14	953	1.38E-71	3.0027	1.6454	0.44825	37.938	19	17189000	3728300	13461000
9	15	33.3	33.3	33.3	32.575	294	7.91E-101	1.5621	1.6308	0.45114	82.122	26	75931000	28766000	47165000
7	13	49.7	49.7	49.7	17.776	157	1.56E-31	0.87009	1.6291	0.45147	19.91	9	18756000	10041000	8715200
14	16	36.1	36.1	36.1	51.156	463	1.45E-75	2.0835	1.6246	0.45237	31.755	14	18934000	6047400	12887000
4	4	8.5	8.5	8.5	66.9	613	2.86E-19	1.7929	1.6238	0.45253	62.616	4	2702500	827640	1874800
21	35	44.5	44.5	44.5	64.324	569	3.64E-145	1.989	1.6226	0.45276	15.198	26	76185000	25087000	51098000
51	85	64.9	64.9	64.9	104.85	911	0	2.8349	1.6208	0.45312	43.986	67	148660000	38011000	110650000
12	21	73.9	73.9	73.9	17.818	165	4.18E-137	0.93344	1.6182	0.45364	31.63	32	459950000	235340000	224610000
5	7	11.6	11.6	11.6	57.805	517	6.20E-15	1.8365	1.6117	0.45495	8.1619	6	4769300	1652500	3116800
1	2	14.7	3	1.7	72.39	660	9.97E-70	1.6321	1.6098	0.45533	4.7505	2	1572800	555970	1016800

3	5	29	29	29	18.749	176	1.48E-14	0.82885	1.6085	0.45559	22.583	4	5862600	2987100	2875500
11	13	49.1	49.1	49.1	18.491	161	1.01E-24	1.5924	1.6042	0.45646	13.022	11	10598000	4045000	6553100
30	32	24.4	24.4	24.4	157.9	1394	1.41E-139	3.9366	1.6039	0.45652	50.269	31	23151000	4166100	18985000
24	43	66.8	61.4	61.4	36.638	334	1.02E-156	1.2214	1.5985	0.4576	16.763	35	190510000	83667000	106840000
6	6	6.8	6.8	6.8	123.38	1071	4.64E-34	3.1202	1.5978	0.45776	16.45	5	1311900	235200	1076700
2	3	8.8	8.8	8.8	29.299	261	5.50E-09	1.104	1.5887	0.45961	34.31	2	2343800	1189100	1154700
6	6	7.9	7.9	7.9	117.97	1052	1.35E-13	2.7403	1.5652	0.46444	93.054	6	1818500	723990	1094500
7	11	58.6	58.6	58.6	17.138	152	1.33E-23	0.73772	1.5645	0.46459	14.993	7	6860400	3912200	2948200
4	5	19.5	19.5	9.4	47.655	425	8.25E-25	2.0488	1.5568	0.46619	23.562	9	10201000	3226100	6974700
5	5	7.8	7.8	6.4	97.717	874	1.77E-21	3.4596	1.5532	0.46695	38.423	6	3222000	373370	2848600
4	8	75.1	75.1	9.4	57.936	531	0	1.9093	1.5494	0.46773	14.078	64	439410000	147060000	292360000
4	4	5.2	5.2	5.2	103.28	919	3.26E-16	3.4487	1.5483	0.46797	67.107	4	1664700	362910	1301700
2	3	22.9	22.9	22.9	9.1113	83	3.15E-05	0.61443	1.5468	0.46828	3.7375	2	1006900	615240	391640
4	4	5.2	5.2	5.2	119.52	1038	1.00E-16	3.0619	1.5467	0.46831	85.685	3	1367900	425450	942470
4	4	4.8	4.8	4.8	95.907	853	1.51E-10	3.5907	1.5447	0.46874	44.703	4	2328600	510340	1818300
9	9	19.6	19.6	8.7	112.89	1023	1.29E-113	3.6699	1.5326	0.47128	115.53	18	19841000	8057800	11783000
9	9	10.9	10.9	10.9	110.5	1020	4.51E-51	3.282	1.531	0.47163	28.134	8	6451400	1424900	5026500
3	3	9.9	9.9	9.9	45.796	403	1.07E-23	3.5543	1.5293	0.47199	35.53	3	1923600	291790	1631800
21	28	29.2	29.2	29.2	100.2	908	1.48E-116	2.8053	1.528	0.47226	32.873	24	30393000	7477400	22915000
3	3	5	5	5	66.193	606	2.40E-17	1.8556	1.5276	0.47236	13.333	3	2250700	763870	1486800
4	5	7.2	7.2	7.2	73.46	669	5.63E-16	1.8464	1.5268	0.47253	7.703	4	3478700	1131200	2347500
2	2	1.6	1.6	1.6	148.42	1278	0.0001467	3.7482	1.5234	0.47325	45.162	2	586580	44185	542390
18	20	18.3	18.3	18.3	139.76	1262	2.42E-138	3.7921	1.5178	0.47445	141.19	18	18005000	7248100	10757000
3	5	62.9	38.2	38.2	10.366	89	2.64E-25	0.73504	1.5175	0.47452	22.831	3	3311200	1886100	1425000
11	20	61.8	61.8	61.8	28.804	254	3.02E-63	0.90758	1.5126	0.47557	14.127	16	33723000	17408000	16314000
3	5	7.7	7.7	7.7	48.227	443	8.49E-13	1.7177	1.5067	0.47683	7.1701	4	2892800	1025700	1867100
17	26	31.7	31.7	31.7	71.496	625	3.27E-86	1.5387	1.5043	0.47735	54.217	19	36417000	13279000	23137000
3	3	13.1	13.1	13.1	28.787	251	1.12E-11	1.0446	1.5026	0.47772	26.501	3	2789000	1440100	1349000
10	19	42.4	42.4	29.8	26.707	238	2.85E-132	0.86586	1.4985	0.47861	73.787	42	1078200000	563730000	514510000
5	9	11.1	11.1	11.1	59.075	523	5.99E-51	1.034	1.4828	0.48204	5.9694	5	12987000	6518500	6468400
2	3	5.2	5.2	5.2	47.731	440	3.92E-20	1.5295	1.4741	0.48397	7.1596	2	729110	298840	430270
1	2	9.5	9.5	9.5	24.385	210	0.016673	1.0515	1.4659	0.48577	57.471	2	621110	286340	334780
2	2	2	2	2	144.73	1338	0.0017902	3.6851	1.4602	0.48704	21.494	2	621360	124720	496640
2	4	18.9	18.9	18.9	16.253	148	4.66E-17	0.62181	1.4587	0.48739	21.318	4	3153800	1872900	1280900
4	5	7	7	7	80.651	704	3.53E-14	1.5836	1.4567	0.48784	130.84	5	3363000	1439000	1924000
6	6	8.3	8.3	8.3	87.679	759	3.64E-13	3.6592	1.4514	0.48902	70.535	6	1507800	98441	1409400
12	12	24.1	24.1	24.1	75.491	694	3.51E-54	3.7161	1.449	0.48955	51.976	14	7871700	1737600	6134100
4	4	4.9	4.9	4.9	96.725	837	1.10E-12	3.6493	1.4475	0.4899	44.293	4	1192100	440590	751470
4	8	37.3	37.3	37.3	13.57	126	6.24E-56	1.4663	1.4436	0.49077	25.458	8	28706000	11539000	17167000
2	4	25	25	25	8.544	76	5.67E-06	0.57254	1.4414	0.49128	7.6601	2	3216300	2011200	1205100
5	9	44.6	44.6	44.6	17.276	148	1.00E-23	0.65542	1.4389	0.49184	16.542	5	6482800	3778900	2703900
6	7	17.1	17.1	17.1	49.741	451	4.47E-26	1.9117	1.4382	0.49199	18.915	6	5703100	1846300	3856800
2	3	10	5.7	5.7	46.437	420	9.27E-15	1.2027	1.4381	0.49201	10.747	2	1153000	535420	617530
2	4	35.7	35.7	5.3	51.79	473	4.90E-117	1.4708	1.4357	0.49257	39.248	19	123270000	52262000	71007000
20	37	54.3	54.3	54.3	37.482	335	1.40E-118	0.99204	1.4326	0.49326	13.492	28	125670000	58963000	66705000
3	3	3.1	3.1	3.1	113.89	1086	1.12E-05	2.8327	1.431	0.49364	59.113	3	1212800	284580	928240
12	22	55.1	55.1	55.1	27.692	256	4.90E-115	1.2509	1.4294	0.49399	23.065	25	236910000	101520000	135390000
2	2	50.4	12	12	41.272	375	2.31E-109	1.3882	1.4148	0.49734	6.3766	2	7550200	3039500	4510700
5	6	7	7	7	96.557	863	1.42E-19	3.4249	1.4089	0.49871	23.466	5	2586000	429070	2157000
6	6	12.6	12.6	12.6	63.541	587	4.66E-17	3.9475	1.4087	0.49876	11.782	5	1560900	186170	1374800
25	45	45.6	45.6	45.6	68.813	631	2.22E-146	1.9532	1.4033	0.5	57.73	32	80362000	26077000	54285000
5	6	9.8	9.8	9.8	71.122	661	7.76E-25	3.0852	1.4003	0.49921	31.999	6	3472900	807600	2665300
5	6	30.4	30.4	30.4	14.226	125	2.02E-09	1.1788	1.3996	0.499	145.12	7	12821000	5620800	7200200
3	3	3.2	3.2	3.2	109.29	992	7.97E-14	2.5529	1.3894	0.4963	11.35	4	995110	236810	758300
1	2	18.2	18.2	3.4	76.569	697	1.66E-76	1.1861	1.3746	0.49232	21.748	10	26320000	11449000	14871000
23	39	55.2	55.2	35.8	83.263	724	0	3.4005	1.3733	0.49196	54.968	56	335600000	74775000	260820000
3	6	21.4	21.4	21.4	21.689	196	9.66E-16	0.57493	1.3711	0.49137	13.086	3	5520500	3437900	2082600
15	19	35.1	35.1	35.1	64.615	592	3.50E-67	1.2796	1.3625	0.48903	40.742	15	13554000	5738400	7815600
6	7	6.6	6.6	6.6	112.42	998	9.36E-19	2.5756	1.359	0.48808	14.155	6	2326300	639960	1686300
7	11	60.4	60.4	14.2	68.996	647	0	1.7125	1.3587	0.48801	58.452	176	2248600000	821260000	1427400000
2	2	3.1	3.1	3.1	104.64	949	0.00082707	3.0259	1.3585	0.48794	40.4	2	664130	145070	519060
9	15	35.5	35.5	35.5	38.627	352	9.52E-85	1.0539	1.3523	0.48624	8.6053	10	27317000	13133000	14185000
15	26	41.9	41.9	41.9	38.746	372	4.22E-152	1.0141	1.3486	0.48523	26.467	18	35680000	17374000	18307000
9	15	38.3	38.3	38.3	31.387	290	4.27E-84	0.76412	1.3473	0.48486	23.811	11	16051000	8821600	7229300
2	3	8.3	8.3	8.3	29.965	277	0.035245	0.76772	1.3372	0.48208	11.66	2	660850	344340	316510

