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isomerase activity, GO:0016853
                                           ficolin-1-rich granule lumen, GO:1904813
                                           unfolded protein binding, GO:0051082
                                           melanosome, GO:0042470
                                           regulation of transcription from RNA polymerase II promoter in response to hypoxia, GO:0061418
                                           macroautophagy, GO:0016236
                                           SCF-dependent proteasomal ubiquitin-dependent protein catabolic process, GO:0031146
                                           secretory granule lumen, GO:0034774
                                           response to endoplasmic reticulum stress, GO:0034976
                                           NIK/NF-kappaB signaling, GO:0038061
                                           Wnt signaling pathway, GO:0060071
                                           ubiquitin-dependent ERAD pathway, GO:0030433
                                           chaperone binding, GO:0051087
                                           negative regulation of G2/M transition of mitotic cell cycle, GO:0010972
                                           endoplasmic reticulum-Golgi intermediate compartment, GO:0005793
                                           negative regulation of canonical Wnt signaling pathway, GO:0090090
                                           tumor necrosis factor-mediated signaling pathway, GO:0033209
                                           endosomal transport, GO:0016197
                                           transforming growth factor beta receptor signaling pathway, GO:0007179
                                           response to unfolded protein, GO:0006986
                                           cell redox homeostasis, GO:0045454
                                           positive regulation of protein binding, GO:0032092
                                           cell body, GO:0044297
                                           ATPase binding, GO:0051117
                                           positive regulation of protein ubiquitination, GO:0031398
                                           I-kappaB kinase/NF-kappaB signaling, GO:0007249
                                           GTPase binding, GO:0051020
                                           endoplasmic reticulum unfolded protein response, GO:0030968
                                           global genome nucleotide-excision repair, GO:0070911
                                           cellular iron ion homeostasis, GO:0006879
                                           signal transducer activity, GO:0005057
                                           negative regulation of neuron projection development, GO:0010977
                                           Wnt signaling pathway, GO:0007223
                                           JNK cascade, GO:0007254
                                           Notch signaling pathway, GO:0007219
                                           Hsp90 protein binding, GO:0051879
                                           negative regulation of transforming growth factor beta receptor signaling pathway, GO:0030512
                                           Hsp70 protein binding, GO:0030544
                                           PcG protein complex, GO:0031519
                                           chaperone-mediated protein folding, GO:0061077
                                           phosphatidylcholine biosynthetic process, GO:0006656
                                           response to stress, GO:0006950
                                           toxin transport, GO:1901998
                                           positive regulation of ATPase activity, GO:0032781
                                           retrograde protein transport, GO:0030970
                                           protein disulfide isomerase activity, GO:0003756
                                           peptide binding, GO:0042277
                                           developmental process, GO:0032502
                                           ATPase activator activity, GO:0001671
                                           DNA polymerase binding, GO:0070182
                                           smooth endoplasmic reticulum, GO:0005790
                                           positive regulation of protein secretion, GO:0050714
                                           protein disulfide oxidoreductase activity, GO:0015035
                                           ATP metabolic process, GO:0046034
                                           antigen processing and presentation of peptide antigen via MHC class I, GO:0002474
                                           MHC class II protein complex binding, GO:0023026
                                           ER to Golgi transport vesicle, GO:0030134
                                           apoptotic mitochondrial changes, GO:0008637
                                           protein localization to nucleus, GO:0034504
                                           protein binding involved in protein folding, GO:0044183
                                           polyubiquitin binding, GO:0031593
                                           chaperone mediated protein folding requiring cofactor, GO:0051085
                                           disordered domain specific binding, GO:0097718
                                           protein localization to cell surface, GO:0034394
                                           spectrin binding, GO:0030507
                                           regulation of blood pressure, GO:0008217
                                           cell, GO:0005623
                                           release of sequestered calcium ion into cytosol, GO:0051209
                                           'de novo' protein folding, GO:0006458
                                           regulation of type I interferon-mediated signaling pathway, GO:0060338
                                           chaperone-mediated protein complex assembly, GO:0051131
                                           protein refolding, GO:0042026
                                           protein folding in endoplasmic reticulum, GO:0034975
                                           acrosomal vesicle, GO:0001669
                                           apoptotic cell clearance, GO:0043277
                                           regulation of G-protein coupled receptor protein signaling pathway, GO:0008277
                                           positive regulation of nitric oxide biosynthetic process, GO:0045429
                                           dolichol-linked oligosaccharide biosynthetic process, GO:0006488
