



Functional Annotation Chart

[Help and Manual](#)

Current Gene List: condition_specific_gene_list
Current Background: Homo sapiens
2052 DAVID IDs

Options

Rerun Using Options

Create Sublist

501 chart records

Sublist	Category	Term
<input type="checkbox"/>	REACTOME_PATHWAY	L13a-mediated translational silencing of Ceruloplasmin expression
<input type="checkbox"/>	REACTOME_PATHWAY	GTP hydrolysis and joining of the 60S ribosomal subunit
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of a pool of free 40S subunits
<input type="checkbox"/>	REACTOME_PATHWAY	SRP-dependent cotranslational protein targeting to membrane
<input type="checkbox"/>	REACTOME_PATHWAY	Eukaryotic Translation Initiation
<input type="checkbox"/>	REACTOME_PATHWAY	Cap-dependent Translation Initiation
<input type="checkbox"/>	REACTOME_PATHWAY	Eukaryotic Translation Elongation
<input type="checkbox"/>	REACTOME_PATHWAY	Viral mRNA Translation
<input type="checkbox"/>	REACTOME_PATHWAY	Peptide chain elongation
<input type="checkbox"/>	REACTOME_PATHWAY	Metabolism of RNA
<input type="checkbox"/>	REACTOME_PATHWAY	Viral Infection Pathways
<input type="checkbox"/>	REACTOME_PATHWAY	Infectious disease
<input type="checkbox"/>	REACTOME_PATHWAY	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
<input type="checkbox"/>	REACTOME_PATHWAY	Selenocysteine synthesis
<input type="checkbox"/>	REACTOME_PATHWAY	Eukaryotic Translation Termination
<input type="checkbox"/>	REACTOME_PATHWAY	Nonsense-Mediated Decay (NMD)
<input type="checkbox"/>	REACTOME_PATHWAY	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)
<input type="checkbox"/>	REACTOME_PATHWAY	Response of EIF2AK4 (GCN2) to amino acid deficiency
<input type="checkbox"/>	REACTOME_PATHWAY	Influenza Infection
<input type="checkbox"/>	REACTOME_PATHWAY	Influenza Viral RNA Transcription and Replication
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of expression of SLITs and ROBOs
<input type="checkbox"/>	REACTOME_PATHWAY	Translation
<input type="checkbox"/>	REACTOME_PATHWAY	Cellular response to starvation
<input type="checkbox"/>	REACTOME_PATHWAY	Selenoamino acid metabolism
<input type="checkbox"/>	REACTOME_PATHWAY	Cellular responses to stress
<input type="checkbox"/>	REACTOME_PATHWAY	Cellular responses to stimuli
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by ROBO receptors
<input type="checkbox"/>	REACTOME_PATHWAY	Major pathway of rRNA processing in the nucleolus and cytosol
<input type="checkbox"/>	REACTOME_PATHWAY	rRNA processing in the nucleus and cytosol
<input type="checkbox"/>	REACTOME_PATHWAY	Disease
<input type="checkbox"/>	REACTOME_PATHWAY	rRNA processing
<input type="checkbox"/>	REACTOME_PATHWAY	Translation initiation complex formation
<input type="checkbox"/>	REACTOME_PATHWAY	Ribosomal scanning and start codon recognition
<input type="checkbox"/>	REACTOME_PATHWAY	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S
<input type="checkbox"/>	REACTOME_PATHWAY	Metabolism of proteins
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of the ternary complex, and subsequently, the 43S complex
<input type="checkbox"/>	REACTOME_PATHWAY	Immune System
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV Infections
<input type="checkbox"/>	REACTOME_PATHWAY	Processing of Capped Intron-Containing Pre-mRNA
<input type="checkbox"/>	REACTOME_PATHWAY	Metabolism of amino acids and derivatives
<input type="checkbox"/>	REACTOME_PATHWAY	mRNA Splicing - Major Pathway
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-1-host interactions
<input type="checkbox"/>	REACTOME_PATHWAY	mRNA Splicing
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-1 modulates host translation machinery
<input type="checkbox"/>	REACTOME_PATHWAY	Neutrophil degranulation
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-1 Infection

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RT	Genes	Count	%	P-Value	Benjamini
RT		93	4.5	1.4E-61	2.5E-58
RT		93	4.5	6.4E-61	5.9E-58
RT		87	4.2	1.6E-59	8.5E-57
RT		92	4.5	1.9E-59	8.5E-57
RT		93	4.5	1.3E-56	3.8E-54
RT		93	4.5	1.3E-56	3.8E-54
RT		81	3.9	4.6E-56	1.2E-53
RT		78	3.8	2.4E-54	4.9E-52
RT		78	3.8	2.4E-54	4.9E-52
RT		254	12.4	1.6E-53	2.9E-51
RT		276	13.5	2.4E-53	4.0E-51
RT		311	15.2	4.9E-51	7.5E-49
RT		78	3.8	3.6E-50	5.1E-48
RT		77	3.8	5.2E-50	6.4E-48
RT		77	3.8	5.2E-50	6.4E-48
RT		85	4.1	2.4E-48	2.5E-46
RT		85	4.1	2.4E-48	2.5E-46
RT		79	3.8	5.7E-48	5.8E-46
RT		97	4.7	4.9E-45	4.7E-43
RT		87	4.2	4.2E-42	3.8E-40
RT		98	4.8	3.6E-41	3.1E-39
RT		132	6.4	7.7E-41	6.4E-39
RT		92	4.5	5.1E-40	4.1E-38
RT		79	3.8	6.0E-40	4.6E-38
RT		238	11.6	5.2E-36	3.8E-34
RT		239	11.6	3.6E-35	2.5E-33
RT		104	5.1	2.0E-34	1.3E-32
RT		93	4.5	3.0E-33	1.9E-31
RT		95	4.6	1.4E-32	9.0E-31
RT		407	19.8	1.9E-31	1.2E-29
RT		96	4.7	3.5E-31	2.1E-29
RT		45	2.2	9.8E-27	5.4E-25
RT		45	2.2	9.8E-27	5.4E-25
RT		45	2.2	3.2E-26	1.7E-24
RT		427	20.8	1.3E-24	6.7E-23
RT		40	1.9	5.4E-24	2.8E-22
RT		419	20.4	2.3E-23	1.1E-21
RT		127	6.2	1.5E-20	7.1E-19
RT		99	4.8	2.7E-20	1.3E-18
RT		117	5.7	1.3E-19	5.8E-18
RT		79	3.8	4.7E-19	2.1E-17
RT		49	2.4	4.5E-18	2.0E-16
RT		79	3.8	6.1E-18	2.6E-16
RT		29	1.4	9.4E-18	3.9E-16
RT		133	6.5	2.3E-17	9.2E-16
RT		60	2.9	4.8E-17	1.9E-15