4	7	23.1	23.1	23.1	37.895	350	4.46E-11	1.1074	1.3309	0.48031	41.338	4	4979900	2246000	2734000
3	3	3.8	3.8	3.8	106.9	954	1.24E-11	2.424	1.3266	0.47912	16.417	3	477720	84652	393060
18	26	49.5	49.5	49.5	47.517	430	1.06E-150	3.1635	1.3251	0.47871	84.162	19	62689000	14145000	48544000
2	2	12.7	12.7	12.7	17.977	158	3.79E-06	0.68954	1.3239	0.47837	25.035	2	1925600	1010900	914670
2	3	12.6	12.6	12.6	23.63	206	2.96E-16	1.177	1.318	0.47671	0.48179	2	1989500	912140	1077400
3	3	7.3	7.3	7.3	49.997	450	8.64E-13	1.6999	1.3159	0.47612	18.391	2	1334700	514010	820700
2	2	6.2	6.2	6.2	35.744	325	3.91E-09	1.0365	1.31	0.47445	8.8415	2	973310	394820	578500
7	7	9.5	9.5	9.5	83.471	751	7.42E-18	3.2982	1.3082	0.47395	29.489	7	3358300	762420	2595900
4	4	6.4	6.4	6.4	87.343	783	1.69E-06	2.2922	1.2997	0.47153	39.218	2	1326300	154790	1171500
3	4	27.2	27.2	27.2	14.199	125	3.70E-22	0.58812	1.294	0.46991	6.0969	3	2039900	1291400	748490
3	3	7.4	7.4	7.4	38.418	351	0.050686	1.1316	1.2829	0.46672	5.17	3	1190700	565850	624820
15	27	64	64	64	35.076	317	1.08E-123	1.0407	1.2818	0.46641	10.851	16	43528000	20655000	22873000
3	5	32.7	32.7	32.7	12.259	104	2.89E-07	0.52143	1.2773	0.4651	21.022	5	6455400	4221900	2233400
16	28	57.5	57.5	57.5	33.172	301	5.83E-131	1.012	1.2746	0.46431	33.315	22	58908000	29444000	29463000
11	20	36.9	36.9	36.9	43.062	390	4.60E-81	1.2823	1.2738	0.46407	14.768	12	26188000	11539000	14649000
3	3	11.1	11.1	11.1	53.844	496	1.15E-07	1.3077	1.2646	0.4614	55.849	3	2233900	983720	1250200
6	9	34.5	34.5	34.5	19.823	174	2.21E-20	0.57449	1.2631	0.46097	87.376	7	33293000	21805000	11488000
2	2	2.6	2.6	2.6	107.6	993	0.00061093	1.943	1.2491	0.45685	31.588	2	1267900	461010	806880
36	66	54.9	54.9	54.9	73.68	679	0	1.2628	1.249	0.4568	29.965	54	356260000	154470000	201790000
14	17	23.8	23.8	23.8	89.321	806	3.71E-60	2.2005	1.2477	0.45642	41.399	16	16662000	5114600	11547000
2	4	15.4	15.4	15.4	19.015	169	2.03E-17	0.66987	1.2443	0.45543	7.103	2	1115400	635520	479850
5	8	28.4	28.4	28.4	26.56	229	3.28E-14	0.68058	1.2437	0.45525	19.978	6	5578900	3093500	2485400
7	12	35.3	35.3	35.3	26.411	241	1.20E-63	0.67745	1.232	0.45176	14.705	7	10932000	6484200	4448100
3	6	5.7	5.7	5.7	53.488	475	7.41E-35	1.5741	1.2284	0.45068	20.146	3	1424000	485370	938610
7	9	8	8	8	97.459	860	5.19E-11	1.9207	1.2231	0.44909	25.628	7	3678400	1119200	2559200
18	28	51.2	51.2	51.2	51.153	449	2.85E-157	1.5252	1.2184	0.44768	35.946	19	22707000	8442300	14265000
2	3	15.3	7.5	7.5	50.822	439	2.60E-17	1.643	1.218	0.44755	32.01	2	1191400	427360	764070
16	30	56.8	56.8	56.8	35.503	338	3.43E-167	0.94702	1.2124	0.44585	20.376	20	100510000	50315000	50193000
11	13	15.3	13.6	13.6	92.468	803	7.68E-36	2.142	1.2058	0.44382	107.65	11	11538000	4130400	7407500
8	13	18.1	18.1	18.1	57.293	520	2.53E-72	1.4911	1.2016	0.44255	4.9302	8	13195000	5330500	7864600
9	15	41.5	41.5	41.5	27.399	246	2.30E-31	0.69049	1.1913	0.43939	14.959	10	19441000	11381000	8059800
3	4	15.8	15.8	15.8	32.745	285	7.02E-06	0.83052	1.1905	0.43914	1.0549	3	2303500	1238900	1064700
15	26	67.1	67.1	67.1	26.21	228	7.08E-119	0.75491	1.1904	0.43911	14.864	27	149260000	84915000	64347000
2	4	24.4	24.4	24.4	9.7251	86	9.25E-18	0.47065	1.1849	0.43741	6.3246	2	638990	429150	209850
8	13	51.3	40.6	40.6	30.54	271	4.18E-61	0.6513	1.1815	0.43635	15.312	9	20129000	11574000	8555000
6	11	24	24	24	36.724	342	8.19E-58	2.8832	1.1799	0.43586	11.366	8	31650000	8570200	23080000
14	21	19.8	19.8	19.8	117.85	1058	7.48E-53	2.2239	1.1754	0.43447	16.608	18	9425600	2893600	6531900
6	12	35.1	35.1	35.1	31.362	282	7.23E-82	0.67822	1.1749	0.4343	15.946	13	85993000	50915000	35079000
1	1	49.6	33.1	5.6	32.865	284	7.07E-106	0.83668	1.1734	0.43384	13.145	13	62051000	32033000	30017000
13	25	36.5	36.5	22.6	70.67	636	6.36E-142	1.1621	1.1706	0.43297	30.348	23	70468000	33524000	36944000
21	40	52.7	52.7	54.177	54.177	509	0	1.5498	1.1692	0.43252	51.04	65	229940000	99359000	130580000
8	13	53.8	39.9	39.9	32.949	286	1.81E-95	0.99558	1.1638	0.43084	10.612	8	31331000	15465000	15866000
4	5	12.2	9.1	9.1	48.162	419	1.79E-10	1.2031	1.1635	0.43074	10.732	4	2807300	1163500	1643900
3	3	3.7	3.7	3.7	109.43	972	1.01E-08	2.2933	1.1585	0.42915	10.949	3	788280	166410	621880
6	10	8.4	8.4	8.4	58.993	547	1.09E-19	0.5819	1.1579	0.42898	28.876	6	16191000	9437300	6753900
7	12	19.8	19.8	19.8	44.131	398	1.44E-27	2.8113	1.1555	0.42821	70.889	7	12445000	3140900	9304000
5	10	18.8	18.8	18.8	29.483	261	7.06E-18	0.80408	1.1539	0.42772	6.5613	5	28576000	16128000	12448000
1	1	35.6	12.8	5.9	35.904	320	1.75E-84	1.3786	1.1531	0.42746	0.68343	2	1072600	426700	645900
3	3	5.8	5.8	5.8	67.454	608	0.00022093	1.2055	1.1506	0.42667	3.3846	3	1417800	609330	808460
2	2	7.4	7.4	7.4	27.547	258	0.00090973	0.6477	1.15	0.42648	17.632	2	1151900	713890	437980
28	49	61.1	61.1	61.1	59.366	543	2.00E-253	1.4152	1.1468	0.42546	15.606	35	123100000	49321000	73784000
6	7	7	7	7	105.84	953	7.24E-15	3.1761	1.1455	0.42505	54.721	7	5554200	1239500	4314700
7	14	53.4	53.4	53.4	17.259	148	1.84E-94	0.65722	1.1435	0.42441	11.399	11	36439000	21679000	14760000
3	5	36.6	36.6	36.6	12.107	112	9.84E-21	0.55146	1.1433	0.42434	12.535	4	2540300	1606800	933580
3	4	13.4	13.4	13.4	33.712	305	2.05E-21	0.79533	1.1363	0.42212	27.015	3	3524900	1935300	1589600
5	8	41.6	41.6	41.6	16.648	154	1.38E-37	0.51757	1.1361	0.42205	21.72	5	8061300	5294400	2766900
34	64	57.9	57.9	57.9	49.679	451	1.75E-298	1.2166	1.1335	0.42121	40.035	53	750170000	336140000	414030000
2	3	6.6	6.6	6.6	39.611	350	1.68E-20	0.79201	1.1322	0.42078	21.63	2	2726500	1506800	1219700
7	11	34	34	34	24.701	212	7.89E-26	0.70044	1.13	0.42007	9.9266	7	11080000	6237600	4842400
11	16	21.5	21.5	21.5	56.44	494	8.63E-31	1.3743	1.1296	0.41996	19.959	12	9875000	3960400	5914600
9	15	31.2	31.2	31.2	48.141	417	3.04E-44	0.76662	1.1294	0.41988	39.862	12	19655000	10745000	8910600
2	3	6	6	6	35.853	316	0.0057215	0.93321	1.1205	0.41702	11.859	2	1382300	688870	693420
21	35	81.9	81.9	66.8	22.11	199	9.58E-162	0.99483	1.1188	0.41645	58.095	63	1773800000	876800000	896990000
4	4	5.2	5.2	5.2	92.888	821	1.18E-06	3.1199	1.1091	0.41329	18.11	2	1230500	179420	1051100
16	26	59.3	59.3	59.3	34.333	300	8.20E-57	0.80129	1.1042	0.41169	26.723	28	40745000	22232000	18513000

8	14	30.4	28.7	28.7	39.638	349	3.50E-60	0.84152	1.0999	0.41028	17.097	10	17028000	9088300	7940200
31	55	64.7	64.7	64.7	57.488	535	0	1.3584	1.0945	0.4085	17.561	41	136000000	59288000	76707000
11	17	58.2	58.2	58.2	28.768	261	5.03E-79	0.76693	1.0926	0.40786	10.2	11	34329000	18918000	15412000
11	18	33.4	33.4	33.4	39.287	353	1.57E-61	0.85359	1.0916	0.40754	15.679	13	22688000	12152000	10536000
10	13	14.8	14.8	14.8	99.028	873	1.22E-28	2.1976	1.0909	0.4073	46.698	11	8583200	2376600	6206600
6	10	14.2	12.5	12.5	54.231	471	5.56E-15	1.311	1.0821	0.40438	11.843	6	3812300	1620900	2191400
14	23	59.2	59.2	59.2	20.17	184	8.99E-82	0.47072	1.0813	0.40411	28.179	25	186690000	124540000	62146000
3	5	20.4	20.4	20.4	24.763	225	2.63E-65	0.74102	1.0805	0.40385	8.136	4	40220000	22462000	17758000
8	11	27.5	27.5	27.5	40.542	367	9.46E-40	2.453	1.076	0.40236	67.598	9	8162800	2061700	6101100
14	26	55.6	55.6	55.6	27.887	248	2.39E-101	0.6119	1.0717	0.4009	22.466	19	62363000	37933000	24430000
5	9	30.4	23.9	11.3	63.923	586	3.72E-124	1.0891	1.0692	0.40005	29.277	24	23255000	10131000	13124000
7	12	20.7	20.7	20.7	53.9	492	8.90E-59	1.1052	1.0688	0.39992	29.478	7	9766900	4010700	5756300
3	5	25	25	25	22.406	200	1.69E-15	0.68993	1.0659	0.39897	14.111	3	2308000	1325000	982950
13	15	25	25	25	59.143	528	4.29E-15	1.2615	1.0653	0.39874	18.949	15	9574000	3914500	5659500
2	3	15.8	15.8	15.8	16.937	152	1.69E-08	0.53886	1.0611	0.39732	16.1	3	1260800	773370	487400
42	66	38.6	38.6	38.6	135.65	1197	1.68E-200	2.4957	1.0607	0.39719	44.717	49	83439000	23064000	60376000
2	3	19	19	5.2	50.679	443	2.65E-36	1.162	1.0598	0.39689	34.264	9	13224000	6207200	7016500
3	4	36.2	36.2	36.2	34.834	318	1.99E-44	0.92921	1.0561	0.39564	21.041	13	12882000	6540600	6341600
3	4	9.2	7.8	7.8	64.319	599	2.82E-09	1.2128	1.0441	0.39154	117.42	3	2568500	368900	2196900
21	35	67.9	67.9	67.9	17.965	156	4.54E-90	0.43467	1.0425	0.39101	99.502	56	369780000	248560000	121220000
2	4	12.6	12.6	12.6	24.49	206	0.02873	0.93223	1.0412	0.39055	20.781	2	1239400	604850	634530
2	3	16.7	16.7	16.7	19.608	180	2.10E-05	0.92737	1.0385	0.38962	7.7627	2	960900	463330	497570
1	2	15.8	3.6	3.6	34.097	303	4.57E-59	0.7262	1.033	0.38773	0.81308	2	32856000	18771000	14085000
6	6	9	9	9	84.228	725	1.11E-10	2.6658	1.0318	0.3873	43.114	6	2632500	610210	2022300
10	17	15	15	15	85.223	760	1.51E-30	2.6332	1.0265	0.38546	38.034	11	9923000	2583700	7339300
4	5	23.4	23.4	23.4	21.834	197	6.96E-18	0.91611	1.0259	0.38526	27.963	5	5518900	2950800	2568100
13	20	18.4	10.2	10.2	10.2	910	1.30E-46	2.0102	1.0247	0.38484	15.493	13	7775400	2400100	5375300
2	2	26.6	26.6	26.6	13.623	124	0.00048191	0.38197	1.0231	0.3843	7.3521	2	2283200	1606500	676730
8	14	54.3	39.9	39.9	22.764	208	4.07E-81	0.60755	1.023	0.38427	12.747	11	42856000	25724000	17131000
42	80	69.5	69.5	69.5	70.897	646	0	1.0169	1.0205	0.3834	31.128	77	110760000	54377000	56380000
4	5	5.6	5.6	5.6	78.365	709	1.95E-20	1.7987	1.0198	0.38316	29.151	4	2529800	844800	1685100
13	23	66.9	66.9	66.9	28.521	248	2.83E-236	0.70344	1.0177	0.38243	25.965	65	285600000	163130000	122470000
2	3	17.6	17.6	17.6	11.845	102	0.013583	0.45528	1.0017	0.37681	13.061	2	1939600	1323900	615680
8	13	32.2	32.2	32.2	30.886	267	9.70E-49	0.69893	1.0015	0.37672	23.828	9	19959000	12066000	7893500
2	2	10.8	10.8	10.8	21.119	186	4.52E-09	0.89175	0.99386	0.37403	18.863	2	1307500	651160	656380
6	6	9.5	9.5	9.5	91.706	796	2.20E-23	2.5037	0.99308	0.37375	21.285	7	2349600	536180	1813400
5	9	64	64	18.5	32.642	292	2.56E-109	0.43551	0.9921	0.3734	37.873	32	290150000	198570000	91580000
3	3	8.6	8.6	8.6	33.824	302	0.0030672	0.87395	0.99084	0.37295	11.486	3	1706100	910450	795660
3	6	34.6	34.6	34.6	9.0714	81	3.29E-29	0.38119	0.97741	0.36815	4.515	5	9710400	6853200	2857200
19	33	35.8	21.7	21.7	98.16	854	4.92E-227	2.1887	0.96851	0.36495	60.085	30	83220000	24931000	58288000
5	7	15.7	15.7	12.9	51.281	451	3.69E-15	1.0056	0.96636	0.36417	11.964	7	9006900	4183300	4823600
6	8	29.9	29.9	29.9	19.208	177	3.02E-20	0.52734	0.96254	0.36278	35.545	7	8916200	5730700	3185400
1	2	56.5	7.9	7.9	19.653	177	1.06E-77	0.42659	0.9607	0.36212	5.4493	2	17398000	12114000	5284400
43	71	40.7	40.7	40.7	126.97	1140	7.93E-168	1.7518	0.95482	0.35998	29.57	51	154150000	52760000	101390000
16	24	32.4	32.4	32.4	65.308	589	3.37E-48	1.1324	0.95124	0.35867	18.081	16	18813000	8694300	10119000
10	14	15.6	15.6	15.6	88.549	835	1.61E-35	1.8144	0.94794	0.35746	42.908	11	6004800	1951200	4053600
2	2	2.8	2.8	2.8	68.671	637	0.010752	0.94596	0.9455	0.35656	1.7316	2	1396600	678590	718000
6	10	20.2	20.2	20.2	38.242	331	1.85E-19	1.0038	0.94208	0.35531	39.903	8	10807000	5375200	5431600
3	5	33.6	33.6	33.6	12.405	110	2.19E-31	0.59537	0.94202	0.35529	19.683	3	1755600	1080000	675570
2	2	13.3	13.3	13.3	20.462	180	0.069862	0.64693	0.93985	0.35449	15.328	3	763050	444370	318670
28	52	56.2	56.2	56.2	57.924	539	1.01E-283	1.1521	0.93755	0.35364	16.885	39	193840000	87825000	106020000
6	9	39	39	39	20.105	172	2.84E-16	0.83963	0.93217	0.35165	38.903	7	11094000	5753800	5340700
6	11	36.8	36.8	36.8	22.836	201	8.06E-51	0.8329	0.93108	0.35124	23.347	7	12849000	7055600	5793200
2	2	15.5	15.5	15.5	17.385	155	0.0050093	0.37331	0.92969	0.35073	17.533	2	1636900	1147700	489140
4	4	9.3	9.3	9.3	36.588	334	8.56E-15	1.9106	0.9286	0.35032	19.454	4	7184300	2940700	4243600
19	31	34.9	34.9	34.9	59.67	541	5.44E-115	1.1023	0.92666	0.3496	58.211	36	54323000	25292000	29031000
4	4	27.8	27.8	27.8	23.449	205	3.27E-14	0.72378	0.92355	0.34845	25.397	4	2086400	1189300	897130
3	3	3	3	3	123.11	1134	1.28E-07	2.2856	0.91772	0.34627	10.599	3	859730	146500	713230
2	2	28.6	28.6	28.6	19.661	175	7.37E-05	0.41244	0.91492	0.34522	29.776	2	848750	549780	298970
10	11	14.5	14.5	14.5	94.33	840	3.65E-69	1.733	0.91023	0.34346	33.235	10	7077600	2263000	4814600
18	33	68	68	68	28.068	244	2.31E-134	0.5454	0.90678	0.34216	30.541	24	54134000	33200000	20935000
5	7	13.7	13.7	13.7	54.416	483	8.11E-10	1.3063	0.90544	0.34165	57.002	7	4314900	1889300	2425600
6	7	15.2	15.2	15.2	39.681	363	1.58E-19	2.3164	0.90334	0.34086	13.37	5	5704200	1272000	4432200
3	4	18.4	18.4	18.4	13.459	114	0.0028442	0.57529	0.89914	0.33927	25.135	3	3141600	1976600	1164900
2	2	2.1	2.1	2.1	74.698	676	0.29778	0.92748	0.89694	0.33843	8.2025	2	1622200	758240	863990

