

_PATHWAY, GO_ERAD_PATHWAY

GO_UBIQUITIN_DEPENDENT_ERAD_PATHWAY, GO_UBIQUITIN_DEPENDENT_ERAD_PATHWAY

GO_DE_NOVO_PROTEIN_FOLDING, GO_DE_NOVO_PROTEIN_FOLDING

GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY, GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY

GO_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEINS, GO_PROTEIN_QUALITY_CONTROL_FOR_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEINS

GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT, GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT

GO_HRD1P_UBIQUITIN_LIGASE_ERAD_L_COMPLEX, GO_HRD1P_UBIQUITIN_LIGASE_ERAD_L_COMPLEX

GO_MANNOSIDASE_ACTIVITY, GO_MANNOSIDASE_ACTIVITY

GO_CELL_REDOX_HOMEOSTASIS, GO_CELL_REDOX_HOMEOSTASIS

GO_ENDOPLASMIC_RETICULUM_ORGANIZATION, GO_ENDOPLASMIC_RETICULUM_ORGANIZATION

GO_CHAPERONE_COFACTOR_DEPENDENT_PROTEIN_REFOLDING, GO_CHAPERONE_COFACTOR_DEPENDENT_PROTEIN_REFOLDING

GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS, GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS

GO_PROTEIN_DEGLYCOSYLATION, GO_PROTEIN_DEGLYCOSYLATION

GO_ER_UBIQUITIN_LIGASE_COMPLEX, GO_ER_UBIQUITIN_LIGASE_COMPLEX