

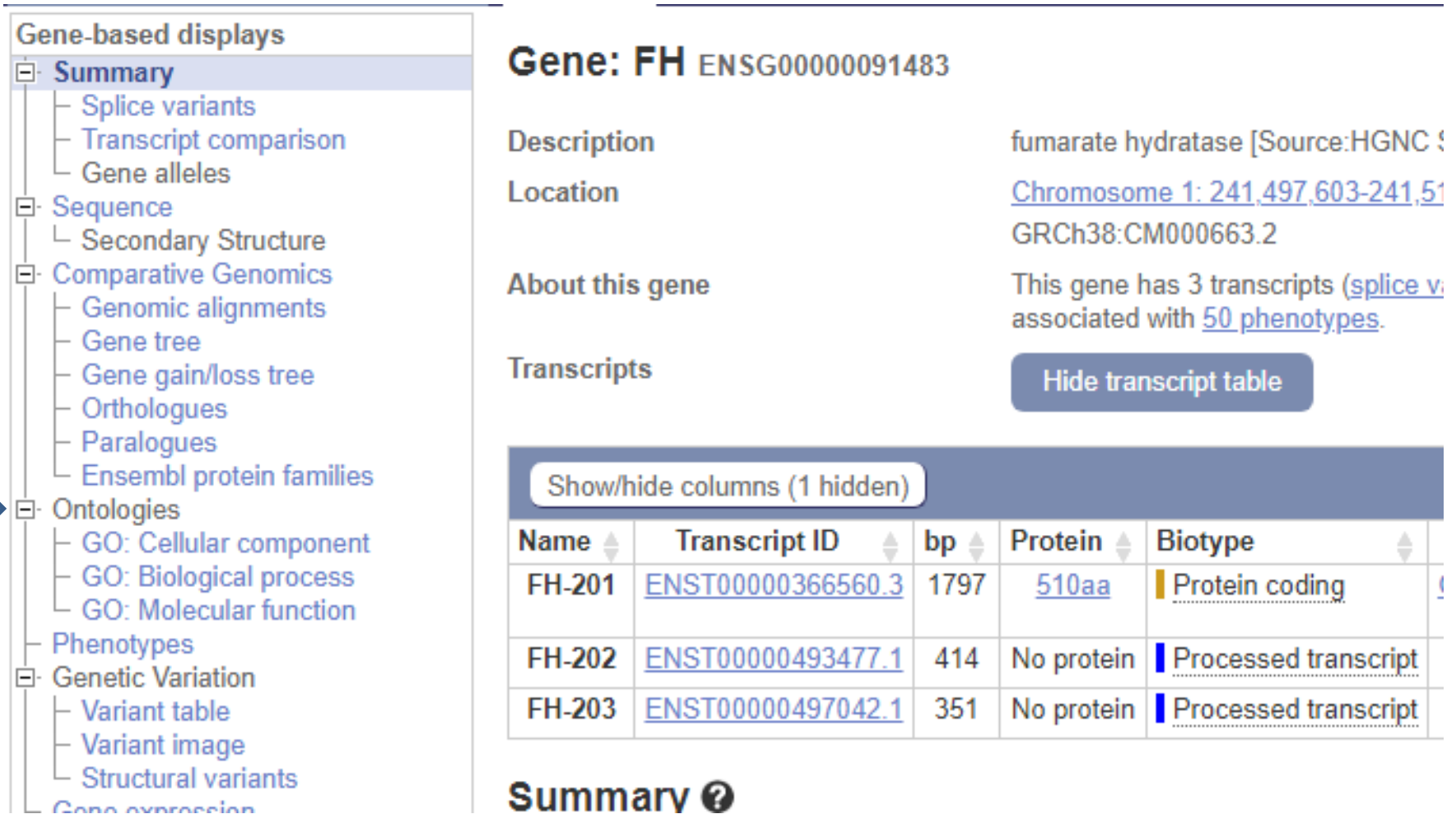
Ch2-L5.2

Accessories

GO

Gene Ontology

When you are in the [ENSEMBL browser](#) on some human gene, please note that on the left menu there are Gene Ontologies.



Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
- Comparative Genomics
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
 - Ensembl protein families
- Ontologies**
 - GO: Cellular component
 - GO: Biological process
 - GO: Molecular function
- Phenotypes
- Genetic Variation
 - Variant table
 - Variant image
 - Structural variants
 - Gene expression

Gene: FH ENSG00000091483

Description fumarate hydratase [Source:HGNC ;

Location [Chromosome 1: 241,497,603-241,51](#)
GRCh38:CM000663.2

About this gene This gene has 3 transcripts ([splice v](#) associated with [50 phenotypes](#).

Transcripts [Hide transcript table](#)

Show/hide columns (1 hidden)				
Name	Transcript ID	bp	Protein	Biotype
FH-201	ENST00000366560.3	1797	510aa	Protein coding
FH-202	ENST00000493477.1	414	No protein	Processed transcript
FH-203	ENST00000497042.1	351	No protein	Processed transcript

Summary ?

Click on the three terms and have a look

Ontologies are established and organized by the Gene Ontology Consortium

Project: **Gene Ontology**

Definition of controlled terms to describe genes

Gene Ontology

<http://www.geneontology.org/>



Current release 2019-03-18: 45.007 GO terms | 6.265.373 annotations
1.140.892 gene products | 4.431 species

THE GENE ONTOLOGY RESOURCE

The mission of the GO Consortium is to develop a comprehensive, **computational model of biological systems**, ranging from the molecular to the organism level, across the multiplicity of species in the tree of life.

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.

Search GO term or Gene Product in AmiGO ...



- Any
- Ontology
- Gene Product

GO Enrichment Analysis ?

Powered by PANTHER

Your gene IDs here...

biological process

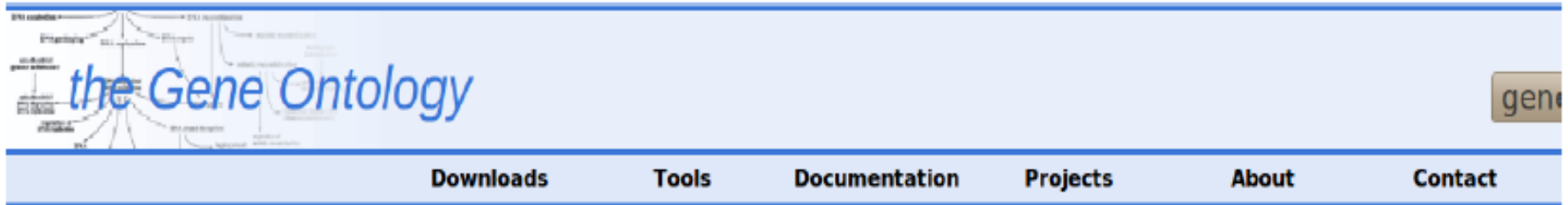
Homo sapiens

Examples

Launch >

Hint: can use UniProt ID/AC, Gene Name, Gene Symbols, MOD IDs

Aim:



Welcome to the Gene Ontology website!

The Gene Ontology project is a major bioinformatics initiative with the aim of standardizing the representation of gene and gene product attributes across species and databases. The project provides [a controlled vocabulary of terms](#) for describing gene product characteristics and [gene product annotation data](#) from GO Consortium members, as well as [tools to access and process this data](#). [Read more about the Gene Ontology...](#)

Aim:

Biologists tend to use different names for the same concept:

eg: ***translation*** vs ***protein synthesis***

The Gene Ontology (GO) project is a collaborative effort to address the need for consistent descriptions of gene products in different databases.

→ ***a unified (universal) vocabulary for biology***







The GO project has developed three structured controlled vocabularies (**ontologies**) that describe gene products and defined logical relationships between them.

Ontology: vocabulary

The GO consortium has defined three different structured vocabularies (ontologies):

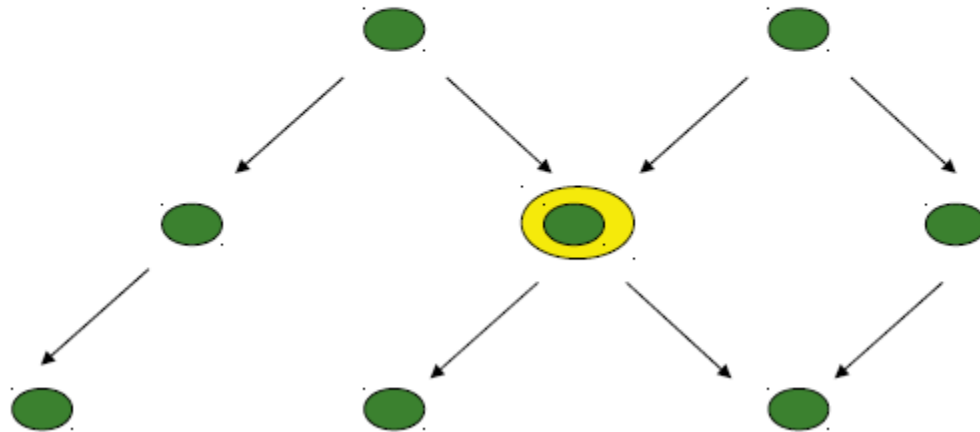
- *Molecular Function*: elemental activity or task
DNA binding, catalysis of a reaction
- *Biological Process*: broad objective or goal
mitosis, signal transduction, metabolism
- *Cellular Component*: location or complex
nucleus, ribosome

Today, March 29, 2019

		biological_process	921699
		cellular_component	878687
		molecular_function	874714

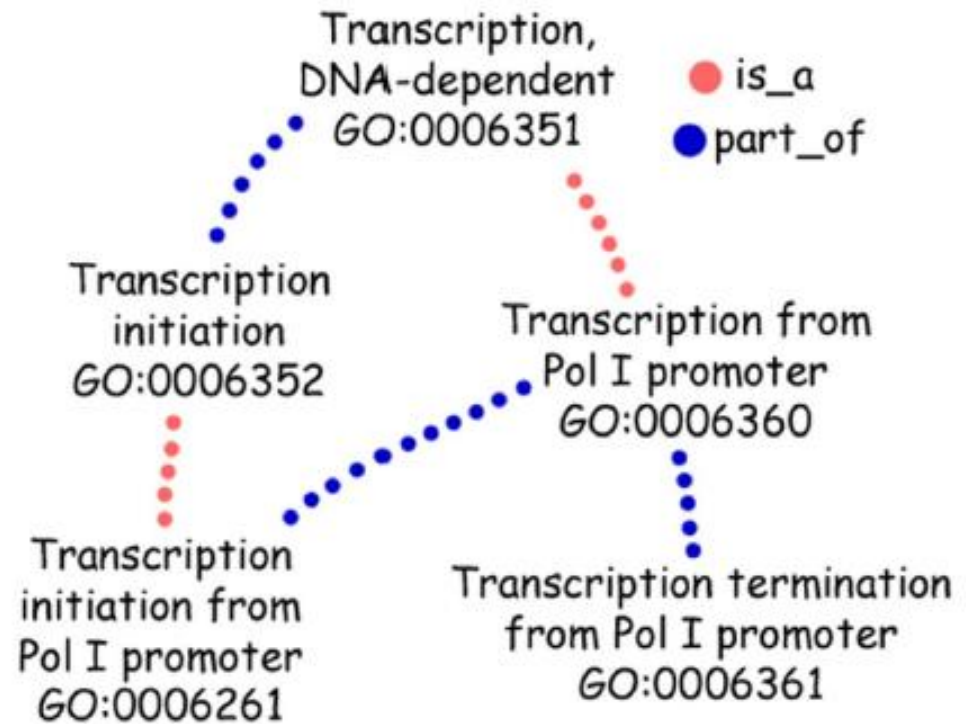


The ontologies are structured as directed acyclic graphs, which are similar to hierarchies but differ in that a child, or more specialized, term can have many parents, or less specialized, terms.