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	REACTOME_PATHWAY	Innate Immune System	RT	<div></div>	237	11.5	4.9E-17	1.9E-15
<input type="checkbox"/>	REACTOME_PATHWAY	HIV Infection	RT	<div></div>	78	3.8	3.1E-15	1.2E-13
<input type="checkbox"/>	REACTOME_PATHWAY	Cytokine Signaling in Immune system	RT	<div></div>	179	8.7	1.2E-13	4.3E-12
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-2 Infection	RT	<div></div>	89	4.3	1.3E-13	4.8E-12
<input type="checkbox"/>	REACTOME_PATHWAY	Axon guidance	RT	<div></div>	136	6.6	4.3E-13	1.5E-11
<input type="checkbox"/>	REACTOME_PATHWAY	Nervous system development	RT	<div></div>	138	6.7	3.0E-12	1.1E-10
<input type="checkbox"/>	REACTOME_PATHWAY	TCR signaling	RT	<div></div>	47	2.3	5.2E-12	1.8E-10
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-2-host interactions	RT	<div></div>	65	3.2	1.2E-11	3.9E-10
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-2 modulates host translation machinery	RT	<div></div>	28	1.4	1.8E-11	6.1E-10
<input type="checkbox"/>	REACTOME_PATHWAY	Programmed Cell Death	RT	<div></div>	66	3.2	4.0E-11	1.3E-9
<input type="checkbox"/>	REACTOME_PATHWAY	Downstream TCR signaling	RT	<div></div>	40	1.9	5.7E-11	1.8E-9
<input type="checkbox"/>	REACTOME_PATHWAY	Adaptive Immune System	RT	<div></div>	166	8.1	8.3E-11	2.6E-9
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by ALK in cancer	RT	<div></div>	37	1.8	3.8E-10	1.2E-8
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by ALK fusions and activated point mutants	RT	<div></div>	37	1.8	3.8E-10	1.2E-8
<input type="checkbox"/>	REACTOME_PATHWAY	Membrane Trafficking	RT	<div></div>	140	6.8	7.3E-10	2.2E-8
<input type="checkbox"/>	REACTOME_PATHWAY	Diseases of signal transduction by growth factor receptors and second messengers	RT	<div></div>	109	5.3	9.5E-10	2.8E-8
<input type="checkbox"/>	REACTOME_PATHWAY	Host Interactions of HIV factors	RT	<div></div>	45	2.2	1.6E-9	4.8E-8
<input type="checkbox"/>	REACTOME_PATHWAY	Interferon Signaling	RT	<div></div>	72	3.5	6.2E-9	1.8E-7
<input type="checkbox"/>	REACTOME_PATHWAY	Vesicle-mediated transport	RT	<div></div>	143	7.0	6.9E-9	1.9E-7
<input type="checkbox"/>	REACTOME_PATHWAY	Regulated Necrosis	RT	<div></div>	27	1.3	1.1E-8	3.0E-7
<input type="checkbox"/>	REACTOME_PATHWAY	Translocation of ZAP-70 to Immunological synapse	RT	<div></div>	14	0.7	5.1E-8	1.4E-6
<input type="checkbox"/>	REACTOME_PATHWAY	HIV Life Cycle	RT	<div></div>	46	2.2	5.7E-8	1.5E-6
<input type="checkbox"/>	REACTOME_PATHWAY	Phosphorylation of CD3 and TCR zeta chains	RT	<div></div>	15	0.7	6.1E-8	1.6E-6
<input type="checkbox"/>	REACTOME_PATHWAY	Transcriptional Regulation by TP53	RT	<div></div>	85	4.1	1.5E-7	4.0E-6
<input type="checkbox"/>	REACTOME_PATHWAY	mRNA 3'-end processing	RT	<div></div>	25	1.2	1.7E-7	4.5E-6
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by Interleukins	RT	<div></div>	103	5.0	3.6E-7	9.1E-6
<input type="checkbox"/>	REACTOME_PATHWAY	Apoptosis	RT	<div></div>	50	2.4	5.2E-7	1.3E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Respiratory syncytial virus (RSV) genome replication, transcription and translation	RT	<div></div>	12	0.6	5.4E-7	1.3E-5
<input type="checkbox"/>	REACTOME_PATHWAY	ER-Phagosome pathway	RT	<div></div>	31	1.5	9.2E-7	2.3E-5
<input type="checkbox"/>	REACTOME_PATHWAY	RNA Polymerase II Transcription Termination	RT	<div></div>	26	1.3	9.5E-7	2.3E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Antigen processing-Cross presentation	RT	<div></div>	34	1.7	1.2E-6	2.9E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Costimulation by the CD28 family	RT	<div></div>	26	1.3	1.3E-6	3.0E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Nuclear events mediated by NFE2L2	RT	<div></div>	32	1.6	1.7E-6	4.0E-5
<input type="checkbox"/>	REACTOME_PATHWAY	KEAP1-NFE2L2 pathway	RT	<div></div>	38	1.9	1.8E-6	4.1E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Cellular response to chemical stress	RT	<div></div>	55	2.7	2.2E-6	4.9E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Potential therapeutics for SARS	RT	<div></div>	32	1.6	2.8E-6	6.2E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Unfolded Protein Response (UPR)	RT	<div></div>	31	1.5	3.3E-6	7.3E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Interferon gamma signaling	RT	<div></div>	31	1.5	4.2E-6	9.1E-5
<input type="checkbox"/>	REACTOME_PATHWAY	Late Phase of HIV Life Cycle	RT	<div></div>	39	1.9	4.9E-6	1.1E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of TNFR1 signaling	RT	<div></div>	20	1.0	5.4E-6	1.1E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Downstream signaling events of B Cell Receptor (BCR)	RT	<div></div>	28	1.4	5.4E-6	1.1E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Antigen Presentation: Folding, assembly and peptide loading of class I MHC	RT	<div></div>	15	0.7	5.9E-6	1.2E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-12 family signaling	RT	<div></div>	22	1.1	6.7E-6	1.4E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Post-translational protein modification	RT	<div></div>	251	12.2	6.9E-6	1.4E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Class I MHC mediated antigen processing & presentation	RT	<div></div>	82	4.0	1.0E-5	2.0E-4
