

Resource Summary Report

Generated by T1D on Sep 4, 2026

Structure

RRID:SCR_021634

Type: Tool

Proper Citation

Structure (RRID:SCR_021634)

Resource Information

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

Proper Citation: Structure (RRID:SCR_021634)

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.

Resource Type: software toolkit, software resource

Defining Citation: [PMID:10835412](#)

Keywords: Multi locus genotype data, investigate population structure

Availability: Free, Available for download, Freely available

Resource Name: Structure

Resource ID: SCR_021634

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260903T235716+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 60 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Rengefors K, et al. (2024) Population genomic analyses reveal that salinity and geographic isolation drive diversification in a free-living protist. *Scientific reports*, 14(1), 4986.

Soares LS, et al. (2024) The phylogeographic journey of a plant species from lowland to highlands during the Pleistocene. *Scientific reports*, 14(1), 3825.

Butterworth NJ, et al. (2023) The blowfly *Chrysomya latifrons* inhabits fragmented rainforests, but shows no population structure. *Oecologia*, 201(3), 703.

Ally HM, et al. (2023) Genetic diversity, distribution, and structure of *Bemisia tabaci* whitefly species in potential invasion and hybridization regions of East Africa. *PloS one*, 18(5), e0285967.

Hackney CM, et al. (2023) A previously unrecognized superfamily of macro-conotoxins includes an inhibitor of the sensory neuron calcium channel Cav2.3. *PLoS biology*, 21(8), e3002217.

Detcharoen M, et al. (2023) Complete Genome of Rose Myrtle, *Rhodomyrtus tomentosa*, and Its Population Genetics in Thai Peninsula. *Plants (Basel, Switzerland)*, 12(8).

Fathifar Z, et al. (2023) New approaches in developing medicinal herbs databases. *Database : the journal of biological databases and curation*, 2023.

Degu HD, et al. (2023) Genetic diversity and population structure of barley landraces from Southern Ethiopia's Gumer district: Utilization for breeding and conservation. *PloS one*, 18(1), e0279737.

Okunlola G, et al. (2023) Genome-wide association studies of *Striga* resistance in extra-early maturing quality protein maize inbred lines. *G3 (Bethesda, Md.)*, 13(2).

Gowda RSR, et al. (2023) Genome wide association studies and candidate gene mining for understanding the genetic basis of straw silica content in a set of *Oryza nivara* (Sharma et Shastry) accessions. *Frontiers in plant science*, 14, 1174266.

Alekseeva M, et al. (2023) A Set of Highly Polymorphic Microsatellite Markers for Genetic Diversity Studies in the Genus *Origanum*. *Plants (Basel, Switzerland)*, 12(4).

Assis J, et al. (2023) Past climate-driven range shifts structuring intraspecific biodiversity levels of the giant kelp (*Macrocystis pyrifera*) at global scales. *Scientific reports*, 13(1), 12046.

Quandt E, et al. (2023) CDK6 is activated by the atypical cyclin I to promote E2F-mediated gene expression and cancer cell proliferation. *Molecular oncology*.

Perfilyeva A, et al. (2023) Kazakh national dog breed Tazy: What do we know? *PloS one*, 18(3), e0282041.

Silva MC, et al. (2023) Contrasting patterns of population structure of Bulwer's petrel (*Bulweria bulwerii*) between oceans revealed by statistical phylogeography. *Scientific reports*, 13(1), 1939.

Sapkota D, et al. (2023) Genotyping of Jujube (*Ziziphus* spp.) Germplasm in New Mexico and Southwestern Texas. *Plants* (Basel, Switzerland), 12(13).

Perera MF, et al. (2023) Genetic diversity and population structure of *Saccharum* hybrids. *PloS one*, 18(8), e0289504.

Gedil M, et al. (2023) Genetic structure analysis and identifying key founder inbred lines in diverse elite sub-tropical maize inbred lines. *Scientific reports*, 13(1), 11695.

Soleimani B, et al. (2023) Identification of Markers Associated with Wheat Dwarf Virus (WDV) Tolerance/Resistance in Barley (*Hordeum vulgare* ssp. *vulgare*) Using Genome-Wide Association Studies. *Viruses*, 15(7).

Brown MR, et al. (2023) Is there hybridization between diploid and tetraploid *Euphrasia* in a secondary contact zone? *American journal of botany*, 110(1), e16100.