



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

564 chart records

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Sublist	Category	Term
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cytoplasmic translation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">translation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">apoptotic process</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA splicing</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA splicing, via spliceosome</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein stabilization</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">translational initiation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA processing</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein folding</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ribosomal small subunit biogenesis</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">multivesicular body assembly</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">proteasome-mediated ubiquitin-dependent protein catabolic process</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of I-kappaB kinase/NF-kappaB signaling</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chaperone-mediated protein folding</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein transport</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription from RNA polymerase II promoter</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription, DNA-templated</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to virus</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ubiquitin-dependent protein catabolic process</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of apoptotic process</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell cycle</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intracellular protein transport</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ESCRT III complex disassembly</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">rRNA processing</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">autophagosome maturation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of translation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of RNA splicing</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">autophagy</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">vesicle-mediated transport</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">formation of cytoplasmic translation initiation complex</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chaperone mediated protein folding requiring cofactor</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription, DNA-templated</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of mRNA splicing, via spliceosome</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chromatin organization</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell receptor signaling pathway</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell division</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of viral genome replication</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">innate immune response</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to endoplasmic reticulum stress</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">multivesicular body sorting pathway</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to unfolded protein</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">macroautophagy</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of translation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">alternative mRNA splicing, via spliceosome</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of alternative mRNA splicing, via spliceosome</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell activation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K63-linked ubiquitination</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of protein stability</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">membrane fission</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral budding via host ESCRT complex</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleus organization</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of translation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endoplasmic reticulum unfolded protein response</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to DNA damage stimulus</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mitotic spindle assembly</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of centrosome duplication</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ERAD pathway</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ribosomal large subunit biogenesis</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein ubiquitination</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to UV</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ER to Golgi vesicle-mediated transport</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chromatin remodeling</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of exosomal secretion</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of cytoplasmic translation</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intrinsic apoptotic signaling pathway</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">defense response to virus</a>
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of T cell activation</a>

RT	Genes	Count	%	P-Value	Benjamini
<a href="#">RT</a>		77	3.8	1.1E-61	5.9E-58
<a href="#">RT</a>		97	4.7	1.3E-39	3.4E-36
<a href="#">RT</a>		122	5.9	2.5E-14	4.2E-11
<a href="#">RT</a>		61	3.0	3.2E-14	4.2E-11
<a href="#">RT</a>		59	2.9	4.1E-14	4.4E-11
<a href="#">RT</a>		63	3.1	2.2E-13	1.9E-10
<a href="#">RT</a>		27	1.3	2.1E-12	1.6E-9
<a href="#">RT</a>		61	3.0	3.0E-12	2.0E-9
<a href="#">RT</a>		50	2.4	1.5E-11	9.0E-9
<a href="#">RT</a>		30	1.5	5.3E-11	2.8E-8
<a href="#">RT</a>		19	0.9	1.3E-10	5.8E-8
<a href="#">RT</a>		23	1.1	1.3E-10	5.8E-8
<a href="#">RT</a>		57	2.8	1.7E-10	6.8E-8
<a href="#">RT</a>		54	2.6	4.4E-10	1.7E-7
<a href="#">RT</a>		21	1.0	1.1E-9	3.7E-7
<a href="#">RT</a>		89	4.3	2.2E-9	7.2E-7
<a href="#">RT</a>		189	9.2	2.4E-9	7.2E-7
<a href="#">RT</a>		124	6.0	2.5E-9	7.2E-7
<a href="#">RT</a>		34	1.7	3.3E-9	8.2E-7
<a href="#">RT</a>		55	2.7	3.4E-9	8.2E-7
<a href="#">RT</a>		95	4.6	3.4E-9	8.2E-7
<a href="#">RT</a>		73	3.6	3.4E-9	8.2E-7
<a href="#">RT</a>		62	3.0	6.8E-9	1.5E-6
<a href="#">RT</a>		10	0.5	9.7E-9	2.1E-6
<a href="#">RT</a>		37	1.8	1.5E-8	3.2E-6
<a href="#">RT</a>		21	1.0	2.6E-8	5.1E-6
<a href="#">RT</a>		28	1.4	2.6E-8	5.1E-6
<a href="#">RT</a>		26	1.3	3.8E-8	7.1E-6
<a href="#">RT</a>		41	2.0	4.5E-8	8.1E-6
<a href="#">RT</a>		49	2.4	5.3E-8	9.3E-6
<a href="#">RT</a>		12	0.6	7.5E-8	1.3E-5
<a href="#">RT</a>		16	0.8	1.2E-7	1.9E-5
<a href="#">RT</a>		98	4.8	2.0E-7	3.2E-5
<a href="#">RT</a>		13	0.6	5.0E-7	7.8E-5
<a href="#">RT</a>		49	2.4	5.4E-7	8.2E-5
<a href="#">RT</a>		32	1.6	6.6E-7	9.6E-5
<a href="#">RT</a>		71	3.5	8.5E-7	1.2E-4
<a href="#">RT</a>		14	0.7	1.5E-6	2.0E-4
<a href="#">RT</a>		89	4.3	1.6E-6	2.0E-4
<a href="#">RT</a>		27	1.3	1.6E-6	2.0E-4
<a href="#">RT</a>		13	0.6	1.6E-6	2.0E-4
<a href="#">RT</a>		20	1.0	1.6E-6	2.0E-4
