	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	181/10723	2.53062E-51	1.23494E-48	8.00476E-49	96
3	Cells	R-HSA-72172	mRNA Splicing	96/1008	189/10723	4.22204E-49	1.37357E-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	3.04194E-45	107
5	Cells	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	81/1008	170/10723	8.15164E-39	1.5912E-36	1.0314E-36	81
6	Cells	R-HSA-376176	Signaling by ROBO receptors	89/1008	216/10723	2.40292E-36	3.90876E-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-72706	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-156827	L13a-mediated translational silencing of Ceruloplasmin expression	61/1008	111/10723	5.01135E-34	4.89108E-32	3.17034E-32	61
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-72764	Eukaryotic Translation Termination	55/1008	93/10723	4.52228E-33	3.15268E-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	5.11439E-29	3.31509E-29	53
18	Cells	R-HSA-1799339	SRP-dependent cotranslational protein targeting to membrane	58/1008	112/10723	1.55374E-30	8.42474E-29	5.46082E-29	58
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	5.43576E-28	3.52339E-28	52
22	Cells	R-HSA-2408522	Selenoamino acid metabolism	58/1008	117/10723	3.28308E-29	1.45649E-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	7.76179E-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-1428517	The citric acid (TCA) cycle and respiratory electron transport	64/1008	178/10723	1.68441E-22	6.32301E-21	4.0985E-21	64
27	Cells	R-HSA-8868773	rRNA processing in the nucleus and cytosol	65/1008	192/10723	3.36417E-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-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	61/1008	182/10723	1.03213E-19	3.35785E-18	2.17652E-18	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-72649	Translation initiation complex formation	30/1008	58/10723	2.28747E-16	6.20159E-15	4.01979E-15	30
36	Cells	R-HSA-72702	Ribosomal scanning and start codon recognition	30/1008	58/10723	2.28747E-16	6.20159E-15	4.01979E-15	30
37	Cells	R-HSA-6798695	Neutrophil degranulation	100/1008	474/10723	2.70259E-15	7.12899E-14	4.62093E-14	100
38	Cells	R-HSA-72187	mRNA 3'-end processing	28/1008	57/10723	1.28811E-14	3.3084E-13	2.14447E-13	28
39	Cells	R-HSA-5389840	Mitochondrial translation elongation	34/1008	87/10723	9.00339E-14	2.25316E-12	1.46047E-12	34
40	Cells	R-HSA-5368287	Mitochondrial translation	35/1008	93/10723	1.47174E-13	3.59103E-12	2.32767E-12	35
41	Cells	R-HSA-611105	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	33/1008	87/10723	5.66762E-13	1.28642E-11	8.3384E-12	33
44	Cells	R-HSA-5368286	Mitochondrial translation initiation	32/1008	87/10723	3.39811E-12	7.53763E-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	1.60596E-09	1.04096E-09	30
47	Cells	R-HSA-8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	19/1008	37/10723	8.968555E-11	1.86241E-09	1.20719E-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	2.01114E-10	3.92575E-09	2.54463E-09	54
51	Cells	R-HSA-72165	mRNA Splicing - Minor Pathway	22/1008	52/10723	3.55149E-10	6.79658E-09	4.40546E-09	22
52	Cells	R-HSA-72202	Transport of Mature Transcript to Cytoplasm	28/1008	82/10723	5.73537E-10	1.07649E-08	6.97765E-09	28
53	Cells	R-HSA-9020591	Interleukin-12 signaling	20/1008	46/10723	1.2587E-09	2.31791E-08	1.50244E-08	20
54	Cells	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	27/1008	80/10723	1.56622E-09	2.8308E-08	1.83489E-08	27
55	Cells	R-HSA-8932339	ROS sensing by NFE2L2	22/1008	56/10723	1.94749E-09	3.4559E-08	2.24007E-08	22
56	Cells	R-HSA-9609507	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	3.07585E-09	5.26673E-08	3.41383E-08	14
58	Cells	R-HSA-180585	Vif-mediated degradation of APOBEC3G	21/1008	53/10723	3.78305E-09	6.36595E-08	4.12634E-08	21
59	Cells	R-HSA-109581	Apoptosis	43/1008	178/10723	4.36398E-09	7.21906E-08	4.67931E-08	43
60	Cells	R-HSA-162909	Host Interactions of HIV factors	35/1008	129/10723	4.87027E-09	7.92231E-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-5357801	Programmed Cell Death	47/1008	207/10723	7.15771E-09	1.12676E-07	7.30353E-08	47
63	Cells	R-HSA-180534	Vpu mediated degradation of CD4	20/1008	51/10723	1.10077E-08	1.70532E-07	1.10537E-07	20
64	Cells	R-HSA-447115	Interleukin-12 family signaling	21/1008	56/10723	1.21686E-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	2.14141E-08	3.16669E-07	2.05261E-07	19
67	Cells	R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	20/1008	53/10723	2.39227E-08	3.4336E-07	2.22562E-07	20
68	Cells	R-HSA-9604323	Negative regulation of NOTCH4 signaling	20/1008	53/10723	2.39227E-08	3.4336E-07	2.22562E-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-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	19/1008	49/10723	3.19228E-08	4.38826E-07	2.84442E-07	19
72	Cells	R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	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-350562	Regulation of ornithine decarboxylase (ODC)	19/1008	50/10723	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	7.9733E-07	5.1682E-07	25
79	Cells	R-HSA-349425	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-69601	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-75815	Ubiquitin-dependent degradation of Cyclin D	19/1008	51/10723	6.83613E-08	8.03863E-07	5.21054E-07	19
84	Cells	R-HSA-5687128	MAPK6/MAPK4 signaling	26/1008	88/10723	7.10315E-08	8.25319E-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	1.11328E-06	7.21614E-07	19
87	Cells	R-HSA-6799198	Complex I biogenesis	20/1008	57/10723	9.9237E-08	1.11328E-06	7.21614E-07	20
88	Cells	R-HSA-71403	Citric acid cycle (TCA cycle)	12/1008	22/10723	1.18487E-07	1.31413E-06	8.51803E-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	NIK-->noncanonical NF-kB signaling	20/1008	58/10723	1.38234E-07	1.48259E-06	9.60999E-07	20
92	Cells	R-HSA-5607764	CLEC7A (Dectin-1) signaling	27/1008	97/10723	1.56649E-07	1.66185E-06	1.07719E-06	27
93	Cells	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	29/1008	109/10723	1.60395E-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(Skp2)-mediated degradation of p27/p21	20/1008	59/10723	1.90856E-07	1.88157E-06	1.21961E-06	20
96	Cells	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB 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	54/10723	1.97023E-07	1.92294E-06	1.24643E-06	19
101	Cells	R-HSA-68886	M Phase	67/1008	379/10723	2.31952E-07	2.24143E-06	1.45287E-06	67
102	Cells	R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	21/1008	65/10723	2.40602E-07	2.30223E-06	1.49228E-06	21
103	Cells	R-HSA-5678895	Defective CFTR causes cystic fibrosis	20/1008	60/10723	2.61283E-07	2.46666E-06	1.59886E-06	20
104	Cells	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	32/1008	130/10723	2.62841E-07	2.46666E-06	1.59886E-06	32
105	Cells	R-HSA-4641258	Degradation of DVL	19/1008	56/10723	3.79613E-07	3.49531E-06	2.26562E-06	19
106	Cells	R-HSA-69541	Stabilization of p53	19/1008	56/10723	3.79613E-07	3.49531E-06	2.26562E-06	19
107	Cells	R-HSA-379724	tRNA Aminoacylation	16/1008	42/10723	5.22493E-07	4.76591E-06	3.08921E-06	16
108	Cells	R-HSA-68882	Mitotic Anaphase	46/1008	230/10723	5.687E-07	5.13936E-06	3.33127E-06	46
109	Cells	R-HSA-2555396	Mitotic Metaphase and Anaphase	46/1008	231/10723	6.47231E-07	5.79539E-06	3.7565E-06	46
110	Cells	R-HSA-68827	CDT1 association with the CDC6:ORC:origin complex	19/1008	58/10723	7.05693E-07	6.26143E-06	4.05858E-06	19
111	Cells	R-HSA-1236975	Antigen processing-Cross presentation	27/1008	104/10723	7.26276E-07	6.386E-06	4.13933E-06	27
112	Cells	R-HSA-6807878	COPI-mediated anterograde transport	26/1008	98/10723	7.3911E-07	6.44082E-06	4.17486E-06	26
113	Cells	R-HSA-71406	Pyruvate metabolism and Citric Acid (TCA) cycle	18/1008	55/10723	1.40459E-06	1.21317E-05	7.86361E-06	18
114	Cells	R-HSA-1169091	Activation of NF-kappaB in B cells	20/1008	66/10723	1.46543E-06	1.25462E-05	8.13227E-06	20
115	Cells	R-HSA-4086400	PCP/CE pathway	24/1008	91/10723	2.19914E-06	1.8664E-05	1.20978E-05	24
116	Cells	R-HSA-1234174	Cellular response to hypoxia	21/1008	74/10723	2.63533E-06	2.19836E-05	1.42495E-05	21
117	Cells	R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	21/1008	74/10723	2.63533E-06	2.19836E-05	1.42495E-05	21
118	Cells	R-HSA-2871837	FCERI mediated NF-kB activation	22/1008	80/10723	2.72728E-06	2.25578E-05	1.46217E-05	22
119	Cells	R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	19/1008	63/10723	2.8967E-06	2.35599E-05	1.52712E-05	19
120	Cells	R-HSA-4608870	Asymmetric localization of PCP proteins	19/1008	63/10723	2.8967E-06	2.35599E-05	1.52712E-05	19
121	Cells	R-HSA-3299685	Detoxification of Reactive Oxygen Species	14/1008	37/10723	2.97085E-06	2.39632E-05	1.55327E-05	14
122	Cells	R-HSA-199977	ER to Golgi Anterograde Transport	33/1008	151/10723	3.06591E-06	2.45273E-05	1.58983E-05	33
123	Cells	R-HSA-68949	Orc1 removal from chromatin	20/1008	70/10723	4.05113E-06	3.21455E-05	2.08363E-05	20
124	Cells	R-HSA-69563	p53-Dependent G1 DNA Damage Response	19/1008	65/10723	4.85288E-06	3.76017E-05	2.4373E-05	19
125	Cells	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	19/1008	65/10723	4.85288E-06	3.76017E-05	2.4373E-05	19
126	Cells	R-HSA-446203	Asparagine N-linked glycosylation	53/1008	301/10723	4.85432E-06	3.76017E-05	2.4373E-05	53
127	Cells	R-HSA-195721	Signaling by WNT	52/1008	296/10723	6.38124E-06	4.904E-05	3.17872E-05	52
128	Cells	R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	20/1008	72/10723	6.50799E-06	4.91298E-05	3.18453E-05	20
129	Cells	R-HSA-8939902	Regulation of RUNX2 expression and activity	20/1008	72/10723	6.50799E-06	4.91298E-05	3.18453E-05	20
130	Cells	R-HSA-69002	DNA Replication Pre-Initiation	22/1008	84/10723	6.54393E-06	4.91298E-05	3.18453E-05	22
131	Cells	R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	39/1008	199/10723	6.8161E-06	5.07825E-05	3.29166E-05	39
132	Cells	R-HSA-174154	APC/C:Cdc20 mediated degradation of Securin	19/1008	67/10723	7.93045E-06	5.77621E-05	3.74407E-05	19
133	Cells	R-HSA-68867	Assembly of the pre-replicative complex	19/1008	67/10723	7.93045E-06	5.77621E-05	3.74407E-05	19
134	Cells	R-HSA-69615	G1/S DNA Damage Checkpoints	19/1008	67/10723	7.93045E-06	5.77621E-05	3.74407E-05	19

135	Cells	R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	20/1008	73/10723	8.18347E-06	5.91634E-05	3.8349E-05	20
136	Cells	R-HSA-5621481	C-type lectin receptors (CLRs)	30/1008	138/10723	9.53765E-06	6.84467E-05	4.43663E-05	30
137	Cells	R-HSA-6803529	FGFR2 alternative splicing	11/1008	26/10723	9.83161E-06	7.00413E-05	4.53999E-05	11
138	Cells	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	21/1008	80/10723	1.01646E-05	7.18885E-05	4.65973E-05	21
139	Cells	R-HSA-9013408	RHOG GTPase cycle	20/1008	74/10723	1.02383E-05	7.18893E-05	4.65978E-05	20
140	Cells	R-HSA-8949613	Cristae formation	12/1008	31/10723	1.16008E-05	8.08739E-05	5.24215E-05	12
141	Cells	R-HSA-9013694	Signaling by NOTCH4	21/1008	81/10723	1.25262E-05	8.67062E-05	5.6202E-05	21
