

Resource Summary Report

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

QuickGO

RRID:SCR_004608

Type: Tool

Proper Citation

QuickGO (RRID:SCR_004608)

Resource Information

URL: <http://www.ebi.ac.uk/QuickGO/>

Proper Citation: QuickGO (RRID:SCR_004608)

Description: A web-based browser for Gene Ontology terms and annotations, which is provided by the UniProtKB-GOA group at the EBI. It is able to offer a range of facilities including bulk downloads of GO annotation data which can be extensively filtered by a range of different parameters and GO slim set generation. The software for QuickGO is freely available under the Apache 2 license. QuickGO can supply GO term information and GO annotation data via REST web services.

Abbreviations: QuickGO

Synonyms: Quick GO

Resource Type: data or information resource, ontology, controlled vocabulary, data access protocol, database, software resource, web service

Defining Citation: [PMID:19744993](#), [PMID:20157483](#)

Keywords: gene, ontology, annotation, browser, visualization, search engine, slimmer-type tool, ontology or annotation browser, ontology or annotation search engine, ontology or annotation visualization, database or data warehouse, windows, mac os x, linux, unix, gold standard, bio.tools

Funding: BBSRC BB/E023541/1

Availability: Apache License, v2, Free for academic use

Resource Name: QuickGO

Resource ID: SCR_004608

Alternate IDs: biotools:quickgo, nlx_60318, OMICS_02276

Alternate URLs: <https://bio.tools/quickgo>

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260801T190238+0000

Ratings and Alerts

No rating or validation information has been found for QuickGO.

No alerts have been found for QuickGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 523 mentions in open access literature.

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

Castro-Arnau J, et al. (2025) Post-testicular spermatozoa of a marine teleost can conduct de novo cytoplasmic and mitochondrial translation. *iScience*, 28(1), 111537.

Kennard AS, et al. (2025) Tubulin sequence divergence is associated with the use of distinct microtubule regulators. *Current biology : CB*, 35(2), 233.

Qush A, et al. (2025) Insects in agricultural greenhouses: a metagenomic analysis of microbes in *Trialeurodes vaporariorum* infesting tomato and cucumber crops. *Frontiers in plant science*, 16, 1581707.

Gazit Shimoni N, et al. (2025) Changes in neurotensin signalling drive hedonic devaluation in obesity. *Nature*, 641(8065), 1238.

Rani V, et al. (2025) Identification and characterization of Eco-miR 169-EcNF-YA13 gene regulatory network reveal their role in conferring tolerance to dehydration and salinity stress in finger millet. *Scientific reports*, 15(1), 12338.

Lin JD, et al. (2025) A bacterial toxin-antitoxin system involved in an unusual response to genotoxic stress. *EMBO reports*, 26(18), 4532.

Song J, et al. (2025) Identification of progression markers for prostate cancer. *Cell cycle (Georgetown, Tex.)*, 24(17-20), 382.

Choudhary S, et al. (2025) Repurposing FDA approved drugs for psoriasis indications through integrated molecular docking, one-SVM algorithm, and molecular dynamics simulation approaches. *Scientific reports*, 15(1), 21211.

Salazar-Alemán DA, et al. (2025) *Escherichia coli* growing under antimicrobial gallium nitrate stress reveals new processes of tolerance and toxicity. *Scientific reports*, 15(1), 1389.

Brenes-Álvarez M, et al. (2025) R-DeeP/TripepSVM identifies the RNA-binding OB-fold-like protein PatR as regulator of heterocyst patterning. *Nucleic acids research*, 53(3).

Pozzoli U, et al. (2025) *Mycobacterium tuberculosis* uses intrinsically disordered, fast evolving proteins to interact with conserved host factors. *Genome biology*, 26(1), 387.

Alshammari SO, et al. (2025) AI-assisted identification of innovative phytochemicals from *Aizoon canariense* aimed at brachyury protein in chordoma: a computational strategy. *Scientific reports*, 15(1), 44161.

Mora-Márquez F, et al. (2025) gymnotoa-db: a database and application to optimize functional annotation in gymnosperms. *Database : the journal of biological databases and curation*, 2025.

Genievskaya Y, et al. (2025) Identification of QTLs associated with grain yield-related traits of spring barley. *BMC plant biology*, 25(1), 554.

Szathmári B, et al. (2025) *Orthrus*: a *Pumilio*-family gene involved in fruiting body and dark stipe development in *Coprinopsis cinerea*. *Frontiers in fungal biology*, 6, 1633301.

Treccarichi S, et al. (2025) MAN2A2-related glycosylation defects in autism and cognitive delay. *Scientific reports*, 15(1), 24471.

Tian D, et al. (2025) The Histidine-25-Arginine Mutation in the Rice MACPF Protein OsCAD1 Induces Cell Death and Activates Defense Responses in the Lesion Mimic Mutant spl17. *Rice (New York, N.Y.)*, 18(1), 68.

Qu Z, et al. (2025) ITGB3 and associated molecules as critical biomarkers in Cesarean Scar Pregnancy. *BMC pregnancy and childbirth*, 25(1), 629.

Xie Y, et al. (2025) Spatial transcriptomics reveals distinct cell type dynamics following opioid dependence in mice with the common human variant in the μ -opioid receptor, Oprm1 A118G. *Research square*.

Gardiner CEC, et al. (2025) Sex-Linked Differentiation in Commercially Exploited Fishes: Rethinking Population Structure in Dynamic Marine Environments. *Global change biology*, 31(10), e70556.