

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on May 11, 2025

## EMINIM

RRID:SCR\_010790

Type: Tool

---

### Proper Citation

EMINIM (RRID:SCR\_010790)

---

### Resource Information

**URL:** <http://genetics.cs.ucla.edu/eminim/>

**Proper Citation:** EMINIM (RRID:SCR\_010790)

**Description:** A software tool for imputation of unobserved genotypes using a set of reference haplotype panel at a higher-density SNP set such as HapMap, and lower-density genotypes of a target individual using such as genotyping arrays.

**Abbreviations:** EMINIM

**Synonyms:** Expectation-Maximized INtegrative Imputation, Expectation-Maximized INtegrative IMputation (EMINIM)

**Resource Type:** software resource

**Funding:**

**Resource Name:** EMINIM

**Resource ID:** SCR\_010790

**Alternate IDs:** OMICS\_00196

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20250420T014509+0000

---

### Ratings and Alerts

No rating or validation information has been found for EMINIM.

No alerts have been found for EMINIM.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

Chen PB, et al. (2024) Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior. Cell genomics, 4(5), 100545.