

mitochondrial outer membrane, GO:0005741

- positive regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043123
- mitochondrial membrane, GO:0031966
- peroxisome, GO:0005777
- fatty acid metabolic process, GO:0006631
- mitochondrion organization, GO:0007005
- defense response to virus, GO:0051607
- activation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0006919
- apoptotic signaling pathway, GO:0097190
- response to lipopolysaccharide, GO:0032496
- fatty acid beta-oxidation, GO:0006635
- peptidyl-threonine phosphorylation, GO:0018107
- phospholipid biosynthetic process, GO:0008654
- positive regulation of protein targeting to mitochondrion, GO:1903955
- extrinsic apoptotic signaling pathway, GO:0097191
- cellular response to mechanical stimulus, GO:0071260
- execution phase of apoptosis, GO:0097194
- hydrogen ion transmembrane transporter activity, GO:0015078
- protein targeting to mitochondrion, GO:0006626
- response to nutrient, GO:0007584
- cellular response to organic cyclic compound, GO:0071407
- cristae formation, GO:0042407
- ATP synthesis coupled proton transport, GO:0015986
- cellular response to glucose stimulus, GO:0071333
- extrinsic apoptotic signaling pathway via death domain receptors, GO:0008625
- mitochondrial ATP synthesis coupled proton transport, GO:0042776
- response to tumor necrosis factor, GO:0034612
- mitochondrial proton-transporting ATP synthase complex, GO:0005753
- proton-transporting ATP synthase activity, GO:0046933
- 2 iron, GO:0051537
- phosphotransferase activity, GO:0016773
- programmed cell death, GO:0012501
- heme biosynthetic process, GO:0006783
- canonical glycolysis, GO:0061621
- xenobiotic metabolic process, GO:0006805
- cellular response to drug, GO:0035690
- integral component of mitochondrial outer membrane, GO:0031307
- nuclear outer membrane, GO:0005640
- reactive oxygen species metabolic process, GO:0072593
- cellular calcium ion homeostasis, GO:0006874
- protein import into nucleus, GO:0000060
- organelle membrane, GO:0031090
- carbohydrate phosphorylation, GO:0046835
- negative regulation of autophagosome assembly, GO:1902902
- acyl-CoA metabolic process, GO:0006637
- activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway, GO:0097296
- fatty acid transport, GO:0015908
- regulation of proteasomal protein catabolic process, GO:0061136
- mitochondrial proton-transporting ATP synthase complex, GO:0000276
- response to progesterone, GO:0032570
- TORC2 complex, GO:0031932
- decidualization, GO:0046697
- proton-transporting ATP synthase complex, GO:0045263
- cardiac muscle contraction, GO:0060048
- steroid biosynthetic process, GO:0006694
- necroptotic process, GO:0070266
- regulation of mitochondrion organization, GO:0010821
- negative regulation of endothelial cell proliferation, GO:0001937
- positive regulation of transcription factor import into nucleus, GO:0042993
- maternal process involved in female pregnancy, GO:0060135
- heme binding, GO:0020037
- cellular lipid metabolic process, GO:0044255
- death-inducing signaling complex assembly, GO:0071550
- triglyceride metabolic process, GO:0006641
- 3-hydroxyacyl-CoA dehydrogenase activity, GO:0003857
- cellular response to exogenous dsRNA, GO:0071360
- alpha-linolenic acid metabolic process, GO:0036109
- triglyceride biosynthetic process, GO:0019432
- sarcoplasm, GO:0016528
- phosphatidic acid biosynthetic process, GO:0006654
- ‘de novo’ pyrimidine nucleobase biosynthetic process, GO:0006207
- protein channel activity, GO:0015266
- glutathione transferase activity, GO:0004364
- positive regulation of glial cell proliferation, GO:0060252
- biotin metabolic process, GO:0006768
- negative regulation of innate immune response, GO:0045824
- regulation of anion transmembrane transport, GO:1903959
- O-acyltransferase activity, GO:0008374
- protein homotrimerization, GO:0070207
- negative regulation of interferon-beta production, GO:0032688
- long-chain fatty acid metabolic process, GO:0001676
- proton-transporting two-sector ATPase complex, GO:0033177
- CDP-diacylglycerol biosynthetic process, GO:0016024
- glucose binding, GO:0005536
- long-chain fatty-acyl-CoA biosynthetic process, GO:0035338
- ATP transport, GO:0015867
- glutathione binding, GO:0043295
- response to osmotic stress, GO:0006970
- protein localization to membrane, GO:0072657
- gap junction assembly, GO:0016264
- cAMP catabolic process, GO:0006198
- glucose 6-phosphate metabolic process, GO:0051156
- anion transmembrane transport, GO:0098656
- activation of innate immune response, GO:0002218
- positive regulation of necrotic cell death, GO:0010940
- cellular response to leucine, GO:0071233
- coenzyme biosynthetic process, GO:0009108
- long-chain fatty acid-CoA ligase activity, GO:0004467
- monooxygenase activity, GO:0004497
- positive regulation of cysteine-type endopeptidase activity, GO:2001056
- glycerolipid metabolic process, GO:0046486
- neuron projection regeneration, GO:0031102
- heme transporter activity, GO:0015232
- enoyl-CoA hydratase activity, GO:0004300
- NAD biosynthetic process, GO:0009435