

Resource Summary Report

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ADMIXTOOLS

RRID:SCR_018495

Type: Tool

Proper Citation

ADMIXTOOLS (RRID:SCR_018495)

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,
<https://bio.tools/admixtools>

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260821T194148+0000

Ratings and Alerts

No rating or validation information has been found for ADMIXTOOLS.

No alerts have been found for ADMIXTOOLS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 222 mentions in open access literature.

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

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.