0.00
5.00
10.00
id
58929 - White Muscle
47141 - Skeletal Muscle
36339 - Skeletal Muscle
84288 - White Muscle
id
cytoplasmic translation (GO:0002181)
translation (GO:0006412)
positive regulation of response to stimulus (GO:0048584)
cell junction maintenance (GO:0034331)
adherens junction maintenance (GO:0034334)
rRNA methylation (GO:0031167)
regulation of translation (GO:0006417)
formation of translation preinitiation complex (GO:0001731)
positive regulation of cellular amide metabolic process (GO:0034250)
glucosamine-containing compound catabolic process (GO:1901072)
embryonic epithelial tube formation (GO:0001838)
nuclear import (GO:0051170)
positive regulation of cellular protein metabolic process (GO:0032270)
negative regulation of multicellular organismal process (GO:0051241)
ribosome assembly (GO:0042255)
ribosomal large subunit biogenesis (GO:0042273)
positive regulation of cell cycle (GO:0045787)
regulation of cyclin-dependent protein kinase activity (GO:1904029)
ribosomal small subunit assembly (GO:0000028)
regulation of cyclin-dependent protein serine/threonine kinase activity (GO:0000079)
hemoglobin metabolic process (GO:0020027)
regulation of protein serine/threonine kinase activity (GO:0071900)
ribosomal small subunit biogenesis (GO:0042274)
regulation of nuclear division (GO:0051783)
cellular macromolecule biosynthetic process (GO:0034645)
regulation of cell cycle process (GO:0010564)
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043154)
ribosomal large subunit assembly (GO:0000027)
ribonucleoprotein complex assembly (GO:0022618)
embryo development ending in birth or egg hatching (GO:0009792)
peptide biosynthetic process (GO:0043043)
maturation of LSU-rRNA (GO:0000470)
apoptotic process (GO:0006915)
intrinsic apoptotic signaling pathway in response to DNA damage (GO:0008630)
regulation of mitotic nuclear division (GO:0007088)
cellular response to organic substance (GO:0071310)
hemoglobin biosynthetic process (GO:0042541)
erythrocyte maturation (GO:0043249)
inhibition of cysteine-type endopeptidase activity involved in apoptotic process (GO:1990001)
chordate embryonic development (GO:0043009)
negative regulation of cell development (GO:0010721)
cellular response to oxidative stress (GO:0034599)
positive regulation of cellular process (GO:0048522)
regulation of cell proliferation (GO:0042127)
mRNA catabolic process (GO:0006402)
iron ion homeostasis (GO:0055072)
positive regulation of transcription from RNA polymerase II promoter in response to stress (GO:0036003)
inhibition of cysteine-type endopeptidase activity (GO:0097340)
stress-activated MAPK cascade (GO:0051403)
positive regulation of G1/S transition of mitotic cell cycle (GO:1900087)
regulation of mitochondrial membrane permeability (GO:0046902)
hydrogen peroxide catabolic process (GO:0042744)
intrinsic apoptotic signaling pathway (GO:0097193)
hydrogen peroxide metabolic process (GO:0042743)
T cell activation (GO:0042110)
fin regeneration (GO:0031101)
nucleocytoplasmic transport (GO:0006913)
positive regulation of cell cycle G1/S phase transition (GO:1902808)
B cell receptor signaling pathway (GO:0050853)
erythrocyte development (GO:0048821)
modification-dependent macromolecule catabolic process (GO:0043632)
purine ribonucleoside biosynthetic process (GO:0046129)
gene expression (GO:0010467)
regulation of programmed cell death (GO:0043067)
mitochondrial membrane organization (GO:0007006)
response to metal ion (GO:0010038)
cellular protein metabolic process (GO:0044267)
ribosome biogenesis (GO:0042254)
defense response to bacterium (GO:0042742)
response to yeast (GO:0001878)
hematopoietic stem cell migration (GO:0035701)
regulation of TORC1 signaling (GO:1903432)
cellular response to UV (GO:0034644)
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000463)
purine nucleobase salvage (GO:0043096)
regulation of cell cycle (GO:0051726)
cellular respiration (GO:0045333)
erythrocyte differentiation (GO:0030218)
myeloid cell differentiation (GO:0030099)
regulation of muscle contraction (GO:0006937)
nuclear transport (GO:0051169)
regulation of blood vessel endothelial cell migration (GO:0043535)
negative regulation of translational initiation (GO:0045947)
regulation of muscle system process (GO:0090257)
retinol metabolic process (GO:0042572)
ganglion development (GO:0061548)
endodermal cell differentiation (GO:0035987)
adenosine metabolic process (GO:0046085)
ventricular cardiac muscle cell development (GO:0055015)
regulation of cell migration involved in sprouting angiogenesis (GO:0090049)
protein stabilization (GO:0050821)
neuron apoptotic process (GO:0051402)
primary alcohol metabolic process (GO:0034308)
regulation of intrinsic apoptotic signaling pathway (GO:2001242)
regulation of response to DNA damage stimulus (GO:2001020)
tRNA splicing, via endonucleolytic cleavage and ligation (GO:0006388)
phosphatidylcholine metabolic process (GO:0046470)
positive regulation of response to external stimulus (GO:0032103)
positive regulation of macroautophagy (GO:0016239)
regulation of transmembrane transport (GO:0034762)
regulation of ion transmembrane transport (GO:0034765)
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000462)
regulation of insulin secretion (GO:0050796)
regulation of ion transport (GO:0043269)
semaphorin-plexin signaling pathway involved in axon guidance (GO:1902287)
semaphorin-plexin signaling pathway involved in neuron projection guidance (GO:1902285)
maturation of SSU-rRNA (GO:0030490)
negative regulation of cell adhesion (GO:0007162)
positive regulation of cell morphogenesis involved in differentiation (GO:0010770)
stem cell differentiation (GO:0048863)
cellular response to amino acid stimulus (GO:0071230)
hematopoietic stem cell differentiation (GO:0060218)