

ligase activity, GO:0016874

- protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:0042787
- fatty acid metabolic process, GO:0006631
- cellular protein modification process, GO:0006464
- tRNA aminoacylation for protein translation, GO:0006418
- positive regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032436
- aminoacyl-tRNA ligase activity, GO:0004812
- peroxisomal membrane, GO:0005778
- protein K48-linked ubiquitination, GO:0070936
- androgen receptor signaling pathway, GO:0030521
- regulation of protein stability, GO:0031647
- protein autoubiquitination, GO:0051865
- protein destabilization, GO:0031648
- mitochondrial translation, GO:0032543
- liver development, GO:0001889
- cellular amino acid metabolic process, GO:0006520
- protein monoubiquitination, GO:0006513
- response to nutrient, GO:0007584
- fatty acid biosynthetic process, GO:0006633
- tricarboxylic acid cycle, GO:0006099
- cellular amino acid biosynthetic process, GO:0008652
- positive regulation of protein catabolic process, GO:0045732
- negative regulation of type I interferon production, GO:0032480
- branched-chain amino acid catabolic process, GO:0009083
- glutamine metabolic process, GO:0006541
- protein catabolic process, GO:0030163
- positive regulation of mitotic cell cycle, GO:0045931
- response to nutrient levels, GO:0031667
- nitrogen compound metabolic process, GO:0006807
- protein K63-linked ubiquitination, GO:0070534
- SUMO transferase activity, GO:0019789
- regulation of translational fidelity, GO:0006450
- purine nucleotide biosynthetic process, GO:0006164
- cellular response to fibroblast growth factor stimulus, GO:0044344
- purine ribonucleoside monophosphate biosynthetic process, GO:0009168
- cullin family protein binding, GO:0097602
- positive regulation of insulin secretion, GO:0032024
- axoneme assembly, GO:0035082
- positive regulation of protein serine/threonine kinase activity, GO:0071902
- response to steroid hormone, GO:0048545
- ERAD pathway, GO:0036503
- dendritic spine development, GO:0060996
- aminoacyl-tRNA synthetase multienzyme complex, GO:0017101
- cellular response to organic substance, GO:0071310
- hydrolase activity, GO:0016810
- organelle membrane, GO:0031090
- regulation of canonical Wnt signaling pathway, GO:0060828
- regulation of protein ubiquitination, GO:0031396
- aminoacyl-tRNA editing activity, GO:0002161
- fatty acid transport, GO:0015908
- pyrimidine nucleotide biosynthetic process, GO:0006221
- hepatocyte differentiation, GO:0070365
- neuromuscular process, GO:0050905
- small protein activating enzyme binding, GO:0044388
- amino acid binding, GO:0016597
- ubiquitin protein ligase activity involved in ERAD pathway, GO:1904264
- regulation of protein processing, GO:0070613
- regulation of cilium assembly, GO:1902017
- response to amino acid, GO:0043200
- negative regulation of androgen receptor signaling pathway, GO:0060766
- urea cycle, GO:0000050
- coenzyme A biosynthetic process, GO:0015937
- glutamate metabolic process, GO:0006536
- carnitine shuttle, GO:0006853
- long-chain fatty-acyl-CoA biosynthetic process, GO:0035338
- succinate metabolic process, GO:0006105
- tRNA-splicing ligase complex, GO:0072669
- ubiquitin-like protein transferase activity, GO:0019787
- protein lipoylation, GO:0009249
- alpha-linolenic acid metabolic process, GO:0036109
- acyl-CoA metabolic process, GO:0006637
- response to starvation, GO:0042594
- negative regulation of JNK cascade, GO:0046329
- biotin metabolic process, GO:0006768
- tRNA aminoacylation, GO:0043039
- bile acid biosynthetic process, GO:0006699
- protein neddylation, GO:0045116
- cellular response to electrical stimulus, GO:0071257
- learning, GO:0007612
- phosphate ion binding, GO:0042301
- fatty-acyl-CoA biosynthetic process, GO:0046949
- arginine binding, GO:0034618
- glutathione binding, GO:0043295
- negative regulation of innate immune response, GO:0045824
- protein targeting to lysosome, GO:0006622
- positive regulation of heart growth, GO:0060421
- NAD biosynthetic process, GO:0009435
- epithelial cilium movement, GO:0003351
- cellular response to hepatocyte growth factor stimulus, GO:0035729
- protein polyglutamylation, GO:0018095
- PRC1 complex, GO:0035102
- VCB complex, GO:0030891
- AMP biosynthetic process, GO:0006167
- phospholipase binding, GO:0043274
- regulation of dopamine metabolic process, GO:0042053
- embryonic viscerocranium morphogenesis, GO:0048703
- sperm axoneme assembly, GO:0007288
- CTP biosynthetic process, GO:0006241
- ketone body biosynthetic process, GO:0046951
- Cul5-RING ubiquitin ligase complex, GO:0031466
- cellular response to leucine, GO:0071233
- coenzyme biosynthetic process, GO:0009108
- ribonucleoside monophosphate biosynthetic process, GO:0009156
- negative regulation of protein processing, GO:0010955
- response to molecule of bacterial origin, GO:0002237
- positive regulation of macromitophagy in response to mitochondrial depolarization, GO:0098779
- SUMO ligase activity, GO:0061665
- tubulin-glutamic acid ligase activity, GO:0070740
- positive regulation of tumor necrosis factor-mediated signaling pathway, GO:1903265
- cellular response to testosterone stimulus, GO:0071394
- cellular response to cholesterol, GO:0071397
- cellular response to prostaglandin E stimulus, GO:0071380
- cellular response to antibiotic, GO:0071236
- protein K11-linked deubiquitination, GO:0035871
- L-ascorbic acid metabolic process, GO:0019852
- positive regulation of vascular associated smooth muscle cell migration, GO:1904754
- pyridine nucleotide biosynthetic process, GO:0019363
- cellular response to manganese ion, GO:0071287
- ‘de novo’ IMP biosynthetic process, GO:0006189
- positive regulation of mitotic metaphase/anaphase transition, GO:0045842
- regulation of glucose metabolic process, GO:0010906
- very long-chain fatty acid metabolic process, GO:0000038
- negative regulation of lipid catabolic process, GO:0050995