# Resource Summary Report

Generated by RRID on Apr 11, 2025

## FASTSLINK

RRID:SCR_008664
Type: Tool

### Proper Citation

FASTSLINK (RRID:SCR_008664)

### Resource Information

**URL:** http://watson.hgen.pitt.edu/register/soft_doc.html

**Proper Citation:** FASTSLINK (RRID:SCR_008664)

**Description:** Software application that is a faster version of SLINK (entry from Genetic Analysis Software)

**Abbreviations:** FASTSLINK

**Synonyms:** faster SLINK

**Resource Type:** software resource, software application

**Keywords:** gene, genetic, genomic, c, unix, bio.tools

**Funding:**

**Resource Name:** FASTSLINK

**Resource ID:** SCR_008664

**Alternate IDs:** nlx_154312, biotools:snpcaller

**Alternate URLs:** https://bio.tools/snpcaller

**Record Creation Time:** 20220129T080248+0000

**Record Last Update:** 20250411T055224+0000

### Ratings and Alerts

No rating or validation information has been found for FASTSLINK.

No alerts have been found for FASTSLINK.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 12 mentions in open access literature.

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


Posadas-Cantera S, et al. (2024) The effect of HLA genotype on disease onset and severity in CTLA-4 insufficiency. Frontiers in immunology, 15, 1447995.

Ghaleb Y, et al. (2022) Whole Exome/Genome Sequencing Joint Analysis of a Family with Oligogenic Familial Hypercholesterolemia. Metabolites, 12(3).

Andres EM, et al. (2020) Pedigree-Based Gene Mapping Supports Previous Loci and Reveals Novel Suggestive Loci in Specific Language Impairment. Journal of speech, language, and hearing research : JSLHR, 63(12), 4046.

Koohiyan M, et al. (2019) Screening of 10 DFNB Loci Causing Autosomal Recessive Non-Syndromic Hearing Loss in Two Iranian Populations Negative for GJB2 Mutations. Iranian journal of public health, 48(9), 1704.

Nikkola E, et al. (2017) Family-specific aggregation of lipid GWAS variants confers the susceptibility to familial hypercholesterolemia in a large Austrian family. Atherosclerosis, 264, 58.

Wight JE, et al. (2016) Chromosome loci vary by juvenile myoclonic epilepsy subsyndromes: linkage and haplotype analysis applied to epilepsy and EEG 3.5-6.0 Hz polyspike waves. Molecular genetics & genomic medicine, 4(2), 197.

Reiisi S, et al. (2016) Screening of DFNB3 in Iranian families with autosomal recessive non-syndromic hearing loss reveals a novel pathogenic mutation in the MyTh4 domain of the MYO15A gene in a linked family. Iranian journal of basic medical sciences, 19(7), 772.

Brugger M, et al. (2016) Estimation of Trait-Model Parameters in a MOD Score Linkage Analysis. Human heredity, 82(3-4), 103.

Moosmann J, et al. (2015) Novel loci for non-syndromic coarctation of the aorta in sporadic and familial cases. PloS one, 10(5), e0126873.

Garnai SJ, et al. (2014) Congenital cataracts: de novo gene conversion event in CRYBB2.

Molecular vision, 20, 1579.

Elston RC, et al. (2004) A review of the 'Statistical Analysis for Genetic Epidemiology' (S.A.G.E.) software package. Human genomics, 1(6), 456.

Long JR, et al. (2004) Patterns of linkage disequilibrium and haplotype distribution in disease candidate genes. BMC genetics, 5, 11.