The vocabulary: relationships

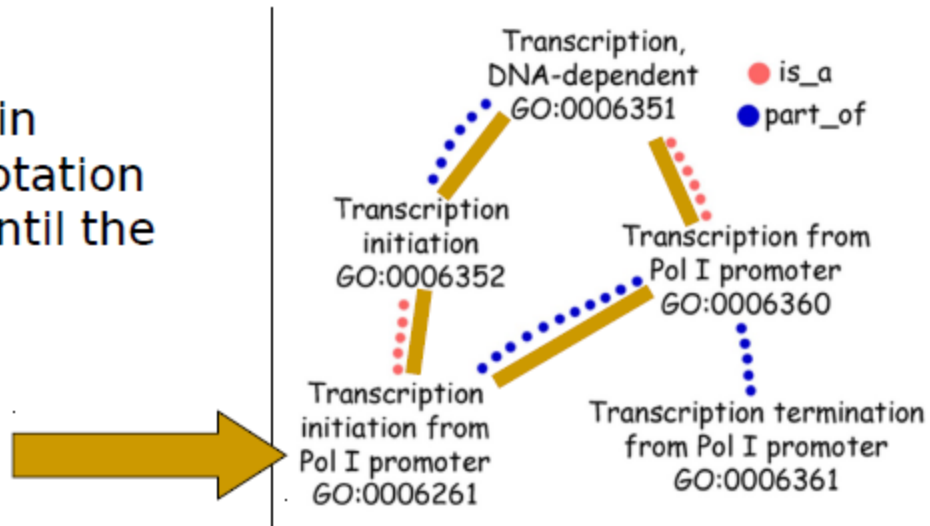
The terms in an ontology are linked by different types of relationships, like *is_a* and *part_of*.



