

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
- regulation of translation, GO:0006417
- cytosolic large ribosomal subunit, GO:0022625
- translation initiation factor activity, GO:0003743
- rRNA binding, GO:0019843
- cytosolic small ribosomal subunit, GO:0022627
- ribosome binding, GO:0043022
- ribosomal large subunit biogenesis, GO:0042273
- DNA damage response, GO:0042769
- cytoplasmic stress granule, GO:0010494
- positive regulation of translation, GO:0045727
- polysome, GO:0005844
- regulation of translational initiation, GO:0006446
- maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000462
- negative regulation of translation, GO:0017148
- small ribosomal subunit, GO:0015935
- nucleotide-excision repair, GO:0000715
- error-prone translesion synthesis, GO:0042276
- cytoplasmic translation, GO:0002181
- nucleotide-excision repair, GO:0006297
- endoplasmic reticulum quality control compartment, GO:0044322
- ribosomal large subunit assembly, GO:0000027
- error-free translesion synthesis, GO:0070987
- ribosomal small subunit biogenesis, GO:0042274
- myelination, GO:0042552
- translation factor activity, GO:0008135
- response to glucose, GO:0009749
- nuclear-transcribed mRNA poly(A) tail shortening, GO:0000289
- MyD88-dependent toll-like receptor signaling pathway, GO:0002755
- eukaryotic translation initiation factor 3 complex, GO:0005852
- glycogen biosynthetic process, GO:0005978
- endoplasmic reticulum mannose trimming, GO:1904380
- formation of translation preinitiation complex, GO:0001731
- stress-activated MAPK cascade, GO:0051403
- Notch signaling pathway, GO:0007219
- negative regulation of epidermal growth factor receptor signaling pathway, GO:0042059
- large ribosomal subunit, GO:0015934
- nucleotide-binding oligomerization domain containing signaling pathway, GO:0070423
- translation initiation factor binding, GO:0031369
- mitotic cell cycle checkpoint, GO:0007093
- mRNA 5'-UTR binding, GO:0048027
- liver regeneration, GO:0097421
- ERBB2 signaling pathway, GO:0038128
- virion assembly, GO:0019068
- response to peptide hormone, GO:0043434
- IRES-dependent viral translational initiation, GO:0075522
- TOR signaling, GO:0031929
- response to heat, GO:0009408
- regulation of necroptotic process, GO:0060544
- ribosomal small subunit binding, GO:0043024
- positive regulation of NIK/NF-kappaB signaling, GO:1901224
- 90S preribosome, GO:0030686
- mRNA cap binding complex, GO:0005845
- positive regulation of translational initiation, GO:0045948
- regulation of type I interferon production, GO:0032479
- eukaryotic 43S preinitiation complex, GO:0016282
- eukaryotic 48S preinitiation complex, GO:0033290
- entry of bacterium into host cell, GO:0035635
- positive regulation of transcription from RNA polymerase III promoter, GO:0045945
- miRNA binding, GO:0035198
- negative regulation of autophagy, GO:0010507
- endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000447
- ribosomal small subunit assembly, GO:0000028
- positive regulation of epidermal growth factor receptor signaling pathway, GO:0045742
- negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:2000059
- translational termination, GO:0006415
- maturation of LSU-rRNA, GO:0000470
- positive regulation of T cell receptor signaling pathway, GO:0050862
- ribosomal large subunit binding, GO:0043023
- ribosome disassembly, GO:0032790
- production of siRNA involved in RNA interference, GO:0030422
- RNA 7-methylguanosine cap binding, GO:0000340
- miRNA mediated inhibition of translation, GO:0035278
- exit from mitosis, GO:0010458
- pre-miRNA processing, GO:0031054
- small ribosomal subunit rRNA binding, GO:0070181
- ribosomal protein import into nucleus, GO:0006610
- maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000463
- mRNA stabilization, GO:0048255
- eukaryotic translation initiation factor 3 complex, GO:0071541
- oligodendrocyte development, GO:0014003
- RISC complex, GO:0016442
- siRNA binding, GO:0035197
- RNA cap binding, GO:0000339
- TORC2 complex, GO:0031932
- MyD88-independent toll-like receptor signaling pathway, GO:0002756
- negative regulation of translational initiation, GO:0045947
- NEDD8-specific protease activity, GO:0019784
- regulation of translational fidelity, GO:0006450
- regulation of JNK cascade, GO:0046328
- TORC1 complex, GO:0031931
- supercoiled DNA binding, GO:0097100
- viral translational termination-reinitiation, GO:0075525
- ribosome assembly, GO:0042255
- cellular metabolic process, GO:0044237
- behavioral fear response, GO:0001662
- retinal ganglion cell axon guidance, GO:0031290
- positive regulation of cellular component movement, GO:0051272
- production of miRNAs involved in gene silencing by miRNA, GO:0035196
- posttranscriptional gene silencing by RNA, GO:0035194
- middle ear morphogenesis, GO:0042474
- PERK-mediated unfolded protein response, GO:0036499
- cellular response to interleukin-4, GO:0071353
- astrocyte development, GO:0014002
- transcription coactivator binding, GO:0001223
- erythrocyte homeostasis, GO:0034101
- acute inflammatory response, GO:0002526
- ribosomal small subunit export from nucleus, GO:0000056
- dosage compensation by inactivation of X chromosome, GO:0009048
- micro-ribonucleoprotein complex, GO:0035068
- polysomal ribosome, GO:0042788
- eukaryotic translation initiation factor 4F complex, GO:0016281
- ovarian follicle development, GO:0001541
- negative regulation of peptidyl-threonine phosphorylation, GO:0010801
- positive regulation of energy homeostasis, GO:2000507
- positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage, GO:1902231
- TORC1 signaling, GO:0038202
- transcription initiation from RNA polymerase III promoter, GO:0006384
- eukaryotic translation initiation factor 2B complex, GO:0005851
- cellular response to dexamethasone stimulus, GO:0071549
- 5S rRNA binding, GO:0008097