

**lyase activity, GO:0016829**

- protein homotetramerization, GO:0051289
- glycolytic process, GO:0006096
- peroxisomal matrix, GO:0005782
- biosynthetic process, GO:0009058
- canonical glycolysis, GO:0061621
- pyridoxal phosphate binding, GO:0030170
- carboxy-lyase activity, GO:0016831
- fatty acid beta-oxidation using acyl-CoA oxidase, GO:0033540
- entrainment of circadian clock by photoperiod, GO:0043153
- DNA-(apurinic or apyrimidinic site) lyase activity, GO:0003906
- tRNA splicing, GO:0006388
- very long-chain fatty acid biosynthetic process, GO:0042761
- presynaptic active zone, GO:0048786
- sphingolipid metabolic process, GO:0006665
- enoyl-CoA hydratase activity, GO:0004300
- phosphorus-oxygen lyase activity, GO:0016849
- pentose-phosphate shunt, GO:0006098
- fatty-acyl-CoA binding, GO:0000062
- guanylate cyclase activity, GO:0004383
- guanylate cyclase complex, GO:0008074
- bicarbonate transport, GO:0015701
- cyclic nucleotide biosynthetic process, GO:0009190
- polyamine biosynthetic process, GO:0006596
- alpha-linolenic acid metabolic process, GO:0036109
- carboxylic acid metabolic process, GO:0019752
- fatty acid elongation, GO:0030497
- pyruvate metabolic process, GO:0006090
- oxidative demethylation, GO:0070989
- transaminase activity, GO:0008483
- lipoxin metabolic process, GO:2001300
- adenylate cyclase activity, GO:0004016
- cyclooxygenase pathway, GO:0019371
- fibroblast migration, GO:0010761
- DNA dealkylation involved in DNA repair, GO:0006307
- regulation of blood vessel diameter, GO:0097746
- positive regulation of renal sodium excretion, GO:0035815
- inhibitory synapse, GO:0060077
- acrosome reaction, GO:0007340
- 3-hydroxyacyl-CoA dehydratase activity, GO:0018812
- isocitrate metabolic process, GO:0006102
- 3-hydroxyacyl-CoA dehydrogenase activity, GO:0003857
- isoprenoid biosynthetic process, GO:0008299
- glycine binding, GO:0016594