

Pathways	#Genes	#Genes enriched	expected	Fold Enrichment	+/	raw P value	Pathway database
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	76	3	0.47	6.4	+	0.0116	Reactome
Activation, myristoylation of BID and translocation to mitochondria	4	1	0.02	40.51	+	0.0245	Reactome
Alzheimer disease-presenilin pathway	127	3	0.78	3.83	+	0.0441	Panther pathway
Antigen processing-Cross presentation	106	3	0.65	4.59	+	0.028	Reactome
APC/C:Cdc20 mediated degradation of mitotic proteins	75	3	0.46	6.48	+	0.0112	Reactome
APC/C:Cdc20 mediated degradation of Securin	67	3	0.41	7.26	+	0.00825	Reactome
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	73	3	0.45	6.66	+	0.0104	Reactome
APC/C-mediated degradation of cell cycle proteins	87	3	0.54	5.59	+	0.0167	Reactome
APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	73	3	0.45	6.66	+	0.0104	Reactome
Apoptosis	173	4	1.07	3.75	+	0.0224	Reactome
Aryl hydrocarbon receptor signalling	7	1	0.04	23.15	+	0.0424	Reactome
Assembly of the pre-replicative complex	110	3	0.68	4.42	+	0.0307	Reactome
Asymmetric localization of PCP proteins	63	3	0.39	7.72	+	0.00696	Reactome
AUF1 (hnRNP D0) binds and destabilizes mRNA	53	2	0.33	6.11	+	0.0424	Reactome
Autodegradation of Cdh1 by Cdh1:APC/C	63	3	0.39	7.72	+	0.00696	Reactome
Autodegradation of the E3 ubiquitin ligase COP1	51	2	0.31	6.35	+	0.0396	Reactome
Cdc20:Phospho-APC/C mediated degradation of Cyclin A	72	3	0.44	6.75	+	0.01	Reactome
CDC42 GTPase cycle	154	4	0.95	4.21	+	0.0153	Reactome
CDK-mediated phosphorylation and removal of Cdc6	72	3	0.44	6.75	+	0.01	Reactome
Cell cycle	22	2	0.14	14.73	+	0.00805	Panther pathway
Cellular response to hypoxia	74	3	0.46	6.57	+	0.0108	Reactome
Citric acid cycle (TCA cycle)	22	2	0.14	14.73	+	0.00805	Reactome
Class B/2 (Secretin family receptors)	93	3	0.57	5.23	+	0.0199	Reactome
CLEC7A (Dectin-1) signaling	96	3	0.59	5.06	+	0.0216	Reactome
Coenzyme A biosynthesis	7	1	0.04	23.15	+	0.0424	Reactome
Coenzyme A biosynthesis	8	1	0.05	20.26	+	0.0483	Panther pathway
Cross-presentation of soluble exogenous antigens (endosomes)	49	2	0.3	6.61	+	0.0368	Reactome
C-type lectin receptors (CLRs)	138	4	0.85	4.7	+	0.0106	Reactome
Dectin-1 mediated noncanonical NF-kB signaling	59	3	0.36	8.24	+	0.0058	Reactome
Degradation of AXIN	54	2	0.33	6	+	0.0439	Reactome
Degradation of DVL	56	2	0.35	5.79	+	0.0469	Reactome
DNA Replication Pre-Initiation	127	3	0.78	3.83	+	0.0441	Reactome
FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	54	2	0.33	6	+	0.0439	Reactome
GSK3B and BTIRC:CUL1-mediated-degradation of NFE2L2	51	2	0.31	6.35	+	0.0396	Reactome
Hedgehog 'on' state	84	3	0.52	5.79	+	0.0152	Reactome
Hh mutants abrogate ligand secretion	58	2	0.36	5.59	+	0.0499	Reactome
Hh mutants are degraded by ERAD	55	2	0.34	5.89	+	0.0454	Reactome
Host Interactions of HIV factors	125	3	0.77	3.89	+	0.0424	Reactome
Interferon alpha/beta signaling	76	3	0.47	6.4	+	0.0116	Reactome
Interleukin-1 signaling	112	3	0.69	4.34	+	0.0322	Reactome
Intra-Golgi traffic	43	2	0.27	7.54	+	0.0289	Reactome
IRE1alpha activates chaperones	49	2	0.3	6.61	+	0.0368	Reactome
Ligand-receptor interactions	8	1	0.05	20.26	+	0.0483	Reactome
Metabolism of polyamines	57	2	0.35	5.69	+	0.0484	Reactome
