

ficolin-1-rich granule lumen, GO:1904813

protein folding, GO:0006457
secretory granule lumen, GO:0034774
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051436
anaphase-promoting complex-dependent catabolic process, GO:0031145
positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, GO:0051437
myelin sheath, GO:0043209
regulation of mRNA stability, GO:0043488
regulation of catalytic activity, GO:0050790
regulation of hematopoietic stem cell differentiation, GO:1902036
negative regulation of canonical Wnt signaling pathway, GO:0090090
proteasome complex, GO:0000502
actin filament binding, GO:0051015
isomerase activity, GO:0016853
antigen processing and presentation of exogenous peptide antigen via MHC class I, GO:0002479
unfolded protein binding, GO:0051082
response to oxidative stress, GO:0006979
NIK/NF-kappaB signaling, GO:0038061
Wnt signaling pathway, GO:0060071
tumor necrosis factor-mediated signaling pathway, GO:0033209
regulation of transcription from RNA polymerase II promoter in response to hypoxia, GO:0061418
cysteine-type peptidase activity, GO:0008234
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process, GO:0031146
protein phosphatase binding, GO:0019903
regulation of cellular response to heat, GO:1900034
stimulatory C-type lectin receptor signaling pathway, GO:0002223
aging, GO:0007568
positive regulation of canonical Wnt signaling pathway, GO:0090263
negative regulation of G2/M transition of mitotic cell cycle, GO:0010972
vesicle, GO:0031982
lyase activity, GO:0016829
response to unfolded protein, GO:0006986
azurophil granule lumen, GO:0035578
regulation of cellular amino acid metabolic process, GO:0006521
response to hypoxia, GO:0001666
platelet degranulation, GO:0002576
cellular response to oxidative stress, GO:0034599
protein homotetramerization, GO:0051289
movement of cell or subcellular component, GO:0006928
cysteine-type endopeptidase activity, GO:0004197
lysosomal lumen, GO:0043202
proteolysis involved in cellular protein catabolic process, GO:0051603
specific granule lumen, GO:0035580
disordered domain specific binding, GO:0097718
response to stress, GO:0006950
hydrolase activity, GO:0016798
response to toxic substance, GO:0009636
viral entry into host cell, GO:0046718
proteasome accessory complex, GO:0022624
response to hydrogen peroxide, GO:0042542
protein methylation, GO:0006479
glucose metabolic process, GO:0006006
endopeptidase activity, GO:0004175
response to estradiol, GO:0032355
glycosphingolipid metabolic process, GO:0006687
cytoskeletal protein binding, GO:0008092
heat shock protein binding, GO:0031072
platelet alpha granule lumen, GO:0031093
ER to Golgi transport vesicle, GO:0030134
positive regulation of telomere maintenance via telomerase, GO:0032212
podosome, GO:0002102
cellular oxidant detoxification, GO:0098869
regulation of sequence-specific DNA binding transcription factor activity, GO:0051090
response to ethanol, GO:0045471
tertiary granule lumen, GO:1904724
gluconeogenesis, GO:0006094
telomere maintenance via telomerase, GO:0007004
protease binding, GO:0002020
positive regulation of apoptotic signaling pathway, GO:2001235
protein heterooligomerization, GO:0051291
response to nutrient, GO:0007584
response to hormone, GO:0009725
intrinsic apoptotic signaling pathway, GO:0097193
translation elongation factor activity, GO:0003746
polyubiquitin binding, GO:0031593
negative regulation of cell death, GO:0060548
protein binding involved in protein folding, GO:0044183
drug binding, GO:0008144
pentose-phosphate shunt, GO:0006098
ATP biosynthetic process, GO:0006754
extracellular vesicle, GO:1903561
nucleotide metabolic process, GO:0009117
ATP metabolic process, GO:0046034
hydrolase activity, GO:0004553
proteasome regulatory particle, GO:0008540
positive regulation of protein import into nucleus, GO:0042307
