Resource Summary Report

Generated by nidm-terms on Jul 28, 2026

MINIMAC

RRID:SCR_009292
Type: Tool

Proper Citation

MINIMAC (RRID:SCR_009292)

Resource Information

URL: http://genome.sph.umich.edu/wiki/Minimac

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Description: Software application that is a low memory, computationally efficient implementation of the MaCH algorithm for genotype imputation. It is designed to work on phased genotypes and can handle very large reference panels with hundreds or thousands of haplotypes. The name has two parts. The first, mini, refers to the modest amount of computational resources it requires. The second, mac, is short hand for MaCH, our widely used algorithm for genotype imputation. (entry from Genetic Analysis Software)

Abbreviations: MINIMAC

Synonyms: MACH

Resource Type: software application, software resource

Defining Citation: DOI:10.1038/ng.3656

Keywords: gene, genetic, genomic

Resource Name: MINIMAC

Resource ID: SCR_009292

Alternate IDs: nlx_154483, OMICS_08953

Alternate URLs: https://sources.debian.org/src/minimac4/

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260727T040448+0000

Ratings and Alerts

No rating or validation information has been found for MINIMAC.

No alerts have been found for MINIMAC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 187 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Davis CN, et al. (2025) Utility of Candidate Genes From an Algorithm Designed to Predict Genetic Risk for Opioid Use Disorder. JAMA network open, 8(1), e2453913.

Charles M, et al. (2025) Functional impact of splicing variants in the elaboration of complex traits in cattle. Nature communications, 16(1), 3893.

Farashi S, et al. (2025) HTRA1/lncRNA HTRA1-AS1 dominates in age-related macular degeneration reticular pseudodrusen genetic risk with no complement involvement. Nature communications, 16(1), 10854.

Zheng R, et al. (2025) A genome-wide association study identified PRKCB as a causal gene and therapeutic target for Mycobacterium avium complex disease. Cell reports. Medicine, 6(2), 101923.

Mulder RH, et al. (2025) Interactive effects of genotype with prenatal stress on DNA methylation at birth. Molecular psychiatry, 30(12), 5749.

Vilar-Ribó L, et al. (2025) Sex-Specific Genetic Architecture and Comorbidities of Alcohol Use Behaviors. medRxiv : the preprint server for health sciences.

Zhu B, et al. (2025) Multiple strategies association revealed functional candidate FASN gene for fatty acid composition in cattle. Communications biology, 8(1), 208.

Gu P, et al. (2025) Gene-Smoking Interaction in Insulin Sensitivity and ?-Cell Function Among Normal Glucose Tolerance Individuals. Journal of diabetes, 17(7), e70131.

Cheng C, et al. (2025) Genetic mapping of serum metabolome to chronic diseases among Han Chinese. Cell genomics, 5(2), 100743.

Squires S, et al. (2025) The impact of ancestry on performance of type 1 diabetes genetic risk scores: high discrimination performance is maintained in African ancestry populations, but population specific thresholds may improve risk prediction. medRxiv : the preprint server for health sciences.

Fouéré C, et al. (2025) Genetic regulation of sperm DNA methylation in cattle through meQTL mapping. BMC genomics, 26(1), 771.

He W, et al. (2025) Large-scale GWAS of strabismus identifies risk loci and provides support for a link with maternal smoking. Nature communications, 16(1), 7890.

Strati P, et al. (2025) Germline determinants of toxicity and efficacy in patients with large B-cell lymphoma treated with CAR T-cell therapy. Journal for immunotherapy of cancer, 13(10).

Huang J, et al. (2025) The impact of blood MCP-1 levels on Alzheimer's disease with genetic variation at the NAV3 and UNC5C loci. Translational psychiatry, 15(1), 296.

Zhang B, et al. (2025) Epigenetic clocks and longitudinal plasma biomarkers of Alzheimer's disease. medRxiv : the preprint server for health sciences.

Kirmani S, et al. (2025) Epigenome-wide DNA methylation association study of CHIP provides insight into perturbed gene regulation. Nature communications, 16(1), 4678.

Clifford RE, et al. (2024) Genetic architecture distinguishes tinnitus from hearing loss. Nature communications, 15(1), 614.

Levy D, et al. (2024) Epigenome-wide DNA Methylation Association Study of CHIP Provides Insight into Perturbed Gene Regulation. Research square.

Li X, et al. (2024) Genome-wide association identifies novel ROP risk loci in a multiethnic cohort. Communications biology, 7(1), 107.

Berger M, et al. (2024) IL-6 and hsCRP predict cardiovascular mortality in patients with heart failure with preserved ejection fraction. ESC heart failure, 11(6), 3607.