

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

Blast2GO

RRID:SCR_005828

Type: Tool

Proper Citation

Blast2GO (RRID:SCR_005828)

Resource Information

URL: <http://www.blast2go.com/b2ghome>

Proper Citation: Blast2GO (RRID:SCR_005828)

Description: An ALL in ONE tool for functional annotation of (novel) sequences and the analysis of annotation data. Blast2GO (B2G) joins in one universal application similarity search based GO annotation and functional analysis. B2G offers the possibility of direct statistical analysis on gene function information and visualization of relevant functional features on a highlighted GO direct acyclic graph (DAG). Furthermore B2G includes various statistics charts summarizing the results obtained at BLASTing, GO-mapping, annotation and enrichment analysis (Fisher's Exact Test). All analysis process steps are configurable and data import and export are supported at any stage. The application also accepts pre-existing BLAST or annotation files and takes them to subsequent steps. The tool offers a very suitable platform for high throughput functional genomics research in non-model species. B2G is a species-independent, intuitive and interactive desktop application which allows monitoring and comprehending the whole annotation and analysis process supported by additional features like GO Slim integration, evidence code (EC) consideration, a Batch-Mode or GO-Multilevel-Pies. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: B2G

Synonyms: Blast2GO (B2G)

Resource Type: software resource, software application

Defining Citation: [PMID:16081474](#)

Keywords: annotation, visualization, analysis, functional genomics, editor, statistical analysis, slimmer-type tool, ontology or annotation editor, functional analysis, direct acyclic graph, analysis, high throughput, functional genomics

Funding: MCyT GEN 2001 - 4885-C05-03;
eTumour Project FP6-2002-LIFESCIHEALTH 503094

Availability: Free for academic use

Resource Name: Blast2GO

Resource ID: SCR_005828

Alternate IDs: OMICS_01475, nlx_149335

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260801T191038+0000

Ratings and Alerts

No rating or validation information has been found for Blast2GO.

No alerts have been found for Blast2GO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8422 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Wu K, et al. (2026) Deciphering the role of ThHSF1 in the differential expression regulation of laccase isozymes in the white-rot fungus *Trametes hirsuta*. *Microbiology spectrum*, 14(1), e0100425.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte (Hong Kong, China)*, 2025, gigabyte149.

De La Forest Divonne S, et al. (2025) Diversity and functional specialization of oyster immune cells uncovered by integrative single-cell level investigations. *eLife*, 13.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phyllobates terribilis*. *GigaByte (Hong Kong, China)*, 2025, gigabyte157.

Perrier C, et al. (2025) Transposable element accumulation drives genome size increase in *Hylesia metabus* (Lepidoptera: Saturniidae), an urticating moth species from South America. *The Journal of heredity*, 116(3), 344.

Song N, et al. (2025) ZmHSFA2B self-regulatory loop is critical for heat tolerance in maize. *Plant biotechnology journal*, 23(1), 284.

Liu T, et al. (2025) Transcriptomic analysis reveals the crucial role of YABBY genes family in hormonal induced parthenocarpy in *Cucumis sativus* L. *BMC plant biology*, 25(1), 45.

Huang J, et al. (2025) Unveiling immunogenic characteristics and neoantigens in endometrial cancer with POLE hotspot mutations for improved immunotherapy. *Frontiers in immunology*, 16, 1528532.

Du H, et al. (2025) Transcriptomic and metabolomic analyses of Tartary buckwheat roots during cadmium stress. *Scientific reports*, 15(1), 5100.

Durand K, et al. (2025) Divergent Selection Promotes Intraspecific Genomic Differentiation in *Spodoptera littoralis* With Possible Involvement in Detoxification. *Ecology and evolution*, 15(3), e70917.

Zhang Z, et al. (2025) Functional evidence supports the potential role of Tbx4-HLEA in the hindlimb degeneration of cetaceans. *EvoDevo*, 16(1), 3.

Tahir Ul Qamar M, et al. (2025) Comparative genomics profiling of Citrus species reveals the diversity and disease responsiveness of the GLP pangenomes family. *BMC plant biology*, 25(1), 388.

Deng K, et al. (2025) Decoding Pecan's Fungal Foe: A Genomic Insight into *Colletotrichum plurivorum* Isolate W-6. *Journal of fungi (Basel, Switzerland)*, 11(3).

Jiao LL, et al. (2025) Comparisons of Whole Saliva and Cell Free Saliva by DIA-Based Proteome Profiling. *Proteomics. Clinical applications*, 19(1), e202400031.

Soler-Garzón A, et al. (2025) Mapping resistance to *Sclerotinia* white mold in two pinto bean recombinant inbred line populations. *The plant genome*, 18(1), e20538.

Castellan M, et al. (2025) Immunological findings of West Caucasian bat virus in an accidental host. *Journal of virology*, 99(2), e0191424.

Vysakh VG, et al. (2025) The transcriptomic footprint of *Mytella strigata*: de novo transcriptome assembly of a major invasive species. *Scientific data*, 12(1), 201.

Cheng Y, et al. (2025) Endothelial AGGF1 promotes retinal angiogenesis by coordinating TNFSF12/FN14 signalling. *Nature communications*, 16(1), 1332.

Ríos N, et al. (2025) Transcriptomic Divergence and Associated Markers Between Genomic Lineages of Silver Catfish (*Rhamdia quelen*). *Ecology and evolution*, 15(3), e71021.