

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

[genehunter-imprinting](#)

RRID:SCR_009104

Type: Tool

Proper Citation

genehunter-imprinting (RRID:SCR_009104)

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 resource, software application

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: 20260801T191055+0000

Ratings and Alerts

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

No alerts have been found for genehunter-imprinting.

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 [RRID](#) .

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.