National Institutes of Health
DAVID Bioinformatics

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

111 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
☐	KEGG_PATHWAY	Ribosome	RT		82	4.0	8.2E-30	2.8E-27
☐	KEGG_PATHWAY	Coronavirus disease - COVID-19	RT		96	4.7	3.2E-28	5.5E-26
☐	KEGG_PATHWAY	Protein processing in endoplasmic reticulum	RT		64	3.1	1.3E-16	1.4E-14
☐	KEGG_PATHWAY	Th17 cell differentiation	RT		47	2.3	4.9E-15	4.1E-13
☐	KEGG_PATHWAY	Endocytosis	RT		78	3.8	1.0E-14	7.0E-13
☐	KEGG_PATHWAY	Epstein-Barr virus infection	RT		67	3.3	3.9E-14	2.2E-12
☐	KEGG_PATHWAY	Human T-cell leukemia virus 1 infection	RT		71	3.5	4.8E-14	2.3E-12
☐	KEGG_PATHWAY	Influenza A	RT		54	2.6	1.3E-10	5.4E-9
☐	KEGG_PATHWAY	PD-L1 expression and PD-1 checkpoint pathway in cancer	RT		35	1.7	6.4E-10	2.4E-8
☐	KEGG_PATHWAY	Amyotrophic lateral sclerosis	RT		88	4.3	9.1E-10	3.1E-8
☐	KEGG_PATHWAY	Th1 and Th2 cell differentiation	RT		35	1.7	1.8E-9	5.1E-8
☐	KEGG_PATHWAY	Measles	RT		45	2.2	1.8E-9	5.1E-8
☐	KEGG_PATHWAY	Apoptosis	RT		44	2.1	3.7E-9	9.6E-8
☐	KEGG_PATHWAY	Antigen processing and presentation	RT		31	1.5	5.4E-9	1.3E-7
☐	KEGG_PATHWAY	Salmonella infection	RT		65	3.2	8.6E-9	1.9E-7
☐	KEGG_PATHWAY	Human immunodeficiency virus 1 infection	RT		58	2.8	1.0E-8	2.1E-7
☐	KEGG_PATHWAY	T cell receptor signaling pathway	RT		40	1.9	1.1E-8	2.1E-7
☐	KEGG_PATHWAY	Viral carcinogenesis	RT		56	2.7	1.6E-8	3.1E-7
☐	KEGG_PATHWAY	Kaposi sarcoma-associated herpesvirus infection	RT		54	2.6	1.8E-8	3.3E-7
☐	KEGG_PATHWAY	Autophagy - animal	RT		48	2.3	2.9E-8	4.9E-7
☐	KEGG_PATHWAY	Huntington disease	RT		72	3.5	1.2E-7	2.0E-6
☐	KEGG_PATHWAY	Parkinson disease	RT		65	3.2	1.3E-7	2.0E-6
☐	KEGG_PATHWAY	Viral life cycle - HIV-1	RT		25	1.2	2.3E-7	3.3E-6
☐	KEGG_PATHWAY	Pathways of neurodegeneration - multiple diseases	RT		99	4.8	2.7E-7	3.8E-6
☐	KEGG_PATHWAY	Hepatitis B	RT		45	2.2	3.6E-7	4.9E-6
☐	KEGG_PATHWAY	Necroptosis	RT		44	2.1	6.7E-7	8.7E-6
☐	KEGG_PATHWAY	NOD-like receptor signaling pathway	RT		48	2.3	1.4E-6	1.8E-5
☐	KEGG_PATHWAY	Phagosome	RT		41	2.0	2.9E-6	3.5E-5
☐	KEGG_PATHWAY	Human cytomegalovirus infection	RT		54	2.6	3.1E-6	3.6E-5
☐	KEGG_PATHWAY	Prion disease	RT		62	3.0	3.2E-6	3.6E-5
☐	KEGG_PATHWAY	Viral myocarditis	RT		24	1.2	3.4E-6	3.7E-5
☐	KEGG_PATHWAY	Toxoplasmosis	RT		33	1.6	3.6E-6	3.8E-5
☐	KEGG_PATHWAY	Oxidative phosphorylation	RT		37	1.8	5.4E-6	5.6E-5
☐	KEGG_PATHWAY	Shigellosis	RT		57	2.8	5.7E-6	5.6E-5
☐	KEGG_PATHWAY	Cellular senescence	RT		41	2.0	5.8E-6	5.6E-5
☐	KEGG_PATHWAY	Alzheimer disease	RT		78	3.8	1.5E-5	1.4E-4
☐	KEGG_PATHWAY	Tuberculosis	RT		44	2.1	1.8E-5	1.6E-4
