Resource Summary Report

Generated by NIF on Apr 18, 2025

International HapMap Project

RRID:SCR_002846
Type: Tool

Proper Citation

International HapMap Project (RRID:SCR_002846)

Resource Information

URL: http://hapmap.ncbi.nlm.nih.gov/

Proper Citation: International HapMap Project (RRID:SCR_002846)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 22, 2016. A multi-country collaboration among scientists and funding agencies to develop a public resource where genetic similarities and differences in human beings are identified and catalogued. Using this information, researchers will be able to find genes that affect health, disease, and individual responses to medications and environmental factors. All of the information generated by the Project will be released into the public domain. Their goal is to compare the genetic sequences of different individuals to identify chromosomal regions where genetic variants are shared. Public and private organizations in six countries are participating in the International HapMap Project. Data generated by the Project can be downloaded with minimal constraints. HapMap project related data, software, and documentation include: bulk data on genotypes, frequencies, LD data, phasing data, allocated SNPs, recombination rates and hotspots, SNP assays, Perlegen amplicons, raw data, inferred genotypes, and mitochondrial and chrY haplogroups; Generic Genome Browser software; protocols and information on assay design, genotyping and other protocols used in the project; and documentation of samples/individuals and the XML format used in the project.

Abbreviations: HapMap

Synonyms: HapMap Project

Resource Type: database, narrative resource, experimental protocol, data or information resource

Defining Citation: PMID:14685227

Keywords: genetic variant, disease, genetic sequence, genetic variation, single nucleotide polymorphism, genetic diversity, dna, sequence, catalog, genome, chromosome, bio.tools

Funding: Chinese Academy of Sciences ;
Chinese Ministry of Science and Technology ;
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Japanese Ministry of Education Culture Sports Science and Technology MEXT ;
National Natural Science Foundation of China ;
SNP Consortium ;
University Grants Committee of Hong Kong ;
Wellcome Trust ;
W. M. Keck Foundation ;
NIH

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: International HapMap Project

Resource ID: SCR_002846

Alternate IDs: nif-0000-02940, biotools:int_hapmap_project, OMICS_00273

Alternate URLs: http://www.hapmap.org/, https://bio.tools/int_hapmap_project

Old URLs: http://snp.cshl.org

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250418T055006+0000

Ratings and Alerts

No rating or validation information has been found for International HapMap Project.

No alerts have been found for International HapMap Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6793 mentions in open access literature.

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

Vermani L, et al. (2025) A Haplotype GWAS in Syndromic Familial Colorectal Cancer. International journal of molecular sciences, 26(2).

Zhou J, et al. (2025) Deep learning predicts DNA methylation regulatory variants in specific brain cell types and enhances fine mapping for brain disorders. Science advances, 11(1), eadn1870.

Pan Q, et al. (2025) A genome-wide association study identifies genetic variants associated with hip pain in the UK Biobank cohort (N?=?221,127). Scientific reports, 15(1), 2812.

Pampari A, et al. (2025) ChromBPNet: bias factorized, base-resolution deep learning models of chromatin accessibility reveal cis-regulatory sequence syntax, transcription factor footprints and regulatory variants. bioRxiv : the preprint server for biology.

Malomane DK, et al. (2025) Patterns of population structure and genetic variation within the Saudi Arabian population. bioRxiv : the preprint server for biology.

Reppell M, et al. (2025) HLA-DQA1*05 Associates With Anti-Tumor Necrosis Factor Immunogenicity and Low Adalimumab Trough Concentrations in Inflammatory Bowel Disease Patients From the SERENE Ulcerative Colitis and Crohn's Disease Studies. Journal of Crohn's & colitis, 19(1).

Akerele AT, et al. (2025) Uterine fibroids show evidence of shared genetic architecture with blood pressure traits. Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing, 30, 281.

Mahaman Mourtala IZ, et al. (2025) Genetic diversity and population structure studies of West African sweetpotato [Ipomoea batatas (L.) Lam] collection using DArTseq. PloS one, 20(1), e0312384.

Mukuze C, et al. (2025) Genome-wide association mapping of bruchid resistance loci in soybean. PloS one, 20(1), e0292481.

Zahid A, et al. (2025) Identifying genetic susceptibility loci associated with human coronary artery disease. PloS one, 20(1), e0315460.

Li S, et al. (2025) Transcriptome-wide association study identifies genes associated with bladder cancer risk. Scientific reports, 15(1), 1390.

Trang KB, et al. (2025) 3D genomic features across >50 diverse cell types reveal insights into the genomic architecture of childhood obesity. eLife, 13.

Pariès M, et al. (2025) The clinical value and most informative threshold of polygenic risk score in the Quebec City Case-Control Asthma Cohort. BMC pulmonary medicine, 25(1), 21.

Zhou J, et al. (2025) Circulating tumour DNA in predicting and monitoring survival of patients with locally advanced rectal cancer undergoing multimodal treatment: long-term results from a prospective multicenter study. EBioMedicine, 112, 105548.

Tihagam RD, et al. (2025) The TRIM37 variant rs57141087 contributes to triple-negative breast cancer outcomes in Black women. EMBO reports, 26(1), 245.

Matt GY, et al. (2024) St. Jude Survivorship Portal: Sharing and Analyzing Large Clinical and Genomic Datasets from Pediatric Cancer Survivors. Cancer discovery, 14(8), 1403.

Qiu Y, et al. (2024) The GC-content at the 5' ends of human protein-coding genes is undergoing mutational decay. Genome biology, 25(1), 219.

Paniri A, et al. (2024) Genetic variations in IKZF3, LET7-a2, and CDKN2B-AS1: Exploring associations with metabolic syndrome susceptibility and clinical manifestations. Journal of clinical laboratory analysis, 38(1-2), e24999.

Maihofer AX, et al. (2024) Effects of genetically predicted posttraumatic stress disorder on autoimmune phenotypes. Translational psychiatry, 14(1), 172.

Conery M, et al. (2024) GWAS-informed data integration and non-coding CRISPRi screen illuminate genetic etiology of bone mineral density. bioRxiv : the preprint server for biology.