<a href="#">RT</a>		23	1.1	1.7E-6	2.1E-4
<a href="#">RT</a>		27	1.3	2.4E-6	2.9E-4
<a href="#">RT</a>		13	0.6	2.7E-6	3.2E-4
<a href="#">RT</a>		20	1.0	2.9E-6	3.2E-4
<a href="#">RT</a>		20	1.0	2.9E-6	3.2E-4
<a href="#">RT</a>		19	0.9	4.0E-6	4.4E-4
<a href="#">RT</a>		25	1.2	4.2E-6	4.5E-4
<a href="#">RT</a>		16	0.8	5.4E-6	5.7E-4
<a href="#">RT</a>		12	0.6	7.7E-6	7.8E-4
<a href="#">RT</a>		12	0.6	7.7E-6	7.8E-4
<a href="#">RT</a>		14	0.7	8.9E-6	8.8E-4
<a href="#">RT</a>		26	1.3	9.8E-6	9.6E-4
<a href="#">RT</a>		17	0.8	1.1E-5	1.0E-3
<a href="#">RT</a>		55	2.7	1.2E-5	1.2E-3
<a href="#">RT</a>		12	0.6	1.2E-5	1.2E-3
<a href="#">RT</a>		11	0.5	1.3E-5	1.2E-3
<a href="#">RT</a>		25	1.2	1.4E-5	1.3E-3
<a href="#">RT</a>		14	0.7	1.9E-5	1.7E-3
<a href="#">RT</a>		77	3.8	2.1E-5	1.9E-3
<a href="#">RT</a>		18	0.9	3.0E-5	2.5E-3
<a href="#">RT</a>		29	1.4	3.0E-5	2.5E-3
<a href="#">RT</a>		59	2.9	3.0E-5	2.5E-3
<a href="#">RT</a>		9	0.4	3.6E-5	2.8E-3
<a href="#">RT</a>		9	0.4	3.6E-5	2.8E-3
<a href="#">RT</a>		14	0.7	3.8E-5	3.0E-3
<a href="#">RT</a>		45	2.2	4.0E-5	3.1E-3
<a href="#">RT</a>		13	0.6	5.0E-5	3.9E-3

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">circadian regulation of gene expression</a>	RT		20	1.0	5.5E-5	4.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">retrograde transport, endosome to Golgi</a>	RT		23	1.1	5.5E-5	4.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">lysosomal lumen acidification</a>	RT		11	0.5	5.5E-5	4.1E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">tumor necrosis factor-mediated signaling pathway</a>	RT		18	0.9	6.1E-5	4.4E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription elongation from RNA polymerase II promoter</a>	RT		10	0.5	6.3E-5	4.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear envelope reassembly</a>	RT		10	0.5	6.3E-5	4.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral budding from plasma membrane</a>	RT		9	0.4	6.5E-5	4.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of viral genome replication</a>	RT		15	0.7	6.7E-5	4.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitophagy</a>	RT		15	0.7	6.7E-5	4.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay</a>	RT		7	0.3	6.7E-5	4.5E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">erythrocyte differentiation</a>	RT		17	0.8	7.0E-5	4.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">proteolysis involved in cellular protein catabolic process</a>	RT		16	0.8	8.0E-5	5.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cell cycle</a>	RT		45	2.2	9.1E-5	5.9E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interleukin-2 production</a>	RT		13	0.6	9.8E-5	6.2E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomere maintenance</a>	RT		9	0.4	1.1E-4	7.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-alpha production</a>	RT		11	0.5	1.2E-4	7.7E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">activation of innate immune response</a>	RT		13	0.6	1.3E-4	8.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of proteasomal ubiquitin-dependent protein catabolic process</a>	RT		13	0.6	1.3E-4	8.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of translational initiation</a>	RT		12	0.6	1.3E-4	8.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of apoptotic process</a>	RT		43	2.1	1.4E-4	8.6E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of signal transduction by p53 class mediator</a>	RT		7	0.3	1.5E-4	9.0E-3
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">plasma membrane repair</a>	RT		11	0.5	1.8E-4	1.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrial ATP synthesis coupled proton transport</a>	RT		18	0.9	1.8E-4	1.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">autophagosome assembly</a>	RT		19	0.9	1.8E-4	1.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of RNA splicing</a>	RT		8	0.4	1.9E-4	1.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">stress granule assembly</a>	RT		11	0.5	2.5E-4	1.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitotic metaphase plate congression</a>	RT		14	0.7	2.8E-4	1.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to epidermal growth factor stimulus</a>	RT		14	0.7	2.8E-4	1.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral release from host cell</a>	RT		9	0.4	2.9E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">multivesicular body-lysosome fusion</a>	RT		7	0.3	3.1E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">CRD-mediated mRNA stabilization</a>	RT		7	0.3	3.1E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein localization to chromosome, telomeric region</a>	RT		7	0.3	3.1E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">vesicle fusion with vacuole</a>	RT		7	0.3	3.1E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">IRES-dependent viral translational initiation</a>	RT		7	0.3	3.1E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay</a>	RT		8	0.4	3.3E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ribosomal small subunit assembly</a>	RT		8	0.4	3.3E-4	1.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein deubiquitination</a>	RT		21	1.0	3.4E-4	1.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">macromolecular complex assembly</a>	RT		29	1.4	3.6E-4	1.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ubiquitin-dependent ERAD pathway</a>	RT		19	0.9	3.8E-4	1.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein polyubiquitination</a>	RT		32	1.6	3.9E-4	1.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">extrinsic apoptotic signaling pathway via death domain receptors</a>	RT		13	0.6	4.1E-4	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation of peptide or polysaccharide antigen via MHC class II</a>	RT		9	0.4	4.4E-4	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">barbed-end actin filament capping</a>	RT		9	0.4	4.4E-4	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">late endosome to lysosome transport</a>	RT		9	0.4	4.4E-4	2.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of ER-associated ubiquitin-dependent protein catabolic process</a>	RT		6	0.3	4.5E-4	2.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription from RNA polymerase I promoter</a>	RT		6	0.3	4.5E-4	2.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of type I interferon production</a>	RT		12	0.6	4.5E-4	2.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of TORC1 signaling</a>	RT		15	0.7	4.8E-4	2.1E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of protein ubiquitination</a>	RT		16	0.8	4.9E-4	2.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein targeting to ER</a>	RT		8	0.4	5.3E-4	2.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptide antigen assembly with MHC class II protein complex</a>	RT		8	0.4	5.3E-4	2.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K48-linked ubiquitination</a>	RT		19	0.9	5.3E-4	2.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative thymic T cell selection</a>	RT		7	0.3	5.7E-4	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to nitrogen starvation</a>	RT		7	0.3	5.7E-4	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">platelet aggregation</a>	RT		14	0.7	5.7E-4	2.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">tricarboxylic acid cycle</a>	RT		12	0.6	5.9E-4	2.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">signal transduction</a>	RT		162	7.9	6.3E-4	2.