2	2	6.2	2.8	2.8	73.502	677	4.25E-11	0.98911	0.8958	0.338	56.386	2	1212800	611060	601690
5	9	47.1	47.1	47.1	13.714	119	4.97E-25	0.46966	0.89565	0.33794	29.433	12	57134000	38445000	18689000
3	3	22.5	22.5	22.5	23.845	222	0.0003289	0.51781	0.89523	0.33778	54.592	3	2084500	1208500	876030
17	28	72.7	66.1	18.506	66.1	165	4.07E-108	0.40177	0.89434	0.33744	42.907	25	118370000	83326000	35048000
5	5	7.2	7.2	7.2	90.069	792	7.58E-13	2.2511	0.89287	0.33689	47.198	5	2430900	618140	1812700
4	6	22.8	22.8	22.8	26.922	241	9.18E-26	0.62188	0.89188	0.33651	10.247	4	5452700	3288500	2164300
17	31	46.1	46.1	46.1	43.135	393	1.28E-84	0.90422	0.88637	0.33441	99.48	19	37872000	22611000	15261000
7	13	56.8	56.8	56.8	14.515	132	1.25E-38	0.53864	0.88548	0.33407	18.53	11	146400000	94093000	52310000
12	20	23.9	23.9	23.9	63.111	556	2.42E-35	0.49666	0.88242	0.33289	87.129	14	32941000	15921000	17020000
5	8	24.5	24.5	21.6	31.279	282	2.60E-25	0.66387	0.88085	0.33229	44.12	7	10007000	5737000	4270000
3	4	6.8	6.8	6.8	59.755	527	7.08E-07	1.078	0.88085	0.33229	48.016	2	1323400	652070	671360
9	11	5.2	5.2	5.2	213.47	2080	2.76E-36	1.546	0.87566	0.33029	41.969	11	7169300	2420400	4748800
8	11	39.6	39.6	39.6	26.697	240	3.06E-60	0.61228	0.87494	0.33002	15.261	8	25936000	15553000	10383000
9	13	27.6	27.6	27.6	36.112	315	6.21E-27	0.73892	0.87463	0.3299	17.306	8	7250400	4087300	3163000
8	13	38	38	38	16.762	150	1.72E-33	0.39534	0.86986	0.32806	35.58	19	48976000	34891000	14085000
9	17	63.2	63.2	63.2	19.81	174	7.07E-43	0.62288	0.86935	0.32786	32.683	19	46903000	28129000	18774000
1	2	6.4	6.4	6.4	21.042	188	0.0001501	0.77535	0.86825	0.32743	19.947	2	846190	393610	452570
11	19	40.8	40.8	40.8	43.66	395	5.15E-104	0.89479	0.86635	0.3267	23.062	12	23315000	12189000	11127000
2	3	7.4	7.4	7.4	32.485	284	5.95E-14	0.47646	0.86337	0.32554	3.4217	2	1578700	1045300	533370
4	6	29.7	29.7	16.495	148	5.10E-07	0.37602	0.86049	0.32442	0.32442	26.325	6	7352600	5246500	2106100
31	57	65	65	65	59.62	548	1.87E-234	1.0678	0.85981	0.32416	9.439	35	154060000	72568000	81493000
2	2	13.8	13.8	13.8	14.365	130	0.00087843	0.34193	0.85869	0.32372	5.6825	2	621520	470460	151500
2	2	2.1	2.1	2.1	90.193	812	0.00015311	2.2777	0.85694	0.32304	43.648	2	344840	28909	315930
10	18	21	21	21	61.626	552	4.10E-41	1.0318	0.84449	0.31833	15.409	11	14042000	7722900	6319300
15	30	44.5	44.5	44.5	50.227	456	9.52E-154	1.1236	0.84461	0.31821	20.147	20	48976000	22991000	25985000
8	10	10	10	10	93.741	844	2.04E-28	2.1703	0.84411	0.31801	29.857	10	4814900	1317100	3497800
9	15	39	39	39	24.682	223	6.48E-53	0.56737	0.84319	0.31765	24.213	12	41862000	25571000	16291000
20	27	30.8	30.8	30.8	82.593	744	1.74E-83	2.1818	0.84167	0.31705	44.491	21	24372000	10346000	14026000
4	4	8.8	5.7	5.7	81.067	737	1.90E-34	1.929	0.83908	0.31603	15.406	4	863740	139280	724470
2	2	3.9	3.9	3.9	87.334	750	3.86E-05	2.227	0.83783	0.31554	76.775	2	501990	0	501990
4	6	13.5	13.5	13.5	50.388	467	9.55E-37	1.2106	0.83762	0.31545	35.16	5	4649900	2121000	2528900
2	2	18.5	18.5	18.5	23.026	211	0.0074603	0.50528	0.83516	0.31448	53.738	2	1737400	1143000	594430
6	10	42.9	42.9	17.5	46.153	406	1.51E-106	0.8427	0.83028	0.31255	11.564	16	26525000	13859000	12666000
9	14	37.8	37.8	37.8	26.489	241	2.78E-26	0.69774	0.82833	0.31177	21.152	12	18952000	11142000	7809800
4	4	4.8	4.8	4.8	89.333	817	9.08E-07	0.89621	0.8217	0.30913	105.96	4	1160000	334120	825840
5	6	14.6	14.6	14.6	35.808	314	1.53E-07	0.44193	0.81888	0.308	24.707	5	4137300	2759800	1377500
6	8	20.5	20.5	20.5	45.46	396	1.32E-57	1.9937	0.81473	0.30634	10.849	5	5446300	1797900	3648500
5	8	61.9	61.9	61.9	17.49	168	6.91E-34	0.39541	0.81152	0.30505	16.598	8	25513000	18728000	6785000
3	3	6	21	21	23.787	214	4.12E-17	0.449	0.81033	0.30457	8.0845	3	4558000	3123900	1434100
3	3	4.2	4.2	4.2	109.96	962	6.19E-09	2.2746	0.80859	0.30388	15.322	2	633290	68144	565140
3	3	4.9	4.9	4.9	61.89	546	0.026761	0.79079	0.80599	0.30283	18.994	3	1187200	492040	695180
3	4	29.1	29.1	29.1	16.32	151	5.94E-09	0.46378	0.80492	0.30239	17.68	3	5650400	3876900	1773500
13	18	44.9	44.9	44.9	44.508	403	9.08E-119	2.0503	0.79958	0.30024	13.777	16	46627000	14814000	31813000
13	17	41.6	41.6	41.6	39.777	363	1.15E-73	1.9247	0.79831	0.29972	56.221	13	20068000	6561200	13507000
4	7	17.5	17.5	12.3	46.937	416	9.18E-41	0.82404	0.79691	0.29915	11.183	7	7087700	3849300	3238400
3	4	8.8	8.8	8.8	32.604	294	0.021565	0.5253	0.79536	0.29852	27.057	3	1779000	1102300	676770
17	27	40.1	40.1	38.5	55.804	514	1.59E-162	0.97611	0.79396	0.29796	19.162	27	75039000	37833000	37206000
3	5	7.8	7.8	7.8	40.763	370	2.46E-14	0.83351	0.79379	0.29789	10.347	3	3650600	2448500	1202100
1	1	6.2	6.2	6.2	26.145	226	5.81E-05	0.55161	0.79161	0.297	12.458	2	988110	650280	337840
3	4	4.5	4.5	4.5	88.885	793	4.00E-14	1.5344	0.79032	0.29648	26.259	3	2292100	932820	1359200
1	1	6.7	6.7	6.7	29.999	268	0.0043285	0.52695	0.78884	0.29587	15.875	2	1818000	1069100	748890
8	14	59.4	59.4	45.5	32.922	286	6.66E-168	0.63839	0.78717	0.29519	24.507	20	130310000	77570000	52735000
3	4	12.4	12.4	12.4	42.592	380	1.49E-26	0.81614	0.78692	0.29509	7.5578	4	4238000	2382700	1855300
15	25	39.4	39.4	39.4	51.028	464	2.60E-140	0.96443	0.78517	0.29438	40.243	18	43036000	19564000	23472000
11	19	35.4	35.4	35.4	38.388	333	1.01E-54	0.80329	0.78453	0.29411	10.352	12	19199000	10570000	8628900
3	5	26.3	26.3	10.9	51.901	475	1.91E-22	0.93227	0.78397	0.29388	56.159	11	7469400	3618900	3850500
3	6	11.8	11.8	11.8	41.079	380	7.76E-17	0.82496	0.7832	0.29357	12.122	3	3788100	2006100	1782000
9	14	42	42	42	14.306	119	1.36E-62	0.33333	0.7822	0.29316	41.404	14	20108000	14974000	5134500
2	2	35.2	10	10	35.054	321	2.05E-56	0.68971	0.78196	0.29306	11.198	2	1017600	604640	412910
12	21	62.6	57.1	57.1	21.892	198	1.30E-132	0.68816	0.78132	0.2928	34.654	15	148100000	86474000	61624000
5	8	17.8	17.8	17.8	37.495	331	6.13E-38	0.50023	0.78014	0.29231	22.494	5	5556300	3701900	1854400
38	66	70.9	70.9	70.9	56.559	529	0	1.3104	0.77735	0.29117	40.374	53	683780000	287050000	396720000
4	8	9.3	9.3	9.3	52.693	494	3.08E-36	0.94223	0.77597	0.2906	32.15	6	7641000	3925700	3715300
5	5	43.2	43.2	43.2	13.53	111	4.35E-21	0.45856	0.77494	0.29018	23.193	5	3353100	2264300	1088800
3	4	13.1	13.1	13.1	38.809	358	2.44E-23	0.53413	0.77117	0.28862	9.4869	3	2275400	1357500	917900

