

Resource Summary Report

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HAPLOPAINTER

RRID:SCR_001710

Type: Tool

Proper Citation

HAPLOPAINTER (RRID:SCR_001710)

Resource Information

URL: <http://haplopainter.sourceforge.net/>

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Description: A pedigree drawing program, suitable in processing haplotype outputs from GENEHUNTER, ALLEGRO, MERLIN, and SIMWALK (entry from Genetic Analysis Software)

Abbreviations: HaploPainter

Resource Type: software application, software resource

Defining Citation: [PMID:15377505](#)

Keywords: gene, genetic, genomic, perl, pedigree, haplotype, draw, bio.tools

Availability: Free, Freely Available

Resource Name: HAPLOPAINTER

Resource ID: SCR_001710

Alternate IDs: nlx_154062, OMICS_00209, biotools:haplopainter

Alternate URLs: <https://bio.tools/haplopainter>

Old URLs: <http://haplopainter.sourceforge.net/html/ManualIndex.htm>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260821T193629+0000

Ratings and Alerts

No rating or validation information has been found for HAPLOPAINTER.

No alerts have been found for HAPLOPAINTER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Maltese PE, et al. (2026) Exclusion of CLIC5 as a Candidate Gene and Identification of NEFM as a Possible Novel Gene Correlated With Autosomal Recessive Pure Cerebellar Ataxia in a Highly Consanguineous Family. *Molecular genetics & genomic medicine*, 14(4), e70199.

Ahmad S, et al. (2025) Pathogenic variants identification in primary congenital glaucoma patients using whole exome sequencing. *Scientific reports*, 15(1), 11066.

Khan A, et al. (2025) Exome Sequencing of Consanguineous Pashtun Families With Familial Epilepsy Reveals Causative and Candidate Variants in TSEN54, MOCS2, and OPHN1. *Clinical genetics*, 107(1), 98.

Simchoni N, et al. (2025) The common HAQ STING allele prevents clinical penetrance of COPA syndrome. *The Journal of experimental medicine*, 222(4).

Qian M, et al. (2024) A rare missense p.C125Y mutation in the TNFRSF1A gene identified in a Chinese family with tumor necrosis factor receptor-associated periodic fever syndrome. *Frontiers in genetics*, 15, 1413641.

Abdel-Salam GMH, et al. (2023) Biallelic MAD2L1BP (p31comet) mutation is associated with mosaic aneuploidy and juvenile granulosa cell tumors. *JCI insight*, 8(22).

Okashah S, et al. (2022) Investigation of Genetic Causes in Patients with Congenital Heart Disease in Qatar: Findings from the Sidra Cardiac Registry. *Genes*, 13(8).

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

Khan NM, et al. (2021) Updates on Clinical and Genetic Heterogeneity of ASPM in 12 Autosomal Recessive Primary Microcephaly Families in Pakistani Population. *Frontiers in pediatrics*, 9, 695133.

Emmert DB, et al. (2021) Genetic and Metabolic Determinants of Atrial Fibrillation in a General Population Sample: The CHRIS Study. *Biomolecules*, 11(11).

Xiomerisiou G, et al. (2021) SORL1 mutation in a Greek family with Parkinson's disease and dementia. *Annals of clinical and translational neurology*, 8(10), 1961.

Waseem SS, et al. (2021) A Homozygous AKNA Frameshift Variant Is Associated with Microcephaly in a Pakistani Family. *Genes*, 12(10).

Hartl D, et al. (2020) A rare loss-of-function variant of ADAM17 is associated with late-onset familial Alzheimer disease. *Molecular psychiatry*, 25(3), 629.

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

Xie W, et al. (2020) Clinical features and genetic analysis of two Chinese families with X-linked ichthyosis. *The Journal of international medical research*, 48(10), 300060520962292.

Pang P, et al. (2019) DDX24 Mutations Associated With Malformations of Major Vessels to the Viscera. *Hepatology (Baltimore, Md.)*, 69(2), 803.

Pr??ss H, et al. (2019) Linkage Evidence for a Two-Locus Inheritance of LQT-Associated Seizures in a Multigenerational LQT Family With a Novel KCNQ1 Loss-of-Function Mutation. *Frontiers in neurology*, 10, 648.

Freder V, et al. (2019) Pathogenicity of new BEST1 variants identified in Italian patients with best vitelliform macular dystrophy assessed by computational structural biology. *Journal of translational medicine*, 17(1), 330.

Nedeljkovic I, et al. (2018) A Genome-Wide Linkage Study for Chronic Obstructive Pulmonary Disease in a Dutch Genetic Isolate Identifies Novel Rare Candidate Variants. *Frontiers in genetics*, 9, 133.

Pourreza MR, et al. (2018) Applying Two Different Bioinformatic Approaches to Discover Novel Genes Associated with Hereditary Hearing Loss via Whole-Exome Sequencing: ENDEAVOUR and HomozygosityMapper. *Advanced biomedical research*, 7, 141.