

guanyl-nucleotide exchange factor activity, GO:0005085
endocytosis, GO:0006897
actin cytoskeleton organization, GO:0030036
regulation of small GTPase mediated signal transduction, GO:0051056
small GTPase mediated signal transduction, GO:0007264
cell-cell junction, GO:0005911
ruffle, GO:0001726
neuron projection development, GO:0031175
trans-Golgi network, GO:0005802
positive regulation of cell migration, GO:0030335
growth cone, GO:0030426
exocytosis, GO:0006887
cell-cell adherens junction, GO:0005913
cell cycle arrest, GO:0007050
negative regulation of protein kinase activity, GO:0006469
peptidyl-tyrosine phosphorylation, GO:0018108
ruffle membrane, GO:0032587
axon guidance, GO:0007411
regulation of cell shape, GO:0008360
SH3 domain binding, GO:0017124
regulation of Rho protein signal transduction, GO:0035023
ephrin receptor signaling pathway, GO:0048013
regulation of GTPase activity, GO:0043087
Rho guanyl-nucleotide exchange factor activity, GO:0005089
positive regulation of protein phosphorylation, GO:0001934
calmodulin binding, GO:0005516
dendritic spine, GO:0043197
neural tube closure, GO:0001843
phosphatase activity, GO:0016791
phagocytic vesicle membrane, GO:0030670
bicellular tight junction, GO:0005923
cell cortex, GO:0005938
Z disc, GO:0030018
cell leading edge, GO:0031252
negative regulation of cell migration, GO:0030336
actin filament organization, GO:0007015
peptidyl-tyrosine dephosphorylation, GO:0035335
kinase binding, GO:0019900
platelet activation, GO:0030168
adherens junction, GO:0005912
sarcolemma, GO:0042383
protein oligomerization, GO:0051259
positive regulation of protein binding, GO:0032092
Rac GTPase binding, GO:0048365
epidermal growth factor receptor signaling pathway, GO:0007173
cellular response to insulin stimulus, GO:0032869
microvillus, GO:0005902
SNARE complex, GO:0031201
positive regulation of neuron projection development, GO:0010976
actin filament, GO:0005884
extrinsic component of cytoplasmic side of plasma membrane, GO:0031234
SNAP receptor activity, GO:0005484
cytoskeleton organization, GO:0007010
single organismal cell-cell adhesion, GO:0016337
regulation of protein phosphorylation, GO:0001932
animal organ morphogenesis, GO:0009887
beta-catenin binding, GO:0008013
negative regulation of neuron projection development, GO:0010977
cerebral cortex development, GO:0021987
integrin-mediated signaling pathway, GO:0007229
regulation of phosphatidylinositol 3-kinase signaling, GO:0014066
vascular endothelial growth factor receptor signaling pathway, GO:0048010
neuron differentiation, GO:0030182
wound healing, GO:0042060
execution phase of apoptosis, GO:0097194
T cell costimulation, GO:0031295
positive regulation of axon extension, GO:0045773
COP9 signalosome, GO:0008180
stress fiber, GO:0001725
synapse assembly, GO:0007416
regulation of cell migration, GO:0030334
phagocytosis, GO:0006909
virus receptor activity, GO:0001618
actin cytoskeleton reorganization, GO:0031532
integrin binding, GO:0005178
peptidyl-tyrosine autophosphorylation, GO:0038083
filopodium, GO:0030175
cellular response to mechanical stimulus, GO:0071260
blood vessel morphogenesis, GO:0048514
presynaptic membrane, GO:0042734
establishment of protein localization to plasma membrane, GO:0090002
activation of GTPase activity, GO:0090630
substrate adhesion-dependent cell spreading, GO:0034446
cell body, GO:004297
regulation of cell adhesion, GO:0030155
neuron projection morphogenesis, GO:0048812
cardiac muscle cell differentiation, GO:0055007
SNARE binding, GO:0000149
perikaryon, GO:0043204
cellular response to nerve growth factor stimulus, GO:1990090
presynapse, GO:0098793
negative regulation of GTPase activity, GO:0034260
endocytic vesicle, GO:0030139
cardiac muscle contraction, GO:0060048
muscle contraction, GO:0006936
dendrite morphogenesis, GO:0048813
lateral plasma membrane, GO:0016328
response to insulin, GO:0032868
positive regulation of neuron death, GO:1901216
non-membrane spanning protein tyrosine kinase activity, GO:0004715
regulation of actin cytoskeleton organization, GO:0032956
positive regulation of peptidyl-serine phosphorylation, GO:0033138
