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: portal, radio, podcast, training resource, organization portal, narrative resource, data or information 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: 20260805T044135+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 772 mentions in open access literature.

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

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.

Li JJ, et al. (2026) NSD2 targeting reverses plasticity and drug resistance in prostate cancer. Nature, 649(8095), 216.

Hartill V, et al. (2025) Molecular diagnoses and candidate gene identification in the congenital heart disease cohorts of the 100,000 genomes project. European journal of human genetics : EJHG, 33(6), 793.

Gallo-Ter??n J, et al. (2025) Sensorineural Hearing Loss in Patients With the m.1555A>G Mutation in the MTRNR1 Gene. The Laryngoscope, 135(2), 901.

Mittal P, et al. (2025) Comprehensive characterization of MCL-1 in patients with colorectal cancer: Expression, molecular profiles, and outcomes. International journal of cancer, 156(8), 1583.

Watson BR, et al. (2025) Spatial transcriptomics of healthy and fibrotic human liver at single-cell resolution. Nature communications, 16(1), 319.

Stafford-Smith B, et al. (2025) "I'm quite proud of how we've handled it": health professionals' experiences of returning additional findings from the 100,000 genomes project. European journal of human genetics : EJHG, 33(8), 1025.

Huang H, et al. (2025) Kupffer cell programming by maternal obesity triggers fatty liver disease. Nature, 644(8077), 790.

West CE, et al. (2025) Medullary Thyroid Cancer Risk and Mortality in Carriers of Incidentally Identified MEN2A RET Variants. JAMA network open, 8(6), e2517937.

Hou S, et al. (2025) Single-cell transcriptomic atlas of different endometriosis indicating that an interaction between endometriosis-associated mesothelial cells (EAMCs) and ectopic stromal cells may influence progesterone resistance. Clinical and translational medicine, 15(2), e70216.

Yoon JW, et al. (2025) Th1-poised naive CD4 T cell subpopulation reflects anti-tumor immunity and autoimmune disease. Nature communications, 16(1), 1962.

Feng Z, et al. (2025) Modeling combinatorial regulation from single-cell multi-omics provides regulatory units underpinning cell type landscape using cRegulon. Genome biology, 26(1), 220.

Kaplanis J, et al. (2025) Assessment of the variant prioritization strategy for genomic newborn screening in the Generation Study. Genetics in medicine : official journal of the American College of Medical Genetics, 27(10), 101532.

Barbati F, et al. (2025) Monogenic Common Variable Immunodeficiency (Mo-CVID) Score for Optimizing the Genetic Diagnosis in Pediatric CVID Cohort. European journal of immunology, 55(3), e202451433.

Schmidt A, et al. (2025) Inflammatory conditions shape phenotypic and functional characteristics of lung-resident memory T cells in mice. Nature communications, 16(1), 3612.

Stenton SL, et al. (2025) Mitochondrial DNA variant detection in over 6,500 rare disease families by the systematic analysis of exome and genome sequencing data resolves undiagnosed cases. HGG advances, 6(3), 100441.

Xu X, et al. (2025) T cell-mediated SIV dissemination into the CNS: a single-cell transcriptomic analysis. Research square.

Noh MY, et al. (2025) Mutations in NEK1 cause ciliary dysfunction as a novel pathogenic mechanism in amyotrophic lateral sclerosis. Molecular neurodegeneration, 20(1), 59.

Nguyen H, et al. (2025) WNT Mimetic-Induced Lacrimal Gland Regeneration Reverses Aqueous Tear Deficiency. Translational vision science & technology, 14(6), 19.

Jalali P, et al. (2025) Bioinformatics analysis reveals shared molecular pathways for relationship between ulcerative colitis and primary sclerosing cholangitis. Genomics & informatics, 23(1), 12.