

DASE_COMPLEX, GO_PEPTIDASE_COMPLEX

- GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS, GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS
- GO_PROTEIN_ACETYLTRANSFERASE_COMPLEX, GO_PROTEIN_ACETYLTRANSFERASE_COMPLEX
- GO_ENDOPEPTIDASE_COMPLEX, GO_ENDOPEPTIDASE_COMPLEX
- GO_MODIFICATION_DEPENDENT_PROTEIN_BINDING, GO_MODIFICATION_DEPENDENT_PROTEIN_BINDING
- GO_RNA_POLYMERASE_COMPLEX, GO_RNA_POLYMERASE_COMPLEX
- GO_FICOLIN_1_RICH_GRANULE, GO_FICOLIN_1_RICH_GRANULE
- GO_UBIQUITIN_LIKE_PROTEIN_BINDING, GO_UBIQUITIN_LIKE_PROTEIN_BINDING
- GO_ENDOPEPTIDASE_REGULATOR_ACTIVITY, GO_ENDOPEPTIDASE_REGULATOR_ACTIVITY
- GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY, GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY
- GO_UBIQUITIN_BINDING, GO_UBIQUITIN_BINDING
- GO_RNA_POLYMERASE_II_HOLOENZYME, GO_RNA_POLYMERASE_II_HOLOENZYME
- GO_FC_RECEPTOR_SIGNALING_PATHWAY, GO_FC_RECEPTOR_SIGNALING_PATHWAY
- GO_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY, GO_INTERLEUKIN_1_MEDIATED_SIGNALING_PATHWAY
- GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA, GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA
- GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GO_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I, GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I
- GO_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GO_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GO_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS, GO_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS
- GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I, GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I
- GO_ADA2_GCN5_ADA3_TRANSCRIPTION_ACTIVATOR_COMPLEX, GO_ADA2_GCN5_ADA3_TRANSCRIPTION_ACTIVATOR_COMPLEX
- GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS, GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS
- GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS, GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS
- GO_ERAD_PATHWAY, GO_ERAD_PATHWAY
- GO_PROTEASOME_ACCESSORY_COMPLEX, GO_PROTEASOME_ACCESSORY_COMPLEX
- GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY, GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY
- GO_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION, GO_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION
- GO_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION, GO_HEMATOPOIETIC_STEM_CELL_DIFFERENTIATION
- GO_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_BINDING, GO_GENERAL_TRANSCRIPTION_INITIATION_FACTOR_BINDING
- GO_NUCLEAR_RECEPTOR_TRANSCRIPTION_COACTIVATOR_ACTIVITY, GO_NUCLEAR_RECEPTOR_TRANSCRIPTION_COACTIVATOR_ACTIVITY
- GO_UNFOLDED_PROTEIN_BINDING, GO_UNFOLDED_PROTEIN_BINDING
- GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS, GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS
- GO_TRANSCRIPTION_FACTOR_TFIID_COMPLEX, GO_TRANSCRIPTION_FACTOR_TFIID_COMPLEX
- GO_TBP_CLASS_PROTEIN_BINDING, GO_TBP_CLASS_PROTEIN_BINDING
- GO_SAGA_TYPE_COMPLEX, GO_SAGA_TYPE_COMPLEX
- GO_PROTEASOME_BINDING, GO_PROTEASOME_BINDING
- GO_POLYUBIQUITIN_MODIFICATION_DEPENDENT_PROTEIN_BINDING, GO_POLYUBIQUITIN_MODIFICATION_DEPENDENT_PROTEIN_BINDING
- GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY, GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY
- GO_PROTEASOME_REGULATORY_PARTICLE_BASE_SUBCOMPLEX, GO_PROTEASOME_REGULATORY_PARTICLE_BASE_SUBCOMPLEX
- GO_TRANSCRIPTION_PREINITIATION_COMPLEX_ASSEMBLY, GO_TRANSCRIPTION_PREINITIATION_COMPLEX_ASSEMBLY
- GO_POSITIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GO_POSITIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GO_MORPHOGENESIS_OF_A_POLARIZED_EPITHELIUM, GO_MORPHOGENESIS_OF_A_POLARIZED_EPITHELIUM
- GO_POSITIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULAR_PROTEIN_CATABOLIC_PROCESS, GO_POSITIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULAR_PROTEIN_CATABOLIC_PROCESS
- GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS, GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS
- GO_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PROCESS, GO_PROTEASOMAL_UBIQUITIN_INDEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GO_POSITIVE_REGULATION_OF_COAGULATION, GO_POSITIVE_REGULATION_OF_COAGULATION
- GO_REGULATION_OF_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER, GO_REGULATION_OF_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER
- GO_RNA_POLYMERASE_II_PREINITIATION_COMPLEX_ASSEMBLY, GO_RNA_POLYMERASE_II_PREINITIATION_COMPLEX_ASSEMBLY
- GO_PROTEIN_K63_LINKED_DEUBIQUITINATION, GO_PROTEIN_K63_LINKED_DEUBIQUITINATION
- GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_OXIDATIVE_STRESS, GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_OXIDATIVE_STRESS
- GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY, GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY
- GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY, GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY