

# Resource Summary Report

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## FlashPCA

RRID:SCR\_021680

Type: Tool

### Proper Citation

FlashPCA (RRID:SCR\_021680)

### Resource Information

**URL:** <https://github.com/gabraham/flashpca>

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**Description:** Software tool as fast principal component analysis of large scale genome wide data. FlashPCA performs fast principal component analysis (PCA) of single nucleotide polymorphism (SNP) data. FlashPCA2 used for principal component analysis of biobank scale genotype datasets.

**Synonyms:** FlashPCA2

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

**Defining Citation:** [DOI:10.1093/bioinformatics/btx299](https://doi.org/10.1093/bioinformatics/btx299),  
[DOI:10.1371/journal.pone.0093766](https://doi.org/10.1371/journal.pone.0093766)

**Keywords:** Principal component analysis, large scale genome wide data, single nucleotide polymorphism data, biobank scale genotype datasets

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

**Resource Name:** FlashPCA

**Resource ID:** SCR\_021680

**License:** GNU General Public License

**Record Creation Time:** 20220129T080356+0000

**Record Last Update:** 20260804T043727+0000

### Ratings and Alerts

No rating or validation information has been found for FlashPCA.

**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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Derkx I, et al. (2025) The genetic demographic history of the last hunter-gatherer population of the Himalayas. Scientific reports, 15(1), 1505.

Douville NJ, et al. (2025) Clinical and Genetic Factors Associated with Intraoperative Minimum Alveolar Concentration Ratio: A Single-center Retrospective Cohort and Genome-wide Association Study. Anesthesiology, 143(3), 541.

Nicolas A, et al. (2025) Transferability of European-derived Alzheimer's disease polygenic risk scores across multiancestry populations. Nature genetics, 57(7), 1598.

Katzourou IK, et al. (2025) Contributions of common and rare genetic variation to different measures of mood and anxiety disorder in the UK Biobank. BJPsych open, 11(3), e97.

Beneker O, et al. (2025) Urbanization and genetic homogenization in the medieval Low Countries revealed through a ten-century paleogenomic study of the city of Sint-Truiden. Genome biology, 26(1), 127.

Bhérier C, et al. (2025) Frequency enrichment of coding variants in a French-Canadian founder population and its implication for inflammatory bowel diseases. medRxiv : the preprint server for health sciences.

Milind N, et al. (2025) Buffering and non-monotonic behavior of gene dosage response curves for human complex traits. medRxiv : the preprint server for health sciences.

Wang Z, et al. (2025) The APOE ?4 allele affects the survival of patients with Parkinson's disease independent of dementia. Journal of translational medicine, 23(1), 1094.

Gao Y, et al. (2024) Reconstructing the ancestral gene pool to uncover the origins and genetic links of Hmong-Mien speakers. BMC biology, 22(1), 59.

Venkateswaran V, et al. (2024) Polygenic scores for tobacco use provide insights into systemic health risks in a diverse EHR-linked biobank in Los Angeles. Translational psychiatry, 14(1), 38.

Chia R, et al. (2024) Genome sequence analyses identify novel risk loci for multiple system atrophy. *Neuron*, 112(13), 2142.

Tissink E, et al. (2023) The Genetic Architectures of Functional and Structural Connectivity Properties within Cerebral Resting-State Networks. *eNeuro*, 10(4).

Dattani S, et al. (2023) Common and rare variant associations with latent traits underlying depression, bipolar disorder, and schizophrenia. *Translational psychiatry*, 13(1), 46.

Sadler KV, et al. (2023) Genome-wide association analysis identifies a susceptibility locus for sporadic vestibular schwannoma at 9p21. *Brain : a journal of neurology*, 146(7), 2861.

Walters RG, et al. (2023) Genotyping and population characteristics of the China Kadoorie Biobank. *Cell genomics*, 3(8), 100361.

Zhou H, et al. (2023) Multi-ancestry study of the genetics of problematic alcohol use in over 1 million individuals. *Nature medicine*, 29(12), 3184.

Venkateswaran V, et al. (2023) Interplay Of Serum Bilirubin and Tobacco Smoking with Lung and Head and Neck Cancers in a Diverse, EHR-linked Los Angeles Biobank. *Research square*.

Venkateswaran V, et al. (2023) Interplay Of Serum Bilirubin and Tobacco Smoking with Lung and Head and Neck Cancers in a Diverse, EHR-linked Los Angeles Biobank. *medRxiv : the preprint server for health sciences*.

Bao J, et al. (2023) Brain-wide genome-wide colocalization study for integrating genetics, transcriptomics and brain morphometry in Alzheimer's disease. *NeuroImage*, 280, 120346.

Actkins KV, et al. (2023) Sex modifies the effect of genetic risk scores for polycystic ovary syndrome on metabolic phenotypes. *PLoS genetics*, 19(5), e1010764.