Resource Summary Report

Generated by nidm-terms on Jul 30, 2026

HGNC

RRID:SCR_002827
Type: Tool

Proper Citation

HGNC (RRID:SCR_002827)

Resource Information

URL: https://genenames.org

Proper Citation: HGNC (RRID:SCR_002827)

Description: Only worldwide authority that provides standardized nomenclature, i.e. gene names and symbols (short form abbreviations), for all known human genes, and stores all approved symbols in the HGNC database. Approved human gene nomenclature. Database of gene symbols and names. Manually curated genes into groups based on shared characteristics such as homology, function or phenotype. Data for protein-coding genes, pseudogenes and non-coding RNAs.

Synonyms: HUGO symbols, HGNC Database, HGNC - HUGO Gene Nomenclature Committee, HUGO Gene Nomenclature Committee, Human Genome Organization Gene Symbols

Resource Type: controlled vocabulary, data or information resource, database

Defining Citation: PMID:36243972, PMID:32747822, PMID:34615987, PMID:33152070

Keywords: gene, owl, gene symbol, phenotype, nomenclature, gene family, gene groups, genomic, proteomic, ortholog, web service, locus, protein coding, genetics, gold standard, bio.tools, FASEB list, GCBR, ELIXIR Core Data Resource, DRKB

Funding: NHGRI U24HG003345

Availability: Free, Freely available

Resource Name: HGNC

Resource ID: SCR_002827

Alternate IDs: biotools:genenames.org, nif-0000-02955, r3d100010901

Alternate URLs: http://bioportal.bioontology.org/ontologies/HUGO, https://bio.tools/genenames.org, https://doi.org/10.17616/R3XC80

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Record Creation Time: 20220129T080215+0000

Record Last Update: 20260729T044031+0000

Ratings and Alerts

No rating or validation information has been found for HGNC.

No alerts have been found for HGNC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 974 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Leban T, et al. (2026) Multiomics Data Synthesis of FAM83H in Amelogenesis Imperfecta. International dental journal, 76(1), 109293.

Park J, et al. (2026) A robust pleiotropy method with applications to lipid traits and to inflammatory bowel disease subtypes with sample overlap. HGG advances, 7(1), 100501.

Yuan Z, et al. (2026) Mucin 2 and unfolded protein response reshape the mucus barrier in inflammatory bowel disease (Review). Molecular medicine reports, 33(1).

Rusche JR, et al. (2026) Modulating ACVRL1 Expression in HMEC1 Cells as a Simplified In Vitro Model for Hereditary Hemorrhagic Telangiectasia (HHT) Type 2 Studies. In vivo (Athens, Greece), 40(1), 64.

Kim S, et al. (2025) Pathogenic roles of immunoproteasomes in fibrosis. Essays in biochemistry, 69(5).

Fu C, et al. (2025) k-mer manifold approximation and projection for visualizing DNA sequences. Genome research, 35(5), 1234.

Elloumi F, et al. (2025) Protocol to set up the CellMinerCDB pharmacogenomics analysis web application with custom cell line data. STAR protocols, 6(4), 104076.

Karjalainen A, et al. (2025) Cell-type-specific requirement for TYK2 in murine immune cells under steady state and challenged conditions. Cellular and molecular life sciences : CMLS, 82(1), 98.

Carli F, et al. (2025) Learning and actioning general principles of cancer cell drug sensitivity. Nature communications, 16(1), 1654.

Zalewski D, et al. (2025) Profiling of main regulators of angiogenesis and inflammation in human PBMC and plasma revealed associations with lower extremity artery disease. Scientific reports, 15(1), 41779.

Zheng D, et al. (2025) Dynamic molecular and cellular characteristics of VSX2-positive retinal progenitor cells in human retinal organoids. Stem cell research & therapy, 16(1), 589.

Madsen TD, et al. (2025) Map of the neuronal O-glycoproteome reveals driver functions in the regulated secretory pathway. The Journal of biological chemistry, 301(7), 110313.

Drago P, et al. (2025) DHFR2 RNA directly regulates dihydrofolate reductase and its expression level impacts folate one carbon metabolism. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(4), e70391.

Arnoldus T, et al. (2025) Cytidine diphosphate diacylglycerol synthase 2 is a synthetic lethal target in mesenchymal-like cancers. Nature genetics, 57(7), 1659.

Liu X, et al. (2025) HCDT 2.0: A Highly Confident Drug-Target Database for Experimentally Validated Genes, RNAs, and Pathways. Scientific data, 12(1), 695.

Sakthivelu V, et al. (2025) Functional synapses between neurons and small cell lung cancer. Nature, 646(8087), 1243.

Zhang J, et al. (2025) Unraveling CBS Mutations and Their Clinical Impact in a Chinese Family With Classical Homocystinuria. Molecular genetics & genomic medicine, 13(9), e70132.

Tweedie S, et al. (2025) Towards an official gene nomenclature for Populus trichocarpa. Tree physiology, 45(13), 149.

Rotte N, et al. (2025) Genotype-specific differences in infertile men due to loss-of-function variants in M1AP or ZZS genes. EMBO molecular medicine, 17(6), 1417.

Li Y, et al. (2025) Deep generative optimization of mRNA codon sequences for enhanced mRNA translation and therapeutic efficacy. Nature communications, 16(1), 9957.