Resource Summary Report

Generated by dkNET on Apr 16, 2025

MULTIPOPTAGSELECT

RRID:SCR_009307
Type: Tool

Proper Citation

MULTIPOPTAGSELECT (RRID:SCR_009307)

Resource Information

URL: http://droog.gs.washington.edu/multiPopTagSelect.html

Proper Citation: MULTIPOPTAGSELECT (RRID:SCR_009307)

Description: Software program that selects a near-minimal set of tagging single-nucleotide polymorphisms (tagSNPs) that account for all observed patterns of linkage disequilibrium (LD) in multiple populations. (entry from Genetic Analysis Software)

Abbreviations: MULTIPOPTAGSELECT

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, perl

Funding:

Resource Name: MULTIPOPTAGSELECT

Resource ID: SCR_009307

Alternate IDs: nlx_154497

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063543+0000

Ratings and Alerts

No rating or validation information has been found for MULTIPOPTAGSELECT.

No alerts have been found for MULTIPOPTAGSELECT.

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 dkNET.

Abbott D, et al. (2012) An international collaborative family-based whole genome quantitative trait linkage scan for myopic refractive error. Molecular vision, 18, 720.