

Resource Summary Report

Generated by [nidm-terms](#) on Sep 20, 2026

Entrez Gene

RRID:SCR_002473

Type: Tool

Proper Citation

Entrez Gene (RRID:SCR_002473)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/gene>

Proper Citation: Entrez Gene (RRID:SCR_002473)

Description: Database for genomes that have been completely sequenced, have active research community to contribute gene-specific information, or that are scheduled for intense sequence analysis. Includes nomenclature, map location, gene products and their attributes, markers, phenotypes, and links to citations, sequences, variation details, maps, expression, homologs, protein domains and external databases. All entries follow NCBI's format for data collections. Content of Entrez Gene represents result of curation and automated integration of data from NCBI's Reference Sequence project (RefSeq), from collaborating model organism databases, and from many other databases available from NCBI. Records are assigned unique, stable and tracked integers as identifiers. Content is updated as new information becomes available.

Abbreviations: NCBI_Gene, NCBI Genen NCBI Entrez

Synonyms: NCBI Gene, Gene - Gene mapped phenotypes, Gene - Gene and mapped phenotypes, Gene Database, GeneID

Resource Type: data or information resource, database

Defining Citation: [PMID:17148475](#), [PMID:21115458](#)

Keywords: gene, gene expression, gene location, gene map, gene prediction, genome, genome sequence analysis, phenotype, nomenclature, gene mapping, protein, genetic code, function, annotation, gold standard, bio.tools

Availability: Free, Freely available

Resource Name: Entrez Gene

Resource ID: SCR_002473

Alternate IDs: nif-0000-02801, biotools:entrez_gene, OMICS_01651, r3d100010650

Alternate URLs: <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene>,
<http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene>, https://bio.tools/entrez_gene,
<https://doi.org/10.17616/R3603S>

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260919T195636+0000

Ratings and Alerts

No rating or validation information has been found for Entrez Gene.

No alerts have been found for Entrez Gene.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2912 mentions in open access literature.

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

Li S, et al. (2026) PRECISE: A Prognostic Thyrocyte-Derived Gene Signature for Papillary Thyroid Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(13), 2667.

Yu X, et al. (2026) miR-339-5p impairs myogenic proliferation and differentiation by repressing contractile gene programs in skeletal muscle. American journal of physiology. Cell physiology, 331(2), C425.

White SL, et al. (2026) Global multi-ancestry genome-wide analyses identify genes and biological pathways associated with thyroid cancer and benign thyroid diseases. Nature genetics, 58(2), 307.

Chen T, et al. (2026) Assessment of dispersion metrics for estimating single-cell transcriptional variability. PLoS computational biology, 22(3), e1014030.

Han L, et al. (2026) Targeting the RNF31-TFEB-NLRP3 Axis With a Curcumin Analog to Restore Autophagy and Alleviate Intestinal Inflammation. Food science & nutrition, 14(5), e71916.

Dwivedi K, et al. (2026) A fusion-based multiomics classification approach for enhanced gene discovery in non-small cell lung cancer. Bioinformatics advances, 6(1), vbag131.

Xhumari J, et al. (2026) Cross-species systems analysis distinguishes inflammatory remodeling from primary mucus secretory failure in inflammatory bowel disease. Frontiers

in immunology, 17, 1813019.

Gao H, et al. (2026) TWAS atlas 2.0: an updated data resource for transcriptome-wide association studies. *Nucleic acids research*, 54(D1), D1321.

Xu Y, et al. (2026) CQMUH-011 mitigated LPS-induced acute lung injury in neonatal rabbits. *Scientific reports*, 16(1).

Taylor-Bateman V, et al. (2026) Repurposing drugs for the prevention of vascular dementia using evidence from drug target Mendelian randomization. *Nature aging*, 6(4), 905.

Canzler S, et al. (2026) From toxicogenomics data to cumulative assessment groups: a framework for chemical grouping. *Archives of toxicology*, 100(1), 173.

Harazim M, et al. (2026) Genome-Wide Association Reveals Signalling-Linked Infection Tolerance in Hibernating Bats. *Pathogens (Basel, Switzerland)*, 15(2).

Chamchoy K, et al. (2026) Resolving haplotypes of the glucose-6-phosphate dehydrogenase gene using long-range polymerase chain reaction and Oxford Nanopore sequencing. *Biology methods & protocols*, 11(1), bpag008.

Laskin GR, et al. (2026) Increasing indices of frailty in aged female mice are associated with impaired skeletal muscle resilience to downhill running stress. *GeroScience*, 48(2), 1665.

Hu S, et al. (2026) MVGAE: A Multi-View Graph Auto-Encoder Model for Drug Prediction of Non-Small Cell Lung Cancer Based on Synthetic Lethality. *Current issues in molecular biology*, 48(3).

Lyu J, et al. (2026) Alpha-1B Glycoprotein Is a Novel Hepatocyte-Derived Host Factor Associated with In Vitro Inhibition of HBV Replication and Hepatocellular Carcinoma Progression. *Cancers*, 18(4).

Wang Z, et al. (2026) Identifying Cytokine Motif-Containing, Immunomodulatory Bacterial Proteins in Human Gut Microbiome. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(29), e20332.

Pereira IC, et al. (2026) Ovarian structures modulate cellular aggregation and gene expression in oviductal isthmus cells. *Animal reproduction*, 23(1), e20250075.

Li X, et al. (2026) Decoding the hub gene blueprint for broiler liver development: A synergistic histomorphological and transcriptomic investigation during the neonatal phase. *Poultry science*, 105(7), 106938.

Hu Y, et al. (2026) DIOPT: the DRSC Integrative Ortholog Prediction Tool, 2026 update. *bioRxiv : the preprint server for biology*.