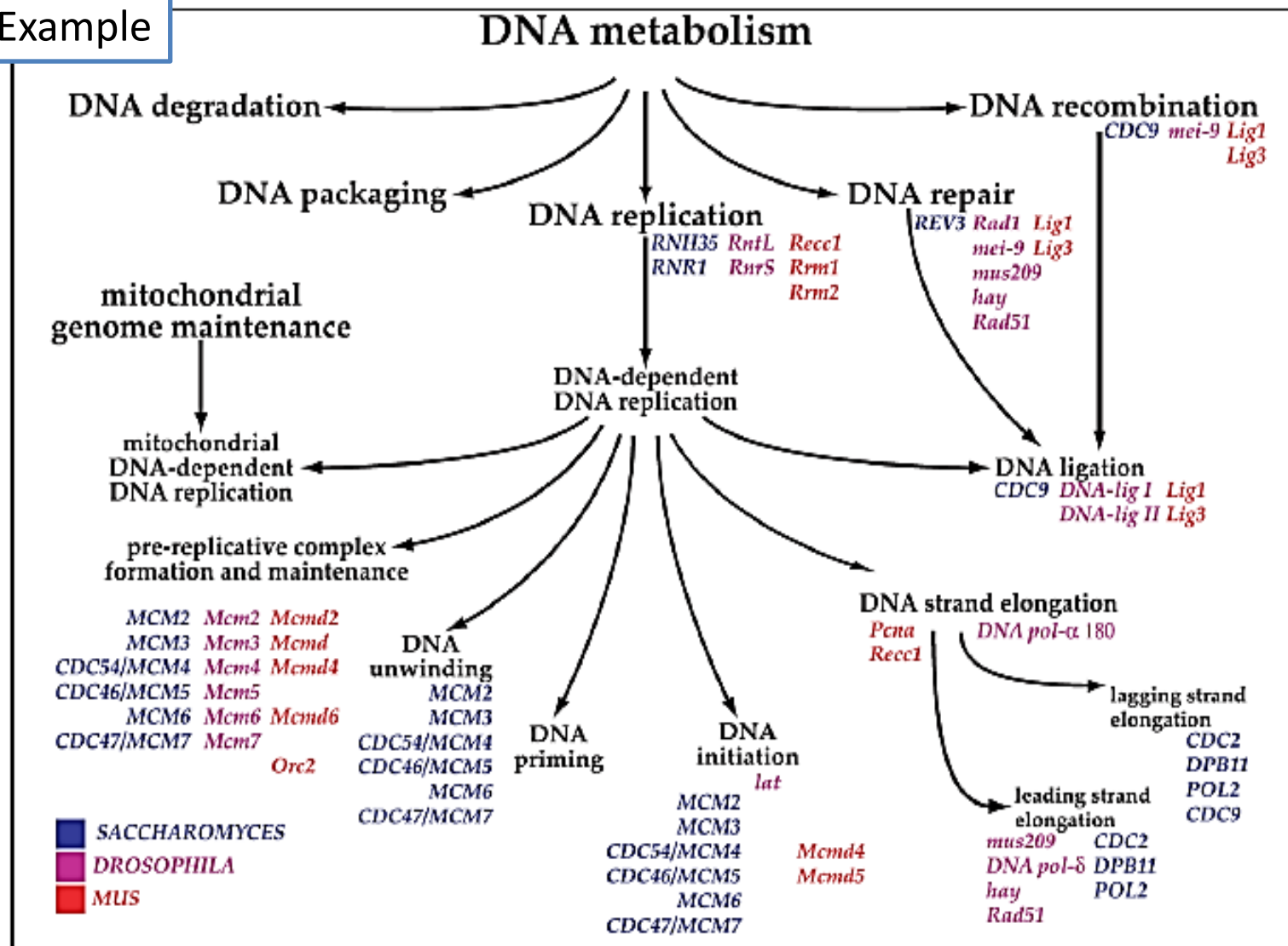
The vocabulary: true path rule

If the child term describes a gene product, then all its parent terms must also apply to that gene product.

Annotation to a certain GO term implies annotation to all the ancestors until the root GO term.



Example



Example

molecular function

