

Cluster	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	Count
1	Cells	R-HSA-72766 Translation	128/1008	291/10723	2.85268E-56	2.78422E-53	1.8047E-53	128
2	Cells	R-HSA-72163 mRNA Splicing - Major Pathway	96/1008	201/10723	2.53062E-51	1.23494E-48	8.0047E-49	96
3	Cells	R-HSA-72172 mRNA Splicing	96/1008	189/10723	4.22204E-49	1.3737E-46	8.90333E-47	96
4	Cells	R-HSA-72203 Processing of Capped Intron-Containing Pre-mRNA	107/1008	241/10723	1.92336E-47	4.69299E-45	3.00419E-45	107
5	Cells	R-HSA-9010553 Regulation of expression of SLTs and RBOs	81/1008	270/10723	8.15104E-39	1.5912E-36	1.0314E-36	81
6	Cells	R-HSA-376176 Signaling by RBO/89/1008	89/1008	240/10723	2.40292E-36	3.00876E-34	2.53361E-34	89
7	Cells	R-HSA-72613 Eukaryotic Translation Initiation	64/1008	119/10723	6.7786E-35	8.2699E-33	5.36045E-33	64
8	Cells	R-HSA-72737 Cap-dependent Translation Initiation	64/1008	119/10723	6.7786E-35	8.2699E-33	5.36045E-33	64
9	Cells	R-HSA-72705 GTP hydrolysis and joining of the 60S ribosomal subunit	62/1008	112/10723	8.06694E-35	8.74815E-33	5.67045E-33	62
10	Cells	R-HSA-72764 L13-dependent translational silencing of Ceruloplasmin expression	62/1008	111/10723	5.01335E-34	4.89108E-32	3.17034E-32	62
11	Cells	R-HSA-927802 Nonsense-Mediated Decay (NMD)	62/1008	115/10723	6.45753E-34	5.25212E-32	3.40436E-32	62
12	Cells	R-HSA-975957 Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	62/1008	115/10723	6.45753E-34	5.25212E-32	3.40436E-32	62
13	Cells	R-HSA-975956 Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	56/1008	95/10723	1.51006E-33	1.13371E-31	7.34855E-32	56
14	Cells	R-HSA-92764 Eukaryotic translation termination	55/1008	93/10723	4.52228E-33	3.1288E-31	2.04353E-31	55
15	Cells	R-HSA-72689 Formation of a pool of free 40S subunits	56/1008	101/10723	1.35284E-31	8.80245E-30	5.70564E-30	56
16	Cells	R-HSA-71291 Metabolism of amino acids and derivatives	113/1008	371/10723	1.53523E-31	9.3649E-30	6.07022E-30	113
17	Cells	R-HSA-156842 Eukaryotic Translation Elongation	53/1008	93/10723	8.90826E-31	5.1439E-29	3.13509E-29	53
18	Cells	R-HSA-179937 SRP-dependent cotranslational protein targeting to membrane	53/1008	117/10723	3.28309E-29	1.4566E-27	9.44083E-28	53
19	Cells	R-HSA-156902 Peptide chain elongation	51/1008	89/10723	8.14662E-30	3.97555E-28	2.57691E-28	51
20	Cells	R-HSA-192823 Viral mRNA Translation	51/1008	89/10723	8.14662E-30	3.97555E-28	2.57691E-28	51
21	Cells	R-HSA-2408557 Selenocysteine synthesis	52/1008	93/10723	1.16958E-29	5.4357E-28	3.5239E-28	52
22	Cells	R-HSA-2408522 Selenoamino acid metabolism	58/1008	117/10723	3.28309E-29	1.4566E-27	9.44083E-28	58
23	Cells	R-HSA-168255 Influenza Infection	66/1008	155/10723	3.66392E-28	1.55478E-26	1.00779E-26	66
24	Cells	R-HSA-168273 Influenza Viral RNA Transcription and Replication	61/1008	135/10723	7.76197E-28	3.15646E-26	2.04598E-26	61
25	Cells	R-HSA-9633012 Response of EIF2AK4 (GCN2) to amino acid deficiency	51/1008	101/10723	2.64315E-26	1.03188E-24	6.68855E-25	51
26	Cells	R-HSA-1781075 The citric acid (TCA) cycle and respiratory electron transport	64/1008	178/10723	1.6841E-22	4.09856E-21	2.9443E-21	64
27	Cells	R-HSA-8868773 rRNA processing in the nucleolus and cytosol	65/1008	192/10723	3.36447E-21	1.21609E-19	7.88252E-20	65
28	Cells	R-HSA-72312 rRNA processing	66/1008	202/10723	1.47655E-20	5.14684E-19	3.33612E-19	66
29	Cells	R-HSA-9711097 Cellular response to starvation	56/1008	156/10723	8.64043E-20	2.90795E-18	1.8849E-18	56
30	Cells	R-HSA-72662 Major pathway of RNA processing in the nucleolus and cytosol	61/1008	182/10723	1.02313E-19	1.14239E-15	7.40485E-16	61
31	Cells	R-HSA-163200 Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	48/1008	127/10723	3.35928E-18	1.05763E-16	6.85543E-17	48
32	Cells	R-HSA-8873719 RAB geranylgeranylation	33/1008	64/10723	8.07176E-18	2.46189E-16	1.59577E-16	33
33	Cells	R-HSA-73856 RNA Polymerase II Transcription Termination	33/1008	66/10723	2.7243E-17	8.05733E-16	5.22267E-16	33
34	Cells	R-HSA-72662 Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	31/1008	59/10723	3.97965E-17	1.14239E-15	7.40485E-16	31
35	Cells	R-HSA-72662 Translation initiation complex formation	30/1008	58/10723	2.2847E-16	6.20159E-15	4.01979E-15	30
36	Cells	R-HSA-72702 Ribosomal scanning and start codon recognition	30/1008	58/10723	2.2847E-16	6.20159E-15	4.01979E-15	30
37	Cells	R-HSA-6798695 Neurotrophin degradation	100/1008	474/10723	2.70259E-15	1.72899E-14	4.62093E-14	100
38	Cells	R-HSA-72187 mRNA 3'-end processing	28/1008	57/10723	1.28811E-14	3.2084E-13	2.14447E-13	28
39	Cells	R-HSA-5389840 Mitochondrial translation elongation	34/1008	87/10723	6.96762E-13	1.2864E-11	8.3384E-12	34
40	Cells	R-HSA-5368287 Mitochondrial translation initiation	35/1008	93/10723	1.47147E-13	3.59103E-12	2.32767E-12	35
41	Cells	R-HSA-6111005 Respiratory electron transport	37/1008	103/10723	1.61188E-13	3.83705E-12	2.48713E-12	37
42	Cells	R-HSA-72695 Formation of the ternary complex, and subsequently, the 43S complex	25/1008	51/10723	3.64074E-13	8.46039E-12	5.48392E-12	25
43	Cells	R-HSA-5419276 Mitochondrial translation termination	31/1008	87/10723	5.67827E-13	1.2864E-11	8.3384E-12	31
44	Cells	R-HSA-5368286 Mitochondrial translation initiation	32/1008	87/10723	3.9811E-12	7.5763E-11	4.8858E-11	32
45	Cells	R-HSA-9711123 Cellular response to chemical stress	45/1008	158/10723	4.98529E-12	1.08125E-10	7.00856E-11	45
46	Cells	R-HSA-450531 Regulation of mRNA stability by proteins that bind AU-rich elements	30/1008	86/10723	7.56907E-11	1.6059E-09	1.0409E-09	30
47	Cells	R-HSA-49005 Gene and protein expression by RAS/RAF signaling after Interleukin-12 stimulation	19/1008	37/10723	8.98565E-11	1.8624E-09	1.2071E-09	19
48	Cells	R-HSA-450408 AUF1 (hnRNP D0) binds and destabilizes mRNA	23/1008	54/10723	1.19381E-10	2.42741E-09	1.57342E-09	23
49	Cells	R-HSA-159236 Transport of Mature mRNA derived from an Intron-Containing Transcript	27/1008	73/10723	1.45038E-10	2.88892E-09	1.87256E-09	27
50	Cells	R-HSA-162906 HIV Infection	54/1008	232/10723	2.0114E-10	3.9257E-09	2.54463E-09	54
51	Cells	R-HSA-72662 mRNA Splicing - Minor Pathway	54/1008	232/10723	3.5249E-10	6.8769E-09	4.40546E-09	54
52	Cells	R-HSA-72202 Transport of Mature Transcript to Cytoplasm	28/1008	82/10723	5.7537E-10	1.07649E-08	6.9775E-09	28
53	Cells	R-HSA-9020591 Interleukin-12 signaling	20/1008	46/10723	1.2587E-09	2.31791E-08	1.5024E-08	20
54	Cells	R-HSA-1168372 Downstream signaling events of E Cell Receptor (BCR)	27/1008	80/10723	1.56622E-09	2.8308E-08	1.8348E-08	27
55	Cells	R-HSA-992316 ROS sensing by p53	26/1008	60/10723	1.94749E-09	3.4559E-08	2.20507E-08	26
56	Cells	R-HSA-960507 Protein localization	41/1008	163/10723	2.80234E-09	4.88408E-08	3.1658E-08	41
57	Cells	R-HSA-379716 Cytosolic tRNA aminoacylation	14/1008	24/10723	3.07758E-09	5.26673E-08	3.41383E-08	14
58	Cells	R-HSA-180585 Virus-mediated degradation of APOBEC3G	21/1008	53/10723	3.78305E-09	6.36595E-08	4.12634E-08	21
59	Cells	R-HSA-12151 Apoptosis	59/1008	278/10723	4.36389E-08	7.2190E-08	4.7931E-08	59
60	Cells	R-HSA-162909 Host Interactions of HIV factors	35/1008	129/10723	4.80727E-09	7.9231E-08	5.13515E-08	35
61	Cells	R-HSA-9707587 Regulation of HMOX1 expression and activity	23/1008	64/10723	6.42794E-09	1.02847E-07	6.66643E-08	23
62	Cells	R-HSA-537801 Programmed Cell Death	47/1008	207/10723	7.15771E-09	1.12676E-07	7.30335E-08	47
63	Cells	R-HSA-49004 Ypu mediated degradation of CD4	21/1008	51/10723	1.10077E-09	1.7031E-07	1.1053E-07	21
64	Cells	R-HSA-447115 Interleukin-12 family signaling	21/1008	56/10723	1.21685E-08	1.85572E-07	1.20285E-07	21
65	Cells	R-HSA-1236974 ER-Phagosome pathway	27/1008	89/10723	2.13914E-08	3.16669E-07	2.05261E-07	27
66	Cells	R-HSA-1236978 Cross-presentation of soluble exogenous antigens (endosomes)	19/1008	48/10723	2.1444E-08	3.16669E-07	2.05261E-07	19
67	Cells	R-HSA-954509 FBX7 down-regulates AuroraB during mitotic entry and in early mitosis	20/1008	53/10723	2.82227E-08	3.4336E-07	2.22502E-07	20