142	Cells	R-HSA-176409	APC/C:Cdc20 mediated degradation of mitotic proteins	20/1008	75/10723	1.27466E-05	8.76101E-05	5.67878E-05	20
143	Cells	R-HSA-75153	Apoptotic execution phase	16/1008	52/10723	1.31728E-05	8.99063E-05	5.82762E-05	16
144	Cells	R-HSA-195258	RHO GTPase Effectors	50/1008	288/10723	1.34064E-05	9.08656E-05	5.8898E-05	50
145	Cells	R-HSA-69202	Cyclin E associated events during G1/S transition	21/1008	82/10723	1.53713E-05	0.000102992	6.67582E-05	21
146	Cells	R-HSA-9020702	Interleukin-1 signaling	24/1008	101/10723	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	20/1008	76/10723	1.57941E-05	0.000104156	6.75124E-05	20
148	Cells	R-HSA-5619084	ABC transporter disorders	20/1008	76/10723	1.57941E-05	0.000104156	6.75124E-05	20
149	Cells	R-HSA-5689603	UCH proteinases	23/1008	95/10723	1.66625E-05	0.000108417	7.02749E-05	23
150	Cells	R-HSA-8878159	Transcriptional regulation by RUNX3	23/1008	95/10723	1.66625E-05	0.000108417	7.02749E-05	23
151	Cells	R-HSA-8856688	Golgi-to-ER retrograde transport	28/1008	130/10723	2.2468E-05	0.000145157	9.40892E-05	28
152	Cells	R-HSA-162587	HIV Life Cycle	31/1008	151/10723	2.2858E-05	0.000145157	9.40892E-05	31
153	Cells	R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	21/1008	84/10723	2.28656E-05	0.000145157	9.40892E-05	21
154	Cells	R-HSA-75067	Processing of Capped Intronless Pre-mRNA	11/1008	28/10723	2.29039E-05	0.000145157	9.40892E-05	11
155	Cells	R-HSA-5696398	Nucleotide Excision Repair	25/1008	110/10723	2.34175E-05	0.00014651	9.49659E-05	25
156	Cells	R-HSA-68875	Mitotic Prophase	25/1008	110/10723	2.34175E-05	0.00014651	9.49659E-05	25
157	Cells	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	23/1008	97/10723	2.39248E-05	0.00014873	9.64049E-05	23
158	Cells	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	19/1008	72/10723	2.45519E-05	0.000151663	9.83058E-05	19
159	Cells	R-HSA-6811436	COPI-independent Golgi-to-ER retrograde traffic	15/1008	49/10723	2.61873E-05	0.000160747	0.000104194	15
160	Cells	R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	19/1008	73/10723	3.03112E-05	0.00018375	0.000119104	19
161	Cells	R-HSA-5654738	Signaling by FGFR2	19/1008	73/10723	3.03112E-05	0.00018375	0.000119104	19
162	Cells	R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	21/1008	87/10723	4.03025E-05	0.000241321	0.000156421	21
163	Cells	R-HSA-453276	Regulation of mitotic cell cycle	21/1008	87/10723	4.03025E-05	0.000241321	0.000156421	21
164	Cells	R-HSA-432720	Lysosome Vesicle Biogenesis	12/1008	35/10723	4.81075E-05	0.000286298	0.000185575	12
165	Cells	R-HSA-191859	snRNP Assembly	15/1008	52/10723	5.69027E-05	0.000332557	0.00021556	15
166	Cells	R-HSA-194441	Metabolism of non-coding RNA	15/1008	52/10723	5.69027E-05	0.000332557	0.00021556	15
167	Cells	R-HSA-3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	15/1008	52/10723	5.69027E-05	0.000332557	0.00021556	15
168	Cells	R-HSA-5627123	RHO GTPases activate PAKs	9/1008	21/10723	5.72772E-05	0.000332753	0.000215687	9
169	Cells	R-HSA-69206	G1/S Transition	27/1008	130/10723	6.13386E-05	0.00035424	0.000229614	27
170	Cells	R-HSA-202424	Downstream TCR signaling	22/1008	96/10723	6.23171E-05	0.000357773	0.000231904	22
171	Cells	R-HSA-5663213	RHO GTPases Activate WASPs and WAVEs	12/1008	36/10723	6.60461E-05	0.000376965	0.000244344	12
172	Cells	R-HSA-6807070	PTEN Regulation	28/1008	138/10723	6.98022E-05	0.000396087	0.000256739	28
173	Cells	R-HSA-8878171	Transcriptional regulation by RUNX1	37/1008	205/10723	7.56551E-05	0.000426817	0.000276658	37
174	Cells	R-HSA-2995410	Nuclear Envelope (NE) Reassembly	18/1008	72/10723	8.65136E-05	0.000485271	0.000314547	18
175	Cells	R-HSA-9609523	Insertion of tail-anchored proteins into the endoplasmic reticulum membrane	9/1008	22/10723	8.88858E-05	0.000495729	0.000321325	9
176	Cells	R-HSA-445355	Smooth Muscle Contraction	12/1008	37/10723	8.94703E-05	0.000496153	0.000321601	12
177	Cells	R-HSA-8878166	Transcriptional regulation by RUNX2	25/1008	119/10723	9.34493E-05	0.000515291	0.000334005	25
178	Cells	R-HSA-5696395	Formation of Incision Complex in GG-NER	13/1008	43/10723	0.00010379	0.000569095	0.00036888	13
179	Cells	R-HSA-69481	G2/M Checkpoints	29/1008	149/10723	0.000114021	0.000621702	0.00040298	29
180	Cells	R-HSA-429914	Deadenylation-dependent mRNA decay	15/1008	55/10723	0.000115478	0.000626148	0.000405862	15
181	Cells	R-HSA-9013418	RHOBTB2 GTPase cycle	9/1008	23/10723	0.000133919	0.000720176	0.00046681	9
182	Cells	R-HSA-8854214	TBC/RABGAPs	13/1008	44/10723	0.000134792	0.000720176	0.00046681	13
183	Cells	R-HSA-3371453	Regulation of HSF1-mediated heat shock response	17/1008	68/10723	0.000135033	0.000720176	0.00046681	17
184	Cells	R-HSA-9009391	Extra-nuclear estrogen signaling	18/1008	75/10723	0.000152265	0.000807668	0.000523521	18
185	Cells	R-HSA-382556	ABC-family proteins mediated transport	22/1008	102/10723	0.000161718	0.000853173	0.000553017	22
186	Cells	R-HSA-948021	Transport to the Golgi and subsequent modification	33/1008	182/10723	0.000166098	0.00087157	0.000564942	33
187	Cells	R-HSA-8856828	Clathrin-mediated endocytosis	28/1008	145/10723	0.000170994	0.000892461	0.000578483	28
188	Cells	R-HSA-162599	Late Phase of HIV Life Cycle	27/1008	138/10723	0.000177117	0.000919499	0.000596009	27
189	Cells	R-HSA-5610787	Hedgehog 'off' state	23/1008	110/10723	0.000189369	0.000977908	0.000633868	23
190	Cells	R-HSA-9679506	SARS-CoV Infections	28/1008	146/10723	0.000193047	0.00099165	0.000642776	28
191	Cells	R-HSA-69052	Switching of origins to a post-replicative state	20/1008	90/10723	0.000207199	0.001058776	0.000686286	20
192	Cells	R-HSA-5632684	Hedgehog 'on' state	19/1008	84/10723	0.000232278	0.001174631	0.000761382	19
193	Cells	R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	19/1008	84/10723	0.000232278	0.001174631	0.000761382	19
194	Cells	R-HSA-532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	11/1008	35/10723	0.000240412	0.001209497	0.000783982	11
195	Cells	R-HSA-453279	Mitotic G1 phase and G1/S transition	28/1008	148/10723	0.000244882	0.001225664	0.000794461	28
196	Cells	R-HSA-69239	Synthesis of DNA	24/1008	119/10723	0.000247335	0.001231627	0.000798326	24
197	Cells	R-HSA-15869	Metabolism of nucleotides	21/1008	98/10723	0.000248696	0.001232116	0.000798643	21
198	Cells	R-HSA-2467813	Separation of Sister Chromatids	33/1008	186/10723	0.0002529	0.001246619	0.000808044	33
199	Cells	R-HSA-210991	Basigin interactions	9/1008	25/10723	0.000281662	0.001381419	0.000895419	9
200	Cells	R-HSA-199992	trans-Golgi Network Vesicle Budding	17/1008	72/10723	0.000284202	0.001386905	0.000898975	17
201	Cells	R-HSA-1592230	Mitochondrial biogenesis	20/1008	93/10723	0.000329466	0.001599797	0.001036969	20
202	Cells	R-HSA-3928662	EPHB-mediated forward signaling	12/1008	42/10723	0.000343453	0.001659454	0.001075639	12
203	Cells	R-HSA-389661	Glyoxylate metabolism and glycine degradation	10/1008	31/10723	0.000363114	0.001745807	0.001131612	10
204	Cells	R-HSA-190236	Signaling by FGFR	19/1008	87/10723	0.000374646	0.001792426	0.001161829	19
205	Cells	R-HSA-70895	Branched-chain amino acid catabolism	8/1008	21/10723	0.000395552	0.001883214	0.001220677	8
206	Cells	R-HSA-3371556	Cellular response to heat stress	19/1008	88/10723	0.000436569	0.002068406	0.001340716	19
207	Cells	R-HSA-391251	Protein folding	20/1008	95/10723	0.000442374	0.002085782	0.001351979	20
208	Cells	R-HSA-69275	G2/M Transition	33/1008	192/10723	0.0004593	0.002155177	0.00139696	33
209	Cells	R-HSA-8876198	RAB GEFs exchange GTP for GDP on RABs	19/1008	89/10723	0.000507176	0.002368439	0.001535194	19
210	Cells	R-HSA-202403	TCR signaling	23/1008	118/10723	0.000550446	0.002558262	0.001658235	23
211	Cells	R-HSA-453274	Mitotic G2-G2/M phases	33/1008	194/10723	0.000555567	0.002569825	0.00166573	33
212	Cells	R-HSA-392170	ADP signalling through P2Y purinoceptor 12	8/1008	22/10723	0.00057079	0.002627789	0.001703301	8
213	Cells	R-HSA-111885	Opioid Signalling	19/1008	90/10723	0.000587452	0.002691797	0.001744791	19
214	Cells	R-HSA-392518	Signal amplification	10/1008	33/10723	0.000636908	0.002904777	0.001882842	10
215	Cells	R-HSA-9013405	RHOD GTPase cycle	13/1008	51/10723	0.000665048	0.003019008	0.001956885	13
216	Cells	R-HSA-69306	DNA Replication	24/1008	127/10723	0.000672975	0.003040851	0.001971043	24
217	Cells	R-HSA-2682334	EPH-Ephrin signaling	19/1008	91/10723	0.000678463	0.003051519	0.001977959	19
218	Cells	R-HSA-9007101	Rab regulation of trafficking	23/1008	121/10723	0.000793646	0.003553203	0.002303144	23
219	Cells	R-HSA-167238	Pausing and recovery of Tat-mediated HIV elongation	10/1008	34/10723	0.000827297	0.003653585	0.00236821	10
220	Cells	R-HSA-167243	Tat-mediated HIV elongation arrest and recovery	10/1008	34/10723	0.000827297	0.003653585	0.00236821	10
221	Cells	R-HSA-5673000	RAF activation	10/1008	34/10723	0.000827297	0.003653585	0.00236821	10
222	Cells	R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	20/1008	100/10723	0.000881823	0.003876842	0.002512923	20
223	Cells	R-HSA-9664407	Parasite infection	14/1008	59/10723	0.000907836	0.003937992	0.002552559	14
224	Cells	R-HSA-9664417	Leishmania phagocytosis	14/1008	59/10723	0.000907836	0.003937992	0.002552559	14
225	Cells	R-HSA-9664422	FCGR3A-mediated phagocytosis	14/1008	59/10723	0.000907836	0.003937992	0.002552559	14
226	Cells	R-HSA-69620	Cell Cycle Checkpoints	42/1008	273/10723	0.000926973	0.00400321	0.002594833	42
227	Cells	R-HSA-9706574	RHOBTB GTPase Cycle	10/1008	35/10723	0.001062051	0.004566354	0.002959856	10
228	Cells	R-HSA-180024	DARPP-32 events	8/1008	24/10723	0.00110742	0.004740534	0.003072758	8
229	Cells	R-HSA-389958	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	9/1008	30/10723	0.001282709	0.005466916	0.00354359	9
230	Cells	R-HSA-9012999	RHO GTPase cycle	61/1008	442/10723	0.001347841	0.005673246	0.00367733	61
231	Cells	R-HSA-167287	HIV elongation arrest and recovery	10/1008	36/10723	0.001348558	0.005673246	0.00367733	10
232	Cells	R-HSA-167290	Pausing and recovery of HIV elongation	10/1008	36/10723	0.001348558	0.005673246	0.00367733	10
233	Cells	R-HSA-390466	Chaperonin-mediated protein folding	18/1008	89/10723	0.001369449	0.005736405	0.003718269	18
234	Cells	R-HSA-983170	Antigen Presentation: Folding, assembly and peptide loading of class I MHC	8/1008	25/10723	0.001496012	0.006239775	0.004044548	8
235	Cells	R-HSA-5625740	RHO GTPases activate PKNs	14/1008	62/10723	0.001521777	0.00632023	0.004096698	14
236	Cells	R-HSA-917729	Endosomal Sorting Complex Required For Transport (ESCRT)	9/1008	31/10723	0.001658967	0.006860563	0.004446936	9
237	Cells	R-HSA-77289	Mitochondrial Fatty Acid Beta-Oxidation	10/1008	37/10723	0.001694894	0.006979816	0.004524234	10
238	Cells	R-HSA-201681	TCF dependent signaling in response to WNT	32/1008	199/10723	0.001755137	0.007197535	0.004665356	32
239	Cells	R-HSA-389957	Prefoldin mediated transfer of substrate to CCT/TriC	8/1008	26/10723	0.001985273	0.008107223	0.005255006	8