extracellular matrix disassembly, GO:0022617
ADP binding, GO:0043531
establishment of protein localization, GO:0045184
positive regulation of telomerase activity, GO:0051973
glutathione metabolic process, GO:0006749
protein catabolic process, GO:0030163
cortical actin cytoskeleton, GO:0030864
proteasome assembly, GO:0043248
positive regulation of interleukin-1 beta secretion, GO:0050718
NADP binding, GO:0050661
cellular response to epidermal growth factor stimulus, GO:0071364
central nervous system development, GO:0007417
glycosaminoglycan catabolic process, GO:0006027
glycogen catabolic process, GO:0005980
positive regulation of DNA binding, GO:0043388
purine nucleotide biosynthetic process, GO:0006164
TBP-class protein binding, GO:0017025
positive regulation of interferon-beta production, GO:0032728
DNA polymerase binding, GO:0070182
collagen binding, GO:0005518
programmed cell death, GO:0012501
regulation of protein catabolic process, GO:0042176
RNA polymerase II carboxy-terminal domain kinase activity, GO:0008353
platelet aggregation, GO:0070527
regulation of cytoskeleton organization, GO:0051493
lipopolysaccharide-mediated signaling pathway, GO:0031663
negative regulation of fibroblast proliferation, GO:0048147
enzyme activator activity, GO:0008047
positive regulation of protein serine/threonine kinase activity, GO:0071902
response to cadmium ion, GO:0046686
cell, GO:0005623
proteasome regulatory particle, GO:0005838
canonical glycolysis, GO:0061621
cysteine-type endopeptidase activator activity involved in apoptotic process, GO:0008656
apoptotic DNA fragmentation, GO:0006309
aggresome, GO:0016235
toll-like receptor signaling pathway, GO:0002224
purine-containing compound salvage, GO:0043101
cellular response to heat, GO:0034605
cellular response to cadmium ion, GO:0071276
regulation of neuron death, GO:1901214
lysosomal transport, GO:0007041
zona pellucida receptor complex, GO:0002199
double-stranded telomeric DNA binding, GO:0003691
response to muramyl dipeptide, GO:0032495
hemostasis, GO:0007599
modulation by virus of host process, GO:0019054
proteasome regulatory particle, GO:0008541
receptor catabolic process, GO:0032801
positive regulation of transforming growth factor beta receptor signaling pathway, GO:0030511
regulation of protein ubiquitination, GO:0031396
protein kinase activator activity, GO:0030295
response to nutrient levels, GO:0031667
Fc-gamma receptor signaling pathway involved in phagocytosis, GO:0038096
cellular response to interleukin-4, GO:0071353
cellular response to reactive oxygen species, GO:0034614
negative regulation of DNA damage response, GO:0043518
positive regulation of telomerase RNA localization to Cajal body, GO:1904874
cytosolic proteasome complex, GO:0031597
retrograde protein transport, GO:0030970
ubiquitin-specific protease binding, GO:1990381
Derlin-1 retrotranslocation complex, GO:0036513
positive chemotaxis, GO:0050918
positive regulation of peptidyl-threonine phosphorylation, GO:0010800
B cell receptor signaling pathway, GO:0050853
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:1902166
embryo implantation, GO:0007566
enzyme regulator activity, GO:0030234
glycolytic process, GO:0006096
regulation of mitotic spindle assembly, GO:1901673
response to testosterone, GO:0033574
autolysosome, GO:0044754
histone ubiquitination, GO:0016574
barbed-end actin filament capping, GO:0051016
inclusion body, GO:0016234
invadopodium, GO:0071437
phosphatidylserine binding, GO:0001786
negative regulation of intrinsic apoptotic signaling pathway, GO:2001243
cornified envelope, GO:0001533
response to vitamin E, GO:0033197
response to estrogen, GO:0043627
protein localization to cell surface, GO:0034394
positive regulation of protein localization to Cajal body, GO:1904871
nuclear proteasome complex, GO:0031595
peptidyl-prolyl cis-trans isomerase activity, GO:0003755
