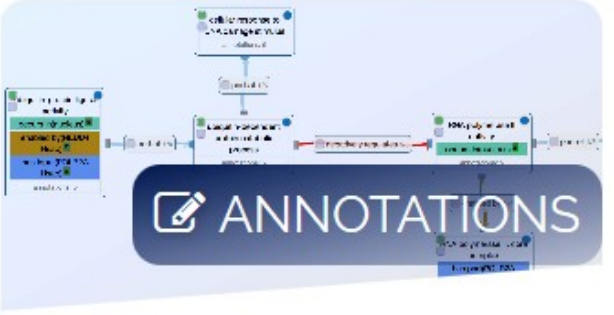
THE GENE ONTOLOGY RESOURCE

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.

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.

GO Ontology Overview
Browse in AmiGO
Download



Statements, based on specific, traceable scientific evidence, asserting that a specific gene product is a real exemplar of a particular GO class.

GO Annotations Overview
View in AmiGO
Download

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.

GO Tools Overview
GO APIs Guide
GO GitHub

http://geneontology.org/

Qué es GO

Es una representación formal del conocimiento biológico.

Es un conjunto de términos o conceptos relacionados.


Science
The End of
PRIVACY
QUICK
MANEUVERS
Flapping-wing robot models
insect flight pp. 1073 & 1089
Science
Science
Science
ILLUMINATING
THE BRAIN
Science
HIDDEN
CONFLICTS?

GO

Together, the ontology and annotations provide a comprehensive model of biological systems. Currently, the GO includes experimental findings from over 150,000 published papers, represented as over 700,000 experimentally-supported annotations. These provide the core dataset for additional inference of over 6 million functional annotations for a diverse set of organisms spanning the tree of life.

- mRNA expression data analysis
- Proteomics data analysis
- Genetic data analysis
- DNA methylation data analysis
- Other uses, primarily in computational biology and biomedical informatics literature

GO agrupa el conocimiento biológico en tres aspectos:

