

Resource Summary Report

Generated by [RRID](#) on Sep 20, 2026

HAPAR

RRID:SCR_009218

Type: Tool

Proper Citation

HAPAR (RRID:SCR_009218)

Resource Information

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

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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: 20260919T195801+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 found 1 mentions in open access literature.

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

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.