Resource Summary Report

Generated by SPARC SAWG on Aug 10, 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: database, data or information resource, controlled vocabulary

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: 20260808T185747+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 1134 mentions in open access literature.

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

Chen X, et al. (2026) Molecular heterogeneity of the non-human primate cochlea. Nature communications, 17(1), 1633.

Gabr MM, et al. (2026) MGMT, NUPR1, NDRG2, and GLI1 Gene Promoter Methylation in Glioblastoma Tissues and Association with Clinical Characteristics and Therapeutic Outcomes. International journal of molecular sciences, 27(2).

Sen P, et al. (2026) From kidney injury to cardiac dysfunction: the central role of oxidative stress in diabetes and CKD. Basic research in cardiology, 121(1), 93.

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

Seal RL, et al. (2026) Genenames.org: the HGNC and PGNC resources in 2026. Nucleic acids research, 54(D1), D1098.

El-Merahbi R, et al. (2026) Endothelial ADGRF5(GPR116) governs vascular adaptation required for sustained thermogenic remodeling of brown adipose tissue. Molecular metabolism, 107, 102346.

Al-Mohannadi A, et al. (2026) A curated list of immune system associated genes related to cancer. BMC genomic data, 27(1).

Roets LE, et al. (2026) Current perspectives on KMT2A fusion proteins and menin inhibition in paediatric acute myeloid leukaemia. The FEBS journal, 293(8), 2159.

Zhang L, et al. (2026) Decoding the role of RPL38 in lung adenocarcinoma: a multi-omics approach. Frontiers in immunology, 17, 1778481.

Zheng B, et al. (2026) Proteomic landscape analysis of undifferentiated pleomorphic sarcoma. Genome medicine, 18(1).

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

Azmi MB, et al. (2026) Computational identification of rare pathogenic genomic variants in esophageal cancer markers: Transcript-level analysis, sequence-based insights, and structural-functional impacts of non-synonymous SNPs. Biochemistry and biophysics reports, 45, 102503.

Oommen AM, et al. (2026) An Integrative Network Analysis Framework for Identifying Altered Glycosylation Pathways Associated with Autism Spectrum Disorder. Genes, 17(4).

Zhang W, et al. (2026) Non-invasive profiling of the tumour microenvironment with spatial ecotypes. Nature, 654(8120), 1076.

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.

Jim??nez-Gracia L, et al. (2026) Interpretable inflammation landscape of circulating immune cells. Nature medicine, 32(2), 633.

Braschi B, et al. (2026) Naming the alpha-2-macroglobulin gene family across vertebrates. Human genomics, 20(1), 31.

Ogino S, et al. (2026) Unique role of the prospective cohort incident-tumor biobank method in etiological research. Lancet regional health. Americas, 53, 101290.

Zhang C, et al. (2026) CuAgent provides a RAG-assisted intelligent framework to investigate cuproptosis. Scientific reports, 16(1).

Emam O, et al. (2026) Small-nucleolar RNA host gene3 (SNHG3) and leukemia-associated non-coding IGF1R activator RNA 1 (LUNAR1) correlated with CRC patients' clinical features: a step-toward ncRNA-precision. Scientific reports, 16(1).