

# Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

## ADMIXTOOLS

RRID:SCR\_018495

Type: Tool

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### Proper Citation

ADMIXTOOLS (RRID:SCR\_018495)

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### Resource Information

**URL:** <https://github.com/DReichLab/AdmixTools>

**Proper Citation:** ADMIXTOOLS (RRID:SCR\_018495)

**Description:** Software package that supports formal tests of whether admixture occurred, and makes it possible to infer admixture proportions and dates.

**Resource Type:** software resource, software toolkit

**Defining Citation:** [PMID:22960212](#)

**Keywords:** Formal test support, admixture, infer admixture proportion, infer admixture date, bio.tools

**Funding:** NIGMS GM100233;  
U.S. National Science Foundation HOMINID

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

**Resource Name:** ADMIXTOOLS

**Resource ID:** SCR\_018495

**Alternate IDs:** biotools:admixtools

**Alternate URLs:** [http://genetics.med.harvard.edu/reich/Reich\\_Lab/Software.html](http://genetics.med.harvard.edu/reich/Reich_Lab/Software.html),  
<https://bio.tools/admixtools>

**Record Creation Time:** 20220129T080340+0000

**Record Last Update:** 20260905T133304+0000

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### Ratings and Alerts

No rating or validation information has been found for ADMIXTOOLS.

No alerts have been found for ADMIXTOOLS.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 222 mentions in open access literature.

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

Marsh WA, et al. (2026) Dogs were widely distributed across western Eurasia during the Palaeolithic. *Nature*, 651(8107), 995.

Tomarovsky AA, et al. (2026) Genomics of Sable (*Martes zibellina*) ?? Pine Marten (*Martes martes*) Hybridization. *Genome biology and evolution*, 18(3).

Power RI, et al. (2026) Population genomics reveals an ancient origin of heartworms in canids. *Communications biology*, 9(1), 68.

Higasa K, et al. (2026) Whole-genome sequencing of 3135 individuals representing the genetic diversity of the Japanese population. *Journal of human genetics*, 71(4), 223.

Cuesta-Aguirre DR, et al. (2026) The genetic landscape of northeastern Iberian communities from the early to late Iron Age. *iScience*, 29(6), 116186.

Guo YQ, et al. (2026) Incomplete lineage sorting shaped mixed traits during a colobine primate radiation. *Proceedings of the National Academy of Sciences of the United States of America*, 123(5), e2524833123.

Yin Z, et al. (2026) Exploring the genomic population structure and history of Austroasiatic speakers in Mainland Southeast Asia. *Communications biology*, 9(1).

Erterek E, et al. (2026) Clinical Evaluation of Three KRS Families and Cellular Analysis of Distinct ATP13A2 Mutations Reveal Different Levels of Iron Accumulation. *Journal of neurochemistry*, 170(4), e70418.

Ketchum RN, et al. (2026) Genomic signatures of speciation and adaptation in the ctenophore *Mnemiopsis*. *BMC biology*, 24(1).

Luo X, et al. (2026) Genomic divergence, adaptation, and the genetic basis of quality traits in ancient walnut landraces and wild relatives. *Horticulture research*, 13(7), uhag082.

Sirak K, et al. (2026) First Lithic Age Caribbean genomes document pre-Ceramic genetic continuity and affinities to Central America and northern South America. *bioRxiv : the preprint server for biology*.

Jain R, et al. (2026) Layers in the sand: The genetic imprint of migration, culture, and Indus craft in the Thar Desert. *HGG advances*, 7(3), 100623.

Zhang G, et al. (2026) Ancient genomes provide insight into the Paleolithic-to-Neolithic transition in northern East Asia. *Current biology : CB*, 36(6), 1399.

Xu Y, et al. (2026) Reconstructing the west-east genetic division in Indonesia using ancient genomes. *iScience*, 29(6), 115974.

Roca-Rada X, et al. (2025) The genetic history of Portugal over the past 5,000 years. *Genome biology*, 26(1), 248.

Amjadi MA, et al. (2025) Ancient DNA indicates 3,000 years of genetic continuity in the Northern Iranian Plateau, from the Copper Age to the Sassanid Empire. *Scientific reports*, 15(1), 16530.

Chen G, et al. (2025) Population Genomic Analysis Provides Insights Into the Evolution and Conservation of Two Critically Endangered Musk Deer Species. *Evolutionary applications*, 18(8), e70134.

Chen Z, et al. (2025) Ancient DNA from Shimao city records kinship practices in Neolithic China. *Nature*, 648(8094), 659.

Scarsbrook L, et al. (2025) A 120-y time series of genomes reveals the consequences of closed breeding in German Shepherd Dogs. *Proceedings of the National Academy of Sciences of the United States of America*, 122(48), e2421755122.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.