240	Cells	R-HSA-5358351	Signaling by Hedgehog	25/1008	146/10723	0.002260276	0.009189284	0.005956385	25
241	Cells	R-HSA-445144	Signal transduction by L1	7/1008	21/10723	0.002269075	0.009189284	0.005956385	7
242	Cells	R-HSA-446652	Interleukin-1 family signaling	24/1008	139/10723	0.002446229	0.009865783	0.006394883	24
243	Cells	R-HSA-5628897	TP53 Regulates Metabolic Genes	17/1008	87/10723	0.002705022	0.01086461	0.007042314	17
244	Cells	R-HSA-8939211	ESR-mediated signaling	30/1008	189/10723	0.002938496	0.011753984	0.007618792	30
245	Cells	R-HSA-8862803	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	7/1008	22/10723	0.003061608	0.012146869	0.007873456	7
246	Cells	R-HSA-8863678	Neurodegenerative Diseases	7/1008	22/10723	0.003061608	0.012146869	0.007873456	7
247	Cells	R-HSA-9679191	Potential therapeutics for SARS	16/1008	81/10723	0.003178563	0.012559827	0.00814113	16
248	Cells	R-HSA-162588	Budding and maturation of HIV virion	8/1008	28/10723	0.003334946	0.01308818	0.008483602	8
249	Cells	R-HSA-187687	Signalling to ERKs	9/1008	34/10723	0.003339095	0.01308818	0.008483602	9
250	Cells	R-HSA-1445148	Translocation of SLC2A4 (GLUT4) to the plasma membrane	14/1008	68/10723	0.00379622	0.014778592	0.009579308	14
251	Cells	R-HSA-2029482	Regulation of actin dynamics for phagocytic cup formation	13/1008	61/10723	0.003800642	0.014778592	0.009579308	13
252	Cells	R-HSA-167242	Abortive elongation of HIV-1 transcript in the absence of Tat	7/1008	23/10723	0.004049405	0.015621419	0.010125618	7
253	Cells	R-HSA-8949215	Mitochondrial calcium ion transport	7/1008	23/10723	0.004049405	0.015621419	0.010125618	7
254	Cells	R-HSA-499943	Interconversion of nucleotide di- and triphosphates	8/1008	29/10723	0.004232678	0.016200367	0.010500885	8
255	Cells	R-HSA-5205647	Mitophagy	8/1008	29/10723	0.004232678	0.016200367	0.010500885	8
256	Cells	R-HSA-9609646	HCMV Infection	21/1008	122/10723	0.004589818	0.01749868	0.011342436	21
257	Cells	R-HSA-9035034	RHOF GTPase cycle	10/1008	42/10723	0.004652496	0.017668623	0.011452591	10
258	Cells	R-HSA-3214858	RMTs methylate histone arginines	11/1008	49/10723	0.004955098	0.018744865	0.012150198	11
259	Cells	R-HSA-400685	Sema4D in semaphorin signaling	7/1008	24/10723	0.00526081	0.019824521	0.012850018	7
260	Cells	R-HSA-9663891	Selective autophagy	15/1008	78/10723	0.005477636	0.020562201	0.013328174	15
261	Cells	R-HSA-2029480	Fcgamma receptor (FCGR) dependent phagocytosis	16/1008	86/10723	0.005868488	0.021944997	0.014224486	16
262	Cells	R-HSA-6806834	Signaling by MET	15/1008	79/10723	0.006190091	0.023059271	0.014946745	15
263	Cells	R-HSA-5619115	Disorders of transmembrane transporters	27/1008	174/10723	0.00631216	0.023424594	0.015183543	27
264	Cells	R-HSA-449147	Signaling by Interleukins	58/1008	446/10723	0.006535009	0.024159729	0.015660049	58
265	Cells	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	52/1008	392/10723	0.006621583	0.024387416	0.015807633	52
266	Cells	R-HSA-5696394	DNA Damage Recognition in GG-NER	9/1008	38/10723	0.007381732	0.02698341	0.017490325	9
267	Cells	R-HSA-6814122	Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding	9/1008	38/10723	0.007381732	0.02698341	0.017490325	9
268	Cells	R-HSA-4615885	SUMOylation of DNA replication proteins	10/1008	45/10723	0.00779739	0.028396464	0.01840625	10
269	Cells	R-HSA-2980766	Nuclear Envelope Breakdown	11/1008	52/10723	0.007926234	0.028758382	0.018640841	11

270	Cells	R-HSA-456926	Thrombin signalling through proteinase activated receptors (PARs)	8/1008	32/10723	0.00805879	0.029131032	0.018882388	8
271	Cells	R-HSA-69242	S Phase	25/1008	161/10723	0.008304989	0.029728073	0.019269383	25
272	Cells	R-HSA-167044	Signalling to RAS	6/1008	20/10723	0.008315332	0.029728073	0.019269383	6
273	Cells	R-HSA-416572	Sema4D induced cell migration and growth-cone collapse	6/1008	20/10723	0.008315332	0.029728073	0.019269383	6
274	Cells	R-HSA-4086398	Ca2+ pathway	12/1008	60/10723	0.008999543	0.032056766	0.020778814	12
275	Cells	R-HSA-167169	HIV Transcription Elongation	10/1008	46/10723	0.009145859	0.032109204	0.020812804	10
276	Cells	R-HSA-167200	Formation of HIV-1 elongation complex containing HIV-1 Tat	10/1008	46/10723	0.009145859	0.032109204	0.020812804	10
277	Cells	R-HSA-167246	Tat-mediated elongation of the HIV-1 transcript	10/1008	46/10723	0.009145859	0.032109204	0.020812804	10
278	Cells	R-HSA-4570464	SUMOylation of RNA binding proteins	10/1008	46/10723	0.009145859	0.032109204	0.020812804	10
279	Cells	R-HSA-180910	Vpr-mediated nuclear import of PICs	8/1008	33/10723	0.009781856	0.034096755	0.022101111	8
280	Cells	R-HSA-5663084	Diseases of carbohydrate metabolism	8/1008	33/10723	0.009781856	0.034096755	0.022101111	8
281	Cells	R-HSA-70326	Glucose metabolism	16/1008	91/10723	0.010160181	0.035289453	0.022874203	16
282	Cells	R-HSA-8848021	Signaling by PTK6	11/1008	54/10723	0.010571597	0.036458934	0.023632247	11
283	Cells	R-HSA-9006927	Signaling by Non-Receptor Tyrosine Kinases	11/1008	54/10723	0.010571597	0.036458934	0.023632247	11
284	Cells	R-HSA-5683057	MAPK family signaling cascades	43/1008	321/10723	0.010860043	0.037321838	0.024191571	43
285	Cells	R-HSA-4085377	SUMOylation of SUMOylation proteins	8/1008	34/10723	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	48/10723	0.012369633	0.042212452	0.027361609	10
287	Cells	R-HSA-9645723	Diseases of programmed cell death	13/1008	70/10723	0.012512433	0.042550991	0.027581046	13
288	Cells	R-HSA-6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	14/1008	78/10723	0.013107505	0.044419878	0.028792436	14
289	Cells	R-HSA-9665686	Signaling by ERBB2 TMD/JMD mutants	6/1008	22/10723	0.01361092	0.045966289	0.029794801	6
290	Cells	R-HSA-5689880	Ub-specific processing proteases	29/1008	202/10723	0.013790562	0.046412375	0.030083949	29
291	Cells	R-HSA-157118	Signaling by NOTCH	29/1008	203/10723	0.014695857	0.049289197	0.031948671	29
292	Cells&Exosomes	R-HSA-9609690	HCMV Early Events	39/162	98/10723	1.21863E-46	7.56767E-44	2.15505E-44	39
293	Cells&Exosomes	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	37/162	97/10723	2.21474E-43	6.87676E-41	1.9583E-41	37
294	Cells&Exosomes	R-HSA-68886	M Phase	57/162	379/10723	2.88816E-42	5.30431E-40	1.51051E-40	57
295	Cells&Exosomes	R-HSA-9609646	HCMV Infection	39/162	122/10723	3.41663E-42	5.30431E-40	1.51051E-40	39
296	Cells&Exosomes	R-HSA-5625740	RHO GTPases activate PKNs	30/162	62/10723	4.32755E-39	5.37482E-37	1.53059E-37	30
297	Cells&Exosomes	R-HSA-73728	RNA Polymerase I Promoter Opening	24/162	31/10723	8.23046E-39	8.51853E-37	2.42582E-37	24
298	Cells&Exosomes	R-HSA-195258	RHO GTPase Effectors	49/162	288/10723	1.13076E-38	1.00314E-36	2.85665E-37	49
299	Cells&Exosomes	R-HSA-171306	Packaging Of Telomere Ends	24/162	32/10723	3.2514E-38	2.5239E-36	7.18731E-37	24
300	Cells&Exosomes	R-HSA-5334118	DNA methylation	24/162	33/10723	1.17741E-37	8.12413E-36	2.31351E-36	24
301	Cells&Exosomes	R-HSA-5625886	Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	24/162	35/10723	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	36/10723	3.68093E-36	1.63276E-34	4.6496E-35	24
303	Cells&Exosomes	R-HSA-110331	Cleavage of the damaged purine	24/162	36/10723	3.68093E-36	1.63276E-34	4.6496E-35	24
304	Cells&Exosomes	R-HSA-427359	SIRT1 negatively regulates rRNA expression	24/162	36/10723	3.68093E-36	1.63276E-34	4.6496E-35	24
305	Cells&Exosomes	R-HSA-73927	Depurination	24/162	36/10723	3.68093E-36	1.63276E-34	4.6496E-35	24
306	Cells&Exosomes	R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	29/162	74/10723	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	41/10723	4.1883E-34	1.30047E-32	3.70334E-33	24
308	Cells&Exosomes	R-HSA-110329	Cleavage of the damaged pyrimidine	24/162	41/10723	4.1883E-34	1.30047E-32	3.70334E-33	24
309	Cells&Exosomes	R-HSA-212300	PRC2 methylates histones and DNA	24/162	41/10723	4.1883E-34	1.30047E-32	3.70334E-33	24
310	Cells&Exosomes	R-HSA-73928	Depyrimidination	24/162	41/10723	4.1883E-34	1.30047E-32	3.70334E-33	24
311	Cells&Exosomes	R-HSA-9710421	Defective pyroptosis	24/162	41/10723	4.1883E-34	1.30047E-32	3.70334E-33	24
312	Cells&Exosomes	R-HSA-2299718	Condensation of Prophase Chromosomes	24/162	42/10723	9.65155E-34	2.8541E-32	8.12767E-33	24
313	Cells&Exosomes	R-HSA-73929	Base-Excision Repair, AP Site Formation	24/162	43/10723	2.15722E-33	6.08923E-32	1.73403E-32	24
314	Cells&Exosomes	R-HSA-427389	ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	24/162	44/10723	4.68703E-33	1.2655E-31	3.60376E-32	24
315	Cells&Exosomes	R-HSA-606279	Deposition of new CENPA-containing nucleosomes at the centromere	25/162	53/10723	2.81376E-32	6.98938E-31	1.99036E-31	25
316	Cells&Exosomes	R-HSA-774815	Nucleosome assembly	25/162	53/10723	2.81376E-32	6.98938E-31	1.99036E-31	25
317	Cells&Exosomes	R-HSA-9670095	Inhibition of DNA recombination at telomere	24/162	47/10723	4.1337E-32	9.87318E-31	2.81158E-31	24
318	Cells&Exosomes	R-HSA-977225	Amyloid fiber formation	28/162	78/10723	6.00871E-32	1.382E-30	3.93553E-31	28
319	Cells&Exosomes	R-HSA-9645723	Diseases of programmed cell death	27/162	70/10723	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	199/10723	9.6594E-32	2.06844E-30	5.89031E-31	38
321	Cells&Exosomes	R-HSA-2559582	Senescence-Associated Secretory Phenotype (SASP)	28/162	80/10723	1.39737E-31	2.89256E-30	8.23715E-31	28
322	Cells&Exosomes	R-HSA-157118	Signaling by NOTCH	38/162	203/10723	2.12797E-31	4.26281E-30	1.21392E-30	38
323	Cells&Exosomes	R-HSA-1221632	Meiotic synapsis	25/162	59/10723	8.74996E-31	1.59815E-29	4.55106E-30	25
324	Cells&Exosomes	R-HSA-3214815	HDACs deacetylate histones	25/162	59/10723	8.74996E-31	1.59815E-29	4.55106E-30	25
325	Cells&Exosomes	R-HSA-5250924	B-WICH complex positively regulates rRNA expression	25/162	59/10723	8.74996E-31	1.59815E-29	4.55106E-30	25
326	Cells&Exosomes	R-HSA-2559586	DNA Damage/Telomere Stress Induced Senescence	25/162	60/10723	1.48148E-30	2.62857E-29	7.48536E-30	25
327	Cells&Exosomes	R-HSA-912446	Meiotic recombination	24/162	54/10723	3.29516E-30	5.63748E-29	1.60539E-29	24
328	Cells&Exosomes	R-HSA-5689880	Ub-specific processing proteases	37/162	202/10723	3.35889E-30	5.63748E-29	1.60539E-29	37
329	Cells&Exosomes	R-HSA-8878171	Transcriptional regulation by RUNX1	37/162	205/10723	5.913E-30	9.66309E-29	2.75176E-29	37
330	Cells&Exosomes	R-HSA-69481	G2/M Checkpoints	33/162	149/10723	8.49628E-30	1.35287E-28	3.85256E-29	33
331	Cells&Exosomes	R-HSA-2559580	Oxidative Stress Induced Senescence	28/162	92/10723	1.33314E-29	2.06969E-28	5.89386E-29	28
332	Cells&Exosomes	R-HSA-9616222	Transcriptional regulation of granulopoiesis	24/162	58/10723	2.86769E-29	4.34351E-28	1.2369E-28	24
333	Cells&Exosomes	R-HSA-201722	Formation of the beta-catenin:TCF transactivating complex	24/162	59/10723	4.77411E-29	6.89471E-28	1.9634E-28	24
334	Cells&Exosomes	R-HSA-73772	RNA Polymerase I Promoter Escape	24/162	59/10723	4.77411E-29	6.89471E-28	1.9634E-28	24
