autophagy, GO:0006914 cytoplasmic vesicle membrane, GO:0030659 recycling endosome, GO:0055037 trans-Golgi network, GO:0005802 Wnt signaling pathway, GO:0060071 phosphatidylinositol biosynthetic process, GO:0006661 phagocytic vesicle membrane, GO:0030670 early endosome membrane, GO:0031901 endosomal transport, GO:0016197 phosphatidylinositol binding, GO:0035091 positive regulation of protein phosphorylation, GO:0001934 lipid transport, GO:0006869 negative regulation of protein phosphorylation, GO:0001933 GDP binding, GO:0019003 phagocytic vesicle, GO:0045335 synaptic vesicle, GO:0008021 axon guidance, GO:0007411 regulation of autophagy, GO:0010506 membrane coat, GO:0030117 phagocytosis, GO:0006909 clathrin-coated pit, GO:0005905 GTPase binding, GO:0051020 receptor complex, GO:0043235 phosphatidylinositol phosphorylation, GO:0046854 phosphatidylinositol-4, GO:0005546 regulation of protein phosphorylation, GO:0001932 cholesterol metabolic process, GO:0008203 membrane fusion, GO:0061025 protein localization to plasma membrane, GO:0072659 clathrin-coated vesicle, GO:0030136 chemotaxis, GO:0006935 viral entry into host cell, GO:0046718 autophagosome assembly, GO:0000045 positive regulation of protein binding, GO:0032092 endocytic recycling, GO:0032456 virus receptor activity, GO:0001618 steroid metabolic process, GO:0008202 positive regulation of autophagy, GO:0010508 phosphoprotein binding, GO:0051219 transferrin transport, GO:0033572 phospholipid transport, GO:0015914 positive regulation of peptidyl-tyrosine phosphorylation, GO:0050731 SH2 domain binding, GO:0042169 epidermal growth factor receptor signaling pathway, GO:0007173 phosphatidylinositol-mediated signaling, GO:0048015 amyloid-beta binding, GO:0001540 adherens junction, GO:0005912 scavenger receptor activity, GO:0005044 retromer complex, GO:0030904 endosome to lysosome transport, GO:0008333 neuromuscular junction, GO:0031594 peptide binding, GO:0042277 caveola, GO:0005901 protein K48-linked deubiquitination, GO:0071108 extrinsic component of membrane, GO:0019898 cellular response to nerve growth factor stimulus, GO:1990090 synaptic vesicle membrane, GO:0030672 presynaptic membrane, GO:0042734 presynapse, GO:0098793 vesicle organization, GO:0016050 clathrin-dependent endocytosis, GO:0072583 protein localization, GO:0008104 phosphatidylinositol-3-phosphate biosynthetic process, GO:0036092 clathrin-coated vesicle membrane, GO:0030665 canonical Wnt signaling pathway, GO:0060070 regulation of endocytosis, GO:0030100 synapse organization, GO:0050808 forebrain development, GO:0030900 receptor internalization, GO:0031623 phosphatidylinositol 3-kinase signaling, GO:0014065 toxin transport, GO:1901998 osteoclast differentiation, GO:0030316 synapse assembly, GO:0007416 phosphatidylinositol-3-phosphate binding, GO:0032266 central nervous system development, GO:0007417 embryonic digit morphogenesis, GO:0042733 postsynapse, GO:0098794 single organismal cell-cell adhesion, GO:0016337 beta-catenin destruction complex disassembly, GO:1904886 iron ion homeostasis, GO:0055072 early endosome to late endosome transport, GO:0045022 ephrin receptor binding, GO:0046875 brush border, GO:0005903 negative regulation of interleukin-6 production, GO:0032715 terminal bouton, GO:0043195 phagocytic cup, GO:0001891 Golgi to endosome transport, GO:0006895 proline-rich region binding, GO:0070064 cellular response to low-density lipoprotein particle stimulus, GO:0071404 negative regulation of neuron death, GO:1901215 apoptotic cell clearance, GO:0043277 protein targeting to membrane, GO:0006612 clathrin-coated endocytic vesicle membrane, GO:0030669 odontogenesis of dentin-containing tooth, GO:0042475 positive regulation of macroautophagy, GO:0016239 positive regulation of neuron death, GO:1901216 Golgi to plasma membrane transport, GO:0006893 pre-autophagosomal structure, GO:0000407 receptor signaling complex scaffold activity, GO:0030159 mitogen-activated protein kinase binding, GO:0051019 insulin receptor binding, GO:0005158 leukocyte cell-cell adhesion, GO:0007159 cholesterol homeostasis, GO:0042632 regulation of long-term