<input type="checkbox"/>	REACTOME_PATHWAY	PD-1 signaling	RT	<div></div>	13	0.6	1.0E-5	2.0E-4
<input type="checkbox"/>	REACTOME_PATHWAY	RHOBTB2 GTPase cycle	RT	<div></div>	13	0.6	1.0E-5	2.0E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-1 signaling	RT	<div></div>	34	1.7	1.1E-5	2.1E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Generation of second messenger molecules	RT	<div></div>	16	0.8	1.1E-5	2.1E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Interferon alpha/beta signaling	RT	<div></div>	26	1.3	1.2E-5	2.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	The citric acid (TCA) cycle and respiratory electron transport	RT	<div></div>	46	2.2	1.3E-5	2.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Cell Cycle	RT	<div></div>	132	6.4	1.3E-5	2.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	CLEC7A (Dectin-1) signaling	RT	<div></div>	31	1.5	1.3E-5	2.4E-4
<input type="checkbox"/>	REACTOME_PATHWAY	TNFR2 non-canonical NF-kB pathway	RT	<div></div>	31	1.5	1.6E-5	2.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-1 family signaling	RT	<div></div>	41	2.0	1.6E-5	2.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Mitotic Anaphase	RT	<div></div>	56	2.7	1.7E-5	3.0E-4
<input type="checkbox"/>	REACTOME_PATHWAY	RHOBTB GTPase Cycle	RT	<div></div>	16	0.8	1.7E-5	3.0E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Asparagine N-linked glycosylation	RT	<div></div>	68	3.3	1.8E-5	3.1E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of mRNA stability by proteins that bind AU-rich elements	RT	<div></div>	28	1.4	1.8E-5	3.2E-4
<input type="checkbox"/>	REACTOME_PATHWAY	G2/M Transition	RT	<div></div>	49	2.4	1.9E-5	3.2E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Mitotic Metaphase and Anaphase	RT	<div></div>	56	2.7	1.9E-5	3.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Mitochondrial protein degradation	RT	<div></div>	30	1.5	2.0E-5	3.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	MHC class II antigen presentation	RT	<div></div>	35	1.7	2.0E-5	3.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	IRE1alpha activates chaperones	RT	<div></div>	20	1.0	2.1E-5	3.5E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Transport of Mature Transcript to Cytoplasm	RT	<div></div>	27	1.3	2.2E-5	3.6E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Fc epsilon receptor (FCERI) signaling	RT	<div></div>	37	1.8	2.2E-5	3.6E-4
<input type="checkbox"/>	REACTOME_PATHWAY	RIPK1-mediated regulated necrosis	RT	<div></div>	15	0.7	2.4E-5	3.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Endosomal Sorting Complex Required For Transport (ESCRT)	RT	<div></div>	15	0.7	2.4E-5	3.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of necroptotic cell death	RT	<div></div>	15	0.7	2.4E-5	3.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Mitotic G2-G2/M phases	RT	<div></div>	49	2.4	2.5E-5	3.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	TNF signaling	RT	<div></div>	21	1.0	2.5E-5	4.0E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Autophagy	RT	<div></div>	40	1.9	2.8E-5	4.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Activation of NF-kappaB in B cells	RT	<div></div>	23	1.1	3.3E-5	5.1E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Nuclear events stimulated by ALK signaling in cancer	RT	<div></div>	15	0.7	3.7E-5	5.7E-4
<input type="checkbox"/>	REACTOME_PATHWAY	FCERI mediated NF-kB activation	RT	<div></div>	26	1.3	4.1E-5	6.3E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by the B Cell Receptor (BCR)	RT	<div></div>	32	1.6	4.4E-5	6.6E-4
<input type="checkbox"/>	REACTOME_PATHWAY	ER to Golgi Anterograde Transport	RT	<div></div>	40	1.9	4.5E-5	6.6E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-21 signaling	RT	<div></div>	8	0.4	6.2E-5	9.2E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Cellular response to heat stress	RT	<div></div>	27	1.3	6.6E-5	9.6E-4
<input type="checkbox"/>	REACTOME_PATHWAY	AUF1 (hnRNP D0) binds and destabilizes mRNA	RT	<div></div>	20	1.0	6.9E-5	9.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Maturation of hRSV A proteins	RT	<div></div>	9	0.4	6.9E-5	9.9E-4
<input type="checkbox"/>	REACTOME_PATHWAY	Transport of Mature mRNA derived from an Intron-Containing Transcript	RT	<div></div>	24	1.2	7.5E-5	1.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	GSK3B and BTRC:CUL1-mediated-degradation of NFE2L2	RT	<div></div>	19	0.9	7.9E-5	1.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor 3 (TLR3) Cascade	RT	<div></div>	30	1.5	7.9E-5	1.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	M-decay: degradation of maternal mRNAs by maternally stored factors	RT	<div></div>	12	0.6	1.1E-4	1.5E-3