335	Cells&Exosomes	R-HSA-1912408	Pre-NOTCH Transcription and Translation	24/162	61/10723	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	65/10723	8.13674E-28	1.1108E-26	3.16322E-27	24
337	Cells&Exosomes	R-HSA-5250913	Positive epigenetic regulation of rRNA expression	25/162	74/10723	8.40701E-28	1.1108E-26	3.16322E-27	25
338	Cells&Exosomes	R-HSA-5578749	Transcriptional regulation by small RNAs	25/162	74/10723	8.40701E-28	1.1108E-26	3.16322E-27	25
339	Cells&Exosomes	R-HSA-195721	Signaling by WNT	40/162	296/10723	2.48846E-27	3.21944E-26	9.168E-27	40
340	Cells&Exosomes	R-HSA-5688426	Deubiquitination	39/162	279/10723	3.33398E-27	4.2253E-26	1.20324E-26	39
341	Cells&Exosomes	R-HSA-9610379	HCMV Late Events	25/162	80/10723	8.08794E-27	1.00452E-25	2.86058E-26	25
342	Cells&Exosomes	R-HSA-73884	Base Excision Repair	24/162	71/10723	1.00688E-26	1.22603E-25	3.49136E-26	24
343	Cells&Exosomes	R-HSA-9646399	Aggrephagy	20/162	40/10723	1.22867E-26	1.46732E-25	4.17848E-26	20
344	Cells&Exosomes	R-HSA-427413	NoRC negatively regulates rRNA expression	24/162	74/10723	3.20753E-26	3.75826E-25	1.07024E-25	24
345	Cells&Exosomes	R-HSA-1500620	Meiosis	25/162	86/10723	6.35579E-26	7.30915E-25	2.08143E-25	25
346	Cells&Exosomes	R-HSA-1912422	Pre-NOTCH Expression and Processing	24/162	77/10723	9.64707E-26	1.06979E-24	3.04644E-25	24
347	Cells&Exosomes	R-HSA-5250941	Negative epigenetic regulation of rRNA expression	24/162	77/10723	9.64707E-26	1.06979E-24	3.04644E-25	24
348	Cells&Exosomes	R-HSA-73854	RNA Polymerase I Promoter Clearance	24/162	78/10723	1.37615E-25	1.49928E-24	4.26949E-25	24
349	Cells&Exosomes	R-HSA-73864	RNA Polymerase I Transcription	25/162	79/10723	1.95208E-25	2.09007E-24	5.9519E-25	24
350	Cells&Exosomes	R-HSA-437239	Recycling pathway of L1	20/162	45/10723	2.65114E-25	2.79044E-24	7.94632E-25	20
351	Cells&Exosomes	R-HSA-9018519	Estrogen-dependent gene expression	27/162	118/10723	7.46075E-25	7.72188E-24	2.19896E-24	27
352	Cells&Exosomes	R-HSA-211000	Gene Silencing by RNA	26/162	106/10723	8.33861E-25	8.48898E-24	2.41741E-24	26
353	Cells&Exosomes	R-HSA-69275	G2/M Transition	32/162	192/10723	9.04078E-25	9.05537E-24	2.5787E-24	32
354	Cells&Exosomes	R-HSA-5689603	UCH proteinases	25/162	95/10723	1.02663E-24	1.01196E-23	2.88176E-24	25
355	Cells&Exosomes	R-HSA-3214847	HATs acetylate histones	26/162	107/10723	1.08796E-24	1.05566E-23	3.00619E-24	26
356	Cells&Exosomes	R-HSA-453274	Mitotic G2-G2/M phases	32/162	194/10723	1.26703E-24	1.21051E-23	3.44715E-24	32
357	Cells&Exosomes	R-HSA-1445148	Translocation of SLC2A4 (GLUT4) to the plasma membrane	22/162	68/10723	4.5109E-24	4.24434E-23	1.20866E-23	22
358	Cells&Exosomes	R-HSA-5617472	Activation of anterior HOX genes in hindbrain development during early embryogenesis	24/162	89/10723	4.89291E-24	4.46838E-23	1.27246E-23	24
359	Cells&Exosomes	R-HSA-5619507	Activation of HOX genes during differentiation	24/162	89/10723	4.89291E-24	4.46838E-23	1.27246E-23	24
360	Cells&Exosomes	R-HSA-3371497	HSP90 chaperone cycle for steroid hormone receptors (SHR)	20/162	52/10723	9.63875E-24	8.67487E-23	2.47034E-23	20
361	Cells&Exosomes	R-HSA-157579	Telomere Maintenance	24/162	92/10723	1.18087E-23	1.0476E-22	2.98326E-23	24
362	Cells&Exosomes	R-HSA-2559583	Cellular Senescence	29/162	164/10723	3.03628E-23	2.65568E-22	7.56257E-23	29
363	Cells&Exosomes	R-HSA-1474165	Reproduction	25/162	111/10723	7.09718E-23	6.13132E-22	1.74317E-22	25
364	Cells&Exosomes	R-HSA-5626467	RHO GTPases activate IQGAPs	16/162	28/10723	9.0243E-23	7.67683E-22	2.18613E-22	16
365	Cells&Exosomes	R-HSA-212165	Epigenetic regulation of gene expression	25/162	116/10723	2.29982E-22	1.92998E-21	5.49601E-22	25
366	Cells&Exosomes	R-HSA-73886	Chromosome Maintenance	25/162	119/10723	4.52544E-22	3.74706E-21	1.06705E-21	25
367	Cells&Exosomes	R-HSA-5610787	Hedgehog 'off' state	24/162	110/10723	1.23194E-21	9.93555E-21	2.82935E-21	24
368	Cells&Exosomes	R-HSA-68875	Mitotic Prophase	24/162	110/10723	1.23194E-21	9.93555E-21	2.82935E-21	24
369	Cells&Exosomes	R-HSA-9663891	Selective autophagy	21/162	78/10723	4.04959E-21	3.2241E-20	9.18126E-21	21
370	Cells&Exosomes	R-HSA-69620	Cell Cycle Checkpoints	33/162	273/10723	5.66674E-21	4.45449E-20	1.2685E-20	33
371	Cells&Exosomes	R-HSA-5693565	Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	19/162	59/10723	7.2097E-21	5.59653E-20	1.5937E-20	19
372	Cells&Exosomes	R-HSA-5693606	DNA Double Strand Break Response	19/162	60/10723	1.04166E-20	7.98604E-20	2.27418E-20	19
373	Cells&Exosomes	R-HSA-389960	Formation of tubulin folding intermediates by CCT/TriC	14/162	23/10723	1.32743E-20	1.00529E-19	2.86275E-20	14
374	Cells&Exosomes	R-HSA-389958	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	15/162	30/10723	3.22261E-20	2.41113E-19	6.86617E-20	15
375	Cells&Exosomes	R-HSA-190828	Gap junction trafficking	17/162	45/10723	3.63244E-20	2.68541E-19	7.64724E-20	17
376	Cells&Exosomes	R-HSA-5689901	Metalloprotease DUBs	15/162	31/10723	6.1634E-20	4.5029E-19	1.28229E-19	15
377	Cells&Exosomes	R-HSA-9619483	Activation of AMPK downstream of NMDARs	14/162	25/10723	7.0549E-20	5.0943E-19	1.4507E-19	14
378	Cells&Exosomes	R-HSA-69473	G2/M DNA damage checkpoint	20/162	77/10723	8.19013E-20	5.84606E-19	1.66478E-19	20
379	Cells&Exosomes	R-HSA-157858	Gap junction trafficking and regulation	17/162	47/10723	8.79705E-20	6.20792E-19	1.76783E-19	17
380	Cells&Exosomes	R-HSA-5358351	Signaling by Hedgehog	25/162	146/10723	9.14717E-20	6.38246E-19	1.81753E-19	25
381	Cells&Exosomes	R-HSA-389977	Post-chaperonin tubulin folding pathway	13/162	20/10723	9.28808E-20	6.40877E-19	1.82503E-19	13
382	Cells&Exosomes	R-HSA-3247509	Chromatin modifying enzymes	30/162	239/10723	1.42158E-19	9.59569E-19	2.73256E-19	30
383	Cells&Exosomes	R-HSA-4839726	Chromatin organization	30/162	239/10723	1.42158E-19	9.59569E-19	2.73256E-19	30
384	Cells&Exosomes	R-HSA-2467813	Separation of Sister Chromatids	27/162	186/10723	2.41792E-19	1.61454E-18	4.59774E-19	27
385	Cells&Exosomes	R-HSA-8939211	ESR-mediated signaling	27/162	189/10723	3.70935E-19	2.45054E-18	6.97839E-19	27
386	Cells&Exosomes	R-HSA-68882	Mitotic Anaphase	29/162	230/10723	5.41834E-19	3.54188E-18	1.00862E-18	29
387	Cells&Exosomes	R-HSA-9668328	Sealing of the nuclear envelope (NE) by ESCRT-III	14/162	28/10723	6.10679E-19	3.91843E-18	1.11585E-18	14
388	Cells&Exosomes	R-HSA-2555396	Mitotic Metaphase and Anaphase	29/162	231/10723	6.12057E-19	3.91843E-18	1.11585E-18	29
389	Cells&Exosomes	R-HSA-5693607	Processing of DNA double-strand break ends	19/162	80/10723	4.5703E-18	2.89608E-17	8.24717E-18	19
390	Cells&Exosomes	R-HSA-9609736	Assembly and cell surface presentation of NMDA receptors	15/162	39/10723	4.64794E-18	2.91552E-17	8.30253E-18	15
391	Cells&Exosomes	R-HSA-3214858	RMTs methylate histone arginines	16/162	49/10723	7.57032E-18	4.70117E-17	1.33875E-17	16
392	Cells&Exosomes	R-HSA-6798695	Neutrophil degranulation	38/162	474/10723	7.84163E-18	4.82144E-17	1.373E-17	38
393	Cells&Exosomes	R-HSA-190861	Gap junction assembly	14/162	34/10723	1.96008E-17	1.1934E-16	3.39829E-17	14
394	Cells&Exosomes	R-HSA-9612973	Autophagy	23/162	147/10723	2.45104E-17	1.47776E-16	4.20822E-17	23
395	Cells&Exosomes	R-HSA-373760	L1CAM interactions	21/162	117/10723	3.5333E-17	2.10979E-16	6.00804E-17	21
396	Cells&Exosomes	R-HSA-8955332	Carboxyterminal post-translational modifications of tubulin	14/162	39/10723	1.99051E-16	1.17725E-15	3.35244E-16	14
397	Cells&Exosomes	R-HSA-73894	DNA Repair	30/162	311/10723	2.50128E-16	1.46537E-15	4.17295E-16	30
398	Cells&Exosomes	R-HSA-9006931	Signaling by Nuclear Receptors	28/162	265/10723	2.61493E-16	1.51764E-15	4.32177E-16	28
399	Cells&Exosomes	R-HSA-1632852	Macroautophagy	21/162	132/10723	4.6248E-16	2.65926E-15	7.57277E-16	21
400	Cells&Exosomes	R-HSA-5693571	Nonhomologous End-Joining (NHEJ)	15/162	51/10723	5.04558E-16	2.87459E-15	8.18598E-16	15
401	Cells&Exosomes	R-HSA-389957	Prefoldin mediated transfer of substrate to CCT/TriC	12/162	26/10723	7.54295E-16	4.25834E-15	1.21265E-15	12
402	Cells&Exosomes	R-HSA-380320	Recruitment of NuMA to mitotic centrosomes	18/162	91/10723	1.18284E-15	6.61753E-15	1.88447E-15	18
403	Cells&Exosomes	R-HSA-450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	15/162	54/10723	1.31715E-15	7.2385E-15	2.06131E-15	15
404	Cells&Exosomes	R-HSA-8866654	E3 ubiquitin ligases ubiquitinate target proteins	15/162	54/10723	1.31715E-15	7.2385E-15	2.06131E-15	15

405	Cells&Exosomes	R-HSA-5693567	HDR through Homologous Recombination (HRR) or Single Strand Annealing (SSA)	19/162	113/10723	4.35557E-15	2.37264E-14	6.75656E-15	19
406	Cells&Exosomes	R-HSA-2995410	Nuclear Envelope (NE) Reassembly	16/162	72/10723	6.91132E-15	3.73211E-14	1.06279E-14	16
407	Cells&Exosomes	R-HSA-450531	Regulation of mRNA stability by proteins that bind AU-rich elements	17/162	86/10723	7.72269E-15	4.1343E-14	1.17732E-14	17
408	Cells&Exosomes	R-HSA-6811436	COPI-independent Golgi-to-ER retrograde traffic	14/162	49/10723	7.8247E-15	4.15311E-14	1.18268E-14	14
409	Cells&Exosomes	R-HSA-8852135	Protein ubiquitination	16/162	74/10723	1.10044E-14	5.79131E-14	1.64919E-14	16
410	Cells&Exosomes	R-HSA-5693538	Homology Directed Repair	19/162	119/10723	1.1739E-14	6.126E-14	1.7445E-14	19
411	Cells&Exosomes	R-HSA-70263	Gluconeogenesis	12/162	34/10723	3.85937E-14	1.99723E-13	5.68575E-14	12
412	Cells&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	Cells&Exosomes	R-HSA-983189	Kinesins	14/162	57/10723	8.03597E-14	4.09044E-13	1.16483E-13	14
414	Cells&Exosomes	R-HSA-5387390	Hh mutants abrogate ligand secretion	14/162	58/10723	1.04561E-13	5.27904E-13	1.50331E-13	14
415	Cells&Exosomes	R-HSA-5678895	Defective CFTR causes cystic fibrosis	14/162	60/10723	1.74225E-13	8.72532E-13	2.48471E-13	14
416	Cells&Exosomes	R-HSA-109581	Apoptosis	21/162	178/10723	2.1555E-13	1.0634E-12	3.02824E-13	21
417	Cells&Exosomes	R-HSA-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	13/162	49/10723	2.15762E-13	1.0634E-12	3.02824E-13	13
418	Cells&Exosomes	R-HSA-390466	Chaperonin-mediated protein folding	16/162	89/10723	2.37789E-13	1.16273E-12	3.31111E-13	16
419	Cells&Exosomes	R-HSA-438064	Post NMDA receptor activation events	15/162	76/10723	3.24971E-13	1.57662E-12	4.48973E-13	15
420	Cells&Exosomes	R-HSA-180534	Vpu mediated degradation of CD4	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
421	Cells&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	Cells&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	Cells&Exosomes	R-HSA-69610	p53-Independent DNA Damage Response	13/162	51/10723	3.81266E-13	1.76691E-12	5.03163E-13	13
424	Cells&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	Cells&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	Cells&Exosomes	R-HSA-5358346	Hedgehog ligand biogenesis	14/162	64/10723	4.56317E-13	2.09506E-12	5.97748E-13	14
427	Cells&Exosomes	R-HSA-5357801	Programmed Cell Death	22/162	207/10723	4.82532E-13	2.20333E-12	6.27441E-13	22
428	Cells&Exosomes	R-HSA-169911	Regulation of Apoptosis	13/162	52/10723	5.01783E-13	2.27451E-12	6.47711E-13	13
