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## Functional annotation of proteoforms in the mouse genome database using the protein ontology

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The Mouse Genome Informatics (MGI) is the international database resource for the laboratory mouse, providing integrated genetic, genomic and biological data to facilitate the study of human health and disease. MGI uses the Gene Ontology (GO) for functional annotation of mouse genes. However, single eukaryotic genes can encode multiple protein isoforms due to the usage of alternate promoters or polyadenylation sites, alternative splicing of the primary transcript and/or selection of alternative start sites during translation of an mRNA. Proteins can be further subjected to post-translational processing events. As well, the functioning or cellular location of these proteoforms may be quite different. To provide the most accurate level of annotation, MGI curators make literature-based manual GO annotations using proteoform IDs provided by the Protein Ontology (PRO). PRO is an ontological resource that supplies unique identifiers to specific proteoforms. These forms are organized in an ontological framework that explicitly describes how these entities relate both in contexts of taxon-specific genome localization as well as comparatively with other taxa. The ontology currently has over 68,600 isoforms and 6440 modified proteoforms, which are either imported from high-quality sources or added via literature-based annotation along with attributes such as provenance. Among them, there are 17,811 mouse isoforms and 589 manual curated mouse specific PTM forms. The GO annotations to proteoforms are grouped according to the encoding gene, and can be queried for and viewed at MGI, as well as at the Amigo database.

## Biography

Li Ni is a Senior Scientific Curator with the Mouse Genome Informatics (MGI) project at The Jackson Laboratory. The MGI system is a model-organism community database resource that provides integrated information about the genetics, genomics and phenotypes of the laboratory mouse. As a Curator of the Gene Ontology (GO) and Protein Ontology (PRO) Consortium, she has more than fifteen years of annotation experience in controlled structured vocabularies for molecular biology that serve as terminologies, classifications and ontologies to further data integration, analysis and reasoning.

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