myelin sheath, GO:0043209 unfolded protein binding, GO:0051082 melanosome, GO:0042470 macroautophagy, GO:0016236 tumor necrosis factor-mediated signaling pathway, GO:0033209 chaperone binding, GO:0051087 secretory granule lumen, GO:0034774 isomerase activity, GO:0016853 regulation of catalytic activity, GO:0050790 response to unfolded protein, GO:0006986 endoplasmic reticulum-Golgi intermediate compartment, GO:0005793 cell redox homeostasis, GO:0045454 interleukin-12-mediated signaling pathway, GO:0035722 negative regulation of protein ubiquitination, GO:0031397 toxin transport, GO:1901998 beta-tubulin binding, GO:0048487 chaperone-mediated protein folding, GO:0061077 cell body, GO:0044297 polyubiquitin binding, GO:0031593 Hsp90 protein binding, GO:0051879 response to stress, GO:0006950 PcG protein complex, GO:0031519 positive regulation of ATPase activity, GO:0032781 antigen processing and presentation of peptide antigen via MHC class I, GO:0002474 negative regulation of neuron projection development, GO:0010977 ATP metabolic process, GO:0046034 lipid particle organization, GO:0034389 zona pellucida receptor complex, GO:0002199 protein binding involved in protein folding, GO:0044183 phosphatidylcholine biosynthetic process, GO:0006656 developmental process, GO:0032502 endoplasmic reticulum chaperone complex, GO:0034663 cell, GO:0005623 photoreceptor connecting cilium, GO:0032391 positive regulation of protein localization to Cajal body, GO:1904871 protein import into mitochondrial matrix, GO:0030150 protein localization to nucleus, GO:0034504 signal transducer activity, GO:0005057 positive regulation of establishment of protein localization to telomere, GO:1904851 retrograde protein transport, GO:0030970 integral component of lumenal side of endoplasmic reticulum membrane, GO:0071556 regulation of blood pressure, GO:0008217 adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway, GO:0007193 dolichol-linked oligosaccharide biosynthetic process, GO:0006488 regulation of type I interferon-mediated signaling pathway, GO:0060338 ATPase activator activity, GO:0001671 cellular response to prostaglandin E stimulus, GO:0071380 ATPase activity, GO:0042623 chaperonin-containing T-complex, GO:0005832 protein secretion, GO:0009306 release of sequestered calcium ion into cytosol, GO:0051209 guanyl nucleotide binding, GO:0019001 protein disulfide oxidoreductase activity, GO:0015035 cytosolic proteasome complex, GO:0031597 heterotrimeric G-protein complex, GO:0005834 rhodopsin mediated signaling pathway, GO:0016056 protein disulfide isomerase activity, GO:0003756 ATF6-mediated unfolded protein response, GO:0036500 adenyl-nucleotide exchange factor activity, GO:0000774 MHC class II protein complex binding, GO:0023026 DNA polymerase binding, GO:0070182 protein deglycosylation, GO:0006517 acrosomal vesicle, GO:0001669 G-protein beta/gamma-subunit complex binding, GO:0031683 positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress, GO:1990440 ER to Golgi transport vesicle, GO:0030134 protein localization to cell surface, GO:0034394 apoptotic mitochondrial changes, GO:0008637 'de novo' protein folding, GO:0006458 proteasome regulatory particle, GO:0008540 regulation of protein localization to plasma membrane, GO:1903076 phototransduction, GO:0007603 tubulin complex assembly, GO:0007021 FK506 binding, GO:0005528 photoreceptor outer segment membrane, GO:0042622 positive regulation of interferon-alpha production, GO:0032727 binding of sperm to zona pellucida, GO:0007339 protein folding in endoplasmic reticulum, GO:0034975 photoreceptor outer segment, GO:0001750 fucosylation, GO:0036065 response to testosterone, GO:0033574 regulation of atrial cardiac muscle cell membrane repolarization, GO:0060372 cell cortex region, GO:0099738 negative regulation of JUN kinase activity, GO:0043508 cellular response to glucagon stimulus, GO:0071377 NADH metabolic process, GO:0006734 regulation of mitotic spindle organization, GO:0060236 detection of light stimulus involved in visual perception, GO:0050908 phospholipase C activity, GO:0004629 positive regulation of transcription from RNA polymerase II promoter involved in unfolded protein response, GO:0006990 scaRNA localization to Cajal body, GO:0090666 retina development in camera-type eye, GO:0060041 peptide disulfide oxidoreductase activity, GO:0015037 copper ion transport, GO:0006825 chaperone-mediated protein complex assembly, GO:0051131 receptor guanylyl cyclase signaling pathway, GO:0007168 signal recognition particle, GO:0048500 glucocorticoid receptor binding, GO:0035259 transforming growth factor beta-activated receptor activity, GO:0005024 nuclear proteasome complex, GO:0031595 negative regulation of cell-substrate adhesion, GO:0010812

protein stabilization, GO:0050821

protein folding, GO:0006457

ficolin-1-rich granule lumen, GO:1904813

oligosaccharide biosynthetic process, GO:0009312

protein maturation by protein folding, GO:0022417

negative regulation of trophoblast cell migration, GO:1901164

positive regulation of multicellular organism growth, GO:0040018

cellular protein complex assembly, GO:0043623

L-fucose catabolic process, GO:0042355