Resource Summary Report

Generated by ASWG on Apr 30, 2025

Human Genome Project Information

RRID:SCR_013028
Type: Tool

Proper Citation

Human Genome Project Information (RRID:SCR_013028)

Resource Information

URL: http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml

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Description: This resource gives information about the U.S. Human Genome Project, which was was a 13-year effort to to discover all the estimated 20,000-25,000 human genes and make them accessible for further biological study. The primary project goals were to: - identify all the approximately 20,000-25,000 genes in human DNA, - determine the sequences of the 3 billion chemical base pairs that make up human DNA, - store this information in databases, - improve tools for data analysis, - transfer related technologies to the private sector, and - address the ethical, legal, and social issues (ELSI) that may arise from the project. To help achieve these goals, researchers also studied the genetic makeup of several nonhuman organisms. These include the common human gut bacterium Escherichia coli, the fruit fly, and the laboratory mouse. These parallel studies helped to develop technology and interpret human gene function. Sponsors: The DOE Human Genome Program and the NIH National Human Genome Research Institute (NHGRI) together sponsored the U.S. Human Genome Project.

Synonyms: HGP

Resource Type: video resource, topical portal, funding resource, slide, narrative resource, portal, training material, data or information resource

Keywords: escherichia coli, fruit fly, function, gene, genome, genetic, bacterium, base pair, biological, dna, human, mouse, sequence, FASEB list

Funding:

Resource Name: Human Genome Project Information

Resource ID: SCR_013028

Alternate IDs: nif-0000-10252

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250430T055843+0000

Ratings and Alerts

No rating or validation information has been found for Human Genome Project Information.

No alerts have been found for Human Genome Project Information.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

van der Geest MA, et al. (2024) Systematic reanalysis of genomic data by diagnostic laboratories: a scoping review of ethical, economic, legal and (psycho)social implications. European journal of human genetics : EJHG, 32(5), 489.

Chiu P, et al. (2024) Integrating genomics into Canadian oncology nursing policy: Insights from a comparative policy analysis. Journal of advanced nursing, 80(11), 4488.

Wang SY, et al. (2024) Construction of a gene model related to the prognosis of patients with gastric cancer receiving immunotherapy and exploration of COX7A1 gene function. European journal of medical research, 29(1), 180.

Finlay D, et al. (2024) Detection of Genomic Structural Variations Associated with Drug Sensitivity and Resistance in Acute Leukemia. Cancers, 16(2).

Aierken A, et al. (2024) No bidirectional relationship between inflammatory bowel disease and diverticular disease: a genetic correlation and Mendelian randomization study. Frontiers in genetics, 15, 1334473.

Ball EM, et al. (2024) Challenging Misconceptions about Race in Undergraduate Genetics. CBE life sciences education, 23(3), ar32.

Aierken A, et al. (2024) No bidirectional relationship between constipation and colorectal cancer in European and Asian populations: A Mendelian randomization study. Medicine, 103(43), e40206.

Thanprasertsuk S, et al. (2023) Levodopa-induced dyskinesia in early-onset Parkinson's disease (EOPD) associates with glucocerebrosidase mutation: A next-generation sequencing study in EOPD patients in Thailand. PloS one, 18(10), e0293516.

Puddester R, et al. (2023) The Canadian Landscape of Genetics and Genomics in Nursing: A Policy Document Analysis. The Canadian journal of nursing research = Revue canadienne de recherche en sciences infirmieres, 55(4), 494.

Madsen RR, et al. (2023) PI3K signaling through a biochemical systems lens. The Journal of biological chemistry, 299(10), 105224.

Aruna P, et al. (2023) Association between polymorphisms of immune response genes and early childhood caries - systematic review, gene-based, gene cluster, and meta-analysis. Journal, genetic engineering & biotechnology, 21(1), 124.

Chen D, et al. (2023) Development trends of etiological research contents and methods of noncommunicable diseases. Health care science, 2(5), 352.

Ning P, et al. (2022) Rare missense variants in the PPP2R5D gene associated with Parkinson's disease in the Han Chinese population. Neuroscience letters, 776, 136564.

Aleissa M, et al. (2022) Common disease-associated gene variants in a Saudi Arabian population. Annals of Saudi medicine, 42(1), 29.

Eichinger J, et al. (2021) The full spectrum of ethical issues in pediatric genome-wide sequencing: a systematic qualitative review. BMC pediatrics, 21(1), 387.

Pietruszewska W, et al. (2021) Expression of Transcript Variants of PTGS1 and PTGS2 Genes among Patients with Chronic Rhinosinusitis with Nasal Polyps. Diagnostics (Basel, Switzerland), 11(1).

Gavrielatos M, et al. (2021) Benchmarking of next and third generation sequencing technologies and their associated algorithms for de novo genome assembly. Molecular medicine reports, 23(4).

Rosado E, et al. (2021) Using Machine Learning to Collect and Facilitate Remote Access to Biomedical Databases: Development of the Biomedical Database Inventory. JMIR medical informatics, 9(2), e22976.

Tanaka H, et al. (2021) HMGB1 signaling phosphorylates Ku70 and impairs DNA damage repair in Alzheimer's disease pathology. Communications biology, 4(1), 1175.

Jin M, et al. (2021) Prediction and verification of the AD-FTLD common pathomechanism based on dynamic molecular network analysis. Communications biology, 4(1), 961.