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA splice site selection</a>	RT		9	0.4	6.5E-4	2.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation of exogenous peptide antigen via MHC class II</a>	RT		11	0.5	6.5E-4	2.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein maturation</a>	RT		13	0.6	6.7E-4	2.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mitotic cell cycle</a>	RT		17	0.8	8.3E-4	3.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA transcription from RNA polymerase II promoter</a>	RT		14	0.7	8.7E-4	3.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to heat</a>	RT		15	0.7	8.8E-4	3.5E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to organic substance</a>	RT		10	0.5	9.2E-4	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein modification process</a>	RT		25	1.2	9.2E-4	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process</a>	RT		9	0.4	9.3E-4	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">alpha-beta T cell activation</a>	RT		6	0.3	9.3E-4	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of necroptotic process</a>	RT		6	0.3	9.3E-4	3.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">aerobic respiration</a>	RT		17	0.8	9.8E-4	3.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">translational elongation</a>	RT		8	0.4	1.2E-3	4.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mRNA splicing, via spliceosome</a>	RT		8	0.4	1.2E-3	4.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mRNA processing</a>	RT		8	0.4	1.2E-3	4.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell differentiation in thymus</a>	RT		12	0.6	1.2E-3	4.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of apoptotic process</a>	RT		51	2.5	1.3E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of macroautophagy</a>	RT		15	0.7	1.3E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">vacuolar acidification</a>	RT		9	0.4	1.3E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of RNA splicing</a>	RT		5	0.2	1.3E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chaperone-mediated autophagy</a>	RT		5	0.2	1.3E-3	4.7E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of erythrocyte differentiation</a>	RT		11	0.5	1.4E-3	5.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">rhythmic process</a>	RT		18	0.9	1.5E-3	5.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein dephosphorylation</a>	RT		24	1.2	1.5E-3	5.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">maintenance of protein location in nucleus</a>	RT		7	0.3	1.5E-3	5.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrial fragmentation involved in apoptotic process</a>	RT		6	0.3	1.7E-3	5.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Golgi lumen acidification</a>	RT		6	0.3	1.7E-3	5.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to interleukin-4</a>	RT		9	0.4	1.8E-3	6.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to glucocorticoid stimulus</a>	RT		9	0.4	1.8E-3	6.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">3'-UTR-mediated mRNA destabilization</a>	RT		8	0.4	1.8E-3	6.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription initiation from RNA polymerase II promoter</a>	RT		15	0.7	1.8E-3	6.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomere maintenance via telomerase</a>	RT		11	0.5	1.8E-3	6.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">extrinsic apoptotic signaling pathway</a>	RT		14	0.7	1.9E-3	6.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein localization to nucleus</a>	RT		12	0.6	1.9E-3	6.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mRNA stability</a>	RT		12	0.6	1.9E-3	6.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell differentiation</a>	RT		12	0.6	1.9E-3	6.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to cytokine</a>	RT		13	0.6	2.0E-3	6.3E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein kinase activity</a>	RT		13	0.6	2.0E-3	6.3E-2

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">natural killer cell mediated cytotoxicity</a>	RT		10	0.5	2.1E-3	6.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">telomere maintenance</a>	RT		15	0.7	2.2E-3	6.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cellular response to heat</a>	RT		7	0.3	2.3E-3	7.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein import into nucleus</a>	RT		21	1.0	2.4E-3	7.6E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of proteolysis</a>	RT		8	0.4	2.5E-3	7.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein localization to Golgi apparatus</a>	RT		8	0.4	2.5E-3	7.8E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of autophagy</a>	RT		15	0.7	2.6E-3	7.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">MAPK cascade</a>	RT		23	1.1	2.7E-3	8.2E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endocytic recycling</a>	RT		16	0.8	2.8E-3	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">interleukin-9-mediated signaling pathway</a>	RT		5	0.2	2.8E-3	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">interleukin-15-mediated signaling pathway</a>	RT		6	0.3	2.9E-3	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of RIG-I signaling pathway</a>	RT		6	0.3	2.9E-3	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cotranslational protein targeting to membrane</a>	RT		6	0.3	2.9E-3	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">retrograde axonal transport</a>	RT		6	0.3	2.9E-3	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intracellular transport</a>	RT		13	0.6	2.9E-3	8.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chromosome segregation</a>	RT		20	1.0	3.1E-3	9.0E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">I-kappaB kinase/NF-kappaB signaling</a>	RT		16	0.8	3.2E-3	9.4E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription elongation from RNA polymerase II promoter</a>	RT		13	0.6	3.4E-3	9.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ribosomal large subunit assembly</a>	RT		8	0.4	3.4E-3	9.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of B cell differentiation</a>	RT		7	0.3	3.4E-3	9.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">lysosome localization</a>	RT		10	0.5	3.5E-3	9.9E-2
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of mitotic cell cycle phase transition</a>	RT		4	0.2	3.8E-3	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of T cell receptor signaling pathway</a>	RT		9	0.4	4.1E-3	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein refolding</a>	RT		9	0.4	4.1E-3	1.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitotic spindle assembly</a>	RT		12	0.6	4.3E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">membrane fusion</a>	RT		10	0.5	4.4E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator</a>	RT		10	0.5	4.4E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of tyrosine phosphorylation of STAT protein</a>	RT		6	0.3	4.5E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein insertion into ER membrane</a>	RT		6	0.3	4.5E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">late endosome to vacuole transport via multivesicular body sorting pathway</a>	RT		6	0.3	4.5E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">telomere maintenance via telomerase</a>	RT		8	0.4	4.6E-3	1.