protein homotetramerization, GO:0051289 glycolytic process, GO:0006096 peroxisomal matrix, GO:0005782 cholesterol biosynthetic process, GO:0006695 pyridoxal phosphate binding, GO:0030170 RNA phosphodiester bond hydrolysis, GO:0090501 presynaptic active zone, GO:0048786 tertiary granule lumen, GO:1904724 bicarbonate transport, GO:0015701 tRNA splicing, GO:0006388 androgen metabolic process, GO:0008209 fatty acid beta-oxidation using acyl-CoA oxidase, GO:0033540 carboxy-lyase activity, GO:0016831 pyruvate metabolic process, GO:0006090 transaminase activity, GO:0008483 L-phenylalanine catabolic process, GO:0006559 fatty-acyl-CoA binding, GO:0000062 response to light stimulus, GO:0009416 pentose-phosphate shunt, GO:0006098 pyruvate biosynthetic process, GO:0042866 estrogen metabolic process, GO:0008210

lyase activity, GO:0016829

oxygen binding, GO:0019825 cyclooxygenase pathway, GO:0019371 vacuolar proton-transporting V-type ATPase complex assembly, GO:0070072 DNA N-glycosylase activity, GO:0019104 chemoattractant activity, GO:0042056 guanylate cyclase activity, GO:0004383 guanylate cyclase complex, GO:0008074 pantothenate metabolic process, GO:0015939 carboxylic acid binding, GO:0031406 cAMP biosynthetic process, GO:0006171 glycine binding, GO:0016594 isocitrate metabolic process, GO:0006102 cyclic nucleotide biosynthetic process, GO:0009190 positive regulation of interleukin-10 production, GO:0032733 lysine catabolic process, GO:0006554 adenylate cyclase activity, GO:0004016 peptide metabolic process, GO:0006518 regulation of blood vessel diameter, GO:0097746