

# Resource Summary Report

Generated by [NIF](#) on Aug 26, 2026

## genehunter-imprinting

RRID:SCR\_009104

Type: Tool

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### Proper Citation

genehunter-imprinting (RRID:SCR\_009104)

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### Resource Information

**URL:** <http://www.helmholtz-muenchen.de/en/ige/service/software-download/genehunter-imprinting/index.html#c63682>

**Proper Citation:** genehunter-imprinting (RRID:SCR\_009104)

**Description:** Resource no longer in service. Documented on February 23,2021. Software tool as modification of GENEHUNTER software package . Allows for parametric multi-marker linkage analysis of dichotomous traits caused by imprinted genes. By specification of two heterozygote penetrance parameters, paternal and maternal origin of the disease allele can be treated differently in terms of probability of expression of the trait.

**Abbreviations:** GENEHUNTER-TWOLOCUS

**Synonyms:** GENEHUNTER-MODSCORE, GENEHUNTER-PLUS, GENEHUNTER, GENEHUNTER-IMPRINTING

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

**Defining Citation:** [DOI:10.1086/302911](https://doi.org/10.1086/302911)

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

**Availability:** Resource no longer in service. Documented on February 23,2021

**Resource Name:** genehunter-imprinting

**Resource ID:** SCR\_009104

**Alternate IDs:** nlx\_154199, biotools:genehunter-imprinting

**Alternate URLs:** <https://bio.tools/genehunter-imprinting>

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

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260821T193850+0000

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## Ratings and Alerts

No rating or validation information has been found for genehunter-imprinting.

No alerts have been found for genehunter-imprinting.

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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 [NIF](#) .

Wang X, et al. (2011) Genome-wide linkage scan of a pedigree with familial hypercholesterolemia suggests susceptibility loci on chromosomes 3q25-26 and 21q22. PloS one, 6(10), e24838.