68	Cells	R-HSA-9604312 Negative regulation of NOTCH4 signaling	20/1008	53/10723	2.82227E-08	3.4336E-07	2.22502E-07	20
69	Cells	R-HSA-351202 Metabolism of polyamines	21/1008	58/10723	2.51433E-08	3.53578E-07	2.29185E-07	21
70	Cells	R-HSA-3858494 Beta-catenin independent Wnt signaling	36/1008	143/10723	2.53591E-08	3.53578E-07	2.29185E-07	36
71	Cells	R-HSA-11213 Regulation of activated RAS by GAP	19/1008	31/10723	3.15228E-08	4.3882E-07	2.8444E-07	19
72	Cells	R-HSA-174413 SCF-beta-TCP mediated degradation of Em1	20/1008	54/10723	3.46725E-08	4.62093E-07	2.99523E-07	20
73	Cells	R-HSA-8941858 Regulation of RUNX3 expression and activity	20/1008	54/10723	3.46725E-08	4.62093E-07	2.99523E-07	20
74	Cells	R-HSA-1268020 Mitochondrial protein import	22/1008	64/10723	3.50357E-08	4.62093E-07	2.99523E-07	22
75	Cells	R-HSA-30562 Regulation of ornithine decarboxylase (ODC)	19/1008	46/10723	4.69943E-08	6.11552E-07	3.96401E-07	19
76	Cells	R-HSA-5362768 Hh mutants are degraded by ERAD	20/1008	55/10723	4.97221E-08	6.38537E-07	4.13892E-07	20
77	Cells	R-HSA-9707564 Cytoprotection by HMOX1	32/1008	122/10723	5.33421E-08	6.76129E-07	4.38259E-07	32
78	Cells	R-HSA-195253 Degradation of beta-catenin by the destruction complex	25/1008	82/10723	6.37211E-08	7.7833E-07	5.1682E-07	25
79	Cells	R-HSA-349255 Autodegradation of the E3 ubiquitin ligase COP1	19/1008	51/10723	6.83613E-08	8.03863E-07	5.21054E-07	19
80	Cells	R-HSA-690161 Ubiquitin-Mediated Degradation of Phosphorylated Cdc25A	19/1008	51/10723	6.83613E-08	8.03863E-07	5.21054E-07	19
81	Cells	R-HSA-69610 p53-independent DNA Damage Response	19/1008	51/10723	6.83613E-08	8.03863E-07	5.21054E-07	19
82	Cells	R-HSA-69613 p53-independent G1/S DNA Damage checkpoint	19/1008	51/10723	6.83613E-08	8.03863E-07	5.21054E-07	19
83	Cells	R-HSA-75915 Ubiquitin-dependent degradation of Cyclin D	19/1008	51/10723	6.83613E-08	8.03863E-07	5.21054E-07	19
84	Cells	R-HSA-569128 MAPK9/MAPK4 signaling	26/1008	117/10723	7.10315E-08	8.2319E-07	5.34962E-07	26
85	Cells	R-HSA-5658442 Regulation of RAS by GAPs	22/1008	67/10723	8.98253E-08	1.03141E-06	6.68545E-07	22
86	Cells	R-HSA-169911 Regulation of Apoptosis	19/1008	52/10723	9.83228E-08	1.1328E-06	7.21614E-07	19
87	Cells	R-HSA-6799198 Complex Biogenesis	20/1008	57/10723	9.9237E-08	1.1328E-06	7.21614E-07	20
88	Cells	R-HSA-71403 Citric acid cycle (TCA cycle)	12/1008	25/10723	1.18487E-07	1.1411E-06	8.1801E-07	12
89	Cells	R-HSA-8948751 Regulation of PTEN stability and activity	22/1008	68/10723	1.21151E-07	1.32858E-06	8.61169E-07	22
90	Cells	R-HSA-5387390 Hh mutants abrogate ligand secretion	20/1008	58/10723	1.38234E-07	1.48259E-06	9.60999E-07	20
91	Cells	R-HSA-5676590 Non-canonical NF-κB signaling	20/1008	58/10723	1.38234E-07	1.48259E-06	9.60999E-07	20
92	Cells	R-HSA-5676564 CLEC7A (Dectin-3) signaling	21/1008	67/10723	1.56649E-07	1.6618E-06	1.07719E-06	21
93	Cells	R-HSA-983705 Signaling by the E Cell Receptor (BCR)	29/1008	109/10723	1.66395E-07	1.68329E-06	1.09109E-06	29
94	Cells	R-HSA-5358346 Hedgehog ligand biogenesis	21/1008	64/10723	1.7848E-07	1.85315E-06	1.20119E-06	21
95	Cells	R-HSA-187577 SCF(E3) mediated degradation of p27(p21)	20/1008	59/10723	1.90856E-07	1.88157E-06	1.21961E-06	20
96	Cells	R-HSA-5607951 Dectin-3 mediated noncanonical NF-κB signaling	20/1008	59/10723	1.90856E-07	1.88157E-06	1.21961E-06	20
97	Cells	R-HSA-5610780 Degradation of GLI1 by the proteasome	20/1008	59/10723	1.90856E-07	1.88157E-06	1.21961E-06	20
98	Cells	R-HSA-5610783 Degradation of GLI2 by the proteasome	20/1008	59/10723	1.90856E-07	1.88157E-06	1.21961E-06	20
99	Cells	R-HSA-5610785 GLI3 is processed to GLI3R by the proteasome	20/1008	59/10723	1.90856E-07	1.88157E-06	1.21961E-06	20
100	Cells	R-HSA-4641257 Degradation of AXIN	19/1008	57/10723	1.97023E-07	1.92294E-06	1.24663E-06	19
101	Cells	R-HSA-68886 M Phase	67/1008	379/10				

135	Cells	R-HSA-179419	APC/Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	20/10/08	73/10/723	8.18347E-06	5.91634E-05	3.8349E-05	20
136	Cells	R-HSA-5621481	C-type lectin receptors (CLRs)	30/10/08	138/10/723	9.53765E-06	6.84407E-05	4.43663E-05	30
137	Cells	R-HSA-690329	FGFR2 alternative splicing	14/10/08	26/10/723	9.83161E-06	7.00411E-05	4.53999E-05	14
138	Cells	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	21/10/08	80/10/723	1.01646E-05	7.18885E-05	4.65973E-05	21
139	Cells	R-HSA-9013408	RHO GTPase cycle	20/10/08	74/10/723	1.02383E-05	7.18893E-05	4.65978E-05	20
140	Cells	R-HSA-8949613	Cristae formation	12/10/08	31/10/723	1.16008E-05	8.08739E-05	5.24215E-05	12
141	Cells	R-HSA-9013604	Signaling by NOTCH4	21/10/08	84/10/723	1.25262E-05	8.67062E-05	5.62026E-05	21
142	Cells	R-HSA-176409	APC/C.Cdc20 mediated degradation of mitotic proteins	20/10/08	75/10/723	1.27466E-05	8.76101E-05	5.67878E-05	20
143	Cells	R-HSA-75153	Apoptotic execution phase	16/10/08	52/10/723	1.31728E-05	8.99063E-05	5.82762E-05	16
144	Cells	R-HSA-195258	RHO GTPase Effectors	50/10/08	288/10/723	1.34064E-05	9.08656E-05	5.8989E-05	50
145	Cells	R-HSA-690229	Cyclin A-associated events during G1/S transition	21/10/08	91/10/723	1.39248E-05	9.00014873	5.94409E-05	21
146	Cells	R-HSA-9020702	Interleukin-1 signaling	24/10/08	101/10/723	1.54066E-05	0.000102992	6.67582E-05	24
147	Cells	R-HSA-176814	Activation of APC/C and APC/C.Cdc20 mediated degradation of mitotic proteins	20/10/08	76/10/723	1.57941E-05	0.000104156	6.75124E-05	20
148	Cells	R-HSA-5619084	ABC transporter disorders	21/10/08	76/10/723	1.69523E-05	0.000108417	7.02749E-05	21
150	Cells	R-HSA-8878159	Transcriptional regulation by RUNX3	23/10/08	95/10/723	1.66625E-05	0.000108417	7.02749E-05	23
151	Cells	R-HSA-8856688	Golgi-to-ER retrograde transport	28/10/08	130/10/723	2.24688E-05	0.000145157	9.40892E-05	28
152	Cells	R-HSA-162587	HIV Life Cycle	31/10/08	151/10/723	2.2858E-05	0.000145157	9.40892E-05	31
153	Cells	R-HSA-691556	Cyclin A-Cdk2 associated events at S phase entry	14/10/08	84/10/723	2.2858E-05	0.000145157	9.40892E-05	14
154	Cells	R-HSA-75067	Processing of Capped Intronless Pre-mRNA	11/10/08	28/10/723	2.29039E-05	0.000145157	9.40892E-05	11
155	Cells	R-HSA-5696398	Nucleotide Excision Repair	25/10/08	110/10/723	2.34175E-05	0.000145157	9.40892E-05	25
156	Cells	R-HSA-688875	Mitotic Prophase	25/10/08	110/10/723	2.34175E-05	0.000145157	9.40892E-05	25
157	Cells	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	23/10/08	91/10/723	2.39248E-05	0.00014873	9.44409E-05	23
158	Cells	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdk6	19/10/08	72/10/723	2.45539E-05	0.000151663	9.83058E-05	19
159	Cells	R-HSA-6811436	COP1-independent Golgi-to-ER retrograde traffic	15/10/08	49/10/723	2.61873E-05	0.000160747	0.000104194	15
160	Cells	R-HSA-174178	APC/C.Cdh1 mediated degradation of Cdk2 and other APC/C.Cdh1 targeted proteins in late mitosis/early G1	19/10/08	73/10/723	3.03112E-05	0.00018375	0.000119104	19
161	Cells	R-HSA-174178	Signaling by RHP	19/10/08	73/10/723	3.03112E-05	0.00018375	0.000119104	19
162	Cells	R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	21/10/08	87/10/723	4.03025E-05	0.000241321	0.000156421	21
163	Cells	R-HSA-453276	Regulation of mitotic cell cycle	21/10/08	87/10/723	4.03025E-05	0.000241321	0.000156421	21
164	Cells	R-HSA-432720	Lysosome Biogenesis	12/10/08	35/10/723	4.81075E-05	0.000286298	0.000185575	12
165	Cells	R-HSA-162559	snRNP Assembly	15/10/08	56/10/723	5.69027E-05	0.00032557	0.00021556	15
166	Cells	R-HSA-194441	Metabolism of non-coding RNA	15/10/08	52/10/723	5.69027E-05	0.00032557	0.00021556	15
167	Cells	R-HSA-3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	15/10/08	52/10/723	5.69027E-05	0.00032557	0.00021556	15
168	Cells	R-HSA-5627123	RHO GTPase Activate PAKs	9/10/08	21/10/723	5.72727E-05	0.00032753	0.000215687	9
169	Cells	R-HSA-69206	G1/S Transition	27/10/08	130/10/723	6.13866E-05	0.00035424	0.000219614	27
170	Cells	R-HSA-20242	Downstream TCR signaling	22/10/08	61/10/723	6.21161E-05	0.00035773	0.000219024	22
171	Cells	R-HSA-5663213	RHO GTPase Activate WASPs and WAVEs	12/10/08	36/10/723	6.60461E-05	0.00037665	0.000244344	12
