

UBIQUITIN_LIGASE_COMPLEX, GOCC_CULLIN_RING_UBIQUITIN_LIGASE_COMPLEX

- GOBP_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GOBP_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GOBP_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS, GOBP_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS
- GOBP_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GOBP_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GOBP_PROTEIN_MONOUBIQUITINATION, GOBP_PROTEIN_MONOUBIQUITINATION
- GOBP_PROTEIN_K11_LINKED_UBIQUITINATION, GOBP_PROTEIN_K11_LINKED_UBIQUITINATION
- GOBP_ERAD_PATHWAY, GOBP_ERAD_PATHWAY
- GOBP_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GOBP_SCF_DEPENDENT_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GOBP_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL, GOBP_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL
- GOMF_PHOSPHATASE_BINDING, GOMF_PHOSPHATASE_BINDING
- GOBP_UBIQUITIN_DEPENDENT_ERAD_PATHWAY, GOBP_UBIQUITIN_DEPENDENT_ERAD_PATHWAY
- GOBP_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS, GOBP_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS
- GOCC_ANAPHASE_PROMOTING_COMPLEX, GOCC_ANAPHASE_PROMOTING_COMPLEX
- GOBP_PROTEIN_K48_LINKED_UBIQUITINATION, GOBP_PROTEIN_K48_LINKED_UBIQUITINATION
- GOMF_PROTEIN_PHOSPHATASE_BINDING, GOMF_PROTEIN_PHOSPHATASE_BINDING
- GOBP_POSITIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULAR_PROTEIN_CATABOLIC_PROCESS, GOBP_POSITIVE_REGULATION_OF_PROTEOLYSIS_INVOLVED_IN_CELLULAR_PROTEIN_CATABOLIC_PROCESS
- GOBP_COPII_COATED_VESICLE_BUDDING, GOBP_COPII_COATED_VESICLE_BUDDING
- GOBP_VESICLE_TARGETING_TO_FROM_OR_WITHIN_GOLGI, GOBP_VESICLE_TARGETING_TO_FROM_OR_WITHIN_GOLGI
- GOBP_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR, GOBP_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR
- GOBP_POSITIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GOBP_POSITIVE_REGULATION_OF_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GOCC_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX, GOCC_CUL3_RING_UBIQUITIN_LIGASE_COMPLEX
- GOBP_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA, GOBP_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_HYPOXIA
- GOBP_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION, GOBP_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION
- GOBP_PROTEIN_AUTOUBIQUITINATION, GOBP_PROTEIN_AUTOUBIQUITINATION
- HP_PROMINENT_NOSE, HP_PROMINENT_NOSE
- HP_NEMALINE_BODIES, HP_NEMALINE_BODIES
- GOBP_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING, GOBP_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING
- GOCC_CUL4_RING_E3_UBIQUITIN_LIGASE_COMPLEX, GOCC_CUL4_RING_E3_UBIQUITIN_LIGASE_COMPLEX
- GOBP_HISTONE_UBIQUITINATION, GOBP_HISTONE_UBIQUITINATION
- GOBP_POSITIVE_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS, GOBP_POSITIVE_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS
- GOCC_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX, GOCC_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX
- HP_HYPERCHLOREMIC_ACIDOSIS, HP_HYPERCHLOREMIC_ACIDOSIS
- GOBP_PHOTOPERIODISM, GOBP_PHOTOPERIODISM