

Resource Summary Report

Generated by [dkNET](#) on Jul 29, 2026

QuickGO

RRID:SCR_004608

Type: Tool

Proper Citation

QuickGO (RRID:SCR_004608)

Resource Information

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

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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, database, data access protocol, software resource, web service, ontology, controlled vocabulary

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: 20260729T044102+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 [dkNET](#).

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 Shimon 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.