

PHOSPHORYLATION, GO_OXIDATIVE_PHOSPHORYLATION

- GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN, GO_RESPIRATORY_ELECTRON_TRANSPORT_CHAIN
- GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX, GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX
- GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT, GO_ATP_SYNTHESIS_COUPLED_ELECTRON_TRANSPORT
- GO_RESPIRASOME, GO_RESPIRASOME
- GO_CELLULAR_RESPIRATION, GO_CELLULAR_RESPIRATION
- GO_RESPIRATORY_CHAIN_COMPLEX, GO_RESPIRATORY_CHAIN_COMPLEX
- GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY, GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY
- GO_ELECTRON_TRANSPORT_CHAIN, GO_ELECTRON_TRANSPORT_CHAIN
- GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY, GO_NADH_DEHYDROGENASE_COMPLEX_ASSEMBLY
- GO_AEROBIC_RESPIRATION, GO_AEROBIC_RESPIRATION
- GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE, GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE
- GO_OXIDOREDUCTASE_COMPLEX, GO_OXIDOREDUCTASE_COMPLEX
- GO_NADH_DEHYDROGENASE_COMPLEX, GO_NADH_DEHYDROGENASE_COMPLEX
- GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE, GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_NADH_TO_UBIQUINONE
- GO_CYTOCHROME_COMPLEX, GO_CYTOCHROME_COMPLEX
- GO_NADH_DEHYDROGENASE_ACTIVITY, GO_NADH_DEHYDROGENASE_ACTIVITY
- GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION, GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION
- GO_POSITIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION, GO_POSITIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION
- GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION, GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION
- GO_ORGANELLE_ENVELOPE_LUMEN, GO_ORGANELLE_ENVELOPE_LUMEN
- GO_PROTEIN_TARGETING_TO_MITOCHONDRION, GO_PROTEIN_TARGETING_TO_MITOCHONDRION
- GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H
- GO_PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCEPTOR, GO_PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCEPTOR
- GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT, GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT
- GO_AEROBIC_ELECTRON_TRANSPORT_CHAIN, GO_AEROBIC_ELECTRON_TRANSPORT_CHAIN
- GO_PROTON_TRANSPORTING_ATP_SYNTHASE_ACTIVITY_ROTATIONAL_MECHANISM, GO_PROTON_TRANSPORTING_ATP_SYNTHASE_ACTIVITY_ROTATIONAL_MECHANISM
- GO_ELECTRON_TRANSFER_ACTIVITY, GO_ELECTRON_TRANSFER_ACTIVITY
- GO_CRISTAE_FORMATION, GO_CRISTAE_FORMATION
- GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS
- GO_CYTOCHROME_COMPLEX_ASSEMBLY, GO_CYTOCHROME_COMPLEX_ASSEMBLY
- GO_PROTON_CHANNEL_ACTIVITY, GO_PROTON_CHANNEL_ACTIVITY
- 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_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX, GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX
- GO_POSITIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT, GO_POSITIVE_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT
- GO_PROTON_TRANSMEMBRANE_TRANSPORT, GO_PROTON_TRANSMEMBRANE_TRANSPORT
- GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL, GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL
- GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATALYTIC_DOMAIN, GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATALYTIC_DOMAIN
- GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS, GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS
- GO_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY, GO_PROTON_TRANSMEMBRANE_TRANSPORTER_ACTIVITY
- GO_TRICARBOXYLIC_ACID_CYCLE, GO_TRICARBOXYLIC_ACID_CYCLE
- GO_HEME_BIOSYNTHETIC_PROCESS, GO_HEME_BIOSYNTHETIC_PROCESS
- GO_RESPIRATORY_CHAIN_COMPLEX_IV, GO_RESPIRATORY_CHAIN_COMPLEX_IV
- GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS, GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS
- GO_POSITIVE_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION, GO_POSITIVE_REGULATION_OF_AUTOPHAGY_OF_MITOCHONDRION
- GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX, GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX
- GO_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT, GO_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT
- GO_TETRAPYRROLE_BINDING, GO_TETRAPYRROLE_BINDING
- GO_UBIQUINONE_METABOLIC_PROCESS, GO_UBIQUINONE_METABOLIC_PROCESS
- GO_2_IRON_2_SULFUR_CLUSTER_BINDING, GO_2_IRON_2_SULFUR_CLUSTER_BINDING
- GO_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY, GO_RESPIRATORY_CHAIN_COMPLEX_IV_ASSEMBLY
- GO_POSITIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA, GO_POSITIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA
- GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS, GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS
- GO_IRON_ION_TRANSMEMBRANE_TRANSPORT, GO_IRON_ION_TRANSMEMBRANE_TRANSPORT
- GO_DOPAMINE_BIOSYNTHETIC_PROCESS, GO_DOPAMINE_BIOSYNTHETIC_PROCESS
- GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_UBIQUINOL_TO_CYTOCHROME_C, GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_UBIQUINOL_TO_CYTOCHROME_C
- GO_COP9_SIGNALOSOME, GO_COP9_SIGNALOSOME
- GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS, GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS