

Your input list contains 49 genes.

These 1 identifiers were found to be unannotated: YLR264C

These 4 identifiers had no non-root annotations: YBL028C YML018C YGR079W YLR327C

GO Terms from the biological_process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use
rRNA processing (GO:0006364)	YDR449C , YEL026W , YER127W , YGR159C , YHR066W , YHR196W , YJL069C , YLR264W , YMR093W , YNL112W , YNL182C , YOL041C , YOL080C	13 of 48 genes, 27.08%	373 of 6985 annotated genes, 5.34%
ribosomal large subunit biogenesis (GO:0042273)	YCR072C , YDL063C , YHR066W , YIR012W , YJL122W , YNL182C , YOL041C , YOL080C	8 of 48 genes, 16.67%	128 of 6985 annotated genes, 1.83%
organelle assembly (GO:0070925)	YCR072C , YGR159C , YHR066W , YIR012W , YLR180W , YLR264W , YNL182C , YOL080C	8 of 48 genes, 16.67%	214 of 6985 annotated genes, 3.06%
ribosomal small subunit biogenesis (GO:0042274)	YDR449C , YEL026W , YER127W , YGR159C , YHR196W , YJL069C , YLR264W , YMR093W	8 of 48 genes, 16.67%	148 of 6985 annotated genes, 2.12%
ribosome assembly (GO:0042255)	YCR072C , YGR159C , YHR066W , YIR012W , YLR264W , YNL182C , YOL080C	7 of 48 genes, 14.58%	83 of 6985 annotated genes, 1.19%
transmembrane transport (GO:0055085)	YDR536W , YHR094C , YJL107C , YJL108C , YKL120W , YNL065W , YOR271C	7 of 48 genes, 14.58%	491 of 6985 annotated genes, 7.03%
transcription by RNA polymerase I (GO:0006360)	YHR196W , YJL148W , YJR063W , YML043C , YMR093W , YNL248C	6 of 48 genes, 12.50%	78 of 6985 annotated genes, 1.12%
amino acid metabolic process (GO:0006520)	YBL039C , YDR037W , YLR180W , YMR300C	4 of 48 genes, 8.33%	256 of 6985 annotated genes, 3.66%
nucleobase-containing small molecule metabolic process (GO:0055086)	YBL039C , YMR300C , YNL141W , YOL136C	4 of 48 genes, 8.33%	246 of 6985 annotated genes, 3.52%
carbohydrate metabolic process (GO:0005975)	YBR105C , YER062C , YKR097W , YOL136C	4 of 48 genes, 8.33%	291 of 6985 annotated genes, 4.17%
RNA catabolic process (GO:0006401)	YGR159C , YLR264W , YNL112W , YOR359W	4 of 48 genes, 8.33%	180 of 6985 annotated genes, 2.58%
monoatomic ion transport (GO:0006811)	YDR536W , YHR094C , YNR060W , YOR271C	4 of 48 genes, 8.33%	235 of 6985 annotated genes, 3.36%
nuclear transport (GO:0051169)	YDL063C , YHR196W , YLR264W	3 of 48 genes, 6.25%	191 of 6985 annotated genes, 2.73%
protein transport (GO:0015031)	YBR105C , YDL063C , YOR359W	3 of 48 genes, 6.25%	646 of 6985 annotated genes, 9.25%
mRNA processing (GO:0006397)	YEL026W , YGR159C , YPL212C	3 of 48 genes, 6.25%	241 of 6985 annotated genes, 3.45%
regulation of translation (GO:0006417)	YLR264W , YNL112W , YOR359W	3 of 48 genes, 6.25%	240 of 6985 annotated genes, 3.44%
proteolysis involved in protein catabolic process (GO:0051603)	YBR105C , YLR224W	2 of 48 genes, 4.17%	285 of 6985 annotated genes, 4.08%
DNA-templated transcription initiation (GO:0006352)	YML043C , YNL248C	2 of 48 genes, 4.17%	95 of 6985 annotated genes, 1.36%
DNA-templated transcription elongation (GO:0006354)	YJL148W , YNL248C	2 of 48 genes, 4.17%	114 of 6985 annotated genes, 1.63%
RNA modification (GO:0009451)	YOL124C , YPL212C	2 of 48 genes, 4.17%	195 of 6985 annotated genes, 2.79%
DNA-templated transcription termination (GO:0006353)	YJR063W , YNL112W	2 of 48 genes, 4.17%	45 of 6985 annotated genes, 0.64%
nucleobase-containing compound transport (GO:0015931)	YHR196W , YLR264W	2 of 48 genes, 4.17%	184 of 6985 annotated genes, 2.63%
amino acid transport (GO:0006865)	YNL065W , YOR271C	2 of 48 genes, 4.17%	59 of 6985 annotated genes, 0.84%
carbohydrate transport (GO:0008643)	YDR536W , YHR094C	2 of 48 genes, 4.17%	52 of 6985 annotated genes, 0.74%
