

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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 application, software resource

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: 20260905T133251+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 [Kravitz](#) .

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.