

guanyl-nucleotide exchange factor activity, GO:0005085

- lamellipodium, GO:0030027
- small GTPase mediated signal transduction, GO:0007264
- Rab GTPase binding, GO:0017137
- actin cytoskeleton organization, GO:0030036
- regulation of small GTPase mediated signal transduction, GO:0051056
- ruffle, GO:0001726
- retrograde transport, GO:0042147
- ruffle membrane, GO:0032587
- endomembrane system, GO:0012505
- SH3 domain binding, GO:0017124
- growth cone, GO:0030426
- neuron projection development, GO:0031175
- regulation of cell shape, GO:0008360
- Rho guanyl-nucleotide exchange factor activity, GO:0005089
- regulation of macroautophagy, GO:0016241
- ephrin receptor signaling pathway, GO:0048013
- regulation of Rho protein signal transduction, GO:0035023
- regulation of GTPase activity, GO:0043087
- vascular endothelial growth factor receptor signaling pathway, GO:0048010
- Rab guanyl-nucleotide exchange factor activity, GO:0017112
- platelet activation, GO:0030168
- Ras protein signal transduction, GO:0007265
- extrinsic component of cytoplasmic side of plasma membrane, GO:0031234
- Rac GTPase binding, GO:0048365
- dendritic spine, GO:0043197
- filopodium, GO:0030175
- regulation of protein kinase activity, GO:0045859
- activation of MAPKK activity, GO:0000186
- regulation of G-protein coupled receptor protein signaling pathway, GO:0008277
- endocytic vesicle, GO:0030139
- endosome organization, GO:0007032
- lysosome organization, GO:0007040
- regulation of cell growth, GO:0001558
- SH3 /SH2 adaptor activity, GO:0005070
- GTP-dependent protein binding, GO:0030742
- activation of GTPase activity, GO:0090630
- positive regulation of signal transduction, GO:0009967
- neutrophil chemotaxis, GO:0030593
- phospholipid binding, GO:0005543
- phosphatidic acid binding, GO:0070300
- Ras guanyl-nucleotide exchange factor activity, GO:0005088
- Rho GTPase binding, GO:0017048
- protein complex scaffold, GO:0032947
- receptor tyrosine kinase binding, GO:0030971
- positive regulation of TOR signaling, GO:0032008
- post-Golgi vesicle-mediated transport, GO:0006892
- phosphotyrosine residue binding, GO:0001784
- Fc-gamma receptor signaling pathway involved in phagocytosis, GO:0038096
- positive regulation of tumor necrosis factor production, GO:0032760
- regulation of cell migration, GO:0030334
- regulation of defense response to virus by virus, GO:0050690
- negative regulation of cell migration, GO:0030336
- signal transducer activity, GO:0005057
- neuromuscular process controlling balance, GO:0050885
- phosphatidylinositol-3, GO:0005547
- epidermal growth factor receptor binding, GO:0005154
- platelet-derived growth factor receptor signaling pathway, GO:0048008
- positive regulation of peptidyl-serine phosphorylation, GO:0033138
- dendrite morphogenesis, GO:0048813
- T cell differentiation, GO:0030217
- cell growth, GO:0016049
- positive regulation of stress fiber assembly, GO:0051496
- positive regulation of establishment of protein localization to plasma membrane, GO:0090004
- positive regulation of JUN kinase activity, GO:0043507
- Rho protein signal transduction, GO:0007266
- regulation of cell size, GO:0008361
- small GTPase binding, GO:0031267
- Rac guanyl-nucleotide exchange factor activity, GO:0030676
- positive regulation of phagocytosis, GO:0050766
- synaptic vesicle endocytosis, GO:0048488
- positive regulation of substrate adhesion-dependent cell spreading, GO:1900026
- regulation of actin filament polymerization, GO:0030833
- negative regulation of TOR signaling, GO:0032007
- regulation of TOR signaling, GO:0032006
- cAMP-mediated signaling, GO:0019933
- reactive oxygen species metabolic process, GO:0072593
- establishment of endothelial barrier, GO:0061028
- regulation of ERK1 and ERK2 cascade, GO:0070372
- regulation of neuronal synaptic plasticity, GO:0048168
- lamellipodium assembly, GO:0030032
- podosome, GO:0002102
- filopodium assembly, GO:0046847
- B cell homeostasis, GO:0001782
- G-protein coupled receptor binding, GO:0001664
- Ras GTPase binding, GO:0017016
- adult locomotory behavior, GO:0008344
- positive regulation of dendritic spine morphogenesis, GO:0061003
- regulation of actin cytoskeleton organization, GO:0032956
- positive regulation of cytosolic calcium ion concentration, GO:0007204
- positive regulation of phosphatidylinositol 3-kinase activity, GO:0043552
- positive regulation of granulocyte macrophage colony-stimulating factor production, GO:0032725
- detection of mechanical stimulus, GO:0050982
- diacylglycerol binding, GO:0019992
- positive regulation of cell adhesion, GO:0045785
- ARF guanyl-nucleotide exchange factor activity, GO:0005086
- adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway, GO:0007193
- cAMP binding, GO:0030552
- cell chemotaxis, GO:0060326
- ATG1 /ULK1 kinase complex, GO:1990316
- cell-cell contact zone, GO:0044291
- regulation of protein localization to cell surface, GO:2000008
- Rac protein signal transduction, GO:0016601
- glial cell migration, GO:0008347
- myosin binding, GO:0017022
- positive regulation of T cell differentiation in thymus, GO:0033089
- receptor recycling, GO:0001881
- guanyl-nucleotide exchange factor complex, GO:0032045
- marginal zone B cell differentiation, GO:0002315
- MAP-kinase scaffold activity, GO:0005078
- inner ear morphogenesis, GO:0042472
- regulation of synaptic plasticity, GO:0048167
- positive regulation of protein localization to cell surface, GO:2000010
- positive regulation of blood coagulation, GO:0030194
- regulation of ARF protein signal transduction, GO:0032012
- sarcomere, GO:0030017
- lymphocyte homeostasis, GO:0002260
- adenosine receptor signaling pathway, GO:0001973
- protein localization to Golgi apparatus, GO:0034067
- regulation of TORC1 signaling, GO:1903432
- asymmetric synapse, GO:0032279
- substrate-dependent cell migration, GO:0006930
- positive regulation of fibroblast migration, GO:0010763
- insulin secretion, GO:0030073
- G-protein alpha-subunit binding, GO:0001965
- positive regulation of vasculogenesis, GO:2001214
- endosome to melanosome transport, GO:0035646
- positive regulation of growth hormone secretion, GO:0060124
- insulin-responsive compartment, GO:0032593
- type 1 angiotensin receptor binding, GO:0031702
- inositol 1, GO:0070679
- dendritic spine morphogenesis, GO:0060997
- hair cycle process, GO:0022405
- negative regulation of neural precursor cell proliferation, GO:2000178
- adenylate cyclase-activating G-protein coupled receptor signaling pathway, GO:0007189
- neuromuscular junction development, GO:0007528
- pericardium morphogenesis, GO:0003344
- cell projection assembly, GO:0030031
- G-protein coupled purinergic nucleotide receptor activity, GO:0045028
- G-protein coupled purinergic nucleotide receptor signaling pathway, GO:0035589