6	11	18.1	18.1	18.1	49.03	437	1.54E-27	0.90612	0.76868	0.2876	20.155	6	5282300	2709800	2572600
8	12	21.2	21.2	21.2	56.578	523	9.70E-28	0.90548	0.76332	0.28538	11.174	8	5967900	3060000	2908000
2	2	3.4	3.4	3.4	86.86	756	8.55E-15	2.0257	0.76211	0.28488	42.878	2	513490	128300	385190
2	2	1.6	1.6	1.6	98.938	882	0.039578	1.9179	0.76074	0.28431	139.67	2	435130	175000	260130
71	73	54.5	44.4	40.5	231.37	1997	0	16.213	0.75789	0.28313	142.32	131	1462700000	80797000	1381900000
14	23	74.1	74.1	74.1	25.035	224	6.65E-90	0.4428	0.7563	0.28247	22.43	18	23649000	16246000	7403500
1	1	45.7	6.4	1.6	60.066	564	9.48E-164	0.3522	0.75387	0.28145	13.037	3	32184000	23629000	8554900
17	30	55.4	55.4	55.4	28.723	249	1.86E-168	0.52021	0.75358	0.28133	10.858	22	146490000	94233000	52255000
2	3	10.4	10.4	10.4	32.854	288	8.58E-11	0.51702	0.74582	0.27809	6.0574	2	1962000	1250300	711790
5	6	14.2	14.2	14.2	37.434	346	7.67E-09	0.48127	0.74449	0.27753	19.956	5	6026100	2752800	3273300
4	4	6.3	6.3	6.3	74.746	709	1.80E-10	1.6959	0.73975	0.27554	51.72	5	1806700	690160	1116500
4	5	52.6	52.6	52.6	13.459	116	1.86E-23	0.43685	0.73721	0.27447	36.973	4	3039800	1993100	1046700
4	7	34.9	34.9	34.9	16.932	152	7.74E-13	0.30746	0.72301	0.26847	29.629	12	11113000	8333600	2779600
44	78	62.2	58.1	58.1	72.332	654	0	0.70362	0.72076	0.26751	34.63	67	633830000	365050000	268780000
2	2	11.7	11.7	11.7	33.034	282	6.43E-07	0.34646	0.7203	0.26732	53.263	2	686300	581780	104520
4	4	39	39	33.1	18.11	154	1.52E-54	0.31638	0.71923	0.26687	30.245	5	15331000	11682000	3648700
4	4	5.3	5.3	5.3	109	958	1.39E-23	1.2978	0.71528	0.26518	186.42	2	4929700	3943300	986400
39	67	86.5	86.5	86.5	32.66	289	0	0.50929	0.71295	0.26419	38.088	98	1396300000	906760000	489530000
6	11	15.4	15.4	15.4	41.331	369	1.30E-33	0.7408	0.71104	0.26337	34.295	6	7848300	4464400	3383800
4	6	14	14	14	34.482	308	2.01E-41	0.57452	0.70914	0.26256	29.586	4	4168800	2530800	1638000
2	2	2	2	2	84.088	744	0.01468	1.7826	0.70707	0.26167	88.601	2	305290	81078	224210
3	4	11.7	11.7	11.7	40.746	368	2.27E-38	0.55428	0.7066	0.26147	19.658	2	1573100	954230	618850
4	5	10.6	10.6	10.6	42.671	377	1.89E-20	1.7616	0.70553	0.26101	4.0141	4	3804500	1373700	2430800
20	20	4.3	4.3	4.3	532.4	4646	6.79E-49	6.771	0.70517	0.26086	171.39	16	6315400	944550	5370900
2	3	9.5	9.5	9.5	29.204	264	0.012299	0.62855	0.70327	0.26004	43.615	2	1450500	823740	626720
2	4	12.6	12.6	12.6	22.168	206	3.04E-20	0.45633	0.70067	0.25893	53.797	4	8815100	5919500	2895500
2	3	4.5	4.5	4.5	65.947	598	0.00082184	0.76662	0.6943	0.25618	38.158	2	760820	382160	378660
8	14	8.3	8.3	8.3	139.44	1267	2.18E-28	1.3044	0.69138	0.25492	17.149	10	5033800	2044800	2989000
20	30	46.4	46.4	46.4	51.212	457	4.07E-93	0.8217	0.69058	0.25457	37.751	22	36487000	19631000	16856000
2	2	5.7	5.7	5.7	37.198	333	1.85E-08	0.71299	0.68742	0.2532	8.5812	2	1514900	928970	585980
10	13	35.5	35.5	35.5	32.551	293	1.11E-64	0.48192	0.68736	0.25318	24.472	10	29084000	18717000	10367000
6	9	57.8	57.8	57.8	15.936	154	2.37E-85	0.3102	0.68732	0.25316	21.903	10	106090000	79899000	26189000
2	2	6.8	6.8	6.8	40.763	368	3.58E-09	0.57226	0.68259	0.25111	11.441	2	1529900	999140	530810
2	2	6.9	6.9	6.9	27.818	260	1.45E-05	0.47535	0.68243	0.25104	2.0946	2	3918600	2165500	1753100
6	9	21	21	21	51.853	463	5.56E-34	0.55661	0.68217	0.25093	49.234	9	6465300	4088800	2376500
8	9	37.6	37.6	37.6	28.415	255	4.31E-41	0.47526	0.68204	0.25087	33.797	9	11180000	7419800	3760600
7	10	35	35	35	21.825	197	6.94E-63	0.35718	0.67877	0.24945	100.54	11	51263000	24761000	26503000
2	2	15.3	15.3	15.3	24.853	229	2.33E-18	0.41642	0.67625	0.24835	19.972	2	1904100	1302300	601860
10	18	64.1	64.1	64.1	15.649	142	4.22E-119	0.42567	0.67117	0.24613	38.057	18	79169000	54200000	24968000
5	6	14.2	14.2	14.2	41.581	366	2.15E-11	1.5107	0.67047	0.24583	88.67	4	4736700	1742900	2993800
3	6	18.2	12.4	12.4	24.033	209	2.18E-23	0.4419	0.66968	0.24548	16.03	9	18313000	12549000	5763700
4	4	16.3	16.3	16.3	26.535	233	3.91E-11	0.36926	0.6678	0.24466	31.953	5	3298000	2323400	974630
2	3	16	16	16	16.297	144	1.33E-11	0.30999	0.66694	0.24428	20.735	2	3201600	2324800	876760
5	6	29.1	29.1	29.1	26.076	234	1.27E-11	0.38619	0.6663	0.244	9.4357	5	5447400	3857700	1589700
7	12	15.1	15.1	15.1	59.632	557	2.77E-65	0.81292	0.66427	0.24311	23.263	9	11231000	5833600	5397000
5	7	14.8	14.8	14.8	56.068	494	2.61E-23	0.7693	0.66249	0.24233	12.108	5	4497200	2428000	2069100
16	26	35.7	35.7	35.7	53.486	482	4.68E-57	0.76371	0.66133	0.24182	43.492	17	28619000	15788000	12831000
4	7	47.6	47.6	47.6	11.749	105	2.57E-41	0.39949	0.65929	0.24092	35.026	6	15302000	10508000	4794600
17	30	89.2	89.2	89.2	10.932	102	2.90E-64	0.29377	0.65448	0.2388	33.37	40	250910000	192220000	58689000
13	24	33.6	33.6	33.6	48.755	453	1.42E-95	0.82733	0.64877	0.23628	86.019	19	61543000	33690000	27853000
3	4	21.1	21.1	21.1	15.945	142	1.19E-17	0.31829	0.64657	0.23531	15.833	4	3796500	2844600	951870
2	2	11.3	11.3	11.3	26.819	257	0.00041625	0.28472	0.64626	0.23517	95.48	3	629390	491650	137740
5	7	19.4	19.4	19.4	67.017	619	3.58E-38	0.46874	0.64447	0.23438	44.731	11	23786000	15769000	8017100
19	31	52.5	52.5	52.5	44.614	417	1.15E-158	0.66712	0.64157	0.23309	11.166	21	52300000	30954000	21347000
9	13	35.8	35.8	35.8	41.949	372	6.93E-117	1.5461	0.64129	0.23297	47.991	11	18007000	6568000	11439000
8	12	16.9	16.9	16.9	62.656	562	4.58E-61	0.71692	0.63811	0.23155	75.531	8	8709900	4853700	3856200
2	2	8.8	8.8	8.8	25.357	239	1.46E-09	0.56693	0.63486	0.23011	1.7572	2	2264700	1439300	825410
15	24	39.2	39.2	39.2	47.534	423	8.02E-74	0.68443	0.63226	0.22895	13.609	17	23456000	13723000	9733100
8	12	65.7	65.7	65.7	11.737	105	2.48E-45	0.37795	0.63212	0.22889	25.455	11	42889000	29859000	13030000
7	10	36.2	36.2	36.2	28.17	268	2.41E-30	0.37468	0.63049	0.22816	16.629	8	10561000	7647600	2913500
16	25	78.5	78.5	78.5	15.164	135	6.13E-117	0.34305	0.63025	0.22805	49.142	26	193470000	147110000	51756000
9	15	22.9	22.9	22.9	54.636	510	5.80E-49	0.77294	0.62654	0.22639	33.166	10	11313000	6052700	5260000
2	2	13.9	13.9	13.9	14.21	122	0.019761	0.40013	0.62537	0.22587	10.293	2	864280	623240	241040
5	8	50.4	50.4	44.4	13.667	117	5.79E-44	0.39845	0.62469	0.22557	14.423	6	13707000	9723500	3983700
3	5	7.1	7.1	7.1	41.165	382	0.0015815	1.5467	0.62207	0.22439	15.534	4	3211100	1170900	2040200

