

endocytosis, GO:0006897

autophagy, GO:0006914
lamellipodium, GO:0030027
Rab GTPase binding, GO:0017137
small GTPase mediated signal transduction, GO:0007264
phosphatidylinositol binding, GO:0035091
actin cytoskeleton organization, GO:0030036
cytoplasmic vesicle membrane, GO:0030659
actin filament binding, GO:0051015
endosomal transport, GO:0016197
retrograde transport, GO:0042147
ruffle, GO:0001726
ruffle membrane, GO:0032587
early endosome membrane, GO:0031901
trans-Golgi network, GO:0005802
Wnt signaling pathway, GO:0060071
regulation of cell shape, GO:0008360
phagocytic vesicle membrane, GO:0030670
SH3 domain binding, GO:0017124
regulation of autophagy, GO:0010506
phosphatidylinositol biosynthetic process, GO:0006661
platelet activation, GO:0030168
recycling endosome, GO:0055037
ephrin receptor signaling pathway, GO:0048013
cell cortex, GO:0005938
protein transporter activity, GO:0008565
phagocytosis, GO:0006909
negative regulation of protein phosphorylation, GO:0001933
mitotic cytokinesis, GO:0000281
recycling endosome membrane, GO:0055038
positive regulation of protein phosphorylation, GO:0001934
axon guidance, GO:0007411
growth cone, GO:0030426
clathrin-coated pit, GO:0005905
synaptic vesicle, GO:0008021
caveola, GO:0005901
phosphatidylinositol phosphorylation, GO:0046854
receptor complex, GO:0043235
dendritic spine, GO:0043197
clathrin-coated vesicle, GO:0030136
activation of MAPK activity, GO:0000187
membrane fusion, GO:0061025
protein complex scaffold, GO:0032947
Rab guanyl-nucleotide exchange factor activity, GO:0017112
lipid transport, GO:0006869
extrinsic component of cytoplasmic side of plasma membrane, GO:0031234
transferrin transport, GO:0033572
cellular response to nerve growth factor stimulus, GO:1990090
regulation of protein phosphorylation, GO:0001932
phagocytic vesicle, GO:0045335
lysosome organization, GO:0007040
actin filament organization, GO:0007015
phospholipid transport, GO:0015914
epidermal growth factor receptor signaling pathway, GO:0007173
endosome to lysosome transport, GO:0008333
membrane coat, GO:0030117
positive regulation of protein binding, GO:0032092
cellular response to starvation, GO:0009267
phosphatidylinositol-3-phosphate biosynthetic process, GO:0036092
positive regulation of peptidyl-serine phosphorylation, GO:0033138
extrinsic component of membrane, GO:0019898
GTPase binding, GO:0051020
endosome organization, GO:0007032
positive regulation of protein catabolic process, GO:0045732
apical part of cell, GO:0045177
cholesterol metabolic process, GO:0008203
single organismal cell-cell adhesion, GO:0016337
Notch signaling pathway, GO:0007219
platelet-derived growth factor receptor signaling pathway, GO:0048008
viral entry into host cell, GO:0046718
peptide binding, GO:0042277
autophagosome assembly, GO:0000045
regulation of endocytosis, GO:0030100
protein localization to plasma membrane, GO:0072659
mitogen-activated protein kinase binding, GO:0051019
endocytic vesicle, GO:0030139
positive regulation of MAP kinase activity, GO:0043406
negative regulation of protein binding, GO:0032091
negative regulation of neuron apoptotic process, GO:0043524
phospholipid binding, GO:0005543
retromer complex, GO:0030904
protein localization to cilium, GO:0061512
chemotaxis, GO:0006935
vesicle organization, GO:0016050
regulation of cytokinesis, GO:0032465
negative regulation of neuron death, GO:1901215
phosphatidylinositol-4, GO:0005546
phosphatidylinositol 3-kinase signaling, GO:0014065
podosome, GO:0002102
cerebral cortex development, GO:0021987
virus receptor activity, GO:0001618
regulation of defense response to virus by virus, GO:0050690
scavenger receptor activity, GO:0005044