172	Cells	R-HSA-6807070	PTEN Regulation	28/10/08	138/10/723	6.98022E-05	0.000396087	0.000256739	28
173	Cells	R-HSA-8878171	Transcriptional regulation by RUNX1	37/10/08	205/10/723	7.56551E-05	0.000426817	0.000276658	37
174	Cells	R-HSA-29210	Nuclear Envelope (NE) Reassembly	18/10/08	61/10/723	8.65348E-05	0.00045217	0.000284547	18
175	Cells	R-HSA-9609523	Insertion of tail-anchored proteins into the endoplasmic reticulum membrane	9/10/08	22/10/723	8.88858E-05	0.000495729	0.00031325	9
176	Cells	R-HSA-445355	Smooth Muscle Contraction	12/10/08	37/10/723	9.84703E-05	0.000496153	0.000321601	12
177	Cells	R-HSA-8878166	Transcriptional regulation by RUNX2	25/10/08	119/10/723	9.44493E-05	0.000515291	0.000334005	25
178	Cells	R-HSA-5696398	Formation of Inclusion Complex in GG-NER	13/10/08	43/10/723	0.00010379	0.00056095	0.00031888	13
179	Cells	R-HSA-69481	G2/M Checkpoints	29/10/08	149/10/723	0.000114021	0.000621702	0.00040298	29
180	Cells	R-HSA-429914	Deadenylation-dependent mRNA decay	15/10/08	55/10/723	0.000115478	0.000626148	0.000405862	15
181	Cells	R-HSA-9013418	RHO GTPase Cycle	9/10/08	23/10/723	0.000113919	0.000720176	0.00046681	9
182	Cells	R-HSA-8854214	TIC/PAAGAPs	13/10/08	44/10/723	0.000114792	0.000720176	0.00046681	13
183	Cells	R-HSA-3371453	Regulation of HSF1-mediated heat shock response	17/10/08	68/10/723	0.000135033	0.000720176	0.00046681	17
184	Cells	R-HSA-9009391	Extra-nuclear estrogen signaling	18/10/08	75/10/723	0.000152265	0.000807668	0.000523521	18
185	Cells	R-HSA-382556	ABC-family proteins mediated transport	22/10/08	102/10/723	0.000167178	0.000853173	0.00053017	22
186	Cells	R-HSA-492021	Transport to the Golgi and subsequent modification	13/10/08	51/10/723	0.000166088	0.00087157	0.0005494	13
187	Cells	R-HSA-8856828	Citric acid mediated endocytosis	28/10/08	145/10/723	0.000170994	0.000892461	0.000578483	28
188	Cells	R-HSA-162599	Late Phase of HIV Life Cycle	27/10/08	138/10/723	0.000177117	0.000919499	0.000596009	27
189	Cells	R-HSA-5610787	Hedgehog 'off' state	23/10/08	110/10/723	0.000189369	0.000979908	0.000633868	23
190	Cells	R-HSA-9679506	SARS-CoV Infections	28/10/08	146/10/723	0.00019923	0.001096165	0.000642776	28
191	Cells	R-HSA-69052	Switching of origins to a post-replicative state	20/10/08	90/10/723	0.000207199	0.001058776	0.000658266	20
192	Cells	R-HSA-5632684	Hedgehog 'on' state	19/10/08	84/10/723	0.000232278	0.001174631	0.000761382	19
193	Cells	R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	19/10/08	84/10/723	0.000232278	0.001174631	0.000761382	19
194	Cells	R-HSA-56268	Glycan trimming in the Golgi and Calnexin/Calreticulin cycle	13/10/08	56/10/723	0.000234463	0.001209497	0.00073982	13
195	Cells	R-HSA-453279	Mitotic G1 phase and G1/S transition	28/10/08	148/10/723	0.000244882	0.001255664	0.000794661	28
196	Cells	R-HSA-69239	Synthesis of DNA	24/10/08	119/10/723	0.000247335	0.001231627	0.000798326	24
197	Cells	R-HSA-15869	Metabolism of nucleotides	21/10/08	98/10/723	0.000248696	0.001232116	0.000798643	21
198	Cells	R-HSA-621813	Separation of Sister Chromatids	18/10/08	76/10/723	0.000252529	0.001246619	0.000808044	18
199	Cells	R-HSA-210991	Basigin interactions	9/10/08	25/10/723	0.000281662	0.001381419	0.000859119	9
200	Cells	R-HSA-199992	trans-Golgi Network Vesicle Budding	17/10/08	72/10/723	0.000284202	0.001386905	0.00089875	17
201	Cells	R-HSA-159230	Mitochondrial biogenesis	20/10/08	93/10/723	0.000293466	0.001599797	0.001036969	20
202	Cells	R-HSA-392662	EPHB-mediated forward signaling	13/10/08	47/10/723	0.000334363	0.001659454	0.001075639	13
203	Cells	R-HSA-398661	Glyoxylate metabolism and glycine degradation	10/10/08	31/10/723	0.000363114	0.001745807	0.001131612	10
204	Cells	R-HSA-190236	Signaling by FGFR	19/10/08	87/10/723	0.000374646	0.001792426	0.001161829	19
205	Cells	R-HSA-70895	Branch-chain amino acid catabolism	8/10/08	21/10/723	0.000395552	0.001883214	0.001220677	8
206	Cells	R-HSA-3371516	Cellular response to heat stress	8/10/08	21/10/723	0.000395552	0.001883214	0.001220677	8
207	Cells	R-HSA-391251	Protein folding	20/10/08	95/10/723	0.000442374	0.002085782	0.001351979	20
208	Cells	R-HSA-69275	G2/M Transition	28/10/08	148/10/723	0.0004593	0.002155177	0.00139696	28
209	Cells	R-HSA-8876198	RAF GEF exchange GTP for GDP on RABs	19/10/08	84/10/723	0.000507176	0.002384839	0.001531594	19
210	Cells	R-HSA-202403	TCR signaling	13/10/08	51/10/723	0.000550446	0.002528262	0.001658235	13
211	Cells	R-HSA-453274	Mitotic G2-G2/M phases	33/10/08	194/10/723	0.000555667	0.002569825	0.00166573	33
212	Cells	R-HSA-392170	ADP signalling through P2Y purinoreceptor 12	8/10/08	22/10/723	0.00057079	0.002627789	0.001703301	8
213	Cells	R-HSA-111885	Opioid Signaling	19/10/08	90/10/723	0.000587452	0.002691797	0.001744791	19
214	Cells	R-HSA-392518	Signal amplification	10/10/08	33/10/723	0.000686908	0.002904777	0.001882842	10
215	Cells	R-HSA-9013405	RHO GTPase cycle	13/10/08	51/10/723	0.000650548	0.003019008	0.001954885	13
216	Cells	R-HSA-69306	DNA Replication	24/10/08	127/10/723	0.000672975	0.003040851	0.001971043	24
217	Cells	R-HSA-2682334	EPH-Ephrin signaling	19/10/08	91/10/723	0.000678463	0.003051519	0.001977959	19
218	Cells	R-HSA-9007101	Rab regulation of trafficking	23/10/08	121/10/723	0.000793646	0.00355203	0.002303144	23
219	Cells	R-HSA-167238	Pausing and recovery of Tat-mediated HIV elongation	10/10/08	34/10/723	0.000872797	0.003653585	0.00238188	10
220	Cells	R-HSA-167243	Tat-mediated HIV elongation arrest and recovery	10/10/08	34/10/723	0.000872797	0.003653585	0.00238188	10
221	Cells	R-HSA-5673000	RAF activation	10/10/08	34/10/723	0.000872797	0.003653585	0.00238188	10
222	Cells	R-HSA-568541	TNFR2 non-canonical NF- $\kappa$ B pathway	20/10/08	100/10/723	0.000881823	0.003878842	0.002512923	20
223	Cells	R-HSA-964407	Bacterial infection	14/10/08	59/10/723				

270	Cells	R-HSA-456926	Thrombin signalling through protease activated receptors (PARs)	8/1008	32/10/723	0.00805879	0.02911032	0.018882388	8
271	Cells	R-HSA-469242	S Phase	25/1008	161/10/723	0.00839489	0.029728073	0.019269383	25
272	Cells	R-HSA-467044	Signalling to RAS	6/1008	30/10/723	0.00815312	0.029728073	0.019269383	6
273	Cells	R-HSA-416572	Sema4D induced cell migration and growth-cone collapse	6/1008	20/10/723	0.00831532	0.029728073	0.019269383	6
274	Cells	R-HSA-4086398	Ca2+ pathway	12/1008	60/10/723	0.00899543	0.032056766	0.02077814	12
275	Cells	R-HSA-167169	HIV Transcription Elongation	10/1008	46/10/723	0.00914589	0.032109204	0.020812804	10
276	Cells	R-HSA-167200	Formation of HIV-1 elongation complex containing HIV-1 Tat	10/1008	46/10/723	0.00914589	0.032109204	0.020812804	10
277	Cells	R-HSA-167246	Tat-mediated elongation of the HIV-1 transcript	10/1008	46/10/723	0.00914589	0.032109204	0.020812804	10
278	Cells	R-HSA-4570464	SUMOylation of RNA binding proteins	10/1008	46/10/723	0.00914589	0.032109204	0.020812804	10
279	Cells	R-HSA-180910	Vpr-mediated nuclear import of PICs	8/1008	33/10/723	0.00978186	0.034096755	0.022101111	8
280	Cells	R-HSA-563864	Diseases of carbohydrate metabolism	16/1008	81/10/723	0.01160181	0.035289453	0.022874203	16
281	Cells	R-HSA-70326	Glucose metabolism	16/1008	81/10/723	0.01160181	0.035289453	0.022874203	16
282	Cells	R-HSA-8848021	Signaling by PTK6	11/1008	54/10/723	0.010571597	0.036458934	0.023632247	11
283	Cells	R-HSA-9006927	Signaling by Non-Receptor Tyrosine Kinases	11/1008	54/10/723	0.010571597	0.036458934	0.023632247	11
284	Cells	R-HSA-563208	MAPK family signaling cascades	43/1008	312/10/723	0.010860643	0.037321838	0.024251571	43
285	Cells	R-HSA-4085377	SUMOylation of SUMOylation proteins	8/1008	34/10/723	0.011764244	0.040287376	0.026113797	8
286	Cells	R-HSA-167152	Formation of HIV elongation complex in the absence of HIV Tat	10/1008	48/10/723	0.012369633	0.042212452	0.027361609	10
287	Cells	R-HSA-9645723	Diseases of programmed cell death	13/1008	70/10/723	0.012512433	0.042550991	0.027584046	13
288	Cells	R-HSA-4781827	Transcription-Coupled nucleotide excision repair (TC-NER)	14/1008	76/10/723	0.013170505	0.044819978	0.028791636	14
