fatty acid metabolic process, GO:0006631 cellular protein modification process, GO:0006464 protein K48-linked ubiquitination, GO:0070936 fatty acid biosynthetic process, GO:0006633 tRNA aminoacylation for protein translation, GO:0006418 regulation of protein stability, GO:0031647 liver development, GO:0001889 aminoacyl-tRNA ligase activity, GO:0004812 response to nutrient, GO:0007584 cellular amino acid biosynthetic process, GO:0008652 tricarboxylic acid cycle, GO:0006099 protein monoubiquitination, GO:0006513 purine nucleotide biosynthetic process, GO:0006164 dendritic spine development, GO:0060996 hydrolase activity, GO:0016810 branched-chain amino acid catabolic process, GO:0009083 biotin metabolic process, GO:0006768 protein neddylation, GO:0045116 cellular response to fibroblast growth factor stimulus, GO:0044344 cellular amino acid metabolic process, GO:0006520 nitrogen compound metabolic process, GO:0006807 protein catabolic process, GO:0030163 organelle membrane, GO:0031090 glutamine metabolic process, GO:0006541 long-chain fatty-acyl-CoA biosynthetic process, GO:0035338 axoneme assembly, GO:0035082 purine nucleobase biosynthetic process, GO:0009113 aminoacyl-tRNA synthetase multienzyme complex, GO:0017101 cofactor binding, GO:0048037 tRNA aminoacylation, GO:0043039 long-chain fatty acid metabolic process, GO:0001676 purine ribonucleoside monophosphate biosynthetic process, GO:0009168 positive regulation of cellular protein catabolic process, GO:1903364 glutamate metabolic process, GO:0006536 coenzyme binding, GO:0050662 folic acid metabolic process, GO:0046655 tRNA-splicing ligase complex, GO:0072669 'de novo' IMP biosynthetic process, GO:0006189 AMP binding, GO:0016208 ligase activity, GO:0016876 phosphate ion binding, GO:0042301 lipid biosynthetic process, GO:0008610 bile acid biosynthetic process, GO:0006699 fatty-acyl-CoA biosynthetic process, GO:0046949 tubulin-glutamic acid ligase activity, GO:0070740

ligase activity, GO:0016874

rough endoplasmic reticulum membrane, GO:0030867 decanoate--CoA ligase activity, GO:0102391 energy homeostasis, GO:0097009 triglyceride metabolic process, GO:0006641 positive regulation of glial cell proliferation, GO:0060252 ER overload response, GO:0006983 pyrimidine nucleotide biosynthetic process, GO:0006221 motor neuron axon guidance, GO:0008045 long-chain fatty acid-CoA ligase activity, GO:0004467 L-ascorbic acid metabolic process, GO:0019852 ethanol oxidation, GO:0006069 regulation of cilium assembly, GO:1902017 modification-dependent protein catabolic process, GO:0019941 response to starvation, GO:0042594 nucleophagy, GO:0044804 protein ufmylation, GO:0071569 NEDD8 transferase activity, GO:0019788 fatty acid transport, GO:0015908 response to steroid hormone, GO:0048545 cardiolipin biosynthetic process, GO:0032049 glutathione biosynthetic process, GO:0006750 cerebellar Purkinje cell layer development, GO:0021680 neuromuscular process, GO:0050905 atrioventricular valve morphogenesis, GO:0003181 very long-chain fatty acid metabolic process, GO:0000038 cellular response to leucine, GO:0071233 coenzyme biosynthetic process, GO:0009108 ribonucleoside monophosphate biosynthetic process, GO:0009156 tetrahydrofolate biosynthetic process, GO:0046654 regulation of ER to Golgi vesicle-mediated transport, GO:0060628 phenylalanine-tRNA ligase activity, GO:0004826 acetyl-CoA biosynthetic process, GO:0006085 cellular response to leucine starvation, GO:1990253 positive regulation of macrophage chemotaxis, GO:0010759 positive regulation of cellular metabolic process, GO:0031325 ISG15-protein conjugation, GO:0032020 aspartate metabolic process, GO:0006531 positive regulation of mitotic metaphase/anaphase transition, GO:0045842 cellular response to hepatocyte growth factor stimulus, GO:0035729 protein lipoylation, GO:0009249 cellular response to testosterone stimulus, GO:0071394 cardiac septum morphogenesis, GO:0060411