429	Cells&Exosomes	R-HSA-114608	Platelet degranulation	18/162	127/10723	5.13152E-13	2.30918E-12	6.57586E-13	18
430	Cells&Exosomes	R-HSA-180585	Vif-mediated degradation of APOBEC3G	13/162	53/10723	6.56268E-13	2.89037E-12	8.23091E-13	13
431	Cells&Exosomes	R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	13/162	53/10723	6.56268E-13	2.89037E-12	8.23091E-13	13
432	Cells&Exosomes	R-HSA-9604323	Negative regulation of NOTCH4 signaling	13/162	53/10723	6.56268E-13	2.89037E-12	8.23091E-13	13
433	Cells&Exosomes	R-HSA-391251	Protein folding	16/162	95/10723	6.87887E-13	3.0083E-12	8.56672E-13	16
434	Cells&Exosomes	R-HSA-5693532	DNA Double-Strand Break Repair	19/162	148/10723	6.95694E-13	3.02116E-12	8.60336E-13	19
435	Cells&Exosomes	R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	13/162	54/10723	8.53179E-13	3.65396E-12	1.04054E-12	13
436	Cells&Exosomes	R-HSA-4641257	Degradation of AXIN	13/162	54/10723	8.53179E-13	3.65396E-12	1.04054E-12	13
437	Cells&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	Cells&Exosomes	R-HSA-4641258	Degradation of DVL	13/162	56/10723	1.41766E-12	5.90848E-12	1.68256E-12	13
439	Cells&Exosomes	R-HSA-69541	Stabilization of p53	13/162	56/10723	1.41766E-12	5.90848E-12	1.68256E-12	13
440	Cells&Exosomes	R-HSA-8932339	ROS sensing by NFE2L2	13/162	56/10723	1.41766E-12	5.90848E-12	1.68256E-12	13
441	Cells&Exosomes	R-HSA-70171	Glycolysis	14/162	71/10723	2.09566E-12	8.67601E-12	2.47067E-12	14
442	Cells&Exosomes	R-HSA-5676590	NIK-->noncanonical NF-kB signaling	13/162	58/10723	2.30625E-12	9.42223E-12	2.68317E-12	13
443	Cells&Exosomes	R-HSA-68827	CDT1 association with the CDC6:ORC:origin complex	13/162	58/10723	2.30625E-12	9.42223E-12	2.68317E-12	13
444	Cells&Exosomes	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	13/162	59/10723	2.91977E-12	1.16229E-11	3.30986E-12	13
445	Cells&Exosomes	R-HSA-5610780	Degradation of GLI1 by the proteasome	13/162	59/10723	2.91977E-12	1.16229E-11	3.30986E-12	13
446	Cells&Exosomes	R-HSA-5610783	Degradation of GLI2 by the proteasome	13/162	59/10723	2.91977E-12	1.16229E-11	3.30986E-12	13
447	Cells&Exosomes	R-HSA-5610785	GLI3 is processed to GLI3R by the proteasome	13/162	59/10723	2.91977E-12	1.16229E-11	3.30986E-12	13
448	Cells&Exosomes	R-HSA-442755	Activation of NMDA receptors and postsynaptic events	15/162	88/10723	3.10633E-12	1.22868E-11	3.49891E-12	15
449	Cells&Exosomes	R-HSA-4086400	PCP/CE pathway	15/162	91/10723	5.16291E-12	2.02922E-11	5.77861E-12	15
450	Cells&Exosomes	R-HSA-5619084	ABC transporter disorders	14/162	76/10723	5.60652E-12	2.18972E-11	6.23566E-12	14
451	Cells&Exosomes	R-HSA-4608870	Asymmetric localization of PCP proteins	13/162	63/10723	7.16887E-12	2.78242E-11	7.92348E-12	13
452	Cells&Exosomes	R-HSA-162909	Host Interactions of HIV factors	17/162	129/10723	7.88233E-12	3.04033E-11	8.65794E-12	17
453	Cells&Exosomes	R-HSA-9707587	Regulation of HMOX1 expression and activity	13/162	64/10723	8.87991E-12	3.40396E-11	9.69347E-12	13
454	Cells&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	Cells&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	Cells&Exosomes	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	13/162	65/10723	1.09564E-11	4.12358E-11	1.17427E-11	13
457	Cells&Exosomes	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	14/162	80/10723	1.16796E-11	4.36929E-11	1.24424E-11	14
458	Cells&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	Cells&Exosomes	R-HSA-9013694	Signaling by NOTCH4	14/162	81/10723	1.39377E-11	5.15195E-11	1.46712E-11	14
460	Cells&Exosomes	R-HSA-174154	APC/C:Cdc20 mediated degradation of Securin	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
461	Cells&Exosomes	R-HSA-5658442	Regulation of RAS by GAPs	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
462	Cells&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	Cells&Exosomes	R-HSA-69615	G1/S DNA Damage Checkpoints	13/162	67/10723	1.64935E-11	5.95491E-11	1.69578E-11	13
464	Cells&Exosomes	R-HSA-8941858	Regulation of RUNX3 expression and activity	12/162	54/10723	1.86089E-11	6.67985E-11	1.90222E-11	12
465	Cells&Exosomes	R-HSA-5663220	RHO GTPases Activate Formins	17/162	136/10723	1.87576E-11	6.69452E-11	1.9064E-11	17
466	Cells&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	Cells&Exosomes	R-HSA-68949	Orc1 removal from chromatin	13/162	70/10723	2.96747E-11	1.04704E-10	2.98166E-11	13
468	Cells&Exosomes	R-HSA-2132295	MHC class II antigen presentation	16/162	121/10723	3.18319E-11	1.11681E-10	3.18035E-11	16
469	Cells&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	Cells&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	Cells&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	Cells&Exosomes	R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	13/162	73/10723	5.18694E-11	1.76983E-10	5.03994E-11	13
473	Cells&Exosomes	R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	13/162	73/10723	5.18694E-11	1.76983E-10	5.03994E-11	13
474	Cells&Exosomes	R-HSA-187577	SCF(Skp2)-mediated degradation of p27/p21	12/162	59/10723	5.69085E-11	1.93116E-10	5.49935E-11	12
475	Cells&Exosomes	R-HSA-1234174	Cellular response to hypoxia	13/162	74/10723	6.21098E-11	2.09621E-10	5.96937E-11	13
476	Cells&Exosomes	R-HSA-71387	Metabolism of Carbohydrates	23/162	291/10723	6.57812E-11	2.20811E-10	6.28804E-11	23
477	Cells&Exosomes	R-HSA-70326	Glucose metabolism	14/162	91/10723	7.16969E-11	2.39375E-10	6.81668E-11	14
478	Cells&Exosomes	R-HSA-176409	APC/C:Cdc20 mediated degradation of mitotic proteins	13/162	75/10723	7.41613E-11	2.46279E-10	7.01328E-11	13
479	Cells&Exosomes	R-HSA-176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	13/162	76/10723	8.83075E-11	2.91697E-10	8.30664E-11	13
480	Cells&Exosomes	R-HSA-5617833	Cilium Assembly	19/162	198/10723	1.26244E-10	4.148E-10	1.18123E-10	19
481	Cells&Exosomes	R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	12/162	63/10723	1.28767E-10	4.20864E-10	1.1985E-10	12
482	Cells&Exosomes	R-HSA-6811434	COPI-dependent Golgi-to-ER retrograde traffic	14/162	96/10723	1.505E-10	4.88003E-10	1.38968E-10	14
483	Cells&Exosomes	R-HSA-5673001	RAF/MAP kinase cascade	22/162	276/10723	1.5088E-10	4.88003E-10	1.38968E-10	22
484	Cells&Exosomes	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	13/162	80/10723	1.72972E-10	5.5369E-10	1.57674E-10	13
485	Cells&Exosomes	R-HSA-2871837	FCERI mediated NF-kB activation	13/162	80/10723	1.72972E-10	5.5369E-10	1.57674E-10	13
486	Cells&Exosomes	R-HSA-6807878	COPI-mediated anterograde transport	14/162	98/10723	1.99929E-10	6.36697E-10	1.81312E-10	14
487	Cells&Exosomes	R-HSA-9711123	Cellular response to chemical stress	17/162	158/10723	2.09854E-10	6.64893E-10	1.89342E-10	17
488	Cells&Exosomes	R-HSA-5684996	MAPK1/MAPK3 signaling	22/162	282/10723	2.28521E-10	7.20363E-10	2.05138E-10	22
489	Cells&Exosomes	R-HSA-5620924	Intraflagellar transport	11/162	52/10723	2.3561E-10	7.38958E-10	2.10433E-10	11
490	Cells&Exosomes	R-HSA-195253	Degradation of beta-catenin by the destruction complex	13/162	82/10723	2.38568E-10	7.44475E-10	2.12004E-10	13
491	Cells&Exosomes	R-HSA-5632684	Hedgehog 'on' state	13/162	84/10723	3.26066E-10	1.0074E-09	2.86877E-10	13
492	Cells&Exosomes	R-HSA-69002	DNA Replication Pre-Initiation	13/162	84/10723	3.26066E-10	1.0074E-09	2.86877E-10	13
493	Cells&Exosomes	R-HSA-76002	Platelet activation, signaling and aggregation	21/162	261/10723	3.44124E-10	1.05792E-09	3.01265E-10	21
494	Cells&Exosomes	R-HSA-382556	ABC-family proteins mediated transport	14/162	102/10723	3.45869E-10	1.05805E-09	3.01302E-10	14
495	Cells&Exosomes	R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	13/162	87/10723	5.12738E-10	1.55322E-09	4.42311E-10	13
496	Cells&Exosomes	R-HSA-453276	Regulation of mitotic cell cycle	13/162	87/10723	5.12738E-10	1.55322E-09	4.42311E-10	13
497	Cells&Exosomes	R-HSA-5687128	MAPK6/MAPK4 signaling	13/162	88/10723	5.93832E-10	1.79014E-09	5.09779E-10	13
498	Cells&Exosomes	R-HSA-9613829	Chaperone Mediated Autophagy	8/162	22/10723	6.09785E-10	1.82935E-09	5.20945E-10	8
499	Cells&Exosomes	R-HSA-1236974	ER-Phagosome pathway	13/162	89/10723	6.86415E-10	2.04934E-09	5.83591E-10	13
500	Cells&Exosomes	R-HSA-69052	Switching of origins to a post-replicative state	13/162	90/10723	7.91926E-10	2.35304E-09	6.70076E-10	13
501	Cells&Exosomes	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	14/162	109/10723	8.5145E-10	2.51786E-09	7.1701E-10	14
502	Cells&Exosomes	R-HSA-68877	Mitotic Prometaphase	18/162	199/10723	1.05224E-09	3.09689E-09	8.81901E-10	18
503	Cells&Exosomes	R-HSA-9648025	EML4 and NUDC in mitotic spindle formation	14/162	113/10723	1.38249E-09	4.04964E-09	1.15322E-09	14
504	Cells&Exosomes	R-HSA-202424	Downstream TCR signaling	13/162	96/10723	1.79891E-09	5.2447E-09	1.49353E-09	13
505	Cells&Exosomes	R-HSA-5607764	CLEC7A (Dectin-1) signaling	13/162	97/10723	2.05044E-09	5.95011E-09	1.69441E-09	13
506	Cells&Exosomes	R-HSA-5683057	MAPK family signaling cascades	22/162	321/10723	2.66046E-09	7.68439E-09	2.18828E-09	22
507	Cells&Exosomes	R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	13/162	100/10723	3.00822E-09	8.64863E-09	2.46287E-09	13
508	Cells&Exosomes	R-HSA-69202	Cyclin E associated events during G1/S transition	12/162	82/10723	3.12208E-09	8.93461E-09	2.54431E-09	12
509	Cells&Exosomes	R-HSA-9020702	Interleukin-1 signaling	13/162	101/10723	3.40796E-09	9.70799E-09	2.76454E-09	13
510	Cells&Exosomes	R-HSA-3858494	Beta-catenin independent WNT signaling	15/162	143/10723	3.66132E-09	1.03821E-08	2.95651E-09	15
511	Cells&Exosomes	R-HSA-2500257	Resolution of Sister Chromatid Cohesion	14/162	122/10723	3.83441E-09	1.07745E-08	3.06826E-09	14
512	Cells&Exosomes	R-HSA-9707564	Cytoprotection by HMOX1	14/162	122/10723	3.83441E-09	1.07745E-08	3.06826E-09	14
513	Cells&Exosomes	R-HSA-9635486	Infection with Mycobacterium tuberculosis	8/162	27/10723	3.97029E-09	1.11061E-08	3.16268E-09	8
514	Cells&Exosomes	R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	12/162	84/10723	4.14864E-09	1.15529E-08	3.28993E-09	12
515	Cells&Exosomes	R-HSA-1236975	Antigen processing-Cross presentation	13/162	104/10723	4.91279E-09	1.36198E-08	3.87852E-09	13
516	Cells&Exosomes	R-HSA-2565942	Regulation of PLK1 Activity at G2/M Transition	12/162	87/10723	6.26283E-09	1.72854E-08	4.92237E-09	12
517	Cells&Exosomes	R-HSA-8856688	Golgi-to-ER retrograde transport	14/162	130/10723	8.83341E-09	2.42723E-08	6.91203E-09	14
518	Cells&Exosomes	R-HSA-983231	Factors involved in megakaryocyte development and platelet production	15/162	153/10723	9.32812E-09	2.55188E-08	7.26698E-09	15
519	Cells&Exosomes	R-HSA-8878159	Transcriptional regulation by RUNX3	12/162	95/10723	1.73917E-08	4.73695E-08	1.34894E-08	12
520	Cells&Exosomes	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	23/162	392/10723	2.16384E-08	5.86788E-08	1.67099E-08	23
521	Cells&Exosomes	R-HSA-202403	TCR signaling	13/162	118/10723	2.32823E-08	6.28623E-08	1.79013E-08	13
