

spliceosomal complex, GO:0005681

- helicase activity, GO:0004386
- mRNA export from nucleus, GO:0006406
- mRNA transport, GO:0051028
- catalytic step 2 spliceosome, GO:0071013
- termination of RNA polymerase II transcription, GO:0006369
- RNA processing, GO:0006396
- mRNA 3'-end processing, GO:0031124
- nuclear matrix, GO:0016363
- RNA metabolic process, GO:0016070
- RNA export from nucleus, GO:0006405
- ATP-dependent RNA helicase activity, GO:0004004
- Cajal body, GO:0015030
- osteoblast differentiation, GO:0001649
- ribonucleoprotein complex binding, GO:0043021
- spliceosomal complex assembly, GO:0000245
- exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay, GO:0043928
- protein methylation, GO:0006479
- fibroblast growth factor receptor signaling pathway, GO:0008543
- single-stranded RNA binding, GO:0003727
- RNA splicing, GO:0000375
- positive regulation of viral genome replication, GO:0045070
- viral nucleocapsid, GO:0019013
- spliceosomal snRNP assembly, GO:0000387
- interleukin-12-mediated signaling pathway, GO:0035722
- exon-exon junction complex, GO:0035145
- U4/U6 x U5 tri-snRNP complex, GO:0046540
- U12-type spliceosomal complex, GO:0005689
- negative regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032435
- regulation of alternative mRNA splicing, GO:0000381
- peptidyl-prolyl cis-trans isomerase activity, GO:0003755
- protein peptidyl-prolyl isomerization, GO:0000413
- negative regulation of mRNA splicing, GO:0048025
- RNA catabolic process, GO:0006401
- telomerase holoenzyme complex, GO:0005697
- mRNA splice site selection, GO:0006376
- nuclear-transcribed mRNA catabolic process, GO:0000956
- precatalytic spliceosome, GO:0071011
- telomerase RNA binding, GO:0070034
- regulation of RNA splicing, GO:0043484
- regulation of mitophagy, GO:1903146
- U2-type prespliceosome, GO:0071004
- U2 snRNP, GO:0005686
- nuclear hormone receptor binding, GO:0035257
- RNA helicase activity, GO:0003724
- regulation of DNA-templated transcription, GO:0032784
- negative regulation of telomere maintenance via telomerase, GO:0032211
- U5 snRNP, GO:0005682
- U1 snRNP, GO:0005685
- small nuclear ribonucleoprotein complex, GO:0030532
- SMN-Sm protein complex, GO:0034719
- nuclear import, GO:0051170
- cyclosporin A binding, GO:0016018
- DNA replication factor A complex, GO:0005662
- pre-mRNA binding, GO:0036002
- Prp19 complex, GO:0000974
- positive regulation of DNA-templated transcription, GO:0032786
- RNA polymerase II core binding, GO:0000993
- alternative mRNA splicing, GO:0000380
- Gemini of coiled bodies, GO:0097504
- methylosome, GO:0034709
- positive regulation of DNA damage response, GO:0043517
- DNA-templated transcription, GO:0006353
- positive regulation of mRNA splicing, GO:0048026
- U6 snRNA binding, GO:0017070
- CRD-mediated mRNA stability complex, GO:0070937
- leucine zipper domain binding, GO:0043522
- U4 snRNP, GO:0005687
- RNA stem-loop binding, GO:0035613
- mitochondrial fragmentation involved in apoptotic process, GO:0043653
- mRNA destabilization, GO:0061157
- U6 snRNP, GO:0005688
- spliceosomal tri-snRNP complex assembly, GO:0000244
- U4 snRNA binding, GO:0030621
- negative regulation of protein dephosphorylation, GO:0035308
- ribonucleoprotein granule, GO:0035770
- ATPase activity, GO:0042623
- response to vitamin E, GO:0033197
- Leydig cell differentiation, GO:0033327
- histone monoubiquitination, GO:0010390
- small nucleolar ribonucleoprotein complex, GO:0005732
- positive regulation by host of viral genome replication, GO:0044829
- enhancer binding, GO:0035326
- cytoplasmic mRNA processing body assembly, GO:0033962
- cellular response to retinoic acid, GO:0071300
- primary miRNA processing, GO:0031053
- retinoic acid receptor binding, GO:0042974
- viral mRNA export from host cell nucleus, GO:0046784
- histone mRNA metabolic process, GO:0008334
- cellular response to sodium arsenite, GO:1903936
- IgE binding, GO:0019863
- CRD-mediated mRNA stabilization, GO:0070934
- regulation of steroid biosynthetic process, GO:0050810
- regulation of ATPase activity, GO:0043462
- pre-mRNA intronic binding, GO:0097157
- regulation of protein complex assembly, GO:0043254
- C2H2 zinc finger domain binding, GO:0070742
- positive regulation of RNA splicing, GO:0033120
- protein phosphatase 1 binding, GO:0008157
- proteasomal protein catabolic process, GO:0010498
- nuclear export, GO:0051168
- U3 snoRNA binding, GO:0034511
- paraspeckles, GO:0042382
- histone pre-mRNA 3'end processing complex, GO:0071204
- poly(G) binding, GO:0034046
- box C/D snoRNP complex, GO:0031428
- regulation of mRNA splicing, GO:0048024
- snRNA binding, GO:0017069
- N6-methyladenosine-containing RNA binding, GO:1990247
- U2-type spliceosomal complex, GO:0005684
- negative regulation of toll-like receptor signaling pathway, GO:0034122
- protein kinase B binding, GO:0043422
- cellular response to brain-derived neurotrophic factor stimulus, GO:1990416
- primary miRNA binding, GO:0070878
- mRNA 5'-splice site recognition, GO:0000395
- hair cycle, GO:0042633
- U1 snRNA binding, GO:0030619
- commitment complex, GO:0000243
- U2AF, GO:0089701