Proceso Biológico: objetivo específico

mitosis, signal transduction, metabolism

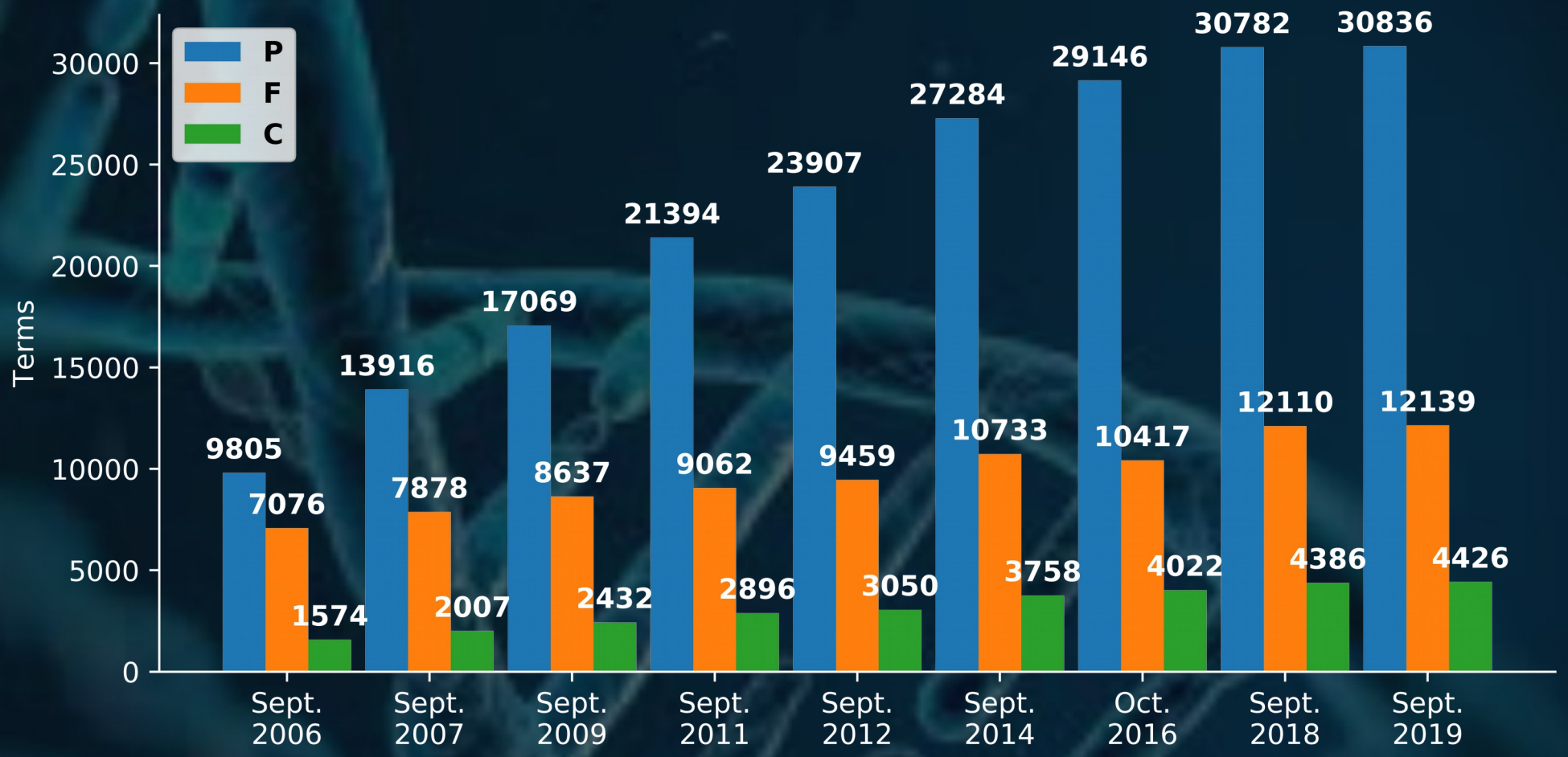
Función Molecular: actividad elemental o tarea