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear migration</a>	RT		7	0.3	4.9E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of ERAD pathway</a>	RT		7	0.3	4.9E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to unfolded protein</a>	RT		7	0.3	4.9E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of T cell proliferation</a>	RT		7	0.3	4.9E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">vesicle transport along microtubule</a>	RT		7	0.3	4.9E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">interleukin-2-mediated signaling pathway</a>	RT		5	0.2	5.2E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">posttranslational protein targeting to membrane, translocation</a>	RT		5	0.2	5.2E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein targeting to mitochondrion</a>	RT		9	0.4	5.2E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">NIK/NF-kappaB signaling</a>	RT		9	0.4	5.2E-3	1.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear-transcribed mRNA catabolic process, nonsense-mediated decay</a>	RT		11	0.5	5.3E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to leukemia inhibitory factor</a>	RT		21	1.0	5.4E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mitochondrial membrane potential</a>	RT		10	0.5	5.4E-3	1.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cell proliferation</a>	RT		26	1.3	5.9E-3	1.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription from RNA polymerase II promoter</a>	RT		38	1.9	6.4E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ribosome biogenesis</a>	RT		11	0.5	6.4E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular respiration</a>	RT		11	0.5	6.4E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of innate immune response</a>	RT		9	0.4	6.6E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to interferon-beta</a>	RT		9	0.4	6.6E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein sumoylation</a>	RT		13	0.6	6.6E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">centrosome localization</a>	RT		7	0.3	6.7E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of T cell receptor signaling pathway</a>	RT		7	0.3	6.7E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive thymic T cell selection</a>	RT		6	0.3	6.7E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">interferon-gamma-mediated signaling pathway</a>	RT		6	0.3	6.7E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of nuclear-transcribed mRNA poly(A) tail shortening</a>	RT		6	0.3	6.7E-3	1.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA polymerase II transcriptional preinitiation complex assembly</a>	RT		14	0.7	7.0E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription from RNA polymerase II promoter</a>	RT		127	6.2	7.0E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">substantia nigra development</a>	RT		12	0.6	7.2E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">defense response</a>	RT		17	0.8	7.3E-3	1.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein import into nucleus</a>	RT		11	0.5	7.7E-3	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">COPII vesicle coating</a>	RT		8	0.4	7.8E-3	1.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein targeting to mitochondrion</a>	RT		10	0.5	8.1E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of lamellipodium assembly</a>	RT		9	0.4	8.2E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of extrinsic apoptotic signaling pathway</a>	RT		9	0.4	8.2E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA repair</a>	RT		45	2.2	8.2E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of erythrocyte differentiation</a>	RT		5	0.2	8.6E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">late endosome to vacuole transport</a>	RT		5	0.2	8.6E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of IRE1-mediated unfolded protein response</a>	RT		4	0.2	8.8E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway</a>	RT		4	0.2	8.8E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of endoplasmic reticulum unfolded protein response</a>	RT		4	0.2	8.8E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">posttranscriptional gene silencing</a>	RT		4	0.2	8.8E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular sphingolipid homeostasis</a>	RT		4	0.2	8.8E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral translational termination-reinitiation</a>	RT		4	0.2	8.8E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">AMP salvage</a>	RT		4	0.2	8.8E-3	1.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of protein ubiquitination</a>	RT		7	0.3	8.9E-3	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endoplasmic reticulum calcium ion homeostasis</a>	RT		7	0.3	8.9E-3	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of gene expression</a>	RT		46	2.2	9.1E-3	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell proliferation</a>	RT		11	0.5	9.2E-3	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell costimulation</a>	RT		11	0.5	9.2E-3	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein ubiquitination</a>	RT		16	0.8	9.3E-3	2.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endosomal lumen acidification</a>	RT		6	0.3	9.6E-3	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intracellular pH reduction</a>	RT		6	0.3	9.6E-3	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">retrograde vesicle-mediated transport, Golgi to ER</a>	RT		12	0.6	9.9E-3	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein peptidyl-prolyl isomerization</a>	RT		8	0.4	9.9E-3	2.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of T cell differentiation</a>	RT		10	0.5	1.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of DNA binding</a>	RT		7	0.3	1.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">immune response</a>	RT		67	3.3	1.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to hypoxia</a>	RT		24	1.2	1.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K11-linked ubiquitination</a>	RT		9	0.4	1.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of macroautophagy</a>	RT		9	0.4	1.2E-2	2.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of double-strand break repair</a>	RT		8	0.4	1.2E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein localization to membrane</a>	RT		8	0.4	1.2E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of cysteine-type endopeptidase activity involved in apoptotic process</a>	RT		11	0.5	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)</a>	RT		6	0.3	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of viral entry into host cell</a>	RT		6	0.3	1.3E-2	2.6E-1



Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomerase RNA localization to Cajal body</a>	RT		6	0.3	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">membrane budding</a>	RT		6	0.3	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">synaptic vesicle transport</a>	RT		6	0.3	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">JAK-STAT cascade involved in growth hormone signaling pathway</a>	RT		5	0.2	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of CD4-positive, alpha-beta T cell proliferation</a>	RT		5	0.2	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of T cell activation</a>	RT		5	0.2	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of establishment of protein localization to telomere</a>	RT		5	0.2	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endosome transport via multivesicular body sorting pathway</a>	RT		5	0.2	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of monocyte differentiation</a>	RT		5	0.2	1.3E-2	2.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phosphorylation</a>	RT		81	3.9	1.4E-2	2.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrial electron transport, NADH to ubiquinone</a>	RT		11	0.5	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">JAK-STAT cascade</a>	RT		11	0.5	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to peptide hormone</a>	RT		11	0.5	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of innate immune response</a>	RT		7	0.3	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of translational initiation</a>	RT		7	0.3	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of translational initiation</a>	RT		7	0.3	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrion morphogenesis</a>	RT		7	0.3	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of immunoglobulin production</a>	RT		8	0.4	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interleukin-4 production</a>	RT		8	0.4	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of circadian rhythm</a>	RT		14	0.7	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein secretion</a>	RT		13	0.6	1.5E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">neuron projection development</a>	RT		21	1.0	1.6E-2	2.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein localization to endoplasmic reticulum</a>	RT		4	0.2	1.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endodermal cell fate commitment</a>	RT		4	0.2	1.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptide antigen assembly with MHC class I protein complex</a>	RT		4	0.2	1.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protection from natural killer cell mediated cytotoxicity</a>	RT		4	0.2	1.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of T cell differentiation in thymus</a>	RT		4	0.2	1.6E-2	3.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">type I interferon signaling pathway</a>	RT		11	0.5	1.7E-2	3.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">retrograde protein transport, ER to cytosol</a>	RT		6	0.3	1.8E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to chemokine</a>	RT		6	0.3	1.8E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear envelope organization</a>	RT		6	0.3	1.8E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein targeting to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway</a>	RT		6	0.3	1.8E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of reactive oxygen species metabolic process</a>	RT		9	0.4	1.8E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to nerve growth factor stimulus</a>	RT		9	0.4	1.8E-2	3.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">DNA methylation</a>	RT		8	0.4	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein targeting to lysosome</a>	RT		8	0.4	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">spliceosomal complex assembly</a>	RT		8	0.4	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">clathrin-dependent endocytosis</a>	RT		8	0.4	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intracellular estrogen receptor signaling pathway</a>	RT		7	0.3	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cytoplasmic translational initiation</a>	RT		5	0.2	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">gamma-delta T cell activation</a>	RT		5	0.2	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of histone acetylation</a>	RT		5	0.2	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein folding in endoplasmic reticulum</a>	RT		5	0.2	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein localization to Cajal body</a>	RT		5	0.2	1.9E-2	3.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cyclin-dependent protein serine/threonine kinase activity</a>	RT		11	0.5	2.0E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein N-linked glycosylation</a>	RT		12	0.6	2.0E-2	3.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein phosphorylation</a>	RT		52	2.5	2.0E-2	3.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress</a>	RT		9	0.4	2.1E-2	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of defense response to virus by host</a>	RT		9	0.4	2.1E-2	3.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endosomal transport</a>	RT		14	0.7	2.2E-2	3.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein catabolic process</a>	RT		16	0.8	2.2E-2	3.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of DNA-templated transcription, elongation</a>	RT		6	0.3	2.3E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">synaptic vesicle lumen acidification</a>	RT		6	0.3	2.3E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to stress</a>	RT		6	0.3	2.3E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of interferon-gamma production</a>	RT		15	0.7	2.3E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to insulin stimulus</a>	RT		17	0.8	2.3E-2	3.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to virus</a>	RT		17	0.8	2.5E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">interleukin-4-mediated signaling pathway</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of granulocyte differentiation</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ATF6-mediated unfolded protein response</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of ERAD pathway</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">purine ribonucleoside salvage</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleophagy</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of endopeptidase activity</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">interleukin-27-mediated signaling pathway</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of histone deacetylation</a>	RT		4	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">telomere capping</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">posttranslational protein targeting to membrane</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of histone H3-K4 methylation</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of gene silencing by miRNA</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear export</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of mRNA catabolic process</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endoplasmic reticulum tubular network organization</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">glycophagy</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to interleukin-7</a>	RT		5	0.2	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to lipopolysaccharide</a>	RT		29	1.4	2.6E-2	4.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of peptidyl-serine phosphorylation of STAT protein</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of cysteine-type endopeptidase activity</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">late endosomal microautophagy</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein K48-linked ubiquitination</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of ER-associated ubiquitin-dependent protein catabolic process</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">small-subunit processome assembly</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of intracellular mRNA localization</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of histone methylation</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein deubiquitination</a>	RT		3	0.1	2.8E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of protein complex assembly</a>	RT		9	0.4	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">proteasomal protein catabolic process</a>	RT		9	0.4	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of multicellular organism growth</a>	RT		7	0.3	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chaperone-mediated protein complex assembly</a>	RT		7	0.3	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of release of cytochrome c from mitochondria</a>	RT		7	0.3	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to xenobiotic stimulus</a>	RT		36	1.8	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of DNA methylation</a>	RT		6	0.3	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">purine nucleotide biosynthetic process</a>	RT		6	0.3	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mitophagy</a>	RT		6	0.3	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">apoptotic mitochondrial changes</a>	RT		6	0.3	2.9E-2	4.3E-1

