

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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 resource, software application

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: 20260731T042814+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 [kravitz2](#) .

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.

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 β -Cell Function Among Normal Glucose Tolerance Individuals. *Journal of diabetes*, 17(7), e70131.

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*.

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.

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).

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

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

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.

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

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

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