

ENASE_ACTIVITY, GO_MONOOXYGENASE_ACTIVITY

- GO_STEROID_HYDROXYLASE_ACTIVITY, GO_STEROID_HYDROXYLASE_ACTIVITY
- GO_EPOXYGENASE_P450_PATHWAY, GO_EPOXYGENASE_P450_PATHWAY
- GO_EXOGENOUS_DRUG_CATABOLIC_PROCESS, GO_EXOGENOUS_DRUG_CATABOLIC_PROCESS
- GO_OXYGEN_BINDING, GO_OXYGEN_BINDING
- GO_ARACHIDONIC_ACID_METABOLIC_PROCESS, GO_ARACHIDONIC_ACID_METABOLIC_PROCESS
- GO_TETRAPYRROLE_BINDING, GO_TETRAPYRROLE_BINDING
- GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_REDUCED_FLAVIN_OR_FLAVOPROTEIN_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_REDUCED_FLAVIN_OR_FLAVOPROTEIN_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN
- GO_ARACHIDONIC_ACID_MONOOXYGENASE_ACTIVITY, GO_ARACHIDONIC_ACID_MONOOXYGENASE_ACTIVITY
- GO_CELLULAR_HORMONE_METABOLIC_PROCESS, GO_CELLULAR_HORMONE_METABOLIC_PROCESS
- GO_COENZYME_BIOSYNTHETIC_PROCESS, GO_COENZYME_BIOSYNTHETIC_PROCESS
- GO_ACTIN_FILAMENT_DEPOLYMERIZATION, GO_ACTIN_FILAMENT_DEPOLYMERIZATION
- GO_DRUG_CATABOLIC_PROCESS, GO_DRUG_CATABOLIC_PROCESS
- GO_ANTIBIOTIC_METABOLIC_PROCESS, GO_ANTIBIOTIC_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_ALPHA_AMINO_ACID_METABOLIC_PROCESS, GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS
- GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_NAD_P_H_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_NAD_P_H_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN
- GO_TERPENOID_METABOLIC_PROCESS, GO_TERPENOID_METABOLIC_PROCESS
- GO_XENOBIOTIC_METABOLIC_PROCESS, GO_XENOBIOTIC_METABOLIC_PROCESS
- GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY, GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY
- GO_RETINOIC_ACID_METABOLIC_PROCESS, GO_RETINOIC_ACID_METABOLIC_PROCESS
- GO_IRON_ION_BINDING, GO_IRON_ION_BINDING
- GO_ICOSANOID_METABOLIC_PROCESS, GO_ICOSANOID_METABOLIC_PROCESS
- GO_CELLULAR_RESPONSE_TO_XENOBIOTIC_STIMULUS, GO_CELLULAR_RESPONSE_TO_XENOBIOTIC_STIMULUS
- GO_ARGININE_METABOLIC_PROCESS, GO_ARGININE_METABOLIC_PROCESS
- GO_FATTY_ACID_CATABOLIC_PROCESS, GO_FATTY_ACID_CATABOLIC_PROCESS
- GO_AROMATASE_ACTIVITY, GO_AROMATASE_ACTIVITY
- GO_VITAMIN_D_METABOLIC_PROCESS, GO_VITAMIN_D_METABOLIC_PROCESS
- GO_TESTOSTERONE_BIOSYNTHETIC_PROCESS, GO_TESTOSTERONE_BIOSYNTHETIC_PROCESS
- GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS, GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS
- GO_MINERALOCORTICOID_METABOLIC_PROCESS, GO_MINERALOCORTICOID_METABOLIC_PROCESS
- GO_CELLULAR_RESPONSE_TO_VITAMIN_D, GO_CELLULAR_RESPONSE_TO_VITAMIN_D
- GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H, GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H