                                           Derlin-1 retrotranslocation complex, GO:0036513
                                           negative regulation of cell cycle arrest, GO:0071157
                                           ER-associated misfolded protein catabolic process, GO:0071712
protein folding, GO:0006457
                                           G-protein coupled receptor binding, GO:0001664
                                           supramolecular fiber organization, GO:0097435
                                           ubiquitin-ubiquitin ligase activity, GO:0034450
                                           regulation of interferon-gamma-mediated signaling pathway, GO:0060334
                                           lipid particle organization, GO:0034389
                                           protein deglycosylation, GO:0006517
                                           regulation of phosphoprotein phosphatase activity, GO:0043666
                                           regulation of protein secretion, GO:0050708
                                           detection of light stimulus involved in visual perception, GO:0050908
                                           FK506 binding, GO:0005528
                                           chaperonin-containing T-complex, GO:0005832
                                           response to testosterone, GO:0033574
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                                           positive regulation of protein localization to Cajal body, GO:1904871
                                           integral component of lumenal side of endoplasmic reticulum membrane, GO:0071556
                                           virion binding, GO:0046790
                                           zona pellucida receptor complex, GO:0002199
                                           tubulin complex assembly, GO:0007021
                                           adenylate cyclase-modulating G-protein coupled receptor signaling pathway, GO:0007188
                                           misfolded or incompletely synthesized protein catabolic process, GO:0006515
                                           protein kinase regulator activity, GO:0019887
                                           binding of sperm to zona pellucida, GO:0007339
                                           mannose binding, GO:0005537
                                           positive regulation of interferon-alpha production, GO:0032727
                                           ubiquitin-specific protease binding, GO:1990381
                                           copper ion transport, GO:0006825
                                           cellular protein complex assembly, GO:0043623
                                           apolipoprotein binding, GO:0034185
                                           peptidase activator activity, GO:0016504
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                                           G-protein coupled acetylcholine receptor signaling pathway, GO:0007213
                                           NADH metabolic process, GO:0006734
                                           protein maturation by protein folding, GO:0022417
                                           signal recognition particle, GO:0048500
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                                           prefoldin complex, GO:0016272
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                                           protein tyrosine kinase binding, GO:1990782
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                                           endoplasmic reticulum chaperone complex, GO:0034663
                                           negative regulation of release of cytochrome c from mitochondria, GO:0090201
                                           GTPase activating protein binding, GO:0032794
                                           positive regulation of cell size, GO:0045793
                                           VCP-NPL4-UFD1 AAA ATPase complex, GO:0034098
                                           vascular endothelial growth factor receptor 2 binding, GO:0043184
                                           disulfide oxidoreductase activity, GO:0015036
                                           peptide disulfide oxidoreductase activity, GO:0015037
                                           nuclear proteasome complex, GO:0031595
                                           negative regulation of wound healing, GO:0061045
                                           type I transforming growth factor beta receptor binding, GO:0034713
                                           prostate gland development, GO:0030850
                                           G-protein beta/gamma-subunit complex binding, GO:0031683
                                           heterotrimeric G-protein complex, GO:0005834
                                           negative regulation of cell-substrate adhesion, GO:0010812
                                           regulation of protein localization to plasma membrane, GO:1903076
                                           face development, GO:0060324
                                           retinal cone cell development, GO:0046549
                                           positive regulation of viral entry into host cell, GO:0046598
                                           signal recognition particle receptor complex, GO:0005785
                                           cellular response to glucagon stimulus, GO:0071377
                                           retina development in camera-type eye, GO:0060041
                                           mitochondrion transport along microtubule, GO:0047497
                                           SMAD protein complex assembly, GO:0007183
                                           protein retention in ER lumen, GO:0006621
                                           L-fucose catabolic process, GO:0042355
                                           negative regulation of synaptic transmission, GO:0050805
                                           proteasome binding, GO:0070628
                                           collagen metabolic process, GO:0032963
                                           glycoprotein metabolic process, GO:0009100
                                           negative regulation of viral process, GO:0048525
                                           viral release from host cell, GO:0019076
                                           regulation of protein transport, GO:0051223
                                           regulation of ubiquitin-protein transferase activity, GO:0051438
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cell cortex region, GO:0099738

sphingosine biosynthetic process, GO:0046512

protein stabilization, GO:0050821

myelin sheath, GO:0043209