Resource Summary Report

Generated by dkNET on Apr 30, 2025

LOKI

RRID:SCR_009260
Type: Tool

Proper Citation

LOKI (RRID:SCR_009260)

Resource Information

URL: http://www.stat.washington.edu/thompson/Genepi/Loki.shtml

Proper Citation: LOKI (RRID:SCR_009260)

Description: Software program for analyses a quantitative trait observed on large pedigrees using Markov chain Monte Carlo multipoint linkage and segregation analysis. The trait may be determined by multiple loci. (entry from Genetic Analysis Software)

Abbreviations: LOKI

Synonyms: PANGAEA

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, (solaris 2.5, osf1 3.2, and others), linux, (2.0.30)

Funding:

Resource Name: LOKI

Resource ID: SCR_009260

Alternate IDs: nlx_154439

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250429T055318+0000

Ratings and Alerts

No rating or validation information has been found for LOKI.

No alerts have been found for LOKI.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Wang L, et al. (2025) Novel loci for triglyceride/HDL-C ratio longitudinal change among subjects without T2D. Journal of lipid research, 66(1), 100702.

Wang L, et al. (2024) Novel Loci (EIF4A2, ADIPOQ, TPRG1) for Triglyceride / High-density Lipoprotein Cholesterol Ratio Longitudinal Change (?THR) among Subjects without Type 2 Diabetes: Evidence from the Long Life Family Study (LLFS) and the Framingham Heart Study (FHS) Offspring Cohort (OS). medRxiv : the preprint server for health sciences.

Weiß JF, et al. (2024) Unprecedented insights into extents of biological responses to physical forcing in an Arctic sub-mesoscale filament by combining high-resolution measurement approaches. Scientific reports, 14(1), 8192.

Snoeijs-Leijonmalm P, et al. (2022) Unexpected fish and squid in the central Arctic deep scattering layer. Science advances, 8(7), eabj7536.

Feitosa MF, et al. (2020) Gene discovery for high-density lipoprotein cholesterol level change over time in prospective family studies. Atherosclerosis, 297, 102.

Zhang X, et al. (2019) Real world scenarios in rare variant association analysis: the impact of imbalance and sample size on the power in silico. BMC bioinformatics, 20(1), 46.

Oh JJ, et al. (2019) An exome-wide rare variant analysis of Korean men identifies three novel genes predisposing to prostate cancer. Scientific reports, 9(1), 17173.

Best LG, et al. (2019) Genetic analysis of hsCRP in American Indians: The Strong Heart Family Study. PloS one, 14(10), e0223574.

Shivakumar M, et al. (2019) Exome-Wide Rare Variant Analysis From the DiscovEHR Study Identifies Novel Candidate Predisposition Genes for Endometrial Cancer. Frontiers in oncology, 9, 574.

Landefeld CC, et al. (2018) Effects on gene expression and behavior of untagged short tandem repeats: the case of arginine vasopressin receptor 1a (AVPR1a) and externalizing

behaviors. Translational psychiatry, 8(1), 72.

Blue EE, et al. (2018) Variants regulating ZBTB4 are associated with age-at-onset of Alzheimer's disease. Genes, brain, and behavior, 17(6), e12429.

Verma SS, et al. (2018) Rare variants in drug target genes contributing to complex diseases, phenome-wide. Scientific reports, 8(1), 4624.

Miller JE, et al. (2018) Rare variants in the splicing regulatory elements of EXOC3L4 are associated with brain glucose metabolism in Alzheimer's disease. BMC medical genomics, 11(Suppl 3), 76.

Woodbury-Smith M, et al. (2017) Combined genome-wide linkage and targeted association analysis of head circumference in autism spectrum disorder families. Journal of neurodevelopmental disorders, 9, 5.

Hall MA, et al. (2017) PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature communications, 8(1), 1167.

Kim D, et al. (2017) Knowledge-driven binning approach for rare variant association analysis: application to neuroimaging biomarkers in Alzheimer's disease. BMC medical informatics and decision making, 17(Suppl 1), 61.

Mathias SR, et al. (2016) Recurrent major depression and right hippocampal volume: A bivariate linkage and association study. Human brain mapping, 37(1), 191.

Rao TJ, et al. (2016) A Framework for Interpreting Type I Error Rates from a Product-Term Model of Interaction Applied to Quantitative Traits. Genetic epidemiology, 40(2), 144.

Hall MA, et al. (2015) Biology-Driven Gene-Gene Interaction Analysis of Age-Related Cataract in the eMERGE Network. Genetic epidemiology, 39(5), 376.

Gomez F, et al. (2015) Admixture mapping of coronary artery calcification in African Americans from the NHLBI family heart study. BMC genetics, 16, 42.