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	REACTOME_PATHWAY	trans-Golgi Network Vesicle Budding	RT	<div></div>	23	1.1	1.1E-4	1.6E-3
<input type="checkbox"/>	REACTOME_PATHWAY	NFE2L2 regulates pentose phosphate pathway genes	RT	<div></div>	7	0.3	1.2E-4	1.7E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Negative regulation of NOTCH4 signaling	RT	<div></div>	19	0.9	1.4E-4	1.9E-3
<input type="checkbox"/>	REACTOME_PATHWAY	PTEN Regulation	RT	<div></div>	36	1.8	1.4E-4	1.9E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Cell Cycle, Mitotic	RT	<div></div>	106	5.2	1.4E-4	1.9E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Endosomal/Vacuolar pathway	RT	<div></div>	8	0.4	1.5E-4	2.0E-3
<input type="checkbox"/>	REACTOME_PATHWAY	NIK-->noncanonical NF-kB signaling	RT	<div></div>	20	1.0	1.5E-4	2.0E-3
<input type="checkbox"/>	REACTOME_PATHWAY	XBP1(S) activates chaperone genes	RT	<div></div>	18	0.9	1.6E-4	2.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Transport to the Golgi and subsequent modification	RT	<div></div>	44	2.1	1.6E-4	2.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of HSF1-mediated heat shock response	RT	<div></div>	22	1.1	1.7E-4	2.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by TGF-beta Receptor Complex	RT	<div></div>	27	1.3	1.8E-4	2.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Budding and maturation of HIV virion	RT	<div></div>	13	0.6	1.8E-4	2.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	TRIF(TICAM1)-mediated TLR4 signaling	RT	<div></div>	30	1.5	1.9E-4	2.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	MyD88-independent TLR4 cascade	RT	<div></div>	30	1.5	1.9E-4	2.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Dectin-1 mediated noncanonical NF-kB signaling	RT	<div></div>	20	1.0	1.9E-4	2.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Death Receptor Signaling	RT	<div></div>	38	1.9	2.2E-4	2.8E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	RT	<div></div>	15	0.7	2.3E-4	2.8E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Hh mutants are degraded by ERAD	RT	<div></div>	19	0.9	2.3E-4	2.8E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Antiviral mechanism by IFN-stimulated genes	RT	<div></div>	37	1.8	2.4E-4	2.9E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-12 signaling	RT	<div></div>	17	0.8	2.4E-4	2.9E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Defective CFTR causes cystic fibrosis	RT	<div></div>	20	1.0	2.5E-4	3.0E-3
<input type="checkbox"/>	REACTOME_PATHWAY	SUMO E3 ligases SUMOylate target proteins	RT	<div></div>	43	2.1	2.5E-4	3.0E-3
<input type="checkbox"/>	REACTOME_PATHWAY	SUMOylation	RT	<div></div>	44	2.1	2.6E-4	3.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Metabolism	RT	<div></div>	335	16.3	2.8E-4	3.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Toll-like Receptor Cascades	RT	<div></div>	40	1.9	3.2E-4	3.8E-3
<input type="checkbox"/>	REACTOME_PATHWAY	DDX58/IFIH1-mediated induction of interferon-alpha/beta	RT	<div></div>	24	1.2	3.3E-4	3.8E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor 4 (TLR4) Cascade	RT	<div></div>	36	1.8	3.4E-4	3.9E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Respiratory electron transport	RT	<div></div>	28	1.4	3.5E-4	4.0E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Macroautophagy	RT	<div></div>	34	1.7	3.9E-4	4.5E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Degradation of beta-catenin by the destruction complex	RT	<div></div>	24	1.2	4.0E-4	4.5E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Respiratory Syncytial Virus Infection Pathway	RT	<div></div>	31	1.5	4.1E-4	4.7E-3
<input type="checkbox"/>	REACTOME_PATHWAY	MAP3K8 (TPL2)-dependent MAPK1/3 activation	RT	<div></div>	9	0.4	4.7E-4	5.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Hh mutants abrogate ligand secretion	RT	<div></div>	19	0.9	4.7E-4	5.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	C-type lectin receptors (CLRs)	RT	<div></div>	35	1.7	4.8E-4	5.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Cytosolic sensors of pathogen-associated DNA	RT	<div></div>	20	1.0	4.9E-4	5.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of PTEN stability and activity	RT	<div></div>	21	1.0	5.0E-4	5.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	The role of Nef in HIV-1 replication and disease pathogenesis	RT	<div></div>	12	0.6	5.7E-4	6.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Pyroptosis	RT	<div></div>	12	0.6	5.7E-4	6.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Intrinsic Pathway for Apoptosis	RT	<div></div>	18	0.9	5.7E-4	6.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	RT	<div></div>	18	0.9	5.7E-4	6.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Deadenylation of mRNA	RT	<div></div>	11	0.5	5.8E-4	6.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	GLI3 is processed to GLI3R by the proteasome	RT	<div></div>	19	0.9	5.9E-4	6.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	SCF(Skp2)-mediated degradation of p27/p21	RT	<div></div>	19	0.9	5.9E-4	6.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Degradation of GLI2 by the proteasome	RT	<div></div>	19	0.9	5.9E-4	6.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	COPI-mediated anterograde transport	RT	<div></div>	27	1.3	6.1E-4	6.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	TBC/RABGAPs	RT	<div></div>	16	0.8	6.3E-4	6.5E-3
<input type="checkbox"/>	REACTOME_PATHWAY	M Phase	RT	<div></div>	80	3.9	6.3E-4	6.5E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of ornithine decarboxylase (ODC)	RT	<div></div>	17	0.8	6.9E-4	7.0E-3
