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

**EASY AND LOW MAINTENANCE**
Perform the whole annotation process within Blast2GO and in an interactive and transparent way. Zero maintenance.

**USER-FRIENDLY**
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.

**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, Mapping to retrieve GO terms and Annotation 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.
- Access to CloudBlast

**Blast2GO® PRO**
Functional annotation and genome-wide analysis of your sequence data

**Contact:** sales@blast2go.com
**Support:** support@blast2go.com

**www.blast2go.com**
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.

SYSTEM REQUIREMENTS

Blast2GO is available for Mac (10.7+), Windows (XP+) and Linux systems (optimised for and tested on Ubuntu 12.12+). We recommend at least 1GB of RAM. A working internet connection is required to use many of the application features. Blast2GO supports automatic updates (write permissions required). If Blast2GO is run in Basic mode an open network port (3006) for direct MySQL connections is required.

For evaluation please get a FREE TRIAL and test Blast2GO PRO for 1 week

For more information visit www.blast2go.com

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
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