

Resource Summary Report

Generated by NIF on Sep 5, 2026

MIXSCORE

RRID:SCR_009076

Type: Tool

Proper Citation

MIXSCORE (RRID:SCR_009076)

Resource Information

URL: <http://www.hsph.harvard.edu/faculty/alkes-price/software/>

Proper Citation: MIXSCORE (RRID:SCR_009076)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 16,2023. Software application using a method for combining SNP association and admixture association statistics to increase power in GWAS in admixed populations. (entry from Genetic Analysis Software)

Abbreviations: MIXSCORE

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MIXSCORE

Resource ID: SCR_009076

Alternate IDs: nlx_154074

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260904T000439+0000

Ratings and Alerts

No rating or validation information has been found for MIXSCORE.

No alerts have been found for MIXSCORE.

Data and Source Information

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Raj T, et al. (2017) Genetic architecture of age-related cognitive decline in African Americans. *Neurology. Genetics*, 3(1), e125.

Hinks A, et al. (2013) Dense genotyping of immune-related disease regions identifies 14 new susceptibility loci for juvenile idiopathic arthritis. *Nature genetics*, 45(6), 664.

Liu Y, et al. (2013) Softwares and methods for estimating genetic ancestry in human populations. *Human genomics*, 7(1), 1.

Zaitlen N, et al. (2012) Informed conditioning on clinical covariates increases power in case-control association studies. *PLoS genetics*, 8(11), e1003032.

Pasaniuc B, et al. (2011) Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARE and a Breast Cancer Consortium. *PLoS genetics*, 7(4), e1001371.

Price AL, et al. (2011) Single-tissue and cross-tissue heritability of gene expression via identity-by-descent in related or unrelated individuals. *PLoS genetics*, 7(2), e1001317.