neuronal synaptic plasticity, GO:0048169 1-phosphatidylinositol-3-kinase activity, GO:0016303 negative regulation of GTPase activity, GO:0034260 positive regulation of muscle cell differentiation, GO:0051149 phagosome acidification, GO:0090383 cellular response to starvation, GO:0009267 cholesterol binding, GO:0015485 synaptic vesicle transport, GO:0048489 viral release from host cell, GO:0019076 protein targeting to lysosome, GO:0006622 positive regulation of mesenchymal cell proliferation, GO:0002053 positive regulation of intrinsic apoptotic signaling pathway, GO:2001244 mitochondrial fission, GO:0000266 disordered domain specific binding, GO:0097718 basal plasma membrane, GO:0009925 phosphatidylinositol dephosphorylation, GO:0046856 clathrin binding, GO:0030276 modulation of synaptic transmission, GO:0050804 clathrin adaptor complex, GO:0030131 trans-Golgi network transport vesicle, GO:0030140 phospholipid translocation, GO:0045332 low-density lipoprotein particle clearance, GO:0034383 regulation of neuron death, GO:1901214 regulation of multicellular organism growth, GO:0040014 olfactory bulb development, GO:0021772 protein K63-linked deubiquitination, GO:0070536 positive regulation of filopodium assembly, GO:0051491 positive regulation of protein kinase B signaling, GO:0051897 phospholipid-translocating ATPase activity, GO:0004012 phosphatidylinositol 3-kinase complex, GO:0005942 dendrite cytoplasm, GO:0032839 low-density lipoprotein receptor activity, GO:0005041 negative regulation of Wnt signaling pathway, GO:0030178 endosomal vesicle fusion, GO:0034058 protein localization to cilium, GO:0061512 clathrin adaptor activity, GO:0035615 endocytosis, GO:0006897 brush border membrane, GO:0031526 Wnt-protein binding, GO:0017147 phosphatidylinositol metabolic process, GO:0046488 autolysosome, GO:0044754 viral RNA genome replication, GO:0039694 positive regulation of cell differentiation, GO:0045597 phosphatidylinositol 3-kinase complex, GO:0035032 coronary vasculature development, GO:0060976 ventricular septum development, GO:0003281 anterior/posterior pattern specification, GO:0009952 phosphatidylinositol-3, GO:0052629 response to lead ion, GO:0010288 endolysosome membrane, GO:0036020 insulin-like growth factor receptor signaling pathway, GO:0048009 pseudopodium, GO:0031143 ciliary membrane, GO:0060170 postsynaptic membrane assembly, GO:0097104 Bergmann glial cell differentiation, GO:0060020 actin filament-based movement, GO:0030048 negative regulation of macroautophagy, GO:0016242 limb development, GO:0060173 inositol phosphate dephosphorylation, GO:0046855 myosin complex, GO:0016459 modulation by virus of host morphology or physiology, GO:0019048 negative regulation of protein localization to plasma membrane, GO:1903077 positive regulation of autophagosome assembly, GO:2000786 cholesterol transport, GO:0030301 oxaloacetate metabolic process, GO:0006107 insulin receptor substrate binding, GO:0043560 positive regulation of membrane protein ectodomain proteolysis, GO:0051044 protein kinase C-activating G-protein coupled receptor signaling pathway, GO:0007205 Notch binding, GO:0005112 inositol-1, GO:0052659 succinate metabolic process, GO:0006105 negative regulation of release of cytochrome c from mitochondria, GO:0090201 phosphatidylinositol-4, GO:0004439 phosphoric ester hydrolase activity, GO:0042578 plasma membrane tubulation, GO:0097320 membrane invagination, GO:0010324 macromitophagy, GO:0000423 positive regulation of receptor-mediated endocytosis, GO:0048260 transition metal ion binding, GO:0046914 insulin-like growth factor receptor binding, GO:0005159 negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage, GO:1902230 peptidase activator activity, GO:0016504 cellular response to cholesterol, GO:0071397 angiogenesis involved in wound healing, GO:0060055 low-density lipoprotein particle receptor binding, GO:0050750 positive regulation of dendrite development, GO:1900006 phosphatidylinositol-3, GO:0043325 regulation of cellular senescence, GO:2000772 positive regulation of endocytosis, GO:0045807 adherens junction assembly, GO:0034333 