

mitochondrial membrane, GO:0031966

mitochondrial respiratory chain complex I assembly, GO:0032981
mitochondrion organization, GO:0007005
respiratory chain, GO:0070469
mitochondrial intermembrane space, GO:0005758
mitochondrial respiratory chain complex I, GO:0005747
mitochondrial electron transport, GO:0006120
NADH dehydrogenase (ubiquinone) activity, GO:0008137
cristae formation, GO:0042407
defense response to virus, GO:0051607
activation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0006919
proton transport, GO:0015992
mitochondrial transport, GO:0006839
ATP biosynthetic process, GO:0006754
intrinsic apoptotic signaling pathway, GO:0097193
mitochondrial proton-transporting ATP synthase complex, GO:0005753
male gonad development, GO:0008584
flavin adenine dinucleotide binding, GO:0050660
negative regulation of intrinsic apoptotic signaling pathway, GO:2001243
mitochondrial ATP synthesis coupled proton transport, GO:0042776
integral component of mitochondrial inner membrane, GO:0031305
phospholipid metabolic process, GO:0006644
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043280
aerobic respiration, GO:0009060
antiporter activity, GO:0015297
hydrogen ion transmembrane transport, GO:1902600
heme biosynthetic process, GO:0006783
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress, GO:0070059
proton-transporting ATP synthase activity, GO:0046933
response to cold, GO:0009409
mitochondrial fission, GO:0000266
steroid biosynthetic process, GO:0006694
ATP synthesis coupled proton transport, GO:0015986
oxidoreductase activity, GO:0016627
2 iron, GO:0051537
blood vessel remodeling, GO:0001974
mitochondrial electron transport, GO:0006123
negative regulation of viral genome replication, GO:0045071
cellular nitrogen compound metabolic process, GO:0034641
1-acylglycerol-3-phosphate O-acyltransferase activity, GO:0003841
iron ion homeostasis, GO:0055072
cellular respiration, GO:0045333
transmembrane transporter activity, GO:0022857
mitochondrial proton-transporting ATP synthase complex, GO:0000276
mitochondrial calcium ion transmembrane transport, GO:0006851
regulation of mitochondrial membrane permeability, GO:0046902
iron ion binding, GO:0005506
phosphatidic acid biosynthetic process, GO:0006654
extrinsic apoptotic signaling pathway via death domain receptors, GO:0008625
hydrogen ion transmembrane transporter activity, GO:0015078
respiratory electron transport chain, GO:0022904
proton-transporting ATP synthase complex, GO:0045263
response to insulin, GO:0032868
response to glucocorticoid, GO:0051384
ATP hydrolysis coupled cation transmembrane transport, GO:0099132
homeostasis of number of cells, GO:0048872
regulation of multicellular organism growth, GO:0040014
NADH dehydrogenase activity, GO:0003954
brown fat cell differentiation, GO:0050873
flagellated sperm motility, GO:0030317
generation of precursor metabolites and energy, GO:0006091
respiratory chain complex IV assembly, GO:0008535
cytochrome-c oxidase activity, GO:0004129
growth, GO:0040007
mitochondrial fusion, GO:0008053
phagocytic cup, GO:0001891
mitochondrial respiratory chain complex IV assembly, GO:0033617
acyl-CoA dehydrogenase activity, GO:0003995
regulation of heart contraction, GO:0008016
synaptic vesicle membrane, GO:0030672
calcium-dependent phospholipid binding, GO:0005544
mitochondrial respiratory chain complex IV, GO:0005751
clathrin binding, GO:0030276
ATP hydrolysis coupled proton transport, GO:0015991
release of cytochrome c from mitochondria, GO:0001836
phosphotransferase activity, GO:0016780
positive regulation of extrinsic apoptotic signaling pathway in absence of ligand, GO:2001241
monooxygenase activity, GO:0004497
lysine catabolic process, GO:0006554
response to nicotine, GO:0035094
insulin secretion involved in cellular response to glucose stimulus, GO:0035773
Lys48-specific deubiquitinase activity, GO:1990380
receptor internalization, GO:0031623
cellular lipid metabolic process, GO:0044255
sterol metabolic process, GO:0016125
iron ion transport, GO:0006826
lipid phosphorylation, GO:0046834
oxidoreductase activity, GO:0016651
negative regulation of peptidyl-serine phosphorylation, GO:0033137
fatty acid beta-oxidation using acyl-CoA dehydrogenase, GO:0033539
mitochondrial respiratory chain, GO:0005746
oxidoreductase activity, GO:0016705
lysophospholipase activity, GO:0004622
phospholipid catabolic process, GO:0009395
mitochondrial respiratory chain complex III assembly, GO:0034551
limb morphogenesis, GO:0035108
head morphogenesis, GO:0060323
striatum development, GO:0021756
cytolysis, GO:0019835
regulation of intracellular estrogen receptor signaling pathway, GO:0033146
response to superoxide, GO:0000303
glycerolipid metabolic process, GO:0046486
pore complex, GO:0046930
heart contraction, GO:0060047
nuclear outer membrane, GO:0005640
diacylglycerol kinase activity, GO:0004143
CARD domain binding, GO:0050700
glycerophospholipid catabolic process, GO:0046475
ion transmembrane transporter activity, GO:0015075
proton-transporting ATP synthase complex, GO:0045261
spermatid differentiation, GO:0048515
CDP-diacylglycerol biosynthetic process, GO:0016024
negative regulation of calcium ion import, GO:0090281
positive regulation of calcium ion transport into cytosol, GO:0010524
channel activity, GO:0015267
presynaptic membrane, GO:0042734
positive regulation of cAMP biosynthetic process, GO:0030819
ubiquinol-cytochrome-c reductase activity, GO:0008121
mitochondrial calcium uptake, GO:0036444
2-acylglycerol-3-phosphate O-acyltransferase activity, GO:0047144
response to herbicide, GO:0009635
B cell apoptotic process, GO:0001783
negative regulation of mitochondrial membrane potential, GO:0010917
establishment or maintenance of transmembrane electrochemical gradient, GO:0010248
cholesterol transporter activity, GO:0017127
calcium ion homeostasis, GO:0055074
non-canonical Wnt signaling pathway, GO:0035567
protoporphyrinogen IX biosynthetic process, GO:0006782
ear development, GO:0043583
mesenchymal cell development, GO:0014031
positive regulation of protein homooligomerization, GO:0032464
nucleoside diphosphate kinase activity, GO:0004550
O-acyltransferase activity, GO:0008374
sulfate transport, GO:0008272
positive regulation of uterine smooth muscle contraction, GO:0070474