Resource Summary Report

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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/

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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

Funding:

Resource Name: National Human Genome Research Institute

Resource ID: SCR_011416

Alternate IDs: nlx_inv_1005098, Crossref funder ID: 100000051, SCR_003205, Wikidata: Q1634459, nlx_143900, OMICS_01554, SCR_006475, ISNI: 0000 0001 2233 9230, grid.280128.1

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

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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 116 mentions in open access literature.

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

Thomas R, et al. (2024) Hepatozoon (Eucoccidiorida: Hepatozoidae) in wild mammals of the Americas: a systematic review. Parasites & vectors, 17(1), 108.

Liu Y, et al. (2024) Comprehensive pan-cancer analysis reveals the versatile role of GALNT7 in epigenetic alterations and immune modulation in cancer. Heliyon, 10(11), e31515.

Yuan W, et al. (2024) UBR1 is a prognostic biomarker and therapeutic target associated with immune cell infiltration in gastric cancer. Aging, 16(16), 12029.

Song T, et al. (2024) Bulk and single-cell RNA sequencing reveal the contribution of laminin ?2 -CD44 to the immune resistance in lymphocyte-infiltrated squamous lung cancer subtype. Heliyon, 10(10), e31299.

Masaki N, et al. (2024) Simultaneous estimation of genotype error and uncalled deletion rates in whole genome sequence data. PLoS genetics, 20(5), e1011297.

Du N, et al. (2024) Identification of a Novel Homozygous Mutation in MTMR2 Gene Causes Very Rare Charcot-Marie-Tooth Disease Type 4B1. The application of clinical genetics, 17, 71.

Scarano A, et al. (2024) Animal Models for Investigating Osseointegration: An Overview of Implant Research over the Last Three Decades. Journal of functional biomaterials, 15(4).

Zhao T, et al. (2024) Characterizing PANoptosis gene signature in prognosis and chemosensitivity of colorectal cancer. Journal of gastrointestinal oncology, 15(5), 2129.

Yang P, et al. (2024) PSMD14 stabilizes estrogen signaling and facilitates breast cancer progression via deubiquitinating ER?. Oncogene, 43(4), 248.

Shakyawar SK, et al. (2024) iCluF: an unsupervised iterative cluster-fusion method for patient stratification using multiomics data. Bioinformatics advances, 4(1), vbae015.

Zhuang T, et al. (2024) USP36 promotes tumorigenesis and tamoxifen resistance in breast cancer by deubiquitinating and stabilizing ER?. Journal of experimental & clinical cancer research : CR, 43(1), 249.

Zhang H, et al. (2024) Unveiling the therapeutic potential of IHMT-337 in glioma treatment: targeting the EZH2-SLC12A5 axis. Molecular medicine (Cambridge, Mass.), 30(1), 91.

Svyatova G, et al. (2024) Genetic Predisposition to Prediabetes in the Kazakh Population. Current issues in molecular biology, 46(10), 10913.

He X, et al. (2024) Comprehensive analysis of clinical features, mRNA splicing, and immunological role of REEP5 in esophageal squamous cell carcinoma. Scientific reports, 14(1), 25675.

Mao B, et al. (2024) Identification and functional characterization of a novel heterozygous splice?site mutation in the calpain 3 gene causes rare autosomal dominant limb?girdle muscular dystrophy. Experimental and therapeutic medicine, 27(3), 97.

Tushoski-Alemán GW, et al. (2024) Infiltration of CD3+ and CD8+ lymphocytes in association with inflammation and survival in pancreatic cancer. PloS one, 19(2), e0297325.

Zhuang X, et al. (2024) MT1E in AML: a gateway to understanding regulatory cell death and immunotherapeutic responses. Journal of leukocyte biology, 116(6), 1515.

Duong D, et al. (2024) Comparison of clinical geneticist and computer visual attention in assessing genetic conditions. PLoS genetics, 20(2), e1011168.

Gao Y, et al. (2023) Animal-SNPAtlas: a comprehensive SNP database for multiple animals. Nucleic acids research, 51(D1), D816.

Zhang C, et al. (2023) Upregulation of FAM83F by c-Myc promotes cervical cancer growth and aerobic glycolysis via Wnt/?-catenin signaling activation. Cell death & disease, 14(12), 837.