289	Cells	R-HSA-9665686	Signaling by ERBB2 TMD/IMD mutants	6/1008	22/10/723	0.01361092	0.045966289	0.029794801	6
290	Cells	R-HSA-5689880	Ub-specific processing proteases	29/1008	202/10/723	0.013790562	0.046412375	0.030083949	29
291	Cells	R-HSA-157118	Signaling by NOTCH	29/1008	203/10/723	0.014658567	0.049289197	0.031948671	29
292	Cells/Exosomes	R-HSA-9009090	HCMV Early Events	39/162	98/10/723	1.21863E+46	7.50767E+44	2.15056E+44	39
293	Cells/Exosomes	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	37/162	97/10/723	2.21474E+43	6.87676E+41	1.9583E+41	37
294	Cells/Exosomes	R-HSA-68886	M Phase	57/162	379/10/723	2.88816E+42	5.30431E+40	1.51051E+40	57
295	Cells/Exosomes	R-HSA-9609646	HCMV Infection	39/162	122/10/723	3.41663E+42	5.30431E+40	1.51051E+40	39
296	Cells/Exosomes	R-HSA-9625240	RHO GTPase activate PKNs	30/162	62/10/723	4.32735E+38	5.37482E+37	1.52059E+37	30
297	Cells/Exosomes	R-HSA-73728	RNA Polymerase I Promoter Opening	24/162	31/10/723	8.23046E+39	8.51853E+37	2.4422E+37	24
298	Cells/Exosomes	R-HSA-195258	RHO GTPase Effectors	49/162	288/10/723	1.13076E+38	1.00314E+36	2.85665E+37	49
299	Cells/Exosomes	R-HSA-171306	Packaging Of Telomere Ends	24/162	32/10/723	3.2514E+38	2.5239E+36	7.18731E+37	24
300	Cells/Exosomes	R-HSA-3351318	DNA methylation	24/162	33/10/723	1.17741E+37	8.12413E+36	2.31531E+36	24
301	Cells/Exosomes	R-HSA-5625886	Activated PKML stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	24/162	33/10/723	1.24237E+36	7.71514E+35	2.19704E+35	24
302	Cells/Exosomes	R-HSA-110330	Recognition and association of DNA glycosylase with site containing an affected purine	24/162	36/10/723	3.68093E+36	1.63276E+34	4.6496E+35	24
303	Cells/Exosomes	R-HSA-110331	Cleavage of the damaged purine	24/162	36/10/723	3.68093E+36	1.63276E+34	4.6496E+35	24
304	Cells/Exosomes	R-HSA-427359	SIRT1 negatively regulates rRNA expression	24/162	36/10/723	3.68093E+36	1.63276E+34	4.6496E+35	24
305	Cells/Exosomes	R-HSA-739271	Depurination	24/162	36/10/723	3.68093E+36	1.63276E+34	4.6496E+35	24
306	Cells/Exosomes	R-HSA-8852276	The role of GISE1 in G2/M progression after G2 checkpoint	29/162	74/10/723	2.05641E+34	8.51356E+33	2.4244E+33	29
307	Cells/Exosomes	R-HSA-110328	Recognition and association of DNA glycosylase with site containing an affected pyrimidine	24/162	41/10/723	4.1883E+34	1.30047E+32	3.70334E+33	24
308	Cells/Exosomes	R-HSA-110329	Cleavage of the damaged pyrimidine	24/162	41/10/723	4.1883E+34	1.30047E+32	3.70334E+33	24
309	Cells/Exosomes	R-HSA-421200	PRC2 methylates histones and DNA	24/162	41/10/723	4.1883E+34	1.30047E+32	3.70334E+33	24
310	Cells/Exosomes	R-HSA-73928	Depyrimidination	24/162	41/10/723	4.1883E+34	1.30047E+32	3.70334E+33	24
311	Cells/Exosomes	R-HSA-9710421	Defective pyroptosis	24/162	41/10/723	4.1883E+34	1.30047E+32	3.70334E+33	24
312	Cells/Exosomes	R-HSA-2299718	Condensation of Prophase Chromosomes	24/162	42/10/723	9.65155E+34	2.8541E+32	8.12762E+33	24
313	Cells/Exosomes	R-HSA-73929	Base-Excision Repair, AP Site Formation	43/10/723	215/10/723	6.8992E+32	1.74043E+32	1.74043E+32	43
314	Cells/Exosomes	R-HSA-427389	ERC6 (CSB) and EHM2 (9p) positively regulate rRNA expression	24/162	44/10/723	4.68703E+33	1.2655E+31	3.60376E+32	24
315	Cells/Exosomes	R-HSA-606279	Deposition of new PCNA-containing nucleosomes at the centromere	25/162	53/10/723	2.81376E+32	6.98938E+31	1.99036E+31	25
316	Cells/Exosomes	R-HSA-774815	Nucleosome assembly	25/162	53/10/723	2.81376E+32	6.98938E+31	1.99036E+31	25
317	Cells/Exosomes	R-HSA-967005	Inhibition of DNA recombination at telomere	24/162	45/10/723	4.13176E+32	9.7918E+31	2.8158E+31	24
318	Cells/Exosomes	R-HSA-977225	Amyloid fiber formation	28/162	78/10/723	6.00871E+32	1.382E+30	3.95353E+31	28
319	Cells/Exosomes	R-HSA-9645723	Diseases of programmed cell death	27/162	70/10/723	7.70712E+32	1.70933E+30	4.86766E+31	27
320	Cells/Exosomes	R-HSA-201681	TCF dependent signaling in response to WNT	38/162	199/10/723	9.6594E+32	2.06844E+30	5.89031E+31	38
321	Cells/Exosomes	R-HSA-259586	Sensence-Associated Secretory Phenotype (SASP)	28/162	80/10/723	2.15727E+31	2.89566E+29	8.23715E+30	28
322	Cells/Exosomes	R-HSA-157118	Signaling by NOTCH	38/162	203/10/723	2.12797E+31	4.26261E+30	1.21392E+30	38
323	Cells/Exosomes	R-HSA-1221632	Meiotic synapsis	25/162	59/10/723	8.74996E+31	1.59815E+29	4.55106E+30	25
324	Cells/Exosomes	R-HSA-3214815	HDMCs deacetylate histones	25/162	59/10/723	8.74996E+31	1.59815E+29	4.55106E+30	25
325	Cells/Exosomes	R-HSA-9609646	D-NHC1 complex positively regulates rRNA expression	25/162	59/10/723	8.74996E+31	1.59815E+29	4.55106E+30	25
326	Cells/Exosomes	R-HSA-259586	DNA Damage/Telomere Stress induced Senescence	25/162	59/10/723	8.74996E+31	1.59815E+29	4.55106E+30	25
327	Cells/Exosomes	R-HSA-912446	Meiotic recombination	24/162	54/10/723	3.29516E+30	5.63748E+29	1.60539E+29	24
328	Cells/Exosomes	R-HSA-5689880	Ub-specific processing proteases	37/162	202/10/723	3.35899E+30	5.63748E+29	1.60539E+29	37
329	Cells/Exosomes	R-HSA-9609646	Transcriptional regulation by RUNX1	37/162	202/10/723	3.35899E+30	5.63748E+29	1.60539E+29	37
330	Cells/Exosomes	R-HSA-69481	G2/M Checkpoints	33/162	149/10/723	8.49628E+30	1.35287E+28	3.85256E+29	33
331	Cells/Exosomes	R-HSA-259580	Oxidative Stress Induced Senescence	28/162	92/10/723	1.33314E+29	2.06699E+28	5.89386E+29	28
332	Cells/Exosomes	R-HSA-9616222	Transcriptional regulation of granulopoiesis	24/162	58/10/723	2.86709E+29	4.34351E+28	1.2369E+28	24
333	Cells/Exosomes	R-HSA-201272	Formation of the basic adenine(TCT) transactivating complex	24/162	58/10/723	4.77411E+29	6.89471E+28	1.9634E+28	24
334	Cells/Exosomes	R-HSA-73772	RNA Polymerase I Promoter Escape	24/162	59/10/723	4.77411E+29	6.89471E+28	1.9634E+28	24
335	Cells/Exosomes	R-HSA-1912408	Pre-NOTCH Transcription and Involvement	24/162	61/10/723	1.27944E+28	1.80576E+27	5.14225E+28	24
336	Cells/Exosomes	R-HSA-8936459	RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	24/162	65/10/723	1.83674E+28	1.1108E+26	3.16322E+27	24
337	Cells/Exosomes	R-HSA-9609646	Positive epigenetic regulation of rRNA expression	25/162	67/10/723	8.40701E+28	1.1108E+26	3.16322E+27	25
338	Cells/Exosomes	R-HSA-5578749	Transcriptional regulation by small RNAs	25/162	74/10/723	8.40701E+28	1.1108E+26	3.16322E+27	25
339	Cells/Exosomes	R-HSA-195721	Signaling by WNT	40/162	296/10/723	2.48846E+27	3.21944E+26	9.168E+27	40
340	Cells/Exosomes	R-HSA-5688426	Deubiquitination	39/162	279/10/723	3.38398E+27	4.2253E+26	1.20324E+26	39
341	Cells/Exosomes	R-HSA-9610379	HCMV Late Events	39/162	279/10/723	3.38398E+27	4.2253E+26	1.20324E+26	39
342	Cells/Exosomes	R-HSA-73884	Base Excision Repair	24/162	71/10/723	1.00688E+26	1.22603E+25	3.49136E+26	24
343	Cells/Exosomes	R-HSA-9646399	Aggregaphy	20/162	40/10/723	1.22867E+26	1.46732E+25	4.17884E+26	20
344	Cells/Exosomes	R-HSA-427413	NoRc1 negatively regulates rRNA expression	24/162	74/10/723	3.20793E+26	3.7826E+25	1.07024E+26	24
345	Cells/Exosomes	R-HSA-150620	Positive epigenetic regulation of rRNA expression	25/162	86/10/723	6.35579E+26	7.10915E+25	2.08130E+26	25
346	Cells/Exosomes	R-HSA-1912422	Pre-NOTCH Expression and Processing	24/162	77/10/723	9.64707E+26	1.06979E+24	3.04644E+25	24
347	Cells/Exosomes	R-HSA-5250941	Negative epigenetic regulation of rRNA expression	24/162	77/10/723	9.64707E+26	1.06979E+24	3.04644E+25	24
348	Cells/Exosomes	R-HSA-73854	RNA Polymerase I Promoter Clearance	24/162	78/10/723	1.37615E+25	1.49907E+24	4.26949E+25	24
349	Cells/Exosomes	R-HSA-73864	RNA Polymerase I Transcription	24/162	79/10/723	1.95208E+25	2.09007E+24	5.9519E+25	24
350	Cells/Exosomes	R-HSA-437329	Recycling pathway of L1	20/162	40/10/723	2.65114E+25	2.79044E+24	7.9463E+25	20
351	Cells/Exosomes	R-HSA-9018519	Estrogen-dependent gene expression	27/162	118/10/723	7.46507E+25	7.72188E+24	2.19896E+24	27
352	Cells/Exosomes	R-HSA-211000	Gene Silencing by RNA	26/162	106/10/723	8.33861E+25	8.48898E+24	2.41741E+24	26
353	Cells/Exosomes	R-HSA-69275	G2/M Transition	32/162	192/10/723	9.04078E+25	9.05537E+24	2.5787E+24	32
