Resource Summary Report

Generated by NIF on Sep 11, 2026

RFMix

RRID:SCR_027030
Type: Tool

Proper Citation

RFMix (RRID:SCR_027030)

Resource Information

URL: https://github.com/slowkoni/rfmix

Proper Citation: RFMix (RRID:SCR_027030)

Description: Software tool for local ancestry and admixture inference. Discriminative Modeling Approach for Rapid and Robust Local-Ancestry Inference.

Resource Type: software application, software resource

Defining Citation: PMID:23910464

Keywords: Discriminative Modeling, local ancestry and admixture inference,

Funding: NHGRI 2R01HG003229;
NLM LM007033;
NSF

Availability: Restricted

Resource Name: RFMix

Resource ID: SCR_027030

Record Creation Time: 20250605T060221+0000

Record Last Update: 20260905T133537+0000

Ratings and Alerts

No rating or validation information has been found for RFMix.

No alerts have been found for RFMix.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Verbitsky M, et al. (2026) Urobiota analysis and genome-wide association study in pediatric recurrent urinary tract infections and vesicoureteral reflux. JCI insight, 11(2).

Liu Y, et al. (2025) Uncovering genetic diversity and admixture of British Africans with HLA alleles inferred from whole genome sequencing. European journal of human genetics : EJHG, 33(8), 1057.

Buonaiuto S, et al. (2025) The Biorepository and Integrative Genomics resource for inclusive genomics: insights from a diverse pediatric and admixed cohort. medRxiv : the preprint server for health sciences.

Im C, et al. (2025) Genome-wide association study of childhood B-cell acute lymphoblastic leukemia reveals novel African ancestry-specific susceptibility loci. Nature communications, 16(1), 8974.

Kim K, et al. (2025) GWAS identifies genetic loci for antibody response to SARS-CoV-2 vaccines in patients with systemic autoimmune diseases and healthy individuals. medRxiv : the preprint server for health sciences.

Del Valle-Per??z M, et al. (2025) Urofacial (Ochoa) syndrome with a founder pathogenic variant in the HPSE2 gene: a case report and mutation origin. Journal of applied genetics, 66(3), 637.

Tan T, et al. (2025) Extending Genome-Wide Association Studies to admixed cohorts with high degrees of relatedness. medRxiv : the preprint server for health sciences.

Wiener P, et al. (2025) Genomic Analysis of Hair Sheep From West/Central Africa Reveals Unique Genetic Diversity and Ancestral Links to Breed Formation in the Caribbean. Molecular ecology, 34(24), e17796.

Oliveira S, et al. (2023) Genome-wide variation in the Angolan Namib Desert reveals unique pre-Bantu ancestry. Science advances, 9(38), eadh3822.