

# Resource Summary Report

Generated by [dkNET](#) on Aug 31, 2026

## GENEHUNTER

RRID:SCR\_009191

Type: Tool

### Proper Citation

GENEHUNTER (RRID:SCR\_009191)

### Resource Information

**URL:** <http://www.broad.mit.edu/ftp/distribution/software/genehunter/>

**Proper Citation:** GENEHUNTER (RRID:SCR\_009191)

**Description:** Software application for multipoint analysis of pedigree data including: non-parametric linkage analysis, LOD-score computation, information-content mapping, haplotype reconstruction (entry from Genetic Analysis Software)

**Abbreviations:** GENEHUNTER

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

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

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

**Resource Name:** GENEHUNTER

**Resource ID:** SCR\_009191

**Alternate IDs:** nlx\_154332

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

**Record Last Update:** 20260829T183107+0000

### Ratings and Alerts

No rating or validation information has been found for GENEHUNTER.

No alerts have been found for GENEHUNTER.

### Data and Source Information

## Usage and Citation Metrics

We found 93 mentions in open access literature.

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

Le PM, et al. (2025)  $\gamma$ -catenin phosphorylation is elevated during mitosis to resist apical rounding and epithelial barrier leak. *Biology open*, 14(1).

Quinn JM, et al. (2024)  $\gamma$ -catenin middle- and actin-binding domain unfolding mutants differentially impact epithelial strength and sheet migration. *Molecular biology of the cell*, 35(5), ar65.

Le PM, et al. (2024)  $\gamma$ -catenin phosphorylation is elevated during mitosis to resist apical rounding and epithelial barrier leak. *bioRxiv : the preprint server for biology*.

Romanelli Tavares VL, et al. (2022) New locus underlying auriculocondylar syndrome (ARCND): 430 kb duplication involving TWIST1 regulatory elements. *Journal of medical genetics*, 59(9), 895.

Neitzel H, et al. (2022) Transmission ratio distortion of mutations in the master regulator of centriole biogenesis PLK4. *Human genetics*, 141(11), 1785.

Majmundar AJ, et al. (2021) Recessive NOS1AP variants impair actin remodeling and cause glomerulopathy in humans and mice. *Science advances*, 7(1).

Chiereghin C, et al. (2021) SLC22A4 Gene in Hereditary Non-syndromic Hearing Loss: Recurrence and Incomplete Penetrance of the p.C113Y Mutation in Northwest Africa. *Frontiers in genetics*, 12, 606630.

Unlu G, et al. (2020) Phenome-based approach identifies RIC1-linked Mendelian syndrome through zebrafish models, biobank associations and clinical studies. *Nature medicine*, 26(1), 98.

Tucker JS, et al. (2020) The Role of Testosterone and Gibberellic Acid in the Melanization of *Cryptococcus neoformans*. *Frontiers in microbiology*, 11, 1921.

Schote AB, et al. (2020) Genome-wide linkage analysis of families with primary hyperhidrosis. *PloS one*, 15(12), e0244565.

Koohiyan M, et al. (2019) Screening of 10 DFNB Loci Causing Autosomal Recessive Non-Syndromic Hearing Loss in Two Iranian Populations Negative for GJB2 Mutations. *Iranian journal of public health*, 48(9), 1704.

Choi YJ, et al. (2019) Mutations of ADAMTS9 Cause Nephronophthisis-Related Ciliopathy. *American journal of human genetics*, 104(1), 45.

Li J, et al. (2019) Linkage Analysis of the Chromosome 5q31-33 Region Identifies JAKMIP2 as a Risk Factor for Graves' Disease in the Chinese Han Population. *Medical*

science monitor : international medical journal of experimental and clinical research, 25, 1439.

Mukhopadhyay N, et al. (2018) Identifying genetic risk loci for diabetic complications and showing evidence for heterogeneity of type 1 diabetes based on complications risk. PloS one, 13(2), e0192696.

van der Ven AT, et al. (2018) A homozygous missense variant in VWA2, encoding an interactor of the Fraser-complex, in a patient with vesicoureteral reflux. PloS one, 13(1), e0191224.

Ashraf S, et al. (2018) Mutations in six nephrosis genes delineate a pathogenic pathway amenable to treatment. Nature communications, 9(1), 1960.

Micheal S, et al. (2018) Identification of TP53BP2 as a Novel Candidate Gene for Primary Open Angle Glaucoma by Whole Exome Sequencing in a Large Multiplex Family. Molecular neurobiology, 55(2), 1387.

Gasser S, et al. (2018) Genomic analysis in patients with myxomatous mitral valve prolapse: current state of knowledge. BMC cardiovascular disorders, 18(1), 41.

Gibson CL, et al. (2018) Glial loss of the metallo  $\beta$ -lactamase domain containing protein, SWIP-10, induces age- and glutamate-signaling dependent, dopamine neuron degeneration. PLoS genetics, 14(3), e1007269.

Urkasemsin G, et al. (2017) Genetics of Hereditary Ataxia in Scottish Terriers. Journal of veterinary internal medicine, 31(4), 1132.