```
regulation of mRNA stability, GO:0043488
protein autophosphorylation, GO:0046777
P-body, GO:0000932
response to endoplasmic reticulum stress, GO:0034976
translation initiation factor activity, GO:0003743
double-stranded RNA binding, GO:0003725
cellular response to insulin stimulus, GO:0032869
gene silencing by miRNA, GO:0035195
negative regulation of translation, GO:0017148
ribosome binding, GO:0043022
gene silencing by RNA, GO:0031047
phosphatidylinositol-mediated signaling, GO:0048015
regulation of translational initiation, GO:0006446
cellular response to hypoxia, GO:0071456
cytoplasmic stress granule, GO:0010494
positive regulation of cell growth, GO:0030307
insulin receptor signaling pathway, GO:0008286
RNA phosphodiester bond hydrolysis, GO:0090503
protein phosphatase binding, GO:0019903
glucose metabolic process, GO:0006006
cellular response to glucose starvation, GO:0042149
cellular response to growth factor stimulus, GO:0071363
nuclear-transcribed mRNA poly(A) tail shortening, GO:0000289
vesicle membrane, GO:0012506
cellular response to amino acid starvation, GO:0034198
3'-5'-exoribonuclease activity, GO:0000175
post-embryonic development, GO:0009791
cellular response to amino acid stimulus, GO:0071230
translation factor activity, GO:0008135
translation initiation factor binding, GO:0031369
lamellipodium assembly, GO:0030032
CCR4-NOT complex, GO:0030014
miRNA metabolic process, GO:0010586
posttranscriptional regulation of gene expression, GO:0010608
regulation of cell migration, GO:0030334
positive regulation of NIK/NF-kappaB signaling, GO:1901224
negative regulation of autophagy, GO:0010507
protein kinase B signaling, GO:0043491
protein phosphatase 2A binding, GO:0051721
Wnt signaling pathway, GO:0007223
calmodulin-dependent protein kinase activity, GO:0004683
receptor tyrosine kinase binding, GO:0030971
response to ischemia, GO:0002931
14-3-3 protein binding, GO:0071889
skeletal system development, GO:0001501
positive regulation of axon extension, GO:0045773
cellular response to epidermal growth factor stimulus, GO:0071364
response to glucocorticoid, GO:0051384
poly(A)-specific ribonuclease activity, GO:0004535
negative regulation of endopeptidase activity, GO:0010951
transcription export complex, GO:0000346
mRNA catabolic process, GO:0006402
stress granule assembly, GO:0034063
perikaryon, GO:0043204
negative regulation of proteolysis, GO:0045861
miRNA mediated inhibition of translation, GO:0035278
regulation of focal adhesion assembly, GO:0051893
extrinsic apoptotic signaling pathway in absence of ligand, GO:0097192
smooth endoplasmic reticulum, GO:0005790
RNA cap binding, GO:0000339
pre-miRNA processing, GO:0031054
piRNA metabolic process, GO:0034587
positive regulation of T cell proliferation, GO:0042102
TOR signaling, GO:0031929
nuclear\mbox{-transcribed mRNA catabolic process, } GO:0000288
negative regulation of transposition, GO:0010529
regulation of stem cell population maintenance, GO:2000036
```

## regulation of translation, GO:0006417

```
positive regulation of dendritic spine development, GO:0060999
developmental growth, GO:0048589
neuronal stem cell population maintenance, GO:0097150
positive regulation of G1/S transition of mitotic cell cycle, GO:1900087
myelination, GO:0042552
mRNA stabilization, GO:0048255
response to glucagon, GO:0033762
regulation of synaptic plasticity, GO:0048167
positive regulation of microtubule polymerization, GO:0031116
eukaryotic translation initiation factor 4F complex, GO:0016281
negative regulation of erythrocyte differentiation, GO:0045647
TORC1 complex, GO:0031931
ligase activity, GO:0016876
RISC complex, GO:0016442
DNA dealkylation involved in DNA repair, GO:0006307
regulation of NMDA receptor activity, GO:2000310
ER overload response, GO:0006983
response to heat, GO:0009408
negative regulation of insulin receptor signaling pathway, GO:0046627
ossification, GO:0001503
cytoskeletal adaptor activity, GO:0008093
positive regulation of glucose import, GO:0046326
negative regulation of intracellular estrogen receptor signaling pathway, GO:0033147
CCR4-NOT core complex, GO:0030015
chondrocyte development, GO:0002063
PERK-mediated unfolded protein response, GO:0036499
positive regulation of nuclear-transcribed mRNA poly(A) tail shortening, GO:0060213
positive regulation of glucose metabolic process, GO:0010907
production of miRNAs involved in gene silencing by miRNA, GO:0035196
pi-body, GO:0071546
eukaryotic 48S preinitiation complex, GO:0033290
deadenylation-dependent decapping of nuclear-transcribed mRNA, GO:0000290
positive regulation of type I interferon-mediated signaling pathway, GO:0060340
protein kinase regulator activity, GO:0019887
MAP kinase kinase activity, GO:0004708
positive regulation of lipid biosynthetic process, GO:0046889
negative regulation of translational initiation in response to stress, GO:0032057
positive regulation of endothelial cell apoptotic process, GO:2000353
positive regulation of cytoplasmic mRNA processing body assembly, GO:0010606
negative regulation of phagocytosis, GO:0050765
positive regulation of sodium ion transport, GO:0010765
tissue homeostasis, GO:0001894
RISC-loading complex, GO:0070578
miRNA loading onto RISC involved in gene silencing by miRNA, GO:0035280
posttranscriptional gene silencing by RNA, GO:0035194
cell morphogenesis involved in neuron differentiation, GO:0048667
positive regulation of neuron differentiation, GO:0045666
RNA 7-methylguanosine cap binding, GO:0000340
neural crest cell development, GO:0014032
long-term memory, GO:0007616
positive regulation of glycogen biosynthetic process, GO:0045725
negative regulation of protein autophosphorylation, GO:0031953
intestinal absorption, GO:0050892
positive regulation of nuclear-transcribed mRNA catabolic process, GO:1900153
positive regulation of ceramide biosynthetic process, GO:2000304
pre-mRNA cleavage required for polyadenylation, GO:0098789
ionotropic glutamate receptor signaling pathway, GO:0035235
```

negative regulation of PERK-mediated unfolded protein response, GO:1903898

cellular response to leucine starvation, GO:1990253

micro-ribonucleoprotein complex, GO:0035068

DNA demethylation, GO:0080111

negative regulation of endoplasmic reticulum stress-induced eIF2 alpha phosphorylation, GO:1903912