522	Cells&Exosomes	R-HSA-376176	Signaling by ROBO receptors	17/162	216/10723	2.57437E-08	6.8762E-08	1.95813E-08	17
523	Cells&Exosomes	R-HSA-69239	Synthesis of DNA	13/162	119/10723	2.57996E-08	6.8762E-08	1.95813E-08	13
524	Cells&Exosomes	R-HSA-8878166	Transcriptional regulation by RUNX2	13/162	119/10723	2.57996E-08	6.8762E-08	1.95813E-08	13
525	Cells&Exosomes	R-HSA-9637690	Response of Mtb to phagocytosis	7/162	23/10723	3.15643E-08	8.37668E-08	2.38543E-08	7
526	Cells&Exosomes	R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	9/162	48/10723	3.32414E-08	8.7842E-08	2.50148E-08	9
527	Cells&Exosomes	R-HSA-6802948	Signaling by high-kinase activity BRAF mutants	8/162	36/10723	4.82134E-08	1.26804E-07	3.61099E-08	8
528	Cells&Exosomes	R-HSA-350562	Regulation of ornithine decarboxylase (ODC)	9/162	50/10723	4.83937E-08	1.26804E-07	3.61099E-08	9
529	Cells&Exosomes	R-HSA-69306	DNA Replication	13/162	127/10723	5.66186E-08	1.47732E-07	4.20696E-08	13
530	Cells&Exosomes	R-HSA-199977	ER to Golgi Anterograde Transport	14/162	151/10723	6.06841E-08	1.57677E-07	4.49017E-08	14
531	Cells&Exosomes	R-HSA-162906	HIV Infection	17/162	232/10723	7.37667E-08	1.90871E-07	5.43544E-08	17
532	Cells&Exosomes	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	13/162	130/10723	7.4885E-08	1.92961E-07	5.49495E-08	13
533	Cells&Exosomes	R-HSA-1852241	Organelle biogenesis and maintenance	19/162	291/10723	7.64119E-08	1.96082E-07	5.58382E-08	19
534	Cells&Exosomes	R-HSA-3371556	Cellular response to heat stress	11/162	88/10723	7.81905E-08	1.9982E-07	5.69028E-08	11
535	Cells&Exosomes	R-HSA-5674135	MAP2K and MAPK activation	8/162	40/10723	1.16404E-07	2.96257E-07	8.4365E-08	8
536	Cells&Exosomes	R-HSA-446203	Asparagine N-linked glycosylation	19/162	301/10723	1.30184E-07	3.29977E-07	9.39676E-08	19
537	Cells&Exosomes	R-HSA-5621481	C-type lectin receptors (CLRs)	13/162	138/10723	1.52207E-07	3.82675E-07	1.08974E-07	13
538	Cells&Exosomes	R-HSA-6807070	PTEN Regulation	13/162	138/10723	1.52207E-07	3.82675E-07	1.08974E-07	13
539	Cells&Exosomes	R-HSA-446652	Interleukin-1 family signaling	13/162	139/10723	1.65739E-07	4.15015E-07	1.18184E-07	13

540	Cells&Exosomes	R-HSA-351202	Metabolism of polyamines	9/162	58/10723	1.85513E-07	4.62665E-07	1.31753E-07	9
541	Cells&Exosomes	R-HSA-449147	Signaling by Interleukins	23/162	446/10723	2.28235E-07	5.66935E-07	1.61446E-07	23
542	Cells&Exosomes	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	14/162	170/10723	2.67443E-07	6.61681E-07	1.88427E-07	14
543	Cells&Exosomes	R-HSA-6802946	Signaling by moderate kinase activity BRAF mutants	8/162	45/10723	3.06005E-07	7.45212E-07	2.12214E-07	8
544	Cells&Exosomes	R-HSA-6802949	Signaling by RAS mutants	8/162	45/10723	3.06005E-07	7.45212E-07	2.12214E-07	8
545	Cells&Exosomes	R-HSA-6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	8/162	45/10723	3.06005E-07	7.45212E-07	2.12214E-07	8
546	Cells&Exosomes	R-HSA-9649948	Signaling downstream of RAS mutants	8/162	45/10723	3.06005E-07	7.45212E-07	2.12214E-07	8
547	Cells&Exosomes	R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	15/162	199/10723	3.12762E-07	7.58693E-07	2.16053E-07	15
548	Cells&Exosomes	R-HSA-112314	Neurotransmitter receptors and postsynaptic signal transmission	15/162	200/10723	3.33747E-07	8.06447E-07	2.29652E-07	15
549	Cells&Exosomes	R-HSA-5619115	Disorders of transmembrane transporters	14/162	174/10723	3.56164E-07	8.57279E-07	2.44127E-07	14
550	Cells&Exosomes	R-HSA-69206	G1/S Transition	12/162	130/10723	5.8155E-07	1.39437E-06	3.97075E-07	12
551	Cells&Exosomes	R-HSA-948021	Transport to the Golgi and subsequent modification	14/162	182/10723	6.16913E-07	1.47347E-06	4.19601E-07	14
552	Cells&Exosomes	R-HSA-3371571	HSF1-dependent transactivation	6/162	23/10723	8.84423E-07	2.10432E-06	5.99246E-07	6
553	Cells&Exosomes	R-HSA-69242	S Phase	13/162	161/10723	9.11665E-07	2.16086E-06	6.15347E-07	13
554	Cells&Exosomes	R-HSA-8982491	Glycogen metabolism	6/162	26/10723	1.94279E-06	4.58735E-06	1.30634E-06	6
555	Cells&Exosomes	R-HSA-9656223	Signaling by RAF1 mutants	7/162	41/10723	2.30318E-06	5.41771E-06	1.5428E-06	7
556	Cells&Exosomes	R-HSA-453279	Mitotic G1 phase and G1/S transition	12/162	148/10723	2.32871E-06	5.4571E-06	1.55402E-06	12
557	Cells&Exosomes	R-HSA-112315	Transmission across Chemical Synapses	16/162	265/10723	2.43802E-06	5.69178E-06	1.62085E-06	16
558	Cells&Exosomes	R-HSA-1169410	Antiviral mechanism by IFN-stimulated genes	9/162	80/10723	3.04225E-06	7.07578E-06	2.01497E-06	9
559	Cells&Exosomes	R-HSA-6802952	Signaling by BRAF and RAF fusions	8/162	65/10723	5.54646E-06	1.28521E-05	3.65988E-06	8
560	Cells&Exosomes	R-HSA-380259	Loss of Nlp from mitotic centrosomes	8/162	69/10723	8.72998E-06	2.0079E-05	5.71788E-06	8
561	Cells&Exosomes	R-HSA-380284	Loss of proteins required for interphase microtubule organization from the centrosome	8/162	69/10723	8.72998E-06	2.0079E-05	5.71788E-06	8
562	Cells&Exosomes	R-HSA-1169408	ISG15 antiviral mechanism	8/162	72/10723	1.20263E-05	2.74571E-05	7.81897E-06	8
563	Cells&Exosomes	R-HSA-8854518	AURKA Activation by TPX2	8/162	72/10723	1.20263E-05	2.74571E-05	7.81897E-06	8
564	Cells&Exosomes	R-HSA-9662361	Sensory processing of sound by outer hair cells of the cochlea	7/162	54/10723	1.5388E-05	3.50036E-05	9.96796E-06	7
565	Cells&Exosomes	R-HSA-8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	6/162	37/10723	1.70984E-05	3.87522E-05	1.10354E-05	6
566	Cells&Exosomes	R-HSA-9013418	RHOBTB2 GTPase cycle	5/162	23/10723	1.99769E-05	4.51114E-05	1.28464E-05	5
567	Cells&Exosomes	R-HSA-380270	Recruitment of mitotic centrosome proteins and complexes	8/162	81/10723	2.88076E-05	6.45831E-05	1.83913E-05	8
568	Cells&Exosomes	R-HSA-380287	Centrosome maturation	8/162	81/10723	2.88076E-05	6.45831E-05	1.83913E-05	8
569	Cells&Exosomes	R-HSA-1643713	Signaling by EGFR in Cancer	5/162	25/10723	3.0781E-05	6.87591E-05	1.95805E-05	5
570	Cells&Exosomes	R-HSA-6802957	Oncogenic MAPK signaling	8/162	82/10723	3.15169E-05	7.01505E-05	1.99768E-05	8
571	Cells&Exosomes	R-HSA-5675221	Negative regulation of MAPK pathway	6/162	43/10723	4.16051E-05	9.22742E-05	2.62769E-05	6
572	Cells&Exosomes	R-HSA-5628897	TP53 Regulates Metabolic Genes	8/162	87/10723	4.84764E-05	0.000107131	3.05077E-05	8
573	Cells&Exosomes	R-HSA-8951664	Neddylation	13/162	232/10723	4.87921E-05	0.000107446	3.05975E-05	13
574	Cells&Exosomes	R-HSA-162588	Budding and maturation of HIV virion	5/162	28/10723	5.48912E-05	0.00012045	3.43006E-05	5
575	Cells&Exosomes	R-HSA-9020591	Interleukin-12 signaling	6/162	46/10723	6.1578E-05	0.000134648	3.83436E-05	6
576	Cells&Exosomes	R-HSA-5213460	RIPK1-mediated regulated necrosis	5/162	29/10723	6.55225E-05	0.000141775	4.03733E-05	5
577	Cells&Exosomes	R-HSA-5675482	Regulation of necroptotic cell death	5/162	29/10723	6.55225E-05	0.000141775	4.03733E-05	5
578	Cells&Exosomes	R-HSA-8863795	Downregulation of ERBB2 signaling	5/162	29/10723	6.55225E-05	0.000141775	4.03733E-05	5
579	Cells&Exosomes	R-HSA-8856828	Clathrin-mediated endocytosis	10/162	145/10723	6.72147E-05	0.000144932	4.12722E-05	10
580	Cells&Exosomes	R-HSA-3371453	Regulation of HSF1-mediated heat shock response	7/162	68/10723	7.05678E-05	0.000151635	4.31812E-05	7
581	Cells&Exosomes	R-HSA-114452	Activation of BH3-only proteins	5/162	30/10723	7.76738E-05	0.000165757	4.72027E-05	5
582	Cells&Exosomes	R-HSA-8866652	Synthesis of active ubiquitin: roles of E1 and E2 enzymes	5/162	30/10723	7.76738E-05	0.000165757	4.72027E-05	5
583	Cells&Exosomes	R-HSA-5620912	Anchoring of the basal body to the plasma membrane	8/162	97/10723	0.000105537	0.000224446	6.39155E-05	8
584	Cells&Exosomes	R-HSA-9659379	Sensory processing of sound	7/162	76/10723	0.000143852	0.000304888	8.68229E-05	7
585	Cells&Exosomes	R-HSA-9615710	Late endosomal microautophagy	5/162	34/10723	0.000144448	0.00030511	8.68862E-05	5
586	Cells&Exosomes	R-HSA-532668	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	5/162	35/10723	0.000166483	0.000349277	9.94636E-05	5
587	Cells&Exosomes	R-HSA-9706574	RHOBTB GTPase Cycle	5/162	35/10723	0.000166483	0.000349277	9.94636E-05	5
588	Cells&Exosomes	R-HSA-1257604	PIP3 activates AKT signaling	13/162	265/10723	0.000186874	0.000390736	0.00011127	13
589	Cells&Exosomes	R-HSA-447115	Interleukin-12 family signaling	6/162	56/10723	0.000188474	0.00039276	0.000111846	6
590	Cells&Exosomes	R-HSA-8876384	Listeria monocytogenes entry into host cells	4/162	20/10723	0.000201357	0.000418204	0.000119092	4
591	Cells&Exosomes	R-HSA-445355	Smooth Muscle Contraction	5/162	37/10723	0.000218167	0.00045069	0.000128343	5
592	Cells&Exosomes	R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	14/162	306/10723	0.00021845	0.00045069	0.000128343	14
593	Cells&Exosomes	R-HSA-4641263	Regulation of FZD by ubiquitination	4/162	21/10723	0.000245823	0.000502158	0.000142999	4
594	Cells&Exosomes	R-HSA-6807004	Negative regulation of MET activity	4/162	21/10723	0.000245823	0.000502158	0.000142999	4
595	Cells&Exosomes	R-HSA-901032	ER Quality Control Compartment (ERQC)	4/162	21/10723	0.000245823	0.000502158	0.000142999	4
596	Cells&Exosomes	R-HSA-5689896	Ovarian tumor domain proteases	5/162	38/10723	0.000248184	0.000503668	0.00014343	5
597	Cells&Exosomes	R-HSA-5696394	DNA Damage Recognition in GG-NER	5/162	38/10723	0.000248184	0.000503668	0.00014343	5
598	Cells&Exosomes	R-HSA-110313	Translesion synthesis by Y family DNA polymerases bypasses lesions on DNA template	5/162	39/10723	0.00028124	0.000568893	0.000162004	5
599	Cells&Exosomes	R-HSA-2979096	NOTCH2 Activation and Transmission of Signal to the Nucleus	4/162	22/10723	0.000296933	0.000592911	0.000168843	4
600	Cells&Exosomes	R-HSA-450321	JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	4/162	22/10723	0.000296933	0.000592911	0.000168843	4
601	Cells&Exosomes	R-HSA-5205685	PINK1-PRKN Mediated Mitophagy	4/162	22/10723	0.000296933	0.000592911	0.000168843	4
602	Cells&Exosomes	R-HSA-912631	Regulation of signaling by CBL	4/162	22/10723	0.000296933	0.000592911	0.000168843	4
603	Cells&Exosomes	R-HSA-2029482	Regulation of actin dynamics for phagocytic cup formation	6/162	61/10723	0.000302904	0.000602895	0.000171686	6
604	Cells&Exosomes	R-HSA-2173795	Downregulation of SMAD2/3:SMAD4 transcriptional activity	4/162	23/10723	0.00035524	0.000700329	0.000199433	4
605	Cells&Exosomes	R-HSA-450302	activated TAK1 mediates p38 MAPK activation	4/162	23/10723	0.00035524	0.000700329	0.000199433	4
606	Cells&Exosomes	R-HSA-937041	IKK complex recruitment mediated by RIP1	4/162	23/10723	0.00035524	0.000700329	0.000199433	4
607	Cells&Exosomes	R-HSA-3769402	Deactivation of the beta-catenin transactivating complex	5/162	42/10723	0.000400645	0.000787344	0.000224212	5
608	Cells&Exosomes	R-HSA-112316	Neuronal System	16/162	405/10723	0.000409235	0.000801687	0.000228296	16
609	Cells&Exosomes	R-HSA-174048	APC/C:Cdc20 mediated degradation of Cyclin B	4/162	24/10723	0.000421302	0.000820152	0.000233555	4
