Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 25, 2025

PSEUDOMARKER

RRID:SCR_009345
Type: Tool

Proper Citation

PSEUDOMARKER (RRID:SCR_009345)

Resource Information

URL: http://www.helsinki.fi/~tsjuntun/pseudomarker/

Proper Citation: PSEUDOMARKER (RRID:SCR_009345)

Description: A linkage analysis software for joint linkage and/or linkage disequilibrium analysis. PSEUDOMARKER can analyze different data structures jointly such as cases-controls, trios, sib-pairs, sib-ships, and extended families. (entry from Genetic Analysis Software)

Abbreviations: PSEUDOMARKER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c/c++, linux

Funding:

Resource Name: PSEUDOMARKER

Resource ID: SCR_009345

Alternate IDs: nlx_154557

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250421T053726+0000

Ratings and Alerts

No rating or validation information has been found for PSEUDOMARKER.

No alerts have been found for PSEUDOMARKER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Postolache TT, et al. (2024) The melatonin receptor genes are linked and associated with the risk of polycystic ovary syndrome. Journal of ovarian research, 17(1), 17.

Wu R, et al. (2024) The melanocortin receptor genes are linked to and associated with the risk of polycystic ovary syndrome in Italian families. Journal of ovarian research, 17(1), 242.

Amin M, et al. (2023) Linkage and association of variants in the dopamine receptor 2 gene (DRD2) with polycystic ovary syndrome. Journal of ovarian research, 16(1), 158.

Hebbar P, et al. (2023) Linkage analysis using whole exome sequencing data implicates SLC17A1, SLC17A3, TATDN2 and TMEM131L in type 1 diabetes in Kuwaiti families. Scientific reports, 13(1), 14978.

Du Y, et al. (2019) A rare TTC30B variant is identified as a candidate for synpolydactyly in a Chinese pedigree. Bone, 127, 503.

Cheng R, et al. (2018) Linkage analysis of multiplex Caribbean Hispanic families loaded for unexplained early-onset cases identifies novel Alzheimer's disease loci. Alzheimer's & dementia (Amsterdam, Netherlands), 10, 554.

Gupta R, et al. (2017) Neuregulin signaling pathway in smoking behavior. Translational psychiatry, 7(8), e1212.

Tommiska J, et al. (2017) Two missense mutations in KCNQ1 cause pituitary hormone deficiency and maternally inherited gingival fibromatosis. Nature communications, 8(1), 1289.

Misiewicz Z, et al. (2016) A genome-wide screen for acrophobia susceptibility loci in a Finnish isolate. Scientific reports, 6, 39345.

Oikkonen J, et al. (2016) Creative Activities in Music--A Genome-Wide Linkage Analysis. PloS one, 11(2), e0148679.

Siwo GH, et al. (2015) Predicting functional and regulatory divergence of a drug resistance transporter gene in the human malaria parasite. BMC genomics, 16(1), 115.

Gertz EM, et al. (2014) PSEUDOMARKER 2.0: efficient computation of likelihoods using NOMAD. BMC bioinformatics, 15, 47.

Sigurdsson S, et al. (2005) Polymorphisms in the tyrosine kinase 2 and interferon regulatory factor 5 genes are associated with systemic lupus erythematosus. American journal of human genetics, 76(3), 528.