

# Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

## MULTIPOPOTAGSELECT

RRID:SCR\_009307

Type: Tool

### Proper Citation

MULTIPOPOTAGSELECT (RRID:SCR\_009307)

### Resource Information

**URL:** <http://droog.gs.washington.edu/multiPopTagSelect.html>

**Proper Citation:** MULTIPOPOTAGSELECT (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:** MULTIPOPOTAGSELECT

**Resource Type:** software resource, software application

**Keywords:** gene, genetic, genomic, perl

**Resource Name:** MULTIPOPOTAGSELECT

**Resource ID:** SCR\_009307

**Alternate IDs:** nlx\_154497

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260731T042818+0000

### Ratings and Alerts

No rating or validation information has been found for MULTIPOPOTAGSELECT.

No alerts have been found for MULTIPOPOTAGSELECT.

### 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 [PRECISE-TBI](#) .

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