

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

Structure Harvester

RRID:SCR_017636

Type: Tool

Proper Citation

Structure Harvester (RRID:SCR_017636)

Resource Information

URL: <http://taylor0.biology.ucla.edu/structureHarvester/>

Proper Citation: Structure Harvester (RRID:SCR_017636)

Description: Web based program for collating results generated by program STRUCTURE. Provides assess and visualize likelihood values across multiple values of K and hundreds of iterations for easier detection of number of genetic groups that best fit data. Reformats data for use in downstream programs, such as CLUMPP. It is complement for using software Structure in genetics population. Website and program for visualizing STRUCTURE output and implementing Evanno method., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16, 2025.

Synonyms: StructureHarvester

Resource Type: analysis service resource, data access protocol, production service resource, service resource, software resource, web service

Defining Citation: [DOI:10.1007/s12686-011-9548-7](https://doi.org/10.1007/s12686-011-9548-7)

Keywords: Visualizing, STRUCTURE, Evanno, method, collating, result, detection, genetic, group, fit, data, reformat

Funding: NCI R21 CA135937;
NCI U24 CA143858

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Structure Harvester

Resource ID: SCR_017636

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260919T195343+0000

Ratings and Alerts

No rating or validation information has been found for Structure Harvester.

No alerts have been found for Structure Harvester.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 337 mentions in open access literature.

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

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Zhou P, et al. (2026) Assessment of Genetic Diversity and Differentiation in *Triadica cochinchinensis* Populations Using SSR Markers. *Plants* (Basel, Switzerland), 15(8).

Liu C, et al. (2026) Characterization of the genetic architecture of adult plant resistance to sharp eyespot in Chinese wheat germplasm. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 139(1), 38.

Patel MK, et al. (2025) Genome-wide association study uncovers key genomic regions governing agro-morphological and quality traits in Indian mustard [*Brassica juncea* (L.) Czern. and Coss.]. *PloS one*, 20(4), e0322120.

Verma VK, et al. (2025) Genetic diversity in male and female landraces of teasel gourd in north-eastern India and strategies for crop improvement through induced monoclity. *BMC plant biology*, 25(1), 383.

Teklewold TH, et al. (2025) Genetic diversity and population structure of Ethiopian Sweet Sorghum [*Sorghum bicolor* (L.) Moench] germplasms using SSR markers. *PloS one*, 20(3), e0316549.

Belkina D, et al. (2025) In-depth population genetic study of *Vitis vinifera* ssp. *sylvestris* from the Black Sea region and its virome. *Frontiers in plant science*, 16, 1536862.

Kniesz K, et al. (2025) High genomic connectivity within *Anatoma* at hydrothermal vents along the Central and Southeast Indian Ridge. *Scientific reports*, 15(1), 1971.

Ruppert LS, et al. (2025) Gene Flow Across Large Distances in the Cavity-Nesting Wasp *Deuteragenia subintermedia* in a Central European Forest. *Ecology and evolution*, 15(4), e71294.

Gyawali S, et al. (2025) Genome wide association study of Fusarium wilt resistance in *Spinacia turkestanica*. *Scientific reports*, 15(1), 15486.

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

Ma X, et al. (2025) ddRAD-seq data reveals the significant population structure and potential causes of population divergence in *Bougainvillea*. *Scientific reports*, 15(1), 34200.

Rakshith HS, et al. (2025) Genetic diversity of the zigzag ladybird beetle, *Cheilomenes sexmaculata* (F.) (Coleoptera: Coccinellidae) with its distribution in India and implications for biological control. *Scientific reports*, 15(1), 15629.

Toker TP, et al. (2025) Genomic insights into Mediterranean pepper diversity using ddRADSeq. *PloS one*, 20(3), e0318105.

Taboada S, et al. (2025) Connectivity and Adaptation Patterns of the Deep-Sea Ground-Forming Sponge *Geodia hentscheli* Across Its Entire Distribution. *Molecular biology and evolution*, 42(7).

Shi A, et al. (2025) Genome and GWAS analyses for soybean cyst nematode resistance in USDA world-wide common bean (*Phaseolus vulgaris*) germplasm. *Frontiers in plant science*, 16, 1520087.

Li Y, et al. (2025) Migration of wheat stripe rust from the primary overwintering region to neighboring regions in China. *Communications biology*, 8(1), 350.

Yang H, et al. (2025) Population Genetics of *Halictis discus hannai* in China Inferred Through EST-SSR Markers. *Genes*, 16(1).

Bernard V, et al. (2024) Unlocking the genetic diversity and population structure of the newly introduced two-row spring European Heritage Barley collection (ExHiBiT). *Frontiers in plant science*, 15, 1268847.

Zheng JX, et al. (2024) Species Composition of a Small Mammal Community and Prevalence of *Echinococcus* spp. in the Alpine Pastoral Area of the Eastern Tibetan Plateau. *Pathogens (Basel, Switzerland)*, 13(7).