

# Resource Summary Report

Generated by T1D on Aug 4, 2026

## MARGARITA

RRID:SCR\_009279

Type: Tool

### Proper Citation

MARGARITA (RRID:SCR\_009279)

### Resource Information

**URL:** <http://www.sanger.ac.uk/resources/software/margarita/>

**Proper Citation:** MARGARITA (RRID:SCR\_009279)

**Description:** Software application that infers genealogies from population genotype data and uses these to map disease loci. These genealogies take the form of the Ancestral Recombination Graph (ARG). The ARG defines a genealogical tree for each locus, and as one moves along the chromosome the topologies of consecutive trees shift according to the impact of historical recombination events. (entry from Genetic Analysis Software)

**Abbreviations:** MARGARITA

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

**Keywords:** gene, genetic, genomic, java

**Resource Name:** MARGARITA

**Resource ID:** SCR\_009279

**Alternate IDs:** nlx\_154460

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

**Record Last Update:** 20260801T191058+0000

### Ratings and Alerts

No rating or validation information has been found for MARGARITA.

No alerts have been found for MARGARITA.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Hu T, et al. (2021) Conformational and migrational dynamics of slipped-strand DNA three-way junctions containing trinucleotide repeats. Nature communications, 12(1), 204.

Wang GH, et al. (2014) An-Gong-Niu-Huang Wan protects against cerebral ischemia induced apoptosis in rats: up-regulation of Bcl-2 and down-regulation of Bax and caspase-3. Journal of ethnopharmacology, 154(1), 156.