

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

DHSMAP

RRID:SCR_009160

Type: Tool

Proper Citation

DHSMAP (RRID:SCR_009160)

Resource Information

URL: <http://galton.uchicago.edu/~mcpeek/software/dhsmap/>

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Description: Software application for fine-mapping of qualitative traits by linkage disequilibrium. Given a set of marker haplotypes or genotypes from affected individuals, haplotypes or genotypes from appropriately selected controls, and a genetic map of the markers at which both sets of individuals are typed, DHSMAP estimates the location of the trait-associated variant by maximum likelihood or maximum quasi-likelihood. (entry from Genetic Analysis Software)

Abbreviations: DHSMAP

Synonyms: Decay of Haplotype Sharing MAPping software

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c++, unix, solaris, linux

Resource Name: DHSMAP

Resource ID: SCR_009160

Alternate IDs: nlx_154282

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260805T044218+0000

Ratings and Alerts

No rating or validation information has been found for DHSMAP.

No alerts have been found for DHSMAP.

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](#) .

Molitor J, et al. (2004) A survey of current Bayesian gene mapping methods. Human genomics, 1(5), 371.