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

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

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, SCR_021271
Ratings and Alerts

No rating or validation information has been found for PLINK.

No alerts have been found for PLINK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10547 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Cornes BK, et al. (2023) Protein coding variation in the J:ARC and J:DO outbred laboratory mouse stocks provides a molecular basis for distinct research applications. G3 (Bethesda, Md.), 13(4).

Truong BT, et al. (2023) PRDM1 DNA-binding zinc finger domain is required for normal limb development and is disrupted in split hand/foot malformation. Disease models & mechanisms, 16(4).


Miller JT, et al. (2023) Independently evolved pollution resistance in four killifish populations is largely explained by few variants of large effect. bioRxiv: the preprint server for biology.


Yu X, et al. (2023) Exploring the causal role of the immune response to varicella-zoster virus on multiple traits: a phenome-wide Mendelian randomization study. BMC medicine, 21(1), 143.

Vaitinadin NS, et al. (2023) Genetic susceptibility for autoimmune diseases and white blood cell count. Scientific reports, 13(1), 5852.