Sublist	Category	term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of stem cell differentiation</a>	RT		6	0.3	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of substrate adhesion-dependent cell spreading</a>	RT		10	0.5	2.9E-2	4.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">post-embryonic development</a>	RT		14	0.7	3.0E-2	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">activation of cysteine-type endopeptidase activity involved in apoptotic process</a>	RT		14	0.7	3.0E-2	4.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to hypoxia</a>	RT		27	1.3	3.1E-2	4.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of mRNA splicing, via spliceosome</a>	RT		8	0.4	3.2E-2	4.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">stem cell population maintenance</a>	RT		9	0.4	3.3E-2	4.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to estradiol</a>	RT		15	0.7	3.4E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of I-kappaB kinase/NF-kappaB signaling</a>	RT		13	0.6	3.4E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">RNA splicing, via transesterification reactions</a>	RT		7	0.3	3.5E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">U2-type prespliceosome assembly</a>	RT		7	0.3	3.5E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ceramide metabolic process</a>	RT		7	0.3	3.5E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">decidualization</a>	RT		7	0.3	3.5E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of ATPase activity</a>	RT		7	0.3	3.5E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway</a>	RT		5	0.2	3.5E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation by host of viral transcription</a>	RT		5	0.2	3.5E-2	5.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein localization to plasma membrane</a>	RT		25	1.2	3.6E-2	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to oxidative stress</a>	RT		17	0.8	3.6E-2	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">fibroblast migration</a>	RT		6	0.3	3.6E-2	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway</a>	RT		6	0.3	3.6E-2	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of tumor necrosis factor-mediated signaling pathway</a>	RT		6	0.3	3.6E-2	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulated exocytosis</a>	RT		6	0.3	3.6E-2	5.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to glucose starvation</a>	RT		11	0.5	3.7E-2	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of I-kappaB kinase/NF-kappaB signaling</a>	RT		8	0.4	3.7E-2	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">viral protein processing</a>	RT		8	0.4	3.7E-2	5.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of DNA replication</a>	RT		10	0.5	3.8E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein K63-linked ubiquitination</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of B cell activation</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein depalmitoylation</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">SRP-dependent cotranslational protein targeting to membrane, translocation</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">plasma membrane to endosome transport</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA metabolic process</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mRNA export from nucleus</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein retention in ER lumen</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of adaptive immune response</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">postsynaptic neurotransmitter receptor internalization</a>	RT		4	0.2	3.9E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of canonical Wnt signaling pathway</a>	RT		19	0.9	4.0E-2	5.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein autoubiquitination</a>	RT		14	0.7	4.0E-2	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of T cell proliferation</a>	RT		12	0.6	4.0E-2	5.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of proteasomal ubiquitin-dependent protein catabolic process</a>	RT		15	0.7	4.1E-2	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA transport</a>	RT		15	0.7	4.1E-2	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of transcription from RNA polymerase I promoter</a>	RT		7	0.3	4.1E-2	5.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of telomerase activity</a>	RT		8	0.4	4.3E-2	5.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">macrophage differentiation</a>	RT		8	0.4	4.3E-2	5.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intra-Golgi vesicle-mediated transport</a>	RT		8	0.4	4.3E-2	5.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of immune response</a>	RT		9	0.4	4.4E-2	5.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of NLRP3 inflammasome complex assembly</a>	RT		6	0.3	4.5E-2	5.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrial electron transport, ubiquinol to cytochrome c</a>	RT		5	0.2	4.5E-2	5.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">termination of RNA polymerase II transcription</a>	RT		5	0.2	4.5E-2	5.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">ruffle organization</a>	RT		5	0.2	4.5E-2	5.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitotic G1 DNA damage checkpoint</a>	RT		5	0.2	4.5E-2	5.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">inflammatory response</a>	RT		54	2.6	4.6E-2	6.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">phagocytosis</a>	RT		13	0.6	4.6E-2	6.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of autophagy</a>	RT		13	0.6	4.6E-2	6.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">somatic stem cell population maintenance</a>	RT		11	0.5	4.7E-2	6.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">actin cytoskeleton organization</a>	RT		31	1.5	4.7E-2	6.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">intrinsic apoptotic signaling pathway in response to DNA damage</a>	RT		10	0.5	4.8E-2	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of microtubule polymerization</a>	RT		7	0.3	4.9E-2	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process</a>	RT		7	0.3	4.9E-2	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein dephosphorylation</a>	RT		7	0.3	4.9E-2	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to gamma radiation</a>	RT		7	0.3	4.9E-2	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of cell-matrix adhesion</a>	RT		7	0.3	4.9E-2	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA export from nucleus</a>	RT		12	0.6	4.9E-2	6.