Resource Summary Report

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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 resource, software application

Keywords: gene, genetic, genomic, c, unix

Funding:

Resource Name: GENEHUNTER

Resource ID: SCR_009191

Alternate IDs: nlx_154332

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063539+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

Source: SciCrunch Registry

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) ?-catenin phosphorylation is elevated during mitosis to resist apical rounding and epithelial barrier leak. Biology open, 14(1).

Quinn JM, et al. (2024) ?-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) ? -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.

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

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

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.

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

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

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