Resource Summary Report

Generated by T1D on Sep 15, 2026

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: 20260912T200226+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 T1D .

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.

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.

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

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).

Xiromerisiou 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.

Frecer 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.

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.

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.