

ligase activity, GO:0016874

- protein ubiquitination involved in ubiquitin-dependent protein catabolic process, GO:0042787
- fatty acid metabolic process, GO:0006631
- positive regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032436
- cellular protein modification process, GO:0006464
- tRNA aminoacylation for protein translation, GO:0006418
- protein K48-linked ubiquitination, GO:0070936
- aminoacyl-tRNA ligase activity, GO:0004812
- protein autoubiquitination, GO:0051865
- regulation of protein stability, GO:0031647
- protein destabilization, GO:0031648
- peroxisomal membrane, GO:0005778
- fatty acid biosynthetic process, GO:0006633
- tubulin binding, GO:0015631
- protein monoubiquitination, GO:0006513
- protein K63-linked ubiquitination, GO:0070534
- liver development, GO:0001889
- negative regulation of neuron apoptotic process, GO:0043524
- androgen receptor signaling pathway, GO:0030521
- negative regulation of NF-kappaB transcription factor activity, GO:0032088
- tricarboxylic acid cycle, GO:0006099
- ubiquitin protein ligase activity involved in ERAD pathway, GO:1904264
- cellular amino acid biosynthetic process, GO:0008652
- positive regulation of mitotic cell cycle, GO:0045931
- biosynthetic process, GO:0009058
- glutamine metabolic process, GO:0006541
- SUMO transferase activity, GO:0019789
- branched-chain amino acid catabolic process, GO:0009083
- long-chain fatty acid metabolic process, GO:0001676
- ligase activity, GO:0016876
- ERAD pathway, GO:0036503
- negative regulation of JNK cascade, GO:0046329
- bile acid biosynthetic process, GO:0006699
- cellular amino acid metabolic process, GO:0006520
- aminoacyl-tRNA synthetase multienzyme complex, GO:0017101
- tRNA aminoacylation, GO:0043039
- rough endoplasmic reticulum membrane, GO:0030867
- learning, GO:0007612
- nitrogen compound metabolic process, GO:0006807
- acyl-CoA metabolic process, GO:0006637
- regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032434
- organelle membrane, GO:0031090
- regulation of canonical Wnt signaling pathway, GO:0060828
- long-chain fatty acid-CoA ligase activity, GO:0004467
- cellular response to fibroblast growth factor stimulus, GO:0044344
- sperm axoneme assembly, GO:0007288
- cullin family protein binding, GO:0097602
- AMP binding, GO:0016208
- very long-chain fatty acid-CoA ligase activity, GO:0031957
- purine nucleobase biosynthetic process, GO:0009113
- cellular response to electrical stimulus, GO:0071257
- regulation of glucose metabolic process, GO:0010906
- glutamate metabolic process, GO:0006536
- aminoacyl-tRNA editing activity, GO:0002161
- fatty acid transport, GO:0015908
- folic acid metabolic process, GO:0046655
- ER-mitochondrion membrane contact site, GO:0044233
- response to steroid hormone, GO:0048545
- very long-chain fatty acid metabolic process, GO:0000038
- long-chain fatty-acyl-CoA biosynthetic process, GO:0035338
- positive regulation of lipid storage, GO:0010884
- regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043122
- response to arsenic-containing substance, GO:0046685
- glutathione biosynthetic process, GO:0006750
- response to glucagon, GO:0033762
- negative regulation of viral release from host cell, GO:1902187
- acyl-CoA hydrolase activity, GO:0047617
- response to starvation, GO:0042594
- succinate metabolic process, GO:0006105
- triglyceride metabolic process, GO:0006641
- hydrolase activity, GO:0016810