354	Cells/Exosomes	R-HSA-5689603	UCH1 proteases	24/162	38/10/723	1.02663E+24	1.01189E+24	2.89176E+24	24
355	Cells/Exosomes	R-HSA-3214847	HATS acetylate histones	26/162	107/10/723	1.08796E+24	1.05566E+23	3.00619E+24	26
356	Cells/Exosomes	R-HSA-453274	Mitotic G2-M/Phases	32/162	194/10/723	1.26703E+24	1.21051E+23	3.44715E+24	32
357	Cells/Exosomes</								

405	Cell&Exosomes	R-HSA-5693567	HDR through Homologous Recombination (HRR) or Single-Strand Annealing (SSA)	19/162	113/10723	4.35557E-15	2.37264E-14	6.75566E-15	19
406	Cell&Exosomes	R-HSA-2995410	Nuclear Envelope (NE) Reassembly	18/162	72/10723	6.91132E-15	3.73211E-14	1.06279E-14	16
407	Cell&Exosomes	R-HSA-4545911	Regulation of mRNA stability by proteins that bind AU-rich elements	17/162	66/10723	7.72908E-15	4.13436E-14	1.17732E-14	17
408	Cell&Exosomes	R-HSA-6811436	COP1-independent Golgi-to-ER retrograde traffic	14/162	49/10723	7.8247E-15	4.15311E-14	1.18226E-14	14
409	Cell&Exosomes	R-HSA-8852135	Protein ubiquitination	16/162	74/10723	1.10044E-14	5.79131E-14	1.64919E-14	16
410	Cell&Exosomes	R-HSA-5693538	Homology Directed Repair	19/162	119/10723	1.1739E-14	6.126E-14	1.7445E-14	19
411	Cell&Exosomes	R-HSA-702623	Glucocorticoids	12/162	40/10723	3.89376E-14	1.99721E-13	5.6875E-14	11
412	Cell&Exosomes	R-HSA-5362768	hh mutants are degraded by ERAD	14/162	55/10723	4.66641E-14	2.39491E-13	6.81998E-14	14
413	Cell&Exosomes	R-HSA-983189	Kinesins	14/162	57/10723	8.03597E-14	4.09044E-13	1.16483E-13	14
414	Cell&Exosomes	R-HSA-5387390	hh mutants abrogate ligand secretion	14/162	58/10723	1.04561E-13	5.27904E-13	1.50331E-13	14
415	Cell&Exosomes	R-HSA-567895	Defective CTR causes cystic fibrosis	14/162	60/10723	1.74226E-13	8.72572E-13	2.48017E-13	14
416	Cell&Exosomes	R-HSA-109581	Apoptosis	21/162	178/10723	2.155E-13	1.0634E-12	3.02824E-13	21
417	Cell&Exosomes	R-HSA-211733	Regulation of activated Pak-2/3/4 by proteasome mediated degradation	13/162	49/10723	2.15762E-13	1.0634E-12	3.02824E-13	13
418	Cell&Exosomes	R-HSA-390466	Chaperonin-mediated protein folding	16/162	89/10723	2.37799E-13	1.16273E-12	3.31111E-13	16
419	Cell&Exosomes	R-HSA-313064	Post-NMDA receptor activation events	15/162	76/10723	3.24976E-13	1.57692E-12	4.48973E-13	15
420	Cell&Exosomes	R-HSA-180534	Yvu mediated degradation of CD4	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
421	Cell&Exosomes	R-HSA-349425	Autodegradation of the E3 ubiquitin ligase COP1	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
422	Cell&Exosomes	R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
423	Cell&Exosomes	R-HSA-69610	p53-independent DNA damage response	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
424	Cell&Exosomes	R-HSA-69613	p53-independent G1/S DNA damage checkpoint	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
425	Cell&Exosomes	R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
426	Cell&Exosomes	R-HSA-5358346	Hedgehog ligand biogenesis	14/162	64/10723	4.56317E-13	2.09906E-12	5.97748E-13	14
427	Cell&Exosomes	R-HSA-5357801	Programmed Cell Death	22/162	207/10723	4.82527E-13	2.20336E-12	6.27441E-13	22
428	Cell&Exosomes	R-HSA-169911	Regulation of Apoptosis	13/162	52/10723	5.01783E-13	2.27451E-12	6.47711E-13	13
429	Cell&Exosomes	R-HSA-114608	Platelet degranulation	18/162	127/10723	5.13352E-13	2.30918E-12	6.57586E-13	18
430	Cell&Exosomes	R-HSA-180855	Vf-mediated degradation of APOBEC3G	13/162	53/10723	6.56268E-13	2.89037E-12	8.20391E-13	13
431	Cell&Exosomes	R-HSA-180856	FBX17 down-regulates AURKB during mitotic entry and in early mitosis	13/162	53/10723	6.56268E-13	2.89037E-12	8.20391E-13	13
432	Cell&Exosomes	R-HSA-9604323	Negative regulation of NOTCH4 signaling	13/162	53/10723	6.56268E-13	2.89037E-12	8.20391E-13	13
433	Cell&Exosomes	R-HSA-391251	Protein folding	16/162	95/10723	6.87877E-13	3.0083E-12	8.56672E-13	16
434	Cell&Exosomes	R-HSA-5693532	DNA Double-Strand Break Repair	19/162	148/10723	6.95694E-13	3.02116E-12	8.60336E-13	19
435	Cell&Exosomes	R-HSA-144113	SCF-based TRIP-mediated degradation of Em1	13/162	65/10723	8.53179E-13	3.6539E-12	1.04054E-12	13
436	Cell&Exosomes	R-HSA-4641257	Degradation of AXIN	13/162	54/10723	8.53179E-13	3.6539E-12	1.04054E-12	13
437	Cell&Exosomes	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	18/162	132/10723	1.0137E-12	4.31171E-12	1.22784E-12	18
438	Cell&Exosomes	R-HSA-4641258	Degradation of DVL	13/162	56/10723	1.41766E-12	5.90848E-12	1.68256E-12	13
439	Cell&Exosomes	R-HSA-69541	Stabilization of p53	13/162	56/10723	1.41766E-12	5.90848E-12	1.68256E-12	13
440	Cell&Exosomes	R-HSA-6953239	RDS sensing by NFE2L3	13/162	56/10723	1.41766E-12	5.90848E-12	1.68256E-12	13
441	Cell&Exosomes	R-HSA-70171	Glycolysis	14/162	71/10723	2.09566E-12	8.67601E-12	2.47067E-12	14
442	Cell&Exosomes	R-HSA-5676590	NIK--noncanonical NF-kB signaling	13/162	58/10723	2.30625E-12	9.42223E-12	2.68317E-12	13
443	Cell&Exosomes	R-HSA-68827	CDT1 association with the CDC20-ORC-origins complex	13/162	58/10723	2.30625E-12	9.42223E-12	2.68317E-12	13
444	Cell&Exosomes	R-HSA-5607651	Dectin-1 mediated noncanonical NF-kB signaling	13/162	58/10723	2.30625E-12	9.42223E-12	2.68317E-12	13
445	Cell&Exosomes	R-HSA-5610780	Degradation of GIL1 by the proteasome	13/162	59/10723	2.91977E-12	1.16229E-11	3.30986E-12	13
446	Cell&Exosomes	R-HSA-5610783	Degradation of GIL2 by the proteasome	13/162	59/10723	2.91977E-12	1.16229E-11	3.30986E-12	13
447	Cell&Exosomes	R-HSA-5610785	GIL1 is processed to GIL1B by the proteasome	13/162	59/10723	2.91977E-12	1.16229E-11	3.30986E-12	13
448	Cell&Exosomes	R-HSA-442355	Activation of NMDA receptor channels and postsynaptic events	15/162	88/10723	3.10833E-12	1.23868E-11	3.49891E-12	15
449	Cell&Exosomes	R-HSA-4086400	PCP/CE pathway	15/162	91/10723	5.16291E-12	2.02922E-11	5.77861E-12	15
450	Cell&Exosomes	R-HSA-5619084	ABC transporter disorders	14/162	76/10723	5.60652E-12	2.18972E-11	6.23566E-12	14
451	Cell&Exosomes	R-HSA-4608870	Asymmetric localization of PCP proteins	13/162	63/10723	7.16887E-12	2.78242E-11	7.92348E-12	13
452	Cell&Exosomes	R-HSA-1862909	Host Interaction of HIV/Ty1	13/162	63/10723	7.16887E-12	3.04031E-11	8.6794E-12	13
453	Cell&Exosomes	R-HSA-9707587	Regulation of HMOX1 expression and activity	13/162	64/10723	8.87799E-12	3.40336E-11	9.69374E-12	13
454	Cell&Exosomes	R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	13/162	65/10723	1.09564E-11	4.12358E-11	1.17427E-11	13
455	Cell&Exosomes	R-HSA-69563	p53-Dependent G1 DNA Damage Response	13/162	65/10723	1.09564E-11	4.12358E-11	1.17427E-11	13
456	Cell&Exosomes	R-HSA-69565	p53-Dependent G1/S DNA Damage checkpoint	13/162	65/10723	1.09564E-11	4.12358E-11	1.17427E-11	13
457	Cell&Exosomes	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	14/162	80/10723	1.16795E-11	4.36929E-11	1.24424E-11	14
458	Cell&Exosomes	R-HSA-1169091	Activation of NF-kappaB in B cells	13/162	66/10723	1.34674E-11	5.00793E-11	1.42611E-11	13
459	Cell&Exosomes	R-HSA-9013694	Signaling by NOTCH4	14/162	81/10723	1.93977E-11	5.15195E-11	1.46712E-11	14
460	Cell&Exosomes	R-HSA-174154	APC/Ccdc20 mediated degradation of Securin	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
461	Cell&Exosomes	R-HSA-5658442	Regulation of RAS by GAPs	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
462	Cell&Exosomes	R-HSA-68867	Assembly of the pre-replicative complex	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
463	Cell&Exosomes	R-HSA-69615	G1/S DNA Damage Checkpoints	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
464	Cell&Exosomes	R-HSA-691458	Regulation of RUNX3 expression and activity	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
465	Cell&Exosomes	R-HSA-5663220	RHO GTPase Activity Formins	17/162	136/10723	1.87576E-11	6.69452E-11	1.90644E-11	17
466	Cell&Exosomes	R-HSA-8948751	Regulation of PTEN stability and activity	13/162	68/10723	2.01282E-11	7.14265E-11	2.03401E-11	13
467	Cell&Exosomes	R-HSA-68849	Orcl removal from chromatin	13/162	70/10723	2.96747E-11	1.04704E-10	2.98166E-11	13
