Resource Summary Report

Generated by NIF on May 24, 2025

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

Funding:

Availability: Free, Freely available

Resource Name: Entrez Gene

Resource ID: SCR_002473

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

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

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250523T054243+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 2774 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

Gioiosa S, et al. (2025) Integrated gene expression and alternative splicing analysis in human and mouse models of Rett syndrome. Scientific reports, 15(1), 2778.

Hu Y, et al. (2025) Cross-Species Epitope Sequence Analysis for Discovery of Existing Antibodies Useful for Phospho-Specific Protein Detection in Model Species. International journal of molecular sciences, 26(2).

Pu Y, et al. (2024) A high-quality chromosomal genome assembly of the sea cucumber Chiridota heheva and its hydrothermal adaptation. GigaScience, 13.

Xu X, et al. (2024) Microglia and macrophages alterations in the CNS during acute SIV infection: a single-cell analysis in rhesus macaques. bioRxiv : the preprint server for biology.

Callahan TJ, et al. (2024) An open source knowledge graph ecosystem for the life sciences. Scientific data, 11(1), 363.

Zarrella JA, et al. (2024) Genome-wide transcriptome profiling and development of age prediction models in the human brain. Aging, 16(5), 4075.

Zhang S, et al. (2024) Species -shared and -unique gyral peaks on human and macaque brains. eLife, 12.

Kannon T, et al. (2024) KANPHOS: Kinase-associated neural phospho-signaling database for data-driven research. Frontiers in molecular neuroscience, 17, 1379089.

Barra J, et al. (2024) DMT1-dependent endosome-mitochondria interactions regulate mitochondrial iron translocation and metastatic outgrowth. Oncogene, 43(9), 650.

Pons-Espinal M, et al. (2024) Blocking IL-6 signaling prevents astrocyte-induced neurodegeneration in an iPSC-based model of Parkinson's disease. JCI insight, 9(3).

Akman M, et al. (2024) TFEB controls sensitivity to chemotherapy and immuno-killing in non-small cell lung cancer. Journal of experimental & clinical cancer research : CR, 43(1), 219.

Sharma D, et al. (2024) Genomic analysis of acid tolerance genes and deciphering the function of ydaG gene in mitigating acid tolerance in Priestia megaterium. Frontiers in microbiology, 15, 1414777.

Nguyen H, et al. (2024) CCPA: cloud-based, self-learning modules for consensus pathway analysis using GO, KEGG and Reactome. Briefings in bioinformatics, 25(Supplement_1).

Wu K, et al. (2024) A correctable immune niche for epithelial stem cell reprogramming and post-viral lung diseases. The Journal of clinical investigation, 134(18).

Ghosh Dastidar R, et al. (2024) In vivo vitamin D targets reveal the upregulation of focal adhesion-related genes in primary immune cells of healthy individuals. Scientific reports, 14(1), 17552.

Chen J, et al. (2024) Integration of background knowledge for automatic detection of inconsistencies in gene ontology annotation. Bioinformatics (Oxford, England), 40(Suppl 1), i390.

Xia K, et al. (2024) SETDB1 targeting SESN2 regulates mitochondrial damage and oxidative stress in renal ischemia-reperfusion injury. BMC biology, 22(1), 246.

Zhang Y, et al. (2024) Drug-target interaction prediction by integrating heterogeneous

information with mutual attention network. BMC bioinformatics, 25(1), 361.