Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

EMINIM

RRID:SCR_010790
Type: Tool

Proper Citation

EMINIM (RRID:SCR_010790)

Resource Information

URL: http://genetics.cs.ucla.edu/eminim/

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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 INtegreative Imputation, Expectation-Maximized INtegreative IMputation (EMINIM)

Resource Type: software resource

Resource Name: EMINIM

Resource ID: SCR_010790

Alternate IDs: OMICS_00196

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260905T132646+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 PRECISE-TBI .

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