nucleic acid binding

enzyme

DNA binding

helicase

adenosine triphosphatase

chromatin binding

DNA helicase

ATP-dependent helicase

DNA-dependent adenosine triphosphatase

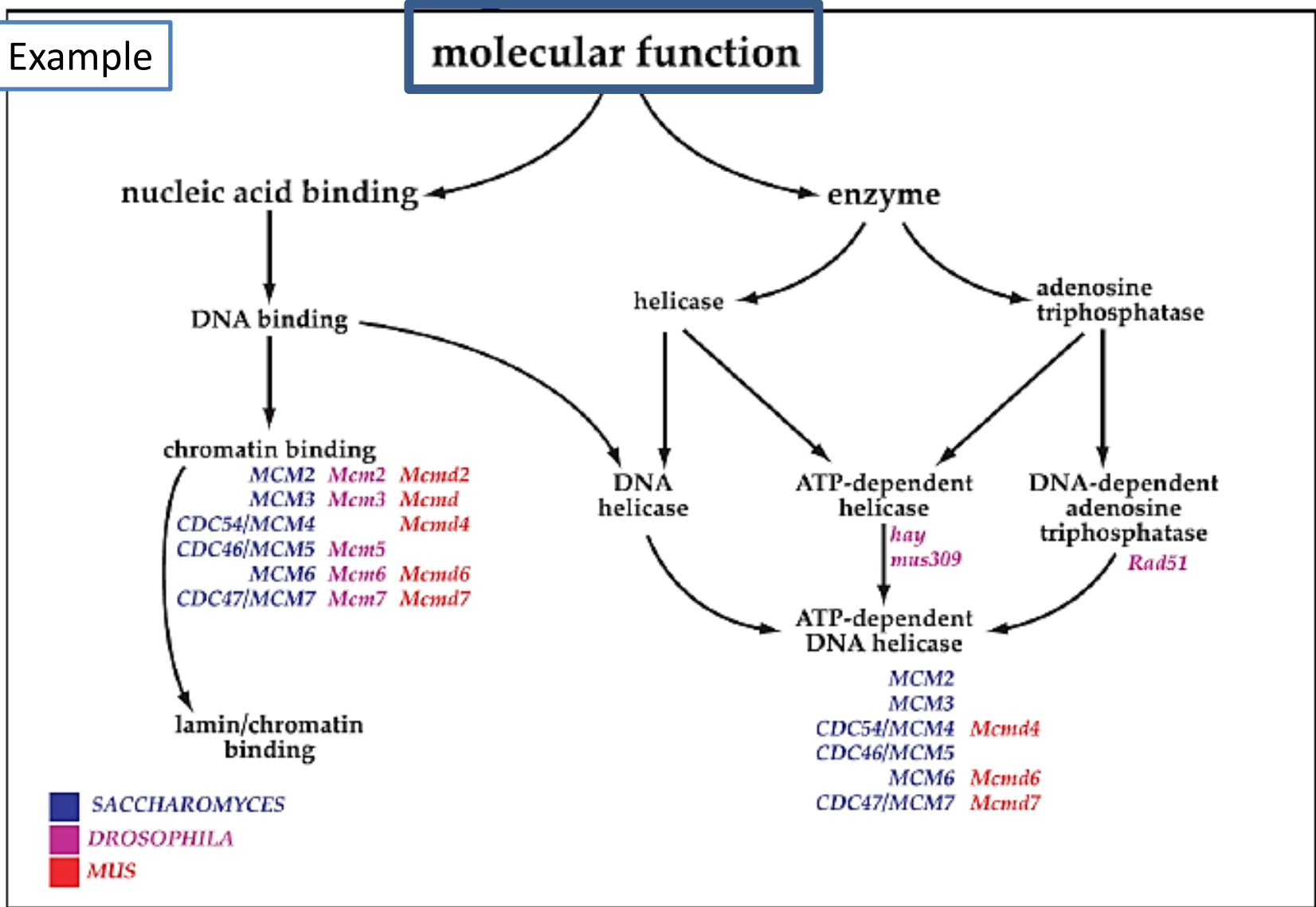
MCM2 Mcm2 Mcmd2
MCM3 Mcm3 Mcmd3
CDC54/MCM4 Mcmd4
CDC46/MCM5 Mcm5
MCM6 Mcm6 Mcmd6
CDC47/MCM7 Mcm7 Mcmd7

