Resource Summary Report

Generated by NIF on Apr 23, 2025

HAPLOT

RRID:SCR_009228
Type: Tool

Proper Citation

HAPLOT (RRID:SCR_009228)

Resource Information

URL: http://info.med.yale.edu/genetics/kkidd/programs.html

Proper Citation: HAPLOT (RRID:SCR_009228)

Description: A simple software program for graphical presentation of haplotype block structures, tagSNP selection and SNP variation. (entry from Genetic Analysis Software)

Abbreviations: HAPLOT

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, fortran, vms

Funding:

Resource Name: HAPLOT

Resource ID: SCR_009228

Alternate IDs: nlx_154385

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250421T053723+0000

Ratings and Alerts

No rating or validation information has been found for HAPLOT.

No alerts have been found for HAPLOT.

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.

Zhang L, et al. (2024) Integrating GWAS, RNA-Seq and functional analysis revealed that BnaA02.SE mediates silique elongation by affecting cell proliferation and expansion in Brassica napus. Plant biotechnology journal, 22(10), 2907.

Gu S, et al. (2018) Recent Selection on a Class I ADH Locus Distinguishes Southwest Asian Populations Including Ashkenazi Jews. Genes, 9(9).

Zanetti D, et al. (2015) Potential Signals of Natural Selection in the Top Risk Loci for Coronary Artery Disease: 9p21 and 10q11. PloS one, 10(8), e0134840.

Zabetian CP, et al. (2003) The structure of linkage disequilibrium at the DBH locus strongly influences the magnitude of association between diallelic markers and plasma dopamine beta-hydroxylase activity. American journal of human genetics, 72(6), 1389.

Zabetian CP, et al. (2001) A quantitative-trait analysis of human plasma-dopamine beta-hydroxylase activity: evidence for a major functional polymorphism at the DBH locus. American journal of human genetics, 68(2), 515.