

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

PLINK/SEQ

RRID:SCR_013193

Type: Tool

Proper Citation

PLINK/SEQ (RRID:SCR_013193)

Resource Information

URL: <https://atgu.mgh.harvard.edu/plinkseq/>

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Description: An open-source C/C++ library for working with human genetic variation data. The specific focus is to provide a platform for analytic tool development for variation data from large-scale resequencing projects, particularly whole-exome and whole-genome studies. However, the library could in principle be applied to other types of genetic studies, including whole-genome association studies of common SNPs. (entry from Genetic Analysis Software)

Resource Type: software toolkit, software resource, software library, software application

Keywords: gene, genetic, genomic, c/c++, r, macos, linux, bio.tools

Availability: Open unspecified license

Resource Name: PLINK/SEQ

Resource ID: SCR_013193

Alternate IDs: nlx_154213, biotools:plink-seq

Alternate URLs: <https://bio.tools/plink-seq>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260731T042858+0000

Ratings and Alerts

No rating or validation information has been found for PLINK/SEQ.

No alerts have been found for PLINK/SEQ.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 77 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ishorst N, et al. (2025) Role of ZFHX4 in orofacial clefting based on human genetic data and zebrafish models. *European journal of human genetics : EJHG*, 33(5), 595.

Lokki AI, et al. (2025) Understanding rare genetic variants within the terminal pathway of complement system in preeclampsia. *Genes and immunity*, 26(1), 22.

Bánfai Z, et al. (2024) Analysis of Gyimes Csango population samples on a high-resolution genome-wide basis. *BMC genomics*, 25(1), 942.

Lokki A, et al. (2024) Rare variants in genes coding for components of the terminal pathway of the complement system in preeclampsia. *Research square*.

Fernandez TV, et al. (2023) Primary complex motor stereotypies are associated with de novo damaging DNA coding mutations that identify KDM5B as a risk gene. *PloS one*, 18(10), e0291978.

Bánfai Z, et al. (2023) Characterization of Danube Swabian population samples on a high-resolution genome-wide basis. *BMC genomics*, 24(1), 9.

Spena S, et al. (2022) Genetic variants at the chromosomal region 2q21.3 underlying inhibitor development in patients with severe haemophilia A. *Haemophilia : the official journal of the World Federation of Hemophilia*, 28(2), 270.

Shin JJ, et al. (2021) Clinical, Radiographic, and Genetic Analyses in a Population-Based Cohort of Adult Spinal Deformity in the Older Population. *Neurospine*, 18(3), 608.

Pagliari MT, et al. (2021) Role of ADAMTS13, VWF and F8 genes in deep vein thrombosis. *PloS one*, 16(10), e0258675.

Mikhaylova AV, et al. (2021) Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. *American journal of human genetics*, 108(10), 1836.

Mahdi H, et al. (2021) Genomic analyses of high-grade neuroendocrine gynecological malignancies reveal a unique mutational landscape and therapeutic vulnerabilities. *Molecular oncology*, 15(12), 3545.

Bis-Brewer DM, et al. (2020) Assessing non-Mendelian inheritance in inherited axonopathies. *Genetics in medicine : official journal of the American College of Medical Genetics*, 22(12), 2114.

Serra EG, et al. (2020) Somatic mosaicism and common genetic variation contribute to the risk of very-early-onset inflammatory bowel disease. *Nature communications*, 11(1), 995.

Bobbili DR, et al. (2020) Excess of singleton loss-of-function variants in Parkinson's disease contributes to genetic risk. *Journal of medical genetics*, 57(9), 617.

Nguyen TH, et al. (2020) mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. *Nature communications*, 11(1), 2929.

Marenne G, et al. (2020) Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. *Cell metabolism*, 31(6), 1107.

Xu C, et al. (2020) Medium-coverage DNA sequencing in the design of the genetic association study. *European journal of human genetics : EJHG*, 28(10), 1459.

Crooks L, et al. (2020) Identification of single nucleotide variants in the Moroccan population by whole-genome sequencing. *BMC genetics*, 21(1), 111.

Witten A, et al. (2020) ADAMTS12, a new candidate gene for pediatric stroke. *PloS one*, 15(8), e0237928.

Monroe TO, et al. (2020) PCM1 is necessary for focal ciliary integrity and is a candidate for severe schizophrenia. *Nature communications*, 11(1), 5903.