cellular response to growth factor stimulus, GO:0071363
adherens junction organization, GO:0034332
platelet-derived growth factor receptor signaling pathway, GO:0048008
Rho protein signal transduction, GO:0007266
axonogenesis, GO:0007409
filamentous actin, GO:0031941
odontogenesis of dentin-containing tooth, GO:0042475
vesicle fusion, GO:0006906
positive regulation of MAPK cascade, GO:0043410
positive regulation of cell growth, GO:0030307
vasculogenesis, GO:0001570
cell morphogenesis, GO:0000902
intercalated disc, GO:0014704
response to mechanical stimulus, GO:0009612
positive regulation of stress fiber assembly, GO:0051496
protein localization to plasma membrane, GO:0072659
positive regulation of MAP kinase activity, GO:0043406
proline-rich region binding, GO:0070064
vesicle organization, GO:0016050
kinesin binding, GO:0019894
cytoplasmic microtubule organization, GO:0031122
cell-matrix adhesion, GO:0007160
protein binding, GO:0030674
lamellipodium assembly, GO:0030032
hippo signaling, GO:0035329
apical part of cell, GO:0045177
positive regulation of actin filament polymerization, GO:0030838
cell chemotaxis, GO:0060326
vacuole, GO:0005773
response to bacterium, GO:0009617
phosphatidylinositol-3, GO:0005547
positive regulation of cell-matrix adhesion, GO:0001954
phagocytic cup, GO:0001891
phosphatidylinositol-4, GO:0005546
phagocytosis, GO:0006911
transforming growth factor beta receptor signaling pathway, GO:0007179
leukocyte cell-cell adhesion, GO:0007159
regulation of cell motility, GO:2000145
positive regulation of protein tyrosine kinase activity, GO:0061098
anatomical structure morphogenesis, GO:0009653
epidermal growth factor receptor binding, GO:0005154
cellular protein localization, GO:0034613
cortical actin cytoskeleton organization, GO:0030866
SH2 domain binding, GO:0042169
calcium-dependent protein binding, GO:0048306
positive regulation of establishment of protein localization to plasma membrane, GO:0090004
positive regulation of neuron apoptotic process, GO:0043525
positive regulation of cell cycle arrest, GO:0071158
plasma membrane raft, GO:0044853
microvillus membrane, GO:0031528
gastrulation with mouth forming second, GO:0001702
positive regulation of protein localization to cell surface, GO:2000010
positive regulation of peptidyl-tyrosine phosphorylation, GO:0050731
calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules, GO:0016339
positive regulation of JUN kinase activity, GO:0043507
positive regulation of endothelial cell migration, GO:0010595
positive regulation of phosphorylation, GO:0042327
myosin binding, GO:0017022
actin filament bundle assembly, GO:0051017
negative regulation of MAPK cascade, GO:0043409
T-tubule, GO:0030315
cellular response to hepatocyte growth factor stimulus, GO:0035729
Rac protein signal transduction, GO:0016601
positive regulation of muscle cell differentiation, GO:0051149
neuronal stem cell population maintenance, GO:0097150
renal system development, GO:0072001
telencephalon development, GO:0021537
regulation of nitric-oxide synthase activity, GO:0050999
regulation of cell morphogenesis, GO:0022604
neuron migration, GO:0001764
positive regulation of cytosolic calcium ion concentration, GO:0007204
receptor internalization, GO:0031623
actin monomer binding, GO:0003785
ruffle organization, GO:0031529
synaptic transmission, GO:0035249
post-Golgi vesicle-mediated transport, GO:0006892
bicellular tight junction assembly, GO:0070830
positive regulation of substrate adhesion-dependent cell spreading, GO:1900026
neuromuscular junction, GO:0031594
positive regulation of osteoblast differentiation, GO:0045669
phosphatidylinositol-3, GO:0043325
synaptic vesicle fusion to presynaptic active zone membrane, GO:0031629
uropod, GO:0001931
brush border, GO:0005903
positive regulation of protein kinase B signaling, GO:0051897
retromer complex, GO:0030904
lamellipodium membrane, GO:0031258
establishment of endothelial barrier, GO:0061028
cell projection membrane, GO:0031253
hepatocyte growth factor receptor signaling pathway, GO:0048012
insulin receptor binding, GO:0005158
regulation of actin filament polymerization, GO:0030833
