

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 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: ontology, data or information resource, web service, controlled vocabulary, data access protocol, software resource, database

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: 20260808T185824+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 556 mentions in open access literature.

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

Khedr T, et al. (2026) Proteomics and Alkaloid Signature of Narrow Leaf Lupin Leaves Reveal Key Enzymes in Quinolizidine Alkaloid Biosynthesis and Transportation. Journal of agricultural and food chemistry, 74(17), 14092.

Akond Z, et al. (2026) Genome-wide identification and characterization of the RNAi gene families in Brassica rapa L. highlighting their regulatory components and underlying functions involving crop improvement. BMC genomic data, 27(1).

Hayward C, et al. (2026) Interactions between the 2C protein of foot-and-mouth disease virus and components of the viral replication machinery are mediated by endoplasmic reticulum-derived membranes. The Journal of general virology, 107(5).

Huang J, et al. (2026) TMT Proteomics-Based Study of Proteins and Pathways Associated with ??-Glucan Degradation in Barley Germination. Metabolites, 16(4).

Valdivia DI, et al. (2026) Regulation of tRNA expression during the social cycle of the amoeba Dictyostelium discoideum. BMC molecular and cell biology, 27(1).

Ji K, et al. (2026) Decoding cryptic defluorinases through a latent generative sequence landscape. Chemical science, 17(28), 13816.

Salinas MD, et al. (2026) Chaperone-mediated autophagy sustains pericyte stemness necessary for brain tissue homeostasis. Journal of advanced research, 80, 155.

Nguyen JL, et al. (2026) Isolation methods influence the biological properties of Wharton's Jelly-derived mesenchymal stem cells: A comparative study of yield, viability, proliferation, differentiation potential, and proteomic profiles. PloS one, 21(3), e0345081.

Tateda S, et al. (2026) Two ferric uptake regulator proteins in *Ralstonia pseudosolanacearum* strain OE1-1 function cooperatively in response to the extracellular iron level under ferrous iron-rich conditions. *Applied and environmental microbiology*, 92(3), e0227625.

Ozcan SC, et al. (2026) Stress adaptation pathways and HA-CD44 signaling maintain the survival of pancreatic cancer cells with centrosome amplification. *Cell communication and signaling : CCS*, 24(1).

Fattel L, et al. (2026) Go Big or go home: a new gene ontology subset that improves plant gene function prediction. *Plant methods*, 22(1).

Ward MH, et al. (2026) Metabolites from plasma-like medium fuel nitrogen metabolism and influence proliferation in *Leptospira interrogans*. *bioRxiv : the preprint server for biology*.

Heller AT, et al. (2026) Interactome Analysis of the CC2D1A Scaffold Reveals Novel Neuronal Interactions and a Postsynaptic Role. *Molecular & cellular proteomics : MCP*, 25(4), 101546.

Furutani Y, et al. (2026) Ligand-dependent Wnt signaling promotes gastric cancer metastasis through hyaluronan expression in microenvironment. *Nature communications*, 17(1).

Listrat A, et al. (2026) Transcriptional profiling of male mouse muscle across aging stages: a gene ontology analysis of the muscle matreotype. *BMC genomics*, 27(1).

Ueyama T, et al. (2026) Contribution of a Novel TetR/AcrR Family Transcriptional Regulator RalT of *Ralstonia pseudosolanacearum* Strain OE1-1 to the Fine-Tuning of Its Virulence. *MicrobiologyOpen*, 15(1), e70229.

Tan SZK, et al. (2026) The Cell Ontology in the age of single-cell omics. *Scientific data*, 13(1).

Ge Y, et al. (2026) Modular Phosphoprotein Signatures Link Rac1 Inhibition to Neurite Morphogenesis in a Dose-Dependent Manner. *Developmental neuroscience*, 1.

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.