Resource Summary Report

Generated by NIF on Apr 27, 2025

frappe

RRID:SCR_001264
Type: Tool

Proper Citation

frappe (RRID:SCR_001264)

Resource Information

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

Proper Citation: frappe (RRID:SCR_001264)

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

Abbreviations: frappe

Resource Type: software resource

Defining Citation: PMID:15712363

Keywords: ancestry, admixture, genome, allele

Funding:

Resource Name: frappe

Resource ID: SCR_001264

Alternate IDs: OMICS_02076

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014024+0000

Ratings and Alerts

No rating or validation information has been found for frappe.

No alerts have been found for frappe.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 53 mentions in open access literature.

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

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.

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.

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.

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.

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.

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.

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.

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

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.

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.

Wang P, et al. (2020) Fine-Scale Population Genetic Structure and Parapatric Cryptic Species of Kuruma Shrimp (Marsupenaeus japonicus), Along the Northwestern Pacific Coast of China. Frontiers in genetics, 11, 118.

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).

Li K, et al. (2020) Incipient sympatric speciation in wild barley caused by geological-edaphic divergence. Life science alliance, 3(12).

Guo F, et al. (2020) A Genome-Wide Association Study Identifies Quantitative Trait Loci Affecting Hematological Traits in Camelus bactrianus. Animals : an open access journal from MDPI, 10(1).