endocytic vesicle membrane, GO:0030666
vascular endothelial growth factor receptor signaling pathway, GO:0048010
protein localization to centrosome, GO:0071539
GTP-dependent protein binding, GO:0030742
disordered domain specific binding, GO:0097718
dendrite morphogenesis, GO:0048813
response to cytokine, GO:0034097
protein K63-linked deubiquitination, GO:0070536
iron ion homeostasis, GO:0055072
mitochondrial fission, GO:0000266
embryonic digit morphogenesis, GO:0042733
response to radiation, GO:0009314
Golgi to endosome transport, GO:0006895
positive regulation of mitotic cell cycle, GO:0045931
substrate adhesion-dependent cell spreading, GO:0034446
adherens junction, GO:0005912
protein K48-linked deubiquitination, GO:0071108
Fc-gamma receptor signaling pathway involved in phagocytosis, GO:0038096
1-phosphatidylinositol-3-kinase activity, GO:0016303
phagosome acidification, GO:0090383
peptide antigen binding, GO:0042605
Rac protein signal transduction, GO:0016601
positive regulation of autophagy, GO:0010508
Golgi to plasma membrane transport, GO:0006893
brush border, GO:0005903
SH2 domain binding, GO:0042169
steroid metabolic process, GO:0008202
regulation of actin cytoskeleton organization, GO:0032956
clathrin-coated endocytic vesicle membrane, GO:0030669
positive regulation of macroautophagy, GO:0016239
clathrin-dependent endocytosis, GO:0072583
phosphatidylinositol dephosphorylation, GO:0046856
cholesterol homeostasis, GO:0042632
positive regulation of peptidyl-tyrosine phosphorylation, GO:0050731
phosphatidylinositol-3, GO:0080025
synaptic vesicle membrane, GO:0030672
anterior/posterior pattern specification, GO:0009952
ephrin receptor binding, GO:0046875
positive regulation of substrate adhesion-dependent cell spreading, GO:1900026
forebrain development, GO:0030900
amyloid-beta binding, GO:0001540
regulation of G-protein coupled receptor protein signaling pathway, GO:0008277
regulation of nitric-oxide synthase activity, GO:0050999
neuron projection morphogenesis, GO:0048812
negative regulation of protein serine/threonine kinase activity, GO:0071901
presynapse, GO:0098793
endocytic recycling, GO:0032456
coronary vasculature development, GO:0060976
positive regulation of receptor-mediated endocytosis, GO:0048260
insulin receptor binding, GO:0005158
basal plasma membrane, GO:0009925
negative regulation of tumor necrosis factor production, GO:0032720
negative regulation of GTPase activity, GO:0034260
G-protein coupled receptor binding, GO:0001664
positive regulation of protein kinase B signaling, GO:0051897
regulation of neuronal synaptic plasticity, GO:0048168
endosomal vesicle fusion, GO:0034058
trans-Golgi network transport vesicle, GO:0030140
cholesterol binding, GO:0015485
proline-rich region binding, GO:0070064
post-Golgi vesicle-mediated transport, GO:0006892
protein localization, GO:0008104
regulation of canonical Wnt signaling pathway, GO:0060828
negative regulation of interleukin-6 production, GO:0032715
clathrin adaptor complex, GO:0030131
pre-autophagosomal structure, GO:0000407
neuromuscular junction, GO:0031594
phosphatidylinositol-3, GO:0043325
phosphatidic acid binding, GO:0070300
phagocytic cup, GO:0001891
early endosome to late endosome transport, GO:0045022
postsynapse, GO:0098794
phosphatidylinositol 3-kinase complex, GO:0005942
vasculogenesis, GO:0001570
protein targeting to lysosome, GO:0006622
pseudopodium, GO:0031143
presynaptic membrane, GO:0042734
Ral GTPase binding, GO:0017160
apoptotic cell clearance, GO:0043277
negative regulation of protein localization to cell surface, GO:2000009
cellular response to dopamine, GO:1903351
regulation of membrane potential, GO:0042391
