

ligase activity, GO:0016874

- cellular protein modification process, GO:0006464
- fatty acid metabolic process, GO:0006631
- positive regulation of proteasomal ubiquitin-dependent protein catabolic process, GO:0032436
- aminoacyl-tRNA ligase activity, GO:0004812
- tRNA aminoacylation for protein translation, GO:0006418
- protein K48-linked ubiquitination, GO:0070936
- regulation of protein stability, GO:0031647
- tricarboxylic acid cycle, GO:0006099
- protein K63-linked ubiquitination, GO:0070534
- protein autoubiquitination, GO:0051865
- fatty acid biosynthetic process, GO:0006633
- cellular amino acid biosynthetic process, GO:0008652
- protein monoubiquitination, GO:0006513
- cellular amino acid metabolic process, GO:0006520
- biosynthetic process, GO:0009058
- tRNA aminoacylation, GO:0043039
- branched-chain amino acid catabolic process, GO:0009083
- organelle membrane, GO:0031090
- purine nucleotide biosynthetic process, GO:0006164
- cellular response to organic substance, GO:0071310
- acyl-CoA metabolic process, GO:0006637
- cullin family protein binding, GO:0097602
- protein catabolic process, GO:0030163
- long-chain fatty-acyl-CoA biosynthetic process, GO:0035338
- cellular response to fibroblast growth factor stimulus, GO:0044344
- myelination, GO:0042552
- regulation of translational fidelity, GO:0006450
- glutamine metabolic process, GO:0006541
- long-chain fatty acid metabolic process, GO:0001676
- folic acid metabolic process, GO:0046655
- pyrimidine nucleotide biosynthetic process, GO:0006221
- aminoacyl-tRNA editing activity, GO:0002161
- purine ribonucleoside monophosphate biosynthetic process, GO:0009168
- negative regulation of JNK cascade, GO:0046329
- ligase activity, GO:0016876
- ERAD pathway, GO:0036503
- dendritic spine development, GO:0060996
- positive regulation of tumor necrosis factor-mediated signaling pathway, GO:1903265
- nitrogen compound metabolic process, GO:0006807
- bile acid biosynthetic process, GO:0006699
- ‘de novo’ IMP biosynthetic process, GO:0006189
- response to steroid hormone, GO:0048545
- ribonucleoside monophosphate biosynthetic process, GO:0009156
- urea cycle, GO:0000050
- aminoacyl-tRNA synthetase multienzyme complex, GO:0017101
- response to starvation, GO:0042594
- negative regulation of phagocytosis, GO:0050765
- very long-chain fatty acid metabolic process, GO:0000038
- ubiquitin-like protein transferase activity, GO:0019787
- amino acid binding, GO:0016597
- motor neuron axon guidance, GO:0008045
- AMP binding, GO:0016208
- protein neddylation, GO:0045116
- ketone body biosynthetic process, GO:0046951
- hepatocyte differentiation, GO:0070365
- MSL complex, GO:0072487
- negative regulation of transporter activity, GO:0032410
- negative regulation of protein transport, GO:0051224
- protein lipoylation, GO:0009249
- negative regulation of DNA damage response, GO:0043518
- ER overload response, GO:0006983
- hydrolase activity, GO:0016810
- xenobiotic catabolic process, GO:0042178
- Derlin-1 retrotranslocation complex, GO:0036513
- phosphate ion binding, GO:0042301
- arginine biosynthetic process, GO:0006526
- ‘de novo’ pyrimidine nucleobase biosynthetic process, GO:0006207
- AMP biosynthetic process, GO:0006167
- positive regulation of mitotic metaphase/anaphase transition, GO:0045842
- acyl-CoA ligase activity, GO:0003996
- triglyceride metabolic process, GO:0006641
- protein K11-linked deubiquitination, GO:0035871
- positive regulation of macrophage activation, GO:0043032
- vinculin binding, GO:0017166
- negative regulation of viral release from host cell, GO:1902187
- tetrahydrofolate biosynthetic process, GO:0046654
- tubulin-glutamic acid ligase activity, GO:0070740
- fatty acid alpha-oxidation, GO:0001561
- decanoate--CoA ligase activity, GO:0102391
- response to vitamin D, GO:0033280
- response to magnesium ion, GO:0032026
- fatty-acyl-CoA biosynthetic process, GO:0046949
- modified amino acid binding, GO:0072341
- homocysteine metabolic process, GO:0050667
- ISG15-protein conjugation, GO:0032020
- biotin metabolic process, GO:0006768