

Resource Summary Report

Generated by T1D on Aug 2, 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: 20260801T190906+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 2830 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Campbell AS, et al. (2025) Opposing roles for Bmp signalling during the development of electrosensory lateral line organs. *eLife*, 14.

Mutai H, et al. (2025) Genetic landscape in undiagnosed patients with syndromic hearing loss revealed by whole exome sequencing and phenotype similarity search. *Human genetics*, 144(1), 93.

Maier BD, et al. (2025) Data-Driven Extraction of Human Kinase-Substrate Relationships From Omics Datasets. *Molecular & cellular proteomics : MCP*, 24(8), 100994.

Gorenflo MP, et al. (2025) Amphetamine use and Parkinson's disease: integration of artificial intelligence prediction, clinical corroboration, and mechanism of action analyses. *PloS one*, 20(5), e0323761.

K??kenek ??nal TD, et al. (2025) Impact of neoadjuvant therapy on cancer stem cell gene expression and miRNA profiles in breast cancer patients: Implications for therapy resistance and survival, a cross-sectional observational study. *Medicine*, 104(26), e43077.

Sun Q, et al. (2025) Knockdown of LncRNA H19 inhibits vascularization and endochondral ossification via the MiRNA-21a-5p-Smad7/p-Smad2/3 pathway in fracture repair. *Scientific reports*, 15(1), 26054.

Uberti A, et al. (2025) Molecular breeding approaches for the improvement of oil content and fatty acid composition in exotic-derived maize germplasm. *The New phytologist*,

248(4), 1920.

Liu R, et al. (2025) Integrating single-cell RNA sequencing and Mendelian randomization analysis to identify potential drug targets for dilated cardiomyopathy. *Hereditas*, 162(1), 211.

Liu L, et al. (2025) Co-infection of *Helicobacter pylori* with Epstein-Barr virus in gastric organoids enhances cell proliferation and morphogenesis. *Journal of virology*, 99(9), e0092825.

Lobov A, et al. (2025) Similar, but not the same: multiomics comparison of human valve interstitial cells and osteoblast osteogenic differentiation expanded with an estimation of data-dependent and data-independent PASEF proteomics. *GigaScience*, 14.

Kouvaraki M, et al. (2025) Prognostic and predictive implications of sterile alpha motif and HD domain-containing protein 1 (SAMHD1) expression in breast cancer. *International journal of cancer*, 156(8), 1621.

Kuchenbecker LA, et al. (2025) Novel set of plasma proteins classifies Alzheimer's dementia in African American individuals with high accuracy. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(7), e70505.

Liu H, et al. (2025) Integrating network pharmacology and molecular docking to explore the pharmacological mechanism of tanshinone IIA in improving chronic obstructive pulmonary disease. *Medicine*, 104(12), e41638.

Battaglia R, et al. (2025) Up-regulated microRNAs in blastocoel fluid of human implanted embryos could control circuits of pluripotency and be related to embryo competence. *Journal of assisted reproduction and genetics*, 42(5), 1635.

Davis JL, et al. (2025) Cocaine perturbs neurodevelopment and increases neuroinflammation in a prenatal cerebral organoid model. *Translational psychiatry*, 15(1), 94.

Wang G, et al. (2025) Hyperopia may exert a protective effect against senile cataracts: Evidence from a Mendelian randomization study. *Medicine*, 104(11), e41794.

Flandreau EI, et al. (2025) Effect of Chronic Stress on Whole Blood Transcriptome: A Meta-Analysis of Publicly Available Datasets from Rodent Models. *bioRxiv : the preprint server for biology*.

Maung JN, et al. (2025) Effects of FGF21, soluble TGFBR2, and environmental temperature on metabolic dysfunction in lipodystrophic mice. *JCI insight*, 10(16).

Ruan X, et al. (2025) Genome-wide screening and validation of exosome-derived TLN1 as a regulator of epithelial-mesenchymal transition in lung cancer. *Scientific reports*, 15(1), 11453.

Gao X, et al. (2025) An updated comparison of microarray and RNA-seq for concentration response transcriptomic study: case studies with two cannabinoids, cannabichromene and cannabinal. *BMC genomics*, 26(1), 392.