



# Functional Analysis

High-Throughput Blast and InterProScan  
Blast2GO Annotation  
Functional Analysis

The OmicsBox Functional Analysis Module allows you to generate high-quality functional annotations via the Blast2GO methodology as well as to perform complex functional analysis in an intuitive way. Main features are:

## High-Throughput Blast and InterProScan

Use CloudBlast and CloudInterProScan to perform fast sequence alignments and domain searches against a reference dataset of your choice.

## Gene Ontology Mapping

Well-curated Uniprot and Gene Ontology databases are used to link potential homologs and domains to up-to-date functional annotations.

## Blast2GO Annotation

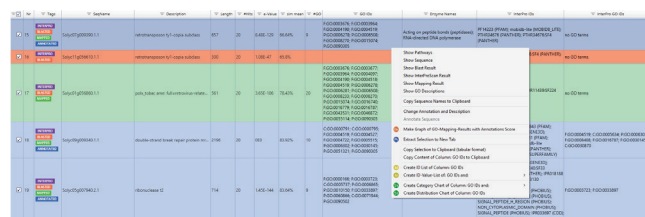
The Blast2GO methodology allows to flexibly assign the most reliable functional labels to novel sequence datasets, taking into account source-annotation qualities and the Gene Ontology hierarchy.

## Enrichment Analysis

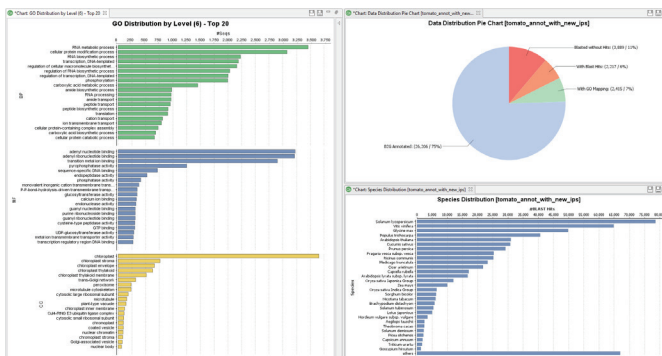
Use different enrichment analysis approaches (Fisher Exact Test and GSEA) to identify over- and under-represented biological functions.

## Functional Interpretation

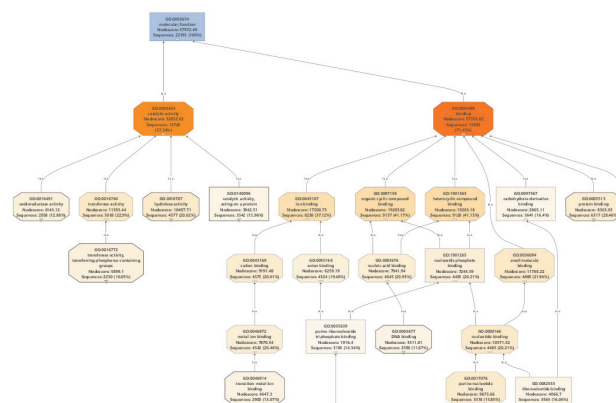
Many different visualizations allow to evaluate the annotation process and to help with the biological interpretation of experimental and functional analysis results.



Start with a FASTA file and analyze it step by step with the Blast2GO methodology to obtain high-quality functional labels with full control over all analysis parameters.



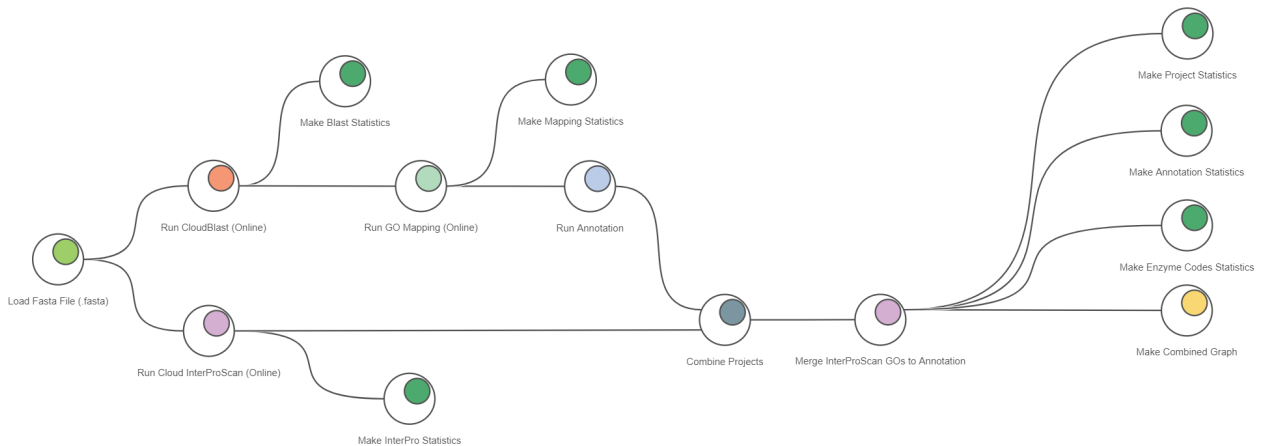
Convenient histograms and distribution charts help you to evaluate every step of your analysis and to get the most out of your data. Visualize annotations as GO graphs. Filter and trim graphs to highlight most abundant functions.





# Functional Analysis

High-Throughput Blast and InterProScan  
Blast2GO Annotation  
Functional Analysis



## Gene Ontology Annotation

This example shows a Gene Ontology annotation workflow which combines fast, cloud-based Blast and InterProScan searches with GO Mapping to obtain high-quality functional annotation labels via the Blast2GO methodology.

Detailed statistics of every step are generated to summarize results. Combined graphs for the three GO categories are generated. The final project contains the combined results of all steps and can be exported in many different formats.

## About Blast2GO



The Blast2GO methodology is the most cited tool for the automatic functional annotation of novel genomes and is internationally recognized by the scientific community with over 10 000 peer-reviewed research citations.

Blast2GO is now part of OmicsBox.

## About OmicsBox and BioBam

BioBam is a leading bioinformatics solution provider which accelerates research in disciplines such as agricultural genomics, microbiology or environmental NGS studies.

OmicsBox is a user-friendly bioinformatics desktop application for industry, academic and governmental research biologists from top private and public research institutions worldwide. It allows to gain biological insights fast and easy even for completely novel genomes.