## **Resource Summary Report**

Generated by NIF on Apr 19, 2025

# HAP 1

RRID:SCR\_000837

Type: Tool

### **Proper Citation**

HAP 1 (RRID:SCR\_000837)

#### **Resource Information**

URL: http://research.calit2.net/hap/

Proper Citation: HAP 1 (RRID:SCR\_000837)

**Description:** Software application (entry from Genetic Analysis Software)

**Abbreviations: HAP 1** 

Synonyms: haplotype resolution using imperfect phylogeny

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

**Funding:** 

Resource Name: HAP 1

Resource ID: SCR\_000837

Alternate IDs: nlx\_154371

**Record Creation Time:** 20220129T080203+0000

**Record Last Update:** 20250419T054805+0000

### **Ratings and Alerts**

No rating or validation information has been found for HAP 1.

No alerts have been found for HAP 1.

#### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 3 mentions in open access literature.

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

Kalis M, et al. (2007) Variants in the FFAR1 gene are associated with beta cell function. PloS one, 2(11), e1090.

Marchini J, et al. (2006) A comparison of phasing algorithms for trios and unrelated individuals. American journal of human genetics, 78(3), 437.

Scheet P, et al. (2006) A fast and flexible statistical model for large-scale population genotype data: applications to inferring missing genotypes and haplotypic phase. American journal of human genetics, 78(4), 629.