receptor clustering, GO:0043113
calcium ion import, GO:0070509
myelination in peripheral nervous system, GO:0022011
stereocilium, GO:0032420
semaphorin-plexin signaling pathway, GO:0071526
positive regulation of focal adhesion assembly, GO:0051894
visual learning, GO:0008542
protein targeting to plasma membrane, GO:0072661
establishment of cell polarity, GO:0030010
positive regulation of lamellipodium assembly, GO:0010592
positive regulation of phosphatidylinositol 3-kinase activity, GO:0043552
ionotropic glutamate receptor binding, GO:0035255
positive regulation of myelination, GO:0031643
actin filament polymerization, GO:0030041
regulation of cell size, GO:0008361
cytoskeleton-dependent intracellular transport, GO:0030705
cell periphery, GO:0007144
cell motility, GO:0048870
actomyosin structure organization, GO:0031032
endothelial cell migration, GO:0043542
osteoclast differentiation, GO:0030316
regulation of establishment of cell polarity, GO:2000114
cerebellum development, GO:0021549
sprouting angiogenesis, GO:0002040
cellular defense response, GO:0006968
aorta development, GO:0035904
sarcomere, GO:0030017
axon extension, GO:0048675
branching involved in ureteric bud morphogenesis, GO:0001658
protein phosphatase 1 binding, GO:0008157
coronary vasculature development, GO:0060976
thioesterase binding, GO:0031996
structural constituent of muscle, GO:0008307
diacylglycerol metabolic process, GO:0046339
myoblast migration, GO:0051451
positive regulation of excitatory postsynaptic potential, GO:2000463
protein kinase B signaling, GO:0043491
focal adhesion assembly, GO:0048041
positive regulation of T cell migration, GO:2000406
calcium-mediated signaling, GO:0019722
regulation of postsynaptic membrane potential, GO:0060078
corpus callosum development, GO:0022038
positive regulation of filopodium assembly, GO:0051491
cellular response to cytokine stimulus, GO:0071345
hair follicle placode formation, GO:0060789
apical junction complex, GO:0043296
cell-cell contact zone, GO:0044291
terminal bouton, GO:0043195
nitric-oxide synthase binding, GO:0050998
vesicle docking, GO:0048278
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand, GO:2001241
axon regeneration, GO:0031103
bleb, GO:0032059
filopodium tip, GO:0032433
negative regulation of cell adhesion, GO:0007162
regulation of angiogenesis, GO:0045765
synaptic vesicle endocytosis, GO:0048488
regulation of mast cell degradation, GO:0043304
Wnt signalosome, GO:1990909
receptor recycling, GO:0001881
negative regulation of organ growth, GO:0046621
small GTPase binding, GO:0031267
regulation of focal adhesion assembly, GO:0051893
morphogenesis of an epithelial sheet, GO:0002011
nerve growth factor signaling pathway, GO:0038180
positive regulation of protein targeting to membrane, GO:0090314
negative regulation of macroautophagy, GO:0016242
negative regulation of epithelial cell migration, GO:0010633
filopodium assembly, GO:0046847
Rac guanyl-nucleotide exchange factor activity, GO:0030676
positive regulation of receptor recycling, GO:0001921
GTPase activating protein binding, GO:0032794
SCAR complex, GO:0031209
positive regulation of early endosome to late endosome transport, GO:2000643
endodermal cell fate commitment, GO:0001711
GDP metabolic process, GO:0046710
guanylate kinase activity, GO:0004385
cell projection assembly, GO:0030031
negative regulation of axonogenesis, GO:0050771
positive regulation of cell adhesion, GO:0045785
fibroblast migration, GO:0010761
WASH complex, GO:0071203
dystrophin-associated glycoprotein complex, GO:0016010
positive regulation of G1/S transition of mitotic cell cycle, GO:1900087
mesodermal cell differentiation, GO:0048333
negative regulation of smooth muscle cell proliferation, GO:0048662
angiogenesis involved in wound healing, GO:0060055
actinin binding, GO:0042805
regulation of lamellipodium assembly, GO:0010591
cytoskeletal adaptor activity, GO:0008093
basement membrane organization, GO:0071711
bone resorption, GO:0045453
regulation of axonogenesis, GO:0050770
channel activity, GO:0001527
regulation of neurogenesis, GO:0050767

lamellipodium, GO:0030027