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein targeting</a>	RT		9	0.4	5.0E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA catabolic process</a>	RT		8	0.4	5.0E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein export from nucleus</a>	RT		8	0.4	5.0E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of translation in response to endoplasmic reticulum stress</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">exosomal secretion</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of leukocyte migration</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of CD4-positive, alpha-beta T cell activation</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of CD8-positive, alpha-beta T cell proliferation</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">insulin receptor recycling</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of T-helper cell differentiation</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">chemokine (C-C motif) ligand 21 signaling pathway</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">establishment of Sertoli cell barrier</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of ceramide biosynthetic process</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">clathrin coat disassembly</a>	RT		3	0.1	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to ethanol</a>	RT		17	0.8	5.3E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">hematopoietic stem cell differentiation</a>	RT		6	0.3	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA destabilization</a>	RT		6	0.3	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of stem cell population maintenance</a>	RT		6	0.3	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of myelination</a>	RT		6	0.3	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">establishment of endothelial barrier</a>	RT		6	0.3	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitotic cytokinesis</a>	RT		12	0.6	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of natural killer cell differentiation</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of retrograde protein transport, ER to cytosol</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleobase-containing small molecule interconversion</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">deadenylation-dependent decapping of nuclear-transcribed mRNA</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to arsenic-containing substance</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of endoplasmic reticulum calcium ion concentration</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">lysosomal protein catabolic process</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">vesicle fusion with Golgi apparatus</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">CD4-positive, alpha-beta T cell proliferation</a>	RT		4	0.2	5.4E-2	6.3E-1

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">endothelial tube morphogenesis</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">L-serine transport</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of protein dephosphorylation</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">autophagosome docking</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">postreplication repair</a>	RT		4	0.2	5.4E-2	6.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of pri-miRNA transcription from RNA polymerase II promoter</a>	RT		7	0.3	5.7E-2	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of interferon-beta production</a>	RT		5	0.2	5.7E-2	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">calcineurin-NFAT signaling cascade</a>	RT		5	0.2	5.7E-2	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell mediated cytotoxicity</a>	RT		5	0.2	5.7E-2	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of mitotic cell cycle</a>	RT		8	0.4	5.7E-2	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitochondrion organization</a>	RT		17	0.8	5.7E-2	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of cell proliferation</a>	RT		63	3.1	5.8E-2	6.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to growth factor stimulus</a>	RT		11	0.5	6.3E-2	7.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nuclear-transcribed mRNA poly(A) tail shortening</a>	RT		6	0.3	6.4E-2	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of telomere maintenance via telomerase</a>	RT		6	0.3	6.4E-2	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of mitochondrion organization</a>	RT		6	0.3	6.4E-2	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cholesterol biosynthetic process</a>	RT		8	0.4	6.5E-2	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of double-strand break repair via homologous recombination</a>	RT		8	0.4	6.5E-2	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">localization</a>	RT		8	0.4	6.5E-2	7.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of innate immune response</a>	RT		7	0.3	6.6E-2	7.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">liver development</a>	RT		14	0.7	6.7E-2	7.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of autophagy</a>	RT		14	0.7	6.7E-2	7.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cell proliferation</a>	RT		22	1.1	6.9E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of DNA repair</a>	RT		11	0.5	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation of endogenous peptide antigen via MHC class Ib</a>	RT		5	0.2	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-independent</a>	RT		5	0.2	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA cis splicing, via spliceosome</a>	RT		5	0.2	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of myoblast fusion</a>	RT		5	0.2	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of viral transcription</a>	RT		5	0.2	7.0E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of NIK/NF-kappaB signaling</a>	RT		12	0.6	7.1E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">G1/S transition of mitotic cell cycle</a>	RT		12	0.6	7.1E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of DNA-templated transcription, elongation</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of ubiquitin protein ligase activity</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">peptidyl-serine dephosphorylation</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of inclusion body assembly</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of alpha-beta T cell differentiation</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of lamellipodium assembly</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">establishment of protein localization to membrane</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of T cell apoptotic process</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to interferon-alpha</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to cholesterol</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mitotic nuclear envelope reassembly</a>	RT		4	0.2	7.2E-2	7.