

histone binding, GO:0042393

- regulation of hematopoietic stem cell differentiation, GO:1902036
- nucleosome assembly, GO:0006334
- nucleosome, GO:0000786
- positive regulation of gene expression, GO:0045815
- chromatin remodeling, GO:0006338
- thiol-dependent ubiquitin-specific protease activity, GO:0004843
- negative regulation of gene expression, GO:0045814
- nuclear chromosome, GO:0000228
- histone deacetylase binding, GO:0042826
- thiol-dependent ubiquitinyl hydrolase activity, GO:0036459
- chromatin organization, GO:0006325
- protein autoubiquitination, GO:0051865
- chromatin silencing at rDNA, GO:0000183
- nucleosomal DNA binding, GO:0031492
- multicellular organism growth, GO:0035264
- protein heterotetramerization, GO:0051290
- telomere organization, GO:0032200
- RNA polymerase II distal enhancer sequence-specific DNA binding, GO:0000980
- beta-catenin-TCF complex assembly, GO:1904837
- interleukin-7-mediated signaling pathway, GO:0038111
- cysteine-type endopeptidase activity, GO:0004197
- DNA-templated transcription, GO:0006352
- DNA replication-independent nucleosome assembly, GO:0006336
- phosphoprotein binding, GO:0051219
- transcription cofactor activity, GO:0003712
- protein-DNA complex, GO:0032993
- chromatin silencing, GO:0006342
- nuclear nucleosome, GO:0000788
- negative regulation of cell growth, GO:0030308
- Ran GTPase binding, GO:0008536
- histone deacetylase complex, GO:0000118
- nucleocytoplasmic transport, GO:0006913
- telomere capping, GO:0016233
- nucleosome binding, GO:0031491
- histone H4 acetylation, GO:0043967
- male gonad development, GO:0008584
- transcriptional repressor complex, GO:0017053
- palate development, GO:0060021
- cellular senescence, GO:0090398
- lysine-acetylated histone binding, GO:0070577
- nucleus organization, GO:0006997
- ATP-dependent chromatin remodeling, GO:0043044
- histone demethylase activity, GO:0032452
- muscle organ development, GO:0007517
- activation of JUN kinase activity, GO:0007257
- positive regulation of transcription elongation from RNA polymerase II promoter, GO:0032968
- non-membrane spanning protein tyrosine kinase activity, GO:0004715
- negative regulation of megakaryocyte differentiation, GO:0045653
- vasculature development, GO:0001944
- SWI/SNF complex, GO:0016514
- intermediate filament cytoskeleton, GO:0045111
- transcriptionally active chromatin, GO:0035327
- activating transcription factor binding, GO:0033613
- spermatid development, GO:0007286
- cellular response to interleukin-4, GO:0071353
- canonical Wnt signaling pathway, GO:0060070
- nuclear replication fork, GO:0043596
- npBAF complex, GO:0071564
- cyclin-dependent protein serine/threonine kinase regulator activity, GO:0016538
- negative regulation of DNA binding, GO:0043392
- beta-catenin binding, GO:0008013
- positive regulation of transcription from RNA polymerase III promoter, GO:0045945
- ribosomal large subunit export from nucleus, GO:0000055
- regulation of gene silencing, GO:0060968
- response to hydroperoxide, GO:0033194
- hydrolase activity, GO:0016817
- positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway, GO:1902237
- seminiferous tubule development, GO:0072520
- negative regulation of transcription elongation from RNA polymerase II promoter, GO:0034244
- positive regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045737
- histone deubiquitination, GO:0016578
- positive regulation of phosphatidylinositol 3-kinase signaling, GO:0014068
- K63-linked polyubiquitin binding, GO:0070530
- regulation of interferon-gamma-mediated signaling pathway, GO:0060334
- negative regulation of cellular senescence, GO:2000773
- nBAF complex, GO:0071565
- negative regulation of androgen receptor signaling pathway, GO:0060766
- positive regulation by host of viral transcription, GO:0043923
- tau protein binding, GO:0048156
- histone H2B ubiquitination, GO:0033523
- regulation of mRNA processing, GO:0050684
- ribosomal small subunit binding, GO:0043024
- regulation of protein ubiquitination, GO:0031396
- condensin complex, GO:0000796
- RNA polymerase II transcription coactivator activity, GO:0001105
- positive regulation of histone acetylation, GO:0035066
- cysteine-type endopeptidase inhibitor activity involved in apoptotic process, GO:0043027
- histone H3-K4 demethylation, GO:0034720
- muscle cell differentiation, GO:0042692
- ribosome assembly, GO:0042255
- cytoplasmic sequestering of transcription factor, GO:0042994
- inclusion body, GO:0016234
- embryo implantation, GO:0007566
- synaptic vesicle transport, GO:0048489
- FAD binding, GO:0071949
- histone ubiquitination, GO:0016574
- negative regulation of cell-cell adhesion, GO:0022408
- H4 histone acetyltransferase activity, GO:0010485
- hematopoietic stem cell proliferation, GO:0071425
- ribosomal large subunit binding, GO:0043023
- Tat protein binding, GO:0030957
- acetylcholine receptor binding, GO:0033130
- regulation of myeloid cell differentiation, GO:0045637
- homeostasis of number of cells, GO:0048872
- positive regulation of centrosome duplication, GO:0010825
- regulation of mammary gland epithelial cell proliferation, GO:0033599
- mitochondrial ATP synthesis coupled electron transport, GO:0042775
- microglial cell activation, GO:0001774
- enzyme linked receptor protein signaling pathway, GO:0007167
- cellular response to thyroid hormone stimulus, GO:0097067
- tongue development, GO:0043586
- mammary gland development, GO:0030879
- RNA polymerase I CORE element sequence-specific DNA binding, GO:0001164
- phosphatidylinositol 3-kinase binding, GO:0043548
- platelet alpha granule membrane, GO:0031092
- lipoprotein transport, GO:0042953
- neural retina development, GO:0003407
- histone H2A monoubiquitination, GO:0035518
- positive regulation of innate immune response, GO:0045089
- detection of bacterium, GO:0016045
- positive regulation of B cell receptor signaling pathway, GO:0050861
- RNA polymerase I core binding, GO:0001042
- regulation of triglyceride metabolic process, GO:0090207
- negative regulation of protein kinase activity by regulation of protein phosphorylation, GO:0044387
- negative regulation of mRNA polyadenylation, GO:1900364
- cellular response to fibroblast growth factor stimulus, GO:0044344
- cellular response to epinephrine stimulus, GO:0071872
- supramolecular fiber organization, GO:0097435
- positive regulation of endocytosis, GO:0045807