

PHOSPHORYLATION, GO_OXIDATIVE_PHOSPHORYLATION

- GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX, GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX
- GO_CELLULAR_RESPIRATION, GO_CELLULAR_RESPIRATION
- GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY, GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY
- GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT, GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT
- GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN, GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN
- GO_RESPIRASOME, GO_RESPIRASOME
- GO_AEROBIC_RESPIRATION, GO_AEROBIC_RESPIRATION
- GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT, GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT
- GO_ORGANELLE_ENVELOPE_LUMEN, GO_ORGANELLE_ENVELOPE_LUMEN
- GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY, GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY
- GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE, GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE
- GO_RESPIRATORY_CHAIN_COMPLEX, GO_RESPIRATORY_CHAIN_COMPLEX
- GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION, GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION
- GO_CYTOCHROME_COMPLEX_ASSEMBLY, GO_CYTOCHROME_COMPLEX_ASSEMBLY
- GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX, GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX
- GO_OXIDOREDUCTASE_COMPLEX, GO_OXIDOREDUCTASE_COMPLEX
- GO_ELECTRON_TRANSPORT_CHAIN, GO_ELECTRON_TRANSPORT_CHAIN
- GO_NADH_DEHYDROGENASE_COMPLEX, GO_NADH_DEHYDROGENASE_COMPLEX
- GO_CRISTAE_FORMATION, GO_CRISTAE_FORMATION
- GO_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY, GO_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY
- GO_NADH_DEHYDROGENASE_ACTIVITY, GO_NADH_DEHYDROGENASE_ACTIVITY
- GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA, GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA
- GO_PROTON_TRANSMEMBRANE_TRANSPORT, GO_PROTON_TRANSMEMBRANE_TRANSPORT
- GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION, GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION
- GO_POSITIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT, GO_POSITIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT
- GO_PURINE_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS, GO_PURINE_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS
- GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX, GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX
- GO_ADP_BINDING, GO_ADP_BINDING
- GO_POSITIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION, GO_POSITIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION
- GO_HEME_BIOSYNTHETIC_PROCESS, GO_HEME_BIOSYNTHETIC_PROCESS
- GO_CATECHOLAMINE_METABOLIC_PROCESS, GO_CATECHOLAMINE_METABOLIC_PROCESS
- GO_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY, GO_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY
- GO_PROTON_TRANSPORTING_ATP_SYNTHASE_ACTIVITY_ROTATIONAL_MECHANISM, GO_PROTON_TRANSPORTING_ATP_SYNTHASE_ACTIVITY_ROTATIONAL_MECHANISM
- GO_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY, GO_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY
- GO_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT, GO_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT
- GO_APOPTOTIC_MITOCHONDRIAL_CHANGES, GO_APOPTOTIC_MITOCHONDRIAL_CHANGES
- GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN, GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN
- GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS, GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS
- GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR
- GO_RIBONUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS, GO_RIBONUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS
- GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS, GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS
- GO_METENCEPHALON_DEVELOPMENT, GO_METENCEPHALON_DEVELOPMENT
- GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS, GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS
- GO_NAD_BINDING, GO_NAD_BINDING
- GO_DOPAMINE_METABOLIC_PROCESS, GO_DOPAMINE_METABOLIC_PROCESS
- GO_DOPAMINE_TRANSPORT, GO_DOPAMINE_TRANSPORT