

Resource Summary Report

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MARGARITA

RRID:SCR_009279

Type: Tool

Proper Citation

MARGARITA (RRID:SCR_009279)

Resource Information

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

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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 application, software resource

Keywords: gene, genetic, genomic, java

Resource Name: MARGARITA

Resource ID: SCR_009279

Alternate IDs: nlx_154460

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260805T044221+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](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.