



BIOINFORMATICS
DATABASE

DAVID Bioinformatics Resources 6.8
Laboratory of Human Retrovirology and Immunoinformatics (LHRI)

*** Welcome to DAVID 6.8 ***
*** If you are looking for DAVID 6.7, please visit our [development site](#). ***

Functional Annotation Clustering

[Help and Manual](#)

Current Gene List: **high_rho**
Current Background: **Background_4**
39 DAVID IDs

Options Classification Stringency Medium

7 Cluster(s)

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Annotation Cluster 1		Enrichment Score: 0.56				Count	P_Value	Benjamini
KEGG_PATHWAY	Glycerolipid metabolism	RT	<div></div>			3	6.7E-2	8.8E-1
GOTERM_BP_DIRECT	phospholipid biosynthetic process	RT	<div></div>			3	1.5E-1	1.0E0
UP_KEYWORDS	Phospholipid metabolism	RT	<div></div>			3	2.8E-1	1.0E0
UP_KEYWORDS	Phospholipid biosynthesis	RT	<div></div>			3	2.8E-1	1.0E0
KEGG_PATHWAY	Glycerophospholipid metabolism	RT	<div></div>			3	3.1E-1	1.0E0
UP_KEYWORDS	Lipid biosynthesis	RT	<div></div>			4	5.0E-1	1.0E0
UP_KEYWORDS	Lipid metabolism	RT	<div></div>			4	5.0E-1	1.0E0
KEGG_PATHWAY	Biosynthesis of secondary metabolites	RT	<div></div>			7	5.4E-1	9.5E-1
Annotation Cluster 2		Enrichment Score: 0.47				Count	P_Value	Benjamini
UP_SEQ_FEATURE	nucleotide phosphate-binding region: GTP	RT	<div></div>			4	2.5E-1	1.0E0
UP_KEYWORDS	GTP-binding	RT	<div></div>			4	2.9E-1	1.0E0
GOTERM_MF_DIRECT	GTPase activity	RT	<div></div>			4	2.9E-1	1.0E0
GOTERM_MF_DIRECT	GTP binding	RT	<div></div>			4	2.9E-1	1.0E0
INTERPRO	Small GTP-binding protein domain	RT	<div></div>			3	3.5E-1	1.0E0
INTERPRO	P-loop containing nucleoside triphosphate hydrolase	RT	<div></div>			5	7.0E-1	1.0E0
Annotation Cluster 3		Enrichment Score: 0.42				Count	P_Value	Benjamini
UP_KEYWORDS	Cell membrane	RT	<div></div>			8	1.6E-1	1.0E0
UP_KEYWORDS	Membrane	RT	<div></div>			8	1.8E-1	1.0E0
GOTERM_CC_DIRECT	plasma membrane	RT	<div></div>			6	4.2E-1	9.9E-1
GOTERM_CC_DIRECT	Integral component of membrane	RT	<div></div>			4	5.4E-1	9.9E-1
UP_KEYWORDS	Transmembrane helix	RT	<div></div>			4	5.5E-1	1.0E0
UP_KEYWORDS	Transmembrane	RT	<div></div>			4	5.5E-1	1.0E0
UP_SEQ_FEATURE	transmembrane region	RT	<div></div>			4	5.6E-1	1.0E0
Annotation Cluster 4		Enrichment Score: 0.3				Count	P_Value	Benjamini
KEGG_PATHWAY	Purine metabolism	RT	<div></div>			4	4.0E-1	9.8E-1
KEGG_PATHWAY	Pyrimidine metabolism	RT	<div></div>			4	4.9E-1	9.8E-1
UP_KEYWORDS	Nucleotidyltransferase	RT	<div></div>			3	6.5E-1	1.0E0
Annotation Cluster 5		Enrichment Score: 0.14				Count	P_Value	Benjamini
UP_KEYWORDS	Protein biosynthesis	RT	<div></div>			7	3.8E-1	1.0E0
KEGG_PATHWAY	Aminoacyl-tRNA biosynthesis	RT	<div></div>			5	5.3E-1	9.6E-1
UP_KEYWORDS	Nucleotide binding	RT	<div></div>			12	7.3E-1	1.0E0
UP_KEYWORDS	Aminoacyl-tRNA synthetase	RT	<div></div>			3	8.8E-1	1.0E0
UP_KEYWORDS	Ligase	RT	<div></div>			5	9.0E-1	1.0E0

GOTERM_MF_DIRECT	ATP.binding	RT	<div></div>	8	9.5E-1	1.0E0
UP_KEYWORDS	ATP-binding	RT	<div></div>	7	9.7E-1	1.0E0
Annotation Cluster 6		Enrichment Score: 0.13	<div></div>	Count	P_Value	Benjamini
GOTERM_MF_DIRECT	metal ion binding	RT	<div></div>	4	5.9E-1	1.0E0
UP_KEYWORDS	Magnesium	RT	<div></div>	5	7.0E-1	1.0E0
UP_KEYWORDS	Metal:binding	RT	<div></div>	5	9.5E-1	1.0E0
Annotation Cluster 7		Enrichment Score: 0.06	<div></div>	Count	P_Value	Benjamini
GOTERM_BP_DIRECT	translation	RT	<div></div>	8	6.3E-1	1.0E0
KEGG_PATHWAY	Ribosome	RT	<div></div>	6	8.3E-1	1.0E0
UP_KEYWORDS	Ribosomal protein	RT	<div></div>	5	9.4E-1	1.0E0
GOTERM_MF_DIRECT	structural constituent of ribosome	RT	<div></div>	5	9.5E-1	1.0E0
UP_KEYWORDS	Ribonucleoprotein	RT	<div></div>	5	9.5E-1	1.0E0
UP_KEYWORDS	rRNA:binding	RT	<div></div>	3	9.9E-1	1.0E0

were not clustered.