

THE GENE ONTOLOGY HANDBOOK%0A

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[The Gene Ontology Handbook | SpringerLink](#)

This book provides a practical and self-contained overview of the Gene Ontology (GO), the leading project to organize biological knowledge on genes and their products across genomic resources.

[The Gene Ontology Handbook - chapters.indigo.ca](#)

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[Gene Ontology Resource](#)

The Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes. This knowledge is both human-readable and machine-readable, and is a foundation for computational analysis of large-scale molecular biology and genetics experiments in biomedical research.

[Gene ontology - Wikipedia](#)

The Gene Ontology Consortium is the set of biological databases and research groups actively involved in the gene ontology project. This includes a number of model organism databases and multi-species protein databases, software development groups, and a dedicated editorial office.

[The Gene Ontology Handbook | Christophe Dessimoz | Springer](#)

This book is open access under a CC BY 4.0 license. This book provides a practical and self-contained overview of the Gene Ontology (GO), the leading project to organize biological knowledge on genes and their products across genomic resources.

[Gene Ontology: tool for the unification of biology](#)

A dynamic gene ontology The GO Consortium is a joint project of three model organism databases: FlyBase 16, Mouse Genome Informatics 17, 18 (MGI) and the Saccharomyces Genome Database 19 (SGD). It is expected that other organism databases will join in the near future.

[Download Annotations | Gene Ontology Consortium Overview](#). The gene association files ingested from GO Consortium members are shown in the table below. Files

are in the GO annotation file format and are compressed using the UNIX gzip utility.

Gene Ontology (GO) TOOLS

"The Gene Ontology (GO) project was established to provide a common language to describe aspects of a gene product's biology. The use of a consistent vocabulary allows genes from different species to be compared based on their GO annotations. The objective of GO is to provide controlled vocabularies for the description of the

Gene Ontology - DNASTAR

Gene Ontology. ArrayStar's Gene Ontology view, accessed via the Data > Show Gene Ontology command, aids you in determining the biological significance of a gene selection by displaying currently selected genes in relation to a designated annotation field.

Gene Ontology Term Enrichment - Wikipedia

Gene Ontology (GO) term enrichment is a technique for interpreting sets of genes making use of the Gene Ontology system of classification, in which genes are assigned to a set of predefined bins depending on their functional characteristics.

Gene Ontology (GO) - uniprot.org

Used when information about the genomic context of a gene product forms part of the evidence for a particular annotation. Genomic context includes, but is not limited to, such things as identity of neighboring genes (i.e. synteny), operon structure, and phylogenetic or other whole genome analysis.

Gene ontology | Wiki | Everipedia

The Gene Ontology Consortium is the set of biological databases and research groups actively involved in the gene ontology project. [29] This includes a number of model organism databases and multi-species protein databases, software development groups, and a dedicated editorial office.

Gene ontology - Wikipedia

Gene ontology (GO) is a major bioinformatics initiative to unify the representation of gene and gene product attributes across all species. More specifically, the project aims to: 1) maintain and develop its controlled vocabulary of gene and gene product attributes; 2) annotate genes and gene products, and assimilate and disseminate annotation data; and 3) provide tools for easy access to all

GO enrichment analysis - geneontology.org

GO enrichment analysis. One of the main uses of the GO is to perform enrichment analysis on gene sets. For example, given a set of genes that are up-regulated under certain conditions, an enrichment analysis will find which

GO terms are over-represented (or under-represented) using annotations for that gene set.