



Functional Annotation Chart

[Help and Manual](#)

Current Gene List: List_1

Current Background: Homo sapiens

417 DAVID IDs

Options

Rerun Using Options

Create Sublist

66 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
<input type="checkbox"/>	KEGG_PATHWAY	Pathways in cancer	RT		70	16.8	3.1E-24	3.5E-22
<input type="checkbox"/>	KEGG_PATHWAY	Neurotrophin signaling pathway	RT		32	7.7	3.2E-13	1.8E-11
<input type="checkbox"/>	KEGG_PATHWAY	Prostate cancer	RT		27	6.5	5.8E-13	2.2E-11
<input type="checkbox"/>	KEGG_PATHWAY	Chronic myeloid leukemia	RT		24	5.8	4.3E-12	1.2E-10
<input type="checkbox"/>	KEGG_PATHWAY	Glioma	RT		22	5.3	6.3E-12	1.4E-10
<input type="checkbox"/>	KEGG_PATHWAY	ErbB signaling pathway	RT		25	6.0	1.8E-11	3.4E-10
<input type="checkbox"/>	KEGG_PATHWAY	Acute myeloid leukemia	RT		20	4.8	9.4E-11	1.5E-9
<input type="checkbox"/>	KEGG_PATHWAY	Pancreatic cancer	RT		22	5.3	1.1E-10	1.6E-9
<input type="checkbox"/>	KEGG_PATHWAY	Focal adhesion	RT		37	8.9	1.4E-10	1.8E-9
<input type="checkbox"/>	KEGG_PATHWAY	Colorectal cancer	RT		23	5.5	4.0E-10	4.5E-9
<input type="checkbox"/>	KEGG_PATHWAY	Non-small cell lung cancer	RT		18	4.3	1.9E-9	1.9E-8
<input type="checkbox"/>	KEGG_PATHWAY	T cell receptor signaling pathway	RT		25	6.0	2.4E-9	2.2E-8
<input type="checkbox"/>	KEGG_PATHWAY	Small cell lung cancer	RT		22	5.3	2.6E-9	2.2E-8
<input type="checkbox"/>	KEGG_PATHWAY	Endometrial cancer	RT		17	4.1	8.4E-9	6.8E-8
<input type="checkbox"/>	KEGG_PATHWAY	Toll-like receptor signaling pathway	RT		23	5.5	1.7E-8	1.3E-7
<input type="checkbox"/>	KEGG_PATHWAY	Adherens junction	RT		20	4.8	1.9E-8	1.3E-7
<input type="checkbox"/>	KEGG_PATHWAY	Renal cell carcinoma	RT		19	4.6	2.3E-8	1.5E-7
<input type="checkbox"/>	KEGG_PATHWAY	Cell cycle	RT		25	6.0	5.1E-8	3.2E-7
<input type="checkbox"/>	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT		26	6.2	7.6E-8	4.5E-7
<input type="checkbox"/>	KEGG_PATHWAY	Apoptosis	RT		20	4.8	1.6E-7	9.0E-7
<input type="checkbox"/>	KEGG_PATHWAY	Regulation of actin cytoskeleton	RT		32	7.7	5.5E-7	2.9E-6
<input type="checkbox"/>	KEGG_PATHWAY	Melanoma	RT		17	4.1	1.0E-6	5.1E-6
<input type="checkbox"/>	KEGG_PATHWAY	Oocyte meiosis	RT		21	5.0	1.7E-6	8.4E-6
<input type="checkbox"/>	KEGG_PATHWAY	Wnt signaling pathway	RT		25	6.0	2.0E-6	9.2E-6
<input type="checkbox"/>	KEGG_PATHWAY	Adipocytokine signaling pathway	RT		16	3.8	2.4E-6	1.1E-5
<input type="checkbox"/>	KEGG_PATHWAY	Progesterone-mediated oocyte maturation	RT		18	4.3	3.2E-6	1.4E-5
<input type="checkbox"/>	KEGG_PATHWAY	TGF-beta signaling pathway	RT		18	4.3	3.8E-6	1.6E-5
<input type="checkbox"/>	KEGG_PATHWAY	NOD-like receptor signaling pathway	RT		15	3.6	4.7E-6	1.9E-5
<input type="checkbox"/>	KEGG_PATHWAY	Chemokine signaling pathway	RT		27	6.5	9.4E-6	3.6E-5
<input type="checkbox"/>	KEGG_PATHWAY	B cell receptor signaling pathway	RT		16	3.8	1.1E-5	4.0E-5
<input type="checkbox"/>	KEGG_PATHWAY	Insulin signaling pathway	RT		22	5.3	1.2E-5	4.5E-5
<input type="checkbox"/>	KEGG_PATHWAY	mTOR signaling pathway	RT		13	3.1	1.8E-5	6.3E-5
<input type="checkbox"/>	KEGG_PATHWAY	VEGF signaling pathway	RT		15	3.6	4.7E-5	1.6E-4
<input type="checkbox"/>	KEGG_PATHWAY	Endocytosis	RT		25	6.0	6.1E-5	2.0E-4
<input type="checkbox"/>	KEGG_PATHWAY	Leukocyte transendothelial migration	RT		19	4.6	6.9E-5	2.2E-4
<input type="checkbox"/>	KEGG_PATHWAY	Axon guidance	RT		20	4.8	7.1E-5	2.2E-4
<input type="checkbox"/>	KEGG_PATHWAY	Thyroid cancer	RT		9	2.2	1.2E-4	3.7E-4
<input type="checkbox"/>	KEGG_PATHWAY	Spliceosome	RT		19	4.6	1.6E-4	4.8E-4
<input type="checkbox"/>	KEGG_PATHWAY	Fc epsilon RI signaling pathway	RT		14	3.4	2.9E-4	8.4E-4
<input type="checkbox"/>	KEGG_PATHWAY	MAPK signaling pathway	RT		30	7.2	3.0E-4	8.4E-4
<input type="checkbox"/>	KEGG_PATHWAY	RIG-I-like receptor signaling pathway	RT		13	3.1	4.4E-4	1.2E-3

