

structural constituent of ribosome, GO:0003735

- translational initiation, GO:0006413
- nuclear-transcribed mRNA catabolic process, GO:0000184
- viral transcription, GO:0019083
- SRP-dependent cotranslational protein targeting to membrane, GO:0006614
- mitochondrial translational termination, GO:0070126
- mRNA binding, GO:0003729
- mitochondrial translational elongation, GO:0070125
- cytosolic large ribosomal subunit, GO:0022625
- cytosolic small ribosomal subunit, GO:0022627
- mitochondrial large ribosomal subunit, GO:0005762
- rRNA binding, GO:0019843
- cytoplasmic translation, GO:0002181
- ribosomal large subunit biogenesis, GO:0042273
- small ribosomal subunit, GO:0015935
- DNA damage response, GO:0042769
- maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000462
- polysome, GO:0005844
- mitochondrial translation, GO:0032543
- positive regulation of translation, GO:0045727
- mitochondrial small ribosomal subunit, GO:0005763
- mitochondrial ribosome, GO:0005761
- mRNA 3'-UTR binding, GO:0003730
- mRNA 5'-UTR binding, GO:0048027
- ribosomal large subunit assembly, GO:0000027
- large ribosomal subunit, GO:0015934
- error-prone translesion synthesis, GO:0042276
- ribosomal small subunit assembly, GO:0000028
- nucleotide-excision repair, GO:0006297
- liver regeneration, GO:0097421
- nucleotide-binding oligomerization domain containing signaling pathway, GO:0070423
- ribosomal small subunit biogenesis, GO:0042274
- error-free translesion synthesis, GO:0070987
- endoplasmic reticulum mannose trimming, GO:1904380
- negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:2000059
- nucleotide-excision repair, GO:0000717
- cytoplasmic ribonucleoprotein granule, GO:0036464
- 90S preribosome, GO:0030686
- glycogen biosynthetic process, GO:0005978
- maturation of SSU-rRNA, GO:0030490
- negative regulation of epidermal growth factor receptor signaling pathway, GO:0042059
- stress-activated MAPK cascade, GO:0051403
- TRIF-dependent toll-like receptor signaling pathway, GO:0035666
- translational elongation, GO:0006414
- erythrocyte differentiation, GO:0030218
- 5S rRNA binding, GO:0008097
- maturation of LSU-rRNA, GO:0000470
- small ribosomal subunit rRNA binding, GO:0070181
- positive regulation of epidermal growth factor receptor signaling pathway, GO:0045742
- endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000447
- regulation of necroptotic process, GO:0060544
- transcription from mitochondrial promoter, GO:0006390
- negative regulation of ubiquitin protein ligase activity, GO:1904667
- ribosomal protein import into nucleus, GO:0006610
- polysomal ribosome, GO:0042788
- positive regulation of cellular component movement, GO:0051272
- entry of bacterium into host cell, GO:0035635
- mitochondrial genome maintenance, GO:0000002
- ubiquitin ligase inhibitor activity, GO:1990948
- regulation of type I interferon production, GO:0032479
- DNA-(apurinic or apyrimidinic site) lyase activity, GO:0003906
- cotranslational protein targeting to membrane, GO:0006613
- fibroblast growth factor binding, GO:0017134
- blastocyst formation, GO:0001825
- positive regulation of signal transduction by p53 class mediator, GO:1901798
- maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000463
- erythrocyte homeostasis, GO:0034101
- virion assembly, GO:0019068
- MyD88-independent toll-like receptor signaling pathway, GO:0002756
- negative regulation of cell cycle arrest, GO:0071157