468	Cell&Exosomes	R-HSA-1832295	MHC class II antigen presentation	14/162	82/10723	3.18319E-11	1.11681E-10	3.18035E-11	14
469	Cell&Exosomes	R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	13/162	72/10723	4.31909E-11	1.49008E-10	4.24331E-11	13
470	Cell&Exosomes	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	13/162	72/10723	4.31909E-11	1.49008E-10	4.24331E-11	13
471	Cell&Exosomes	R-HSA-8939902	Regulation of RUNX2 expression and activity	13/162	72/10723	4.31909E-11	1.49008E-10	4.24331E-11	13
472	Cell&Exosomes	R-HSA-1832295	APC/C mediated degradation of Cdc20 and other APC/C/Dhl1 targeted proteins in late mitosis/early G1	13/162	73/10723	5.18984E-11	1.76983E-10	5.03994E-11	13
473	Cell&Exosomes	R-HSA-179419	APC/Ccdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	13/162	73/10723	5.18984E-11	1.76983E-10	5.03994E-11	13
474	Cell&Exosomes	R-HSA-187577	SCF(Skp2) mediated degradation of p27/cip1	12/162	59/10723	5.69085E-11	1.93116E-10	5.49935E-11	12
475	Cell&Exosomes	R-HSA-1234174	Cellular response to hypoxia	13/162	74/10723	6.21098E-11	2.09621E-10	5.96937E-11	13
476	Cell&Exosomes	R-HSA-71307	Metabolism of carbohydrates	23/162	91/10723	6.57812E-11	2.20811E-10	6.28004E-11	23
477	Cell&Exosomes	R-HSA-70326	Glucose metabolism	14/162	81/10723	7.36969E-11	2.39375E-10	6.81668E-11	14
478	Cell&Exosomes	R-HSA-176409	APC/Ccdc20 mediated degradation of mitotic proteins	13/162	75/10723	7.46133E-11	2.46279E-10	7.10318E-11	13
479	Cell&Exosomes	R-HSA-176814	Activation of APC/C and APC/Ccdc20 mediated degradation of mitotic proteins	13/162	76/10723	8.83075E-11	2.91697E-10	8.30664E-11	13
480	Cell&Exosomes	R-HSA-187183	Citium Assembly	19/162	198/10723	9.25244E-10	4.1448E-09	1.18121E-10	19
481	Cell&Exosomes	R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	12/162	63/10723	1.28767E-10	4.20844E-10	1.1985E-10	12
482	Cell&Exosomes	R-HSA-6811434	COP1-dependent Golgi-to-ER retrograde traffic	14/162	96/10723	1.505E-10	4.88003E-10	1.38968E-10	14
483	Cell&Exosomes	R-HSA-5673001	RAF/MAP kinase cascade	22/162	276/10723	1.5088E-10	4.88003E-10	1.38968E-10	22
484	Cell&Exosomes	R-HSA-179408	Regulation of APC/C activators between G1/S and early anaphase	13/162	80/10723	1.73972E-10	5.5369E-10	1.57674E-10	13
485	Cell&Exosomes	R-HSA-2871837	FcER1 mediated NF-kB activation	13/162	68/10723	1.73972E-10	5.5369E-10	1.57674E-10	13
486	Cell&Exosomes	R-HSA-6807878	COP1-mediated anterograde transport	14/162	98/10723	1.99929E-10	6.36697E-10	1.8132E-10	14
487	Cell&Exosomes	R-HSA-9711123	Cellular response to chemical stress	17/162	158/10723	2.09854E-10	6.64893E-10	1.89342E-10	17
488	Cell&Exosomes	R-HSA-5684959	MAPK1/MAPK3 signaling	22/162	282/10723	2.28521E-10	7.20363E-10	2.05139E-10	22
489	Cell&Exosomes	R-HSA-5620924	Intracellular transport	13/162	56/10723	2.3501E-10	7.38989E-10	2.04331E-10	13
490	Cell&Exosomes	R-HSA-195253	Degradation of beta-catenin by the destruction complex	13/162	82/10723	2.35858E-10	7.44		

540	Cell&Exosomes	R-HSA-351202	Metabolism of polyamines	9/162	58/10723	1.85513E07	4.62665E07	1.31753E07	9
541	Cell&Exosomes	R-HSA-449147	Signaling by Interleukins	23/162	446/10723	2.28235E07	5.60935E07	1.61446E07	23
542	Cell&Exosomes	R-HSA-901053	Regulation of expression of SUTs and RORs	14/162	170/10723	2.67443E07	6.16816E07	1.89247E07	14
543	Cell&Exosomes	R-HSA-6802946	Signaling by moderate kinase activity BRAF mutants	8/162	45/10723	3.06005E07	7.45212E07	1.21224E07	8
544	Cell&Exosomes	R-HSA-6802949	Signaling by RAS mutants	8/162	45/10723	3.06005E07	7.45212E07	1.21224E07	8
545	Cell&Exosomes	R-HSA-6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	8/162	45/10723	3.06005E07	7.45212E07	1.21224E07	8
546	Cell&Exosomes	R-HSA-6904948	Signaling downstream of RAS mutants	8/162	50/10723	3.06005E07	7.45212E07	1.21224E07	8
547	Cell&Exosomes	R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	15/162	199/10723	3.11762E07	7.58693E07	1.16053E07	15
548	Cell&Exosomes	R-HSA-112314	Neurotransmitter receptors and postsynaptic signal transduction	15/162	200/10723	3.33747E07	8.06447E07	2.29552E07	15
549	Cell&Exosomes	R-HSA-5619115	Disorders of transmembrane transporters	14/162	174/10723	3.56164E07	8.57299E07	2.44127E07	14
550	Cell&Exosomes	R-HSA-69206	G1/S transition	12/162	130/10723	5.8155E07	1.20437E06	3.97075E07	12
551	Cell&Exosomes	R-HSA-948021	Transport to the Golgi and subsequent modification	14/162	182/10723	6.16913E07	1.47347E06	4.19601E07	14
552	Cell&Exosomes	R-HSA-3371571	HSP1-dependent transactivation	6/162	23/10723	8.84423E07	2.10432E06	5.99246E07	6
553	Cell&Exosomes	R-HSA-69242	SPhase	13/162	161/10723	9.11665E07	2.16086E06	6.15347E07	13
554	Cell&Exosomes	R-HSA-892491	Glycogen metabolism	6/162	26/10723	1.94239E06	4.58751E06	1.30634E06	6
555	Cell&Exosomes	R-HSA-9656223	Signaling by RAF1 mutants	7/162	41/10723	2.30318E06	5.41771E06	1.5428E06	7
556	Cell&Exosomes	R-HSA-453279	Mitotic G1 phase and G1/S transition	12/162	148/10723	2.32871E06	5.4571E06	1.55402E06	12
557	Cell&Exosomes	R-HSA-112315	Transmission across Chemical Synapses	18/162	265/10723	2.48302E06	5.69178E06	1.62085E06	18
558	Cell&Exosomes	R-HSA-2159400	Involvement of tyrosine phosphorylation in cell cycle	9/162	80/10723	3.04223E06	7.07579E06	2.01497E06	9
559	Cell&Exosomes	R-HSA-6802952	Signaling by BRAF and RAF fusion	8/162	65/10723	5.54646E06	1.28521E05	3.65898E06	8
560	Cell&Exosomes	R-HSA-380259	Loss of Nip from mitotic centrosomes	8/162	69/10723	8.72998E06	2.0079E05	5.71788E06	8
561	Cell&Exosomes	R-HSA-380284	Loss of proteins required for interphase microtubule organization from the centrosome	8/162	69/10723	8.72998E06	2.0079E05	5.71788E06	8
562	Cell&Exosomes	R-HSA-1159408	ISC15 antiviral mechanism	8/162	72/10723	1.20263E05	2.74571E05	7.81897E06	8
563	Cell&Exosomes	R-HSA-8854518	AURKA Activation by TPX2	8/162	72/10723	1.20263E05	2.74571E05	7.81897E06	8
564	Cell&Exosomes	R-HSA-9662361	Sensory processing of sound by outer hair cells of the cochlea	7/162	54/10723	1.5388E05	3.50036E05	9.96796E06	7
565	Cell&Exosomes	R-HSA-8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	6/162	37/10723	1.70984E05	3.87522E05	1.10354E05	6
566	Cell&Exosomes	R-HSA-8866552	Budding and G2/M phase cycle	5/162	30/10723	1.99797E05	4.51114E05	1.28464E05	5
567	Cell&Exosomes	R-HSA-380270	Recruitment of mitotic centrosome proteins and complexes	8/162	81/10723	2.88076E05	6.45831E05	1.83913E05	8
568	Cell&Exosomes	R-HSA-380287	Centrosome maturation	8/162	81/10723	2.88076E05	6.45831E05	1.83913E05	8
569	Cell&Exosomes	R-HSA-1643713	Signaling by EGFR in Cancer	5/162	25/10723	3.0781E05	6.87591E05	1.9805E05	5
570	Cell&Exosomes	R-HSA-6802957	Oncogenic MAPK signaling	5/162	82/10723	3.15109E05	7.0155E05	1.9978E05	5
571	Cell&Exosomes	R-HSA-5675212	Negative regulation of MAPK pathway	6/162	43/10723	4.16051E05	9.22742E05	2.62769E05	6
572	Cell&Exosomes	R-HSA-5628897	TP53 Regulates Metabolic Genes	8/162	87/10723	4.84764E05	0.000107131	3.05077E05	8
573	Cell&Exosomes	R-HSA-8951664	Neddylation	13/162	232/10723	4.87921E05	0.000107446	3.05975E05	13
574	Cell&Exosomes	R-HSA-162588	Budding and maturation of HIV virion	5/162	28/10723	5.48912E05	0.00012045	3.43006E05	5
575	Cell&Exosomes	R-HSA-902051	Interleukin-12 signaling	6/162	60/10723	6.15787E05	0.000134648	3.83436E05	6
576	Cell&Exosomes	R-HSA-5213460	RIPI1-mediated regulated necrosis	5/162	29/10723	6.55225E05	0.000141775	4.07333E05	5
577	Cell&Exosomes	R-HSA-5675482	Regulation of necrotic cell death	5/162	29/10723	6.55225E05	0.000141775	4.07333E05	5
578	Cell&Exosomes	R-HSA-8863795	Downregulation of ERBB2 signaling	5/162	29/10723	6.55225E05	0.000141775	4.07333E05	5
579	Cell&Exosomes	R-HSA-886380	Citric acid metabolism	10/162	145/10723	6.72147E05	0.000149812	4.16426E05	10
580	Cell&Exosomes	R-HSA-3371453	Regulation of HSP1-mediated heat shock response	7/162	68/10723	7.05678E05	0.000151635	4.31812E05	7
581	Cell&Exosomes	R-HSA-114452	Synthesis of BHA-oligomers	5/162	30/10723	7.76738E05	0.000165757	4.70272E05	5
