

Blast2GO® is a complete framework for functional annotation of novel sequences and the analysis of

#### EASY AND LOW MAINTENANCE

Perform the whole annotation process within Blast2-GO and in an interactive and transparent way. Zero maintenance.

#### **USER-FRIENDLY**

annotation data.

Blast2GO is designed for experimentalists. An intuitive design, many graphical options and a detailed documentation makes the use of this plugin possible from the first try.

# HIGH-THROUGHPUT AND INTERACTIVE

Blast2GO can annotate thousands of sequences in one session. Users can follow and modify the annotation process at any stage.

#### HIGHLY CONFIGURABLE

Blast2GO is a functional annotation framework which allows you to design your custom annotation style through the many configurable parameters. Statistical charts are available to guide you during the annotation process.

#### **DATA MINING**

Blast2GO does not only generate functional annotations. You can interrogate the biological meaning of your data with different graphical and statistical functions.

# Blast2G0<sup>®</sup> PRO

Functional annotation and genome-wide analysis of your sequence data



#### MAIN BLAST2GO PRO FEATURES

- Handle tens of thousand of sequences in one project.
- Sequence annotation data presented in spread-sheet format.
- Functional annotation is done in 3 steps: BLAST to find homologus sequences, MAP-PING to retrieve GO terms and ANNOTA-TION to select reliable functions.
- Different annotation databases are supported:
  GO, Enzyme Codes and InterPro
- Configurable annotation settings to adapt to your data.
- Statistical charts to monitor your annotation progress.
- Graphical display of annotation data through GO graphs, pie and bar charts.
- Select sequences based on keywords and functional information
- Functional Enrichment Analysis
- Tools to manipulate GO graphs.





## **TESTIMONIAL**

"Blast2Go provides a convenient, intuitive yet flexible interface for the annotation of large-scale transcript and DNA sequence data [...] We have been using Blast2Go to annotate and explore de novo assemblies of spider transcriptomes and can not imagine how much slower we would have been without it. Blast2Go has been and will continue to be central to our work with transcriptome data. The support team is quick to respond positively. In short, Blast2Go is an indispensable tool for the analysis of next generation DNA sequence data.

> Dr. Peter Croucher Research Fellow The University of Birmingham, UK

#### **DEVELOPED BY**

Blast2GO is developed and maintained by BioBam Bioinformatics which is internationally recognised for its expertise in functional annotation and genome analysis - and demonstrated by over 1000 citations. With our solutions we transform the process of complex data analysis into an attractive and interactive task for biologists reducing the gap between experimental work, bioinformatics analysis, and applied research.

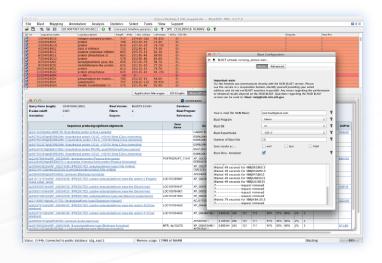
### **TESTIMONIAL**

"I have found Blast2Go very helpful in my work for blasting and annotating various sequences. The versatile and user-friendly interface makes small and large blast-annotations jobs easy and provides a very comprehensive collection of tools needed for doing the work.

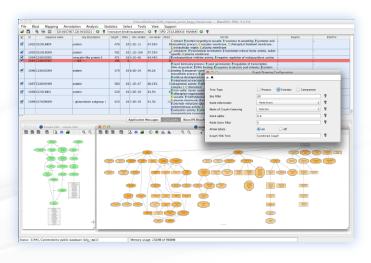
Dr. Knut Erik Tollefsen Senior researcher in Ecotoxicology and adjunct Professor Norwegian Institute for Water Research (NIVA) and University of Life Sciences, Norway

### SYSTEM REQUIREMENTS

Blast2GO is a platform independent Java Application and works on Mac, Windows and Linux systems. All systems have to have Java from Sun/Oracle (version 1.6 or higher) installed. We recommend at least 1GB of ram. Also a working Internet connection is required to use the PRO account and most of the other features of the application.







For evaluation please get a

# FREE TRIAL

and test Blast2GO PRO for 1 week

For more information visit

www.blast2go.com