<input type="checkbox"/>	REACTOME_PATHWAY	DEX/H-box helicases activate type I IFN and inflammatory cytokines production	RT	<div></div>	6	0.3	7.0E-4	7.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	RHO GTPase cycle	RT	<div></div>	85	4.1	7.1E-4	7.1E-3
<input type="checkbox"/>	REACTOME_PATHWAY	RNA Polymerase II Pre-transcription Events	RT	<div></div>	23	1.1	7.1E-4	7.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Clathrin-mediated endocytosis	RT	<div></div>	35	1.7	7.2E-4	7.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Golgi Associated Vesicle Biogenesis	RT	<div></div>	18	0.9	7.2E-4	7.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	TNFR1-induced NF-kappa-B signaling pathway	RT	<div></div>	13	0.6	7.3E-4	7.2E-3
<input type="checkbox"/>	REACTOME_PATHWAY	TNFR1-induced proapoptotic signaling	RT	<div></div>	11	0.5	8.5E-4	8.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by NOTCH4	RT	<div></div>	23	1.1	8.6E-4	8.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Apoptotic cleavage of cellular proteins	RT	<div></div>	14	0.7	8.7E-4	8.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Ypu mediated degradation of CD4	RT	<div></div>	17	0.8	8.7E-4	8.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Translation of Structural Proteins	RT	<div></div>	18	0.9	9.0E-4	8.7E-3
<input type="checkbox"/>	REACTOME_PATHWAY	APC/C:Cdc20 mediated degradation of Securin	RT	<div></div>	20	1.0	9.1E-4	8.8E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of PLK1 Activity at G2/M Transition	RT	<div></div>	24	1.2	9.8E-4	9.3E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Deubiquitination	RT	<div></div>	60	2.9	9.9E-4	9.4E-3
<input type="checkbox"/>	REACTOME_PATHWAY	Bacterial Infection Pathways	RT	<div></div>	21	1.0	1.1E-3	1.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of RUNX2 expression and activity	RT	<div></div>	21	1.0	1.1E-3	1.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Attenuation phase	RT	<div></div>	8	0.4	1.1E-3	1.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Autodegradation of Cdh1 by Cdh1:APC/C	RT	<div></div>	19	0.9	1.1E-3	1.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	RT	<div></div>	31	1.5	1.1E-3	1.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Gene expression (Transcription)	RT	<div></div>	246	12.0	1.2E-3	1.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Downregulation of TGF-beta receptor signaling	RT	<div></div>	11	0.5	1.2E-3	1.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	N-glycan trimming in the ER and Calnexin/Calreticulin cycle	RT	<div></div>	13	0.6	1.3E-3	1.2E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Vif-mediated degradation of APOBEC3G	RT	<div></div>	17	0.8	1.4E-3	1.2E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Metabolism of polyamines	RT	<div></div>	18	0.9	1.4E-3	1.2E-2
<input type="checkbox"/>	REACTOME_PATHWAY	STAT3 nuclear events downstream of ALK signaling	RT	<div></div>	7	0.3	1.4E-3	1.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Cyclin A:Cdk2-associated events at S phase entry	RT	<div></div>	23	1.1	1.4E-3	1.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Nuclear Envelope (NE) Reassembly	RT	<div></div>	21	1.0	1.6E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Cellular response to hypoxia	RT	<div></div>	21	1.0	1.6E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Circadian Clock	RT	<div></div>	20	1.0	1.6E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Hedgehog ligand biogenesis	RT	<div></div>	19	0.9	1.7E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Degradation of GLI1 by the proteasome	RT	<div></div>	18	0.9	1.7E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Pyruvate metabolism and Citric Acid (TCA) cycle	RT	<div></div>	17	0.8	1.7E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	HSP90 chaperone cycle for steroid hormone receptors (SHR) in the presence of ligand	RT	<div></div>	17	0.8	1.7E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of RUNX3 expression and activity	RT	<div></div>	17	0.8	1.7E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	SCF-beta-TrCP mediated degradation of Emi1	RT	<div></div>	17	0.8	1.7E-3	1.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor 5 (TLR5) Cascade	RT	<div></div>	25	1.2	1.7E-3	1.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MyD88 cascade initiated on plasma membrane	RT	<div></div>	25	1.2	1.7E-3	1.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor 10 (TLR10) Cascade	RT	<div></div>	25	1.2	1.7E-3	1.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Initiation of Nuclear Envelope (NE) Reformation	RT	<div></div>	9	0.4	1.9E-3	1.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	RT	<div></div>	19	0.9	2.0E-3	1.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-2 activates/modulates innate and adaptive immune responses	RT	<div></div>	30	1.5	2.1E-3	1.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MyD88 dependent cascade initiated on endosome	RT	<div></div>	26	1.3	2.2E-3	1.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	S Phase	RT	<div></div>	36	1.8	2.4E-3	2.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Cyclin E associated events during G1/S transition	RT	<div></div>	22	1.1	2.5E-3	2.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor 7/8 (TLR7/8) Cascade	RT	<div></div>	26	1.3	2.5E-3	2.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Z-decay: degradation of maternal mRNAs by zygotically expressed factors	RT	<div></div>	7	0.3	2.5E-3	2.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	HSF1 activation	RT	<div></div>	7	0.3	2.5E-3	2.0E-2