positive regulation of feeding behavior, GO:2000253 Golgi to lysosome transport, GO:0090160 protein localization to endosome, GO:0036010positive regulation of protein tyrosine kinase activity, GO:0061098 extrinsic component of plasma membrane, GO:0019897 striated muscle cell differentiation, GO:0051146 regulation of synaptic transmission, GO:0051966 vasculature development, GO:0001944 neural tube formation, GO:0001841 positive regulation of skeletal muscle tissue development, GO:0048643 regulation of membrane potential, GO:0042391 Wnt signalosome, GO:1990909 positive regulation of protein metabolic process, GO:0051247 citrate metabolic process, GO:0006101 1-phosphatidylinositol binding, GO:0005545 regulation of mitochondrial membrane permeability, GO:0046902 diacylglycerol kinase activity, GO:0004143 transport vesicle membrane, GO:0030658 release of cytochrome c from mitochondria, GO:0001836 Wnt-activated receptor activity, GO:0042813 regulation of protein secretion, GO:0050708 guanyl nucleotide binding, GO:0019001 response to mitochondrial depolarisation, GO:0098780 establishment of Golgi localization, GO:0051683 growth hormone receptor signaling pathway, GO:0060396 adult walking behavior, GO:0007628 cellular response to amyloid-beta, GO:1904646 cellular lipid metabolic process, GO:0044255 acetylcholine receptor activity, GO:0015464 regulation of lamellipodium assembly, GO:0010591 dendritic cell chemotaxis, GO:0002407 regulation of dendritic spine morphogenesis, GO:0061001 type I transforming growth factor beta receptor binding, GO:0034713 negative regulation of protein processing, GO:0010955 positive regulation of SMAD protein import into nucleus, GO:0060391 glucose import, GO:0046323 hair follicle placode formation, GO:0060789 epithelial cell proliferation involved in salivary gland morphogenesis, GO:0060664 phosphatidylinositol 3-kinase activity, GO:0035004 varicosity, GO:0043196 animal organ development, GO:0048513 dorsal/ventral neural tube patterning, GO:0021904 osteoblast development, GO:0002076 neuron projection terminus, GO:0044306 keratinocyte development, GO:0003334 deoxyribonuclease activity, GO:0004536 integral component of synaptic vesicle membrane, GO:0030285 calcium ion regulated exocytosis, GO:0017156 mitogen-activated protein kinase kinase binding, GO:0031434 regulation of insulin receptor signaling pathway, GO:0046626 low-density lipoprotein particle, GO:0034362 virion binding, GO:0046790 diacylglycerol metabolic process, GO:0046339 positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway, GO:1901030 glycoprotein metabolic process, GO:0009100 clathrin coat assembly, GO:0048268 phosphatidylinositol-3, GO:0043813 branching involved in prostate gland morphogenesis, GO:0060442 cellular response to lipid, GO:0071396 SMAD protein import into nucleus, GO:0007184 synaptic vesicle maturation, GO:0016188 positive regulation of early endosome to late endosome transport, GO:2000643 clathrin coat of coated pit, GO:0030132 response to isolation stress, GO:0035900 regulation of calcium ion transmembrane transport, GO:1903169 regulation of cell-matrix adhesion, GO:0001952 phosphatidylinositol-3, GO:0080025 early endosome to Golgi transport, GO:0034498 neuroepithelial cell differentiation, GO:0060563 neurotrophin TRK receptor signaling pathway, GO:0048011 protein localization to pre-autophagosomal structure, GO:0034497 sterol transporter activity, GO:0015248 regulation of smooth muscle cell migration, GO:0014910 cartilage development involved in endochondral bone morphogenesis, GO:0060351 negative regulation of mitochondrial fusion, GO:0010637 positive regulation of striated muscle cell differentiation, GO:0051155 VCB complex, GO:0030891 Bcl-2 family protein complex, GO:0097136 negative regulation of protein localization to cell surface, GO:2000009 inner ear development, GO:0048839 regulation of blood coagulation, GO:0030193 SCAR complex, GO:0031209 behavioral response to ethanol, GO:0048149 positive regulation of pseudopodium assembly, GO:0031274 suckling behavior, GO:0001967 regulation of cell adhesion mediated by integrin, GO:0033628