**MINIMAC**

**RRID:** SCR_009292  
**Type:** Tool

**Proper Citation**

MINIMAC (RRID:SCR_009292)

**Resource Information**

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

**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)

**Resource Name:** MINIMAC

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**Resource Type:** Resource, software resource, software application

**Keywords:** gene, genetic, genomic

**Resource ID:** SCR_009292

**Website Status:** Last checked up

**Alternate IDs:** nlx_154483

**Abbreviations:** MINIMAC

**Mentions Count:** 84

**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 84 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [scicrunch](https://www.sci.crunch).