8	10	46.6	46.6	46.6	20.546	178	2.75E-15	0.55341	0.61881	0.22293	32.451	11	15209000	9247700	5960900
3	5	21.7	21.7	21.7	23.934	212	3.82E-44	0.28717	0.61658	0.22193	25.843	5	6800200	5231100	1569100
7	9	23	23	23	35.554	318	6.11E-25	0.49824	0.61524	0.22133	24.907	7	6301000	4055600	2245400
16	16	8.2	6.7	6.7	271.32	2390	2.54E-49	10.018	0.61416	0.22084	184.81	11	15211000	3719200	14839000
18	29	42.2	42.2	42.2	46.836	408	1.83E-85	0.6725	0.61408	0.22008	58.296	31	57814000	29094000	28720000
3	4	28.6	28.6	28.6	20.455	182	1.93E-15	0.54718	0.61275	0.22021	9.8829	3	45719000	2891700	1680200
13	20	61.4	61.4	61.4	29.126	254	1.76E-137	0.41268	0.61205	0.21989	20.575	17	79474000	56100000	23374000
2	2	1.2	1.2	1.2	114.66	981	0.77746	0.63737	0.60835	0.21822	12.745	2	2052400	1240500	811920
9	14	44.9	44.9	44.9	22.086	214	1.65E-91	0.28444	0.6079	0.21802	13.299	11	25770000	19602000	6167800
9	13	71.8	71.8	71.8	18.72	163	1.38E-98	0.32439	0.60724	0.21772	30.147	22	64399000	47659000	16740000
7	13	50	50	50	14.192	132	1.17E-52	0.35215	0.60415	0.21633	29.237	10	17993000	13316000	4677700
2	2	19.2	19.2	19.2	14.285	125	2.09E-14	0.3251	0.60287	0.21575	23.352	2	1233500	920120	313360
8	13	48.3	48.3	48.3	23.31	201	8.44E-45	0.32659	0.59922	0.2141	29.395	12	53104000	39270000	13834000
6	8	40.9	40.9	40.9	20.363	181	7.41E-20	0.53223	0.59756	0.21335	21.494	6	6513500	4169200	2344400
6	10	31	31	25.5	25.814	216	1.69E-65	0.40227	0.59579	0.21254	19.242	16	62238000	43566000	18672000
2	2	0.3	0.3	0.3	519.18	4636	0.024375	4.871	0.59442	0.21192	72.303	2	40424000	1831600	38592000
11	18	45.2	45.2	45.2	28.993	261	2.14E-68	0.37664	0.59348	0.21149	25.708	16	29988000	21483000	8504800
6	11	41.3	41.3	41.3	20.35	184	1.77E-57	0.33985	0.59316	0.21135	15.414	10	39218000	29233000	9984900
5	8	19	19	19	38.324	357	2.86E-40	1.3925	0.59286	0.21121	91.32	5	4618000	1801200	2816800
8	12	31.6	31.6	31.6	36.067	335	4.58E-55	0.41745	0.59012	0.20997	13.041	9	16986000	11739000	5247100
4	6	17.3	11.4	11.4	46.871	411	1.02E-29	0.61253	0.58865	0.2093	16.317	4	3681500	2196900	1484600
10	17	28.3	28.3	28.3	44.809	406	1.30E-117	0.60506	0.58784	0.20893	13.707	13	18455000	11368000	7086900
5	6	41	41	41	24.722	222	4.36E-18	0.36583	0.58657	0.20835	46.955	5	5482000	3891700	1590400
3	3	16.5	16.5	16.5	25.177	224	3.50E-08	0.36085	0.5864	0.20828	9.8167	3	1376600	989600	387010
2	2	13.4	13.4	13.4	14.395	127	0.052734	0.3362	0.58349	0.20695	2.3295	2	1218000	900950	317020
18	30	59.1	59.1	59.1	43.786	394	4.27E-101	0.59975	0.58	0.20536	17.215	21	52561000	32624000	19936000
1	2	39.3	39.3	6.2	16.363	145	1.96E-25	0.33143	0.57521	0.20317	23.064	5	20894000	15349000	5549000
5	7	46.5	46.5	46.5	12.774	114	4.80E-29	0.33584	0.57447	0.20283	18.246	5	6268800	4583700	1685100
4	8	25.1	25.1	25.1	19.602	175	1.80E-31	0.47385	0.57373	0.20249	29.162	7	13433000	9099800	4332900
6	7	21.8	21.8	21.8	36.908	325	5.98E-15	0.45539	0.57359	0.20243	11.93	6	5815400	3938500	1876900
42	73	73.1	73.1	73.1	61.054	573	0	0.70508	0.57342	0.20235	37.559	88	336660000	194350000	142320000
10	18	45.4	45.4	45.4	37.025	324	6.67E-95	1.4129	0.57124	0.20135	45.412	12	31845000	13059000	18786000
12	19	39.7	39.7	39.7	23.207	204	6.21E-103	0.33411	0.56891	0.20029	19.084	19	136000000	100180000	35813000
29	52	34.1	34.1	34.1	76.613	710	6.70E-212	1.0202	0.56578	0.19885	73.189	55	246220000	118560000	127660000
3	5	6.3	4.8	4.8	89.252	808	3.94E-09	1.1198	0.56567	0.1988	17.807	3	847240	402830	444410
11	14	20.6	20.6	20.6	72.932	645	5.68E-65	0.56059	0.56528	0.19862	14.576	11	11043000	6812800	4230200
3	4	18.3	18.3	18.3	23.264	219	2.64E-07	0.50474	0.56088	0.19659	10.328	3	2362400	1458200	904190
4	7	39.4	33.1	33.1	16.801	142	6.15E-28	0.28833	0.55885	0.19566	44.466	4	5907000	4351000	1556000
5	6	6.6	6.6	6.6	71.223	640	5.25E-06	1.548	0.55241	0.19269	50.865	5	2092500	874920	1217600
3	4	2.9	2.9	2.9	111.33	999	0.010892	1.2725	0.55228	0.19263	39.916	3	1727300	693130	1034200
2	4	14	14	14	14.582	129	0.0026638	0.47457	0.55161	0.19233	22.754	3	2152800	1448600	704180
18	32	74.5	74.5	74.5	18.012	165	1.77E-164	0.29107	0.54904	0.19114	43.016	42	58337000	44844000	13493000
15	25	52.1	52.1	52.1	30.358	286	2.00E-164	0.31942	0.54457	0.18907	17.349	22	145910000	108090000	37818000
13	21	50.2	50.2	50.2	33.269	311	4.66E-122	0.34478	0.53833	0.18619	16.94	17	44664000	32106000	12558000
7	10	26.8	26.8	26.8	34.063	313	2.28E-26	0.44195	0.53781	0.18594	35.623	8	5343100	3444800	1898300
19	29	43.7	43.7	34.5	69.412	586	8.58E-166	0.52305	0.53436	0.18434	15.945	36	117760000	74823000	42934000
2	3	7.3	7.3	7.3	38.534	356	3.38E-08	1.3254	0.53306	0.18374	6.8948	2	1145800	443800	702040
9	12	69.8	69.8	69.8	20.694	189	7.62E-126	0.30333	0.53182	0.18316	162.83	11	32437000	25917000	6520200
43	43	11.3	11.3	11.3	469.08	4128	6.57E-172	7.7292	0.52999	0.18231	192.98	34	39417000	20329000	19088000
2	4	23.2	23.2	23.2	10.839	95	1.09E-13	0.31554	0.52892	0.18182	31.907	6	12840000	9381700	3458100
3	5	14.8	14.8	14.8	25.569	229	1.88E-06	0.30444	0.52803	0.1814	8.3031	3	3709300	2783700	925640
3	3	4.6	4.6	4.6	94.769	855	6.00E-05	1.4785	0.5276	0.1812	9.3548	3	1160700	421000	739670
6	8	33.3	33.3	33.3	20.811	183	1.32E-46	0.48409	0.52117	0.17821	13.732	6	7285300	4760000	2525300
6	9	40.9	40.9	40.9	20.838	193	8.12E-33	0.44623	0.5202	0.17776	18.133	10	21190000	14895000	6294500
3	5	7.4	7.4	7.4	58.075	525	0.0036695	0.63456	0.51763	0.17656	2.7358	3	2912800	1708100	1204700
3	5	18.1	18.1	18.1	21.525	188	4.15E-06	0.51371	0.51704	0.17629	12.698	4	4199600	2754600	1445000
2	2	5.3	5.3	5.3	54.392	468	5.46E-11	0.61683	0.51629	0.17594	8.3808	2	1047700	632900	414770
3	4	26.8	26.8	26.8	13.941	123	7.51E-13	0.33015	0.51601	0.1758	29.294	3	5674100	4410900	1263200
3	6	2	2	2	205.42	2078	2.11E-54	0.39843	0.51593	0.17577	9.4763	6	9595500	6710900	2884600
3	3	22.3	12.9	12.9	31.17	278	1.22E-50	0.27549	0.51013	0.17306	16.563	3	2055500	1576700	478790
2	2	5.3	5.3	5.3	40.513	358	2.83E-05	1.2982	0.50628	0.17126	35.187	2	1591000	731750	859290
7	10	43.5	43.5	31.2	35.924	324	2.12E-187	0.52942	0.50506	0.17069	29.34	17	90489000	58151000	32338000
2	2	2.2	2.2	2.2	88.828	779	0.027036	1.4114	0.50365	0.17003	9.4077	2	535310	195780	339530
7	11	4.1	4.1	4.1	245.44	2297	5.41E-22	1.2317	0.5026	0.16954	7.7569	7	4543800	2099900	2443900
3	4	14.1	14.1	14.1	20.457	184	1.94E-09	0.22711	0.49218	0.16466	12.784	3	2716800	2213000	503800

4	5	28.6	28.6	28.6	20.55	182	9.04E-53	0.44239	0.4896	0.16345	20.874	4	5535900	3646000	1889900
2	2	22.1	22.1	22.1	15.689	145	5.02E-21	0.18099	0.48477	0.16118	9.1378	2	2261500	1982200	279290
9	13	23.8	23.8	23.8	44.468	378	1.02E-46	0.52068	0.48164	0.15971	7.6924	10	17489000	11494000	5995500
2	3	13.3	13.3	13.3	12.597	120	0.43417	0.33186	0.48121	0.15951	15.967	5	69737000	151727000	18010000
2	3	19.4	19.4	19.4	14.665	129	6.66E-10	0.29125	0.47968	0.15879	8.6268	2	460390	400670	59716
6	7	36.1	36.1	36.1	21.195	183	3.82E-07	0.432	0.47939	0.15866	12.273	6	5911400	3987500	1923900
4	4	17.6	17.6	17.6	28.763	250	4.49E-08	0.32991	0.47338	0.15583	26.636	4	3416200	2471900	944340
35	61	61.5	61.5	61.5	54.122	501	3.42E-213	0.45835	0.47166	0.15502	52.986	69	515660000	342200000	173460000
30	50	62.4	62.4	62.4	56.166	519	0	0.6301	0.46882	0.15368	47.736	54	212510000	129360000	83157000
4	4	24.3	24.3	24.3	21.143	185	0.00096954	0.40407	0.46722	0.15293	85.002	5	2099600	1521900	577650
1	2	39.8	39.8	3.4	24.823	236	1.84E-92	0.32452	0.46673	0.1527	51.808	20	143990000	107480000	36509000
5	5	6.5	6.5	6.5	96.771	873	1.89E-14	1.0988	0.46608	0.1524	35.061	4	1153200	546610	606560
2	2	7.2	7.2	7.2	35.964	318	7.97E-10	0.38887	0.46574	0.15223	16.045	2	979990	759420	220560
4	5	18.7	18.7	18.7	23.423	209	1.50E-32	0.30609	0.46345	0.15115	27.005	4	1905700	1407800	497880
2	2	25.4	25.4	25.4	12.895	118	1.47E-32	0.22577	0.46029	0.14967	43.8	2	2807000	2340600	466430
2	2	6.9	6.9	6.9	53.126	480	3.93E-05	0.59731	0.45714	0.14818	35.478	2	1801200	1089100	712130
15	27	67.4	67.4	67.4	26.477	239	1.34E-96	0.30109	0.4563	0.14779	27.075	28	101200000	76385000	24816000
3	3	60.7	60.7	60.7	9.6981	84	1.19E-14	0.18119	0.45615	0.14772	9.0221	3	1420800	1222700	198170
15	27	68.9	68.9	68.9	30.791	286	1.41E-245	0.26344	0.45208	0.1458	22.466	35	133670000	104690000	28979000
16	26	67.7	67.7	24.824	223	288E-55	0.25138	0.45111	0.14534	11.982	20	123200000	98510000	24691000	
6	7	38.3	38.3	38.3	23.98	214	2.51E-15	0.39942	0.44993	0.14479	15.219	6	5904100	4251700	1652400
10	16	62.8	62.8	62.8	19.206	172	3.55E-78	0.21792	0.44355	0.14178	19.938	13	53424000	43300000	10124000
16	28	44.4	44.4	44.4	47.628	432	2.80E-57	0.46027	0.44054	0.14036	15.117	18	39261000	26488000	12773000
7	9	48.3	48.3	48.3	26.182	230	1.64E-44	0.26978	0.4386	0.13945	22.658	8	9265600	7275700	1989900
3	4	18.6	18.6	18.6	13.696	129	1.33E-05	0.27998	0.43759	0.13897	33.851	3	6094000	4571200	1522700
6	7	24.5	24.5	24.5	27.566	241	8.45E-16	0.25537	0.43182	0.13625	19.765	7	8580300	6417400	2162900
14	22	35.9	35.9	35.9	37.54	337	6.36E-72	0.33035	0.42954	0.13518	44.717	21	39929000	29804000	10126000
7	12	13.1	13.1	13.1	65.401	586	1.78E-62	1.0853	0.42797	0.13444	13.849	10	23508000	10919000	12589000
3	3	10.7	10.7	10.7	29.841	253	2.03E-05	0.23932	0.42731	0.13413	23.637	4	2577000	2105400	471570
6	7	23.1	23.1	23.1	38.274	338	2.72E-20	1.0248	0.42388	0.13251	12.403	6	6543800	3421600	3122200
12	17	33.8	24.4	24.4	67.819	577	2.04E-90	0.42346	0.13232	0.13232	22.508	12	12418000	8674400	3743400
4	8	25.4	14.8	14.8	38.651	366	4.74E-74	0.59748	0.4219	0.13158	62.729	8	19007000	11467000	7540200
9	12	74.6	74.6	74.6	13.802	126	7.16E-30	0.20099	0.42017	0.13077	37.62	13	47601000	39291000	8309100
14	23	56.9	56.9	51.5	22.728	204	1.50E-196	0.28403	0.4169	0.12923	43.617	38	205300000	155150000	50153000
2	2	16.2	16.2	16.2	20.925	198	6.38E-10	0.22433	0.41601	0.12881	45.874	2	2777400	2294500	482930
3	4	6.3	6.3	6.3	54.705	490	7.05E-07	0.50795	0.41507	0.12837	18.137	3	1467100	924430	542650
2	2	6.7	6.7	6.7	35.845	315	1.52E-08	0.37049	0.41489	0.12828	32.479	2	5158100	3819500	1338600
5	6	24.4	24.4	24.4	25.007	225	7.26E-22	0.26915	0.40752	0.12482	16.155	5	6014700	4721500	1293200
6	10	17.4	17.4	17.4	50.151	454	1.55E-26	1.0165	0.40338	0.12288	73.465	6	9092300	4344000	4748300
21	35	56.1	56.1	56.1	42.461	371	1.67E-173	0.91327	0.40168	0.12207	71.099	25	89695000	46462000	43233000
3	3	14.2	14.2	14.2	24.428	226	0.014219	0.36089	0.40006	0.12132	46.946	3	2255900	1655800	600080
11	21	60.5	60.5	60.5	23.356	210	6.63E-159	0.36211	0.39807	0.12038	11.047	14	99920000	72996000	26924000
4	6	21.4	21.4	21.4	27.907	252	6.85E-23	0.26643	0.3978	0.12026	28.028	6	6786000	5645200	1140800
2	2	11.6	11.6	11.6	18.795	173	0.0027561	0.20013	0.3958	0.11932	12.845	2	745920	641750	104170
4	6	10	10	10	39.383	350	3.51E-08	0.32789	0.39535	0.11911	219.36	5	2565000	1940300	624680
4	6	22.4	22.4	22.4	26.836	241	2.53E-26	0.35196	0.39413	0.11854	31.104	4	14449000	11831000	2618200
4	5	14	14	14	33.969	301	6.68E-08	0.31976	0.38502	0.11428	24.122	4	3348100	2507900	840190
59	105	86.8	86.8	86.8	70.288	627	0	0.36321	0.38141	0.11259	56.636	118	921630000	664840000	256790000
9	11	34.6	34.6	34.6	37.131	335	1.84E-89	0.32438	0.37905	0.11148	30.453	11	15353000	11202000	4151100
4	4	12.9	12.9	12.9	48.84	458	1.30E-14	0.33349	0.37852	0.11124	68.225	5	5823100	3953100	1870000
14	22	39.5	39.5	39.5	45.355	415	5.26E-94	0.91236	0.37322	0.10877	57.38	14	31585000	16029000	15556000
5	5	22	22	22	34.559	309	1.65E-27	0.32773	0.37318	0.10875	27.771	5	3333400	2594900	738530
26	41	43.2	43.2	43.2	68.08	590	2.40E-229	0.29573	0.37291	0.10863	68.062	38	124390000	94040000	30346000
14	18	33.5	33.5	33.5	57.116	508	1.85E-60	0.45932	0.37274	0.10855	16.609	15	17868000	12179000	5688200
3	3	12.9	12.9	12.9	40.089	372	1.99E-107	0.36222	0.36794	0.10632	32.099	2	2167800	1627200	540620
10	12	13.2	13.2	13.2	85.95	783	1.01E-09	0.89167	0.36608	0.10545	34.508	10	7933600	3954600	3979000
2	3	5.6	5.6	5.6	42.766	374	1.76E-05	0.52919	0.36527	0.10508	22.9	2	1026000	607420	418610
3	3	10.6	10.6	10.6	29.396	264	0.00042244	0.25181	0.36315	0.1041	6.4221	3	2991700	2389900	601790
4	4	6	6	6	87.819	805	0.0012684	0.91535	0.36307	0.10406	23.802	4	1794600	859780	934790
1	2	56.3	56.3	7.1	26.706	252	2.33E-219	0.23139	0.36233	0.10372	36.869	63	407890000	328600000	79290000
5	6	18.4	18.4	18.4	23.819	212	1.13E-08	0.27464	0.35933	0.10233	49.228	5	3538200	2305000	1187700
23	23	13.1	13.1	13.1	274.61	2364	1.86E-167	8.9806	0.35283	0.099329	50.471	20	16955000	1140100	15815000
4	6	24.2	24.2	24.2	17.911	161	1.02E-09	0.20063	0.35153	0.098728	89.54	7	16444000	12584000	3859800
45	73	81.7	81.7	81.7	51.804	459	0	0.40077	0.34431	0.09541	30.4	74	268230000	188070000	80160000
4	4	14.8	14.8	14.8	41.024	365	8.68E-17	0.35794	0.34247	0.094566	99.423	4	4144000	3014600	1129400