<input type="checkbox"/>	KEGG_PATHWAY	Basal transcription factors	RT		9	2.2	5.0E-4	1.3E-3
<input type="checkbox"/>	KEGG_PATHWAY	Bladder cancer	RT		9	2.2	1.8E-3	4.7E-3
<input type="checkbox"/>	KEGG_PATHWAY	Dorso-ventral axis formation	RT		7	1.7	2.0E-3	5.0E-3
<input type="checkbox"/>	KEGG_PATHWAY	Tight junction	RT		17	4.1	2.7E-3	6.7E-3
<input type="checkbox"/>	KEGG_PATHWAY	Long-term potentiation	RT		11	2.6	3.8E-3	9.2E-3
<input type="checkbox"/>	KEGG_PATHWAY	Non-homologous end-joining	RT		5	1.2	4.4E-3	1.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Jak-STAT signaling pathway	RT		18	4.3	4.9E-3	1.1E-2
<input type="checkbox"/>	KEGG_PATHWAY	Fc gamma R-mediated phagocytosis	RT		13	3.1	5.7E-3	1.3E-2
<input type="checkbox"/>	KEGG_PATHWAY	GnRH signaling pathway	RT		13	3.1	7.3E-3	1.6E-2
<input type="checkbox"/>	KEGG_PATHWAY	Melanogenesis	RT		13	3.1	7.9E-3	1.7E-2
<input type="checkbox"/>	KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori infection	RT		10	2.4	1.2E-2	2.5E-2
<input type="checkbox"/>	KEGG_PATHWAY	Type II diabetes mellitus	RT		8	1.9	1.4E-2	2.9E-2
<input type="checkbox"/>	KEGG_PATHWAY	Notch signaling pathway	RT		8	1.9	1.4E-2	2.9E-2
<input type="checkbox"/>	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	RT		15	3.6	1.4E-2	3.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Aldosterone-regulated sodium reabsorption	RT		7	1.7	2.4E-2	4.8E-2
<input type="checkbox"/>	KEGG_PATHWAY	Gap junction	RT		11	2.6	2.4E-2	4.7E-2
<input type="checkbox"/>	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	RT		8	1.9	3.0E-2	5.9E-2
<input type="checkbox"/>	KEGG_PATHWAY	Circadian rhythm	RT		4	1.0	3.2E-2	6.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Nucleotide excision repair	RT		7	1.7	3.2E-2	6.1E-2
<input type="checkbox"/>	KEGG_PATHWAY	p53 signaling pathway	RT		9	2.2	3.3E-2	6.0E-2
<input type="checkbox"/>	KEGG_PATHWAY	Viral myocarditis	RT		9	2.2	4.1E-2	7.3E-2
<input type="checkbox"/>	KEGG_PATHWAY	Prion diseases	RT		6	1.4	4.1E-2	7.4E-2
<input type="checkbox"/>	KEGG_PATHWAY	Homologous recombination	RT		5	1.2	6.6E-2	1.1E-1
<input type="checkbox"/>	KEGG_PATHWAY	Antigen processing and presentation	RT		9	2.2	8.6E-2	1.5E-1
<input type="checkbox"/>	KEGG_PATHWAY	Pathogenic Escherichia coli infection	RT		7	1.7	9.3E-2	1.5E-1

162 gene(s) from your list are not in the output.

Please cite [Nature Protocols 2009; 4\(1\):44 & Genome Biology 2003; 4\(5\):P3](#) within any publication that makes use of any methods inspired by **DAVID**.



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