610	Cells&Exosomes	R-HSA-9648002	RAS processing	4/162	24/10723	0.000421302	0.000820152	0.000233555	4
611	Cells&Exosomes	R-HSA-5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	4/162	25/10723	0.000495687	0.000955968	0.000272231	4
612	Cells&Exosomes	R-HSA-9013507	NOTCH3 Activation and Transmission of Signal to the Nucleus	4/162	25/10723	0.000495687	0.000955968	0.000272231	4
613	Cells&Exosomes	R-HSA-9705462	Inactivation of CSF3 (G-CSF) signaling	4/162	25/10723	0.000495687	0.000955968	0.000272231	4
614	Cells&Exosomes	R-HSA-156842	Eukaryotic Translation Elongation	7/162	93/10723	0.000503201	0.000967455	0.000275502	7
615	Cells&Exosomes	R-HSA-983169	Class I MHC mediated antigen processing & presentation	15/162	374/10723	0.000532553	0.001020727	0.000290672	15
616	Cells&Exosomes	R-HSA-179409	APC-Cdc20 mediated degradation of Nek2A	4/162	26/10723	0.000578967	0.001099506	0.000313106	4
617	Cells&Exosomes	R-HSA-2173788	Downregulation of TGF-beta receptor signaling	4/162	26/10723	0.000578967	0.001099506	0.000313106	4
618	Cells&Exosomes	R-HSA-901042	Calnexin/calreticulin cycle	4/162	26/10723	0.000578967	0.001099506	0.000313106	4
619	Cells&Exosomes	R-HSA-9662360	Sensory processing of sound by inner hair cells of the cochlea	6/162	69/10723	0.000592177	0.001121164	0.000319274	6
620	Cells&Exosomes	R-HSA-9006925	Intracellular signaling by second messengers	13/162	305/10723	0.000718919	0.001356987	0.000386429	13
621	Cells&Exosomes	R-HSA-512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	5/162	48/10723	0.000749808	0.001406739	0.000400597	5
622	Cells&Exosomes	R-HSA-73893	DNA Damage Bypass	5/162	48/10723	0.000749808	0.001406739	0.000400597	5
623	Cells&Exosomes	R-HSA-9682385	FLT3 signaling in disease	4/162	28/10723	0.000774524	0.001444382	0.000411316	4
624	Cells&Exosomes	R-HSA-9683701	Translation of structural proteins	4/162	28/10723	0.000774524	0.001444382	0.000411316	4
625	Cells&Exosomes	R-HSA-5205647	Mitophagy	4/162	29/10723	0.000887964	0.001646046	0.000468744	4
626	Cells&Exosomes	R-HSA-5654732	Negative regulation of FGFR3 signaling	4/162	29/10723	0.000887964	0.001646046	0.000468744	4
627	Cells&Exosomes	R-HSA-1227986	Signaling by ERBB2	5/162	50/10723	0.000905568	0.001668717	0.0004752	5
628	Cells&Exosomes	R-HSA-9678108	SARS-CoV-1 Infection	5/162	50/10723	0.000905568	0.001668717	0.0004752	5
629	Cells&Exosomes	R-HSA-110314	Recognition of DNA damage by PCNA-containing replication complex	4/162	30/10723	0.001012624	0.001849527	0.00052669	4
630	Cells&Exosomes	R-HSA-5357956	TNFR1-induced NFkappaB signaling pathway	4/162	30/10723	0.001012624	0.001849527	0.00052669	4
631	Cells&Exosomes	R-HSA-9674555	Signaling by CSF3 (G-CSF)	4/162	30/10723	0.001012624	0.001849527	0.00052669	4
632	Cells&Exosomes	R-HSA-8856825	Cargo recognition for clathrin-mediated endocytosis	7/162	105/10723	0.001039745	0.001893495	0.00053921	7
633	Cells&Exosomes	R-HSA-182971	EGFR downregulation	4/162	31/10723	0.001149088	0.002068359	0.000589006	4
634	Cells&Exosomes	R-HSA-2122948	Activated NOTCH1 Transmits Signal to the Nucleus	4/162	31/10723	0.001149088	0.002068359	0.000589006	4
635	Cells&Exosomes	R-HSA-5654733	Negative regulation of FGFR4 signaling	4/162	31/10723	0.001149088	0.002068359	0.000589006	4
636	Cells&Exosomes	R-HSA-917729	Endosomal Sorting Complex Required For Transport (ESCRT)	4/162	31/10723	0.001149088	0.002068359	0.000589006	4
637	Cells&Exosomes	R-HSA-6806834	Signaling by MET	6/162	79/10723	0.00121322	0.002177485	0.000620082	6
638	Cells&Exosomes	R-HSA-168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	6/162	80/10723	0.001295475	0.002296357	0.000653933	6
639	Cells&Exosomes	R-HSA-2173789	TGF-beta receptor signaling activates SMADs	4/162	32/10723	0.001297941	0.002296357	0.000653933	4
640	Cells&Exosomes	R-HSA-2173796	SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	4/162	32/10723	0.001297941	0.002296357	0.000653933	4
641	Cells&Exosomes	R-HSA-445989	TAK1 activates NFkB by phosphorylation and activation of IKKs complex	4/162	32/10723	0.001297941	0.002296357	0.000653933	4
642	Cells&Exosomes	R-HSA-5656169	Termination of translesion DNA synthesis	4/162	32/10723	0.001297941	0.002296357	0.000653933	4
643	Cells&Exosomes	R-HSA-109606	Intrinsic Pathway for Apoptosis	5/162	55/10723	0.001399486	0.00246898	0.000703091	5
644	Cells&Exosomes	R-HSA-1980145	Signaling by NOTCH2	4/162	33/10723	0.001459765	0.002546388	0.000725135	4
645	Cells&Exosomes	R-HSA-2559585	Oncogene Induced Senescence	4/162	33/10723	0.001459765	0.002546388	0.000725135	4
646	Cells&Exosomes	R-HSA-5654726	Negative regulation of FGFR1 signaling	4/162	33/10723	0.001459765	0.002546388	0.000725135	4
647	Cells&Exosomes	R-HSA-5663084	Diseases of carbohydrate metabolism	4/162	33/10723	0.001459765	0.002546388	0.000725135	4
648	Cells&Exosomes	R-HSA-71291	Metabolism of amino acids and derivatives	14/162	371/10723	0.001466647	0.002550902	0.00072642	14
649	Cells&Exosomes	R-HSA-168643	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	5/162	56/10723	0.001518213	0.002626212	0.000747866	5
650	Cells&Exosomes	R-HSA-5218859	Regulated Necrosis	5/162	56/10723	0.001518213	0.002626212	0.000747866	5
651	Cells&Exosomes	R-HSA-5654727	Negative regulation of FGFR2 signaling	4/162	34/10723	0.001635141	0.002812805	0.000801002	4
652	Cells&Exosomes	R-HSA-936440	Negative regulators of DDX58/IFIH1 signaling	4/162	34/10723	0.001635141	0.002812805	0.000801002	4
653	Cells&Exosomes	R-HSA-9679506	SARS-CoV Infections	8/162	146/10723	0.001650448	0.002831294	0.000806267	8
654	Cells&Exosomes	R-HSA-917937	Iron uptake and transport	5/162	58/10723	0.001777682	0.003041158	0.00086603	5
655	Cells&Exosomes	R-HSA-5357905	Regulation of TNFR1 signaling	4/162	35/10723	0.001824643	0.003112925	0.000886467	4
656	Cells&Exosomes	R-HSA-2029480	Fcgamma receptor (FCGR) dependent phagocytosis	6/162	86/10723	0.001882087	0.003202125	0.000911869	6
657	Cells&Exosomes	R-HSA-168638	NOD1/2 Signaling Pathway	4/162	36/10723	0.002028851	0.003433015	0.000977619	4
658	Cells&Exosomes	R-HSA-6804757	Regulation of TP53 Degradation	4/162	36/10723	0.002028851	0.003433015	0.000977619	4
659	Cells&Exosomes	R-HSA-6806003	Regulation of TP53 Expression and Degradation	4/162	37/10723	0.002248328	0.003794054	0.001080432	4
660	Cells&Exosomes	R-HSA-168255	Influenza Infection	8/162	155/10723	0.00240417	0.004046043	0.001152191	8
661	Cells&Exosomes	R-HSA-6783310	Fanconi Anemia Pathway	4/162	38/10723	0.002483639	0.004157251	0.00118386	4
662	Cells&Exosomes	R-HSA-9607240	FLT3 Signaling	4/162	38/10723	0.002483639	0.004157251	0.00118386	4
663	Cells&Exosomes	R-HSA-9033241	Peroxisomal protein import	5/162	63/10723	0.002567126	0.004285444	0.001220365	5
664	Cells&Exosomes	R-HSA-373755	Semaphorin interactions	5/162	64/10723	0.002751285	0.004580557	0.001304405	5
665	Cells&Exosomes	R-HSA-5654741	Signaling by FGFR3	4/162	40/10723	0.003003987	0.004987904	0.001420405	4
666	Cells&Exosomes	R-HSA-913531	Interferon Signaling	9/162	198/10723	0.003098633	0.005131335	0.00146125	9
667	Cells&Exosomes	R-HSA-5654743	Signaling by FGFR4	4/162	41/10723	0.00329012	0.005419534	0.00154332	4
668	Cells&Exosomes	R-HSA-5696400	Dual Incision in GG-NER	4/162	41/10723	0.00329012	0.005419534	0.00154332	4
669	Cells&Exosomes	R-HSA-9694516	SARS-CoV-2 Infection	5/162	67/10723	0.003361142	0.005521876	0.001572464	5
670	Cells&Exosomes	R-HSA-1500931	Cell-Cell communication	7/162	129/10723	0.003380554	0.005539113	0.001577373	7
671	Cells&Exosomes	R-HSA-3700989	Transcriptional Regulation by TP53	13/162	365/10723	0.003557236	0.005813273	0.001655445	13
672	Cells&Exosomes	R-HSA-5696395	Formation of Incision Complex in GG-NER	4/162	43/10723	0.003916981	0.006384371	0.001818077	4
673	Cells&Exosomes	R-HSA-8862803	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	3/162	22/10723	0.004221075	0.006844092	0.001948991	3
674	Cells&Exosomes	R-HSA-8863678	Neurodegenerative Diseases	3/162	22/10723	0.004221075	0.006844092	0.001948991	3

675	Cells&Exosomes	R-HSA-2173793	Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	4/162	44/10723	0.004258758	0.006851526	0.001951108	4
676	Cells&Exosomes	R-HSA-75893	TNF signaling	4/162	44/10723	0.004258758	0.006851526	0.001951108	4
677	Cells&Exosomes	R-HSA-9694635	Translation of structural proteins	4/162	44/10723	0.004258758	0.006851526	0.001951108	4
678	Cells&Exosomes	R-HSA-373753	Nephrin family interactions	3/162	23/10723	0.00480095	0.00770385	0.002193824	3
679	Cells&Exosomes	R-HSA-69231	Cyclin D associated events in G1	4/162	47/10723	0.005403573	0.008626269	0.002456502	4
680	Cells&Exosomes	R-HSA-69236	G1 Phase	4/162	47/10723	0.005403573	0.008626269	0.002456502	4
681	Cells&Exosomes	R-HSA-204998	Cell death signalling via NRAGE, NRIF and NADE	5/162	76/10723	0.005769938	0.009187517	0.002616328	5
682	Cells&Exosomes	R-HSA-2122947	NOTCH1 Intracellular Domain Regulates Transcription	4/162	48/10723	0.005826642	0.009254079	0.002635283	4
683	Cells&Exosomes	R-HSA-9012852	Signaling by NOTCH3	4/162	49/10723	0.006271237	0.009934791	0.002829129	4
684	Cells&Exosomes	R-HSA-177929	Signaling by EGFR	4/162	50/10723	0.006737817	0.010619757	0.003024187	4
685	Cells&Exosomes	R-HSA-5654736	Signaling by FGFR1	4/162	50/10723	0.006737817	0.010619757	0.003024187	4
686	Cells&Exosomes	R-HSA-354192	Integrin signaling	3/162	27/10723	0.007587431	0.011928595	0.003396905	3
687	Cells&Exosomes	R-HSA-6781823	Formation of TC-NER Pre-Incision Complex	4/162	53/10723	0.008273896	0.012974974	0.003694882	4
688	Cells&Exosomes	R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	5/162	84/10723	0.008759573	0.013702002	0.003901918	5
689	Cells&Exosomes	R-HSA-8848021	Signaling by PTK6	4/162	54/10723	0.008832788	0.013747272	0.003914809	4
690	Cells&Exosomes	R-HSA-9006927	Signaling by Non-Receptor Tyrosine Kinases	4/162	54/10723	0.008832788	0.013747272	0.003914809	4
691	Cells&Exosomes	R-HSA-397014	Muscle contraction	8/162	194/10723	0.009191918	0.014270453	0.004063795	8
692	Cells&Exosomes	R-HSA-5339562	Uptake and actions of bacterial toxins	3/162	29/10723	0.009272328	0.014359391	0.004089122	3
693	Cells&Exosomes	R-HSA-156902	Peptide chain elongation	5/162	89/10723	0.011093359	0.017135531	0.004879683	5
694	Cells&Exosomes	R-HSA-1236394	Signaling by ERBB4	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
695	Cells&Exosomes	R-HSA-2644602	Signaling by NOTCH1 PEST Domain Mutants in Cancer	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
696	Cells&Exosomes	R-HSA-2644603	Signaling by NOTCH1 in Cancer	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
697	Cells&Exosomes	R-HSA-2644606	Constitutive Signaling by NOTCH1 PEST Domain Mutants	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
698	Cells&Exosomes	R-HSA-2894858	Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
699	Cells&Exosomes	R-HSA-2894862	Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
700	Cells&Exosomes	R-HSA-72649	Translation initiation complex formation	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
