Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

HAPAR

RRID:SCR_009218
Type: Tool

Proper Citation

HAPAR (RRID:SCR_009218)

Resource Information

URL: http://theory.stanford.edu/~xuying/hapar/

Proper Citation: HAPAR (RRID:SCR_009218)

Description: Software application to infer haplotype from genotype data. It uses the parsimony principle, i.e. try to find the minimum number of haplotypes that can reconstruct the input genotypes. (entry from Genetic Analysis Software)

Abbreviations: HAPAR

Synonyms: HAplotype inference by PARsimony

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, ms-window, unix, solaris

Funding:

Resource Name: HAPAR

Resource ID: SCR_009218

Alternate IDs: nlx_154373

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250412T055357+0000

Ratings and Alerts

No rating or validation information has been found for HAPAR.

No alerts have been found for HAPAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.