Resource Summary Report

Generated by dkNET on Apr 16, 2025

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

Funding:

Resource Name: EMINIM

Resource ID: SCR_010790

Alternate IDs: OMICS_00196

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250410T070021+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 dkNET.

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