Resource Summary Report

Generated by T1D on Jul 31, 2026

SNPLINK

RRID:SCR_009403
Type: Tool

Proper Citation

SNPLINK (RRID:SCR_009403)

Resource Information

URL: http://www.icr.ac.uk/cancgen/molgen/MolPopGen_Bioinformatics.htm

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Description: Software application for multipoint linkage analysis of densely distributed SNP data incorporating automated linkage disequilibrium removal. SNPLINK requires these other programs installed on the system: MERLIN (used for nonparametric analysis), ALLEGRO (used for parametric analysis), R and PERL, all are freely available. (entry from Genetic Analysis Software)

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, perl, unix

Resource Name: SNPLINK

Resource ID: SCR_009403

Alternate IDs: nlx_154646

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260731T042809+0000

Ratings and Alerts

No rating or validation information has been found for SNPLINK.

No alerts have been found for SNPLINK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Xie L, et al. (2025) Plasma protein levels and hepatocellular carcinoma: a Mendelian randomization study with drug screening implications. Discover oncology, 16(1), 567.

Karasik D, et al. (2010) Refined QTLs of osteoporosis-related traits by linkage analysis with genome-wide SNPs: Framingham SHARe. Bone, 46(4), 1114.

Arinami T, et al. (2005) Genomewide high-density SNP linkage analysis of 236 Japanese families supports the existence of schizophrenia susceptibility loci on chromosomes 1p, 14q, and 20p. American journal of human genetics, 77(6), 937.

Sellick GS, et al. (2005) A high-density SNP genomewide linkage scan for chronic lymphocytic leukemia-susceptibility loci. American journal of human genetics, 77(3), 420.