

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

MAPMAKER/HOMOZ

RRID:SCR_009282

Type: Tool

Proper Citation

MAPMAKER/HOMOZ (RRID:SCR_009282)

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 application, software resource

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: 20260727T040448+0000

Ratings and Alerts

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

No alerts have been found for MAPMAKER/HOMOZ.

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 [nidm-terms](#) .

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.