

Resource Summary Report

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DnaSP

RRID:SCR_003067

Type: Tool

Proper Citation

DnaSP (RRID:SCR_003067)

Resource Information

URL: <http://www.ub.edu/dnasp/>

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Description: A software package for the analysis of nucleotide polymorphism from aligned DNA sequence data. DnaSP can estimate several measures of DNA sequence variation within and between populations (in noncoding, synonymous or nonsynonymous sites, or in various sorts of codon positions), as well as linkage disequilibrium, recombination, gene flow and gene conversion parameters. DnaSP can also carry out several tests of neutrality: Hudson, Kreitman and Aguad (1987), Tajima (1989), McDonald and Kreitman (1991), Fu and Li (1993), and Fu (1997) tests. Additionally, DnaSP can estimate the confidence intervals of some test-statistics by the coalescent. The results of the analyses are displayed on tabular and graphic form.

Abbreviations: DnaSP

Synonyms: DNA Sequence Polymorphism

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

Defining Citation: [PMID:19346325](#), [PMID:19378153](#), [PMID:14668244](#), [PMID:10089204](#), [PMID:9183537](#), [PMID:8808578](#)

Keywords: genetics, dna, population genetics, sequence, polymorphism, nucleotide polymorphism, dna sequence, population, noncoding, synonymous, nonsynonymous

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Spanish Direccion General de Investigacion Cientifica y Technica BFU2007-6292

Availability: Free, Available for download, Freely available

Resource Name: DnaSP

Resource ID: SCR_003067

Alternate IDs: OMICS_01820, nif-0000-30461

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260803T040333+0000

Ratings and Alerts

No rating or validation information has been found for DnaSP.

No alerts have been found for DnaSP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5935 mentions in open access literature.

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

Zhang RL, et al. (2026) Comparative Plastome Analysis of Artocarpus Species in China: Insight Into Adaptive Evolution and Mutational Hotspot Regions. Ecology and evolution, 16(1), e72881.

Szécsényi-Nagy A, et al. (2025) Ancient DNA reveals diverse community organizations in the 5th millennium BCE Carpathian Basin. Nature communications, 16(1), 5318.

Lu K, et al. (2025) Characterization of Spectrin Family Genes and Their Evolutionary Roles in Domestication and Breeding of the Silkworm Bombyx mori. Insects, 16(6).

Rabelo-Araujo JVDS, et al. (2025) Phylogeny, structural patterns, and polymorphisms in Dyckia spp. from the Espinhaço mountain range based on complete chloroplast genome. Frontiers in plant science, 16, 1549351.

Sereno-Uribe AL, et al. (2025) A phylogeographic study of two acanthocephalan species from aquatic birds distributed in the Nearctic and neotropical region of Mexico and the USA. Parasitology, 152(10), 1027.

Keumeni CR, et al. (2025) Association of knockdown resistance mutations with pyrethroid resistance in Aedes aegypti, a major arbovirus vector in Cameroon. Parasites & vectors, 18(1), 296.

- Arias T, et al. (2025) Plastome phylogenomics of the diverse neotropical orchid genus *Lepanthes* with emphasis on subgenus *Marsiphanthes* (Pleurothallidinae: Orchidaceae). *BMC ecology and evolution*, 25(1), 79.
- Ma R, et al. (2025) Environmental Variation Contributes to Head Phenotypes in Workers of *Camponotus japonicus* (Hymenoptera: Formicidae). *Ecology and evolution*, 15(8), e71940.
- Zhong L, et al. (2025) Phylogenetic investigation and mitochondrial genome description of ten species in nine genera of Cicadellinae from China (Hemiptera: Cicadellidae). *PloS one*, 20(8), e0329906.
- Hayakawa T, et al. (2025) Genome-scale evolution in local populations of wild chimpanzees. *Scientific reports*, 15(1), 548.
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- Zhang R, et al. (2025) Comparative organelle genomics in Daphniophyllaceae reveal phylogenetic position and organelle structure evolution. *BMC genomics*, 26(1), 40.
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- Das PJ, et al. (2025) Complete mitochondrial genome sequence analysis revealed double matrilineal components in Indian Ghoongroo pigs. *Scientific reports*, 15(1), 2219.
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- Krause-Kyora B, et al. (2025) Neolithic introgression of IL23R-related protection against chronic inflammatory bowel diseases in modern Europeans. *EBioMedicine*, 113, 105591.
- Kidd SE, et al. (2025) *Sporothrix davidellisii* : A new pathogenic species belonging to the *Sporothrix pallida* complex. *Medical mycology*, 63(4).
- Ouyang HB, et al. (2025) Mutations in the signal peptide of effector gene Pi04314 contribute to the adaptive evolution of the *Phytophthora infestans*. *BMC ecology and evolution*, 25(1), 21.
- Matoso DA, et al. (2025) Is there hidden genetic variability in the species of *Steindachneridion* Garavello, 2005 (Siluriformes: Pimelodidae)? *PeerJ*, 13, e18193.
- Wu P, et al. (2025) OGU: A Toolbox for Better Utilising Organelle Genomic Data. *Molecular ecology resources*, 25(3), e14044.