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: low_rho
Current Background: Background_4
27 DAVID IDs

Options   **Classification Stringency**   Medium

4 Cluster(s)

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Annotation Cluster 1	Enrichment Score: 3.91	G		Count	P_Value	Benjamini
GOTERM_BP_DIRECT	cell division	RT		9	2.8E-5	8.7E-4
KEGG_PATHWAY	Peptidoglycan biosynthesis	RT		8	3.1E-5	5.5E-4
UP_KEYWORDS	Cell cycle	RT		9	1.1E-4	5.9E-3
UP_KEYWORDS	Cell division	RT		9	1.1E-4	5.9E-3
UP_KEYWORDS	Cell shape	RT		9	1.1E-4	5.9E-3
GOTERM_BP_DIRECT	cell cycle	RT		8	1.8E-4	2.7E-3
GOTERM_BP_DIRECT	peptidoglycan biosynthetic process	RT		8	1.8E-4	2.7E-3
GOTERM_BP_DIRECT	regulation of cell shape	RT		9	1.8E-4	1.9E-3
UP_KEYWORDS	Peptidoglycan synthesis	RT		8	1.8E-4	5.0E-3
GOTERM_BP_DIRECT	cell wall organization	RT		9	3.0E-4	2.3E-3
UP_KEYWORDS	Cell wall biogenesis/degradation	RT		9	3.1E-4	5.7E-3
Annotation Cluster 2	**Enrichment Score: 0.75**	G		Count	P_Value	Benjamini
UP_KEYWORDS	rRNA-binding	RT		8	5.9E-2	5.6E-1
GOTERM_MF_DIRECT	rRNA binding	RT		7	1.1E-1	9.8E-1
UP_KEYWORDS	Ribosomal protein	RT		8	1.7E-1	8.6E-1
UP_KEYWORDS	Ribonucleoprotein	RT		8	1.9E-1	8.4E-1
UP_KEYWORDS	RNA-binding	RT		8	2.3E-1	8.2E-1
GOTERM_MF_DIRECT	structural constituent of ribosome	RT		8	2.4E-1	9.9E-1
KEGG_PATHWAY	Ribosome	RT		8	2.8E-1	8.6E-1
GOTERM_BP_DIRECT	translation	RT		7	3.8E-1	9.5E-1
Annotation Cluster 3	**Enrichment Score: 0.53**	G		Count	P_Value	Benjamini
INTERPRO	Mur ligase, N-terminal	RT		3	4.0E-2	9.8E-1
INTERPRO	Mur ligase, central	RT		3	7.4E-2	9.8E-1
INTERPRO	Mur ligase, C-terminal	RT		3	7.4E-2	9.8E-1
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	RT		4	6.1E-1	1.0E0
UP_KEYWORDS	Ligase	RT		5	6.5E-1	9.8E-1
UP_KEYWORDS	ATP-binding	RT		7	7.6E-1	9.9E-1
GOTERM_MF_DIRECT	ATP binding	RT		7	8.7E-1	1.0E0
UP_KEYWORDS	Nucleotide-binding	RT		7	9.1E-1	1.0E0
Annotation Cluster 4	**Enrichment Score: 0.36**	G		Count	P_Value	Benjamini
UP_KEYWORDS	Cell membrane	RT		6	2.1E-1	8.4E-1
UP_KEYWORDS	Membrane	RT		6	2.4E-1	8.0E-1
GOTERM_CC_DIRECT	plasma membrane	RT		5	4.2E-1	1.0E0

UP_SEQ_FEATURE	transmembrane region	**RT**		3	6.0E-1	1.0E0
UP_KEYWORDS	Transmembrane	**RT**		3	6.1E-1	9.8E-1
UP_KEYWORDS	Transmembrane helix	**RT**		3	6.1E-1	9.8E-1
GOTERM_CC_DIRECT	integral component of membrane	**RT**		3	6.7E-1	1.0E0

were not clustered.