phosphatidylinositol metabolic process, GO:0046488
phospholipid translocation, GO:0045332
positive regulation of membrane protein ectodomain proteolysis, GO:0051044
positive regulation of intrinsic apoptotic signaling pathway, GO:2001244
low-density lipoprotein receptor activity, GO:0005041
dynactin binding, GO:0034452
mannose binding, GO:0005537
peptidyl-tyrosine autophosphorylation, GO:0038083
heart looping, GO:0001947
central nervous system development, GO:0007417
response to peptide hormone, GO:0043434
receptor internalization, GO:0031623
epidermal growth factor receptor binding, GO:0005154
uropod, GO:0001931
negative regulation of release of cytochrome c from mitochondria, GO:0090201
receptor signaling complex scaffold activity, GO:0030159
clathrin adaptor activity, GO:0035615
regulation of neuron death, GO:1901214
low-density lipoprotein particle clearance, GO:0034383
extrinsic component of plasma membrane, GO:0019897
beta-catenin destruction complex disassembly, GO:1904886
protein targeting to membrane, GO:0006612
regulation of clathrin-dependent endocytosis, GO:2000369
positive regulation of early endosome to late endosome transport, GO:2000643
plasma membrane to endosome transport, GO:0048227
WW domain binding, GO:0050699
vesicle fusion with Golgi apparatus, GO:0048280
AP-2 adaptor complex binding, GO:0035612
positive regulation of viral process, GO:0048524
lung-associated mesenchyme development, GO:0060484
positive regulation of autophagosome assembly, GO:0000786
positive regulation of filopodium assembly, GO:0051491
limb development, GO:0060173
synapse assembly, GO:0007416
cellular response to amyloid-beta, GO:1904646
positive regulation of cell differentiation, GO:0045597
terminal bouton, GO:0043195
osteoclast differentiation, GO:0030316
negative regulation of neuron differentiation, GO:0045665
release of cytochrome c from mitochondria, GO:0001836
cholesterol transport, GO:0030301
detection of temperature stimulus involved in sensory perception of pain, GO:0050965
dopaminergic neuron differentiation, GO:0071542
low-density lipoprotein particle, GO:0034362
negative regulation of TOR signaling, GO:0032007
neural crest formation, GO:0014029
nerve growth factor signaling pathway, GO:0038180
Bcl-2 family protein complex, GO:00097136
hair follicle placode formation, GO:0060789
positive regulation of protein localization to cell surface, GO:2000010
cellular response to cholesterol, GO:0071397
synaptic vesicle maturation, GO:0016188
regulation of calcium ion transmembrane transport, GO:1903169
Arp2/3 complex binding, GO:0071933
positive regulation of receptor internalization, GO:0002092
regulation of long-term neuronal synaptic plasticity, GO:0048169
embryonic morphogenesis, GO:0048598
positive regulation of protein metabolic process, GO:0051247
positive regulation of programmed cell death, GO:0043068
deoxyribonuclease activity, GO:0004536
neutrophil chemotaxis, GO:0030593
apolipoprotein binding, GO:0034185
protein localization to Golgi apparatus, GO:0034067
negative regulation of phosphatidylinositol 3-kinase signaling, GO:0014067
clathrin coat assembly, GO:0048268
integral component of synaptic vesicle membrane, GO:0030285
positive regulation of osteoblast proliferation, GO:0033690
phosphatidylinositol 3-kinase activity, GO:0035004
thioesterase binding, GO:0031996
positive regulation of triglyceride biosynthetic process, GO:0010867
synaptic vesicle endocytosis, GO:0048488
synaptic membrane, GO:0097060
nitric-oxide synthase binding, GO:0050998
cytokine production, GO:0001816
dendrite extension, GO:0097484
peroxisome fission, GO:0016559
protein localization to endosome, GO:0036010
cellular protein localization, GO:0034613
