

spliceosomal complex, GO:0005681

helicase activity, GO:0004386
catalytic step 2 spliceosome, GO:0071013
mRNA export from nucleus, GO:0006406
mRNA binding, GO:0003729
RNA processing, GO:0006396
mRNA transport, GO:0051028
termination of RNA polymerase II transcription, GO:0006369
nuclear matrix, GO:0016363
mRNA 3'-end processing, GO:0031124
RNA metabolic process, GO:0016070
ATP-dependent RNA helicase activity, GO:0004004
Cajal body, GO:0015030
RNA export from nucleus, GO:0006405
RNA splicing, GO:0000375
osteoblast differentiation, GO:0001649
spliceosomal complex assembly, GO:0000245
U12-type spliceosomal complex, GO:0005689
RNA secondary structure unwinding, GO:0010501
protein methylation, GO:0006479
exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay, GO:0043928
spliceosomal snRNP assembly, GO:0000387
fibroblast growth factor receptor signaling pathway, GO:0008543
ribonucleoprotein complex binding, GO:0043021
viral nucleocapsid, GO:0019013
U4/U6 x U5 tri-snRNP complex, GO:0046540
positive regulation of viral genome replication, GO:0045070
exon-exon junction complex, GO:0035145
regulation of mitophagy, GO:1903146
androgen receptor binding, GO:0050681
regulation of alternative mRNA splicing, GO:0000381
regulation of RNA splicing, GO:0043484
maturation of SSU-rRNA, GO:0030490
telomerase holoenzyme complex, GO:0005697
mRNA 3'-UTR binding, GO:0003730
precatalytic spliceosome, GO:0071011
small nuclear ribonucleoprotein complex, GO:0030532
nuclear hormone receptor binding, GO:0035257
peptidyl-prolyl cis-trans isomerase activity, GO:0003755
protein peptidyl-prolyl isomerization, GO:0000413
single-stranded RNA binding, GO:0003727
U2 snRNP, GO:0005686
nuclear-transcribed mRNA catabolic process, GO:0000956
negative regulation of mRNA splicing, GO:0048025
positive regulation of mRNA splicing, GO:0048026
telomerase RNA binding, GO:0070034
U2-type prespliceosome, GO:0071004
negative regulation of telomere maintenance via telomerase, GO:0032211
nuclear import, GO:0051170
U1 snRNP, GO:0005685
U5 snRNP, GO:0005682
SMN-Sm protein complex, GO:0034719
U6 snRNA binding, GO:0017070
Prp19 complex, GO:0000974
mRNA splice site selection, GO:0006376
alternative mRNA splicing, GO:0000380
pre-mRNA binding, GO:0036002
methylosome, GO:0034709
cytoplasmic ribonucleoprotein granule, GO:0036464
positive regulation of RNA splicing, GO:0033120
negative regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032435
RNA catabolic process, GO:0006401
spliceosomal tri-snRNP complex assembly, GO:0000244
DNA replication factor A complex, GO:0005662
histone mRNA metabolic process, GO:0008334
RNA helicase activity, GO:0003724
cellular response to tumor necrosis factor, GO:0071356
poly(U) RNA binding, GO:0008266
C2H2 zinc finger domain binding, GO:0070742
negative regulation of nucleic acid-templated transcription, GO:1903507
U4 snRNP, GO:0005687
G-rich strand telomeric DNA binding, GO:0098505
viral mRNA export from host cell nucleus, GO:0046784
box C/D snoRNP assembly, GO:0000492
chaperone mediated protein folding requiring cofactor, GO:0051085
positive regulation of DNA damage response, GO:0043517
cytoplasmic mRNA processing body assembly, GO:0033962
leucine zipper domain binding, GO:0043522
mRNA destabilization, GO:0061157
positive regulation of production of miRNAs involved in gene silencing by miRNA, GO:1903800
poly(A) binding, GO:0008143
maturation of 5.8S rRNA, GO:0000460
U4 snRNA binding, GO:0030621
U6 snRNP, GO:0005688
small nucleolar ribonucleoprotein complex, GO:0005732
U2-type spliceosomal complex, GO:0005684
DNA-templated transcription, GO:0006353
RNA stem-loop binding, GO:0035613
snRNA binding, GO:0017069
positive regulation of nuclear-transcribed mRNA poly(A) tail shortening, GO:0060213
transcription corepressor binding, GO:0001222
cellular response to brain-derived neurotrophic factor stimulus, GO:1990416
negative regulation of protein dephosphorylation, GO:0035308
pre-mRNA intronic binding, GO:0097157
protein kinase B binding, GO:0043422
commitment complex, GO:0000243
Ral GTPase binding, GO:0017160
histone monoubiquitination, GO:0010390
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N6-methyladenosine-containing RNA binding, GO:1990247
enhancer binding, GO:0035326
RS domain binding, GO:0050733
mRNA cis splicing, GO:0045292
U2 snRNA binding, GO:0030620
G-quadruplex DNA unwinding, GO:0044806
histone pre-mRNA 3'end processing complex, GO:0071204
poly(G) binding, GO:0034046
RNA polymerase II core binding, GO:0000993
positive regulation of DNA-templated transcription, GO:0032786
cellular response to interferon-beta, GO:0035458
response to vitamin E, GO:0033197
myoblast differentiation, GO:0045445
U7 snRNP, GO:0005683
fibroblast growth factor binding, GO:0017134
positive regulation of DNA biosynthetic process, GO:2000573
Lsm1-7-Pat1 complex, GO:1990726
prespliceosome, GO:0071010
negative regulation of RNA splicing, GO:0033119
positive regulation of DNA topoisomerase (ATP-hydrolyzing) activity, GO:2000373
U1 snRNA binding, GO:0030619
transcription factor activity, GO:0001135
regulation of protein complex stability, GO:0061635
U2AF, GO:0089701
pre-mRNA 3'-splice site binding, GO:0030628
intracellular estrogen receptor signaling pathway, GO:0030520
positive regulation of astrocyte differentiation, GO:0048711
negative regulation of toll-like receptor signaling pathway, GO:0034122
U3 snoRNA binding, GO:0034511
mRNA 3'-splice site recognition, GO:0000389
pICln-Sm protein complex, GO:0034715
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paraspeckles, GO:0042382
CRD-mediated mRNA stability complex, GO:0070937
box C/D snoRNP complex, GO:0031428
positive regulation of intracellular estrogen receptor signaling pathway, GO:0033148
positive regulation of nuclear-transcribed mRNA catabolic process, GO:1900153
positive regulation of G1/S transition of mitotic cell cycle, GO:1900087
regulation of T cell proliferation, GO:0042129