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of T cell mediated cytotoxicity</a>	RT		8	0.4	7.4E-2	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of intrinsic apoptotic signaling pathway</a>	RT		8	0.4	7.4E-2	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">establishment of mitotic spindle orientation</a>	RT		8	0.4	7.4E-2	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of G1/S transition of mitotic cell cycle</a>	RT		10	0.5	7.4E-2	7.9E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">melanosome transport</a>	RT		6	0.3	7.5E-2	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of calcium ion transport</a>	RT		6	0.3	7.5E-2	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">release of cytochrome c from mitochondria</a>	RT		6	0.3	7.5E-2	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of telomere maintenance</a>	RT		6	0.3	7.5E-2	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein targeting to membrane</a>	RT		7	0.3	7.6E-2	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">Golgi to plasma membrane protein transport</a>	RT		7	0.3	7.6E-2	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">mRNA polyadenylation</a>	RT		7	0.3	7.6E-2	8.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">apoptotic signaling pathway</a>	RT		12	0.6	7.7E-2	8.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of protein catabolic process</a>	RT		9	0.4	7.9E-2	8.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">osteoclast differentiation</a>	RT		9	0.4	7.9E-2	8.2E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of inflammatory response</a>	RT		17	0.8	8.1E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">connective tissue replacement involved in inflammatory response wound healing</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein K69-linked ufmylation</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of steroid metabolic process</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">granulocyte colony-stimulating factor signaling pathway</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein monoubiquitination</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to sodium arsenite</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">hair follicle placode formation</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">constitutive secretory pathway</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">citrate metabolic process</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">lymphocyte differentiation</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">snoRNA localization</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">GMP salvage</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of hematopoietic stem cell differentiation</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">electron transport coupled proton transport</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of ceramide biosynthetic process</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">nucleoside triphosphate biosynthetic process</a>	RT		3	0.1	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of immune response</a>	RT		8	0.4	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">T cell homeostasis</a>	RT		8	0.4	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">gene expression</a>	RT		21	1.0	8.3E-2	8.3E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">insulin receptor signaling pathway</a>	RT		12	0.6	8.4E-2	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to steroid hormone stimulus</a>	RT		5	0.2	8.5E-2	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">homeostasis of number of cells</a>	RT		5	0.2	8.5E-2	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">respiratory burst</a>	RT		5	0.2	8.5E-2	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of cardiac muscle hypertrophy</a>	RT		5	0.2	8.5E-2	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">embryonic hemopoiesis</a>	RT		5	0.2	8.5E-2	8.4E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">in utero embryonic development</a>	RT		30	1.5	8.5E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">anterograde axonal transport</a>	RT		7	0.3	8.6E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">heterochromatin assembly</a>	RT		7	0.3	8.6E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of stem cell population maintenance</a>	RT		9	0.4	8.7E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">androgen receptor signaling pathway</a>	RT		6	0.3	8.8E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of macromolecule metabolic process</a>	RT		6	0.3	8.8E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of type I interferon-mediated signaling pathway</a>	RT		6	0.3	8.8E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of reactive oxygen species metabolic process</a>	RT		6	0.3	8.8E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">blastocyst development</a>	RT		6	0.3	8.8E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein N-linked glycosylation via asparagine</a>	RT		6	0.3	8.8E-2	8.5E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of protein phosphorylation</a>	RT		29	1.4	8.8E-2	8.6E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of fibroblast proliferation</a>	RT		10	0.5	9.0E-2	8.7E-1



Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to stress</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein localization to endosome</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of telomere maintenance via telomere lengthening</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of smooth muscle cell proliferation</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to interferon-alpha</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">SRP-dependent cotranslational protein targeting to membrane</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein deneddylation</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">response to interferon-beta</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">protein maturation by iron-sulfur cluster transfer</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of T cell cytokine production</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway</a>	<b>RT</b>		4	0.2	9.1E-2	8.7E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">transcription elongation from RNA polymerase II promoter</a>	<b>RT</b>		8	0.4	9.3E-2	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to interferon-gamma</a>	<b>RT</b>		16	0.8	9.3E-2	8.8E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to tumor necrosis factor</a>	<b>RT</b>		20	1.0	9.5E-2	9.0E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of DNA repair</a>	<b>RT</b>		9	0.4	9.6E-2	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">regulation of embryonic development</a>	<b>RT</b>		9	0.4	9.6E-2	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">negative regulation of apoptotic signaling pathway</a>	<b>RT</b>		7	0.3	9.7E-2	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">positive regulation of vascular endothelial growth factor production</a>	<b>RT</b>		7	0.3	9.7E-2	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to fibroblast growth factor stimulus</a>	<b>RT</b>		7	0.3	9.7E-2	9.1E-1
<input type="checkbox"/>	GOTERM_BP_DIRECT	<a href="#">cellular response to amino acid stimulus</a>	<b>RT</b>		11	0.5	9.9E-2	9.2E-1

339 gene(s)

 from your list are not in the output.

Please [cite DAVID](#) within any publication that makes use of any methods inspired by **DAVID**.