structural constituent of ribosome, GO:0003735

translational initiation, GO:0006413 nuclear-transcribed mRNA catabolic process, GO:0000184 mitochondrial translational termination, GO:0070126 mitochondrial translational elongation, GO:0070125 SRP-dependent cotranslational protein targeting to membrane, GO:0006614 mitochondrial large ribosomal subunit, GO:0005762 cytosolic large ribosomal subunit, GO:0022625 polysome, GO:0005844 mitochondrial translation, GO:0032543 cytosolic small ribosomal subunit, GO:0022627 rRNA binding, GO:0019843 mitochondrial ribosome, GO:0005761 maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000462 ribosomal large subunit biogenesis, GO:0042273 small ribosomal subunit, GO:0015935 mRNA 5'-UTR binding, GO:0048027 endoplasmic reticulum quality control compartment, GO:0044322 cytoplasmic translation, GO:0002181 mitochondrial small ribosomal subunit, GO:0005763 MyD88-dependent toll-like receptor signaling pathway, GO:0002755 ribosomal large subunit assembly, GO:0000027 TRIF-dependent toll-like receptor signaling pathway, GO:0035666 Notch signaling pathway, GO:0007219 nucleotide-excision repair, GO:0000715 nucleotide-excision repair, GO:0000717 endoplasmic reticulum mannose trimming, GO:1904380 translational elongation, GO:0006414 maturation of LSU-rRNA, GO:0000470 large ribosomal subunit, GO:0015934 liver regeneration, GO:0097421 ribosomal small subunit biogenesis, GO:0042274 regulation of type I interferon production, GO:0032479 glycogen biosynthetic process, GO:0005978 90S preribosome, GO:0030686 ribosomal small subunit assembly, GO:0000028 virion assembly, GO:0019068 regulation of necroptotic process, GO:0060544 ribosomal protein import into nucleus, GO:0006610 fibroblast growth factor binding, GO:0017134 ERBB2 signaling pathway, GO:0038128 cotranslational protein targeting to membrane, GO:0006613 entry of bacterium into host cell, GO:0035635 negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:2000059 blastocyst formation, GO:0001825 TOR signaling, GO:0031929 5S rRNA binding, GO:0008097 MyD88-independent toll-like receptor signaling pathway, GO:0002756 maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, GO:0000463 translation regulator activity, GO:0045182 erythrocyte homeostasis, GO:0034101 ATP synthesis coupled electron transport, GO:0042773 ribosomal small subunit export from nucleus, GO:0000056 small ribosomal subunit rRNA binding, GO:0070181 positive regulation of epidermal growth factor receptor signaling pathway, GO:0045742 antibacterial humoral response, GO:0019731 innate immune response in mucosa, GO:0002227

middle ear morphogenesis, GO:0042474