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-35 Signalling	RT	<div></div>	7	0.3	2.5E-3	2.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Apoptotic execution phase	RT	<div></div>	16	0.8	2.6E-3	2.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Ubiquitin-dependent degradation of Cyclin D	RT	<div></div>	16	0.8	2.6E-3	2.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	ABC transporter disorders	RT	<div></div>	21	1.0	2.6E-3	2.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	RT	<div></div>	20	1.0	2.7E-3	2.2E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-9 signaling	RT	<div></div>	6	0.3	3.3E-3	2.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Nef Mediated CD4 Down-regulation	RT	<div></div>	6	0.3	3.3E-3	2.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MAPK family signaling cascades	RT	<div></div>	62	3.0	3.3E-3	2.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MyD88:MAL(TIRAP) cascade initiated on plasma membrane	RT	<div></div>	27	1.3	3.4E-3	2.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor TLR6:TLR2 Cascade	RT	<div></div>	27	1.3	3.4E-3	2.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of APC/C activators between G1/S and early anaphase	RT	<div></div>	21	1.0	3.6E-3	2.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Intra-Golgi and retrograde Golgi-to-ER traffic	RT	<div></div>	42	2.0	3.7E-3	2.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Separation of Sister Chromatids	RT	<div></div>	40	1.9	3.7E-3	2.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor 9 (TLR9) Cascade	RT	<div></div>	26	1.3	3.7E-3	2.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	PKR-mediated signaling	RT	<div></div>	20	1.0	3.8E-3	2.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	APC/C:Cdc20 mediated degradation of mitotic proteins	RT	<div></div>	20	1.0	3.8E-3	2.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	RT	<div></div>	122	5.9	4.0E-3	3.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Nef-mediates down modulation of cell surface receptors by recruiting them to clathrin adapters	RT	<div></div>	9	0.4	4.0E-3	3.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	RT	<div></div>	25	1.2	4.1E-3	3.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	RAB geranylgeranylation	RT	<div></div>	18	0.9	4.2E-3	3.2E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	RT	<div></div>	20	1.0	4.5E-3	3.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	APC/C-mediated degradation of cell cycle proteins	RT	<div></div>	22	1.1	4.5E-3	3.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of mitotic cell cycle	RT	<div></div>	22	1.1	4.5E-3	3.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Negative regulators of DDX58/IFIH1 signaling	RT	<div></div>	12	0.6	4.5E-3	3.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Degradation of AXIN	RT	<div></div>	16	0.8	4.6E-3	3.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Deadenylation-dependent mRNA decay	RT	<div></div>	16	0.8	4.6E-3	3.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-1 activates/modulates innate immune responses	RT	<div></div>	13	0.6	4.7E-3	3.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	RHOU GTPase cycle	RT	<div></div>	13	0.6	4.7E-3	3.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of activated PAK-2p34 by proteasome mediated degradation	RT	<div></div>	15	0.7	4.7E-3	3.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by Rho GTPases	RT	<div></div>	119	5.8	4.9E-3	3.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MAPK1/MAPK3 signaling	RT	<div></div>	55	2.7	4.9E-3	3.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor 2 (TLR2) Cascade	RT	<div></div>	27	1.3	5.0E-3	3.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Toll Like Receptor TLR1:TLR2 Cascade	RT	<div></div>	27	1.3	5.0E-3	3.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	RAF/MAP kinase cascade	RT	<div></div>	54	2.6	5.0E-3	3.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	The role of GTSE1 in G2/M progression after G2 checkpoint	RT	<div></div>	20	1.0	5.2E-3	3.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	PIP3 activates AKT signaling	RT	<div></div>	52	2.5	5.2E-3	3.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of actin dynamics for phagocytic cup formation	RT	<div></div>	17	0.8	5.3E-3	3.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Protein localization	RT	<div></div>	35	1.7	5.5E-3	3.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	CDK-mediated phosphorylation and removal of Cdc6	RT	<div></div>	19	0.9	5.6E-3	3.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	RT	<div></div>	19	0.9	5.6E-3	3.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Citric acid cycle (TCA cycle)	RT	<div></div>	9	0.4	5.6E-3	3.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Insertion of tail-anchored proteins into the endoplasmic reticulum membrane	RT	<div></div>	9	0.4	5.6E-3	3.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	RT	<div></div>	15	0.7	5.7E-3	3.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of WDR5-containing histone-modifying complexes	RT	<div></div>	13	0.6	5.9E-3	4.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MAPK6/MAPK4 signaling	RT	<div></div>	22	1.1	5.9E-3	4.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Cargo recognition for clathrin-mediated endocytosis	RT	<div></div>	25	1.2	6.0E-3	4.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by cytosolic FGFR1 fusion mutants	RT	<div></div>	8	0.4	6.2E-3	4.2E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Rab regulation of trafficking	RT	<div></div>	28	1.4	6.4E-3	4.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	RT	<div></div>	19	0.9	6.5E-3	4.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Early Phase of HIV Life Cycle	RT	<div></div>	7	0.3	6.5E-3	4.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-15 signaling	RT	<div></div>	7	0.3	6.5E-3	4.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Antigen processing: Ubiquitination & Proteasome degradation	RT	<div></div>	58	2.8	6.5E-3	4.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Degradation of DVL	RT	<div></div>	16	0.8	6.6E-3	4.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Stabilization of p53	RT	<div></div>	16	0.8	6.6E-3	4.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Autodegradation of the E3 ubiquitin ligase COP1	RT	<div></div>	15	0.7	6.9E-3	4.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	RT	<div></div>	15	0.7	6.9E-3	4.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	p53-Independent DNA Damage Response	RT	<div></div>	15	0.7	6.9E-3	4.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	p53-Independent G1/S DNA damage checkpoint	RT	<div></div>	15	0.7	6.9E-3	4.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of RAS by GAPs	RT	<div></div>	18	0.9	6.9E-3	4.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	COPII-mediated vesicle transport	RT	<div></div>	18	0.9	6.9E-3	4.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Mitotic G1 phase and G1/S transition	RT	<div></div>	32	1.6	7.4E-3	4.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Switching of origins to a post-replicative state	RT	<div></div>	22	1.1	7.8E-3	4.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of RNA Pol II elongation complex	RT	<div></div>	16	0.8	7.8E-3	4.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	RNA Polymerase II Transcription Elongation	RT	<div></div>	16	0.8	7.8E-3	4.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of paraxial mesoderm	RT	<div></div>	18	0.9	8.1E-3	5.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of Apoptosis	RT	<div></div>	15	0.7	8.2E-3	5.2E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Activation, myristolyation of BID and translocation to mitochondria	RT	<div></div>	4	0.2	8.6E-3	5.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	TP53 Regulates Transcription of Cell Cycle Genes	RT	<div></div>	14	0.7	8.6E-3	5.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MAP kinase activation	RT	<div></div>	17	0.8	8.7E-3	5.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	PCP/CE pathway	RT	<div></div>	22	1.1	8.8E-3	5.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Golgi-to-ER retrograde transport	RT	<div></div>	29	1.4	9.0E-3	5.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	E3 ubiquitin ligases ubiquitinate target proteins	RT	<div></div>	16	0.8	9.2E-3	5.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Ub-specific processing proteases	RT	<div></div>	43	2.1	9.3E-3	5.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Late SARS-CoV-2 Infection Events	RT	<div></div>	18	0.9	9.4E-3	5.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Transcription of the HIV genome	RT	<div></div>	18	0.9	9.4E-3	5.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Chromatin organization	RT	<div></div>	51	2.5	9.6E-3	5.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Chromatin modifying enzymes	RT	<div></div>	51	2.5	9.6E-3	5.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	TP53 Regulates Metabolic Genes	RT	<div></div>	21	1.0	9.6E-3	5.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-27 signaling	RT	<div></div>	6	0.3	9.7E-3	5.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Mitochondrial protein import	RT	<div></div>	17	0.8	1.0E-2	6.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Cross-presentation of soluble exogenous antigens (endosomes)	RT	<div></div>	14	0.7	1.0E-2	6.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Intracellular signaling by second messengers	RT	<div></div>	57	2.8	1.1E-2	6.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Nucleotide Excision Repair	RT	<div></div>	25	1.2	1.1E-2	6.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-2 family signaling	RT	<div></div>	13	0.6	1.1E-2	6.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Orc1 removal from chromatin	RT	<div></div>	18	0.9	1.1E-2	6.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	SUMOylation of DNA damage response and repair proteins	RT	<div></div>	19	0.9	1.1E-2	6.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Somitogenesis	RT	<div></div>	15	0.7	1.2E-2	6.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	p53-Dependent G1 DNA Damage Response	RT	<div></div>	17	0.8	1.2E-2	6.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	p53-Dependent G1/S DNA damage checkpoint	RT	<div></div>	17	0.8	1.2E-2	6.8E-2
<input type="checkbox"/>	REACTOME_PATHWAY	TP53 regulates transcription of additional cell cycle genes whose exact role in the p53 pathway remain uncertain	RT	<div></div>	8	0.4	1.2E-2	6.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Protein hydroxylation	RT	<div></div>	8	0.4	1.2E-2	6.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by TGFB family members	RT	<div></div>	27	1.3	1.2E-2	7.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	RNA Polymerase II Transcription	RT	<div></div>	212	10.3	1.2E-2	7.0E-2

