

Resource Summary Report

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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: production service resource, data or information resource, database, service resource, data analysis service, analysis 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: nif-0000-20935, OMICS_02266

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

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260803T040328+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 1242 mentions in open access literature.

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

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

Ennis CS, et al. (2025) Plasma exosomes from individuals with type 2 diabetes drive breast cancer aggression in patient-derived organoids. Communications biology, 8(1), 1276.

Boucherie C, et al. (2025) Aut2 enhances neurogenesis and promotes expansion of the cerebral cortex. Journal of advanced research, 72, 151.

Lin T, et al. (2025) Identification of RNA processing factor LSM5 as a new adverse biomarker in nasopharyngeal carcinoma. Scientific reports, 15(1), 9901.

Vimonish R, et al. (2025) Transcriptomic analysis of Rhipicephalus microplus hemocytes from female ticks infected with Babesia bovis or Babesia bigemina. Parasites & vectors, 18(1), 37.

Chen J, et al. (2025) Construction of a Prognostic Model Using RNA Processing Factor Genes and the Key Role of NSUN6 in Glioma Outcomes. Journal of cellular and molecular medicine, 29(12), e70668.

Zheng B, et al. (2025) Integrated bioinformatics analysis reveals novel PANoptosis biomarkers and therapeutic response in clear cell renal cell carcinoma. Clinical and experimental medicine, 25(1), 338.

Si W, et al. (2025) SARDH in the 1-C metabolism sculpts the T-cell fate and serves as a potential cancer therapeutic target. Cellular & molecular immunology, 22(11), 1363.

Lee Y, et al. (2025) Therapeutic potential of Bacillus sonorensis PMC204 membrane vesicles against drug-resistant Mycobacterium tuberculosis. Medical microbiology and

immunology, 214(1), 43.

Tsunoda Y, et al. (2025) Comparative omics profiling reveals differences in biomass, energy production, and vesicle transport between CHO and fast-growing CHL-YN cells. *Scientific reports*, 15(1), 39784.

Li J, et al. (2025) Integrated bioinformatics analysis and machine learning identifies FZD4, SRPX2, and COL8A1 as angiogenesis hub genes in endometriosis. *Medicine*, 104(43), e45341.

Hu M, et al. (2025) Myogenic enhancer snatching promotes adipogenic differentiation during epigenetic reprogramming mediated by lineage-specific transcription factors. *Cellular and molecular life sciences : CMLS*, 82(1), 412.

Liu J, et al. (2025) Exploring biomarkers related to coagulation and immunity in myocardial infarction based on bioinformatics. *Scientific reports*, 15(1), 40700.

Yan R, et al. (2025) Convergent flow-mediated mesenchymal force drives embryonic foregut constriction and splitting. *Nature communications*, 16(1), 10643.

Kennedy L, et al. (2025) A hybrid machine learning framework for functional annotation of mitochondrial glutathione transport and metabolism proteins in cancers. *BMC bioinformatics*, 26(1), 48.

Ho Ching Chan B, et al. (2025) A stable NTN1 fluorescent reporter chicken reveals cell specific molecular signatures during optic fissure closure. *Scientific reports*, 15(1), 10096.

Baty SM, et al. (2025) Strong Signatures of Selection on Candidate Genes Underlying Core Speciation Mechanisms in Desert Tortoises. *Molecular ecology resources*, 25(6), e14098.

Wang J, et al. (2025) Expression, prognosis and preliminary investigation of the mechanism of action of ACTR6, a member of the ARPs gene family, in hepatocellular carcinoma. *Frontiers in medicine*, 12, 1513233.

Yang S, et al. (2025) Detection of positive selection on depression-associated genes. *Heredity*, 134(5), 263.

Huang C, et al. (2025) Downregulation of tropomyosin 2 promotes the progression of lung adenocarcinoma by regulating neutrophil infiltration through neutrophil elastase. *Cell death & disease*, 16(1), 264.