

**regulation of mRNA stability, GO:0043488**

- regulation of hematopoietic stem cell differentiation, GO:1902036
- proteasome complex, GO:0000502
- regulation of transcription from RNA polymerase II promoter in response to hypoxia, GO:0061418
- P-body, GO:0000932
- negative regulation of canonical Wnt signaling pathway, GO:0090090
- antigen processing and presentation of exogenous peptide antigen via MHC class I, GO:0002479
- regulation of cellular amino acid metabolic process, GO:0006521
- endopeptidase activity, GO:0004175
- protein export from nucleus, GO:0006611
- RNA phosphodiester bond hydrolysis, GO:0090503
- proteolysis involved in cellular protein catabolic process, GO:0051603
- nuclear localization sequence binding, GO:0008139
- proteasome accessory complex, GO:0022624
- proteasome regulatory particle, GO:0005838
- exosome (RNase complex), GO:0000178
- proteasome core complex, GO:0005839
- 3'-5'-exoribonuclease activity, GO:0000175
- cellular response to transforming growth factor beta stimulus, GO:0071560
- threonine-type endopeptidase activity, GO:0004298
- proteasome regulatory particle, GO:0008540
- positive regulation of mRNA catabolic process, GO:0061014
- protein import into nucleus, GO:0000060
- regulation of G1/S transition of mitotic cell cycle, GO:2000045
- 14-3-3 protein binding, GO:0071889
- mRNA catabolic process, GO:0006402
- poly(A)-specific ribonuclease activity, GO:0004535
- nuclear exosome (RNase complex), GO:0000176
- positive regulation of blood vessel endothelial cell migration, GO:0043536
- 3'-UTR-mediated mRNA destabilization, GO:0061158
- somatic stem cell division, GO:0048103
- regulation of protein catabolic process, GO:0042176
- embryonic morphogenesis, GO:0048598
- proteasome core complex, GO:0019774
- positive regulation of proteasomal protein catabolic process, GO:1901800
- AU-rich element binding, GO:0017091
- positive regulation of tumor necrosis factor biosynthetic process, GO:0042535
- blastocyst development, GO:0001824
- negative regulation of smooth muscle cell migration, GO:0014912
- nuclear mRNA surveillance, GO:0071028
- positive regulation of glucose import in response to insulin stimulus, GO:2001275
- cellular response to vascular endothelial growth factor stimulus, GO:0035924
- nitric oxide biosynthetic process, GO:0006809
- regulation of stem cell population maintenance, GO:2000036
- positive regulation of cellular protein metabolic process, GO:0032270
- mRNA 3'-UTR AU-rich region binding, GO:0035925
- posttranscriptional regulation of gene expression, GO:0010608
- deadenylation-dependent decapping of nuclear-transcribed mRNA, GO:0000290
- proteasome core complex, GO:0019773
- regulation of neuron projection development, GO:0010975
- cytoplasmic exosome (RNase complex), GO:0000177
- nuclear-transcribed mRNA catabolic process, GO:0034427
- calcium-dependent protein serine/threonine kinase activity, GO:0009931
- uracil DNA N-glycosylase activity, GO:0004844
- negative regulation of insulin secretion, GO:0046676
- regulation of myotube differentiation, GO:0010830
- DNA demethylation, GO:0080111