Resource Summary Report

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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: data or information resource, database, experimental protocol, narrative 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 ;
Delores Dore Eccles Foundation ;
Genome Canada ;
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Hong Kong Innovation and Technology Commission ;
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, r3d100011835, OMICS_00273

Alternate URLs: http://www.hapmap.org/, https://bio.tools/int_hapmap_project, https://doi.org/10.17616/R3H06Q

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260905T132454+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 6854 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

?or?evi? N, et al. (2026) Protective association of the HIF-1? rs11549465 polymorphism with metabolic syndrome in people living with HIV on antiretroviral therapy. Frontiers in

medicine, 13, 1802450.

Gan X, et al. (2026) CTNNB1 Genetic Variation and Its Interaction With DLK1 in Type 2 Diabetes Mellitus. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(8), e71782.

Wang Y, et al. (2026) Association of SMAD4 gene polymorphisms with human papillomavirus infection and risk of cervical cancer: a case-control study. BMC cancer, 26(1), 213.

Liao X, et al. (2026) Impact of Hypoxia-Inducible Factor-1? Gene Polymorphisms on Renal Cell Carcinoma Susceptibility in a Chinese Han Population. Lifestyle genomics, 19(1), 1.

Luo S, et al. (2026) Association between maternal MTHFR and MTRR gene polymorphisms and the risk of congenital heart disease in newborns. BMC pediatrics, 26(1).

Deiana G, et al. (2025) Brain-wide pleiotropy investigation of alcohol drinking and tobacco smoking behaviors. Translational psychiatry, 15(1), 61.

Zheng Q, et al. (2025) Genetic basis of partner choice. bioRxiv : the preprint server for biology.

Chen X, et al. (2025) Old vs. New Local Ancestry Inference in HCHS/SOL: A Comparative Study. bioRxiv : the preprint server for biology.

Mukiti HM, et al. (2025) Optimizing breeding strategies for early-maturing white maize through genetic diversity and population structure. PloS one, 20(2), e0316793.

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

Li X, et al. (2025) Do CRP gene variants and smoking elevate recurrent stroke risk in minor ischemic stroke patients? European journal of medical research, 30(1), 179.

Wu F, et al. (2025) Association of IL-1RAcP rs16865597 gene polymorphism with susceptibility to essential hypertension: a case-control study in the Chinese Han population. BMC cardiovascular disorders, 25(1), 172.

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.

Tan MM, et al. (2025) Polygenic scores for disease risk are not associated with clinical outcomes in Parkinson's disease. medRxiv : the preprint server for health sciences.

Jin J, et al. (2025) PennPRS: a centralized cloud computing platform for efficient polygenic risk score training in precision medicine. medRxiv : the preprint server for health sciences.

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.

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.

Wang X, et al. (2025) EMcnv: enhancing CNV detection performance through ensemble strategies with heterogeneous meta-graph neural networks. Briefings in bioinformatics, 26(2).

Deng J, et al. (2025) The genetic susceptibility of SOD2 gene polymorphism in sudden sensorineural hearing loss (SSNHL). Global medical genetics, 12(1), 100021.

Cavalcante-Leão B, et al. (2025) Involvement of the gene encoding the collagen type II alpha 1 chain in mandibular mobility. BMC oral health, 25(1), 958.