701	Cells&Exosomes	R-HSA-72702	Ribosomal scanning and start codon recognition	4/162	58/10723	0.011313314	0.017135531	0.004879683	4
702	Cells&Exosomes	R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	4/162	59/10723	0.01199654	0.018126159	0.005161784	4
703	Cells&Exosomes	R-HSA-2682334	EPH-Ephrin signaling	5/162	91/10723	0.012135288	0.018247007	0.005196198	5
704	Cells&Exosomes	R-HSA-446728	Cell junction organization	5/162	91/10723	0.012135288	0.018247007	0.005196198	5
705	Cells&Exosomes	R-HSA-72766	Translation	10/162	291/10723	0.012846854	0.019270282	0.005487596	10
706	Cells&Exosomes	R-HSA-180746	Nuclear import of Rev protein	3/162	33/10723	0.013250741	0.019828217	0.005646479	3
707	Cells&Exosomes	R-HSA-1834949	Cytosolic sensors of pathogen-associated DNA	4/162	63/10723	0.014992014	0.022326236	0.00635784	4
708	Cells&Exosomes	R-HSA-450294	MAP kinase activation	4/162	63/10723	0.014992014	0.022326236	0.00635784	4
709	Cells&Exosomes	R-HSA-193704	p75 NTR receptor-mediated signalling	5/162	97/10723	0.015655273	0.023258193	0.006623233	5
710	Cells&Exosomes	R-HSA-6782210	Gap-filling DNA repair synthesis and ligation in TC-NER	4/162	64/10723	0.015808062	0.023429133	0.006671912	4
711	Cells&Exosomes	R-HSA-6782135	Dual incision in TC-NER	4/162	65/10723	0.016651553	0.02456203	0.006994527	4
712	Cells&Exosomes	R-HSA-9614085	FOXO-mediated transcription	4/162	65/10723	0.016651553	0.02456203	0.006994527	4
713	Cells&Exosomes	R-HSA-177243	Interactions of Rev with host cellular proteins	3/162	36/10723	0.016780735	0.024635547	0.007015462	3
714	Cells&Exosomes	R-HSA-390522	Striated Muscle Contraction	3/162	36/10723	0.016780735	0.024635547	0.007015462	3
715	Cells&Exosomes	R-HSA-5685942	HDR through Homologous Recombination (HRR)	4/162	66/10723	0.017522749	0.025664214	0.007308396	4
716	Cells&Exosomes	R-HSA-3299685	Detoxification of Reactive Oxygen Species	3/162	37/10723	0.018063006	0.026393239	0.007516	3
717	Cells&Exosomes	R-HSA-162599	Late Phase of HIV Life Cycle	6/162	138/10723	0.018183878	0.026507483	0.007548533	6
718	Cells&Exosomes	R-HSA-400253	Circadian Clock	4/162	69/10723	0.020304993	0.029530213	0.008409316	4
719	Cells&Exosomes	R-HSA-76009	Platelet Aggregation (Plug Formation)	3/162	39/10723	0.020786967	0.030160529	0.008588811	3
720	Cells&Exosomes	R-HSA-448424	Interleukin-17 signaling	4/162	71/10723	0.022302576	0.032284149	0.009193554	4
721	Cells&Exosomes	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	3/162	41/10723	0.023723991	0.034261857	0.009756745	3
722	Cells&Exosomes	R-HSA-170834	Signaling by TGF-beta Receptor Complex	4/162	73/10723	0.02441618	0.035098259	0.009994927	4
723	Cells&Exosomes	R-HSA-5654738	Signaling by FGFR2	4/162	73/10723	0.02441618	0.035098259	0.009994927	4
724	Cells&Exosomes	R-HSA-3928662	EPHB-mediated forward signaling	3/162	42/10723	0.025272431	0.036161704	0.010297765	3
725	Cells&Exosomes	R-HSA-9035034	RHOF GTPase cycle	3/162	42/10723	0.025272431	0.036161704	0.010297765	3
726	Cells&Exosomes	R-HSA-5696398	Nucleotide Excision Repair	5/162	110/10723	0.025474304	0.036344044	0.010349689	5
727	Cells&Exosomes	R-HSA-1980143	Signaling by NOTCH1	4/162	74/10723	0.025516913	0.036344044	0.010349689	4
728	Cells&Exosomes	R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	5/162	111/10723	0.026361575	0.037461186	0.010667818	5
729	Cells&Exosomes	R-HSA-162587	HIV Life Cycle	6/162	151/10723	0.026908609	0.038151247	0.010864327	6
730	Cells&Exosomes	R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	5/162	112/10723	0.027268398	0.038573291	0.010984512	5
731	Cells&Exosomes	R-HSA-6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	4/162	78/10723	0.030216014	0.042645783	0.012144235	4
732	Cells&Exosomes	R-HSA-72613	Eukaryotic Translation Initiation	5/162	119/10723	0.034173064	0.048012382	0.013672481	5
733	Cells&Exosomes	R-HSA-72737	Cap-dependent Translation Initiation	5/162	119/10723	0.034173064	0.048012382	0.013672481	5
734	Exosomes	R-HSA-3000178	ECM proteoglycans	19/89	75/10723	7.51596E-24	1.26268E-21	7.35773E-22	19
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	125/10723	2.9708E-22	2.49547E-20	1.45413E-20	21
736	Exosomes	R-HSA-8957275	Post-translational protein phosphorylation	19/89	108/10723	1.40559E-20	7.87131E-19	4.58666E-19	19
737	Exosomes	R-HSA-1474244	Extracellular matrix organization	25/89	300/10723	9.1732E-19	3.85274E-17	2.24502E-17	25
738	Exosomes	R-HSA-216083	Integrin cell surface interactions	16/89	85/10723	6.16184E-18	2.07038E-16	1.20642E-16	16
739	Exosomes	R-HSA-3000171	Non-integrin membrane-ECM interactions	14/89	59/10723	2.49928E-17	6.99799E-16	4.07778E-16	14
740	Exosomes	R-HSA-114608	Platelet degranulation	17/89	127/10723	2.19917E-16	5.278E-15	3.07553E-15	17
741	Exosomes	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	17/89	132/10723	4.29222E-16	9.01367E-15	5.25232E-15	17
742	Exosomes	R-HSA-76002	Platelet activation, signaling and aggregation	20/89	261/10723	2.27863E-14	4.25344E-13	2.47851E-13	20
743	Exosomes	R-HSA-977606	Regulation of Complement cascade	11/89	46/10723	7.17377E-14	1.20519E-12	7.02274E-13	11
744	Exosomes	R-HSA-166658	Complement cascade	11/89	57/10723	9.21598E-13	1.40753E-11	8.20178E-12	11
745	Exosomes	R-HSA-8874081	MET activates PTK2 signaling	9/89	30/10723	1.53329E-12	2.14661E-11	1.25084E-11	9
746	Exosomes	R-HSA-1474228	Degradation of the extracellular matrix	14/89	139/10723	6.49915E-12	8.3989E-11	4.8941E-11	14
747	Exosomes	R-HSA-140877	Formation of Fibrin Clot (Clotting Cascade)	9/89	39/10723	2.13731E-11	2.56477E-10	1.49451E-10	9
748	Exosomes	R-HSA-3000170	Syndecan interactions	8/89	27/10723	3.1902E-11	3.57303E-10	2.08203E-10	8
749	Exosomes	R-HSA-8875878	MET promotes cell motility	9/89	41/10723	3.4861E-11	3.66041E-10	2.13294E-10	9
750	Exosomes	R-HSA-140875	Common Pathway of Fibrin Clot Formation	7/89	22/10723	3.29142E-10	3.25269E-09	1.89537E-09	7
751	Exosomes	R-HSA-6806834	Signaling by MET	10/89	79/10723	8.34693E-10	7.79046E-09	4.53956E-09	10
752	Exosomes	R-HSA-186797	Signaling by PDGF	9/89	58/10723	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	41/10723	1.24934E-09	1.04945E-08	6.11521E-09	8
754	Exosomes	R-HSA-975634	Retinoid metabolism and transport	8/89	43/10723	1.87067E-09	1.49654E-08	8.72042E-09	8
755	Exosomes	R-HSA-8948216	Collagen chain trimerization	8/89	44/10723	2.27101E-09	1.73423E-08	1.01055E-08	8
756	Exosomes	R-HSA-6806667	Metabolism of fat-soluble vitamins	8/89	47/10723	3.9487E-09	2.88427E-08	1.68068E-08	8
757	Exosomes	R-HSA-140837	Intrinsic Pathway of Fibrin Clot Formation	6/89	23/10723	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	61/10723	3.36484E-08	2.26118E-07	1.3176E-07	8
759	Exosomes	R-HSA-1442490	Collagen degradation	8/89	64/10723	4.95622E-08	3.20248E-07	1.86611E-07	8
760	Exosomes	R-HSA-1650814	Collagen biosynthesis and modifying enzymes	8/89	67/10723	7.15723E-08	4.45339E-07	2.59502E-07	8
761	Exosomes	R-HSA-8963899	Plasma lipoprotein remodeling	6/89	30/10723	1.39491E-07	8.36945E-07	4.87693E-07	6
762	Exosomes	R-HSA-1474290	Collagen formation	8/89	90/10723	7.28459E-07	4.22004E-06	2.45904E-06	8
763	Exosomes	R-HSA-419037	NCAM1 interactions	6/89	42/10723	1.13785E-06	6.37197E-06	3.71299E-06	6
764	Exosomes	R-HSA-2187338	Visual phototransduction	8/89	98/10723	1.40125E-06	7.59386E-06	4.425E-06	8
765	Exosomes	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	7/89	69/10723	1.51894E-06	7.97444E-06	4.64676E-06	7
766	Exosomes	R-HSA-3781865	Diseases of glycosylation	9/89	141/10723	2.36995E-06	1.20652E-05	7.03049E-06	9
767	Exosomes	R-HSA-196854	Metabolism of vitamins and cofactors	10/89	187/10723	3.15379E-06	1.55834E-05	9.08058E-06	10
768	Exosomes	R-HSA-3000157	Laminin interactions	5/89	30/10723	4.25518E-06	2.04249E-05	1.19017E-05	5
769	Exosomes	R-HSA-375165	NCAM signaling for neurite out-growth	6/89	63/10723	1.28194E-05	5.98238E-05	3.48597E-05	6
770	Exosomes	R-HSA-76009	Platelet Aggregation (Plug Formation)	5/89	39/10723	1.62105E-05	7.36044E-05	4.28898E-05	5
771	Exosomes	R-HSA-3560782	Diseases associated with glycosaminoglycan metabolism	5/89	40/10723	1.84057E-05	8.13728E-05	4.74165E-05	5
772	Exosomes	R-HSA-5668914	Diseases of metabolism	9/89	242/10723	0.000172877	0.000744703	0.000433943	9
773	Exosomes	R-HSA-8935690	Digestion	3/89	20/10723	0.000568895	0.002389359	0.001392295	3
774	Exosomes	R-HSA-166663	Initial triggering of complement	3/89	22/10723	0.000759341	0.003111446	0.001813061	3
775	Exosomes	R-HSA-8963743	Digestion and absorption	3/89	25/10723	0.001113869	0.004455475	0.002596235	3
776	Exosomes	R-HSA-2022854	Keratan sulfate biosynthesis	3/89	27/10723	0.001399684	0.005468532	0.003186551	3
777	Exosomes	R-HSA-1638074	Keratan sulfate/keratin metabolism	3/89	33/10723	0.002518801	0.009403525	0.005479498	3
778	Exosomes	R-HSA-8964043	Plasma lipoprotein clearance	3/89	33/10723	0.002518801	0.009403525	0.005479498	3
779	Exosomes	R-HSA-156590	Glutathione conjugation	3/89	36/10723	0.003237709	0.011573089	0.006743717	3
780	Exosomes	R-HSA-5083635	Defective B3GALTL causes Peters-plus syndrome (PpS)	3/89	36/10723	0.003237709	0.011573089	0.006743717	3
781	Exosomes	R-HSA-5173214	O-glycosylation of TSR domain-containing proteins	3/89	37/10723	0.003502428	0.012089991	0.00704492	3
782	Exosomes	R-HSA-1630316	Glycosaminoglycan metabolism	5/89	123/10723	0.003526247	0.012089991	0.00704492	5
783	Exosomes	R-HSA-2129379	Molecules associated with elastic fibres	3/89	38/10723	0.003780021	0.012700872	0.007400884	3
784	Exosomes	R-HSA-977225	Amyloid fiber formation	4/89	78/10723	0.003963551	0.013056402	0.007608054	4
785	Exosomes	R-HSA-198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	5/89	130/10723	0.004465199	0.014426027	0.008406144	5
786	Exosomes	R-HSA-202733	Cell surface interactions at the vascular wall	5/89	137/10723	0.005570363	0.017657	0.010288853	5
787	Exosomes	R-HSA-1566948	Elastic fibre formation	3/89	45/10723	0.006098632	0.01897352	0.011055999	3
788	Exosomes	R-HSA-9707616	Heme signaling	3/89	46/10723	0.006485429	0.019810038	0.011543443	3
789	Exosomes	R-HSA-983231	Factors involved in megakaryocyte development and platelet production	5/89	153/10723	0.008798889	0.026396667	0.015381517	5
790	Exosomes	R-HSA-3560783	Defective B4GALT7 causes EDS, progeroid type	2/89	20/10723	0.011744933	0.0334432	0.019487579	2
791	Exosomes	R-HSA-3560801	Defective B3GAT3 causes JDSSDHD	2/89	20/10723	0.011744933	0.0334432	0.019487579	2
792	Exosomes	R-HSA-4420332	Defective B3GALT6 causes EDSP2 and SEMDJL1	2/89	20/10723	0.011744933	0.0334432	0.019487579	2
793	Exosomes	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	4/89	108/10723	0.012346711	0.03457079	0.020144633	4
794	Exosomes	R-HSA-5686938	Regulation of TLR by endogenous ligand	2/89	21/10723	0.012911796	0.035560356	0.02072126	2
795	Exosomes	R-HSA-2024096	HS-GAG degradation	2/89	22/10723	0.014127041	0.038279725	0.022305855	2
796	Exosomes	R-HSA-3906995	Diseases associated with O-glycosylation of proteins	3/89	67/10723	0.01807272	0.048193921	0.028082924	3