

protein C-terminus binding, GO:0008022

protein stabilization, GO:0050821
histone deacetylase binding, GO:0042826
protein complex assembly, GO:0006461
rhythmic process, GO:0048511
centriole, GO:0005814
macroautophagy, GO:0016236
transcription factor complex, GO:0005667
protein N-terminus binding, GO:0047485
protein tyrosine kinase activity, GO:0004713
transcription initiation from RNA polymerase II promoter, GO:0006367
negative regulation of cell growth, GO:0030308
endosomal transport, GO:0016197
response to organic cyclic compound, GO:0014070
cell adhesion molecule binding, GO:0050839
cellular response to hypoxia, GO:0071456
ion channel binding, GO:0044325
positive regulation of catalytic activity, GO:0043085
cellular response to glucose starvation, GO:0042149
intraciliary transport involved in cilium assembly, GO:0035735
transcriptional repressor complex, GO:0017053
global genome nucleotide-excision repair, GO:0070911
protein self-association, GO:0043621
positive regulation of type I interferon production, GO:0032481
response to organic substance, GO:0010033
positive regulation of sequence-specific DNA binding transcription factor activity, GO:0051091
protein complex scaffold, GO:0032947
protein kinase C binding, GO:0005080
repressing transcription factor binding, GO:0070491
ciliary tip, GO:0097542
transcription factor TFIID complex, GO:0005669
transcription cofactor activity, GO:0003712
forebrain development, GO:0030900
lung development, GO:0030324
sensory perception of sound, GO:0007605
estrogen receptor binding, GO:0030331
positive regulation of JNK cascade, GO:0046330
core promoter sequence-specific DNA binding, GO:0001046
response to cytokine, GO:0034097
membrane coat, GO:0030117
regulation of protein localization, GO:0032880
circadian rhythm, GO:0007623
multivesicular body assembly, GO:0036258
basement membrane, GO:0005604
thymus development, GO:0048538
regulation of circadian rhythm, GO:0042752
negative regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043124
transcription elongation from RNA polymerase I promoter, GO:0006362
caveola, GO:0005901
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043280
postsynapse, GO:0098794
beta-catenin-TCF complex assembly, GO:1904837
potassium channel regulator activity, GO:0015459
regulation of molecular function, GO:0065009
regulation of cholesterol biosynthetic process, GO:0045540
ERBB2 signaling pathway, GO:0038128
protein-DNA complex, GO:0032993
protein localization, GO:0008104
positive regulation of epithelial to mesenchymal transition, GO:0010718
protein targeting, GO:0006605
neuromuscular process controlling balance, GO:0050885
termination of RNA polymerase I transcription, GO:0006363
embryonic digit morphogenesis, GO:0042733
transcription initiation from RNA polymerase I promoter, GO:0006361
negative regulation of ERK1 and ERK2 cascade, GO:0070373
immunological synapse, GO:0001772
response to wounding, GO:0009611
clathrin-dependent endocytosis, GO:0072583
UV protection, GO:0009650
canonical Wnt signaling pathway, GO:0060070
mitochondrial calcium ion transmembrane transport, GO:0006851
scaffold protein binding, GO:0097110
positive regulation of ATPase activity, GO:0032781
nucleus organization, GO:0006997
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:0042771
positive regulation of epithelial cell proliferation, GO:0050679
regulation of endocytosis, GO:0030100
phosphoprotein binding, GO:0051219
voltage-gated potassium channel complex, GO:0008076
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway, GO:0043162
fat cell differentiation, GO:0045444
basal plasma membrane, GO:0009925
positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, GO:1900740
regulation of membrane potential, GO:0042391
mitogen-activated protein kinase binding, GO:0051019
negative regulation of sequence-specific DNA binding transcription factor activity, GO:0043433
histone H4 acetylation, GO:0043967
negative regulation of Wnt signaling pathway, GO:0030178
activating transcription factor binding, GO:0033613
glucose homeostasis, GO:0042593
acrosomal vesicle, GO:0001669
ATPase activator activity, GO:0001671
excitatory synapse, GO:0060076
protein targeting to membrane, GO:0006612
T cell differentiation in thymus, GO:0033077
