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, data analysis software, software resource, 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: 20260729T044024+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 15344 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

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.

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.

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

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.

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

Taylor RS, et al. (2026) Accurate Runs of Homozygosity Estimation From Low Coverage Genome Sequences in Non-Model Species. Molecular ecology resources, 26(1), e70083.

Gao X, et al. (2026) Single-Cell Genetic Mapping of Gasdermin Expression Across Immune-Mediated Inflammatory Diseases. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(1), e71328.

Anastasi F, et al. (2026) Proteomic polygenic risk scores of age-related plasma protein levels reveal a role for Metalloproteinase inhibitor 2 (TIMP2) in cognitive performance.

Neurobiology of aging, 157, 68.

Liu Y, et al. (2026) Telomere length, aging, and cognitive function in the Midwestern Amish. HGG advances, 7(1), 100533.

Li R, et al. (2026) Whole-genome sequence-based association analysis of African American individuals with bipolar disorder and schizophrenia. HGG advances, 7(1), 100499.

Han Y, et al. (2026) Linkage disequilibrium score regression identifies genetic correlations between hepatocellular carcinoma and clinically relevant traits. International journal of cancer, 158(5), 1193.

Jacques A, et al. (2026) Optimising the Use of Cryopreserved Genetic Resources for the Selection and Conservation of Animal Populations. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 143(1), 50.

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. Molecular ecology, 35(1), e70218.

Langie J, et al. (2026) The impact of Indigenous American-like ancestry on the risk of acute lymphoblastic leukemia in Hispanic/Latino children. HGG advances, 7(1), 100534.

Estand??a A, et al. (2026) The Genetic Consequences of Dispersal and Immigration in a Wild Great Tit Population. Molecular ecology, 35(1), e70206.

Teng CS, et al. (2026) Actomyosin contractility and a threshold of cadherin cell adhesion are required during tissue fusion. The Journal of cell biology, 225(1).

Schnelle A, et al. (2026) Using Historic and Contemporary Genomes to Assess the Genetic Consequences of a Population Decline in an Endangered Tern Population. Evolutionary applications, 19(1), e70192.

Zeigler LP, et al. (2026) Detailed assessment of rare and common TERT variation in a family with a telomere biology disorder. HGG advances, 7(1), 100536.

Onabanjo O, et al. (2026) Genomic prediction of feed efficiency in boars by deep learning. G3 (Bethesda, Md.), 16(1).

Cruz DE, et al. (2026) Admixture-mapping analysis reveals genetic determinants of the human plasma proteome. HGG advances, 7(1), 100529.