4	4	16.7	16.7	16.7	25.855	228	4.38E-07	0.27408	0.33708	0.092102	37.928	6	4307900	3335500	972440	
8	10	46.9	46.9	46.9	22.04	207	1.27E-25	0.29775	0.33509	0.091195	25.88	7	11860000	9033300	2826900	
16	21	31.4	30.3	30.3	67.56	644	5.01E-51	0.32569	0.33317	0.090323	17.29	16	28205000	21107000	7097900	
5	5	14.9	14.9	14.9	41.694	368	1.20E-14	0.83868	0.32956	0.088681	5.707	5	3397000	1715600	1681400	
1	1	2.2	2.2	2.2	46.941	417	0.0018819					0	233930	233930	0	+
1	1	6	6	6	24.536	234	0.0010672					0	706650	706650	0	+
1	1	4.8	4.8	2.1	49.423	436	0.019792					0	689920	689920	0	+
2	2	11.1	11.1	11.1	22.975	199	0.00010159					0	415450	415450	0	+
1	1	8.8	1.9	1.9	61.901	578	2.18E-21					1	98295	63095	35201	+
1	1	1.8	1.8	1.8	54.176	487	2.34E-05					0	0	0	0	+
4	4	8.3	8.3	8.3	73.449	683	1.29E-21					0	1528800	0	1528800	
1	1	9.8	9.8	9.8	17.162	163	2.93E-08					1	400370	345460	54911	
1	1	2.9	2.9	2.9	49.451	441	3.05E-13					1	487280	82201	405080	
1	1	2.5	2.5	2.5	58.768	522	0.019081					1	342800	167710	175090	
1	1	2.9	2.9	2.9	49.797	447	1.01E-08					0	339340	0	339340	
1	2	13.8	13.8	13.8	9.1275	80	0.00019884					1	231640	100840	130800	
1	1	1.1	1.1	1.1	73.011	704	0.046957					1	138810	103990	34818	
1	1	5.6	5.6	5.6	22.367	198	2.70E-06					1	1105000	336710	768250	
1	1	2.5	2.5	2.5	36.214	322	0.0033474					1	969270	698450	270830	
1	1	2.4	1	1	97.621	871	1.35E-12					1	114860	22611	92246	
1	1	1.5	1.5	1.5	81.613	717	0.031982					0	0	0	0	
1	2	7.4	7.4	7.4	19.767	175	1.05E-10					1	426560	215320	211250	
1	1	6.5	6.5	6.5	20.878	184	0.025709					1	298620	131420	167210	
1	2	7.4	7.4	7.4	12.274	108	0.14239					1	503640	151010	352640	
1	1	2.3	2.3	2.3	48.55	432	0.015771					0	220980	0	220980	
1	1	2.3	2.3	2.3	47.46	429	0.002075					1	1005300	357150	648110	
1	1	2	2	2	61.992	549	0.025712					1	351260	24873	326390	
1	2	4.4	4.4	4.4	20.274	180	0.0033474					1	439230	177300	261940	
1	1	6.1	6.1	6.1	22.519	197	2.95E-06					1	337950	256800	81145	
1	1	5	5	5	29.172	258	3.52E-07					1	714430	358590	355840	
1	1	10.5	10.5	10.5	26.215	237	8.58E-35					1	1551600	555690	995950	
1	1	4.9	4.9	4.9	28.466	247	0.035245					1	594920	380160	214770	
1	1	6.8	6.8	6.8	15.908	148	0.00016571					1	610000	400660	209330	
1	1	6.9	6.9	6.9	20.374	174	6.95E-08					1	303460	203980	99479	
1	1	2.8	2.8	2.8	32.287	282	0.014046					1	229370	30319	199050	
2	2	8.4	8.4	8.4	24.158	215	0.01342					0	180930	180930	0	
1	1	6.5	6.5	6.5	24.593	215	5.81E-05					1	208020	0	208020	
1	1	12.5	12.5	12.5	10.449	88	0.10595					1	82053	54821	27232	
1	1	2.8	2.8	2.8	38.806	352	0.002075					1	348020	53806	294210	
1	1	2.4	2.4	2.4	68.303	617	0.0112					1	217550	0	217550	
1	1	4.4	4.4	4.4	24.347	225	1.01E-08					1	268060	69343	198720	
1	1	2.9	2.9	2.9	56.5	511	1.36E-08					1	376900	45211	331680	
1	1	7	7	7	25.868	243	1.25E-16					1	1219900	972760	247180	
1	2	0.3	0.3	0.3	273.6	2335	0.00046123					1	471810	230890	240920	
1	1	3.6	3.6	3.6	35.594	309	7.37E-17					1	719000	130570	588430	
1	2	14	14	14	11.514	114	2.93E-08					1	1193900	331370	862510	
2	2	4.9	4.9	4.9	52.356	451	4.23E-06					1	895980	104570	791410	
1	1	3.4	3.4	3.4	32.381	290	0.018707					1	651820	321500	330330	
1	1	2.1	2.1	2.1	68.965	661	0.0017083					1	239190	89798	149390	
1	1	10.6	10.6	10.6	11.662	104	0.10023					0	48592	48592	0	
2	2	10	10	10	23.705	210	0.00013696					1	568860	8505.8	560350	
1	1	2.6	2.6	2.6	47.34	416	0.033369					1	212220	46174	166050	
1	2	8.6	8.6	8.6	20.108	175	4.45E-10					1	4031400	2084900	1946500	
1	1	3.9	3.9	3.9	32.55	307	0.012564					1	415280	26660	388620	
1	1	2.5	2.5	2.5	43.618	404	0.002075					1	109320	0	109320	
1	1	1.7	1.7	1.7	80.379	721	0.012564					1	354850	0	354850	
1	1	1.9	1.9	1.9	113.28	1019	9.88E-05					0	821260	821260	0	
1	2	2.1	2.1	2.1	69.697	616	2.65E-06					1	378070	157940	220130	
1	1	5.9	5.9	5.9	18.681	170	0.018707					1	377400	224220	153170	
1	1	1.8	1.8	1.8	47.535	440	0.0033474					1	355680	124730	230950	
1	1	6.1	6.1	6.1	19.652	179	0.0063888					1	104120	47130	56986	
2	2	2.2	2.2	2.2	170.59	1512	2.32E-16					1	813930	44338	769600	
1	2	6.6	6.6	6.6	21.21	181	2.95E-06					1	238020	97716	140300	
1	1	11.7	11.7	11.7	18.243	163	6.82E-10					1	842540	590450	252090	
3	3	11.6	11.6	11.6	27.679	242	3.02E-07					1	1431000	1431000	0	

1	1	2	2	2	51.922	442	6.54E-12	0	0	0	0
1	1	1.3	1.3	1.3	87.498	776	0.015771	1	367310	75530	291780
1	1	2.6	2.6	2.6	44.301	385	0.015771	0	84211	0	84211
1	1	12.4	12.4	12.4	12.823	113	1.48E-13	1	495560	377530	118030
1	1	12.7	12.7	12.7	9.6601	79	0.16245	1	132500	106170	26333
1	1	51.1	7.1	7.1	20.825	184	8.44E-67	1	1302400	117850	1184600
1	1	3.3	3.3	3.3	35.943	330	0.0017954	1	535140	171830	363310
1	1	1.7	1.7	1.7	53.293	469	0.028553	0	0	0	0
1	1	3.7	3.7	3.7	34.291	295	0.013216	1	179380	111700	67674
1	1	2.3	2.3	2.3	71.607	646	0.019346	1	195600	89686	105920
1	1	4.5	4.5	4.5	22.761	201	0.34515	1	58787	21921	36866
1	1	5.3	5.3	5.3	26.748	228	6.51E-07	1	471940	357240	114700
1	1	2.3	2.3	2.3	56.256	522	0.0017687	1	2002500	1530300	472240
1	1	1.6	1.6	1.6	83.353	739	5.77E-09	1	419810	0	419810
1	1	3.2	3.2	3.2	46.649	411	8.15E-16	1	975030	340110	634920
1	1	5.4	2.8	2.8	44.078	386	9.52E-09	1	161090	55326	105770
1	1	1.2	1.2	1.2	106.25	952	0.0012222	1	239040	33534	205500
1	1	5.7	5.7	5.7	24.422	212	5.77E-09	0	234690	0	234690
1	1	1.9	1.9	1.9	86.396	787	0.08858	1	3174600	1517200	1657500
1	1	8.3	8.3	8.3	35.597	314	0.77958	1	11788000	8771800	3016300
1	1	4.4	4.4	4.4	26.183	228	0.00016571	1	684530	409260	275270
1	1	7.2	7.2	7.2	21.445	194	0.0010672	0	0	0	0
1	1	0.7	0.3	0.3	289.06	2564	0.00025565	1	493820	200990	292830
1	1	2.9	2.9	2.9	38.215	344	0.00016571	1	397610	162160	235450
2	2	9.8	9.8	9.8	33.58	305	7.81E-13	1	477600	125220	352380
1	1	8.8	8.8	8.8	12.452	113	0.015771	1	202510	133200	69315
1	1	15.4	2.4	2.4	42.208	370	3.92E-25	1	3072100	2298100	774010
1	1	2.3	2.3	2.3	42.2	385	0.010901	0	177790	177790	0
1	1	1.8	1.8	1.8	79.685	736	1.19E-16	1	626650	479230	147420
1	1	7.4	7.4	7.4	16.893	149	0.025712	1	783360	528750	254610
1	1	1.5	1.5	1.5	67.699	604	0.0481	0	0	0	0
1	1	4.1	4.1	4.1	33.043	291	0.16489	1	103120	0	103120
1	1	2.4	2.4	2.4	61.829	592	0.0017083	1	172670	78360	94308
1	1	10.6	5.5	5.5	23.48	218	3.65E-18	0	646600	0	646600
1	1	8.6	8.6	8.6	14.96	140	0.025709	1	814620	426700	387930
1	1	2.8	2.8	2.8	58.896	509	1.06E-08	1	282150	42803	239350
1	1	1	1	1	124	1114	0.0044179	0	168910	0	168910
1	2	0.9	0.9	0.9	141.45	1268	0.025709	1	154990	88067	66925
1	1	8	8	8	13.178	112	0.010901	1	350670	92858	257810
1	2	7.6	7.6	7.6	16.442	144	0.013216	1	701930	397770	304160
1	2	4	4	4	33.631	299	6.95E-08	1	883050	455640	427410
1	1	5.7	5.7	5.7	22.574	194	0.00031999	1	87095	65651	21444
2	2	1.6	1.6	1.6	191.61	1675	1.92E-08	1	1263800	33754	1230100
1	1	2.7	2.7	2.7	63.852	601	0.00055641	1	833690	450820	382870
2	3	25.7	25.7	25.7	11.528	101	0.016884	1	631550	295600	335940
1	1	1.7	1.7	1.7	55.873	483	0.046957	1	185420	17541	167880
1	1	1.7	1.7	1.7	52.545	463	0.016913	1	884850	76007	808840
1	1	2.6	2.6	2.6	47.873	423	0.0063888	1	326130	48707	277430
1	1	3.4	3.4	3.4	32.952	296	0.015771	1	903830	903830	0
1	1	11.7	11.7	11.7	25.029	231	0.53384	1	267770	187800	79970
1	1	8	8	8	21.175	188	0.03073	0	321590	0	321590
1	1	1.2	1.2	1.2	160.88	1443	0.00011266	0	235100	0	235100
1	1	3.5	3.5	3.5	37.208	346	0.0027867	1	469300	297280	172020
1	1	0.3	0.3	0.3	310.36	2806	0.0481	0	0	0	0
1	1	2.2	2.2	2.2	56.23	498	0.0017954	1	570460	145920	424530
1	1	1.1	1.1	1.1	119.91	1047	0.0012222	1	241880	22643	219240
1	1	16.4	11.6	11.6	17.008	146	6.50E-10	1	469070	352480	116590
1	1	29.3	2.6	2.6	38.631	341	3.52E-40	1	917810	206830	710980
2	2	7.1	3.4	3.4	64.132	589	1.34E-22	1	797250	354900	442340
1	1	5	5	5	24.976	219	0.00031999	1	466320	59629	406690
1	1	6.5	6.5	6.5	24.635	217	5.81E-05	0	0	0	0
1	1	2.2	2.2	2.2	41.337	370	0.028553	1	996160	996160	0
1	2	0.7	0.7	0.7	110.42	983	0.38887	1	4758300	2707700	2050600
1	1	2.8	2.8	2.8	60.663	539	0.0078383	1	204570	21105	183460
1	1	2.7	1.7	1.7	110.4	982	0.0005771	0	122340	0	122340

