

regulation of mRNA stability, GO:0043488

- regulation of hematopoietic stem cell differentiation, GO:1902036
- P-body, GO:0000932
- proteasome complex, GO:0000502
- antigen processing and presentation of exogenous peptide antigen via MHC class I, GO:0002479
- regulation of cellular amino acid metabolic process, GO:0006521
- RNA phosphodiester bond hydrolysis, GO:0090503
- endopeptidase activity, GO:0004175
- 3'-5'-exoribonuclease activity, GO:0000175
- proteasome accessory complex, GO:0022624
- proteasome regulatory particle, GO:0005838
- cellular response to tumor necrosis factor, GO:0071356
- exosome (RNase complex), GO:0000178
- protein export from nucleus, GO:0006611
- proteolysis involved in cellular protein catabolic process, GO:0051603
- T cell differentiation in thymus, GO:0033077
- nuclear exosome (RNase complex), GO:0000176
- proteasome core complex, GO:0005839
- positive regulation of mRNA catabolic process, GO:0061014
- NF-kappaB binding, GO:0051059
- regulation of protein catabolic process, GO:0042176
- AU-rich element binding, GO:0017091
- threonine-type endopeptidase activity, GO:0004298
- cytoplasmic exosome (RNase complex), GO:0000177
- nuclear localization sequence binding, GO:0008139
- intermediate filament cytoskeleton, GO:0045111
- type I interferon signaling pathway, GO:0060337
- mRNA catabolic process, GO:0006402
- response to wounding, GO:0009611
- proteasome assembly, GO:0043248
- proteasome regulatory particle, GO:0008540
- 3'-UTR-mediated mRNA destabilization, GO:0061158
- protein import into nucleus, GO:0000060
- nuclear-transcribed mRNA catabolic process, GO:0034427
- U4 snRNA 3'-end processing, GO:0034475
- P granule, GO:0043186
- deadenylation-dependent decapping of nuclear-transcribed mRNA, GO:0000290
- cytosolic proteasome complex, GO:0031597
- cellular response to peptide, GO:1901653
- nuclear polyadenylation-dependent rRNA catabolic process, GO:0071035
- MDM2/MDM4 family protein binding, GO:0097371
- negative regulation of proteasomal protein catabolic process, GO:1901799
- positive regulation of peptidase activity, GO:0010952
- regulation of G1/S transition of mitotic cell cycle, GO:2000045
- nuclear mRNA surveillance, GO:0071028
- negative regulation of smooth muscle cell migration, GO:0014912
- negative regulation of activated T cell proliferation, GO:0046007
- immunoglobulin mediated immune response, GO:0016064
- mRNA 3'-UTR AU-rich region binding, GO:0035925
- labyrinthine layer blood vessel development, GO:0060716
- negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway, GO:1902236
- neuronal stem cell population maintenance, GO:0097150
- cellular response to glucocorticoid stimulus, GO:0071385
- bHLH transcription factor binding, GO:0043425
- positive regulation of cAMP metabolic process, GO:0030816
- negative regulation of glial cell apoptotic process, GO:0034351
- 7S RNA binding, GO:0008312
- nuclear polyadenylation-dependent mRNA catabolic process, GO:0071042
- exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000467
- nuclear polyadenylation-dependent tRNA catabolic process, GO:0071038
- regulation of cytokine biosynthetic process, GO:0042035
- proteasome core complex, GO:0019774
- enzyme regulator activity, GO:0030234
- posttranscriptional regulation of gene expression, GO:0010608
- proteasome core complex, GO:0019773
- negative regulation of insulin secretion, GO:0046676
- nuclear pore central transport channel, GO:0044613
- positive regulation of monocyte differentiation, GO:0045657
- regulation of myoblast differentiation, GO:0045661
- meiosis I, GO:0007127