

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[AmiGO](#)

RRID:SCR_002143

Type: Tool

Proper Citation

AmiGO (RRID:SCR_002143)

Resource Information

URL: <http://amigo.geneontology.org/>

Proper Citation: AmiGO (RRID:SCR_002143)

Description: Web tool to search, sort, analyze, visualize and download data of interest. Along with providing details of the ontologies, gene products and annotations, features a BLAST search, Term Enrichment and GO Slimmer tools, the GO Online SQL Environment and a user help guide. Used at the Gene Ontology (GO) website to access the data provided by the GO Consortium. Developed and maintained by the GO Consortium.

Abbreviations: AmiGO

Synonyms: GO Consortium, AmiGO, AmiGO 2, AmiGene Ontology, Gene Ontology Database, Gene Ontology Consortium, GO Database, The Gene Ontology Consortium

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: [PMID:19033274](#)

Keywords: search, sort, analyze, visualize, data, ontology, gene, annotation, FASEB list

Funding: NHGRI P41 HG002273

Availability: Free, Available for download, Freely available

Resource Name: AmiGO

Resource ID: SCR_002143

Alternate IDs: OMICS_02266, nif-0000-20935

Alternate URLs: <http://sourceforge.net/projects/geneontology/>

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260905T132444+0000

Ratings and Alerts

No rating or validation information has been found for AmiGO.

No alerts have been found for AmiGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1285 mentions in open access literature.

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

, et al. (2026) The Gene Ontology knowledgebase in 2026. Nucleic acids research, 54(D1), D1779.

Rao H, et al. (2026) Ribosome Homeostasis Regulated by SETD2 Preserves Intestinal Epithelial Barrier. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(16), e08168.

Ren X, et al. (2026) CRISPR tiling deletion screens reveal functional enhancers and allelic compensation effects (ACE) on SIN3A transcription. Nature communications, 17(1).

Castro Ramos A, et al. (2026) Omentum-Derived Mesenchymal Stem Cells Promote Antibacterial Effects and Protect Endothelial Functions via PAI-1. Stem cell reviews and reports, 22(5), 2491.

Pescador-Dionisio S, et al. (2026) Quick conversions and de novo synthesis within the entire α - and β -carotenoid branches during non-steady-state light transients. Photosynthesis research, 164(3).

Cao J, et al. (2026) An anoikis-based risk model predicts outcomes and is associated with the immune microenvironment in adrenocortical carcinoma. Frontiers in molecular biosciences, 13, 1779180.

Gu H, et al. (2026) Lipid droplet-associated gene signatures classify metabolic subtypes and identify PLIN3 as a key driver in hepatocellular carcinoma. Genes & diseases, 13(5), 102067.

Azevedo GM, et al. (2026) Reconstruction of the evolutionary landscape of biological processes involved in the early stages of the metastatic cascade. Genetics and molecular biology, 49(suppl 2), e20250197.

Garapati PV, et al. (2026) Comprehensive annotation of the enzymes of *Drosophila melanogaster*. *G3* (Bethesda, Md.), 16(2).

Qin Z, et al. (2026) CAPG serves as a prognostic biomarker and promotes proliferation and migration in pancreatic ductal adenocarcinoma. *PloS one*, 21(3), e0346011.

Dai J, et al. (2026) Functional germline variants together with somatic mutations alter the integrity of cancer hallmark regulatory networks. *Genome medicine*, 18(1).

Kosonocky CW, et al. (2026) Validation and analysis of 12,000 AI-driven CAR-T designs in the Bits to Binders competitions. *bioRxiv : the preprint server for biology*.

Li R, et al. (2026) Fibro-Adipogenic Progenitors Regulate Orofacial Neuromuscular Junction Regeneration via Myostatin. *Journal of cachexia, sarcopenia and muscle*, 17(2), e70264.

Kim W, et al. (2026) Whole genome sequence analysis of pulmonary function and COPD in 44,287 multi-ancestry participants. *Genome biology*, 27(1), 28.

Kashatnikova DA, et al. (2026) Genetic Architectures of Myeloid Dysregulation in Severe COVID-19. *Viruses*, 18(6).

Yang S, et al. (2026) Identification of Notch pathway-related biomarkers in patients with idiopathic pulmonary fibrosis. *PloS one*, 21(1), e0339287.

Santoro DF, et al. (2026) Traversing the effects of ploidy changes in different *Eragrostis curvula* genotypes through high-throughput RNA sequencing. *The plant genome*, 19(2), e70227.

Zhao C, et al. (2026) Dynamic Targetable Extracellular Vesicle Surface Proteins Monitor Depth of Response to CAR T Therapy. *Research square*.

Fernandes VJ, et al. (2026) Predicting groundwater storage from seasonal managed aquifer recharge: insights from machine learning and explainable AI techniques. *Environmental earth sciences*, 85(5), 112.

Lee MJ, et al. (2026) Comparative Transcriptomic Profiling of Mesenchymal Stem Cells from Distinct Tissue Origins and Isolation Methods Highlights the Stability and Immunomodulatory Signature of Umbilical Cord-Derived Smumf Cells. *Tissue engineering and regenerative medicine*, 23(1), 157.