1	1	2.3	2.3	2.3	64.969	561	0.29131	1	58221	25067	33153
2	2	25	25	25	10.803	92	9.21E-05	1	1814500	1033000	781500
1	1	6.4	6.4	6.4	27.388	250	0.00021494	1	587230	367160	220060
2	2	2.3	2.3	2.3	118.58	1068	0.0081755	0	293150	0	293150
6	6	6.3	6.3	6.3	122.76	1070	3.67E-45	1	2475600	0	2475600
1	1	6.2	6.2	6.2	15.225	129	0.10873	1	347050	44317	302740
1	2	6.2	6.2	6.2	22.338	211	1.71E-08	1	608170	340220	267950
1	1	4.9	4.9	4.9	26.21	243	6.95E-08	1	1362800	184970	1177800
1	1	3.1	3.1	3.1	46.374	419	0.00056102	1	261510	220010	41504
1	1	4.6	4.6	4.6	30.757	284	1.36E-05	1	514910	0	514910
1	1	1.2	1.2	1.2	101.27	866	0.015771	1	285290	34490	250800
3	3	52	52	52	11.006	98	2.19E-14	1	5500500	5500500	0
1	1	10	10	10	15.609	150	3.84E-23	1	272090	229300	42791
1	1	6	6	6	20.126	182	0.025712	1	122080	0	122080
1	1	4.3	4.3	4.3	28.97	258	0.025712	1	205950	47091	158860
1	1	4.7	4.7	4.7	27.306	236	0.10852	1	366470	46650	319820
1	1	12.5	12.5	12.5	7.7059	64	0.39777	1	36919	0	36919
1	1	5.3	5.3	5.3	21.77	190	0.015771	1	470710	78879	391830
1	1	3.9	3.9	3.9	42.153	407	6.31E-20	1	1110400	347780	762670
2	2	4.2	4.2	4.2	48.445	425	0.0074461	1	1022300	821780	200540
1	1	2.2	2.2	2.2	98.427	882	0.16212	0	476050	0	476050
1	1	2.6	2.6	2.6	48.283	418	0.00031999	1	22029000	299390	21735000
1	1	1.9	1.9	1.9	65.272	577	0.026993	0	184870	0	184870
1	1	4.8	4.8	4.8	22.739	208	2.72E-16	0	320320	320320	0
1	1	1.2	1.2	1.2	124.19	1066	0.019081	1	3073400	0	3073400
1	2	6	6	6	20.749	184	2.42E-09	1	834560	587180	247380
1	2	6.3	6.3	6.3	21.198	189	0.77746	1	1810500	1204900	605600
1	1	21.6	3.7	3.7	63.451	575	6.27E-67	1	332020	184790	147230
1	1	2.4	2.4	2.4	80.883	715	0.18706	1	2383300	222210	2161100
1	1	0.3	0.2	0.2	437.6	3859	0.014816	1	138680	55984	82693
1	1	2	2	2	70.86	647	1.20E-06	0	0	0	0
1	1	1	1	1	231.32	2044	0.012292	0	283820	0	283820
1	1	2	2	2	82.86	747	0.00080413	0	378240	378240	0
4	4	10.4	10.4	10.4	52.099	453	3.13E-15	1	2103500	55714	2047800
1	1	3.1	3.1	3.1	36.844	323	0.018707	1	369440	110600	258840
1	1	8.1	8.1	8.1	20.776	172	1.24E-06	1	1003300	41006	962310
1	1	1.5	1.5	1.5	47.346	403	0.014816	0	270600	0	270600
1	1	7	7	7	21.645	199	0.017389	1	723940	529910	194030
1	1	7.8	7.8	7.8	18.824	167	0.00056102	0	0	0	0
1	1	1.7	1.7	1.7	70.349	653	0.00031999	1	335170	35268	299900
1	1	3.5	3.5	3.5	35.716	313	0.00031999	1	340070	142090	197980
1	1	0.7	0.7	0.7	129.08	1132	0.21071	0	172360	0	172360
1	1	0.9	0.9	0.9	152.78	1360	0.051309	0	242580	0	242580
1	1	2.9	2.9	2.9	86.752	794	0.12953	1	13389000	275020	13114000
1	1	5.4	1.8	1.8	36.507	332	2.07E-11	1	386980	136630	250360
1	1	2.8	2.8	2.8	33.3	288	0.0033474	1	641360	314960	326400
4	4	8.3	8.3	8.3	72.695	649	3.38E-18	1	1580900	208360	1372500
1	1	2.4	2.4	2.4	43.664	381	0.010901	0	272270	0	272270
2	2	3.5	3.5	3.5	63.704	579	0.011526	1	221030	0	221030
1	1	1.4	1.4	1.4	107.84	948	0.0046858	1	525470	116770	408700
1	1	1.1	1.1	1.1	110.39	1014	0.025712	0	706420	0	706420
1	1	1.8	1.8	1.8	68.822	601	0.0063888	1	235620	0	235620
1	1	3.3	1.6	1.6	73.652	672	2.39E-05	0	51434	0	51434
1	1	7.4	7.4	7.4	21.178	190	9.97E-05	1	382680	271220	111460
1	1	1.3	1.3	1.3	75.022	668	0.12003	1	247260	92694	154560
1	1	2.7	2.7	2.7	49.684	438	3.92E-11	1	779260	420110	359150
1	1	9	1.5	1.5	65.241	588	1.09E-25	1	526090	57339	468750
1	2	8.8	8.8	8.8	20.012	171	4.40E-08	1	685030	389170	295860
1	1	0.2	0.2	0.2	482.14	4376	0.016111	0	63562	0	63562
1	1	2.2	2.2	2.2	63.544	593	0.00012449	1	518250	338850	179400
1	1	2.6	2.6	2.6	120.68	1100	0.31949	0	0	0	0
1	1	1	1	1	121.34	1069	0.025712	0	164430	164430	0
1	1	0.4	0.4	0.4	243.87	2240	0.0481	0	0	0	0
1	1	7	7	7	19.171	171	1.77E-05	1	169660	0	169660
1	1	2.2	2.2	2.2	54.646	494	4.15E-15	1	599320	173420	425900

2	2	3.5	3.5	3.5	75.213	694	6.05E-05	1	341860	15309	326550
1	1	1.7	1.7	1.7	123.51	1096	0.16212	1	502370	0	502370
1	1	20	3.9	3.9	20.511	180	1.82E-12	1	311350	76931	234420
1	1	1	1	1	99.986	894	0.04536	0	126450	126450	0
1	1	12.6	3.4	3.4	27.584	238	1.61E-12	1	330690	148300	182390
1	1	4.3	4.3	4.3	40.063	349	4.70E-11	1	617660	195860	421800
1	1	1.7	1.7	1.7	82.43	719	0.012564	1	424000	41681	382320
2	3	0.6	0.6	0.6	552.04	4870	0.026761	1	1445800	335250	1110500
1	2	6.2	6.2	6.2	23.744	208	2.65E-06	1	1635600	1135200	500380
1	1	1.7	1.7	1.7	79.578	756	0.00056102	1	131900	20216	111690
1	1	5.7	5.7	5.7	23.135	210	0.0001501	1	736190	495130	241060
2	2	3	3	3	85.126	802	2.25E-09	1	228710	15606	213100
1	1	3.4	3.4	3.4	40.589	351	3.07E-09	0	0	0	0
1	1	9.8	9.8	9.8	13.406	122	2.95E-06	1	122470	54224	68245
1	1	16.3	16.3	16.3	10.853	98	0.00055641	1	176620	115320	61305
1	1	2.1	2.1	2.1	87.156	795	1.56E-08	1	176330	43708	132620
1	2	7.4	7.4	7.4	20.33	176	0.032983	1	87689	56279	31409
1	1	0.3	0.3	0.3	293.51	2715	0.099011	0	113670	113670	0
1	1	1.5	1.5	1.5	84.109	749	0.0012222	1	611290	86483	524810
1	1	5.7	5.7	5.7	21.778	194	0.00031999	1	584370	107600	476770
1	2	2.4	2.4	2.4	52.562	455	0.0017954	1	1252700	487940	764730
1	1	4.1	4.1	4.1	35.23	318	0.019081	1	249460	34148	215310
3	3	6.6	6.6	6.6	50.344	438	1.76E-05	0	1577500	0	1577500
1	1	7.8	7.8	7.8	15.208	129	0.0027894	1	341180	99325	241850
1	1	7.3	7.3	7.3	23.015	205	4.44E-08	1	342510	264500	78013
1	1	9.5	9.5	9.5	20.747	190	0.42903	1	1344000	706900	637110
1	1	1.3	1.3	1.3	100.23	895	0.0092395	0	267650	0	267650
1	2	13.1	13.1	13.1	11.261	99	0.00012449	1	191450	137810	53634
1	1	1.9	1.9	1.9	57.673	514	0.015771	1	177110	10813	166290
4	4	0.6	0.6	0.6	798.85	6907	1.51E-13	1	617350	117880	499470
1	1	1	1	1	123.9	1098	0.0063888	1	312560	230240	82319
1	1	1.1	1.1	1.1	89.999	811	0.12003	1	183240	57085	126150
1	2	4.9	4.9	4.9	35.776	309	6.40E-16	1	545710	196270	349430
1	1	0.3	0.3	0.3	513.63	4678	0.00014029	0	0	0	0
1	1	2.7	2.7	2.7	44.049	377	0.015868	0	257230	0	257230
1	1	2.5	2.5	2.5	50.982	473	7.04E-05	1	580350	280310	300030
1	1	1	1	1	116	1030	0.00017195	0	0	0	0
1	1	20.1	4.4	4.4	32.866	298	6.95E-32	1	1126700	134470	992220
3	3	2	2	2	168.59	1508	3.43E-09	1	314740	0	314740
1	1	2.2	2.2	2.2	70.294	643	0.052331	1	557570	0	557570
1	2	4	4	4	31.608	277	2.70E-06	1	1047100	591360	455770
1	2	4.5	4.5	4.5	27.325	244	0.013216	1	711600	421510	290080
1	1	1.1	1.1	1.1	114.71	1024	0.031982	0	0	0	0
1	1	1	1	1	150.25	1332	1.36E-05	0	335190	0	335190
1	1	0.8	0.8	0.8	96.458	870	0.022947	1	2056300	909100	1147200
1	2	5.8	5.8	5.8	45.318	395	0.014998	1	599190	199280	399910
1	2	10.4	10.4	10.4	16.156	144	2.56E-06	1	263920	40867	223050
1	1	3.1	3.1	3.1	83.005	740	0.24289	1	1144400	661600	482800
1	1	2.4	2.4	2.4	50.8	456	2.42E-09	1	781900	192070	589840
2	2	3.9	3.9	3.9	96.753	856	8.25E-05	1	725940	40049	685890
1	1	47.5	2.9	2.9	58.573	512	1.07E-147	1	2056500	113590	1942900
1	1	5.6	5.6	5.6	25.468	234	8.15E-16	1	812700	111360	701340
1	1	1.5	1.5	1.5	115.73	1025	3.96E-05	0	145290	0	145290
1	1	3.9	3.9	3.9	35.932	331	0.0046858	1	116580	0	116580
2	2	2.2	2.2	2.2	97.553	855	5.33E-08	1	1000300	25327	974970
1	1	10	1	1	133.32	1226	4.58E-89	1	403500	0	403500
1	1	3.4	3.4	3.4	36.748	324	0.00019884	1	321430	227940	93495
1	1	1.6	1.6	1.6	85.737	759	0.051309	0	33121	0	33121
2	3	18.4	18.4	18.4	15.892	147	3.75E-09	1	2573600	2057400	516250
1	1	3.5	3.5	3.5	35.548	314	0.0017954	1	583720	322180	261540
1	1	0.9	0.9	0.9	106.92	941	0.00032911	1	132310	57928	74384
3	3	2.5	2.5	2.5	119.16	1056	4.85E-05	1	495730	9823.1	485910
1	1	2.2	2.2	2.2	61.345	554	0.0001501	1	110760	23737	87019
1	1	6.1	6.1	6.1	22.092	198	6.95E-08	1	708800	420590	288220
1	1	1.9	1.9	1.9	66.755	583	0.0012222	1	130710	43530	87178

