

mitochondrial outer membrane, GO:0005741

- mitochondrial membrane, GO:0031966
- positive regulation of I-kappaB kinase/NF-kappaB signaling, GO:0043123
- peroxisome, GO:0005777
- mitochondrion organization, GO:0007005
- activation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0006919
- response to lipopolysaccharide, GO:0032496
- defense response to virus, GO:0051607
- phospholipid biosynthetic process, GO:0008654
- apoptotic signaling pathway, GO:0097190
- fatty acid beta-oxidation, GO:0006635
- protein targeting to mitochondrion, GO:0006626
- cristae formation, GO:0042407
- positive regulation of protein targeting to mitochondrion, GO:1903955
- flavin adenine dinucleotide binding, GO:0050660
- cellular response to mechanical stimulus, GO:0071260
- cellular calcium ion homeostasis, GO:0006874
- mitophagy, GO:0000422
- extrinsic apoptotic signaling pathway via death domain receptors, GO:0008625
- male gonad development, GO:0008584
- execution phase of apoptosis, GO:0097194
- response to organonitrogen compound, GO:0010243
- intrinsic apoptotic signaling pathway by p53 class mediator, GO:0072332
- xenobiotic metabolic process, GO:0006805
- extrinsic apoptotic signaling pathway, GO:0097191
- integral component of mitochondrial outer membrane, GO:0031307
- mitochondrial ATP synthesis coupled proton transport, GO:0042776
- hydrogen ion transmembrane transporter activity, GO:0015078
- regulation of mitochondrial membrane potential, GO:0051881
- mitochondrial proton-transporting ATP synthase complex, GO:0005753
- reactive oxygen species metabolic process, GO:0072593
- ATP synthesis coupled proton transport, GO:0015986
- heme binding, GO:0020037
- monooxygenase activity, GO:0004497
- phosphatidic acid biosynthetic process, GO:0006654
- ATP hydrolysis coupled proton transport, GO:0015991
- canonical glycolysis, GO:0061621
- intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress, GO:0070059
- adipose tissue development, GO:0060612
- negative regulation of intrinsic apoptotic signaling pathway, GO:2001243
- T cell homeostasis, GO:0043029
- response to glucocorticoid, GO:0051384
- 2 iron, GO:0051537
- heme biosynthetic process, GO:0006783
- negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage, GO:1902230
- carbohydrate phosphorylation, GO:0046835
- activation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway, GO:0097296
- TORC2 complex, GO:0031932
- nuclear outer membrane, GO:0005640
- positive regulation of neuron apoptotic process, GO:0043525
- protein channel activity, GO:0015266
- positive regulation of release of cytochrome c from mitochondria, GO:0090200
- protein import into nucleus, GO:0000060
- lactation, GO:0007595
- negative regulation of viral genome replication, GO:0045071
- growth, GO:0040007
- cellular lipid metabolic process, GO:0044255
- positive regulation of transcription factor import into nucleus, GO:0042993
- endoplasmic reticulum calcium ion homeostasis, GO:0032469
- positive regulation of protein homooligomerization, GO:0032464
- phosphotransferase activity, GO:0016773
- programmed cell death, GO:0012501
- proton-transporting ATP synthase activity, GO:0046933
- regulation of mitochondrial membrane permeability, GO:0046902
- mitochondrial outer membrane permeabilization, GO:0097345
- CDP-diacylglycerol biosynthetic process, GO:0016024
- death receptor binding, GO:0005123
- mitochondrial fusion, GO:0008053
- spleen development, GO:0048536
- FAD binding, GO:0071949
- death-inducing signaling complex, GO:0031264
- protein kinase B binding, GO:0043422
- response to iron ion, GO:0010039
- myeloid cell homeostasis, GO:0002262
- triglyceride biosynthetic process, GO:0019432
- cellular response to exogenous dsRNA, GO:0071360
- response to axon injury, GO:0048678
- glutathione transferase activity, GO:0004364
- positive regulation of defense response to virus by host, GO:0002230
- positive regulation of smooth muscle cell migration, GO:0014911
- response to tumor necrosis factor, GO:0034612
- negative regulation of extrinsic apoptotic signaling pathway via death domain receptors, GO:1902042
- blood vessel remodeling, GO:0001974
- lipid phosphorylation, GO:0046834
- P-P-bond-hydrolysis-driven protein transmembrane transporter activity, GO:0015450
- proton-transporting ATP synthase complex, GO:0045263
- transferase activity, GO:0016763
- enoyl-CoA hydratase activity, GO:0004300
- glutathione binding, GO:0043295
- decidualization, GO:0046697
- response to muscle activity, GO:0014850
- cysteine-type endopeptidase activity involved in execution phase of apoptosis, GO:0097200
- chronic inflammatory response, GO:0002544
- multicellular organismal iron ion homeostasis, GO:0060586
- anion transport, GO:0006820
- organelle organization, GO:0006996
- response to progesterone, GO:0032570
- negative regulation of wound healing, GO:0061045
- O-acyltransferase activity, GO:0008374
- regulation of anion transmembrane transport, GO:1903959
- riposome, GO:0097342
- activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c, GO:0008635
- negative regulation of vascular permeability, GO:0043116
- negative regulation of nitric oxide biosynthetic process, GO:0045019
- negative regulation of glycolytic process, GO:0045820
- glucose binding, GO:0005536
- mitochondrial outer membrane translocase complex, GO:0005742
- linoleic acid metabolic process, GO:0043651
- positive regulation of endoplasmic reticulum unfolded protein response, GO:1900103
- regulation of oxidative phosphorylation, GO:0002082
- manganese ion transmembrane transporter activity, GO:0005384
- response to selenium ion, GO:0010269
- negative regulation of mitochondrial membrane potential, GO:0010917
- positive regulation of execution phase of apoptosis, GO:1900119
- energy reserve metabolic process, GO:0006112
- developmental pigmentation, GO:0048066
- positive regulation of glial cell proliferation, GO:0060252
- mitochondrial proton-transporting ATP synthase complex, GO:0000276
- negative regulation of innate immune response, GO:0045824
- anion transmembrane transport, GO:0098656
- protein homotrimerization, GO:0070207
- response to manganese ion, GO:0010042
- negative regulation of endothelial cell proliferation, GO:0001937
- regulation of myotube differentiation, GO:0010830
- manganese ion transmembrane transport, GO:0071421
- glycerolipid metabolic process, GO:0046486
- negative regulation of extrinsic apoptotic signaling pathway in absence of ligand, GO:2001240
- energy homeostasis, GO:0097009
- mitochondrial envelope, GO:0005740
- regulation of mitochondrion organization, GO:0010821
- mammary gland development, GO:0030879
- maternal process involved in female pregnancy, GO:0060135
- protein phosphatase 2B binding, GO:0030346
- regulation of epithelial cell proliferation, GO:0050678
- cellular homeostasis, GO:0019725
- positive regulation of cysteine-type endopeptidase activity, GO:2001056
- mitochondrial ATP synthesis coupled electron transport, GO:0042775
- pore complex, GO:0046930
- cellular response to macrophage colony-stimulating factor stimulus, GO:0036006
- calcium:sodium antiporter activity, GO:0005432
- CD95 death-inducing signaling complex, GO:0031265
- glycerol catabolic process, GO:0019563
- calcium ion transport into cytosol, GO:0060402
- positive regulation of cardiac muscle cell apoptotic process, GO:0010666
- ATP-binding cassette (ABC) transporter complex, GO:0043190