DAVID Bioinformatics Resources 6.7
National Institute of Allergy and Infectious Diseases (NIAID), NIH

Functional Annotation Chart

Help and Manual

Current Gene List: List_1
Current Background: Background_1
2159 DAVID IDs
Options

Rerun Using Options | Create Sublist

90 chart records

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Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	KEGG_PATHWAY	Cell cycle	RT		37	1,7	2,1E-4	2,8E-2
	KEGG_PATHWAY	DNA replication	RT		15	0,7	8,9E-4	5,8E-2
	KEGG_PATHWAY	Spliceosome	RT		33	1,5	1,9E-3	8,2E-2
	KEGG_PATHWAY	Valine, leucine and isoleucine degradation	RT		15	0,7	6,9E-3	2,1E-1
	KEGG_PATHWAY	Glycerolipid metabolism	RT		12	0,6	1,2E-2	2,7E-1
	KEGG_PATHWAY	Fatty acid metabolism	RT		12	0,6	1,2E-2	2,7E-1
	KEGG_PATHWAY	Mismatch repair	RT		9	0,4	1,4E-2	2,7E-1
	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT		18	0,8	1,6E-2	2,7E-1
	KEGG_PATHWAY	Propanoate metabolism	RT		11	0,5	2,0E-2	2,9E-1
	KEGG_PATHWAY	Oocyte meiosis	RT		24	1,1	3,0E-2	3,7E-1
	KEGG_PATHWAY	Nucleotide excision repair	RT		13	0,6	3,4E-2	3,7E-1
	KEGG_PATHWAY	Ascorbate and aldarate metabolism	RT		5	0,2	5,5E-2	5,0E-1
	KEGG_PATHWAY	One carbon pool by folate	RT		6	0,3	5,9E-2	5,0E-1
	KEGG_PATHWAY	Proteasome	RT		13	0,6	7,7E-2	5,7E-1
	KEGG_PATHWAY	Galactose metabolism	RT		7	0,3	1,2E-1	7,0E-1
	KEGG_PATHWAY	Tryptophan metabolism	RT		10	0,5	1,2E-1	6,9E-1
	KEGG_PATHWAY	Arginine and proline metabolism	RT		13	0,6	1,3E-1	6,9E-1
	KEGG_PATHWAY	Ether lipid metabolism	RT		8	0,4	1,5E-1	7,3E-1
	KEGG_PATHWAY	Retinol metabolism	RT		7	0,3	1,7E-1	7,5E-1
	KEGG_PATHWAY	Pentose and glucuronate interconversions	RT		4	0,2	1,9E-1	7,9E-1
	KEGG_PATHWAY	Base excision repair	RT		8	0,4	2,0E-1	7,8E-1
	KEGG_PATHWAY	Methane metabolism	RT		3	0,1	2,1E-1	7,8E-1
	KEGG_PATHWAY	Glycerophospholipid metabolism	RT		12	0,6	2,4E-1	8,2E-1
	KEGG_PATHWAY	Pyruvate metabolism	RT		9	0,4	2,5E-1	8,2E-1
	KEGG_PATHWAY	TGF-beta signaling pathway	RT		16	0,7	3,2E-1	8,8E-1
	KEGG_PATHWAY	Lysosome	RT		20	0,9	3,7E-1	9,2E-1
	KEGG_PATHWAY	Histidine metabolism	RT		5	0,2	3,8E-1	9,2E-1
	KEGG_PATHWAY	Limonene and pinene degradation	RT		4	0,2	4,0E-1	9,2E-1
	KEGG_PATHWAY	Glycine, serine and threonine metabolism	RT		6	0,3	4,1E-1	9,2E-1
	KEGG_PATHWAY	Pentose phosphate pathway	RT		7	0,3	4,2E-1	9,2E-1
	KEGG_PATHWAY	beta-Alanine metabolism	RT		5	0,2	4,3E-1	9,2E-1
	KEGG_PATHWAY	p53 signaling pathway	RT		12	0,6	4,3E-1	9,1E-1
	KEGG_PATHWAY	RNA degradation	RT		11	0,5	4,4E-1	9,1E-1
	KEGG_PATHWAY	Starch and sucrose metabolism	RT		6	0,3	4,4E-1	9,1E-1
	KEGG_PATHWAY	Oxidative phosphorylation	RT		21	1,0	4,5E-1	9,1E-1
	KEGG_PATHWAY	Citrate cycle (TCA cycle)	RT		7	0,3	4,6E-1	9,1E-1
	KEGG_PATHWAY	Cell adhesion molecules (CAMs)	RT		14	0,6	4,9E-1	9,2E-1
	KEGG_PATHWAY	Steroid biosynthesis	RT		4	0,2	5,0E-1	9,2E-1
	KEGG_PATHWAY	Purine metabolism	RT		24	1,1	5,1E-1	9,2E-1
	KEGG_PATHWAY	Ubiquitin mediated proteolysis	RT		20	0,9	5,3E-1	9,3E-1
	KEGG_PATHWAY	Regulation of autophagy	RT		4	0,2	5,4E-1	9,3E-1
	KEGG_PATHWAY	Butanoate metabolism	RT		6	0,3	5,5E-1	9,3E-1
	KEGG_PATHWAY	Gap junction	RT		14	0,6	5,5E-1	9,2E-1
	KEGG_PATHWAY	Cysteine and methionine metabolism	RT		7	0,3	5,8E-1	9,4E-1