

late endosome, GO:0005770

- late endosome membrane, GO:0031902
- lysosomal lumen, GO:0043202
- azurophil granule membrane, GO:0035577
- recycling endosome membrane, GO:0055038
- autophagosome, GO:0005776
- tertiary granule membrane, GO:0070821
- PDZ domain binding, GO:0030165
- phosphatase binding, GO:0019902
- protein processing, GO:0016485
- mitophagy, GO:0000422
- intracellular transport, GO:0046907
- zinc ion transmembrane transporter activity, GO:0005385
- retrograde transport, GO:1990126
- thyroid gland development, GO:0030878
- regulation of centrosome duplication, GO:0010824
- receptor catabolic process, GO:0032801
- cation transport, GO:0006812
- zinc II ion transport, GO:0006829
- autophagosome membrane, GO:0000421
- blood vessel development, GO:0001568
- cation transmembrane transporter activity, GO:0008324
- zinc II ion transmembrane transport, GO:0071577
- ESCRT III complex, GO:0000815
- ATP hydrolysis coupled cation transmembrane transport, GO:0099132
- lysosome localization, GO:0032418
- cellular copper ion homeostasis, GO:0006878
- membrane protein ectodomain proteolysis, GO:0006509
- cellular response to antibiotic, GO:0071236
- vacuole, GO:0005773
- AP-3 adaptor complex, GO:0030123
- copper ion transport, GO:0006825
- cellular response to epinephrine stimulus, GO:0071872
- ATP transport, GO:0015867
- face development, GO:0060324
- HOPS complex, GO:0030897
- vacuolar membrane, GO:0005774
- specific granule, GO:0042581
- myosin V binding, GO:0031489
- exocyst, GO:0000145
- cellular zinc ion homeostasis, GO:0006882
- regulation of sequestering of zinc ion, GO:0061088
- ESCRT I complex, GO:0000813
- collagen fibril organization, GO:0030199
- protein serine/threonine kinase activator activity, GO:0043539
- response to pH, GO:0009268
- regulation of ossification, GO:0030278
- cardiovascular system development, GO:0072358
- positive regulation of T-helper 1 type immune response, GO:0002827
- negative regulation of retrograde protein transport, GO:1904153
- regulation of anion transport, GO:0044070
- reverse cholesterol transport, GO:0043691
- regulation of anion transmembrane transport, GO:1903959
- cerebellar Purkinje cell differentiation, GO:0021702
- vacuolar acidification, GO:0007035
- action potential, GO:0001508
- multicellular organismal iron ion homeostasis, GO:0060586
- iron ion transport, GO:0006826
- cellular response to iron ion, GO:0071281
- chemokine receptor activity, GO:0004950
- antimicrobial humoral response, GO:0019730
- polar body extrusion after meiotic divisions, GO:0040038
- endolysosome lumen, GO:0036021
- positive regulation of skeletal muscle tissue growth, GO:0048633
- lysosomal lumen acidification, GO:0007042
- negative regulation of multicellular organism growth, GO:0040015
- removal of superoxide radicals, GO:0019430
- high-density lipoprotein particle remodeling, GO:0034375
- azurophil granule, GO:0042582
- voltage-gated potassium channel activity involved in cardiac muscle cell action potential repolarization, GO:0086008
- C21-steroid hormone biosynthetic process, GO:0006700
- germinal center formation, GO:0002467
- BLOC-1 complex, GO:0031083
- voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization, GO:1902282
- membrane repolarization during ventricular cardiac muscle cell action potential, GO:0098915
- plus-end-directed vesicle transport along microtubule, GO:0072383
- cholesterol efflux, GO:0033344
- antigen receptor-mediated signaling pathway, GO:0050851
- copper ion transmembrane transporter activity, GO:0005375
- solute:proton antiporter activity, GO:0015299
- beta-2-microglobulin binding, GO:0030881