mRNA Splicing	212	4	1.31	3.06	+	0.0425	Reactome
mRNA splicing	7	1	0.04	23.15	+	0.0424	Panther pathway
mRNA Splicing - Major Pathway	204	4	1.26	3.18	+	0.0378	Reactome
mRNA Splicing - Minor Pathway	50	2	0.31	6.48	+	0.0382	Reactome
Negative regulation of NOTCH4 signaling	52	2	0.32	6.23	+	0.041	Reactome
NIK-->noncanonical NF-kB signaling	58	3	0.36	8.38	+	0.00553	Reactome
Orexin and neuropeptides FF and QRFP bind to their respective receptors	8	1	0.05	20.26	+	0.0483	Reactome
p53-Independent DNA Damage Response	51	2	0.31	6.35	+	0.0396	Reactome
p53-Independent G1/S DNA damage checkpoint	51	2	0.31	6.35	+	0.0396	Reactome
PCP/CE pathway	91	3	0.56	5.34	+	0.0188	Reactome
Programmed Cell Death	205	4	1.27	3.16	+	0.0384	Reactome
PTK6 Regulates Proteins Involved in RNA Processing	5	1	0.03	32.41	+	0.0305	Reactome
Pyruvate metabolism and Citric Acid (TCA) cycle	54	2	0.33	6	+	0.0439	Reactome
RAC1 GTPase cycle	183	4	1.13	3.54	+	0.0269	Reactome
Regulation of activated PAK-2p34 by proteasome mediated degradation	49	2	0.3	6.61	+	0.0368	Reactome
Regulation of APC/C activators between G1/S and early anaphase	80	3	0.49	6.08	+	0.0134	Reactome
Regulation of Apoptosis	52	2	0.32	6.23	+	0.041	Reactome
Regulation of mitotic cell cycle	87	3	0.54	5.59	+	0.0167	Reactome
Regulation of ornithine decarboxylase (ODC)	50	2	0.31	6.48	+	0.0382	Reactome
Regulation of RUNX3 expression and activity	53	2	0.33	6.11	+	0.0424	Reactome
Replication of the SARS-CoV-1 genome	4	1	0.02	40.51	+	0.0245	Reactome
Replication of the SARS-CoV-2 genome	4	1	0.02	40.51	+	0.0245	Reactome
RMTs methylate histone arginines	48	2	0.3	6.75	+	0.0354	Reactome
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known	36	2	0.22	9	+	0.0208	Reactome
RUNX1 regulates transcription of genes involved in differentiation of keratinocytes	8	1	0.05	20.26	+	0.0483	Reactome
SARS-CoV-1 Genome Replication and Transcription	4	1	0.02	40.51	+	0.0245	Reactome
SARS-CoV-2 Genome Replication and Transcription	4	1	0.02	40.51	+	0.0245	Reactome
SCF-beta-TrCP mediated degradation of Emi1	54	2	0.33	6	+	0.0439	Reactome
Somitogenesis	54	2	0.33	6	+	0.0439	Reactome
Stabilization of p53	55	2	0.34	5.89	+	0.0454	Reactome
Switching of origins to a post-replicative state	91	3	0.56	5.34	+	0.0188	Reactome
Synaptic vesicle trafficking	30	2	0.19	10.8	+	0.0147	Panther pathway
Synthesis of DNA	120	3	0.74	4.05	+	0.0383	Reactome
TCF dependent signaling in response to WNT	200	4	1.23	3.24	+	0.0355	Reactome
TNFR2 non-canonical NF-kB pathway	98	3	0.6	4.96	+	0.0228	Reactome
Toxicity of botulinum toxin type C (botC)	3	1	0.02	54.02	+	0.0184	Reactome
Trafficking and processing of endosomal TLR	13	2	0.08	24.93	+	0.00282	Reactome
Transcriptional regulation by RUNX1	202	5	1.25	4.01	+	0.0084	Reactome
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	51	2	0.31	6.35	+	0.0396	Reactome
Ubiquitin proteasome pathway	58	2	0.36	5.59	+	0.0499	Panther pathway
Ubiquitin-dependent degradation of Cyclin D	51	2	0.31	6.35	+	0.0396	Reactome
Vif-mediated degradation of APOBEC3G	52	2	0.32	6.23	+	0.041	Reactome
Vpr-mediated induction of apoptosis by mitochondrial outer membrane permeabilization	3	1	0.02	54.02	+	0.0184	Reactome
Vpu mediated degradation of CD4	51	2	0.31	6.35	+	0.0396	Reactome