# Resource Summary Report

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# HAPLORE

RRID:SCR_009226
Type: Tool

## Proper Citation

HAPLORE (RRID:SCR_009226)

## Resource Information

**URL:** http://bioinformatics.med.yale.edu/group/software.html

**Proper Citation:** HAPLORE (RRID:SCR_009226)

**Description:** Software application for haplotype reconstruction in general pedigree without recombination (entry from Genetic Analysis Software)

**Abbreviations:** HAPLORE

**Synonyms:** HAPLOtype REconstruction in pedigrees

**Resource Type:** software resource, software application

**Keywords:** gene, genetic, genomic

**Funding:**

**Resource Name:** HAPLORE

**Resource ID:** SCR_009226

**Alternate IDs:** nlx_154383

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

**Record Last Update:** 20250503T060108+0000

## Ratings and Alerts

No rating or validation information has been found for HAPLORE.

No alerts have been found for HAPLORE.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 5 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

Diao G, et al. (2020) Statistically efficient association analysis of quantitative traits with haplotypes and untyped SNPs in family studies. BMC genetics, 21(1), 99.

Bountouvi E, et al. (2017) Novel NPC1 mutations with different segregation in two related Greek patients with Niemann-Pick type C disease: molecular study in the extended pedigree and clinical correlations. BMC medical genetics, 18(1), 51.

Lee YC, et al. (2016) Spinocerebellar ataxia type 36 in the Han Chinese. Neurology. Genetics, 2(3), e68.

Kaklamani V, et al. (2011) Polymorphisms of ADIPOQ and ADIPOR1 and prostate cancer risk. Metabolism: clinical and experimental, 60(9), 1234.

Chen M, et al. (2011) Incorporating biological pathways via a Markov random field model in genome-wide association studies. PLoS genetics, 7(4), e1001353.