

autophagy, GO:0006914

- late endosome, GO:0005770
- mitochondrial outer membrane, GO:0005741
- ubiquitin-dependent ERAD pathway, GO:0030433
- regulation of macroautophagy, GO:0016241
- late endosome membrane, GO:0031902
- Rab GTPase binding, GO:0017137
- endomembrane system, GO:0012505
- ubiquitin binding, GO:0043130
- Golgi organization, GO:0007030
- recycling endosome, GO:0055037
- azurophil granule membrane, GO:0035577
- response to endoplasmic reticulum stress, GO:0034976
- retrograde transport, GO:0042147
- negative regulation of protein phosphorylation, GO:0001933
- regulation of autophagy, GO:0010506
- phagocytic vesicle, GO:0045335
- positive regulation of protein ubiquitination, GO:0031398
- trans-Golgi network membrane, GO:0032588
- autophagosome, GO:0005776
- autophagosome assembly, GO:0000045
- GTPase binding, GO:0051020
- regulation of mitochondrial membrane potential, GO:0051881
- recycling endosome membrane, GO:0055038
- lipid particle, GO:0005811
- positive regulation of protein catabolic process, GO:0045732
- axoneme, GO:0005930
- cellular response to amino acid starvation, GO:0034198
- clathrin-coated vesicle, GO:0030136
- syntaxin binding, GO:0019905
- membrane fusion, GO:0061025
- negative regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032435
- mitophagy, GO:0000422
- positive regulation of autophagy, GO:0010508
- endocytic recycling, GO:0032456
- autophagosome maturation, GO:0097352
- autophagosome membrane, GO:0000421
- negative regulation of autophagy, GO:0010507
- ubiquitin conjugating enzyme binding, GO:0031624
- positive regulation of TOR signaling, GO:0032008
- low-density lipoprotein particle clearance, GO:0034383
- endosome to lysosome transport, GO:0008333
- endosome organization, GO:0007032
- cellular calcium ion homeostasis, GO:0006874
- lysosome organization, GO:0007040
- positive regulation of intrinsic apoptotic signaling pathway, GO:2001244
- negative regulation of neuron death, GO:1901215
- regulation of vesicle fusion, GO:0031338
- endoplasmic reticulum organization, GO:0007029
- intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress, GO:0070059
- extrinsic component of membrane, GO:0019898
- intracellular transport, GO:0046907
- regulation of inflammatory response, GO:0050727
- cellular response to starvation, GO:0009267
- histone H3 deacetylation, GO:0070932
- neuron development, GO:0048666
- nucleophagy, GO:0044804
- regulation of autophagosome assembly, GO:2000785
- lysosome localization, GO:0032418
- intra-Golgi vesicle-mediated transport, GO:0006891
- regulation of cytokinesis, GO:0032465
- pre-autophagosomal structure, GO:0000407
- intrinsic apoptotic signaling pathway by p53 class mediator, GO:0072332
- sterol biosynthetic process, GO:0016126
- protein targeting to Golgi, GO:0000042
- ER-associated misfolded protein catabolic process, GO:0071712
- vesicle docking involved in exocytosis, GO:0006904
- protein phosphatase 2A binding, GO:0051721
- positive regulation of release of cytochrome c from mitochondria, GO:0090200
- positive regulation of macroautophagy, GO:0016239
- regulation of exocytosis, GO:0017157
- copper ion binding, GO:0005507
- regulation of centrosome duplication, GO:0010824
- regulation of mitochondrion organization, GO:0010821
- early endosome to late endosome transport, GO:0045022
- phosphatidylinositol-3-phosphate binding, GO:0032266
- positive regulation of reactive oxygen species metabolic process, GO:2000379
- receptor tyrosine kinase binding, GO:0030971
- negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway, GO:1902236
- phosphatidylinositol-3-phosphate biosynthetic process, GO:0036092
- positive regulation of interleukin-6 secretion, GO:2000778
- cytokine production, GO:0001816
- K63-linked polyubiquitin binding, GO:0070530
- histone acetyltransferase binding, GO:0035035
- pre-autophagosomal structure membrane, GO:0034045
- ER overload response, GO:0006983
- endolysosome membrane, GO:0036020
- regulation of cilium assembly, GO:1902017
- negative thymic T cell selection, GO:0045060
- smooth endoplasmic reticulum, GO:0005790
- Tat protein binding, GO:0030957
- regulation of gene expression, GO:0040029
- positive regulation of mitochondrial fission, GO:0090141
- cargo loading into COPII-coated vesicle, GO:0090110
- phagosome acidification, GO:0090383
- cellular protein catabolic process, GO:0044257
- clathrin coat of coated pit, GO:0030132
- rough endoplasmic reticulum, GO:0005791
- negative regulation of reactive oxygen species metabolic process, GO:2000378
- negative regulation of fat cell differentiation, GO:0045599
- Golgi-associated vesicle, GO:0005798
- endoplasmic reticulum calcium ion homeostasis, GO:0032469
- HOPS complex, GO:0030897
- neutrophil chemotaxis, GO:0030593
- negative regulation of apoptotic signaling pathway, GO:2001234
- paranode region of axon, GO:0033270
- phosphatidylinositol 3-kinase signaling, GO:0014065
- SAGA complex, GO:0000124
- regulation of protein localization to plasma membrane, GO:1903076
- phosphatidylinositol-3, GO:0080025
- integral component of mitochondrial outer membrane, GO:0031307
- digestion, GO:0007586
- positive thymic T cell selection, GO:0045059
- regulation of synaptic transmission, GO:0051966
- co-receptor binding, GO:0039706
- neural retina development, GO:0003407
- cardiovascular system development, GO:0072358
- synaptic vesicle priming, GO:0016082
- ATF6-mediated unfolded protein response, GO:0036500
- ESCRT III complex, GO:0000815
- CARD domain binding, GO:0050700
- 1-phosphatidylinositol-3-kinase activity, GO:0016303
- endosomal vesicle fusion, GO:0034058
- establishment of protein localization to membrane, GO:0090150
- bile acid metabolic process, GO:0008206
- regulated exocytosis, GO:0045055
- regulation of energy homeostasis, GO:2000505
- L-glutamate transport, GO:0015813
- adult locomotory behavior, GO:0008344
- vacuolar transport, GO:0007034
- protein deglycosylation, GO:0006517