nuclease, DNA binding, catalytic activity

Componente celular: localización o complejo

nucleus, ribosome, membrane

Actualizaciones de GO



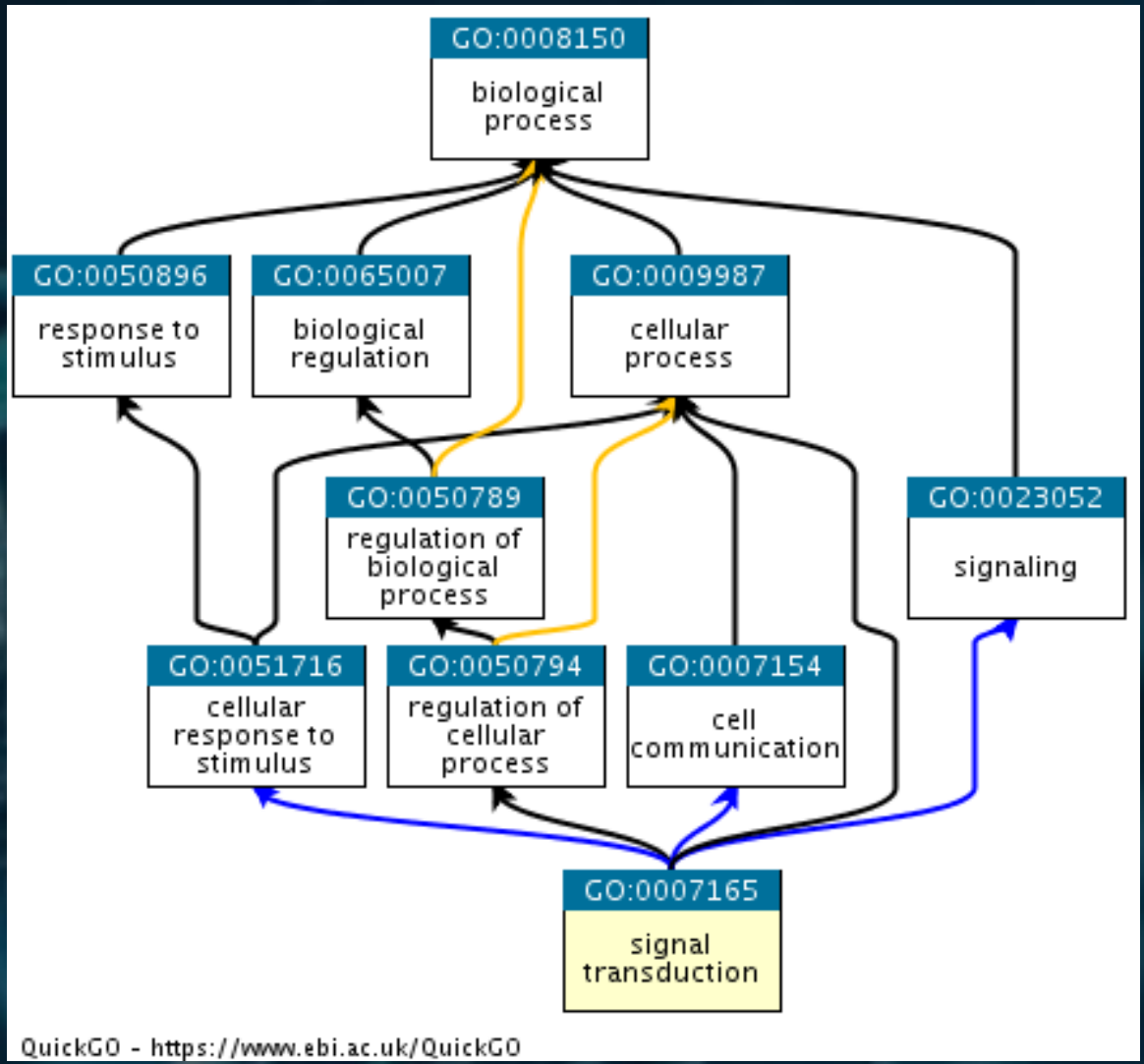
2006 https://academic.oup.com/nar/article/34/suppl_1/D322/1132320
2007 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2238979/
2009 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2808930/
2011 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3245151/
2012 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3531070/
2014 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4383973/
2016 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5210579/