☐	KEGG_PATHWAY	Chemical carcinogenesis - reactive oxygen species	RT		51	2.5	2.5E-5	2.2E-4
☐	KEGG_PATHWAY	Allograft rejection	RT		16	0.8	2.6E-5	2.2E-4
☐	KEGG_PATHWAY	Type I diabetes mellitus	RT		17	0.8	3.3E-5	2.8E-4
☐	KEGG_PATHWAY	Diabetic cardiomyopathy	RT		47	2.3	3.9E-5	3.2E-4
☐	KEGG_PATHWAY	Spliceosome	RT		49	2.4	5.1E-5	4.1E-4
☐	KEGG_PATHWAY	Lysosome	RT		34	1.7	6.5E-5	5.1E-4
☐	KEGG_PATHWAY	Non-alcoholic fatty liver disease	RT		38	1.9	6.9E-5	5.3E-4
☐	KEGG_PATHWAY	Graft-versus-host disease	RT		16	0.8	1.0E-4	7.3E-4
☐	KEGG_PATHWAY	Osteoclast differentiation	RT		34	1.7	1.0E-4	7.3E-4
☐	KEGG_PATHWAY	Legionellosis	RT		19	0.9	1.0E-4	7.3E-4
☐	KEGG_PATHWAY	Chagas disease	RT		28	1.4	1.0E-4	7.3E-4
☐	KEGG_PATHWAY	TNF signaling pathway	RT		30	1.5	1.3E-4	8.7E-4
☐	KEGG_PATHWAY	Lipid and atherosclerosis	RT		47	2.3	1.7E-4	1.1E-3
☐	KEGG_PATHWAY	Protein export	RT		13	0.6	2.1E-4	1.4E-3
☐	KEGG_PATHWAY	Hepatitis C	RT		37	1.8	2.4E-4	1.5E-3
☐	KEGG_PATHWAY	Vibrio cholerae infection	RT		17	0.8	2.6E-4	1.7E-3
☐	KEGG_PATHWAY	Inflammatory bowel disease	RT		20	1.0	2.7E-4	1.7E-3
☐	KEGG_PATHWAY	mRNA surveillance pathway	RT		26	1.3	2.9E-4	1.8E-3
☐	KEGG_PATHWAY	Mitophagy - animal	RT		27	1.3	3.2E-4	1.9E-3
☐	KEGG_PATHWAY	Leishmaniasis	RT		22	1.1	3.8E-4	2.3E-3
☐	KEGG_PATHWAY	Autoimmune thyroid disease	RT		17	0.8	5.5E-4	3.2E-3
☐	KEGG_PATHWAY	Citrate cycle (TCA cycle)	RT		12	0.6	6.6E-4	3.8E-3
☐	KEGG_PATHWAY	Spinocerebellar ataxia	RT		33	1.6	7.1E-4	4.0E-3
☐	KEGG_PATHWAY	Pancreatic cancer	RT		21	1.0	8.6E-4	4.8E-3
☐	KEGG_PATHWAY	Rheumatoid arthritis	RT		24	1.2	9.4E-4	5.1E-3
☐	KEGG_PATHWAY	Proteasome	RT		15	0.7	1.1E-3	5.9E-3
☐	KEGG_PATHWAY	Apoptosis - multiple species	RT		12	0.6	1.2E-3	6.5E-3
☐	KEGG_PATHWAY	Pathogenic Escherichia coli infection	RT		41	2.0	1.4E-3	7.4E-3
☐	KEGG_PATHWAY	Renal cell carcinoma	RT		19	0.9	1.7E-3	8.7E-3
☐	KEGG_PATHWAY	Colorectal cancer	RT		22	1.1	1.8E-3	9.1E-3
☐	KEGG_PATHWAY	Cell cycle	RT		34	1.7	1.8E-3	9.1E-3
☐	KEGG_PATHWAY	NF-kappa B signaling pathway	RT		25	1.2	2.0E-3	1.0E-2
☐	KEGG_PATHWAY	Non-small cell lung cancer	RT		19	0.9	2.8E-3	1.4E-2
☐	KEGG_PATHWAY	Yersinia infection	RT		30	1.5	3.0E-3	1.4E-2
☐	KEGG_PATHWAY	Ferroptosis	RT		13	0.6	4.4E-3	2.1E-2
☐	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT		30	1.5	5.2E-3	2.4E-2
☐	KEGG_PATHWAY	Chronic myeloid leukemia	RT		19	0.9	5.3E-3	2.4E-2
☐	KEGG_PATHWAY	Human papillomavirus infection	RT		58	2.8	7.6E-3	3.4E-2
☐	KEGG_PATHWAY	p53 signaling pathway	RT		18	0.9	9.1E-3	4.0E-2
☐	KEGG_PATHWAY	Epithelial cell signaling in Helicobacter pylori infection	RT		17	0.8	1.2E-2	5.2E-2
☐	KEGG_PATHWAY	Pathways in cancer	RT		85	4.1	1.4E-2	5.9E-2

