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

EASY AND LOW MAINTENANCE
The plugin lets you perform the whole annotation process within the Workbench 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.

DISTRIBUTED BY:

Blast2GO® PRO Plugin
A functional annotation framework for your CLC bio Workbench

MAIN BLAST2GO PRO PLUGIN FEATURES
• Sequence annotation data presented in spread-sheet format.
• Handle tens of thousand of sequences in one project.
• Functional annotation is done in 3 steps: BLAST to find homologous 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
• Completely workflowable
• Access to CloudBlast

Contact: sales@blast2go.com
Support: pluginsupport@blast2go.com

Developed by:
BioBam Bioinformatics S.L.
The Blast2GO PRO Plugin is developed and maintained by BioBam Bioinformatics, a knowledge-based company dedicated to creating user-friendly software for the scientific community. BioBam is internationally recognized for its expertise in functional annotation and genome analysis. For more information about BioBam and Blast2GO please visit them online at www.blast2go.com and www.biobam.com

SYSTEM REQUIREMENTS

- CLC bio Main, Genomics and Biomedical Workbench
  - The amount of required memory depends on the amount of sequences one wants to load into the plugin. However, we recommend a minimum of 1 GB RAM for any scenario.
- The Blast2GO Plugin depends on the CLC bio Workbench requirements.
- A working network (Internet) connection is required.

For more information visit www.blast2go.com

FREE TRIAL

For evaluation please get a FREE TRIAL from within the CLC bio Workbench

TESTIMONIAL

“For us, CLC Genomics Workbench and Blast2GO are crucial tools for the analysis of necessary de novo transcriptome data. The new CLC Blast2GO plugin allows easier integration of these two tools, reducing the ad hoc time from sequence acquisition to annotation results. Furthermore, it has become indispensable in ongoing gene expression profiling studies of non-model species, because it enables us to identify potentially relevant target genes with ease.”

Dr. Ewald Große-Wilde
Department of Evolutionary Neuroethology
Max Planck Institute for Chemical Ecology

“I in my lab we do bioinformatics analyses of transcriptomes data from species for which no or little genome information is available. The combination of CLC Genomics Workbench and the Blast2GO PRO plugin works great since we can assemble our new transcript sequences and send them directly to functional annotation to quickly identify which transcripts are coding and what they’re coding for, which saves time and adds value to our research.”

Ana Conesa, PhD
Head of Genomics of Gene Expression
Centro de Investigación Príncipe Felipe