

translational initiation, GO:0006413

- structural constituent of ribosome, GO:0003735
- viral transcription, GO:0019083
- nuclear-transcribed mRNA catabolic process, GO:0000184
- SRP-dependent cotranslational protein targeting to membrane, GO:0006614
- mRNA binding, GO:0003729
- regulation of translation, GO:0006417
- cytosolic large ribosomal subunit, GO:0022625
- translation initiation factor activity, GO:0003743
- ATP-dependent RNA helicase activity, GO:0004004
- cytoplasmic translation, GO:0002181
- cytosolic small ribosomal subunit, GO:0022627
- RNA secondary structure unwinding, GO:0010501
- ribosome binding, GO:0043022
- rRNA binding, GO:0019843
- positive regulation of translation, GO:0045727
- DNA damage response, GO:0042769
- ribosomal large subunit biogenesis, GO:0042273
- polysome, GO:0005844
- regulation of translational initiation, GO:0006446
- negative regulation of translation, GO:0017148
- mRNA 3'-UTR binding, GO:0003730
- nuclear-transcribed mRNA poly(A) tail shortening, GO:0000289
- maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000462
- small ribosomal subunit, GO:0015935
- cytoplasmic stress granule, GO:0010494
- nucleotide-excision repair, GO:0006297
- nucleotide-excision repair, GO:0000715
- response to glucose, GO:0009749
- translational elongation, GO:0006414
- liver regeneration, GO:0097421
- ribosomal small subunit biogenesis, GO:0042274
- maturation of LSU-rRNA, GO:0000470
- viral life cycle, GO:0019058
- ribosomal large subunit assembly, GO:0000027
- erythrocyte differentiation, GO:0030218
- error-prone translesion synthesis, GO:0042276
- glycogen biosynthetic process, GO:0005978
- mRNA 5'-UTR binding, GO:0048027
- formation of translation preinitiation complex, GO:0001731
- negative regulation of epidermal growth factor receptor signaling pathway, GO:0042059
- large ribosomal subunit, GO:0015934
- endoplasmic reticulum mannose trimming, GO:1904380
- nucleotide-excision repair, GO:0000717
- regulation of tumor necrosis factor-mediated signaling pathway, GO:0010803
- positive regulation of NIK/NF-kappaB signaling, GO:1901224
- cellular response to UV, GO:0034644
- 90S preribosome, GO:0030686
- ribosomal small subunit assembly, GO:0000028
- error-free translesion synthesis, GO:0070987
- negative regulation of neuron differentiation, GO:0045665
- negative regulation of type I interferon production, GO:0032480
- antimicrobial humoral immune response mediated by antimicrobial peptide, GO:0061844
- translation factor activity, GO:0008135
- ovarian follicle development, GO:0001541
- Wnt signaling pathway, GO:0007223
- nucleotide-binding oligomerization domain containing signaling pathway, GO:0070423
- eukaryotic translation initiation factor 3 complex, GO:0005852
- TRIF-dependent toll-like receptor signaling pathway, GO:0035666
- positive regulation of viral genome replication, GO:0045070
- maturation of SSU-rRNA, GO:0030490
- poly(U) RNA binding, GO:0008266
- oligodendrocyte development, GO:0014003
- miRNA mediated inhibition of translation, GO:0035278
- translation initiation factor binding, GO:0031369
- stress-activated MAPK cascade, GO:0051403
- cellular metabolic process, GO:0044237
- cytoplasmic ribonucleoprotein granule, GO:0036464
- 5S rRNA binding, GO:0008097
- endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000447
- NEDD8-specific protease activity, GO:0019784
- myelination, GO:0042552
- eukaryotic translation initiation factor 4F complex, GO:0016281
- negative regulation of translational initiation, GO:0045947
- MyD88-dependent toll-like receptor signaling pathway, GO:0002755
- TOR signaling, GO:0031929
- response to heat, GO:0009408
- pre-miRNA processing, GO:0031054
- hippocampus development, GO:0021766
- protein deneddylation, GO:0000338
- behavioral fear response, GO:0001662
- ribosomal small subunit binding, GO:0043024
- IRES-dependent viral translational initiation, GO:0075522
- production of miRNAs involved in gene silencing by miRNA, GO:0035196
- ribosomal large subunit binding, GO:0043023
- mRNA cap binding complex, GO:0005845
- RISC complex, GO:0016442
- RNA 7-methylguanosine cap binding, GO:0000340
- micro-ribonucleoprotein complex, GO:0035068
- ribosomal protein import into nucleus, GO:0006610
- eukaryotic 43S preinitiation complex, GO:0016282
- eukaryotic 48S preinitiation complex, GO:0033290
- TORC2 complex, GO:0031932
- small ribosomal subunit rRNA binding, GO:0070181
- positive regulation of microtubule polymerization, GO:0031116
- positive regulation of interleukin-2 production, GO:0032743
- siRNA binding, GO:0035197
- PERK-mediated unfolded protein response, GO:0036499
- regulation of necroptotic process, GO:0060544
- production of siRNA involved in RNA interference, GO:0030422
- positive regulation of translational initiation, GO:0045948
- positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage, GO:1902231
- positive regulation of T cell receptor signaling pathway, GO:0050862
- translational termination, GO:0006415
- positive regulation of nuclear-transcribed mRNA poly(A) tail shortening, GO:0060213
- miRNA binding, GO:0035198
- eukaryotic translation initiation factor 3 complex, GO:0071541
- posttranscriptional gene silencing by RNA, GO:0035194
- regulation of translational fidelity, GO:0006450