protein peptidyl-prolyl isomerization, GO:0000413
negative regulation of cell cycle arrest, GO:0071157
proteasome core complex, GO:0005839
mRNA catabolic process, GO:0006402
learning or memory, GO:0007611
positive regulation of proteasomal protein catabolic process, GO:1901800
positive regulation of keratinocyte differentiation, GO:0045618
negative regulation of oxidative stress-induced neuron death, GO:1903204
hyaluronan catabolic process, GO:0030214
MHC class II protein complex binding, GO:0023026
hepatocyte apoptotic process, GO:0097284
response to inorganic substance, GO:0010035
proteasomal protein catabolic process, GO:0010498
cellular response to dopamine, GO:1903351
response to glucocorticoid, GO:0051384
positive regulation of protein import into nucleus, GO:0033160
DNA ligation, GO:0006266
cellular response to nitrogen starvation, GO:0006995
negative regulation of protein tyrosine kinase activity, GO:0061099
nucleoside diphosphate phosphorylation, GO:0006165
Bergmann glial cell differentiation, GO:0060020
chaperonin-containing T-complex, GO:0005832
amyloid fibril formation, GO:1990000
positive regulation of establishment of protein localization to telomere, GO:1904851
DNA topological change, GO:0006265
NADH metabolic process, GO:0006734
sulfuric ester hydrolase activity, GO:0008484
galactose catabolic process, GO:0019388
Arp2/3 complex-mediated actin nucleation, GO:0034314
small protein activating enzyme activity, GO:0008641
DNA damage response, GO:0030330
RAGE receptor binding, GO:0050786
structural constituent of cytoskeleton, GO:0005200
viral genome replication, GO:0019079
calcium-dependent cysteine-type endopeptidase activity, GO:0004198
G-protein coupled receptor binding, GO:0001664
mitogen-activated protein kinase kinase kinase binding, GO:0031435
placenta development, GO:0001890
DNA ligation involved in DNA repair, GO:0051103
endothelial cell proliferation, GO:0001935
negative regulation of endopeptidase activity, GO:0010951
protein targeting to ER, GO:0045047
negative regulation of potassium ion transmembrane transport, GO:1901380
chromatin assembly, GO:0031497
antioxidant activity, GO:0016209
positive regulation of telomere capping, GO:1904355
regulation of stress-activated MAPK cascade, GO:0032872
fatty acid binding, GO:0005504
peroxiredoxin activity, GO:0051920
cyclin/CDK positive transcription elongation factor complex, GO:0008024
proteasome-activating ATPase activity, GO:0036402
positive regulation of tumor necrosis factor-mediated signaling pathway, GO:1903265
threonine-type endopeptidase activity, GO:0004298
glutathione peroxidase activity, GO:0004602
proteasome core complex, GO:0019773
positive regulation of interleukin-8 secretion, GO:2000484
cellular lipid metabolic process, GO:0044255
fatty acid oxidation, GO:0019395
regulation of protein complex assembly, GO:0043254
regulation of ventricular cardiac muscle cell action potential, GO:0098911
keratan sulfate catabolic process, GO:0042340
cell cortex region, GO:0099738
muscle cell cellular homeostasis, GO:0046716
blastocyst development, GO:0001824
chondroitin sulfate catabolic process, GO:0030207
actin filament capping, GO:0051693
protein maturation by protein folding, GO:0022417
zonula adherens, GO:0005915
positive regulation of endopeptidase activity, GO:0010950
positive regulation of alpha-beta T cell differentiation, GO:0046638
cotranslational protein targeting to membrane, GO:0006613
positive regulation of ATP biosynthetic process, GO:2001171
fusion of virus membrane with host plasma membrane, GO:0019064
positive regulation of peptidase activity, GO:0010952
MHC class I protein binding, GO:0042288
positive regulation of dendritic spine morphogenesis, GO:0061003
positive regulation of macrophage chemotaxis, GO:0010759
positive regulation of nitric oxide biosynthetic process, GO:0045429