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- respiratory chain, GO:0070469
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- mitochondrion organization, GO:0007005
- mitochondrial electron transport, GO:0006120
- mitochondrial respiratory chain complex I, GO:0005747
- proton transport, GO:0015992
- NADH dehydrogenase (ubiquinone) activity, GO:0008137
- flavin adenine dinucleotide binding, GO:0050660
- fatty acid beta-oxidation, GO:0006635
- cristae formation, GO:0042407
- ATP biosynthetic process, GO:0006754
- mitochondrial ATP synthesis coupled proton transport, GO:0042776
- hydrogen ion transmembrane transport, GO:1902600
- aerobic respiration, GO:0009060
- intrinsic apoptotic signaling pathway, GO:0097193
- mitochondrial transport, GO:0006839
- male gonad development, GO:0008584
- proton-transporting ATP synthase activity, GO:0046933
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- mitochondrial proton-transporting ATP synthase complex, GO:0005753
- heme binding, GO:0020037
- generation of precursor metabolites and energy, GO:0006091
- response to insulin, GO:0032868
- blood vessel remodeling, GO:0001974
- transmembrane transporter activity, GO:0022857
- antiporter activity, GO:0015297
- ATP synthesis coupled proton transport, GO:0015986
- oxidoreductase activity, GO:0016627
- hydrogen ion transmembrane transporter activity, GO:0015078
- phospholipid metabolic process, GO:0006644
- monooxygenase activity, GO:0004497
- mitochondrial electron transport, GO:0006123
- steroid biosynthetic process, GO:0006694
- brown fat cell differentiation, GO:0050873
- heme biosynthetic process, GO:0006783
- iron ion binding, GO:0005506
- respiratory electron transport chain, GO:0022904
- oxidoreductase activity, GO:0016705
- ATP hydrolysis coupled proton transport, GO:0015991
- negative regulation of intrinsic apoptotic signaling pathway, GO:2001243
- cellular response to hormone stimulus, GO:0032870
- proton-transporting ATP synthase complex, GO:0045263
- 1-acylglycerol-3-phosphate O-acyltransferase activity, GO:0003841
- mitochondrial respiratory chain complex IV assembly, GO:0033617
- nuclear outer membrane, GO:0005640
- cytochrome-c oxidase activity, GO:0004129
- oxidoreductase activity, GO:0016651
- lysophospholipase activity, GO:0004622
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- phosphatidic acid biosynthetic process, GO:0006654
- oxidoreductase activity, GO:0016616
- cellular respiration, GO:0045333
- acyl-CoA dehydrogenase activity, GO:0003995
- NADH dehydrogenase activity, GO:0003954
- neuron development, GO:0048666
- negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway, GO:1902236
- mitochondrial inner membrane presequence translocase complex, GO:0005744
- cellular nitrogen compound metabolic process, GO:0034641
- mitochondrial proton-transporting ATP synthase complex, GO:0000276
- lipid phosphorylation, GO:0046834
- mitochondrial ATP synthesis coupled electron transport, GO:0042775
- myeloid cell homeostasis, GO:0002262
- positive regulation of keratinocyte differentiation, GO:0045618
- fatty acid beta-oxidation using acyl-CoA dehydrogenase, GO:0033539
- mitochondrial respiratory chain complex III assembly, GO:0034551
- mitochondrial fusion, GO:0008053
- proton-transporting ATP synthase complex, GO:0045261
- nerve development, GO:0021675
- nucleoside diphosphate phosphorylation, GO:0006165
- positive regulation of protein homooligomerization, GO:0032464
- protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, GO:0001844
- mitochondrial respiratory chain, GO:0005746
- CDP-diacylglycerol biosynthetic process, GO:0016024
- activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c, GO:0008635
- electron transport chain, GO:0022900
- negative regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress, GO:1990441
- glycerolipid metabolic process, GO:0046486
- negative regulation of cell migration involved in sprouting angiogenesis, GO:0090051
- mitochondrial envelope, GO:0005740
- negative regulation of peptidyl-serine phosphorylation, GO:0033137
- quinone binding, GO:0048038
- mitochondrial calcium ion homeostasis, GO:0051560
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- flagellated sperm motility, GO:0030317
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- cellular response to acidic pH, GO:0071468
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- glycerophospholipid catabolic process, GO:0046475
- protoporphyrinogen IX biosynthetic process, GO:0006782
- endoplasmic reticulum tubular network organization, GO:0071786
- ubiquinone binding, GO:0048039
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- positive regulation of neurotransmitter secretion, GO:0001956