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	REACTOME_PATHWAY	SUMOylation of transcription cofactors	RT	<div></div>	13	0.6	1.3E-2	7.4E-2
<input type="checkbox"/>	REACTOME_PATHWAY	G1/S Transition	RT	<div></div>	28	1.4	1.3E-2	7.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Oncogenic MAPK signaling	RT	<div></div>	20	1.0	1.4E-2	7.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Recognition of DNA damage by PCNA-containing replication complex	RT	<div></div>	10	0.5	1.4E-2	7.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Insulin receptor recycling	RT	<div></div>	10	0.5	1.4E-2	7.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Downregulation of SMAD2/3:SMAD4 transcriptional activity	RT	<div></div>	10	0.5	1.4E-2	7.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Late endosomal microautophagy	RT	<div></div>	11	0.5	1.4E-2	7.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	SHOC2 M1731 mutant abolishes MRAS complex function	RT	<div></div>	5	0.2	1.4E-2	7.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Gain-of-function MRAS complexes activate RAF signaling	RT	<div></div>	5	0.2	1.4E-2	7.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by MRAS-complex mutants	RT	<div></div>	5	0.2	1.4E-2	7.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Transcriptional regulation by RUNX3	RT	<div></div>	22	1.1	1.4E-2	7.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	UCH proteinases	RT	<div></div>	23	1.1	1.5E-2	8.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Synthesis of DNA	RT	<div></div>	26	1.3	1.5E-2	8.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-2 signaling	RT	<div></div>	6	0.3	1.5E-2	8.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	ATF6 (ATF6-alpha) activates chaperones	RT	<div></div>	6	0.3	1.5E-2	8.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Caspase-mediated cleavage of cytoskeletal proteins	RT	<div></div>	6	0.3	1.5E-2	8.1E-2
<input type="checkbox"/>	REACTOME_PATHWAY	G1/S DNA Damage Checkpoints	RT	<div></div>	17	0.8	1.6E-2	8.5E-2
<input type="checkbox"/>	REACTOME_PATHWAY	ZBP1(DAI) mediated induction of type I IFNs	RT	<div></div>	8	0.4	1.6E-2	8.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Negative regulation of MET activity	RT	<div></div>	8	0.4	1.6E-2	8.6E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Transcriptional regulation by RUNX2	RT	<div></div>	26	1.3	1.6E-2	8.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	RAF activation	RT	<div></div>	11	0.5	1.7E-2	9.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Calnexin/calreticulin cycle	RT	<div></div>	9	0.4	1.7E-2	9.0E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Fcgamma receptor (FCGR) dependent phagocytosis	RT	<div></div>	20	1.0	1.7E-2	9.3E-2
<input type="checkbox"/>	REACTOME_PATHWAY	TGF-beta receptor signaling activates SMADs	RT	<div></div>	13	0.6	1.8E-2	9.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Cyclin D associated events in G1	RT	<div></div>	13	0.6	1.8E-2	9.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	G1 Phase	RT	<div></div>	13	0.6	1.8E-2	9.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	Iron uptake and transport	RT	<div></div>	15	0.7	1.8E-2	9.7E-2
<input type="checkbox"/>	REACTOME_PATHWAY	RIP-mediated NFkB activation via ZBP1	RT	<div></div>	7	0.3	1.9E-2	9.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	MECP2 regulates neuronal receptors and channels	RT	<div></div>	7	0.3	1.9E-2	9.9E-2
<input type="checkbox"/>	REACTOME_PATHWAY	NFE2L2 regulating ER-stress associated genes	RT	<div></div>	4	0.2	1.9E-2	1.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Drug-mediated inhibition of CDK4/CDK6 activity	RT	<div></div>	4	0.2	1.9E-2	1.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Transcriptional regulation by RUNX1	RT	<div></div>	44	2.1	2.0E-2	1.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Diseases of mitotic cell cycle	RT	<div></div>	11	0.5	2.0E-2	1.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Maturation of spike protein	RT	<div></div>	11	0.5	2.0E-2	1.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Loss of proteins required for interphase microtubule organization from the centrosome	RT	<div></div>	17	0.8	2.0E-2	1.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Loss of Nlp from mitotic centrosomes	RT	<div></div>	17	0.8	2.0E-2	1.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Chaperone Mediated Autophagy	RT	<div></div>	8	0.4	2.1E-2	1.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Infection with Mycobacterium tuberculosis	RT	<div></div>	9	0.4	2.1E-2	1.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Purine salvage	RT	<div></div>	6	0.3	2.2E-2	1.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Integration of provirus	RT	<div></div>	5	0.2	2.3E-2	1.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of TC-NER Pre-Incision Complex	RT	<div></div>	14	0.7	2.3E-2	1.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	DNA Damage Recognition in GG-NER	RT	<div></div>	11	0.5	2.4E-2	1.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Hedgehog 'off' state	RT	<div></div>	24	1.2	2.4E-2	1.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Neddylation	RT	<div></div>	45	2.2	2.5E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	HIV elongation arrest and recovery	RT	<div></div>	10	0.5	2.6E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Pausing and recovery of HIV elongation	RT	<div></div>	10	0.5	2.6E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-17 signaling	RT	<div></div>	17	0.8	2.6E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Translocation of SLC2A4 (GLUT4) to the plasma membrane	RT	<div></div>	17	0.8	2.6E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Prefoldin mediated transfer of substrate to CCT/TriC	RT	<div></div>	9	0.4	2.6E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	RHOBTB1 GTPase cycle	RT	<div></div>	8	0.4	2.6E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Response of Mtb to phagocytosis	RT	<div></div>	8	0.4	2.6E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Global Genome Nucleotide Excision Repair (GG-NER)	RT	<div></div>	19	0.9	2.7E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Interleukin-4 and Interleukin-13 signaling	RT	<div></div>	23	1.1	2.7E-2	1.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Developmental Biology	RT	<div></div>	193	9.4	2.8E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	AURKA Activation by TPX2	RT	<div></div>	17	0.8	2.9E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	ISG15 antiviral mechanism	RT	<div></div>	17	0.8	2.9E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	RT	<div></div>	18	0.9	3.0E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of IFNG signaling	RT	<div></div>	6	0.3	3.0E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Disorders of Nervous System Development	RT	<div></div>	6	0.3	3.0E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Loss of function of MECP2 in Rett syndrome	RT	<div></div>	6	0.3	3.0E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Disorders of Developmental Biology	RT	<div></div>	6	0.3	3.0E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Pervasive developmental disorders	RT	<div></div>	6	0.3	3.0E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	ABC-family proteins mediated transport	RT	<div></div>	22	1.1	3.0E-2	1.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Mitophagy	RT	<div></div>	9	0.4	3.2E-2	1.5E-1
<input type="checkbox"/>	REACTOME_PATHWAY	NFE2L2 regulating anti-oxidant/detoxification enzymes	RT	<div></div>	7	0.3	3.3E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	HSF1-dependent transactivation	RT	<div></div>	8	0.4	3.3E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Anchoring of the basal body to the plasma membrane	RT	<div></div>	21	1.0	3.3E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	COPI-independent Golgi-to-ER retrograde traffic	RT	<div></div>	13	0.6	3.4E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	MAP2K and MAPK activation	RT	<div></div>	11	0.5	3.4E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	ATF6 (ATF6-alpha) activates chaperone genes	RT	<div></div>	5	0.2	3.4E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Folding of actin by CCT/TriC	RT	<div></div>	5	0.2	3.4E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Uptake and function of diphtheria toxin	RT	<div></div>	4	0.2	3.5E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	RT	<div></div>	14	0.7	3.5E-2	1.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Epigenetic regulation of gene expression	RT	<div></div>	35	1.7	3.7E-2	1.7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Lysosome Vesicle Biogenesis	RT	<div></div>	10	0.5	3.7E-2	1.7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Metabolism of nucleotides	RT	<div></div>	21	1.0	3.7E-2	1.7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by Hedgehog	RT	<div></div>	29	1.4	3.7E-2	1.7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by CSF3 (G-CSF)	RT	<div></div>	9	0.4	3.9E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of TP53 Activity through Acetylation	RT	<div></div>	9	0.4	3.9E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Maturation of nucleoprotein	RT	<div></div>	6	0.3	4.0E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Activation of BAD and translocation to mitochondria	RT	<div></div>	6	0.3	4.0E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Translation of Replicase and Assembly of the Replication Transcription Complex	RT	<div></div>	6	0.3	4.0E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	TRAF3-dependent IRF activation pathway	RT	<div></div>	6	0.3	4.0E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-1 targets host intracellular signalling and regulatory pathways	RT	<div></div>	6	0.3	4.0E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Asymmetric localization of PCP proteins	RT	<div></div>	15	0.7	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Defective Intrinsic Pathway for Apoptosis	RT	<div></div>	8	0.4	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Inactivation of CSF3 (G-CSF) signaling	RT	<div></div>	8	0.4	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Recruitment of mitotic centrosome proteins and complexes	RT	<div></div>	18	0.9	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Centrosome maturation	RT	<div></div>	18	0.9	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by PDGFR in disease	RT	<div></div>	7	0.3	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by KIT in disease	RT	<div></div>	7	0.3	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	RT	<div></div>	7	0.3	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Processing of Intronless Pre-mRNAs	RT	<div></div>	7	0.3	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	TP53 Regulates Transcription of Genes Involved in Cytochrome C Release	RT	<div></div>	7	0.3	4.1E-2	1.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Interactions of Vpr with host cellular proteins	RT	<div></div>	10	0.5	4.3E-2	1.9E-1