lamin/chromatin binding

ATP-dependent DNA helicase

MCM2
MCM3
CDC54/MCM4 Mcmd4
CDC46/MCM5
MCM6 Mcmd6
CDC47/MCM7 Mcmd7

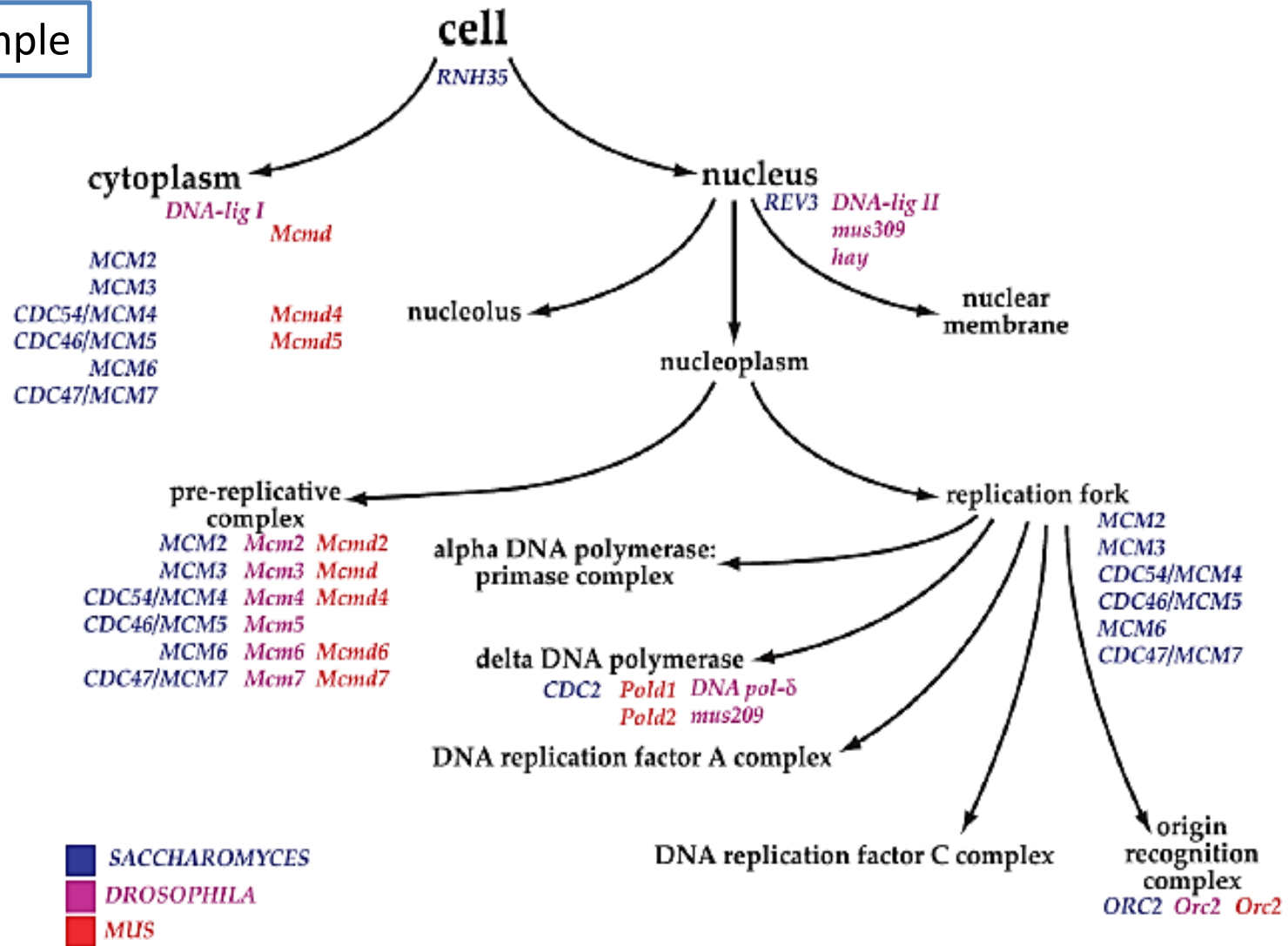
SACCHAROMYCES
DROSOPHILA
MUS



PAUSE

Cell component

Example

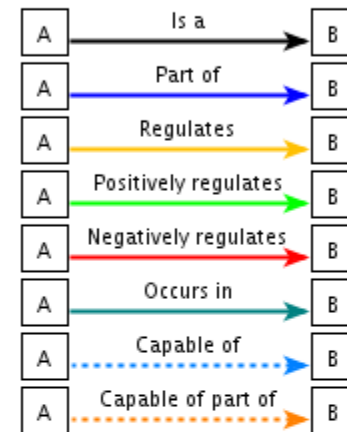
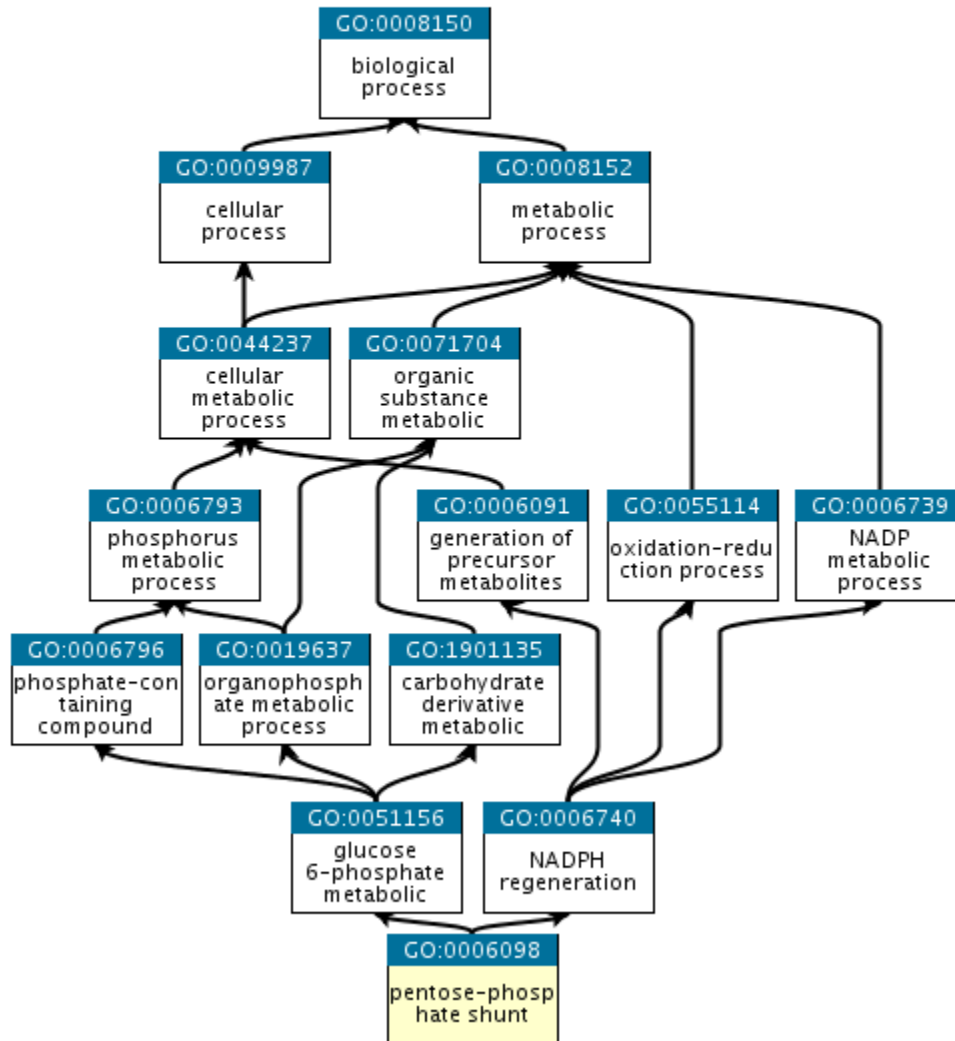


