fibrillar center, GO:0001650 small-subunit processome, GO:0032040 ATPase binding, GO:0051117 negative regulation of protein ubiquitination, GO:0031397 snoRNA binding, GO:0030515 preribosome, GO:0030687 pseudouridine synthesis, GO:0001522 positive regulation of interferon-beta production, GO:0032728 preribosome, GO:0030688 endoribonuclease activity, GO:0004521 positive regulation of telomerase RNA localization to Cajal body, GO:1904874 nuclear export, GO:0051168 histone demethylase activity (H3-K36 specific), GO:0051864 histone H3-K36 demethylation, GO:0070544 TFIID-class transcription factor binding, GO:0001094 ribonucleoprotein granule, GO:0035770 RNA polymerase binding, GO:0070063 positive regulation of transcription from RNA polymerase I promoter, GO:0045943 ribosomal large subunit export from nucleus, GO:0000055 negative regulation of protein complex assembly, GO:0031333 blastocyst formation, GO:0001825 rRNA catabolic process, GO:0016075 positive regulation of establishment of protein localization to telomere, GO:1904851 stem cell division, GO:0017145 pre-snoRNP complex, GO:0070761 cellular response to zinc ion, GO:0071294 histone H3-K4 demethylation, GO:0034720 nuclear export signal receptor activity, GO:0005049 stress granule assembly, GO:0034063

ribosome biogenesis, GO:0042254

cellular response to zinc ion, GO:0071294
histone H3-K4 demethylation, GO:0034720
nuclear export signal receptor activity, GO:0005049
stress granule assembly, GO:0034063
regulation of cellular respiration, GO:0043457
RNA polymerase I CORE element sequence-specific DNA binding, GO:0001164
trophectodermal cell differentiation, GO:0001829
positive regulation of rRNA processing, GO:2000234
endonucleolytic cleavage in 5′-ETS of tricistronic rRNA transcript (SSU-rRNA, GO:0000480
histone demethylase activity (H3-K4 specific), GO:0032453
regulation of transcription from RNA polymerase I promoter, GO:0006356
regulation of aerobic respiration, GO:1903715
box H/ACA snoRNA binding, GO:0034513
rRNA pseudouridine synthesis, GO:0031118
box H/ACA snoRNP complex, GO:0031429
negative regulation of defense response to virus, GO:0050687
DEAD/H-box RNA helicase binding, GO:0017151
protein localization to cytoplasmic stress granule, GO:1903608

negative regulation of amyloid precursor protein biosynthetic process, GO:0042985

negative regulation of phosphatidylinositol 3-kinase signaling, GO:0014067

negative regulation of RIG-I signaling pathway, GO:0039536

positive regulation of dendritic cell chemotaxis, GO:2000510

negative regulation of interleukin-12 production, GO:0032695

negative regulation of protein sumoylation, GO:0033234

negative regulation of cell-cell adhesion, GO:0022408

regulation of axon extension, GO:0030516

T cell mediated immunity, GO:0002456

bone marrow development, GO:0048539

hyaluronic acid binding, GO:0005540

GTP metabolic process, GO:0046039