**PLINK**

**RRID:** SCR_001757  
**Type:** Tool

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**Proper Citation**

PLINK (RRID:SCR_001757)

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**Resource Information**

**URL:** [http://www.nitrc.org/projects/plink](http://www.nitrc.org/projects/plink)

**Proper Citation:** PLINK (RRID:SCR_001757)

**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.

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

**References:** PMID:17701901

**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

**Related resources:** Whap, PLINK/SEQ, Haploview, MendelIHT.jl

**Availability:** Free, Available for download, Freely Available

**Website Status:** Last checked up

**Resource Name:** PLINK

**Resource ID:** SCR_001757
**Alternate IDs:** nlx_154200, OMICS_00206, SCR_021271

**Alternate URLs:** https://www.cog-genomics.org/plink/1.9/general_usage#cite

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

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**Ratings and Alerts**

No rating or validation information has been found for PLINK.

No alerts have been found for PLINK.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 7889 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://www.cog-genomics.org/plink/1.9/general_usage#cite).


da Silva RS, et al. (2021) NCOA3 identified as a new candidate to explain autosomal dominant progressive hearing loss. Human molecular genetics, 29(22), 3691-3705.


