

These 8 identifier(s) represent valid gene names that either could not be mapped to terms in the current GO slim set or are currently annotated to the root node for the slim set being used: YOR360C YBL028C YLR264C-A YML018C YLR327C YGR079W YJL107C YJL108C

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 49 genes, 26.53%	366 of 6443 annotated genes, 5.68%
ribosomal large subunit biogenesis (GO:0042273)	YCR072C , YDL063C , YEL026W , YHR066W , YIR012W , YJL122W , YNL182C , YOL041C , YOL080C	9 of 49 genes, 18.37%	130 of 6443 annotated genes, 2.02%
ribosomal small subunit biogenesis (GO:0042274)	YDR449C , YEL026W , YER127W , YGR159C , YHR196W , YJL069C , YLR264W , YMR093W	8 of 49 genes, 16.33%	146 of 6443 annotated genes, 2.27%
ribosome assembly (GO:0042255)	YCR072C , YGR159C , YHR066W , YIR012W , YLR264W , YNL182C , YOL080C	7 of 49 genes, 14.29%	79 of 6443 annotated genes, 1.23%
transcription by RNA polymerase I (GO:0006360)	YHR196W , YJL148W , YJR063W , YML043C , YMR093W , YNL248C	6 of 49 genes, 12.24%	71 of 6443 annotated genes, 1.10%
ion transport (GO:0006811)	YDR536W , YHR094C , YKL120W , YNL065W , YNR060W , YOR271C	6 of 49 genes, 12.24%	340 of 6443 annotated genes, 5.28%
transmembrane transport (GO:0055085)	YDR536W , YHR094C , YKL120W , YNL065W , YOR271C	5 of 49 genes, 10.20%	468 of 6443 annotated genes, 7.26%
nucleobase-containing small molecule metabolic process (GO:0055086)	YBL039C , YMR300C , YNL141W , YOL136C	4 of 49 genes, 8.16%	220 of 6443 annotated genes, 3.41%
carbohydrate metabolic process (GO:0005975)	YBR105C , YER062C , YKR097W , YOL136C	4 of 49 genes, 8.16%	253 of 6443 annotated genes, 3.93%
RNA catabolic process (GO:0006401)	YLR264W , YNL112W , YOR359W	3 of 49 genes, 6.12%	166 of 6443 annotated genes, 2.58%

cellular amino acid metabolic process (GO:0006520)	YBL039C , YLR180W , YMR300C	3 of 49 genes, 6.12%	218 of 6443 annotated genes, 3.38%
regulation of translation (GO:0006417)	YLR264W , YNL112W , YOR359W	3 of 49 genes, 6.12%	234 of 6443 annotated genes, 3.63%
nucleobase-containing compound transport (GO:0015931)	YHR196W , YLR264W	2 of 49 genes, 4.08%	183 of 6443 annotated genes, 2.84%
proteolysis involved in cellular protein catabolic process (GO:0051603)	YBR105C , YLR224W	2 of 49 genes, 4.08%	265 of 6443 annotated genes, 4.11%
RNA modification (GO:0009451)	YOL124C , YPL212C	2 of 49 genes, 4.08%	186 of 6443 annotated genes, 2.89%
DNA-templated transcription, termination (GO:0006353)	YJR063W , YNL112W	2 of 49 genes, 4.08%	42 of 6443 annotated genes, 0.65%
tRNA processing (GO:0008033)	YOL124C , YPL212C	2 of 49 genes, 4.08%	134 of 6443 annotated genes, 2.08%
response to chemical (GO:0042221)	YLR224W , YNL065W	2 of 49 genes, 4.08%	530 of 6443 annotated genes, 8.23%
transcription by RNA polymerase II (GO:0006366)	YJR063W , YNL112W	2 of 49 genes, 4.08%	556 of 6443 annotated genes, 8.63%
DNA-templated transcription, elongation (GO:0006354)	YJL148W , YNL248C	2 of 49 genes, 4.08%	109 of 6443 annotated genes, 1.69%
lipid metabolic process (GO:0006629)	YBL039C , YOL151W	2 of 49 genes, 4.08%	348 of 6443 annotated genes, 5.40%
amino acid transport (GO:0006865)	YNL065W , YOR271C	2 of 49 genes, 4.08%	56 of 6443 annotated genes, 0.87%
regulation of DNA metabolic process (GO:0051052)	YNL182C , YOR359W	2 of 49 genes, 4.08%	97 of 6443 annotated genes, 1.51%
DNA-templated transcription, initiation (GO:0006352)	YML043C , YNL248C	2 of 49 genes, 4.08%	83 of 6443 annotated genes, 1.29%
carbohydrate transport (GO:0008643)	YDR536W , YHR094C	2 of 49 genes, 4.08%	46 of 6443 annotated genes, 0.71%
organelle assembly (GO:0070925)	YLR180W	1 of 49 genes, 2.04%	125 of 6443 annotated genes, 1.94%
cellular ion homeostasis (GO:0006873)	YNR060W	1 of 49 genes, 2.04%	162 of 6443 annotated genes, 2.51%
protein modification by small protein conjugation or removal (GO:0070647)	YLR224W	1 of 49 genes, 2.04%	223 of 6443 annotated genes, 3.46%
mRNA processing (GO:0006397)	YEL026W	1 of 49 genes, 2.04%	220 of 6443 annotated genes, 3.41%
regulation of organelle organization (GO:0033043)	YLR180W	1 of 49 genes, 2.04%	279 of 6443 annotated genes, 4.33%
RNA splicing (GO:0008380)	YEL026W	1 of 49 genes, 2.04%	153 of 6443 annotated genes, 2.37%
generation of precursor metabolites and energy (GO:0006091)	YOL136C	1 of 49 genes, 2.04%	113 of 6443 annotated genes, 1.75%
response to osmotic stress (GO:0006970)	YER062C	1 of 49 genes, 2.04%	73 of 6443 annotated genes, 1.13%
monocarboxylic acid metabolic process (GO:0032787)	YOL136C	1 of 49 genes, 2.04%	164 of 6443 annotated genes, 2.55%
cytoplasmic translation (GO:0002181)	YLR264W	1 of 49 genes, 2.04%	205 of 6443 annotated genes, 3.18%
tRNA aminoacylation for protein translation (GO:0006418)	YDR037W	1 of 49 genes, 2.04%	37 of 6443 annotated genes, 0.57%
protein targeting (GO:0006605)	YBR105C	1 of 49 genes, 2.04%	256 of 6443 annotated genes, 3.97%
DNA replication (GO:0006260)	YNL182C	1 of 49 genes, 2.04%	151 of 6443 annotated genes, 2.34%
DNA recombination (GO:0006310)	YGR159C	1 of 49 genes, 2.04%	255 of 6443 annotated genes, 3.96%