

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 19, 2026

## frappe

RRID:SCR\_001264

Type: Tool

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### Proper Citation

frappe (RRID:SCR\_001264)

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### Resource Information

**URL:** <http://med.stanford.edu/tanglab/software/frappe.html>

**Proper Citation:** frappe (RRID:SCR\_001264)

**Description:** Software using a frequentist approach for estimating individual ancestry proportion.

**Abbreviations:** frappe

**Resource Type:** software resource

**Defining Citation:** [PMID:15712363](#)

**Keywords:** ancestry, admixture, genome, allele

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

**Resource Name:** frappe

**Resource ID:** SCR\_001264

**Alternate IDs:** OMICS\_02076

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20260912T195522+0000

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### Ratings and Alerts

No rating or validation information has been found for frappe.

No alerts have been found for frappe.

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### Data and Source Information

## Usage and Citation Metrics

We found 56 mentions in open access literature.

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

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.

Reif-Leonhard C, et al. (2025) Effectiveness of a communal, multilevel, interdisciplinary suicide prevention program. *European psychiatry : the journal of the Association of European Psychiatrists*, 68(1), e119.

Zhang BL, et al. (2025) Forward and reverse genomic screens enhance the understanding of phenotypic variation in a large Chinese rhesus macaque cohort. *Nature communications*, 16(1), 8703.

Wang P, et al. (2024) De novo assembling a high-quality genome sequence of Amur grape (*Vitis amurensis* Rupr.) gives insight into *Vitis* divergence and sex determination. *Horticulture research*, 11(6), uhae117.

Zhu L, et al. (2024) Genome-wide association study and genomic selection of flax powdery mildew in Xinjiang Province. *Frontiers in plant science*, 15, 1403276.

Shi S, et al. (2023) Whole genome analyses reveal novel genes associated with chicken adaptation to tropical and frigid environments. *Journal of advanced research*, 47, 13.

Chang G, et al. (2023) The First Crested Duck Genome Reveals Clues to Genetic Compensation and Crest Cushion Formation. *Genomics, proteomics & bioinformatics*, 21(3), 483.

Shi J, et al. (2023) Structural variants involved in high-altitude adaptation detected using single-molecule long-read sequencing. *Nature communications*, 14(1), 8282.

Yao X, et al. (2022) A chromosome-scale genome assembly for the holly (*Ilex polyneura*) provides insights into genomic adaptations to elevation in Southwest China. *Horticulture research*, 9.

Liu Y, et al. (2022) GAIN: A Gated Adaptive Feature Interaction Network for Click-Through Rate Prediction. *Sensors (Basel, Switzerland)*, 22(19).

Wang X, et al. (2022) Selective and comparative genome architecture of Asian cultivated rice (*Oryza sativa* L.) attributed to domestication and modern breeding. *Journal of advanced research*, 42, 1.

Zhang Y, et al. (2021) Genome-wide comparative analyses reveal selection signatures underlying adaptation and production in Tibetan and Poll Dorset sheep. *Scientific reports*, 11(1), 2466.

Wang Y, et al. (2021) Construction of a SNP Fingerprinting Database and Population Genetic Analysis of Cigar Tobacco Germplasm Resources in China. *Frontiers in plant science*, 12, 618133.

Canton G, et al. (2021) Atherosclerotic Burden and Remodeling Patterns of the Popliteal Artery as Detected in the Magnetic Resonance Imaging Osteoarthritis Initiative Data Set. *Journal of the American Heart Association*, 10(11), e018408.

Liu J, et al. (2020) Genetic signatures of high-altitude adaptation and geographic distribution in Tibetan sheep. *Scientific reports*, 10(1), 18332.

Qu Y, et al. (2020) Rapid phenotypic evolution with shallow genomic differentiation during early stages of high elevation adaptation in Eurasian Tree Sparrows. *National science review*, 7(1), 113.

Li Y, et al. (2020) Comparative population genomics reveals genetic divergence and selection in lotus, *Nelumbo nucifera*. *BMC genomics*, 21(1), 146.

Hu JY, et al. (2020) Genomic consequences of population decline in critically endangered pangolins and their demographic histories. *National science review*, 7(4), 798.

Bian C, et al. (2020) Genome and Transcriptome Sequencing of casper and roy Zebrafish Mutants Provides Novel Genetic Clues for Iridophore Loss. *International journal of molecular sciences*, 21(7).

Mei L, et al. (2020) Population genomics and evolution of a fungal pathogen after releasing exotic strains to control insect pests for 20 years. *The ISME journal*, 14(6), 1422.