

protein C-terminus binding, GO:0008022

rhythmic process, GO:0048511
protein complex assembly, GO:0006461
protein N-terminus binding, GO:0047485
cell-cell junction, GO:0005911
kinase binding, GO:0019900
ion channel binding, GO:0044325
transcription initiation from RNA polymerase II promoter, GO:0006367
response to oxidative stress, GO:0006979
transcription factor complex, GO:0005667
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
positive regulation of cell migration, GO:0030335
peroxisomal membrane, GO:0005778
sarcolemma, GO:0042383
hemopoiesis, GO:0030097
regulation of circadian rhythm, GO:0042752
androgen receptor signaling pathway, GO:0030521
integrin binding, GO:0005178
peptidyl-tyrosine phosphorylation, GO:0018108
cell-cell adherens junction, GO:0005913
protein heterooligomerization, GO:0051291
protein tyrosine kinase activity, GO:0004713
cell adhesion molecule binding, GO:0050839
phosphatase binding, GO:0019902
transcription initiation from RNA polymerase I promoter, GO:0006361
termination of RNA polymerase I transcription, GO:0006363
positive regulation of catalytic activity, GO:0043085
multivesicular body assembly, GO:0036258
response to organic cyclic compound, GO:0014070
protease binding, GO:0002020
circadian rhythm, GO:0007623
negative regulation of ERK1 and ERK2 cascade, GO:0070373
transcription factor TFIIID complex, GO:0005669
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transcription elongation from RNA polymerase I promoter, GO:0006362
cytoskeletal protein binding, GO:0008092
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:0042771
negative regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043124
response to antibiotic, GO:0046677
response to wounding, GO:0009611
telomeric DNA binding, GO:0042162
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T-tubule, GO:0030315
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circadian regulation of gene expression, GO:0032922
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043280
response to hydrogen peroxide, GO:0042542
negative regulation of cell death, GO:0060548
intercalated disc, GO:0014704
actin filament, GO:0005884
cortical actin cytoskeleton, GO:0030864
lung development, GO:0030324
peroxisome organization, GO:0007031
positive regulation of protein serine/threonine kinase activity, GO:0071902
glucose homeostasis, GO:0042593
RNA polymerase II transcription factor binding, GO:0001085
viral budding via host ESCRT complex, GO:0039702
cell separation after cytokinesis, GO:0000920
positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, GO:1900740
hippo signaling, GO:0035329
negative regulation of sequence-specific DNA binding transcription factor activity, GO:0043433
positive regulation of protein targeting to membrane, GO:0090314
estrogen receptor binding, GO:0030331
repressing transcription factor binding, GO:0070491
regulation of molecular function, GO:0065009
mitochondrial calcium ion transmembrane transport, GO:0006851
nuclear euchromatin, GO:0005719
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scaffold protein binding, GO:0097110
drug binding, GO:0008144
response to estradiol, GO:0032355
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positive regulation of transforming growth factor beta receptor signaling pathway, GO:0030511
positive regulation of MAPK cascade, GO:0043410
positive regulation of epithelial cell proliferation, GO:0050679
potassium channel regulator activity, GO:0015459
wound healing, GO:0042060
regulation of cardiac conduction, GO:1903779
glycosaminoglycan catabolic process, GO:0006027
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RNA polymerase II carboxy-terminal domain kinase activity, GO:0008353
regulation of cell motility, GO:2000145
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integral component of peroxisomal membrane, GO:0005779
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positive regulation of viral release from host cell, GO:1902188
axonogenesis, GO:0007409
branching involved in ureteric bud morphogenesis, GO:0001658
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negative regulation of cell adhesion, GO:0007162
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actin monomer binding, GO:0003785
SUMO transferase activity, GO:0019789
macromolecular complex binding, GO:0044877
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negative regulation of osteoblast differentiation, GO:0045668
S100 protein binding, GO:0044548
RNA polymerase II activating transcription factor binding, GO:0001102
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T cell differentiation in thymus, GO:0033077
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positive regulation of DNA-templated transcription, GO:2000144
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regulation of axon regeneration, GO:0048679
positive regulation of excitatory postsynaptic potential, GO:2000463
regulation of energy homeostasis, GO:2000505
negative regulation of vascular permeability, GO:0043116
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positive regulation of intracellular signal transduction, GO:1902533
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negative regulation of endothelial cell differentiation, GO:0045602
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cellular response to laminar fluid shear stress, GO:0071499
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MPP7-DLG1-LIN7 complex, GO:0097025
response to superoxide, GO:0000303
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