

ER to Golgi vesicle-mediated transport, GO:0006888

- Golgi organization, GO:0007030
- COPII vesicle coating, GO:0048208
- IRE1-mediated unfolded protein response, GO:0036498
- lipid particle, GO:0005811
- trans-Golgi network membrane, GO:0032588
- secretory granule membrane, GO:0030667
- platelet degranulation, GO:0002576
- exocytosis, GO:0006887
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- Ras guanyl-nucleotide exchange factor activity, GO:0005088
- cis-Golgi network, GO:0005801
- syntaxin binding, GO:0019905
- transport vesicle, GO:0030133
- Golgi cisterna membrane, GO:0032580
- SNARE complex, GO:0031201
- Z disc, GO:0030018
- endoplasmic reticulum-Golgi intermediate compartment membrane, GO:0033116
- Cul3-RING ubiquitin ligase complex, GO:0031463
- ER to Golgi transport vesicle membrane, GO:0012507
- SNAP receptor activity, GO:0005484
- protein oligomerization, GO:0051259
- endoplasmic reticulum-Golgi intermediate compartment, GO:0005793
- SNARE binding, GO:0000149
- protein N-linked glycosylation via asparagine, GO:0018279
- platelet alpha granule lumen, GO:0031093
- endoplasmic reticulum organization, GO:0007029
- antigen processing and presentation of peptide antigen via MHC class I, GO:0002474
- integral component of Golgi membrane, GO:0030173
- vesicle fusion, GO:0006906
- endoplasmic reticulum unfolded protein response, GO:0030968
- ficolin-1-rich granule membrane, GO:0101003
- toxin transport, GO:1901998
- ER to Golgi transport vesicle, GO:0030134
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- vesicle docking, GO:0048278
- protein targeting to plasma membrane, GO:0072661
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- COPI vesicle coat, GO:0030126
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- negative regulation of dendrite morphogenesis, GO:0050774
- cargo loading into COPII-coated vesicle, GO:0090110
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- WASH complex, GO:0071203
- vesicle fusion with Golgi apparatus, GO:0048280
- endoplasmic reticulum exit site, GO:0070971
- TRAPP complex, GO:0030008
- response to calcium ion, GO:0051592
- auditory receptor cell stereocilium organization, GO:0060088
- axolemma, GO:0030673
- spectrin, GO:0008091
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- rough endoplasmic reticulum, GO:0005791
- negative regulation of proteolysis, GO:0045861
- hemostasis, GO:0007599
- cellular response to vitamin D, GO:0071305
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- activation of phospholipase D activity, GO:0031584
- barbed-end actin filament capping, GO:0051016
- copper ion binding, GO:0005507
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- porphyrin-containing compound biosynthetic process, GO:0006779
- pharyngeal arch artery morphogenesis, GO:0061626
- positive regulation of ATP biosynthetic process, GO:2001171
- costamere, GO:0043034
- neural crest cell development, GO:0014032
- NADH metabolic process, GO:0006734
- chloride channel inhibitor activity, GO:0019869
- nuclear envelope reassembly, GO:0031468
- positive regulation of mitochondrial fission, GO:0090141
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- activation of signaling protein activity involved in unfolded protein response, GO:0006987
- positive regulation of blood coagulation, GO:0030194
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- phospholipase activity, GO:0004620
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- positive regulation of sodium ion transport, GO:0010765