



*** Welcome to DAVID (2021 Update) ***

*** If you are looking for [DAVID 6.8](#), it is still accessible on [this server](#). ***

Functional Annotation Chart

Current Gene List: [List_1](#)

Current Background: [Saccharomyces cerevisiae S288C](#)

612 DAVID IDs

Options

Rerun Using Options

Create Sublist

81 chart records

Sublist	Category	Term	RT	Genes
<input type="checkbox"/>	KEGG_PATHWAY	Glycolysis / Gluconeogenesis	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Glycolysis	RT	
<input type="checkbox"/>	INTERPRO	Asparaginase/glutaminase	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	DOMAIN:Asparaginase/glutaminase	RT	
<input type="checkbox"/>	PIR_SUPERFAMILY	L-asparaginase/Glutamyl-tRNA(Gln) amidotransferase subunit D	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Carbon metabolism	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Starch and sucrose metabolism	RT	
<input type="checkbox"/>	SMART	SM00870	RT	
<input type="checkbox"/>	INTERPRO	L-asparaginase, C-terminal domain	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Metabolic pathways	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Biosynthesis of secondary metabolites	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Tyrosine metabolism	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Periplasm	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Kinetochore	RT	
<input type="checkbox"/>	COG_ONTOLOGY	Carbohydrate transport and metabolism	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Secreted	RT	
<input type="checkbox"/>	INTERPRO	Asparaginase/glutaminase, active site 1	RT	
<input type="checkbox"/>	INTERPRO	L-asparaginase, N-terminal	RT	
<input type="checkbox"/>	INTERPRO	Asparaginase/glutaminase, active site 2	RT	
<input type="checkbox"/>	INTERPRO	L-asparaginase, type II	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	BINDING:Glyceraldehyde 3-phosphate	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	ACT_SITE:O-isoaspartyl threonine intermediate	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REGION:Substrate binding	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Mitosis	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Galactose metabolism	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Meiosis	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Fatty acid degradation	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Centromere	RT	
<input type="checkbox"/>	UP_KW_MOLECULAR_FUNCTION	Aminotransferase	RT	
<input type="checkbox"/>	INTERPRO	Galactose mutarotase-like domain	RT	
<input type="checkbox"/>	UP_KW_PTM	Glycoprotein	RT	
<input type="checkbox"/>	SMART	SM00846	RT	
<input type="checkbox"/>	SMART	RL11	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	Chromosome partition	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	BINDING:Substrate	RT	
<input type="checkbox"/>	INTERPRO	Ribosomal protein L11, N-terminal	RT	

Sublist	Category	Term	RT	Genes
<input type="checkbox"/>	SMART	SM01192	RT	
<input type="checkbox"/>	UP_KW_BIOLOGICAL_PROCESS	mRNA splicing	RT	
<input type="checkbox"/>	INTERPRO	Enolase, N-terminal	RT	
<input type="checkbox"/>	INTERPRO	Enolase	RT	
<input type="checkbox"/>	INTERPRO	Enolase, conserved site	RT	
<input type="checkbox"/>	INTERPRO	Enolase, C-terminal	RT	
<input type="checkbox"/>	UP_KW_CELLULAR_COMPONENT	Spliceosome	RT	
<input type="checkbox"/>	UP_KW_LIGAND	Pyridoxal phosphate	RT	
<input type="checkbox"/>	INTERPRO	Pyridoxal phosphate-dependent transferase, major region, subdomain 1	RT	
<input type="checkbox"/>	INTERPRO	Pyridoxal phosphate-dependent transferase	RT	
<input type="checkbox"/>	UP_KW_PTM	GPI-anchor	RT	
<input type="checkbox"/>	INTERPRO	Aminotransferase, class I/classII	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	ACT_SITE:Proton donor	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Biosynthesis of nucleotide sugars	RT	
<input type="checkbox"/>	KEGG_PATHWAY	Phenylalanine metabolism	RT	
<input type="checkbox"/>	PIR_SUPERFAMILY	enolase	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	METAL:Copper	RT	
<input type="checkbox"/>	UP_SEQ_FEATURE	REPEAT:PIR1/2/3	RT	
<input type="checkbox"/>	UP_KW_LIGAND	Heme	RT	
<input type="checkbox"/>	KEGG_PATHWAY	RNA degradation	RT	

372 gene(s)

 from your list are not in the output.