

spliceosomal complex, GO:0005681

- mRNA export from nucleus, GO:0006406
- catalytic step 2 spliceosome, GO:0071013
- RNA processing, GO:0006396
- mRNA binding, GO:0003729
- termination of RNA polymerase II transcription, GO:0006369
- ATP-dependent RNA helicase activity, GO:0004004
- mRNA 3'-end processing, GO:0031124
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- Cajal body, GO:0015030
- RNA metabolic process, GO:0016070
- RNA secondary structure unwinding, GO:0010501
- osteoblast differentiation, GO:0001649
- exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay, GO:0043928
- androgen receptor binding, GO:0050681
- RNA splicing, GO:0000375
- spliceosomal complex assembly, GO:0000245
- spliceosomal snRNP assembly, GO:0000387
- protein methylation, GO:0006479
- U12-type spliceosomal complex, GO:0005689
- fibroblast growth factor receptor signaling pathway, GO:0008543
- single-stranded RNA binding, GO:0003727
- mRNA 3'-UTR binding, GO:0003730
- peptidyl-prolyl cis-trans isomerase activity, GO:0003755
- protein peptidyl-prolyl isomerization, GO:0000413
- U4/U6 x U5 tri-snRNP complex, GO:0046540
- precatalytic spliceosome, GO:0071011
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- exon-exon junction complex, GO:0035145
- negative regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032435
- nuclear hormone receptor binding, GO:0035257
- positive regulation of viral genome replication, GO:0045070
- regulation of alternative mRNA splicing, GO:0000381
- regulation of mitophagy, GO:1903146
- regulation of RNA splicing, GO:0043484
- negative regulation of mRNA splicing, GO:0048025
- nuclear import, GO:0051170
- telomerase holoenzyme complex, GO:0005697
- telomerase RNA binding, GO:0070034
- cytoplasmic mRNA processing body assembly, GO:0033962
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- maturation of SSU-rRNA, GO:0030490
- negative regulation of telomere maintenance via telomerase, GO:0032211
- RNA helicase activity, GO:0003724
- U5 snRNP, GO:0005682
- negative regulation of catalytic activity, GO:0043086
- RNA catabolic process, GO:0006401
- ribonucleoprotein complex binding, GO:0043021
- nuclear-transcribed mRNA catabolic process, GO:0000956
- viral nucleocapsid, GO:0019013
- pre-mRNA binding, GO:0036002
- small nuclear ribonucleoprotein complex, GO:0030532
- alternative mRNA splicing, GO:0000380
- U2-type prespliceosome, GO:0071004
- poly(U) RNA binding, GO:0008266
- positive regulation of RNA splicing, GO:0033120
- methylosome, GO:0034709
- cyclosporin A binding, GO:0016018
- mRNA splice site selection, GO:0006376
- spliceosomal tri-snRNP complex assembly, GO:0000244
- calcium-dependent protein binding, GO:0048306
- cellular response to drug, GO:0035690
- mRNA destabilization, GO:0061157
- histone mRNA metabolic process, GO:0008334
- U1 snRNP, GO:0005685
- positive regulation of mRNA splicing, GO:0048026
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- histone monoubiquitination, GO:0010390
- viral mRNA export from host cell nucleus, GO:0046784
- U6 snRNP, GO:0005688
- Ral GTPase binding, GO:0017160
- cellular response to tumor necrosis factor, GO:0071356
- U4 snRNP, GO:0005687
- nuclear export, GO:0051168
- Prp19 complex, GO:0000974
- ribonucleoprotein granule, GO:0035770
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- U6 snRNA binding, GO:0017070
- U4 snRNA binding, GO:0030621
- negative regulation of interferon-beta production, GO:0032688
- positive regulation of nuclear-transcribed mRNA poly(A) tail shortening, GO:0060213
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- cyclin/CDK positive transcription elongation factor complex, GO:0008024
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- Leydig cell differentiation, GO:0033327
- lipid biosynthetic process, GO:0008610
- transcription corepressor binding, GO:0001222
- protection from non-homologous end joining at telomere, GO:0031848
- positive regulation by host of viral genome replication, GO:0044829
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