

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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, data processing software, software application, software resource

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

Funding: Spanish Direccion General de Investigacion Cientifica y Technica PB91-0245; Spanish Direccion General de Investigacion Cientifica y Technica PB94-0923; Spanish Direccion General de Investigacion Cientifica y Technica PB97-0918; Spanish Direccion General de Investigacion Cientifica y Technica TXT98-1802; Spanish Direccion General de Investigacion Cientifica y Technica BMC2001-2906; Spanish Direccion General de Investigacion Cientifica y Technica BFU2004-02253;

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: 20260905T132457+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 6215 mentions in open access literature.

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

Sánchez-Casiano NE, et al. (2026) Molecular epidemiology and population structure of *Providencia stuartii* obtained from humans and other sources. *Microbiology spectrum*, 14(2), e0203225.

Hoelzel AR, et al. (2026) Balancing selection maintains intraspecific diversity in a deep-sea fish. *Heredity*, 135(1), 13.

Riedelbauch S, et al. (2026) Recurrent innovation of protein-protein interactions in the *Drosophila* piRNA pathway. *The EMBO journal*, 45(6), 1909.

Caviedes-Triana K, et al. (2026) Structure and Diversity of the Microbiome in Amazonian Sand Flies: Insights into Vector-Microbe Interactions. *Microbial ecology*, 89(1), 37.

Zhou X, et al. (2026) Comparative genomic and phylogenetic analyses of the mitogenome of *Graptopetalum Paraguayense* (N. E. Br.) Walth. 1938. *Scientific reports*, 16(1), 4174.

Zhang K, et al. (2026) De novo assembly of the first mitochondrial genome in *Benincasa* reveals structural dynamics and evolutionary insights in Cucurbitaceae. *BMC plant biology*, 26(1).

- Liu W, et al. (2026) Photosynthesis-related genetic and transcriptomic variations contribute to adaptive trait diversity in global *Arabidopsis thaliana* populations. *BMC plant biology*, 26(1).
- Mereu P, et al. (2026) Evolutionary History of the Adult γ -Globin Gene in Wild Sheep: First Sequences From the Argali (*Ovis ammon*) and the Urial (*Ovis vignei*). *Ecology and evolution*, 16(2), e73031.
- Rerkdee S, et al. (2026) Landscape Features Shape Maternal Genetic Structure of Asian Elephants in Thailand: Insights from mtDNA. *Biology*, 15(4).
- Benito AA, et al. (2026) First Detection and Genetic Characterization of Influenza D Virus in Cattle in Spain. *Veterinary sciences*, 13(2).
- Villegas L, et al. (2026) Geographic distribution of nematodes in the Atacama is associated with elevation, climate gradients and parthenogenesis. *Nature communications*, 17(1), 424.
- Feng L, et al. (2026) Comprehensive analysis of the complete chloroplast genome of white pomegranate and phylogenetic relationships within Myrtales. *BMC genomics*, 27(1), 220.
- Salinas NA, et al. (2026) Landscape Genomics and Evolutionary History of *Megamelus scutellaris*, a Biocontrol Agent of the Invasive Water Hyacinth (*Pontederia crassipes*). *Evolutionary applications*, 19(2), e70208.
- Chen JJ, et al. (2026) *Neobythites nanhaiensis* sp. nov. (Ophidiidae, Ophidiiformes) from the South China Sea, with morphology, mitogenome, and its phylogenetic position. *ZooKeys*, 1269, 107.
- Chen EY, et al. (2026) Mitogenomic organization and characteristics of deep-sea pelagic ostracods from both polar regions. *BMC genomics*, 27(1).
- Chinnaiah S, et al. (2026) Resistance breaking: integrated genomic and phenotypic insights into Orthospovirus tomatomaculae strains overcoming Sw-5b and Tsw resistance. *BMC genomics*, 27(1).
- Ma L, et al. (2026) Retention of AnAFP Sequence Variants in *Ammopiptanthus nanus* Ex Situ Collections with Contrasting Management Histories. *Plants (Basel, Switzerland)*, 15(7).
- Lin JR, et al. (2026) Population genetic diversity in the annual breeding area of the *Spodoptera frugiperda* in China. *Scientific reports*, 16(1).
- Ba?usta N, et al. (2026) Genetic diversity and phylogeography of *Chimaera monstrosa* (Linnaeus, 1758) in the Mediterranean Sea: insights from COI mitochondrial DNA analysis. *Scientific reports*, 16(1).
- Zhao L, et al. (2026) Development of a multilocus sequence typing tool for *Balantioides coli* and its genetic diversity in pigs. *Journal of clinical microbiology*, 64(5), e0000426.