

# Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

## fineSTRUCTURE

RRID:SCR\_018170

Type: Tool

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### Proper Citation

fineSTRUCTURE (RRID:SCR\_018170)

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### Resource Information

**URL:** <http://paintmychromosomes.com/>

**Proper Citation:** fineSTRUCTURE (RRID:SCR\_018170)

**Description:** Software tool as algorithm for identifying population structure using dense sequencing data. Can perform model based Bayesian clustering on large datasets, including full resequencing data.

**Synonyms:** FineSTRUCTURE version 2

**Resource Type:** data analysis software, data processing software, software application, software resource

**Keywords:** Identifying population structure, dense sequencing data, Bayesian clustering, large dataset, data, analysis, bio.tools

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

**Resource Name:** fineSTRUCTURE

**Resource ID:** SCR\_018170

**Alternate IDs:** biotools:finestructure

**Alternate URLs:** <https://bio.tools/finestructure>

**Record Creation Time:** 20220129T080339+0000

**Record Last Update:** 20260912T195858+0000

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### Ratings and Alerts

No rating or validation information has been found for fineSTRUCTURE.

No alerts have been found for fineSTRUCTURE.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 23 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Liu S, et al. (2025) Origin and de novo domestication of sweet orange. *Nature genetics*, 57(3), 754.

Henschel A, et al. (2024) Human migration from the Levant and Arabia into Yemen since Last Glacial Maximum. *Scientific reports*, 14(1), 31704.

Howard-McCombe J, et al. (2023) Genetic swamping of the critically endangered Scottish wildcat was recent and accelerated by disease. *Current biology : CB*, 33(21), 4761.

Ladner JT, et al. (2022) The population genetics of the causative agent of snake fungal disease indicate recent introductions to the USA. *PLoS biology*, 20(6), e3001676.

Zhao Z, et al. (2022) Protocol to analyze population structure and migration history based on human genome variation data. *STAR protocols*, 4(1), 101928.

You Y, et al. (2022) Genomic differentiation within East Asian *Helicobacter pylori*. *Microbial genomics*, 8(2).

Zhang Z, et al. (2022) The Tibetan-Yi region is both a corridor and a barrier for human gene flow. *Cell reports*, 39(4), 110720.

Cumer T, et al. (2022) Landscape and Climatic Variations Shaped Secondary Contacts amid Barn Owls of the Western Palearctic. *Molecular biology and evolution*, 39(1).

Capodiferro MR, et al. (2021) Archaeogenomic distinctiveness of the Isthmo-Colombian area. *Cell*, 184(7), 1706.

van Hal SJ, et al. (2021) The global dissemination of hospital clones of *Enterococcus faecium*. *Genome medicine*, 13(1), 52.

Muñoz-Ramirez ZY, et al. (2021) A 500-year tale of co-evolution, adaptation, and virulence: *Helicobacter pylori* in the Americas. *The ISME journal*, 15(1), 78.

Whiting JR, et al. (2021) Drainage-structuring of ancestral variation and a common functional pathway shape limited genomic convergence in natural high- and low-predation guppies. *PLoS genetics*, 17(5), e1009566.

Joseph SJ, et al. (2021) Comparative Genomic and Transcriptomic Analysis of *Naegleria fowleri* Clinical and Environmental Isolates. *mSphere*, 6(4), e0063721.

Flores-Bello A, et al. (2021) Genetic origins, singularity, and heterogeneity of Basques. *Current biology : CB*, 31(10), 2167.

Almarri MA, et al. (2021) The genomic history of the Middle East. *Cell*, 184(18), 4612.

Paim TDP, et al. (2020) Genomic Breed Composition of Selection Signatures in Brangus Beef Cattle. *Frontiers in genetics*, 11, 710.

Paim TDP, et al. (2020) Dynamics of genomic architecture during composite breed development in cattle. *Animal genetics*, 51(2), 224.

Byrne RP, et al. (2020) Dutch population structure across space, time and GWAS design. *Nature communications*, 11(1), 4556.

Easton A, et al. (2020) Molecular evidence of hybridization between pig and human *Ascaris* indicates an interbred species complex infecting humans. *eLife*, 9.

Cui Y, et al. (2020) The landscape of coadaptation in *Vibrio parahaemolyticus*. *eLife*, 9.