

Resource Summary Report

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PLINK

RRID:SCR_001757

Type: Tool

Proper Citation

PLINK (RRID:SCR_001757)

Resource Information

URL: <http://www.nitrc.org/projects/plink>

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Description: Open source whole genome association analysis toolset, designed to perform range of basic, large scale analyses in computationally efficient manner. Used for analysis of genotype/phenotype data. Through integration with gPLINK and Haploview, there is some support for subsequent visualization, annotation and storage of results. PLINK 1.9 is improved and second generation of the software.

Synonyms: PLINK 1.9, PLINK/SEQ, plink - Whole genome association analysis toolset

Resource Type: software application, software resource, data analysis software, data processing software, software toolkit

Defining Citation: [PMID:17701901](#), [DOI:10.1086/519795](#)

Keywords: gene, genetic, genomic, genotype, phenotype, copy number variant, whole-genome association, population, linkage analysis, whole-genome association study, data management, summary statistics, population stratification, association analysis, identity-by-descent estimation

Availability: Free, Available for download, Freely Available

Resource Name: PLINK

Resource ID: SCR_001757

Alternate IDs: nlx_154200, OMICS_00206, SCR_021271

Alternate URLs: <https://zzz.bwh.harvard.edu/plink/>, https://www.cog-genomics.org/plink/1.9/general_usage#cite, <https://sources.debian.org/src/plink/>

Old URLs: <http://pngu.mgh.harvard.edu/~purcell/plink/>

License: GNU General Public License, v2

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260819T044032+0000

Ratings and Alerts

No rating or validation information has been found for PLINK.

Warning: Warning: PCA results may be sensitive to the sample size, population composition, and the number of columns, in which case the results will not be reliable, robust, nor replicable and should not be used to draw conclusions.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16581 mentions in open access literature.

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

Liu Q, et al. (2026) Structural variation drives praziquantel response and host adaptation in *Schistosoma japonicum*. *iScience*, 29(6), 116118.

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

Yeh CM, et al. (2026) A New CA19-9 Cutoff Value Identifies Lewis Antigen Status and Refines Prognostic Stratification in PDAC. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(13), 2722.

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal *Anaerostipes*. *Poultry science*, 105(3), 106388.

Tjader NP, et al. (2026) Association of germline variants with KRAS-mutation status in colorectal cancer. *Scientific reports*, 16(1).

Meng X, et al. (2026) Characterization of Genetic Etiologic Factors for Pediatric Acute Lymphoblastic Leukemia in Large Childhood Cancer Survivorship Cohorts. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(7), 1100.

McFarland LN, et al. (2026) The dilution effect of stocking and the loss of wildness among North American mallards. *Current biology : CB*.

Huang K, et al. (2026) Exploring a genetic basis for the metabolic perturbations in ME/CFS using UK biobank. *iScience*, 29(1), 114316.

Camerini L, et al. (2026) Harsh parenting and rs11621961 at the SERPINA6/1 locus: gene-environment interaction effects on hair cortisol in a Brazilian population-based longitudinal study. *Stress (Amsterdam, Netherlands)*, 29(1), 2611613.

Sigalova OM, et al. (2026) Modeling cis-regulatory variation in human brain enhancers across a large Parkinson's Disease cohort. *bioRxiv : the preprint server for biology*.

Parween S, et al. (2026) Host genome and bacterial taxa shape the Arabidopsis seed microbiome. *EMBO reports*, 27(1), 122.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Kore P, et al. (2026) Interplay between Genetic Ancestry, Self-reported Race and Ethnicity, and Clinical Factors in Pediatric Acute Lymphoblastic Leukemia: A REDIAL Consortium Report. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(5), 710.

Chung C, et al. (2026) Ancestrally Diverse Autologous Patient-Derived Organoid-Immune Cell Coculture Platform for Addressing Immunotherapeutic Outcome Disparities in High-Grade Endometrial Cancer. *Cancer research communications*, 6(3), 657.

Lu Q, et al. (2026) Genomic characterization and pathogenicity validation of *Mycoplasma ovipneumoniae* strains from diseased sheep: insights into potential pathogenic mechanisms of GSWW364. *Veterinary research*, 57(1).

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. *EBioMedicine*, 123, 106111.

Ma Y, et al. (2026) Gene-culture coevolution shapes olfactory receptor gene diversity in Orang Asli populations. *Cell reports*, 117181.

C Dos Santos J, et al. (2026) Persistent viral control status is associated with enhanced innate immune responses in people with HIV-1. *iScience*, 29(3), 114807.

Levey D, et al. (2026) Genetics of SSRI antidepressant use and relationship to psychiatric and medical traits. *HGG advances*, 7(1), 100500.

Klepinowski T, et al. (2026) Epigenome-wide DNA methylation profiling in aneurysmal subarachnoid hemorrhage and delayed ischemic neurologic deficit: a prospective observational study. *International journal of surgery (London, England)*, 112(1), 832.