Ancestor Chart

Ancestor chart for GO:0006098

Chart options ▾

search term «pentose phosphate shunt»



GO does not include:

- Processes, functions or components that are unique to mutants or diseases: e.g. **oncogenesis**
- Attributes of sequence such as intron/exon parameters
- - Protein domains or structural features or interactions
- Evolution and expression information
- Anatomical or histological features

Go back now to the first page of the Gene Ontology website:

<http://geneontology.org/>

The screenshot shows the Gene Ontology website homepage. At the top, there is a navigation bar with the Gene Ontology logo and the tagline "Unifying Biology". The main navigation menu includes "About", "Ontology", "Annotations", "Downloads", and "Help". On the right side, there are social media icons for Facebook, Twitter, and LinkedIn, along with the "ALLIANCE of GENOME RESEARCHERS" logo.

The main content area is divided into four columns, each representing a different aspect of the Gene Ontology project:

- ONTOLOGY:** The network of biological classes describing the current best representation of the "universe" of biology. The molecular functions, cellular locations, and processes gene products may carry out.
- ANNOTATION:** Statements, based on specific, traceable scientific evidence, asserting that a specific gene product is a real exemplar of a particular GO class.
- GO-CAM:** GO Causal Activity Model (GO-CAM) provides a structured framework to link standard GO annotations into a more complete model of a biological system.
- TOOL & GUIDE:** Tools to curate, browse, search, visualize and download both the ontology and annotations. Bioinformatic Guides (Notebooks) and simple API access to integrate GO into your research.

Each section includes a list of links for further exploration:


- ONTOLOGY:** [GO Ontology Overview](#), [Browse in AmiGO](#), [Download](#)
- ANNOTATION:** [GO Annotations Overview](#), [View in AmiGO](#), [Download](#)
- GO-CAM:** [GO-CAM Overview](#), [Browse GO-CAMs](#), [Download](#)
- TOOL & GUIDE:** [GO Tools Overview](#), [GO APIs Guide](#), [GO GitHub](#)

A «tool» to examine single genes and gene groups
(as, for example, when you have a «gene expression profile» or a signature)

AMIGO

<http://amigo.geneontology.org/amigo>

Term Enrichment Service



Powered by PANTHER

Also see Statistics http://amigo.geneontology.org/amigo/base_statistics

Examples: choose a gene name

Go to see it in:

NCBI Gene

ENSEMBL

UniProt

PDB

Gene Ontology

OMIM - <https://www.ncbi.nlm.nih.gov/omim>

Medicine

NIH – National Institutes of health

<https://www.nih.gov/>

OMIM -

<https://www.ncbi.nlm.nih.gov/omim>

OMM site: <https://omim.org/>