

late endosome, GO:0005770

- late endosome membrane, GO:0031902
- ubiquitin binding, GO:0043130
- azurophil granule membrane, GO:0035577
- tertiary granule membrane, GO:0070821
- phosphatase binding, GO:0019902
- lysosomal lumen, GO:0043202
- positive regulation of neuron projection development, GO:0010976
- autophagosome maturation, GO:0097352
- phosphotyrosine residue binding, GO:0001784
- autophagosome membrane, GO:0000421
- ATP hydrolysis coupled cation transmembrane transport, GO:0099132
- response to retinoic acid, GO:0032526
- positive regulation of interferon-gamma production, GO:0032729
- blood vessel development, GO:0001568
- lipopolysaccharide-mediated signaling pathway, GO:0031663
- T cell activation, GO:0042110
- zinc II ion transmembrane transport, GO:0071577
- cation transport, GO:0006812
- metal ion transport, GO:0030001
- regulation of sequence-specific DNA binding transcription factor activity, GO:0051090
- response to zinc ion, GO:0010043
- type I interferon signaling pathway, GO:0060337
- lysosome localization, GO:0032418
- myosin V binding, GO:0031489
- regulation of stress-activated MAPK cascade, GO:0032872
- zinc II ion transport, GO:0006829
- vacuolar membrane, GO:0005774
- vacuolar transport, GO:0007034
- receptor catabolic process, GO:0032801
- renal system process, GO:0003014
- collagen fibril organization, GO:0030199
- regulation of centrosome duplication, GO:0010824
- retrograde transport, GO:1990126
- zinc ion transmembrane transporter activity, GO:0005385
- cellular response to reactive oxygen species, GO:0034614
- negative regulation of epidermal growth factor-activated receptor activity, GO:0007175
- AP-type membrane coat adaptor complex, GO:0030119
- ESCRT III complex, GO:0000815
- melanocyte differentiation, GO:0030318
- regulation of mast cell degranulation, GO:0043304
- positive regulation of macrophage cytokine production, GO:0060907
- toll-like receptor 9 signaling pathway, GO:0034162
- MAP kinase kinase activity, GO:0004708
- negative regulation of ERBB signaling pathway, GO:1901185
- multivesicular body, GO:0005771
- proteasome assembly, GO:0043248
- regulation of ossification, GO:0030278
- potassium:proton antiporter activity, GO:0015386
- cytokine binding, GO:0019955
- solute:proton antiporter activity, GO:0015299
- endosome lumen, GO:0031904
- BLOC-1 complex, GO:0031083
- mRNA transcription from RNA polymerase II promoter, GO:0042789
- regulated exocytosis, GO:0045055
- calcium-transporting ATPase activity, GO:0005388
- Golgi-associated vesicle membrane, GO:0030660
- negative regulation of cell motility, GO:2000146
- sodium:proton antiporter activity, GO:0015385
- positive regulation of T cell mediated cytotoxicity, GO:0001916
- AP-3 adaptor complex, GO:0030123
- cellular response to platelet-derived growth factor stimulus, GO:0036120
- regulation of sequestering of zinc ion, GO:0061088
- cation transmembrane transport, GO:0098655
- detection of temperature stimulus involved in sensory perception of pain, GO:0050965
- exocyst, GO:0000145
- megakaryocyte development, GO:0035855
- positive regulation of calcium ion transport, GO:0051928
- antimicrobial humoral response, GO:0019730
- regulation of chemotaxis, GO:0050920
- chitin binding, GO:0008061
- platelet dense granule organization, GO:0060155
- vacuole, GO:0005773
- thyroid gland development, GO:0030878
- reverse cholesterol transport, GO:0043691
- protein serine/threonine kinase activator activity, GO:0043539
- regulation of cytoskeleton organization, GO:0051493
- positive regulation of interleukin-6 secretion, GO:2000778
- membrane protein ectodomain proteolysis, GO:0006509
- cellular zinc ion homeostasis, GO:0006882
- cation transmembrane transporter activity, GO:0008324
- insulin-like growth factor II binding, GO:0031995
- sympathetic nervous system development, GO:0048485
- high-density lipoprotein particle remodeling, GO:0034375
- endolysosome lumen, GO:0036021
- pyramidal neuron development, GO:0021860
- positive regulation of T-helper 1 type immune response, GO:0002827
- negative regulation of retrograde protein transport, GO:1904153
- positive regulation of collagen biosynthetic process, GO:0032967
- regulation of SNARE complex assembly, GO:0035542
- regulation of endopeptidase activity, GO:0052548
- MAP kinase activity, GO:0004707
- insulin-like growth factor binding, GO:0005520