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	REACTOME_PATHWAY	RHO GTPases Activate WASPs and WAVES	RT	<div></div>	10	0.5	4.3E-2	1.9E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Leishmania infection	RT	<div></div>	31	1.5	4.4E-2	1.9E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Parasitic Infection Pathways	RT	<div></div>	31	1.5	4.4E-2	1.9E-1
<input type="checkbox"/>	REACTOME_PATHWAY	FCGR3A-mediated phagocytosis	RT	<div></div>	14	0.7	4.5E-2	2.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Parasite infection	RT	<div></div>	14	0.7	4.5E-2	2.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Leishmania phagocytosis	RT	<div></div>	14	0.7	4.5E-2	2.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Gap-filling DNA repair synthesis and ligation in TC-NER	RT	<div></div>	15	0.7	4.6E-2	2.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Platelet activation, signaling and aggregation	RT	<div></div>	46	2.2	4.7E-2	2.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Pausing and recovery of Tat-mediated HIV elongation	RT	<div></div>	9	0.4	4.7E-2	2.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Tat-mediated HIV elongation arrest and recovery	RT	<div></div>	9	0.4	4.7E-2	2.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Beta-catenin independent WNT signaling	RT	<div></div>	28	1.4	4.8E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of BACH1 activity	RT	<div></div>	5	0.2	4.8E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Receptor Mediated Mitophagy	RT	<div></div>	5	0.2	4.8E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Defective NEU1 causes sialidosis	RT	<div></div>	3	0.1	4.9E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Beta oxidation of palmitoyl-CoA to myristoyl-CoA	RT	<div></div>	3	0.1	4.9E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Protein folding	RT	<div></div>	20	1.0	4.9E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	DARPP-32 events	RT	<div></div>	8	0.4	5.0E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of TP53 Expression and Degradation	RT	<div></div>	10	0.5	5.1E-2	2.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Dual incision in TC-NER	RT	<div></div>	15	0.7	5.1E-2	2.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	VLDLR internalisation and degradation	RT	<div></div>	6	0.3	5.2E-2	2.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Negative regulation of MAPK pathway	RT	<div></div>	11	0.5	5.3E-2	2.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of Incision Complex in GG-NER	RT	<div></div>	11	0.5	5.3E-2	2.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by Receptor Tyrosine Kinases	RT	<div></div>	85	4.1	5.5E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Release of apoptotic factors from the mitochondria	RT	<div></div>	4	0.2	5.5E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Loss of Function of TGFBR1 in Cancer	RT	<div></div>	4	0.2	5.5E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	IkBA variant leads to FDA-ID	RT	<div></div>	4	0.2	5.5E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	2-LTR circle formation	RT	<div></div>	4	0.2	5.5E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Cooperation of Prefoldin and Tric/CCT in actin and tubulin folding	RT	<div></div>	9	0.4	5.5E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Hedgehog 'on' state	RT	<div></div>	18	0.9	5.6E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Protein ubiquitination	RT	<div></div>	17	0.8	5.6E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Amino acids regulate mTORC1	RT	<div></div>	13	0.6	5.6E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by BRAF and RAF1 fusions	RT	<div></div>	15	0.7	5.7E-2	2.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Association of Tric/CCT with target proteins during biosynthesis	RT	<div></div>	10	0.5	5.9E-2	2.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	RHOV GTPase cycle	RT	<div></div>	10	0.5	5.9E-2	2.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	FLT3 Signaling	RT	<div></div>	10	0.5	5.9E-2	2.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	RHOH GTPase cycle	RT	<div></div>	10	0.5	5.9E-2	2.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Integrin signaling	RT	<div></div>	8	0.4	6.0E-2	2.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	TP53 Regulates Transcription of Cell Death Genes	RT	<div></div>	11	0.5	6.1E-2	2.5E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Neurodegenerative Diseases	RT	<div></div>	7	0.3	6.3E-2	2.5E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	RT	<div></div>	7	0.3	6.3E-2	2.5E-1
<input type="checkbox"/>	REACTOME_PATHWAY	PINK1-PRKN Mediated Mitophagy	RT	<div></div>	7	0.3	6.3E-2	2.5E-1
<input type="checkbox"/>	REACTOME_PATHWAY	TP53 Regulates Transcription of DNA Repair Genes	RT	<div></div>	14	0.7	6.4E-2	2.5E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of MECP2 expression and activity	RT	<div></div>	9	0.4	6.5E-2	2.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	SARS-CoV-2 targets host intracellular signalling and regulatory pathways	RT	<div></div>	5	0.2	6.5E-2	2.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	TICAM1-dependent activation of IRF3/IRF7	RT	<div></div>	5	0.2	6.5E-2	2.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	ALK mutants bind TKIs	RT	<div></div>	5	0.2	6.5E-2	2.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	SUMOylation of immune response proteins	RT	<div></div>	5	0.2	6.5E-2	2.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Removal of the Flap Intermediate from the C-strand	RT	<div></div>	6	0.3	6.6E-2	2.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Selective autophagy	RT	<div></div>	17	0.8	6.8E-2	2.7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Formation of HIV elongation complex in the absence of HIV Tat	RT	<div></div>	11	0.5	7.0E-2	2.7E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Mitotic Prometaphase	RT	<div></div>	36	1.8	7.0E-2	2.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Complex I biogenesis	RT	<div></div>	13	0.6	7.1E-2	2.8E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Nucleotide salvage	RT	<div></div>	7	0.3	7.6E-2	3.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Abortive elongation of HIV-1 transcript in the absence of Tat	RT	<div></div>	7	0.3	7.6E-2	3.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Telomere Extension By Telomerase	RT	<div></div>	7	0.3	7.6E-2	3.0E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of NFE2L2 gene expression	RT	<div></div>	4	0.2	7.9E-2	3.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by TGF-beta Receptor Complex in Cancer	RT	<div></div>	4	0.2	7.9E-2	3.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Nef and signal transduction	RT	<div></div>	4	0.2	7.9E-2	3.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of TP53 Activity	RT	<div></div>	29	1.4	8.0E-2	3.1E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Processing of Capped Intronless Pre-mRNA	RT	<div></div>	8	0.4	8.3E-2	3.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by NTRK1 (TRKA)	RT	<div></div>	22	1.1	8.3E-2	3.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	IRF3-mediated induction of type I IFN	RT	<div></div>	5	0.2	8.4E-2	3.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	WNT5A-dependent internalization of FZD2, FZD5 and ROR2	RT	<div></div>	5	0.2	8.4E-2	3.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Suppression of phagosomal maturation	RT	<div></div>	5	0.2	8.4E-2	3.2E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Aberrant regulation of mitotic cell cycle due to RB1 defects	RT	<div></div>	9	0.4	8.6E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	RAB GEFs exchange GTP for GDP on RABs	RT	<div></div>	18	0.9	8.6E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Chaperonin-mediated protein folding	RT	<div></div>	18	0.9	8.6E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Transcriptional regulation of white adipocyte differentiation	RT	<div></div>	17	0.8	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by moderate kinase activity BRAF mutants	RT	<div></div>	11	0.5	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling downstream of RAS mutants	RT	<div></div>	11	0.5	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by RAS mutants	RT	<div></div>	11	0.5	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Paradoxical activation of RAF signaling by kinase inactive BRAF	RT	<div></div>	11	0.5	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Diseases of nucleotide metabolism	RT	<div></div>	3	0.1	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	TGFBR1 LBD Mutants in Cancer	RT	<div></div>	3	0.1	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	ATF6B (ATF6-beta) activates chaperones	RT	<div></div>	3	0.1	8.9E-2	3.3E-1
<input type="checkbox"/>	REACTOME_PATHWAY	mTORC1-mediated signalling	RT	<div></div>	7	0.3	9.1E-2	3.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	RHO GTPases activate PAKs	RT	<div></div>	7	0.3	9.1E-2	3.4E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Activation of BH3-only proteins	RT	<div></div>	8	0.4	9.6E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Interconversion of nucleotide di- and triphosphates	RT	<div></div>	8	0.4	9.6E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by ALK	RT	<div></div>	8	0.4	9.6E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	RT	<div></div>	9	0.4	9.9E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	ROS and RNS production in phagocytes	RT	<div></div>	9	0.4	9.9E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by high-kinase activity BRAF mutants	RT	<div></div>	9	0.4	9.9E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Interactions of Rev with host cellular proteins	RT	<div></div>	9	0.4	9.9E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Regulation of TP53 Degradation	RT	<div></div>	9	0.4	9.9E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Signaling by FLT3 fusion proteins	RT	<div></div>	6	0.3	9.9E-2	3.6E-1
<input type="checkbox"/>	REACTOME_PATHWAY	Processive synthesis on the C-strand of the telomere	RT	<div></div>	6	0.3	9.9E-2	3.6E-1

649 gene(s)

from your list are not in the output.

