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. The focus of PLINK is purely on analysis of genotype/phenotype data, so there is no support for steps prior to this (e.g. study design and planning, generating genotype or CNV calls from raw data). Through integration with gPLINK and Haploview, there is some support for the subsequent visualization, annotation and storage of results.

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, Open unspecified license

Website Status: Last checked up

Abbreviations: PLINK
Resource Name: PLINK
Resource ID: SCR_001757
Alternate IDs: nlx_154200, OMICS_00206
Old URLs: http://pngu.mgh.harvard.edu/~purcell/plink/

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 7361 mentions in open access literature.

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

Harroud A, et al. (2021) Mendelian randomization study shows no causal effects of serum urate levels on the risk of MS. Neurology(R) neuroimmunology & neuroinflammation, 8(1).


Xu G, et al. (2020) Genome and population sequencing of a chromosome-level genome
assembly of the Chinese tapertail anchovy (Coilia nasus) provides novel insights into migratory adaptation. GigaScience, 9(1).


Pechlivanis S, et al. (2020) Association between lipoprotein(a) (Lp(a)) levels and Lp(a) genetic variants with coronary artery calcification. BMC medical genetics, 21(1), 62.


Liu X, et al. (2020) CACNA1C Gene rs11832738 Polymorphism Influences Depression Severity by Modulating Spontaneous Activity in the Right Middle Frontal Gyrus in Patients With Major Depressive Disorder. Frontiers in psychiatry, 11, 73.