

# Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

## 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

**Resource Name:** HAPAR

**Resource ID:** SCR\_009218

**Alternate IDs:** nlx\_154373

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260912T200242+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](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Agrohi P, et al. (2026) Decoding the multifaceted role of erythrocyte PMCA4b in oxidative stress-mediated malaria protection and artemisinin resistance. mBio, 17(1), e0173825.