

autophagy, GO:0006914

endocytosis, GO:0006897
mitochondrial outer membrane, GO:0005741
late endosome, GO:0005770
recycling endosome, GO:0055037
trans-Golgi network, GO:0005802
kinase binding, GO:0019900
ubiquitin binding, GO:0043130
recycling endosome membrane, GO:0055038
autophagosome, GO:0005776
lysosomal lumen, GO:0043202
axoneme, GO:0005930
positive regulation of protein targeting to mitochondrion, GO:1903955
phagocytic vesicle, GO:0045335
phagocytic vesicle membrane, GO:0030670
cellular response to hypoxia, GO:0071456
mitophagy, GO:0000422
beta-catenin binding, GO:0008013
cysteine-type endopeptidase activity, GO:0004197
core promoter binding, GO:0001047
negative regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043124
negative regulation of cell death, GO:0060548
endosome to lysosome transport, GO:0008333
regulation of protein localization, GO:0032880
protein binding, GO:0030674
regulation of mitochondrial membrane potential, GO:0051881
autophagosome assembly, GO:0000045
cellular response to glucose starvation, GO:0042149
extrinsic component of membrane, GO:0019898
presynapse, GO:0098793
integral component of mitochondrial outer membrane, GO:0031307
repressing transcription factor binding, GO:0070491
positive regulation of release of cytochrome c from mitochondria, GO:0090200
positive regulation of mitochondrial fission, GO:0090141
negative regulation of fat cell differentiation, GO:0045599
cellular calcium ion homeostasis, GO:0006874
RNA polymerase II transcription factor binding, GO:0001085
negative regulation of apoptotic signaling pathway, GO:2001234
protein localization, GO:0008104
regulation of androgen receptor signaling pathway, GO:0060765
regulation of mitochondrion organization, GO:0010821
regulation of autophagosome assembly, GO:2000785
phagosome acidification, GO:0090383
negative regulation of fibroblast proliferation, GO:0048147
K63-linked polyubiquitin binding, GO:0070530
endosomal vesicle fusion, GO:0034058
early endosome to late endosome transport, GO:0045022
endoplasmic reticulum calcium ion homeostasis, GO:0032469
intrinsic apoptotic signaling pathway by p53 class mediator, GO:0072332
social behavior, GO:0035176
receptor catabolic process, GO:0032801
protein targeting to membrane, GO:0006612
vacuole, GO:0005773
autophagosome membrane, GO:0000421
cytokine production, GO:0001816
protein lipidation, GO:0006497
low-density lipoprotein particle clearance, GO:0034383
positive regulation of intrinsic apoptotic signaling pathway, GO:2001244
sulfuric ester hydrolase activity, GO:0008484
positive regulation of autophagosome assembly, GO:2000786
nucleus organization, GO:0006997
phosphatidylinositol-3-phosphate binding, GO:0032266
histone H3 deacetylation, GO:0070932
regulation of vesicle fusion, GO:0031338
aspartic-type endopeptidase activity, GO:0004190
histone acetyltransferase binding, GO:0035035
synapse organization, GO:0050808
phosphatidylinositol-3, GO:0080025
clathrin-dependent endocytosis, GO:0072583
protein targeting to Golgi, GO:0000042
adult locomotory behavior, GO:0008344
nucleophagy, GO:0044804
positive regulation of interferon-alpha secretion, GO:1902741
AP-3 adaptor complex, GO:0030123
positive regulation of interleukin-6 secretion, GO:2000778
chronic inflammatory response, GO:0002544
cellular response to misfolded protein, GO:0071218
positive regulation of immunoglobulin secretion, GO:0051024
cell separation after cytokinesis, GO:0000920
tissue homeostasis, GO:0001894
viral budding via host ESCRT complex, GO:0039702
antioxidant activity, GO:0016209
cellular response to ethanol, GO:0071361
phosphatidylinositol 3-kinase complex, GO:0005942
polysaccharide binding, GO:0030247
cell junction assembly, GO:0034329
regulation of neuron apoptotic process, GO:0043523
regulation of exocytosis, GO:0017157
positive regulation of skeletal muscle tissue development, GO:0048643
1-phosphatidylinositol-4-phosphate 3-kinase activity, GO:0035005
C-terminal protein lipidation, GO:0006501
vesicle transport along actin filament, GO:0030050
response to growth factor, GO:0070848
fatty acid catabolic process, GO:0009062
mitochondrial calcium ion homeostasis, GO:0051560
response to lead ion, GO:0010288
negative regulation of T cell activation, GO:0050868
positive regulation of mitophagy in response to mitochondrial depolarization, GO:1904925
positive regulation of interferon-beta secretion, GO:0035549
positive regulation of wound healing, GO:0090303
mesodermal cell differentiation, GO:0048333
enamel mineralization, GO:0070166
NAD-dependent histone deacetylase activity (H3-K14 specific), GO:0032041
vacuolar transport, GO:0007034
membrane protein proteolysis, GO:0033619
phagosome maturation, GO:0090382
autophagic cell death, GO:0048102
protein localization to endosome, GO:0036010
fatty acid oxidation, GO:0019395
cellular response to nitrogen starvation, GO:0006995
platelet dense granule membrane, GO:0031088
epithelial cell maturation, GO:0002070
digestion, GO:0007586
positive regulation of viral release from host cell, GO:1902188
positive regulation of protein oligomerization, GO:0032461
positive regulation of monocyte chemotaxis, GO:0090026
histone H4 deacetylation, GO:0070933
positive regulation of receptor biosynthetic process, GO:0010870
arylsulfatase activity, GO:0004065
regulation of myeloid cell differentiation, GO:0045637
regulation of oxidative phosphorylation, GO:0002082
negative regulation of p38MAPK cascade, GO:1903753
protein tag, GO:0031386
peroxiredoxin activity, GO:0051920
positive regulation of execution phase of apoptosis, GO:1900119
synaptic vesicle fusion to presynaptic active zone membrane, GO:0031629
negative regulation of myotube differentiation, GO:0010832
melanosome membrane, GO:0033162
RAGE receptor binding, GO:0050786
leukocyte migration involved in inflammatory response, GO:0002523
viral budding, GO:0046755
mitochondrial outer membrane translocase complex, GO:0005742
positive regulation of histone deacetylation, GO:0031065
endolysosome membrane, GO:0036020