

protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:0042787

- ligase activity, GO:0016874
- G2/M transition of mitotic cell cycle, GO:0000086
- 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
- negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051436
- ubiquitin ligase complex, GO:0000151
- SCF-dependent proteasomal ubiquitin-dependent protein catabolic process, GO:0031146
- regulation of transcription from RNA polymerase II promoter in response to hypoxia, GO:0061418
- ubiquitin-dependent ERAD pathway, GO:0030433
- NIK/NF-kappaB signaling, GO:0038061
- negative regulation of G2/M transition of mitotic cell cycle, GO:0010972
- stimulatory C-type lectin receptor signaling pathway, GO:0002223
- ubiquitin binding, GO:0043130
- regulation of protein stability, GO:0031647
- positive regulation of NF-kappaB transcription factor activity, GO:0051092
- negative regulation of canonical Wnt signaling pathway, GO:0090090
- positive regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032436
- protein K48-linked ubiquitination, GO:0070936
- positive regulation of canonical Wnt signaling pathway, GO:0090263
- I-kappaB kinase/NF-kappaB signaling, GO:0007249
- protein destabilization, GO:0031648
- SCF ubiquitin ligase complex, GO:0019005
- viral life cycle, GO:0019058
- positive regulation of protein ubiquitination, GO:0031398
- Cul3-RING ubiquitin ligase complex, GO:0031463
- global genome nucleotide-excision repair, GO:0070911
- JNK cascade, GO:0007254
- intrinsic apoptotic signaling pathway, GO:0097193
- nucleotide-excision repair, GO:0000715
- protein monoubiquitination, GO:0006513
- negative regulation of type I interferon production, GO:0032480
- endoplasmic reticulum quality control compartment, GO:0044322
- regulation of tumor necrosis factor-mediated signaling pathway, GO:0010803
- cellular iron ion homeostasis, GO:0006879
- ubiquitin conjugating enzyme binding, GO:0031624
- endoplasmic reticulum unfolded protein response, GO:0030968
- positive regulation of cell cycle, GO:0045787
- protein K63-linked ubiquitination, GO:0070534
- SMAD binding, GO:0046332
- protein K11-linked ubiquitination, GO:0070979
- negative regulation of transforming growth factor beta receptor signaling pathway, GO:0030512
- ubiquitin conjugating enzyme activity, GO:0061631
- transforming growth factor beta receptor signaling pathway, GO:0007179
- protein catabolic process, GO:0030163
- ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway, GO:0043162
- Hsp70 protein binding, GO:0030544
- protein binding, GO:0030674
- negative regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0045736
- MyD88-dependent toll-like receptor signaling pathway, GO:0002755
- mitophagy, GO:0000422
- negative regulation of JNK cascade, GO:0046329
- ubiquitin-specific protease binding, GO:1990381
- ERBB2 signaling pathway, GO:0038128
- ER-associated misfolded protein catabolic process, GO:0071712
- BMP signaling pathway, GO:0030509
- Cul4-RING E3 ubiquitin ligase complex, GO:0080008
- positive regulation of proteolysis, GO:0045862
- translation elongation factor activity, GO:0003746
- cullin family protein binding, GO:0097602
- positive regulation of ubiquitin-protein transferase activity, GO:0051443
- ubiquitin protein ligase activity involved in ERAD pathway, GO:1904264
- receptor catabolic process, GO:0032801
- cullin-RING ubiquitin ligase complex, GO:0031461
- small protein activating enzyme activity, GO:0008641
- regulation of protein catabolic process, GO:0042176
- cellular response to antibiotic, GO:0071236
- proteasomal protein catabolic process, GO:0010498
- negative regulation of viral release from host cell, GO:1902187
- Derlin-1 retrotranslocation complex, GO:0036513
- Cul4A-RING E3 ubiquitin ligase complex, GO:0031464
- protein neddylation, GO:0045116
- negative regulation of extrinsic apoptotic signaling pathway via death domain receptors, GO:1902042
- regulation of dopamine metabolic process, GO:0042053
- ERAD pathway, GO:0036503
- regulation of autophagosome assembly, GO:2000785
- mitochondrion transport along microtubule, GO:0047497
- response to activity, GO:0014823
- erythrocyte development, GO:0048821
- regulation of proteolysis, GO:0030162
- regulation of membrane repolarization, GO:0060306
- VCP-NPL4-UFD1 AAA ATPase complex, GO:0034098
- negative regulation of viral transcription, GO:0032897
- meiotic spindle, GO:0072687
- myosin binding, GO:0017022
- ventricular cardiac muscle cell action potential, GO:0086005
- positive regulation of protein polyubiquitination, GO:1902916
- ubiquitin-like protein transferase activity, GO:0019787
- positive regulation of tumor necrosis factor-mediated signaling pathway, GO:1903265
- actinin binding, GO:0048185
- atrial septum development, GO:0003283
- positive regulation of mitotic metaphase/anaphase transition, GO:0045842
- mast cell granule, GO:0042629
- negative regulation of BMP signaling pathway, GO:0030514
- positive regulation of peptidyl-threonine phosphorylation, GO:0010800
- regulation of dendrite morphogenesis, GO:0048814
- misfolded or incompletely synthesized protein catabolic process, GO:0006515
- cellular protein catabolic process, GO:0044257
- response to vitamin D, GO:0033280
- positive regulation of neurogenesis, GO:0050769
- regulation of potassium ion transmembrane transporter activity, GO:1901016
- negative regulation of oxidative stress-induced neuron death, GO:1903204
- polar microtubule, GO:0005827
- ubiquitin activating enzyme activity, GO:0004839
- NEDD8 transferase activity, GO:0019788
- negative regulation of tumor necrosis factor-mediated signaling pathway, GO:0010804
- negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway, GO:1902236