

lyase activity, GO:0016829

- peroxisome, GO:0005777
- fatty acid beta-oxidation, GO:0006635
- biosynthetic process, GO:0009058
- tRNA splicing, GO:0006388
- RNA phosphodiester bond hydrolysis, GO:0090501
- gluconeogenesis, GO:0006094
- peroxisomal matrix, GO:0005782
- porphyrin-containing compound biosynthetic process, GO:0006779
- lipid storage, GO:0019915
- pyridoxal phosphate binding, GO:0030170
- fatty acid beta-oxidation using acyl-CoA oxidase, GO:0033540
- phosphatidylethanolamine biosynthetic process, GO:0006646
- sphingolipid metabolic process, GO:0006665
- transaminase activity, GO:0008483
- coenzyme binding, GO:0050662
- fatty-acyl-CoA binding, GO:0000062
- carboxy-lyase activity, GO:0016831
- cGMP-mediated signaling, GO:0019934
- presynaptic active zone, GO:0048786
- cyclooxygenase pathway, GO:0019371
- adenylate cyclase binding, GO:0008179
- polyamine biosynthetic process, GO:0006596
- L-phenylalanine catabolic process, GO:0006559
- NADPH binding, GO:0070402
- pantothenate metabolic process, GO:0015939
- nucleoside metabolic process, GO:0009116
- phosphorus-oxygen lyase activity, GO:0016849
- very long-chain fatty acid biosynthetic process, GO:0042761
- pyruvate metabolic process, GO:0006090
- oxidative demethylation, GO:0070989
- oxaloacetate metabolic process, GO:0006107
- histidine metabolic process, GO:0006547
- isocitrate metabolic process, GO:0006102
- 3-hydroxyacyl-CoA dehydrogenase activity, GO:0003857
- enoyl-CoA hydratase activity, GO:0004300
- tryptophan catabolic process, GO:0006569
- cyclic nucleotide biosynthetic process, GO:0009190
- fatty acid elongation, GO:0030497
- peptide hormone binding, GO:0017046