

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

NGSadmix

RRID:SCR_003208

Type: Tool

Proper Citation

NGSadmix (RRID:SCR_003208)

Resource Information

URL: <http://www.popgen.dk/software/index.php/NgsAdmix>

Proper Citation: NGSadmix (RRID:SCR_003208)

Description: A tool for finding admixture proportions from next generation sequencing (NGS) data that is based on genotype likelihoods. It is a multithreaded c/c++ program.

Abbreviations: NGSadmix

Resource Type: software resource

Defining Citation: [PMID:24026093](#)

Keywords: next generation sequencing, admixture proportion, admixture, genotype, c, c++, admixture, association study, population structure, resequencing

Availability: Acknowledgement requested

Resource Name: NGSadmix

Resource ID: SCR_003208

Alternate IDs: OMICS_01553

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260815T182228+0000

Ratings and Alerts

No rating or validation information has been found for NGSadmix.

No alerts have been found for NGSadmix.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 144 mentions in open access literature.

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

Crego-Walters M, et al. (2026) Targeted Chromosomal Sequencing of Wild Bonobos Identifies a Genetically Distinct Subpopulation East of the Lomami River. *bioRxiv : the preprint server for biology*.

Westbury MV, et al. (2026) Tracing the Drivers of Range-Wide Bowhead Whale Genomic Structure and Diversity. *Molecular ecology*, 35(10), e70378.

Feinauer IS, et al. (2026) Whole genomes reveal subpopulations and isolation-by-distance patterns in the Norwegian lemming. *BMC biology*, 24(1).

Szmato?a T, et al. (2026) Genomic diversity and structure in arabian horses revealed by whole-genome sequencing: establishment of an allele frequency database of common genetic variation. *BMC genomics*, 27(1).

Wang X, et al. (2026) Population structure and domestication history of the Javan banteng. *Current biology : CB*, 36(2), 458.

Witonsky D, et al. (2026) Genomic profiling of active vitamin D colonic responses in African- and European-Americans identifies an ancestry-related regulatory variant of POLB. *PLoS genetics*, 22(1), e1011983.

Tensen L, et al. (2026) Reduced Genetic Load and Inbreeding in Reintroduced African Wild Dogs Reflect the Benefits of Admixture. *Molecular ecology*, 35(12), e70424.

Brand JN, et al. (2026) Stepwise emergence of recombination suppression precedes fissiparous asexuality in the planarian *Schmidtea mediterranea*. *Nature communications*, 17(1).

Tensen L, et al. (2026) Genomic divergence of leopards in the Cape Floristic Region of South Africa: potential drivers for local adaptation. *Heredity*, 135(2), 86.

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

Reeves IM, et al. (2025) Admixture Increases Genetic Diversity and Adaptive Potential in Australasian Killer Whales. *Molecular ecology*, 34(23), e17689.

Blom MPK, et al. (2025) Museomics unravels cryptic diversity in an endemic group of New Guinean songbirds. *Biology letters*, 21(7), 20240611.

Csapó HK, et al. (2025) Genome sequence analysis provides evidence that a boreal crustacean colonised Svalbard well before the ongoing Atlantification of the Arctic. *Heredity*, 134(9), 558.

Battlay P, et al. (2025) Haploblocks contribute to parallel climate adaptation following global invasion of a cosmopolitan plant. *Nature ecology & evolution*, 9(8), 1441.

McCarthy ML, et al. (2025) Range-Wide Genomic Analysis Reveals Regional and Meta-Population Dynamics of Decline and Recovery in the Grey Seal. *Molecular ecology*, 34(14), e17824.

Thörn F, et al. (2025) Frequent Hybridisation Between Parapatric Lekking Bird-of-Paradise Species. *Molecular ecology*, 34(11), e17780.

De Cahsan B, et al. (2025) Road to Extinction? Past and Present Population Structure and Genomic Diversity in the Koala. *Molecular biology and evolution*, 42(4).

Sotka EE, et al. (2025) The genetic legacy of a global marine invader. *Proceedings of the National Academy of Sciences of the United States of America*, 122(15), e2418730122.

Dallaire X, et al. (2025) Leveraging Whole Genomes, Mitochondrial DNA and Haploblocks to Decipher Complex Demographic Histories: An Example From a Broadly Admixed Arctic Fish. *Molecular ecology*, 34(10), e17772.

Kurta K, et al. (2025) Whole Genome Sequencing Reveals How Plasticity and Genetic Differentiation Underlie Sympatric Morphs of Arctic Charr. *Molecular ecology*, 34(19), e70085.