striated muscle cell differentiation, GO:0051146
filopodium assembly, GO:0046847
diacylglycerol binding, GO:0019992
positive regulation of T cell differentiation in thymus, GO:0033089
clathrin complex, GO:0071439
inositol phosphate dephosphorylation, GO:0046855
adherens junction, GO:0034333
profilin binding, GO:0005522
ventricular septum development, GO:0003281
dynamamin family protein polymerization involved in mitochondrial fission, GO:0003374
1-phosphatidylinositol-4-phosphate 3-kinase activity, GO:0035005
phospholipid-translocating ATPase activity, GO:0004012
positive regulation of SMAD protein import into nucleus, GO:0060391
dorsal/ventral neural tube patterning, GO:0021904
phosphatidylinositol-3, GO:0043813
tubular endosome, GO:0097422
establishment of Golgi localization, GO:0051683
ruffle assembly, GO:0097178
phosphatidylinositol-4, GO:0004439
SMAD protein import into nucleus, GO:0007184
mitochondrion localization, GO:0051646
response to isolation stress, GO:0035900
hair follicle morphogenesis, GO:0031069
positive regulation of mitochondrial fission, GO:0090141
creatine metabolic process, GO:0006600
regulation of insulin receptor signaling pathway, GO:0046626
response to lead ion, GO:0010288
guanyl-nucleotide exchange factor complex, GO:0032045
low-density lipoprotein particle binding, GO:0030169
negative regulation of epidermal growth factor-activated receptor activity, GO:0007175
positive regulation of cytosolic calcium ion concentration, GO:0007204
aorta morphogenesis, GO:0035909
insulin-like growth factor receptor signaling pathway, GO:0048009
limb bud formation, GO:0060174
low-density lipoprotein particle receptor catabolic process, GO:0032802
autolysosome, GO:0044754
citrate metabolic process, GO:0006101
secretory granule, GO:0030141
regulation of synaptic vesicle exocytosis, GO:2000300
phosphatidylinositol-3, GO:0052629
glycoprotein metabolic process, GO:0009100
regulation of axon extension, GO:0030516
regulation of microtubule polymerization, GO:0031113
regulation of protein transport, GO:0051223
negative regulation of Wnt signaling pathway, GO:0030178
Bergmann glial cell differentiation, GO:0060020
clathrin coat of coated pit, GO:0030132
positive regulation of peptidase activity, GO:0010952
dorsal/ventral pattern formation, GO:0009953
regulation of multicellular organism growth, GO:0040014
digestive system development, GO:0055123
NAD+ kinase activity, GO:0003951
cell fate specification, GO:0001708
embryonic pattern specification, GO:0009880
transcytosis, GO:0045056
positive regulation of acute inflammatory response, GO:0002675
mast cell degranulation, GO:0043303
regulation of dendritic spine morphogenesis, GO:0061001
positive regulation of alpha-beta T cell differentiation, GO:0046638
early endosome to Golgi transport, GO:0034498
inositol-1, GO:0052659
negative regulation of potassium ion transmembrane transport, GO:1901380
positive regulation of smooth muscle cell apoptotic process, GO:0034393
negative regulation of protein localization to plasma membrane, GO:1903077
positive regulation of cholesterol storage, GO:0010886
phagosome maturation, GO:0090382
negative regulation of ubiquitin-protein transferase activity, GO:0051444
lipid phosphorylation, GO:0046834
regulation of cholesterol metabolic process, GO:0090181
clathrin-coated vesicle membrane, GO:0030665
postsynaptic membrane assembly, GO:0097104
intracellular distribution of mitochondria, GO:0048312
ADP-ribosylation factor binding, GO:0030306
transferrin receptor binding, GO:1990459
ATG1/ULK1 kinase complex, GO:1990316
SCAR complex, GO:0031209
positive regulation of bone resorption, GO:0045780
positive regulation of pseudopodium assembly, GO:0031274