582	Cell&Exosomes	R-HSA-8866552	Activation of active ubiquitin: roles of E1 and E2 enzymes	5/162	30/10723	7.76738E05	0.000165757	4.70272E05	5
583	Cell&Exosomes	R-HSA-5620912	Anchoring of the basal body to the plasma membrane	6/162	70/10723	0.000166483	0.000214446	6.39155E05	6
584	Cell&Exosomes	R-HSA-9659379	Sensory processing of sound	7/162	76/10723	0.000143852	0.000304888	8.8229E05	7
585	Cell&Exosomes	R-HSA-9615710	Late endosomal microautophagy	5/162	34/10723	0.000144448	0.00030511	8.88862E05	5
586	Cell&Exosomes	R-HSA-532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	5/162	35/10723	0.000166483	0.000349277	9.94363E05	5
587	Cell&Exosomes	R-HSA-9705574	RHOBTB GTPase Cyt1	5/162	26/10723	0.000166483	0.000349277	9.94363E05	5
588	Cell&Exosomes	R-HSA-1257604	PIP3 activates Akt signaling	13/162	365/10723	0.000166874	0.000390736	0.00011127	13
589	Cell&Exosomes	R-HSA-447115	Interleukin-12 family signaling	6/162	56/10723	0.000188474	0.00039276	0.000111846	6
590	Cell&Exosomes	R-HSA-8876384	Listeria monocytogenes entry into host cells	4/162	20/10723	0.000201357	0.000418204	0.000119092	4
591	Cell&Exosomes	R-HSA-445355	Smooth Muscle Contraction	7/162	70/10723	0.000218819	0.000450069	0.000123454	7
592	Cell&Exosomes	R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	14/162	306/10723	0.00021845	0.00045069	0.000128343	14
593	Cell&Exosomes	R-HSA-4641263	Regulation of F2D by ubiquitination	4/162	21/10723	0.000245823	0.000502158	0.000142999	4
594	Cell&Exosomes	R-HSA-6807004	Negative regulation of MET activity	4/162	21/10723	0.000245823	0.000502158	0.000142999	4
595	Cell&Exosomes	R-HSA-9010512	ER Quality Control Compartment (ERQC)	5/162	38/10723	0.000248184	0.000503668	0.000143443	5
596	Cell&Exosomes	R-HSA-5689896	Ovarian Tumor domain proteases	5/162	38/10723	0.000248184	0.000503668	0.000143443	5
597	Cell&Exosomes	R-HSA-5696394	DNA Damage Recognition in GG-NER	5/162	38/10723	0.000248184	0.000503668	0.000143443	5
598	Cell&Exosomes	R-HSA-110313	Transduction Synthesis by Y Family DNA polymerases bypasses lesions on DNA template	5/162	39/10723	0.000282124	0.000568893	0.000162004	5
599	Cell&Exosomes	R-HSA-9659379	CIITA Activation and Transcription of Signal to the Nucleus	5/162	39/10723	0.000282124	0.000568893	0.000162004	5
600	Cell&Exosomes	R-HSA-450321	INK (I- $\kappa$ B kinase) phosphorylation and activation mediated by activated human TAK1	4/162	22/10723	0.000286933	0.000592911	0.000168843	4
601	Cell&Exosomes	R-HSA-5205685	PINK1-PRKN Mediated Mitophagy	4/162	22/10723	0.000286933	0.000592911	0.000168843	4
602	Cell&Exosomes	R-HSA-912631	Regulation of signaling by CB1	4/162	22/10723	0.000286933	0.000592911	0.000168843	4
603	Cell&Exosomes	R-HSA-201482	Regulation of actin dynamics for phagocytic cup formation	4/162	23/10723	0.0002894	0.000623854	0.000171686	4
604	Cell&Exosomes	R-HSA-2173795	Downregulation of SMAD2/3/SMAD4 transcriptional activity	4/162	23/10723	0.0003524	0.000700329	0.000194333	4
605	Cell&Exosomes	R-HSA-450302	activated TAK1 mediates p38 MAPK activation	4/162	23/10723	0.0003524	0.000700329	0.000194333	4
606	Cell&Exosomes	R-HSA-937041	IKK complex recruitment mediated by RIP1	4/162	23/10723	0.0003524	0.000700329	0.000194333	4
607	Cell&Exosomes	R-HSA-9659379	Deactivation of the beta-catenin transactivating complex	5/162	40/10723	0.000406645	0.00073744	0.00024212	5
608	Cell&Exosomes	R-HSA-112316	Neuronal System	16/162	400/10723	0.000409235	0.000801687	0.000228256	16
609	Cell&Exosomes	R-HSA-174048	APC/Ccdc20 mediated degradation of Cyclin B	4/162	24/10723	0.000421302	0.000820152	0.000233555	4
610	Cell&Exosomes	R-HSA-9648002	RAS processing	4/162	24/10723	0.000421302	0.000820152	0.000233555	4
611	Cell&Exosomes	R-HSA-5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	4/162	25/10723	0.000456687	0.00095968	0.000272231	4
612	Cell&Exosomes	R-HSA-9013507	NOTCH3 Activation and Transduction of Signal to the Nucleus	4/162	25/10723	0.000456687	0.00095968	0.000272231	4
613	Cell&Exosomes	R-HSA-9705462	Inactivation of CSF3 (G-CSF) signaling	4/162	25/10723	0.000456687	0.00095968	0.000272231	4
614	Cell&Exosomes	R-HSA-156842	Eukaryotic Translation Elongation	7/162	93/10723	0.000503201	0.000967455	0.000275502	7
615	Cell&Exosomes	R-HSA-893169	Class I MHC mediated antigen processing & presentation	15/162	374/10723	0.000523563	0.00103727	0.000296672	15
616	Cell&Exosomes	R-HSA-179409	APC-Cdc20 mediated degradation of Nek2A	4/162	26/10723	0.000578967	0.01099506	0.000311006	4
617	Cell&Exosomes	R-HSA-2173788	Downregulation of TGF-beta receptor signaling	4/162	26/10723	0.000578967	0.01099506	0.000311006	4
618	Cell&Exosomes	R-HSA-901042	Calnexin/Calreticulin cycle	4/162	26/10723	0.000578967	0.01099506	0.000311006	4
619	Cell&Exosomes	R-HSA-9662360	Sensory processing of sound by inner hair cells of the cochlea	6/162	69/10723	0.000592917	0.01111164	0.000319274	6
620	Cell&Exosomes	R-HSA-9006925	Intracellular signaling by second messengers	6/162	69/10723	0.000718919	0.001356987	0.000346429	6
621	Cell&Exosomes	R-HSA-512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	5/162	48/10723	0.000749808	0.01406739	0.000400597	5
622	Cell&Exosomes	R-HSA-73893	DNA Damage Bypass	5/162	48/10723	0.000749808	0.01406739	0.000400597	5
623	Cell&Exosomes	R-HSA-9682285	FLT3 signaling in disease	4/162	28/10723	0.000774524	0.01444382	0.00041316	4
624	Cell&Exosomes	R-HSA-9683701	Translocation of structural proteins	4/162	28/10723	0.000774524	0.01444382	0.00041316	4
625	Cell&Exosomes	R-HSA-5205647	Mitophagy	4/162	29/10723	0.000887964	0.01646046	0.000468744	4
626	Cell&Exosomes	R-HSA-5654732	Negative regulation of FGF3 signaling	4/162	29/10723	0.000887964	0.01646046	0.000468744	4
627	Cell&Exosomes	R-HSA-1227986	Signaling by ERBB2	5/162	50/10723	0.000995568	0		

675	Cell&Exosomes	R-HSA-2173793	Transcriptional activity of SMAD3/SMAD3:SMAD4 heterotrimer	4/162	44/10/723	0.004258758	0.006851526	0.001951108	4
676	Cell&Exosomes	R-HSA-75893	TNF signaling	4/162	44/10/723	0.004258758	0.006851526	0.001951108	4
677	Cell&Exosomes	R-HSA-969435	Translation of structural proteins	4/162	44/10/723	0.004258758	0.006851526	0.001951108	4
678	Cell&Exosomes	R-HSA-373753	Nephrin family interactions	3/162	23/10/723	0.00480095	0.00770385	0.00213824	3
679	Cell&Exosomes	R-HSA-69231	Cyclin D associated events in G1	4/162	47/10/723	0.005403573	0.008626269	0.002456502	4
680	Cell&Exosomes	R-HSA-69236	G1 Phase	4/162	47/10/723	0.005403573	0.008626269	0.002456502	4
681	Cell&Exosomes	R-HSA-204958	Cell death signaling via NLRP6, NLRP1 and NADe	5/162	50/10/723	0.005769384	0.00917517	0.001616328	5
682	Cell&Exosomes	R-HSA-2122947	NOTCH1 Intracellular Domain Regulates Transcription	4/162	48/10/723	0.005826642	0.009254079	0.002635283	4
683	Cell&Exosomes	R-HSA-9012852	Signaling by NOTCH3	4/162	49/10/723	0.006271237	0.009934791	0.002829129	4
684	Cell&Exosomes	R-HSA-177929	Signaling by EGFR	4/162	50/10/723	0.006737817	0.010619757	0.003024187	4
685	Cell&Exosomes	R-HSA-5649736	Signaling by FGFR1	4/162	50/10/723	0.006737817	0.010619757	0.003024187	4
686	Cell&Exosomes	R-HSA-354152	Integrin signaling	3/162	27/10/723	0.007587431	0.011928595	0.003396905	3
687	Cell&Exosomes	R-HSA-6781823	Formation of TC-NER Pre-Incision Complex	4/162	53/10/723	0.008273896	0.012974974	0.003694882	4
688	Cell&Exosomes	R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	5/162	84/10/723	0.008795973	0.013702002	0.003901918	5
689	Cell&Exosomes	R-HSA-8840221	Signaling by PKK6	4/162	54/10/723	0.008832788	0.013747272	0.003914809	4
690	Cell&Exosomes	R-HSA-9006527	Signaling by Non-Receptor Tyrosine Kinases	4/162	54/10/723	0.008832788	0.013747272	0.003914809	4
691	Cell&Exosomes	R-HSA-397014	Muscle contraction	8/162	194/10/723	0.009191918	0.014270453	0.004063795	8
692	Cell&Exosomes	R-HSA-5339562	Uptake and actions of bacterial toxins	3/162	29/10/723	0.009272328	0.014393991	0.004089122	3
693	Cell&Exosomes	R-HSA-2644603	Constitutive Signaling by NOTCH1 PEST Domain Mutants	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
694	Cell&Exosomes	R-HSA-1236394	Signaling by ERBB4	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
