Resource Summary Report

Generated by T1D on Jul 30, 2026

SLINK

RRID:SCR_009397
Type: Tool

Proper Citation

SLINK (RRID:SCR_009397)

Resource Information

URL: http://www.jurgott.org/linkage/SLINK.htm

Proper Citation: SLINK (RRID:SCR_009397)

Description: Software application (entry from Genetic Analysis Software)

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, pascal, ms-dos

Resource Name: SLINK

Resource ID: SCR_009397

Alternate IDs: nlx_154635

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260727T040501+0000

Ratings and Alerts

No rating or validation information has been found for SLINK.

No alerts have been found for SLINK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Bot DM, et al. (2025) FLASC: a flare-sensitive clustering algorithm. PeerJ. Computer science, 11, e2792.

Tsivilskiy I, et al. (2023) Thermal-structural hybrid Lagrangian solver and numerical simulation-based correction of shape deformation of stainless-steel parts produced by laser powder bed fusion. Scientific reports, 13(1), 17535.

Ye XC, et al. (2022) Linkage analysis identifies an isolated strabismus locus at 14q12 overlapping with FOXG1 syndrome region. Journal of medical genetics, 59(1), 46.

Argimón S, et al. (2021) A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at pathogenwatch. Nature communications, 12(1), 2879.

Sánchez-Busó L, et al. (2021) A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of Neisseria gonorrhoeae at Pathogenwatch. Genome medicine, 13(1), 61.

Tabbarah S, et al. (2020) COG5 variants lead to complex early onset retinal degeneration, upregulation of PERK and DNA damage. Scientific reports, 10(1), 21269.

Zou QL, et al. (2018) A powerful parent-of-origin effects test for qualitative traits on X chromosome in general pedigrees. BMC bioinformatics, 19(1), 8.

Li JL, et al. (2017) Generalized disequilibrium test for association in qualitative traits incorporating imprinting effects based on extended pedigrees. BMC genetics, 18(1), 90.

Peter B, et al. (2016) Genetic Candidate Variants in Two Multigenerational Families with Childhood Apraxia of Speech. PloS one, 11(4), e0153864.

Arkema EV, et al. (2016) What to Expect When Expecting With Systemic Lupus Erythematosus (SLE): A Population-Based Study of Maternal and Fetal Outcomes in SLE and Pre-SLE. Arthritis care & research, 68(7), 988.

Arkema EV, et al. (2016) Case definitions in Swedish register data to identify systemic lupus erythematosus. BMJ open, 6(1), e007769.

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

Mitchell AL, et al. (2015) Linkage Analysis in Autoimmune Addison's Disease: NFATC1 as a Potential Novel Susceptibility Locus. PloS one, 10(6), e0123550.

Li X, et al. (2014) Genome-wide linkage study suggests a susceptibility locus for isolated bilateral microtia on 4p15.32-4p16.2. PloS one, 9(7), e101152.

Feng BJ, et al. (2011) Design considerations for massively parallel sequencing studies of complex human disease. PloS one, 6(8), e23221.

Wang X, et al. (2011) Genome-wide linkage scan of a pedigree with familial hypercholesterolemia suggests susceptibility loci on chromosomes 3q25-26 and 21q22. PloS one, 6(10), e24838.

Tabatabaiefar M, et al. (2011) Genetic Linkage Analysis of 15 DFNB Loci in a Group of Iranian Families with Autosomal Recessive Hearing Loss. Iranian journal of public health, 40(2), 34.

Hattersley K, et al. (2010) A novel syndrome of paediatric cataract, dysmorphism, ectodermal features, and developmental delay in Australian Aboriginal family maps to 1p35.3-p36.32. BMC medical genetics, 11, 165.

Li Q, et al. (2010) Genome scan for locus involved in mandibular prognathism in pedigrees from China. PloS one, 5(9).

Kemlink D, et al. (2008) Suggestive evidence for linkage for restless legs syndrome on chromosome 19p13. Neurogenetics, 9(2), 75.