

translational initiation, GO:0006413

- structural constituent of ribosome, GO:0003735
- nuclear-transcribed mRNA catabolic process, GO:0000184
- viral transcription, GO:0019083
- SRP-dependent cotranslational protein targeting to membrane, GO:0006614
- mRNA binding, GO:0003729
- regulation of translation, GO:0006417
- cytosolic large ribosomal subunit, GO:0022625
- cytosolic small ribosomal subunit, GO:0022627
- translation initiation factor activity, GO:0003743
- rRNA binding, GO:0019843
- small ribosomal subunit, GO:0015935
- cytoplasmic translation, GO:0002181
- ribosomal large subunit biogenesis, GO:0042273
- maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000462
- negative regulation of translation, GO:0017148
- RNA secondary structure unwinding, GO:0010501
- ribosome binding, GO:0043022
- polysome, GO:0005844
- cytoplasmic stress granule, GO:0010494
- ribosomal large subunit assembly, GO:0000027
- regulation of translational initiation, GO:0006446
- gene silencing by RNA, GO:0031047
- positive regulation of translation, GO:0045727
- mRNA 3'-UTR binding, GO:0003730
- cytoplasmic ribonucleoprotein granule, GO:0036464
- nucleotide-excision repair, GO:0000715
- stress-activated MAPK cascade, GO:0051403
- nuclear-transcribed mRNA poly(A) tail shortening, GO:0000289
- endoplasmic reticulum quality control compartment, GO:0044322
- ribosomal small subunit biogenesis, GO:0042274
- translation initiation factor binding, GO:0031369
- error-free translesion synthesis, GO:0070987
- response to peptide hormone, GO:0043434
- mRNA 5'-UTR binding, GO:0048027
- nucleotide-excision repair, GO:0000717
- viral life cycle, GO:0019058
- regulation of tumor necrosis factor-mediated signaling pathway, GO:0010803
- translation factor activity, GO:0008135
- error-prone translesion synthesis, GO:0042276
- maturation of SSU-rRNA, GO:0030490
- translational elongation, GO:0006414
- 90S preribosome, GO:0030686
- formation of translation preinitiation complex, GO:0001731
- eukaryotic translation initiation factor 3 complex, GO:0005852
- endoplasmic reticulum mannose trimming, GO:1904380
- nucleotide-binding oligomerization domain containing signaling pathway, GO:0070423
- maturation of LSU-rRNA, GO:0000470
- endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000447
- response to glucose, GO:0009749
- ribosomal small subunit binding, GO:0043024
- negative regulation of epidermal growth factor receptor signaling pathway, GO:0042059
- 5S rRNA binding, GO:0008097
- ERBB2 signaling pathway, GO:0038128
- ribosomal small subunit assembly, GO:0000028
- positive regulation of nuclear-transcribed mRNA poly(A) tail shortening, GO:0060213
- TRIF-dependent toll-like receptor signaling pathway, GO:0035666
- positive regulation of epidermal growth factor receptor signaling pathway, GO:0045742
- myelination, GO:0042552
- glycogen biosynthetic process, GO:0005978
- large ribosomal subunit, GO:0015934
- innate immune response in mucosa, GO:0002227
- liver regeneration, GO:0097421
- positive regulation of nuclear-transcribed mRNA catabolic process, GO:1900153
- MyD88-dependent toll-like receptor signaling pathway, GO:0002755
- endocytic vesicle membrane, GO:0030666
- negative regulation of autophagy, GO:0010507
- mRNA cap binding complex, GO:0005845
- protein deneddylation, GO:0000338
- TOR signaling, GO:0031929
- virion assembly, GO:0019068
- translational termination, GO:0006415
- RNA cap binding, GO:0000339
- poly(A) binding, GO:0008143
- poly(U) RNA binding, GO:0008266
- miRNA mediated inhibition of translation, GO:0035278
- regulation of transcription from RNA polymerase III promoter, GO:0006359
- ovarian follicle development, GO:0001541
- eukaryotic 43S preinitiation complex, GO:0016282
- eukaryotic 48S preinitiation complex, GO:0033290
- regulation of necroptotic process, GO:0060544
- entry of bacterium into host cell, GO:0035635
- RISC complex, GO:0016442
- mRNA stabilization, GO:0048255
- small ribosomal subunit rRNA binding, GO:0070181
- maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000463
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- ubiquitin ligase inhibitor activity, GO:1990948
- micro-ribonucleoprotein complex, GO:0035068
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- ribosomal protein import into nucleus, GO:0006610
- DNA-(apurinic or apyrimidinic site) lyase activity, GO:0003906
- fibroblast growth factor binding, GO:0017134
- positive regulation of microtubule polymerization, GO:0031116
- production of miRNAs involved in gene silencing by miRNA, GO:0035196
- eukaryotic translation initiation factor 4F complex, GO:0016281
- positive regulation of interleukin-2 production, GO:0032743
- polysomal ribosome, GO:0042788
- hydrolase activity, GO:0016818
- transcription initiation from RNA polymerase III promoter, GO:0006384
- ubiquitin-like protein conjugating enzyme binding, GO:0044390
- response to heat, GO:0009408
- negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:2000059
- siRNA binding, GO:0035197
- cytosolic ribosome, GO:0022626
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- postranscriptional gene silencing by RNA, GO:0035194
- cellular metabolic process, GO:0044237
- positive regulation of cellular protein metabolic process, GO:0032270
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- dosage compensation by inactivation of X chromosome, GO:0009048
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- positive regulation of transcription from RNA polymerase III promoter, GO:0045945
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- pre-miRNA processing, GO:0031054
- PERK-mediated unfolded protein response, GO:0036499
- oligodendrocyte development, GO:0014003
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- eukaryotic translation initiation factor 3 complex, GO:0071541
- negative regulation of translational initiation in response to stress, GO:0032057
- ribosomal small subunit export from nucleus, GO:0000056
- antibacterial humoral response, GO:0019731
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- negative regulation of peptidyl-threonine phosphorylation, GO:0010801
- sexual reproduction, GO:0019953
- positive regulation of NIK/NF-kappaB signaling, GO:1901224
- negative regulation of translational initiation, GO:0045947
- retinal ganglion cell axon guidance, GO:0031290
- positive regulation of G1/S transition of mitotic cell cycle, GO:1900087
- astrocyte development, GO:0014002
- negative regulation of ubiquitin protein ligase activity, GO:1904667