

Resource Summary Report

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Public Health Genomics

RRID:SCR_006462

Type: Tool

Proper Citation

Public Health Genomics (RRID:SCR_006462)

Resource Information

URL: <http://www.cdc.gov/genomics/default.htm>

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Description: The Office of Public Health Genomics (OPHG) aims to integrate genomics into public health research, policy, and programs. Doing so could improve interventions designed to prevent and control the country's leading chronic, infectious, environmental, and occupational diseases. OPHG's efforts focus on conducting population-based genomic research, assessing the role of family health history in disease risk and prevention, supporting a systematic process for evaluating genetic tests, translating genomics into public health research and programs, and strengthening capacity for public health genomics in disease prevention programs. Goals: To improve public health interventions of diseases of major public health importance, including chronic, infectious, environmental, and occupational diseases, through six major initiatives: * Evaluation of Genomic Applications in Practice and Prevention (EGAPP), * Human Genome Epidemiology Network (HuGENet), * NHANES Collaborative Genomics Project, * Family History Public Health Initiative, * Genomics Translation Research and Programs, and, * Genomic Applications in Practice and Prevention Network (GAPPNet).

Synonyms: Genomics

Resource Type: data or information resource, narrative resource, organization portal, podcast, portal, radio, training resource

Keywords: environmental, genetics, chronic, disease, genomic, health, infectious, occupational, prevention, research

Resource Name: Public Health Genomics

Resource ID: SCR_006462

Alternate IDs: nif-0000-10186

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260919T195111+0000

Ratings and Alerts

No rating or validation information has been found for Public Health Genomics.

No alerts have been found for Public Health Genomics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 885 mentions in open access literature.

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

Hofer I, et al. (2026) An Extracellular Matrix-Producing Subset of Cancer-Associated Fibroblasts Drives Chemoresistance in Breast Cancer via SRC Activation and G0S2 Upregulation. Cancer research, 86(4), 1054.

Heron C, et al. (2026) Molecular determinants of cardiac lymphatic dysfunction in a chronic pressure-overload model. EMBO molecular medicine, 18(1), 325.

Ma Q, et al. (2026) scSemiPLC: a semi-supervised learning framework for annotating single-cell RNA-Seq data by generating pseudo-labels through clustering. mSystems, 11(1), e0022325.

Chang Y, et al. (2026) NDST3-Induced Epigenetic Reprogramming Reverses Neurodegeneration in Parkinson's Disease. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(14), e07323.

Solomon ED, et al. (2026) Which religious and personal characteristics predict attitudes toward gene editing? Findings from a survey of 4,939 adults in the U.S. Journal of community genetics, 17(3).

Singh S, et al. (2026) Temporal single-cell transcriptional dynamics of murine pancreatic islet remodeling during hyperglycaemia progression. Molecular metabolism, 110, 102387.

Kim D, et al. (2026) Molecular determinants of outcome to gemcitabine, cisplatin, and nab-paclitaxel in patients with advanced biliary tract cancer. Clinical and molecular hepatology, 32(2), 721.

Yan K, et al. (2026) Nurr1 Orchestrates Claustrium Development and Functionality. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(13), e08999.

Hazell Pickering S, et al. (2026) Multimodal epigenetic and enhancer network remodeling shape the transcriptional landscape of human beige adipocytes. *Communications biology*, 9(1), 191.

Patiño M, et al. (2026) Protocol for mapping neural circuit connectivity with START: Single transcriptome assisted rabies tracing. *STAR protocols*, 7(2), 104634.

Raleigh D, et al. (2026) DNA-PKcs inhibition sensitizes glioblastoma to radiotherapy through reprogramming of tumor cell states and immune microenvironment cell types. *Research square*.

Komaravolu RK, et al. (2026) Age-associated chemokine receptor expression profiles in human peripheral blood monocyte subsets predict cardiovascular disease risk. *Frontiers in immunology*, 17, 1749366.

Lawless D, et al. (2026) Application of qualifying variants for genomic analysis. *Bioinformatics (Oxford, England)*, 42(2).

Robbins MD, et al. (2026) Haplotype-resolved chromosome-level genome assembly of creeping bentgrass, *Agrostis stolonifera*. *Scientific data*, 13(1), 241.

Zhang X, et al. (2026) Activation of the impaired NAMPT/SIRT7/SOD2 axis restores alveolar progenitor cell renewal in idiopathic pulmonary fibrosis. *The Journal of clinical investigation*, 136(12).

Chen J, et al. (2026) Integrating single cell- and spatial- resolved transcriptomics unravels the inter-tumor heterogeneity and immunosuppressive landscape in HBV- and *Clonorchis sinensis*-associated hepatocellular carcinoma. *Molecular cancer*, 25(1), 3.

Pan M, et al. (2026) Insights into the potential mechanism of Beiqishen Jiangtang Granule in the treatment of type 2 diabetes nephropathy: A study based on network pharmacology, molecular docking, and biological validation. *Medicine*, 105(7), e47533.

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

Guedes M, et al. (2026) Uropathogenic *Escherichia coli* invade luminal prostate cells via FimH-PPAP receptor binding. *Nature microbiology*, 11(2), 535.

Yu L, et al. (2026) Digit regeneration in mice is stimulated by sequential treatment with FGF2 and BMP2. *Nature communications*, 17(1).