1	1	1.7	1.7	1.7	68.997	585	0.002075	1	492600	293930	198670
1	1	2.4	2.4	2.4	135.37	1202	0.2746	0	0	0	0
1	1	28.9	3.7	3.7	46.489	408	7.87E-87	1	1292100	752410	539660
1	1	1.9	1.9	1.9	63.836	582	0.00031999	1	492850	84978	407880
1	1	1.7	1.7	1.7	95.526	846	1.06E-08	1	536360	172870	363490
1	1	1.7	1.7	1.7	67.213	591	9.05E-14	1	390710	126090	264620
1	1	2.8	2.8	2.8	35.936	320	0.010901	1	436940	320100	116830
1	1	2	2	2	90.577	830	0.0083598	1	665280	122440	542850
2	2	7.3	7.3	7.3	39.336	341	1.80E-06	1	1807300	0	1807300
1	1	6	0.3	0.3	232.01	2036	5.86E-112	1	773270	421210	352050
1	1	1.8	1.8	1.8	81.673	737	1.71E-08	1	353150	79365	273780
1	1	3.5	3.5	3.5	50.927	451	0.016894	0	76486	0	76486
1	1	83.5	7.9	7.9	17.748	164	1.91E-209	1	548180	461090	87089
2	2	2.1	2.1	2.1	128.25	1148	3.07E-10	0	458340	0	458340
1	1	15.2	15.2	15.2	9.9741	92	0.68431	1	1470100	676600	793530
1	2	6.5	6.5	6.5	15.679	138	0.066388	1	4419400	4001400	418040
1	1	6.9	6.9	6.9	25.098	217	0.32933	0	0	0	0
1	1	6	6	6	44.128	399	4.77E-14	1	584050	145240	438810
1	1	2	2	2	69.81	638	0.00056102	0	463520	0	463520
1	1	4.3	1.2	1.2	74.761	678	2.58E-10	1	227910	0	227910
1	1	9	9	9	10.729	100	0.0052705	1	672160	672160	0
1	1	17.3	8.1	8.1	52.314	469	2.36E-18	1	1760200	306270	1453900
1	1	6.1	6.1	6.1	51.537	442	0.35183	0	0	0	0
1	1	1.7	1.7	1.7	58.078	531	0.12003	0	164990	164990	0
4	4	6	6	6	101.43	902	2.44E-21	0	1470900	0	1470900
1	1	0.8	0.8	0.8	137.22	1203	0.015771	1	401930	79824	322110
1	2	1.4	1.4	1.4	65.896	580	0.77745	1	637110	265240	371860
1	1	9.1	9.1	9.1	18.902	164	6.40E-16	1	420790	76458	344330
1	1	3	3	3	48.101	438	3.52E-13	1	633540	115960	517580
1	2	4.7	4.7	4.7	31.918	297	5.46E-11	1	677100	371090	306010
1	1	3.8	3.8	3.8	29.224	263	0.014789	0	0	0	0
1	1	10.6	10.6	10.6	12.551	113	0.012564	1	127140	25877	101260
2	2	2.2	2.2	2.2	113.86	1023	0.00031637	0	176870	0	176870
1	1	8	8	8	15.824	137	0.025712	0	277250	0	277250
1	1	4.3	4.3	4.3	43.963	392	0.0018257	1	403140	0	403140
1	1	4.9	4.9	4.9	37.72	349	0.0024391	0	780700	780700	0
5	5	11	11	11	81.744	745	3.47E-22	0	2488500	2488500	0
1	1	3.5	3.5	3.5	70.858	649	0.00078255	1	1679500	690850	988620
1	1	8.4	8.4	8.4	16.953	154	1.52E-11	1	151150	0	151150
1	1	0.7	0.7	0.7	229.88	2056	0.0078796	1	1691400	187340	1504000
1	1	1.3	1.3	1.3	111.76	993	3.79E-16	1	367750	36146	331600
1	2	15.6	2.1	2.1	77.561	705	3.66E-87	1	5993600	3150900	2842700
1	1	15.3	2.3	2.3	53.696	470	5.41E-35	1	954390	318560	635820
1	2	4.5	4.5	4.5	28.291	268	3.06E-12	1	1080200	713700	366510
1	1	1.5	1.5	1	117.8	1042	0.077136	1	1580500	391400	1189100 +
1	1	4.2	4.2	4.2	26.049	236	0.015771	1	854020	117030	736990
1	2	2.2	2.2	2.2	50.42	448	0.0027894	1	1273400	680370	593060
1	1	39.8	3.4	3.4	25.024	236	1.81E-93	1	1267700	1267700	0
1	2	13	13	13	7.8409	69	0.18987	1	1476100	721340	754750
1	1	0.4	0.4	0.4	250.91	2214	0.0481	0	0	0	0
1	1	4	4	4	25.72	225	0.010901	1	1095200	46846	1048300
1	1	7.3	7.3	7.3	30.941	273	0.099858	0	287180	287180	0
1	1	2	2	2	61.332	563	0.0006486	1	153510	27604	125910
1	1	1.9	1.9	1.9	137.06	1203	0.24289	1	1290900	1242400	48538
1	1	1.8	1.8	1.8	133.91	1250	0.067469	0	700460	0	700460
1	1	1.2	1.2	1.2	96.723	881	0.026993	1	219370	24154	195210
1	1	1.8	1.8	1.8	62.402	569	0.00038378	0	211360	0	211360
1	2	38.2	11.4	11.4	13.519	123	1.87E-42	1	5578100	4358600	1219500
1	2	20	3.2	3.2	33.7	310	2.03E-16	1	334740	191700	143040
1	1	3.9	3.9	3.9	23.493	205	0.046957	1	859180	108290	750890
1	1	1.1	1.1	1.1	146.6	1299	3.23E-18	0	200600	0	200600
1	2	21	4.2	4.2	47.12	433	9.54E-10	1	4710900	2429700	2281200
1	1	24.7	3.4	3.4	33.14	291	1.55E-33	1	1083500	511320	572210
1	1	5.9	5.9	5.9	29.643	272	1.78E-10	1	957920	712040	245880
1	1	2.6	2.6	2.6	52.317	461	0.16489	0	194110	194110	0 +

1	1	0.4	0.4	0.4	537.33	4695	0.092102
1	1	1	1	1	127.52	1118	0.10595
2	3	0.7	0.7	0.7	307.84	2817	0.063576
1	1	1	1	1	139.36	1303	0.019081
1	1	0.5	0.5	0.5	268.16	2488	0.20636
1	1	0.3	0.3	0.3	304.81	2723	0.38194
1	1	3.3	3.3	3.3	51.57	448	0.041826
1	1	0.4	0.4	0.4	552.04	4870	0.076039
1	1	1.4	1.4	1.4	66.408	586	0.1091
1	1	1.1	1.1	1.1	97.695	875	0.056356
1	1	2.5	2.5	2.5	54.953	480	0.051309
1	1	7.2	7.2	7.2	11.694	111	0.16667
1	1	1.6	1.6	1.6	117.82	1032	0.081344
1	1	0.7	0.7	0.7	147.09	1287	0.038152
1	1	0.8	0.8	0.8	140.84	1254	0.50729
1	1	0.9	0.9	0.9	107.96	957	0.0052705
1	1	8.7	8.7	8.7	14.408	127	0.025712
1	1	22.1	22.1	22.1	8.6313	77	0.081344
1	1	2.4	2.4	2.4	38.804	336	0.77745

0	286970	286970	0 +
1	2825000	0	2825000 +
1	4446600	2306300	2140300 +
0	373220	0	373220 +
0	567250	567250	0 +
0	91698	91698	0 +
1	11453000	227610	11226000 +
1	2209600	410010	1799600 +
1	223990	12988	211000 +
1	7600100	0	7600100 +
0	6099500	6099500	0 +
1	1455000	226620	1228400 +
1	1296200	0	1296200 +
1	7204700	0	7204700 +
1	1111700	560920	550770 +
1	401670	57161	344510 +
0	409700	409700	0 +
1	505040	81055	423990 +
1	833900	122150	711740 +

Protein Descriptions	Uniprot	PEP	Mean Ratio H/L	Mean Ratio H/L Normalized	Ratio H/L Significance(A)	Ratio H/L Variability [%]	Ratio H/L Count	STDEV	Gene name
Uncharacterized protein	E1BT08	4.80E-124	1.451	1.2867	0.50694	11.636	14	0.11	HSPH1
hypothetical protein, partial Heat shock 70 kDa protein	Q6ZS10	2.34E-40	1.3033	1.25015	4.06E-02	10.593	10	0.14	CLEC17A
Uncharacterized protein; F-actin-capping protein subunit alpha-1; Uncharacterized protein (Fragment)	P08106;B3VHV2	1.13E-209	1.0481	1.23288	0.37078	11.477	11	0.211	HSP70
F-actin-capping protein subunit alpha-2; Uncharacterized protein (Fragment)	E1BXA2;P13127	2.17E-157	1.3832	1.2106	0.20223	10.822	13	0.14	CapZ-alpha1
Profilin; Uncharacterized protein (Fragment)	P28497;A0M8UC	4.96E-75	1.27643	1.16598	0.0349	10.561	15	0.13	CapZ-alpha2
Uncharacterized protein GDP/GTP exchange factor VAV3	F1NA40;Q5ZL5C	7.71E-58	1.0423	1.15486	0.40471	10.715	29	0.09	PFN
	E1BUJ8	0.0013973	1.1433	1.1324	0.3458	7.1216	12	0.24	CHCHD4
	F1NF39;Q8UUX6	6.84E-10	1.0721	1.08603	0.412687	15.979	4	0.07	Vav3
Isoform 2 of F-actin-capping protein subunit beta isoforms 1 and 2; Isoform 1 of F-actin-capping protein subunit beta isoforms 1 and 2	P14315-2;P14315	1.54E-89	1.3121	1.0273	0.053245	16.704	20	0.12	CapZ-beta

Uncharacterized protein; Serine-threonine phosphatase 2A regulatory subunit (Fragment); Uncharacterized protein (Fragment); Serine/threonine-phosphatase 2A 55 kDa regulatory subunit B delta isoform; Uncharacterized protein (Fragment) Talin-1; Uncharacterized protein; Uncharacterized protein	Q5ZLP4;Q8AWE	2.29E-42	1.0861	0.98845	0.45633	9.085	5	0.21	PP2A
similar to WDR81 protein	F1N971	5.52E-12	1.067	0.97224	0.43148	13.511	11	0.08	WDR81
Growth factor receptor-bound protein 2	Q07883;A3R0S3	1.03E-97	1.2706	0.946	5.41E-02	18.314	18	0.12	Grb2
CIN85	F1NKX7;Q5ZMQ	1.51E-254	1.05231	0.9288	5.80E-02	12.808	33	0.14	SH3KBP1
CD2AP Putative uncharacterized protein	Q5ZJW0;F1NAW	7.04E-110	0.7168	0.9234	6.69E-02	15.074	36	0.22	CD2AP
Uncharacterized protein	F1P338;Q5F357	2.04E-38	1.022	0.92066	0.45199	10.483	15	0.13	AIFM1

similar to Ig
alpha chain -
chicken; 13 kDa
protein; similar
to This CDS
feature is
included to
show the
translation of
the
corresponding
V_region.

Presently
translation
qualifiers on
V_region
features are
illegal; similar
to Ig alpha
chain -
chicken; similar
Uncharacterize
d
protein; Tyrosin
e-protein
kinase BTK
BASH/BLNK N-
terminal
associated
protein 1

A2N881;A2N882	0.0055989	0.92869	0.91822	0.34825	17.913	11	0.15	CD79a
Q5ZLF2;Q8JH64	3.46E-126	0.80631	0.87382	0.054693	10.959	19	0.16	Btk
F1NBR2;Q25QX!	8.41E-48	0.89435	0.84992	0.0024697	11.243	8	0.27	BRI3BP

similar to 1-
phosphatidylinositol-4,5-
bisphosphate
phosphodiester
ase gamma 2

E1C6E1	7.19E-82	0.5128	0.521658	0.00028397	6.1903	16	0.11	PLC-γ2
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