RNA splicing (GO:0008380)	YEL026W , YGR159C	2 of 48 genes, 4.17%	166 of 6985 annotated genes, 2.38%
lipid metabolic process (GO:0006629)	YBL039C , YOL151W	2 of 48 genes, 4.17%	361 of 6985 annotated genes, 5.17%
response to chemical (GO:0042221)	YLR224W , YOR271C	2 of 48 genes, 4.17%	526 of 6985 annotated genes, 7.53%
regulation of DNA metabolic process (GO:0051052)	YNL182C , YOR359W	2 of 48 genes, 4.17%	134 of 6985 annotated genes, 1.92%
transcription by RNA polymerase II (GO:0006366)	YJR063W , YNL112W	2 of 48 genes, 4.17%	566 of 6985 annotated genes, 8.10%
tRNA processing (GO:0008033)	YOL124C , YPL212C	2 of 48 genes, 4.17%	147 of 6985 annotated genes, 2.10%
DNA replication (GO:0006260)	YNL182C	1 of 48 genes, 2.08%	165 of 6985 annotated genes, 2.36%
protein targeting (GO:0006605)	YBR105C	1 of 48 genes, 2.08%	267 of 6985 annotated genes, 3.82%
generation of precursor metabolites and energy (GO:0006091)	YOL136C	1 of 48 genes, 2.08%	227 of 6985 annotated genes, 3.25%
cytoplasmic translation (GO:0002181)	YLR264W	1 of 48 genes, 2.08%	204 of 6985 annotated genes, 2.92%
monocarboxylic acid metabolic process (GO:0032787)	YOL136C	1 of 48 genes, 2.08%	171 of 6985 annotated genes, 2.45%
tRNA aminoacylation for protein translation (GO:0006418)	YDR037W	1 of 48 genes, 2.08%	38 of 6985 annotated genes, 0.54%
DNA recombination (GO:0006310)	YGR159C	1 of 48 genes, 2.08%	268 of 6985 annotated genes, 3.84%
response to osmotic stress (GO:0006970)	YER062C	1 of 48 genes, 2.08%	72 of 6985 annotated genes, 1.03%
regulation of organelle organization (GO:0033043)	YLR180W	1 of 48 genes, 2.08%	269 of 6985 annotated genes, 3.85%
protein modification by small protein conjugation or removal (GO:0070647)	YLR224W	1 of 48 genes, 2.08%	217 of 6985 annotated genes, 3.11%
signaling (GO:0023052)	YOR360C	1 of 48 genes, 2.08%	447 of 6985 annotated genes, 6.40%
intracellular monoatomic ion homeostasis (GO:0006873)	YNR060W	1 of 48 genes, 2.08%	159 of 6985 annotated genes, 2.28%
pseudohyphal growth (GO:0007124)	none	0 of 48 genes, 0%	74 of 6985 annotated genes, 1.06%
conjugation with cellular fusion (GO:0000747)	none	0 of 48 genes, 0%	123 of 6985 annotated genes, 1.76%
cell budding (GO:0007114)	none	0 of 48 genes, 0%	53 of 6985 annotated genes, 0.76%
invasive growth in response to glucose limitation (GO:0001403)	none	0 of 48 genes, 0%	53 of 6985 annotated genes, 0.76%
cell wall organization or biogenesis (GO:0071554)	none	0 of 48 genes, 0%	299 of 6985 annotated genes, 4.28%
protein folding (GO:0006457)	none	0 of 48 genes, 0%	127 of 6985 annotated genes, 1.82%
protein alkylation (GO:0008213)	none	0 of 48 genes, 0%	53 of 6985 annotated genes, 0.76%
organelle inheritance (GO:0048308)	none	0 of 48 genes, 0%	55 of 6985 annotated genes, 0.79%
response to heat (GO:0009408)	none	0 of 48 genes, 0%	51 of 6985 annotated genes, 0.73%
protein acylation (GO:0043543)	none	0 of 48 genes, 0%	80 of 6985 annotated genes, 1.15%
mitochondrion organization (GO:0007005)	none	0 of 48 genes, 0%	302 of 6985 annotated genes, 4.32%
response to oxidative stress (GO:0006979)	none	0 of 48 genes, 0%	127 of 6985 annotated genes, 1.82%
translational initiation (GO:0006413)	none	0 of 48 genes, 0%	83 of 6985 annotated genes, 1.19%
vacuole organization (GO:0007033)	none	0 of 48 genes, 0%	113 of 6985 annotated genes, 1.62%
regulation of cell cycle (GO:0051726)	none	0 of 48 genes, 0%	304 of 6985 annotated genes, 4.35%
transposition (GO:0032196)	none	0 of 48 genes, 0%	110 of 6985 annotated genes, 1.57%
mitotic cell cycle (GO:0000278)	none	0 of 48 genes, 0%	390 of 6985 annotated genes, 5.58%
protein glycosylation (GO:0006486)	none	0 of 48 genes, 0%	86 of 6985 annotated genes, 1.23%