695	Cell&Exosomes	R-HSA-2644602	Signaling by NOTCH1 PEST Domain Mutants in Cancer	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
696	Cell&Exosomes	R-HSA-2644603	Signaling by NOTCH1 in Cancer	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
697	Cell&Exosomes	R-HSA-2644606	Constitutive Signaling by NOTCH1 PEST Domain Mutants	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
698	Cell&Exosomes	R-HSA-2894858	Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
699	Cell&Exosomes	R-HSA-2894862	Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
700	Cell&Exosomes	R-HSA-72649	Translation initiation complex formation	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
701	Cell&Exosomes	R-HSA-72702	Ribosomal scanning and start codon recognition	4/162	58/10/723	0.011133314	0.017135531	0.004879683	4
702	Cell&Exosomes	R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	4/162	59/10/723	0.01199654	0.018126159	0.005161984	4
703	Cell&Exosomes	R-HSA-2682334	Eph-Ephrin signaling	5/162	91/10/723	0.012135288	0.018247007	0.005196198	5
704	Cell&Exosomes	R-HSA-446728	Cell junction organization	5/162	91/10/723	0.012135288	0.018247007	0.005196198	5
705	Cell&Exosomes	R-HSA-72756	Translation	10/162	291/10/723	0.012848654	0.019270262	0.005497596	10
706	Cell&Exosomes	R-HSA-180746	Nuclear import of Rev protein	3/162	33/10/723	0.013250741	0.019828217	0.005646479	3
707	Cell&Exosomes	R-HSA-1834949	Cytosolic sensors of pathogen-associated DNA	4/162	63/10/723	0.014992014	0.022326236	0.006357844	4
708	Cell&Exosomes	R-HSA-450294	MAP kinase activation	4/162	63/10/723	0.014992014	0.022326236	0.006357844	4
709	Cell&Exosomes	R-HSA-193704	p75 NTR receptor-mediated signalling	5/162	97/10/723	0.015653273	0.023528193	0.006623213	5
710	Cell&Exosomes	R-HSA-6782110	Cap-filling DNA repair synthesis and ligation in TC-NER	4/162	60/10/723	0.015800862	0.023429133	0.006671912	4
711	Cell&Exosomes	R-HSA-6782135	Dual incision in TC-NER	4/162	65/10/723	0.016651553	0.02456203	0.006994527	4
712	Cell&Exosomes	R-HSA-9614085	FOXO-mediated transcription	4/162	65/10/723	0.016651553	0.02456203	0.006994527	4
713	Cell&Exosomes	R-HSA-177243	Interactions of Rev with host cellular proteins	3/162	36/10/723	0.016780755	0.024635547	0.007015462	3
714	Cell&Exosomes	R-HSA-39952	Striated Muscle Contraction	4/162	66/10/723	0.016780755	0.024635547	0.007015462	4
715	Cell&Exosomes	R-HSA-5685942	HDR through Homologous Recombination (HRR)	4/162	66/10/723	0.017522749	0.025664214	0.007308396	4
716	Cell&Exosomes	R-HSA-3299685	Detoxification of Reactive Oxygen Species	3/162	37/10/723	0.018063006	0.026393239	0.007516	3
717	Cell&Exosomes	R-HSA-162599	Late Phase of HIV Life Cycle	6/162	138/10/723	0.018183878	0.026507483	0.007548533	6
718	Cell&Exosomes	R-HSA-409253	Circadian Clock	4/162	60/10/723	0.020034983	0.026959213	0.008409316	4
719	Cell&Exosomes	R-HSA-76009	Platelet Aggregation (Plug Formation)	3/162	39/10/723	0.020786967	0.030160529	0.008588111	3
720	Cell&Exosomes	R-HSA-448424	Interleukin-17 signaling	4/162	71/10/723	0.022302576	0.032284149	0.009193554	4
721	Cell&Exosomes	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	3/162	41/10/723	0.023723991	0.034261857	0.009756745	3
722	Cell&Exosomes	R-HSA-170834	Signaling by TGF-beta Receptor Complex	4/162	72/10/723	0.02441618	0.035098229	0.009994927	4
723	Cell&Exosomes	R-HSA-5654738	Signaling by FGFR2	4/162	73/10/723	0.02441618	0.035098229	0.009994927	4
724	Cell&Exosomes	R-HSA-3928662	EPHB-mediated forward signaling	3/162	42/10/723	0.025272431	0.038616704	0.010297765	3
725	Cell&Exosomes	R-HSA-9035034	RHO GTPase cycle	3/162	42/10/723	0.025272431	0.038616704	0.010297765	3
726	Cell&Exosomes	R-HSA-9035034	Nucleotide Excision Repair	4/162	110/10/723	0.025474304	0.038634084	0.010349688	4
727	Cell&Exosomes	R-HSA-1980143	Signaling by NOTCH1	4/162	74/10/723	0.025516913	0.038634084	0.010349688	4
728	Cell&Exosomes	R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	5/162	111/10/723	0.026361575	0.037461186	0.010667818	5
729	Cell&Exosomes	R-HSA-162587	HIV Life Cycle	6/162	151/10/723	0.026990809	0.03811247	0.010864327	6
730	Cell&Exosomes	R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	4/162	112/10/723	0.027183689	0.038573291	0.010981523	4
731	Cell&Exosomes	R-HSA-6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	4/162	78/10/723	0.030216014	0.042645783	0.012144325	4
732	Cell&Exosomes	R-HSA-72613	Eukaryotic Translation Initiation	5/162	119/10/723	0.034173064	0.048012382	0.013672481	5
733	Cell&Exosomes	R-HSA-72737	Cap-dependent Translation Initiation	5/162	119/10/723	0.034173064	0.048012382	0.013672481	5
734	Cell&Exosomes	R-HSA-300278	ECM proteoglycans	13/89	50/10/723	7.5159646E-12	1.162868E-11	7.33773E-12	13
735	Exosomes	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by insulin-like Growth Factor Binding Proteins (IGFBPs)	21/89	125/10/723	2.9708E-22	2.49547E-20	1.45413E-20	21
736	Exosomes	R-HSA-8957275	Post-translational protein phosphorylation	19/89	108/10/723	1.40559E-20	7.8711E-19	4.58666E-19	19
737	Exosomes	R-HSA-1474244	Extracellular matrix organization	25/89	300/10/723	9.1732E-19	3.85274E-17	2.4502E-17	25
738	Exosomes	R-HSA-147424	Integrin cell surface interactions	16/89	65/10/723	6.48991E-16	3.1898E-15	1.2064E-16	16
739	Exosomes	R-HSA-3000171	Non-integrin membrane-ECM interactions	14/89	59/10/723	2.49928E-17	6.95979E-16	4.07778E-16	14
740	Exosomes	R-HSA-114608	Platelet degradation	17/89	127/10/723	2.18917E-16	5.278E-15	3.07553E-15	17
741	Exosomes	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	17/89	132/10/723	4.2922E-16	9.01367E-15	5.25232E-15	17
742	Exosomes	R-HSA-76002	Platelet activation, signaling and aggregation	20/89	261/10/723	2.77863E-14	4.24851E-13	2.47851E-14	20
743	Exosomes	R-HSA-977606	Regulation of Complement cascade	11/89	48/10/723	7.17377E-14	1.20519E-12	7.02274E-13	11
744	Exosomes	R-HSA-166658	Complement cascade	11/89	57/10/723	9.21598E-13	1.40753E-11	8.20178E-12	11
745	Exosomes	R-HSA-8874081	MET activates PI3K signaling	9/89	30/10/723	1.53239E-12	2.44661E-11	1.25084E-11	9
746	Exosomes	R-HSA-147428	Degradation of the extracellular matrix	14/89	139/10/723	6.49915E-12	8.3098E-11	4.4841E-11	14
747	Exosomes	R-HSA-140877	Formation of Fibrin Clot (Clotting Cascade)	9/89	39/10/723	2.13731E-11	2.56477E-10	1.49451E-10	9
748	Exosomes	R-HSA-3000170	Syndecan interactions	8/89	27/10/723	3.1902E-11	3.57030E-10	2.08203E-10	8
749	Exosomes	R-HSA-88875878	MET promotes cell motility	9/89	41/10/723	3.4861E-11	3.66041E-10	2.13294E-10	9
750	Exosomes	R-HSA-162595	Common Pathway of Fibrin Clot Formation	22/89	22/10/723	3.2912E-10	3.2520E-09	1.89537E-09	22
751	Exosomes	R-HSA-6806534	Signaling by MET	10/89	79/10/723	8.34693E-10	7.79046E-09	4.53956E-09	10
752	Exosomes	R-HSA-186797	Signaling by PDGF	9/89	58/10/723	9.44796E-10	8.35398E-09	4.86792E-09	9
753	Exosomes	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	8/89	41/10/723	1.24934E-09	1.04945E-08	6.11521E-09	8
754	Exosomes	R-HSA-975634	Retinoid metabolism and transport	8/89	43/10/723	1.87067E-09	1.94654E-08	8.70242E-09	8
755	Exosomes	R-HSA-8948216	Collagen chain trimerization	8/89	40/10/723	2.7101E-09	1.78423E-08	1.01055E-08	8
756	Exosomes	R-HSA-6806667	Metabolism of fat-soluble vitamins	8/89	47/10/723	3.9487E-09	2.88427E-08	1.68088E-08	8
757	Exosomes	R-HSA-140837	Intrinsic Pathway of Fibrin Clot Formation	6/89	23/10/723	2.48451E-08	1.73916E-07	1.01342E-07	6
758	Exosomes	R-HSA-2022090	Assembly of collagen fibrils and other multimeric structures	8/89	61/10/723	3.64844E-08	2.26118E-07	1.3170E-07	8
759	Exosomes	R-HSA-1442490	Collagen degradation	8/89	64/10/723	4.9562E-08	3.20248E-07	1.89611E-07	8
760	Exosomes	R-HSA-1650814	Collagen biosynthesis and modifying enzymes	8/89	67/10/723	7.15723E-08	4.45339E-07	2.59502E-07	8
761	Exosomes	R-HSA-8963899	Plasma lipoprotein remodeling	8/89	30/10/723	1.39491E-07	8.36945E-07	4.87693E-07	8
762	Exosomes	R-HSA-1474290	Collagen formation	8/89	90/10/723	7.28459E-07	4.2		