

regulation of translation, GO:0006417

- protein autophosphorylation, GO:0046777
- regulation of mRNA stability, GO:0043488
- cell cycle arrest, GO:0007050
- P-body, GO:0000932
- double-stranded RNA binding, GO:0003725
- gene silencing by miRNA, GO:0035195
- translation initiation factor activity, GO:0003743
- response to endoplasmic reticulum stress, GO:0034976
- gene silencing by RNA, GO:0031047
- interleukin-7-mediated signaling pathway, GO:0038111
- negative regulation of translation, GO:0017148
- insulin receptor signaling pathway, GO:0008286
- cellular response to insulin stimulus, GO:0032869
- aging, GO:0007568
- positive regulation of cell growth, GO:0030307
- cellular response to amino acid starvation, GO:0034198
- phosphatidylinositol-mediated signaling, GO:0048015
- negative regulation of protein kinase activity, GO:0006469
- regulation of translational initiation, GO:0006446
- nuclear-transcribed mRNA poly(A) tail shortening, GO:0000289
- Wnt signaling pathway, GO:0007223
- cytoplasmic stress granule, GO:0010494
- translation initiation factor binding, GO:0031369
- translation factor activity, GO:0008135
- glycogen metabolic process, GO:0005977
- 3'-5'-exoribonuclease activity, GO:0000175
- positive regulation of NIK/NF-kappaB signaling, GO:1901224
- glucose metabolic process, GO:0006006
- developmental growth, GO:0048589
- RNA phosphodiester bond hydrolysis, GO:0090503
- cellular response to amino acid stimulus, GO:0071230
- Hsp90 protein binding, GO:0051879
- positive regulation of axon extension, GO:0045773
- miRNA metabolic process, GO:0010586
- transcription export complex, GO:0000346
- vesicle membrane, GO:0012506
- cell growth, GO:0016049
- mRNA cap binding complex, GO:0005845
- positive regulation of translational initiation, GO:0045948
- receptor tyrosine kinase binding, GO:0030971
- eukaryotic translation initiation factor 4F complex, GO:0016281
- SMN complex, GO:0032797
- protein kinase inhibitor activity, GO:0004860
- carbohydrate transport, GO:0008643
- CCR4-NOT complex, GO:0030014
- miRNA mediated inhibition of translation, GO:0035278
- calmodulin-dependent protein kinase activity, GO:0004683
- perikaryon, GO:0043204
- RNA cap binding, GO:0000339
- positive regulation of G1/S transition of mitotic cell cycle, GO:1900087
- extrinsic apoptotic signaling pathway in absence of ligand, GO:0097192
- response to heat, GO:0009408
- mRNA stabilization, GO:0048255
- negative regulation of insulin receptor signaling pathway, GO:0046627
- DNA-(apurinic or apyrimidinic site) lyase activity, GO:0003906
- DNA dealkylation involved in DNA repair, GO:0006307
- posttranscriptional regulation of gene expression, GO:0010608
- miRNA binding, GO:0035198
- cellular response to hydroperoxide, GO:0071447
- regulation of focal adhesion assembly, GO:0051893
- mRNA catabolic process, GO:0006402
- deadenylation-dependent decapping of nuclear-transcribed mRNA, GO:0000290
- glucose import, GO:0046323
- smooth endoplasmic reticulum, GO:0005790
- ionotropic glutamate receptor signaling pathway, GO:0035235
- negative regulation of autophagy, GO:0010507
- positive regulation of glucose import, GO:0046326
- GTPase inhibitor activity, GO:0005095
- striated muscle cell differentiation, GO:0051146
- protein kinase regulator activity, GO:0019887
- nucleotide biosynthetic process, GO:0009165
- negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:1902166
- piRNA metabolic process, GO:0034587
- positive regulation of monocyte differentiation, GO:0045657
- eukaryotic 48S preinitiation complex, GO:0033290
- TORC1 complex, GO:0031931
- SREBP signaling pathway, GO:0032933
- 14-3-3 protein binding, GO:0071889
- negative regulation of cell size, GO:0045792
- protoporphyrinogen IX biosynthetic process, GO:0006782
- positive regulation of lipid biosynthetic process, GO:0046889
- chondrocyte development, GO:0002063
- negative regulation of transposition, GO:0010529
- poly(A)+ mRNA export from nucleus, GO:0016973
- negative regulation of protein autophosphorylation, GO:0031953
- relaxation of cardiac muscle, GO:0055119
- metalloexopeptidase activity, GO:0008235
- cellular response to granulocyte macrophage colony-stimulating factor stimulus, GO:0097011
- positive regulation of type I interferon-mediated signaling pathway, GO:0060340
- axonal growth cone, GO:0044295
- protein kinase B signaling, GO:0043491
- chromatoid body, GO:0033391
- iron ion transport, GO:0006826
- negative regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation, GO:1903912
- nitric oxide biosynthetic process, GO:0006809
- long-term memory, GO:0007616
- negative regulation of peptidyl-serine phosphorylation, GO:0033137
- regulation of tyrosine phosphorylation of STAT protein, GO:0042509
- p38MAPK cascade, GO:0038066
- TORC1 signaling, GO:0038202
- establishment of protein localization to mitochondrion, GO:0072655
- skeletal muscle atrophy, GO:0014732