

Resource Summary Report

Generated by PRECISE-TBI on Aug 9, 2026

National Human Genome Research Institute

RRID:SCR_011416

Type: Tool

Proper Citation

National Human Genome Research Institute (RRID:SCR_011416)

Resource Information

URL: <http://www.genome.gov/>

Proper Citation: National Human Genome Research Institute (RRID:SCR_011416)

Description: One of 27 institutes and centers that make up the NIH, National Human Genome Research Institute (NHGRI) is devoted to advancing health through genome research. The Institute led NIH's contribution to the Human Genome Project, which was successfully completed in 2003 ahead of schedule and under budget. Building on the foundation laid by the sequencing of the human genome, NHGRI's work now encompasses a broad range of research aimed at expanding understanding of human biology and improving human health. The NHGRI's mission has expanded to encompass a broad range of studies aimed at understanding the structure and function of the human genome and its role in health and disease. To that end NHGRI supports the development of resources and technology that will accelerate genome research and its application to human health. A critical part of the NHGRI mission continues to be the study of the ethical, legal and social implications (ELSI) of genome research. NHGRI also supports the training of investigators and the dissemination of genome information to the public and to health professionals.

Abbreviations: NHGRI

Synonyms: NCHGR, National Center for Human Genome Research

Resource Type: institution

Resource Name: National Human Genome Research Institute

Resource ID: SCR_011416

Alternate IDs: nlx_inv_1005098, Crossref funder ID: 100000051, Wikidata: Q1634459, nlx_143900, OMICS_01554, ISNI: 0000 0001 2233 9230, grid.280128.1

Alternate URLs: <https://ror.org/00baak391>

Record Creation Time: 20220129T080304+0000

Record Last Update: 20260808T185930+0000

Ratings and Alerts

No rating or validation information has been found for National Human Genome Research Institute.

No alerts have been found for National Human Genome Research Institute.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 157 mentions in open access literature.

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

Suckiel SA, et al. (2026) Healthcare professionals' experiences returning monogenic, polygenic, and integrated risk results in the eMERGE study. HGG advances, 7(1), 100554.

You Y, et al. (2026) The clinical significance and prognostic implication of autophagy-related gene 13 in human gastric cancer. Frontiers in oncology, 16, 1729996.

Epstein BE, et al. (2026) Comparison of neonatal systemic and intracerebroventricular AAV9 gene therapy delivery demonstrating improved behavioral and phenotypic outcomes in a mouse model of Niemann-Pick disease, type C1. PloS one, 21(3), e0331275.

Mao B, et al. (2026) Mutation in MSH5 Causes Primary Ovarian Insufficiency and Successful Therapeutic Intervention by In Vitro Fertilisation. Journal of cellular and molecular medicine, 30(9), e70745.

Domingo J, et al. (2026) Nonlinear transcriptional responses to gradual modulation of transcription factor dosage. eLife, 13.

Pramanik S, et al. (2026) FAM168B identified as a novel candidate target for chimeric antigen receptor T cell-based cancer therapy. Discover oncology, 17(1), 340.

Lilles S, et al. (2026) Population-Based Study of Drug-Resistant Epilepsy Before Age Two: Predominance of Developmental and Epileptic Encephalopathies. Neurology international, 18(5).

Chen C, et al. (2025) Pan-cancer analysis of ITGB3 as a potential prognostic and immunological biomarker. Discover oncology, 16(1), 522.

Zhou Y, et al. (2025) Clinical and functional significance of SPATA2 in cancer particularly in LIHC. Scientific reports, 15(1), 8392.

Horta P, et al. (2025) Adaptive Introgression as an Evolutionary Force: A Meta-Analysis of Knowledge Trends. *Evolutionary applications*, 18(6), e70103.

Yang Z, et al. (2025) Dicoumarol sensitizes hepatocellular carcinoma cells to ferroptosis induced by imidazole ketone erastin. *Frontiers in immunology*, 16, 1531874.

Yang Y, et al. (2025) Analysis of Whole-Genome for *Alternaria* Species Identification. *Journal of fungi (Basel, Switzerland)*, 11(3).

Le Menestrel T, et al. (2025) Using pre-training and interaction modeling for ancestry-specific disease prediction using multiomics data from the UK Biobank. *PLoS one*, 20(12), e0336861.

Smith CL, et al. (2025) Factors influencing trustworthiness and perceived biases of medical information and genetic testing for Black and White Americans. *PLoS genetics*, 21(10), e1011800.

Cao K, et al. (2025) Case Report: Identification and functional characterization of a novel heterozygous splice-donor (c.647+1G>A) site mutation in the SPTB gene that causes hereditary spherocytosis with hemolytic anemia. *Frontiers in genetics*, 16, 1626155.

Avraham-Davidi I, et al. (2025) Spatially defined multicellular functional units in colorectal cancer revealed from single cell and spatial transcriptomics. *eLife*, 14.

Zhang B, et al. (2025) Implication of CDKN2A in cuproptosis through defining cuproptosis-related gene signature in ovarian cancer. *Journal of Cancer*, 16(11), 3355.

Wei C, et al. (2025) STMN1 regulates the stemness of gastric cancer cells by binding to HN1L to activate the STAT3 signaling pathway. *Discover oncology*, 16(1), 263.

Zhang Z, et al. (2025) Expression of ITGA3 in pan-cancer tissues and its relationship to prognosis and immune infiltration. *Discover oncology*, 16(1), 2115.

Huang B, et al. (2025) Genome-wide selection inference at short tandem repeats. *PLoS genetics*, 21(12), e1011959.