transcription elongation from RNA polymerase II promoter, GO:0006368

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snRNA transcription from RNA polymerase II promoter, GO:0042795
protein N-terminus binding, GO:0047485
positive regulation of gene expression, GO:0045815
transcription initiation from RNA polymerase II promoter, GO:0006367
positive regulation of viral transcription, GO:0050434
transcription factor TFIID complex, GO:0005669
MLL1 complex, GO:0071339
DNA-directed 5'-3' RNA polymerase activity, GO:0003899
mRNA polyadenylation, GO:0006378
transcription from RNA polymerase III promoter, GO:0006383
histone acetyltransferase activity, GO:0004402
DNA-templated transcription, GO:0006352
somatic stem cell population maintenance, GO:0035019
positive regulation of type I interferon production, GO:0032481
transcription elongation factor complex, GO:0008023
RNA polymerase II repressing transcription factor binding, GO:0001103
positive regulation of transcription elongation from RNA polymerase II promoter, GO:0032968
DNA-directed RNA polymerase II, GO:0005665
translation elongation factor activity, GO:0003746
histone H4 acetylation, GO:0043967
DNA-directed RNA polymerase III complex, GO:0005666
vitamin D receptor binding, GO:0042809
transcriptionally active chromatin, GO:0035327
histone deubiquitination, GO:0016578
transcription factor TFTC complex, GO:0033276
RNA polymerase I activity, GO:0001054
RNA polymerase III activity, GO:0001056
nucleosome binding, GO:0031491
negative regulation of transcription elongation from RNA polymerase II promoter, GO:0034244
TBP-class protein binding, GO:0017025
SAGA complex, GO:0000124
negative regulation of myeloid cell differentiation, GO:0045638
DNA-directed RNA polymerase I complex, GO:0005736
nuclear-transcribed mRNA catabolic process, GO:0000288
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:1902166
core TFIIH complex, GO:0000439
poly(A)+ mRNA export from nucleus, GO:0016973
Cdc73/Paf1 complex, GO:0016593
RNA polymerase II activity, GO:0001055
regulation of mRNA processing, GO:0050684
STAGA complex, GO:0030914
positive regulation by host of viral transcription, GO:0043923
positive regulation of cell cycle G1/S phase transition, GO:1902808
pre-mRNA cleavage required for polyadenylation, GO:0098789
positive regulation of cardiac muscle hypertrophy, GO:0010613
positive regulation of neurogenesis, GO:0050769
7SK snRNA binding, GO:0097322
histone H2B ubiquitination, GO:0033523
Elongator holoenzyme complex, GO:0033588
endodermal cell fate commitment, GO:0001711
transcription factor activity, GO:0001076
proteasome regulatory particle, GO:0008541
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