

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
nuclear matrix, GO:0016363
mRNA 3'-end processing, GO:0031124
RNA export from nucleus, GO:0006405
RNA metabolic process, GO:0016070
ATP-dependent RNA helicase activity, GO:0004004
Cajal body, GO:0015030
fibroblast growth factor receptor signaling pathway, GO:0008543
androgen receptor binding, GO:0050681
regulation of alternative mRNA splicing, GO:0000381
RNA secondary structure unwinding, GO:0010501
regulation of RNA splicing, GO:0043484
RNA splicing, GO:0000375
negative regulation of mRNA splicing, GO:0048025
osteoblast differentiation, GO:0001649
spliceosomal complex assembly, GO:0000245
ribonucleoprotein complex binding, GO:0043021
exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay, GO:0043928
precatalytic spliceosome, GO:0071011
exon-exon junction complex, GO:0035145
RNA catabolic process, GO:0006401
U12-type spliceosomal complex, GO:0005689
U4/U6 x U5 tri-snRNP complex, GO:0046540
negative regulation of telomere maintenance via telomerase, GO:0032211
single-stranded RNA binding, GO:0003727
protein methylation, GO:0006479
viral nucleocapsid, GO:0019013
negative regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032435
nuclear hormone receptor binding, GO:0035257
spliceosomal snRNP assembly, GO:0000387
regulation of mitophagy, GO:1903146
alternative mRNA splicing, GO:0000380
peptidyl-prolyl cis-trans isomerase activity, GO:0003755
protein peptidyl-prolyl isomerization, GO:0000413
U2 snRNP, GO:0005686
nuclear-transcribed mRNA catabolic process, GO:0000956
small nuclear ribonucleoprotein complex, GO:0030532
U5 snRNP, GO:0005682
U2-type prespliceosome, GO:0071004
histone mRNA metabolic process, GO:0008334
telomerase RNA binding, GO:0070034
negative regulation of catalytic activity, GO:0043086
Prp19 complex, GO:0000974
positive regulation of mRNA splicing, GO:0048026
DNA replication factor A complex, GO:0005662
spliceosomal tri-snRNP complex assembly, GO:0000244
U1 snRNP, GO:0005685
positive regulation of viral genome replication, GO:0045070
RNA polymerase II core binding, GO:0000993
nuclear import, GO:0051170
pre-mRNA binding, GO:0036002
RNA helicase activity, GO:0003724
telomerase holoenzyme complex, GO:0005697
calcium-dependent protein binding, GO:0048306
negative regulation of nucleic acid-templated transcription, GO:1903507
nuclear export, GO:0051168
poly(U) RNA binding, GO:0008266
mRNA splice site selection, GO:0006376
U4 snRNP, GO:0005687
SMN-Sm protein complex, GO:0034719
histone monoubiquitination, GO:0010390
mRNA destabilization, GO:0061157
DNA-templated transcription, GO:0006353
positive regulation of RNA splicing, GO:0033120
U7 snRNP, GO:0005683
inner cell mass cell proliferation, GO:0001833
U6 snRNA binding, GO:0017070
mRNA cis splicing, GO:0045292
C2H2 zinc finger domain binding, GO:0070742
positive regulation of intracellular estrogen receptor signaling pathway, GO:0033148
pre-mRNA intronic binding, GO:0097157
G-rich strand telomeric DNA binding, GO:0098505
methylosome, GO:0034709
mRNA 3'-splice site recognition, GO:0000389
U4 snRNA binding, GO:0030621
mRNA 5'-splice site recognition, GO:0000395
leucine zipper domain binding, GO:0043522
Leydig cell differentiation, GO:0033327
viral mRNA export from host cell nucleus, GO:0046784
positive regulation of DNA-templated transcription, GO:0032786
regulation of DNA-templated transcription, GO:0032784
negative regulation of protein dephosphorylation, GO:0035308
commitment complex, GO:0000243
ATP-dependent protein binding, GO:0043008
cyclin/CDK positive transcription elongation factor complex, GO:0008024
small nucleolar ribonucleoprotein complex, GO:0005732
cellular response to brain-derived neurotrophic factor stimulus, GO:1990416
transcription factor activity, GO:0001135
positive regulation of mRNA catabolic process, GO:0061014
cytoplasmic mRNA processing body assembly, GO:0033962
P granule, GO:0043186
ubiquitin-ubiquitin ligase activity, GO:0034450
poly(A) binding, GO:0008143
cellular response to retinoic acid, GO:0071300
cellular response to interferon-beta, GO:0035458
protein kinase B binding, GO:0043422
Gemini of coiled bodies, GO:0097504
U2-type spliceosomal complex, GO:0005684
positive regulation of DNA damage response, GO:0043517
intracellular estrogen receptor signaling pathway, GO:0030520
negative regulation of protein refolding, GO:0061084
Lsm1-7-Pat1 complex, GO:1990726
RS domain binding, GO:0050733
U6 snRNP, GO:0005688
positive regulation of DNA biosynthetic process, GO:2000573
protein refolding, GO:0042026
chaperone mediated protein folding requiring cofactor, GO:0051085
histone pre-mRNA 3'end processing complex, GO:0071204
CRD-mediated mRNA stability complex, GO:0070937
regulation of protein complex stability, GO:0061635
3'-UTR-mediated mRNA stabilization, GO:0070935
protein phosphatase 1 binding, GO:0008157
miRNA binding, GO:0035198
eosinophil chemotaxis, GO:0048245
negative regulation of fibroblast apoptotic process, GO:2000270
primary miRNA processing, GO:0031053
cerebral cortex regionalization, GO:0021796
positive regulation by host of viral genome replication, GO:0044829
hair cycle, GO:0042633
IgE binding, GO:0019863
post-mRNA release spliceosomal complex, GO:0071014
RNA-dependent ATPase activity, GO:0008186
primary miRNA binding, GO:0070878