RNA polymerase II activating transcription factor binding, GO:0001102
cellular response to peptide hormone stimulus, GO:0071375
intraciliary transport particle B, GO:0030992
cellular senescence, GO:0090398
glycosaminoglycan metabolic process, GO:0030203
endocytic vesicle membrane, GO:0030666
glucocorticoid receptor binding, GO:0035259
synaptic vesicle exocytosis, GO:0016079
regulation of cardiac conduction, GO:1903779
G-protein alpha-subunit binding, GO:0001965
regulation of ERK1 and ERK2 cascade, GO:0070372
myeloid cell differentiation, GO:0030099
positive regulation of fat cell differentiation, GO:0045600
glycosaminoglycan biosynthetic process, GO:0006024
cell death, GO:0008219
UV-damage excision repair, GO:0070914
receptor signaling complex scaffold activity, GO:0030159
viral budding via host ESCRT complex, GO:0039702
platelet formation, GO:0030220
skin development, GO:0043588
activation of JUN kinase activity, GO:0007257
regulation of protein complex stability, GO:0061635
locomotory behavior, GO:0007626
response to ischemia, GO:0002931
positive regulation of dendritic spine development, GO:0060999
ephrin receptor binding, GO:0046875
response to cAMP, GO:0051591
oligodendrocyte differentiation, GO:0048709
somitogenesis, GO:0001756
regulation of calcium ion transport, GO:0051924
embryonic hindlimb morphogenesis, GO:0035116
negative regulation of DNA binding, GO:0043392
regulation of long-term neuronal synaptic plasticity, GO:0048169
GMP metabolic process, GO:0046037
ESCRT III complex disassembly, GO:1904903
adult behavior, GO:0030534
sodium channel regulator activity, GO:0017080
negative regulation of cellular senescence, GO:2000773
regulation of interferon-gamma-mediated signaling pathway, GO:0060334
RNA polymerase II transcription factor binding, GO:0001085
peroxisome organization, GO:0007031
spinal cord development, GO:0021510
response to lipid, GO:0033993
cell maturation, GO:0048469
regulation of receptor activity, GO:0010469
cellular response to prostaglandin E stimulus, GO:0071380
response to retinoic acid, GO:0032526
phosphatidylinositol 3-kinase binding, GO:0043548
S100 protein binding, GO:0044548
response to antibiotic, GO:0046677
protein tag, GO:0031386
regulation of cellular senescence, GO:2000772
positive regulation of synaptic transmission, GO:0050806
long term synaptic depression, GO:0060292
positive regulation of T cell activation, GO:0050870
negative regulation of osteoblast differentiation, GO:0045668
neurotransmitter secretion, GO:0007269
response to molecule of bacterial origin, GO:0002237
positive regulation of neurogenesis, GO:0050769
intracellular steroid hormone receptor signaling pathway, GO:0030518
glutamate secretion, GO:0014047
regulation of mitotic spindle organization, GO:0060236
cell separation after cytokinesis, GO:0000920
integral component of peroxisomal membrane, GO:0005779
regulation of myelination, GO:0031641
negative regulation of mitotic cell cycle, GO:0045930
retinoid metabolic process, GO:0001523
metanephros development, GO:0001656
protein kinase A catalytic subunit binding, GO:0034236
cellular potassium ion homeostasis, GO:0030007
response to interferon-gamma, GO:0034341
photoreceptor outer segment, GO:0001750
photoreceptor inner segment, GO:0001917
JAK-STAT cascade, GO:0007259
dendritic spine morphogenesis, GO:0060997
intracellular distribution of mitochondria, GO:0048312
neuron projection terminus, GO:0044306
negative regulation of protein serine/threonine kinase activity, GO:0071901
positive regulation of nitric-oxide synthase activity, GO:0051000
voltage-gated calcium channel activity, GO:0005245
low-density lipoprotein particle receptor catabolic process, GO:0032802
positive regulation of viral release from host cell, GO:1902188
negative regulation of epithelial cell proliferation, GO:0050680
regulation of NMDA receptor activity, GO:2000310
fibronectin binding, GO:0001968
nuclear euchromatin, GO:0005719
clathrin adaptor activity, GO:0035615
negative regulation of ubiquitin-protein transferase activity, GO:0051444
positive regulation of viral process, GO:0048524
positive regulation of cell cycle G1/S phase transition, GO:1902808
macrophage derived foam cell differentiation, GO:0010742