

protein C-terminus binding, GO:0008022

protein complex assembly, GO:0006461
actin filament binding, GO:0051015
transcription factor complex, GO:0005667
negative regulation of cell growth, GO:0030308
histone deacetylase binding, GO:0042826
response to organic cyclic compound, GO:0014070
androgen receptor binding, GO:0050681
cell-cell adherens junction, GO:0005913
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:0042771
ciliary tip, GO:0097542
transcription cofactor activity, GO:0003712
single organismal cell-cell adhesion, GO:0016337
cytoskeletal protein binding, GO:0008092
actin filament organization, GO:0007015
movement of cell or subcellular component, GO:0006928
adherens junction, GO:0005912
bicellular tight junction, GO:0005923
basement membrane, GO:0005604
cell-matrix adhesion, GO:0007160
response to estradiol, GO:0032355
protein targeting, GO:0006605
immunological synapse, GO:0001772
protein heterooligomerization, GO:0051291
scaffold protein binding, GO:0097110
response to cytokine, GO:0034097
cell adhesion molecule binding, GO:0050839
potassium ion transport, GO:0006813
sensory perception of sound, GO:0007605
fat cell differentiation, GO:0045444
protease binding, GO:0002020
response to estrogen, GO:0043627
estrogen receptor binding, GO:0030331
protein-DNA complex, GO:0032993
transcriptional repressor complex, GO:0017053
regulation of molecular function, GO:0065009
phosphatase binding, GO:0019902
drug binding, GO:0008144
RNA polymerase II distal enhancer sequence-specific DNA binding, GO:0000980
peroxisome organization, GO:0007031
multivesicular body assembly, GO:0036258
negative regulation of sequence-specific DNA binding transcription factor activity, GO:0043433
extracellular vesicle, GO:1903561
protein self-association, GO:0043621
T-tubule, GO:0030315
cell motility, GO:0048870
cortical actin cytoskeleton, GO:0030864
dendrite development, GO:0016358
negative regulation of cell adhesion, GO:0007162
integral component of peroxisomal membrane, GO:0005779
branching involved in ureteric bud morphogenesis, GO:0001658
synapse assembly, GO:0007416
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway, GO:0043162
positive regulation of excitatory postsynaptic potential, GO:2000463
negative regulation of Wnt signaling pathway, GO:0030178
regulation of cardiac conduction, GO:1903779
lateral plasma membrane, GO:0016328
embryonic digit morphogenesis, GO:0042733
myeloid cell differentiation, GO:0030099
positive regulation of epithelial to mesenchymal transition, GO:0010718
intraciliary transport particle B, GO:0030992
ionotropic glutamate receptor binding, GO:0035255
positive regulation of T cell activation, GO:0050870
UV-damage excision repair, GO:0070914
receptor signaling complex scaffold activity, GO:0030159
potassium ion binding, GO:0030955
platelet formation, GO:0030220
Flemming body, GO:0090543
calcium channel regulator activity, GO:0005246
skin development, GO:0043588
S100 protein binding, GO:0044548
embryonic hindlimb morphogenesis, GO:0035116
apical junction complex, GO:0043296
embryonic forelimb morphogenesis, GO:0035115
positive regulation of early endosome to late endosome transport, GO:2000643
basal plasma membrane, GO:0009925
actin crosslink formation, GO:0051764
voltage-gated calcium channel activity, GO:0005245
microvillus membrane, GO:0031528
GMP metabolic process, GO:0046037
laminin binding, GO:0043236
eating behavior, GO:0042755
metanephros development, GO:0001656
negative regulation of cAMP biosynthetic process, GO:0030818
actinin binding, GO:0042805
actin monomer binding, GO:0003785
positive regulation of muscle cell differentiation, GO:0051149
cortical actin cytoskeleton organization, GO:0030866
protein import into peroxisome matrix, GO:0016558
neurotransmitter secretion, GO:0007269
GDP metabolic process, GO:0046710
guanylate kinase activity, GO:0004385
cellular sodium ion homeostasis, GO:0006883
brain morphogenesis, GO:0048854
oogenesis, GO:0048477
protein kinase A signaling, GO:0010737
ESCRT III complex disassembly, GO:1904903
negative regulation of vascular permeability, GO:0043116
positive regulation of transforming growth factor beta receptor signaling pathway, GO:0030511
glucocorticoid receptor binding, GO:0035259
I-SMAD binding, GO:0070411
clathrin adaptor activity, GO:0035615
locomotory exploration behavior, GO:0035641
inositol-1, GO:0052659
intercellular canaliculus, GO:0046581
sodium ion binding, GO:0031402
fibronectin binding, GO:0001968
intracellular steroid hormone receptor signaling pathway, GO:0030518
synaptic membrane, GO:0097060
ionotropic glutamate receptor complex, GO:0008328
regulation of sensory perception of pain, GO:0051930
response to interferon-gamma, GO:0034341
troponin I binding, GO:0031013
phosphatidylinositol-3, GO:0043813
phosphoric ester hydrolase activity, GO:0042578
hydrolase activity, GO:0016817
regulation of synapse assembly, GO:0051963
positive regulation of ruffle assembly, GO:1900029
cardiac septum development, GO:0003279
positive regulation of urine volume, GO:0035810
filamin binding, GO:0031005
dorsal/ventral pattern formation, GO:0009953
cellular senescence, GO:0090398
vocalization behavior, GO:0071625
neurofilament, GO:0005883
activating transcription factor binding, GO:0033613
morphogenesis of embryonic epithelium, GO:0016331
negative regulation of cell motility, GO:2000146
RNA polymerase II activating transcription factor binding, GO:0001102
1-phosphatidylinositol binding, GO:0005545
catenin complex, GO:0016342
monoamine transport, GO:0015844
telomere maintenance via telomere lengthening, GO:0010833
inositol phosphate dephosphorylation, GO:0046855
positive regulation of hair follicle development, GO:0051798
macrophage derived foam cell differentiation, GO:0010742
thioredoxin peroxidase activity, GO:0008379
somatic recombination of immunoglobulin gene segments, GO:0016447
actin filament depolymerization, GO:0030042
protein targeting to peroxisome, GO:0006625
post-anal tail morphogenesis, GO:0036342
negative regulation of endothelial cell differentiation, GO:0045602
flotillin complex, GO:0016600
uropod, GO:0001931
positive regulation of SMAD protein import into nucleus, GO:0060391
T-helper 1 type immune response, GO:0042088
regulation of Arp2/3 complex-mediated actin nucleation, GO:0034315
maintenance of cell polarity, GO:0030011
sensory perception, GO:0007600
hydrogen peroxide catabolic process, GO:0042744
stabilization of membrane potential, GO:0030322
D1 dopamine receptor binding, GO:0031748
secretion, GO:0046903