

Resource Summary Report

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HAPMINER

RRID:SCR_009233

Type: Tool

Proper Citation

HAPMINER (RRID:SCR_009233)

Resource Information

URL: <http://vorlon.case.edu/~jxl175/HapMiner.html>

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Description: Software application for association mapping based on directly mining the haplotypes from case-control data via a density-based clustering algorithm. HapMiner can be applied to whole-genome screens, as well as candidate-gene studies in small genomic regions. (entry from Genetic Analysis Software)

Abbreviations: HAPMINER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ms-windows, linux

Resource Name: HAPMINER

Resource ID: SCR_009233

Alternate IDs: nlx_154390

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260731T042812+0000

Ratings and Alerts

No rating or validation information has been found for HAPMINER.

No alerts have been found for HAPMINER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.