

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

GENEHUNTER-MODSCORE

RRID:SCR_009069

Type: Tool

Proper Citation

GENEHUNTER-MODSCORE (RRID:SCR_009069)

Resource Information

URL: <https://www.helmholtz-muenchen.de/ige/service/software-download/genehunter-modscore/index.html>

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Description: Software application that is an extension of GENEHUNTER-IMPRINTING, based on the original GENEHUNTER version 2.1 release 6, that allows for a MOD-score analysis, in which parametric LOD scores are maximized over the parameters of the trait model, i.e., the penetrances and disease allele frequency. As of version 2.0, it is possible to use sex-specific recombination frequencies. The genetic positions of markers can be automatically read from a publicly available genetic map. (entry from Genetic Analysis Software)

Abbreviations: GENEHUNTER-MODSCORE

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, sunos, solaris, osf, hpux, aix, ultrix, linux, ms-windows

Resource Name: GENEHUNTER-MODSCORE

Resource ID: SCR_009069

Alternate IDs: nlx_154061

Old URLs: <http://www.staff.uni-marburg.de/~strauchk/software.html>

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260731T042806+0000

Ratings and Alerts

No rating or validation information has been found for GENEHUNTER-MODSCORE.

No alerts have been found for GENEHUNTER-MODSCORE.

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 [kravitz2](#) .

Brugger M, et al. (2016) Estimation of Trait-Model Parameters in a MOD Score Linkage Analysis. Human heredity, 82(3-4), 103.