Estructura

Padre

Especificidad

Hijo



Anotaciones

Anotación Estructural

ORF, Estructura de genes, Motivos, Regiones codificantes

Anotación Funcional

Funciones bioquímicas y biológicas, interacción entre productos de genes

La Anotación Funcional es

una declaración donde el producto de un gen

tiene una **función molecular** particular

o está implicado en un **proceso biológico** particular

o está dentro de cierto **componente celular** particular

como determinado por un **método** particular

como descrito en una **referencia** particular

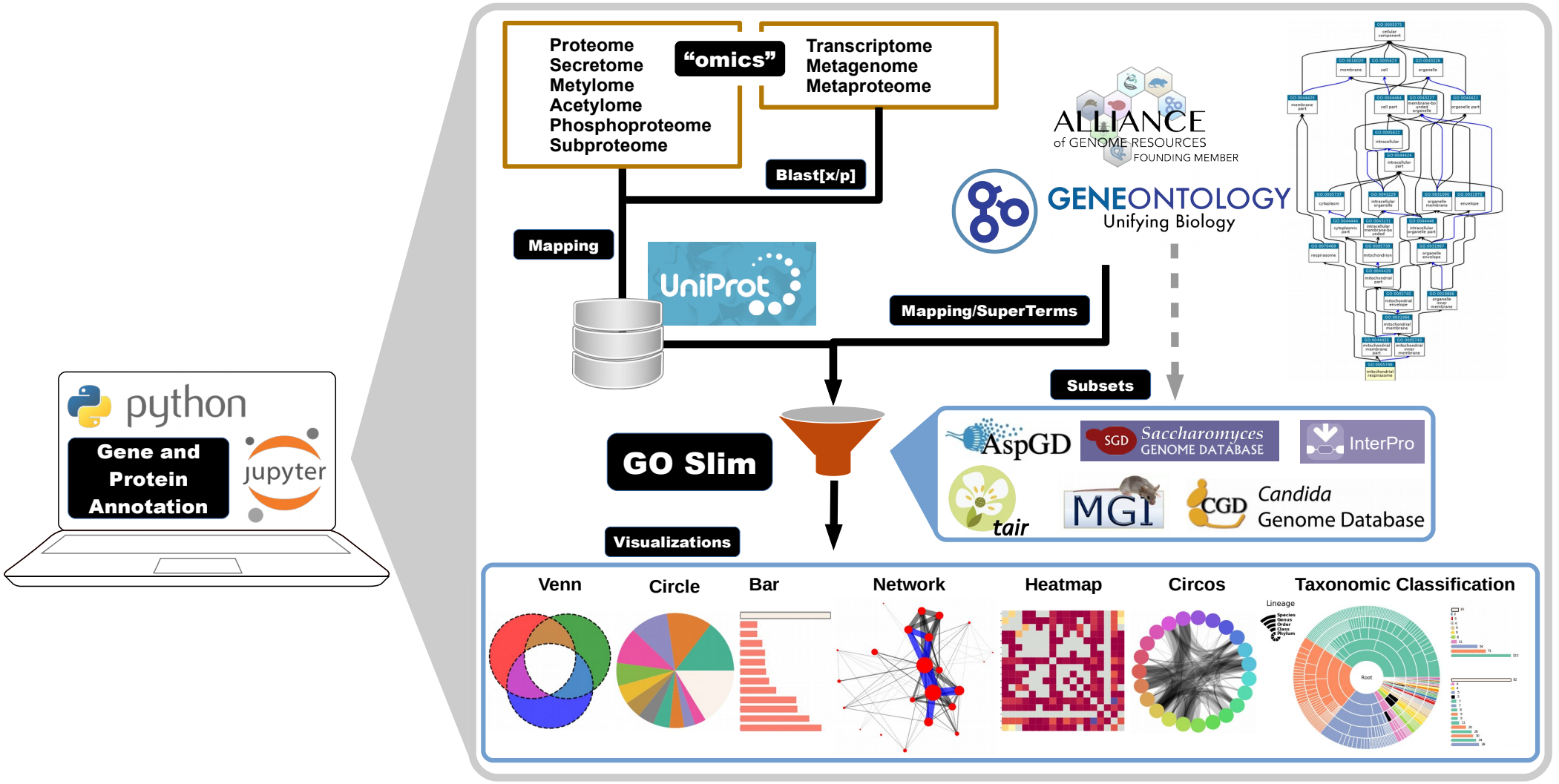
Fuentes de anotación

GENEONTOLOGY
Unifying Biology

Anotación manual
UniProtKB

Anotación automática
UniProt-GOA

http://geneontology.org/page/download-mappings


python
Gene and Protein Annotation
jupyter
Proteome
Secretome
Metylome
Acetylome
Phosphoproteome
Subproteome
"omics"
Transcriptome
Metagenome
Metaproteome
Blast[x/p]
Mapping
UniProt
ALLIANCE
of GENOME RESOURCES
FOUNDING MEMBER
GENEONTOLOGY
Unifying Biology
Mapping/SuperTerms
Subsets
GO Slim
AspGD
SGD Saccharomyces GENOME DATABASE
InterPro
tair
MGI
CGD Candida Genome Database
Visualizations
Venn
Circle
Bar
Network
Heatmap
Circos
Taxonomic Classification
Lineage
Root