

# Resource Summary Report

Generated by RRID on Aug 4, 2026

## MAPMAKER/HOMOZ

RRID:SCR\_009282

Type: Tool

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### Proper Citation

MAPMAKER/HOMOZ (RRID:SCR\_009282)

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### Resource Information

**URL:** <https://github.com/gaow/genetic-analysis-software/blob/master/pages/MAPMAKER%26HOMOZ.md>

**Proper Citation:** MAPMAKER/HOMOZ (RRID:SCR\_009282)

**Description:** Software application that calculates multipoint lod scores in pedigrees with inbreeding loops (entry from Genetic Analysis Software)

**Abbreviations:** MAPMAKER/HOMOZ

**Synonyms:** homozygosity mapping

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

**Keywords:** gene, genetic, genomic, c, unix

**Resource Name:** MAPMAKER/HOMOZ

**Resource ID:** SCR\_009282

**Alternate IDs:** nlx\_154463

**Old URLs:** ftp://ftp-genome.wi.mit.edu/distribution/software/homoz

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

**Record Last Update:** 20260801T191048+0000

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### Ratings and Alerts

No rating or validation information has been found for MAPMAKER/HOMOZ.

No alerts have been found for MAPMAKER/HOMOZ.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Ruiz A, et al. (1998) A major locus for autosomal recessive retinitis pigmentosa on 6q, determined by homozygosity mapping of chromosomal regions that contain gamma-aminobutyric acid-receptor clusters. American journal of human genetics, 62(6), 1452.