chromosome segregation (GO:0007059)	none	0 of 48 genes, 0%	223 of 6985 annotated genes, 3.19%
lipid transport (GO:0006869)	none	0 of 48 genes, 0%	79 of 6985 annotated genes, 1.13%
membrane fusion (GO:0061025)	none	0 of 48 genes, 0%	68 of 6985 annotated genes, 0.97%
meiotic cell cycle (GO:0051321)	none	0 of 48 genes, 0%	327 of 6985 annotated genes, 4.68%
endosomal transport (GO:0016197)	none	0 of 48 genes, 0%	118 of 6985 annotated genes, 1.69%
cell morphogenesis (GO:0000902)	none	0 of 48 genes, 0%	37 of 6985 annotated genes, 0.53%
ribosomal subunit export from nucleus (GO:0000054)	none	0 of 48 genes, 0%	55 of 6985 annotated genes, 0.79%
protein lipidation (GO:0006497)	none	0 of 48 genes, 0%	53 of 6985 annotated genes, 0.76%
telomere organization (GO:0032200)	none	0 of 48 genes, 0%	141 of 6985 annotated genes, 2.02%
chromatin organization (GO:0006325)	none	0 of 48 genes, 0%	309 of 6985 annotated genes, 4.42%
nucleus organization (GO:0006997)	none	0 of 48 genes, 0%	104 of 6985 annotated genes, 1.49%
organelle fission (GO:0048285)	none	0 of 48 genes, 0%	277 of 6985 annotated genes, 3.97%
regulation of protein modification process (GO:0031399)	none	0 of 48 genes, 0%	143 of 6985 annotated genes, 2.05%
histone modification (GO:0016570)	none	0 of 48 genes, 0%	139 of 6985 annotated genes, 1.99%
membrane invagination (GO:0010324)	none	0 of 48 genes, 0%	1 of 6985 annotated genes, 0.01%
Golgi vesicle transport (GO:0048193)	none	0 of 48 genes, 0%	216 of 6985 annotated genes, 3.09%
peroxisome organization (GO:0007031)	none	0 of 48 genes, 0%	59 of 6985 annotated genes, 0.84%
vitamin metabolic process (GO:0006766)	none	0 of 48 genes, 0%	64 of 6985 annotated genes, 0.92%
cytokinesis (GO:0000910)	none	0 of 48 genes, 0%	105 of 6985 annotated genes, 1.50%
protein phosphorylation (GO:0006468)	none	0 of 48 genes, 0%	221 of 6985 annotated genes, 3.16%
oligosaccharide metabolic process (GO:0009311)	none	0 of 48 genes, 0%	54 of 6985 annotated genes, 0.77%
cytoskeleton organization (GO:0007010)	none	0 of 48 genes, 0%	284 of 6985 annotated genes, 4.07%
translational elongation (GO:0006414)	none	0 of 48 genes, 0%	350 of 6985 annotated genes, 5.01%
regulation of transport (GO:0051049)	none	0 of 48 genes, 0%	104 of 6985 annotated genes, 1.49%
vesicle organization (GO:0016050)	none	0 of 48 genes, 0%	114 of 6985 annotated genes, 1.63%
organelle fusion (GO:0048284)	none	0 of 48 genes, 0%	124 of 6985 annotated genes, 1.78%
mitochondrial translation (GO:0032543)	none	0 of 48 genes, 0%	175 of 6985 annotated genes, 2.51%
protein dephosphorylation (GO:0006470)	none	0 of 48 genes, 0%	56 of 6985 annotated genes, 0.80%
endocytosis (GO:0006897)	none	0 of 48 genes, 0%	136 of 6985 annotated genes, 1.95%
cellular respiration (GO:0045333)	none	0 of 48 genes, 0%	122 of 6985 annotated genes, 1.75%
sno(s)RNA processing (GO:0043144)	none	0 of 48 genes, 0%	47 of 6985 annotated genes, 0.67%
cellular response to DNA damage stimulus (GO:0006974)	none	0 of 48 genes, 0%	373 of 6985 annotated genes, 5.34%
peptidyl-amino acid modification (GO:0018193)	none	0 of 48 genes, 0%	201 of 6985 annotated genes, 2.88%
DNA repair (GO:0006281)	none	0 of 48 genes, 0%	323 of 6985 annotated genes, 4.62%
sporulation (GO:0043934)	none	0 of 48 genes, 0%	171 of 6985 annotated genes, 2.45%
response to starvation (GO:0042594)	none	0 of 48 genes, 0%	78 of 6985 annotated genes, 1.12%
protein maturation (GO:0051604)	none	0 of 48 genes, 0%	101 of 6985 annotated genes, 1.45%
transcription by RNA polymerase III (GO:0006383)	none	0 of 48 genes, 0%	48 of 6985 annotated genes, 0.69%
exocytosis (GO:0006887)	none	0 of 48 genes, 0%	50 of 6985 annotated genes, 0.72%