

protein folding, GO:0006457

- ficolin-1-rich granule lumen, GO:1904813
- isomerase activity, GO:0016853
- regulation of transcription from RNA polymerase II promoter in response to hypoxia, GO:0061418
- unfolded protein binding, GO:0051082
- melanosome, GO:0042470
- secretory granule lumen, GO:0034774
- chaperone binding, GO:0051087
- ubiquitin-dependent ERAD pathway, GO:0030433
- cell redox homeostasis, GO:0045454
- positive regulation of protein ubiquitination, GO:0031398
- response to unfolded protein, GO:0006986
- interleukin-12-mediated signaling pathway, GO:0035722
- negative regulation of protein ubiquitination, GO:0031397
- cell body, GO:0044297
- negative regulation of neuron projection development, GO:0010977
- chaperone-mediated protein folding, GO:0061077
- polyubiquitin binding, GO:0031593
- positive regulation of ATPase activity, GO:0032781
- Hsp70 protein binding, GO:0030544
- ATPase activator activity, GO:0001671
- PcG protein complex, GO:0031519
- ATP metabolic process, GO:0046034
- response to stress, GO:0006950
- DNA polymerase binding, GO:0070182
- signal transducer activity, GO:0005057
- dolichol-linked oligosaccharide biosynthetic process, GO:0006488
- cell, GO:0005623
- phosphatidylcholine biosynthetic process, GO:0006656
- protein import into mitochondrial matrix, GO:0030150
- negative regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043154
- response to cold, GO:0009409
- protein disulfide oxidoreductase activity, GO:0015035
- protein binding involved in protein folding, GO:0044183
- ‘de novo’ protein folding, GO:0006458
- protein folding in endoplasmic reticulum, GO:0034975
- ADP binding, GO:0043531
- protein localization to nucleus, GO:0034504
- chaperone mediated protein folding requiring cofactor, GO:0051085
- protein disulfide isomerase activity, GO:0003756
- chaperone-mediated protein complex assembly, GO:0051131
- ER-associated misfolded protein catabolic process, GO:0071712
- positive regulation of protein localization to Cajal body, GO:1904871
- regulation of blood pressure, GO:0008217
- FK506 binding, GO:0005528
- endoplasmic reticulum chaperone complex, GO:0034663
- chaperonin-containing T-complex, GO:0005832
- developmental process, GO:0032502
- zona pellucida receptor complex, GO:0002199
- retrograde protein transport, GO:0030970
- ubiquitin-ubiquitin ligase activity, GO:0034450
- G-protein beta/gamma-subunit complex binding, GO:0031683
- nuclear proteasome complex, GO:0031595
- cGMP biosynthetic process, GO:0006182
- response to testosterone, GO:0033574
- protein deglycosylation, GO:0006517
- apoptotic mitochondrial changes, GO:0008637
- guanyl nucleotide binding, GO:0019001
- retina development in camera-type eye, GO:0060041
- protein maturation by protein folding, GO:0022417
- ATF6-mediated unfolded protein response, GO:0036500
- signal recognition particle, GO:0048500
- fucosyltransferase activity, GO:0008417
- negative regulation of cell cycle arrest, GO:0071157
- heterotrimeric G-protein complex, GO:0005834
- activin binding, GO:0048185
- adenyl-nucleotide exchange factor activity, GO:0000774
- L-fucose catabolic process, GO:0042355
- cardiac myofibril, GO:0097512
- negative regulation of JUN kinase activity, GO:0043508
- prostate gland development, GO:0030850
- chaperone cofactor-dependent protein refolding, GO:0070389
- positive regulation of interferon-alpha production, GO:0032727
- detection of chemical stimulus involved in sensory perception of bitter taste, GO:0001580
- integral component of lumenal side of endoplasmic reticulum membrane, GO:0071556
- Tat protein binding, GO:0030957
- release of sequestered calcium ion into cytosol, GO:0051209
- body fluid secretion, GO:0007589
- response to light intensity, GO:0009642
- signal recognition particle receptor complex, GO:0005785
- inclusion body, GO:0016234
- mannosylation, GO:0097502
- necroptotic process, GO:0070266
- mannosyltransferase activity, GO:0000030
- disulfide oxidoreductase activity, GO:0015036
- regulation of type I interferon-mediated signaling pathway, GO:0060338
- pore complex assembly, GO:0046931
- regulation of ubiquitin-protein transferase activity, GO:0051438
- proteasome-activating ATPase activity, GO:0036402