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
☐	KEGG_PATHWAY	Toll-like receptor signaling pathway	RT		23	1.1	1.4E-2	6.0E-2
☐	KEGG_PATHWAY	Natural killer cell mediated cytotoxicity	RT		26	1.3	1.4E-2	6.0E-2
☐	KEGG_PATHWAY	Polycomb repressive complex	RT		19	0.9	1.5E-2	6.4E-2
☐	KEGG_PATHWAY	RNA degradation	RT		18	0.9	1.7E-2	7.1E-2
☐	KEGG_PATHWAY	Vasopressin-regulated water reabsorption	RT		12	0.6	1.8E-2	7.2E-2
☐	KEGG_PATHWAY	Parathyroid hormone synthesis, secretion and action	RT		22	1.1	2.2E-2	8.8E-2
☐	KEGG_PATHWAY	Nucleocytoplasmic transport	RT		22	1.1	2.7E-2	1.1E-1
☐	KEGG_PATHWAY	Prostate cancer	RT		20	1.0	3.1E-2	1.2E-1
☐	KEGG_PATHWAY	C-type lectin receptor signaling pathway	RT		21	1.0	3.3E-2	1.3E-1
☐	KEGG_PATHWAY	Nucleotide metabolism	RT		18	0.9	3.4E-2	1.3E-1
☐	KEGG_PATHWAY	Long-term potentiation	RT		15	0.7	3.7E-2	1.4E-1
☐	KEGG_PATHWAY	Acute myeloid leukemia	RT		15	0.7	3.7E-2	1.4E-1
☐	KEGG_PATHWAY	cGMP-PKG signaling pathway	RT		30	1.5	4.0E-2	1.5E-1
☐	KEGG_PATHWAY	Primary immunodeficiency	RT		10	0.5	4.2E-2	1.6E-1
☐	KEGG_PATHWAY	Growth hormone synthesis, secretion and action	RT		23	1.1	4.3E-2	1.6E-1
☐	KEGG_PATHWAY	Sphingolipid signaling pathway	RT		23	1.1	4.6E-2	1.7E-1
☐	KEGG_PATHWAY	2-Oxocarboxylic acid metabolism	RT		9	0.4	4.8E-2	1.7E-1
☐	KEGG_PATHWAY	Carbon metabolism	RT		22	1.1	4.9E-2	1.7E-1
☐	KEGG_PATHWAY	RIG-I-like receptor signaling pathway	RT		15	0.7	5.6E-2	2.0E-1
☐	KEGG_PATHWAY	B cell receptor signaling pathway	RT		17	0.8	5.7E-2	2.0E-1
☐	KEGG_PATHWAY	Dopaminergic synapse	RT		24	1.2	6.4E-2	2.2E-1
☐	KEGG_PATHWAY	Hematopoietic cell lineage	RT		19	0.9	6.7E-2	2.3E-1
☐	KEGG_PATHWAY	Platinum drug resistance	RT		15	0.7	6.8E-2	2.3E-1
☐	KEGG_PATHWAY	Various types of N-glycan biosynthesis	RT		10	0.5	7.3E-2	2.4E-1
☐	KEGG_PATHWAY	Thermogenesis	RT		38	1.9	7.4E-2	2.4E-1
☐	KEGG_PATHWAY	Intestinal immune network for IgA production	RT		11	0.5	8.1E-2	2.6E-1
☐	KEGG_PATHWAY	Amphetamine addiction	RT		14	0.7	8.7E-2	2.8E-1
☐	KEGG_PATHWAY	Cytosolic DNA-sensing pathway	RT		16	0.8	9.2E-2	2.9E-1
☐	KEGG_PATHWAY	FoxO signaling pathway	RT		23	1.1	9.4E-2	2.9E-1
☐	KEGG_PATHWAY	JAK-STAT signaling pathway	RT		28	1.4	9.5E-2	2.9E-1
☐	KEGG_PATHWAY	Prolactin signaling pathway	RT		14	0.7	9.5E-2	2.9E-1
☐	KEGG_PATHWAY	Glutathione metabolism	RT		12	0.6	9.5E-2	2.9E-1
☐	KEGG_PATHWAY	Autophagy - other	RT		8	0.4	9.8E-2	3.0E-1

1184 gene(s) from your list are not in the output.

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