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Specific bioinformatic concerns (Gene Ontologies)**

The Gene Ontology (GO) Consortium, a collaboration between model organism databases and other organizations involved in the annotation of gene products, is developing a system to annotate genes and gene products from any species. Having a common language to describe a gene's process, function, or location facilitates comparison of the genes or genomes of different species. The use of a controlled vocabulary and a unique identifier (GO ID number) for each GO term makes this system useful for human interpretation as well as computational analysis of large scale experiments including phenotypic analyses, two-hybrid screens, microarray experiments, and genomic sequence comparisons.

GO itself does not provide a nomenclature for gene products; rather, the vocabulary is derived from terms used in the scientific literature. Therefore, use of a consistent nomenclature representing clearly defined types of kinesin proteins, and applicable to kinesins from any species, within the research literature will help GO developers represent kinesin functions and processes accurately within the ontologies. Such a nomenclature will also improve the ability of annotaters to assign GO terms correctly and consistently. The combination of consistent nomenclature and accurate GO annotations will facilitate bioinformatic analyses of the kinesin family of proteins, including those found in newly sequenced genomes.