

Resource Summary Report

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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](https://doi.org/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: 20260821T193851+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 196 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Mandla R, et al. (2026) Statistical uncertainty explains the poor agreement in polygenic scoring for type 2 diabetes. medRxiv : the preprint server for health sciences.

Dyer WG, et al. (2026) Synergistic Effects of Early Psychosocial Factors and Polygenic Risk for Smoking: a Cross-Sectional Analysis of a Sample of Older Adults in the United States. Developmental psychobiology, 68(3), e70152.

Lapinska S, et al. (2026) Evaluation of the genome-informed risk assessment (GIRA) approach from eMERGE in an independent health system. medRxiv : the preprint server for health sciences.

Hernandez RO, et al. (2026) Preliminary estimates of genetic parameters for bone geometry, strength, and metabolism traits and their relationship with walking ability in turkeys (Meleagris gallopavo). Poultry science, 105(8), 107137.

Wang X, et al. (2026) GS-Impute: A neural network framework for accurate imputation of low-density markers in across-population genomic selection. Plant communications, 7(5), 101821.

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

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.

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.

Zhang Z, et al. (2025) An Advanced Entropy Approach for Minimizing False Discoveries in Imputation-Based Association Analyses. Research square.

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*.

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

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

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).

Jajoo A, et al. (2025) Leveraging genomic and transcriptomic data of diverse ancestry to uncover mechanisms of psychiatric risk in the adult and developing brain. *Nature communications*, 17(1), 1179.

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

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.

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.