

protein folding, GO:0006457

- ficollin-1-rich granule lumen, GO:1904813
- protein stabilization, GO:0050821
- macroautophagy, GO:0016236
- isomerase activity, GO:0016853
- secretory granule lumen, GO:0034774
- melanosome, GO:0042470
- chaperone binding, GO:0051087
- ubiquitin-dependent ERAD pathway, GO:0030433
- unfolded protein binding, GO:0051082
- response to endoplasmic reticulum stress, GO:0034976
- endoplasmic reticulum-Golgi intermediate compartment, GO:0005793
- response to unfolded protein, GO:0006986
- interleukin-12-mediated signaling pathway, GO:0035722
- positive regulation of protein ubiquitination, GO:0031398
- cell body, GO:0044297
- cell redox homeostasis, GO:0045454
- positive regulation of ATPase activity, GO:0032781
- response to stress, GO:0006950
- endoplasmic reticulum unfolded protein response, GO:0030968
- Hsp70 protein binding, GO:0030544
- negative regulation of neuron projection development, GO:0010977
- chaperone-mediated protein folding, GO:0061077
- antigen processing and presentation of peptide antigen via MHC class I, GO:0002474
- retrograde protein transport, GO:0030970
- Wnt signaling pathway, GO:0007223
- protein binding, GO:0030674
- phosphatidylcholine biosynthetic process, GO:0006656
- ATPase activator activity, GO:0001671
- polyubiquitin binding, GO:0031593
- Hsp90 protein binding, GO:0051879
- PcG protein complex, GO:0031519
- ATP metabolic process, GO:0046034
- apoptotic mitochondrial changes, GO:0008637
- protein localization to cell surface, GO:0034394
- ERAD pathway, GO:0036503
- lipid particle organization, GO:0034389
- Derlin-1 retrotranslocation complex, GO:0036513
- DNA polymerase binding, GO:0070182
- protein disulfide isomerase activity, GO:0003756
- protein import into mitochondrial matrix, GO:0030150
- protein binding involved in protein folding, GO:0044183
- ER-associated misfolded protein catabolic process, GO:0071712
- developmental process, GO:0032502
- smooth endoplasmic reticulum, GO:0005790
- protein disulfide oxidoreductase activity, GO:0015035
- ubiquitin-specific protease binding, GO:1990381
- response to cold, GO:0009409
- FK506 binding, GO:0005528
- protein localization to nucleus, GO:0034504
- negative regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043154
- dolichol-linked oligosaccharide biosynthetic process, GO:0006488
- integral component of lumenal side of endoplasmic reticulum membrane, GO:0071556
- cell, GO:0005623
- GTPase activating protein binding, GO:0032794
- protein deglycosylation, GO:0006517
- response to testosterone, GO:0033574
- chaperone-mediated protein complex assembly, GO:0051131
- protein metabolic process, GO:0019538
- ATPase activity, GO:0042623
- ubiquitin-ubiquitin ligase activity, GO:0034450
- endoplasmic reticulum chaperone complex, GO:0034663
- protein folding in endoplasmic reticulum, GO:0034975
- cytosolic proteasome complex, GO:0031597
- heterotrimeric G-protein complex, GO:0005834
- protein kinase regulator activity, GO:0019887
- nuclear proteasome complex, GO:0031595
- cellular protein complex assembly, GO:0043623
- positive regulation of protein localization to Cajal body, GO:1904871
- gonad development, GO:0008406
- glycoprotein catabolic process, GO:0006516
- positive regulation of viral entry into host cell, GO:0046598
- signal recognition particle, GO:0048500
- prefoldin complex, GO:0016272
- Tat protein binding, GO:0030957
- regulation of blood pressure, GO:0008217
- ‘de novo’ protein folding, GO:0006458
- zona pellucida receptor complex, GO:0002199
- L-fucose catabolic process, GO:0042355
- positive regulation of multicellular organism growth, GO:0040018
- regulation of type I interferon-mediated signaling pathway, GO:0060338
- VCP-NPL4-UFD1 AAA ATPase complex, GO:0034098
- protein heterotrimerization, GO:0070208
- negative regulation of JUN kinase activity, GO:0043508
- hormone activity, GO:0005179
- protein retention in ER lumen, GO:0006621
- retina development in camera-type eye, GO:0060041
- proteasome binding, GO:0070628
- regulation of stress fiber assembly, GO:0051492
- regulation of interferon-gamma-mediated signaling pathway, GO:0060334
- cellular response to prostaglandin E stimulus, GO:0071380
- adenyl-nucleotide exchange factor activity, GO:0000774
- cGMP biosynthetic process, GO:0006182
- chaperone cofactor-dependent protein refolding, GO:0070389
- G-protein coupled acetylcholine receptor signaling pathway, GO:0007213
- sphingosine biosynthetic process, GO:0046512
- transforming growth factor beta binding, GO:0050431
- positive regulation of interferon-alpha production, GO:0032727
- oxidoreductase activity, GO:0016671
- acetylcholine receptor binding, GO:0033130
- proteasome-activating ATPase activity, GO:0036402
- alpha-(1->3)-fucosyltransferase activity, GO:0046920
- chaperonin-containing T-complex, GO:0005832
- regulation of peptidyl-tyrosine phosphorylation, GO:0050730
- signal recognition particle receptor complex, GO:0005785
- collagen metabolic process, GO:0032963
- regulation of cGMP metabolic process, GO:0030823
- R2TP complex, GO:0097255
- peptide disulfide oxidoreductase activity, GO:0015037
- negative regulation of adenylate cyclase activity, GO:0007194
- L-ascorbic acid binding, GO:0031418
- inclusion body, GO:0016234
- regulation of smooth muscle cell proliferation, GO:0048660
- vesicle fusion with endoplasmic reticulum-Golgi intermediate compartment (ERGIC) membrane, GO:1990668
- K48-linked polyubiquitin binding, GO:0036435
- binding of sperm to zona pellucida, GO:0007339
- positive regulation of phosphoprotein phosphatase activity, GO:0032516