

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

STRUCTURE

RRID:SCR_017637

Type: Tool

Proper Citation

STRUCTURE (RRID:SCR_017637)

Resource Information

URL: <https://web.stanford.edu/group/pritchardlab/structure.html>

Proper Citation: STRUCTURE (RRID:SCR_017637)

Description: Software package for using multi locus genotype data to investigate population structure. Used for inferring presence of distinct populations, assigning individuals to populations, studying hybrid zones, identifying migrants and admixed individuals, and estimating population allele frequencies in situations where many individuals are migrants or admixed. Can be applied to most of commonly used genetic markers, including SNPS, microsatellites, RFLPs and Amplified Fragment Length Polymorphisms.

Synonyms: structure, Structure

Resource Type: software toolkit, software resource

Defining Citation: [PMID:21564903](#), [PMID:18784791](#), [PMID:12930761](#), [PMID:10835412](#)

Keywords: Multi locus genotype data, investigate population structure, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: STRUCTURE

Resource ID: SCR_017637

Alternate IDs: SCR_021634, nlx_154662, biotools:structure, SCR_002151

Alternate URLs: <https://bio.tools/structure>, <http://pritch.bsd.uchicago.edu/structure.html>,

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260803T040751+0000

Ratings and Alerts

No rating or validation information has been found for STRUCTURE.

No alerts have been found for STRUCTURE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4017 mentions in open access literature.

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

Jimenez A, et al. (2026) Defining Genetic Ancestry: Implications for Nurses. Biological research for nursing, 28(1), 149.

Hagen IJ, et al. (2026) Genetic Markers for Tracing Introgression of Farmed Atlantic Salmon (*Salmo salar*) in Wild Conspecifics. Molecular ecology resources, 26(1), e70065.

Schmidt SA, et al. (2025) Diversity on a small scale: phylogeography of the locally endemic dwarf succulent genus *Oophytum* (Aizoaceae) in the Knersvlakte of South Africa. Annals of botany, 135(4), 735.

Lawrence AJ, et al. (2025) Maintenance of Genetic Diversity Despite Population Fluctuations in the Lesser Prairie-Chicken (*Tympanuchus pallidicinctus*). Ecology and evolution, 15(1), e70879.

Shim D, et al. (2025) Eu-Substituents-Induced Modifications in the Thermoelectric Properties of the Zintl Phase $\text{Ba}_{1-x}\text{Eu}_x\text{Zn}_2\text{Sb}_2$ System. Molecules (Basel, Switzerland), 30(2).

Kumar M, et al. (2025) Identification of resistance sources and genomic regions regulating *Septoria tritici* blotch resistance in South Asian bread wheat germplasm. The plant genome, 18(1), e20531.

Patova A, et al. (2025) Population genomics and connectivity of *Vazella pourtalesii* sponge grounds of the northwest Atlantic with conservation implications of deep sea vulnerable marine ecosystems. Scientific reports, 15(1), 1540.

Dufresnes C, et al. (2025) Speciation and historical invasions of the Asian black-spined toad (*Duttaphrynus melanostictus*). Nature communications, 16(1), 298.

Stafiniak M, et al. (2025) Integrative morphological, phytochemical, and molecular identification of three invasive and medicinal *Reynoutria* species. Scientific reports, 15(1), 6001.

Kim JK, et al. (2025) Genome-wide SNP discovery and phylogeography of sandlances (*Ammodytes japonicus* and *Ammodytes heian*) in the Northwest pacific by MIG-Seq with evolutionary implications. Scientific reports, 15(1), 5998.

Rumberger C, et al. (2025) Selection Over Small and Large Spatial Scales in the Face of High Gene Flow. *Molecular ecology*, 34(6), e17700.

Morinha F, et al. (2025) ???Molecular and morphological data support the synonymy of *Muricanthusradix* Gmelin, 1791 and *Muricanthusambiguus* Reeve, 1845 (Gastropoda, Muricidae). *ZooKeys*, 1239, 281.

Ronchetti F, et al. (2025) The Significance of Genetic Relatedness and Nest Sharing on the Worker-Worker Similarity of Gut Bacterial Microbiome and Cuticular Hydrocarbon Profile in a Sweat Bee. *Ecology and evolution*, 15(6), e71519.

Fish JJ, et al. (2025) Evidence of Fine-Scale Genetic Structure in Tiger Sharks (*Galeocerdo cuvier*) Highlights the Importance of Stratified Sampling Regimes. *Evolutionary applications*, 18(6), e70117.

Engelbrecht E, et al. (2025) Germline polymorphisms in the immunoglobulin kappa and lambda loci explain variation in the expressed light chain antibody repertoire. *bioRxiv : the preprint server for biology*.

Ernst M, et al. (2025) Comparative Phylogeography of West African Rainforest Frogs Reveals Regional Variation in Refugia Dynamics. *Molecular ecology*, 34(17), e70043.

Colli-Silva M, et al. (2025) Wild or Introduced? Investigating the Genetic Landscape of Cacao Populations in South America. *Ecology and evolution*, 15(7), e71746.

Shen-Tu XL, et al. (2025) Size-Dependent Genetic Erosion due to Human Logging and Conservation Recommendation for an Endangered Yew (*Taxus fuana*) in Tibet, China. *Ecology and evolution*, 15(7), e71844.

Wang Q, et al. (2025) Population Patterns and Dynamics of *Ilisha elongata* (Clupeiformes: Pristigasteridae) Revealed by Target Enrichment Data. *Evolutionary applications*, 18(8), e70142.

Roper CD, et al. (2025) Coral thermotolerance retained following year-long exposure to a novel environment. *Science advances*, 11(32), eadu3858.