helicase activity, GO:0004386 catalytic step 2 spliceosome, GO:0071013 mRNA export from nucleus, GO:0006406 RNA processing, GO:0006396 mRNA transport, GO:0051028 nuclear matrix, GO:0016363 termination of RNA polymerase II transcription, GO:0006369 RNA metabolic process, GO:0016070 mRNA 3'-end processing, GO:0031124 Cajal body, GO:0015030 osteoblast differentiation, GO:0001649 RNA export from nucleus, GO:0006405 spliceosomal snRNP assembly, GO:0000387 ribonucleoprotein complex binding, GO:0043021 fibroblast growth factor receptor signaling pathway, GO:0008543 RNA splicing, GO:0000375 precatalytic spliceosome, GO:0071011 exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay, GO:0043928 U2 snRNP, GO:0005686 U12-type spliceosomal complex, GO:0005689 androgen receptor binding, GO:0050681 interleukin-12-mediated signaling pathway, GO:0035722 U4/U6 x U5 tri-snRNP complex, GO:0046540 regulation of mitophagy, GO:1903146 single-stranded RNA binding, GO:0003727 telomerase RNA binding, GO:0070034 small nuclear ribonucleoprotein complex, GO:0030532 negative regulation of mRNA splicing, GO:0048025 viral nucleocapsid, GO:0019013 U2-type prespliceosome, GO:0071004 telomerase holoenzyme complex, GO:0005697 nuclear import, GO:0051170 exon-exon junction complex, GO:0035145 U5 snRNP, GO:0005682 spliceosomal complex assembly, GO:0000245 regulation of alternative mRNA splicing, GO:0000381 DNA replication factor A complex, GO:0005662 nuclear-transcribed mRNA catabolic process, GO:0000956 SMN-Sm protein complex, GO:0034719 RNA catabolic process, GO:0006401 U1 snRNP, GO:0005685 nuclear hormone receptor binding, GO:0035257 RNA helicase activity, GO:0003724 mRNA splice site selection, GO:0006376

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U4 snRNP, GO:0005687

methylosome, GO:0034709

Prp19 complex, GO:0000974

pre-mRNA binding, GO:0036002

poly(A) binding, GO:0008143

alternative mRNA splicing, GO:0000380

regulation of RNA splicing, GO:0043484

histone monoubiquitination, GO:0010390

C2H2 zinc finger domain binding, GO:0070742

histone mRNA metabolic process, GO:0008334

RNA polymerase II core binding, GO:0000993

ATP-dependent helicase activity, GO:0008026

cellular response to retinoic acid, GO:0071300

G-rich strand telomeric DNA binding, GO:0098505

positive regulation of mRNA splicing, GO:0048026

positive regulation of RNA splicing, GO:0033120

small nucleolar ribonucleoprotein complex, GO:0005732

positive regulation by host of viral transcription, GO:0043923

positive regulation of mRNA catabolic process, GO:0061014

negative regulation of telomere maintenance via telomerase, GO:0032211

DNA-templated transcription, GO:0006353

protein kinase B binding, GO:0043422

U7 snRNP, GO:0005683

regulation of ATPase activity, GO:0043462

pre-mRNA intronic binding, GO:0097157

cellular response to tumor necrosis factor, GO:0071356

cytoplasmic mRNA processing body assembly, GO:0033962

positive regulation of DNA-templated transcription, GO:0032786

negative regulation of fibroblast apoptotic process, GO:2000270

spliceosomal tri-snRNP complex assembly, GO:0000244