

Resource Summary Report

Generated by T1D on Aug 2, 2026

ARLEQUIN

RRID:SCR_009051

Type: Tool

Proper Citation

ARLEQUIN (RRID:SCR_009051)

Resource Information

URL: <http://cmpg.unibe.ch/software/arlequin3/>

Proper Citation: ARLEQUIN (RRID:SCR_009051)

Description: An exploratory population genetics software environment able to handle large samples of molecular data (RFLPs, DNA sequences, microsatellites), while retaining the capacity of analyzing conventional genetic data (standard multi-locus data or mere allele frequency data). (entry from Genetic Analysis Software)

Abbreviations: ARLEQUIN

Synonyms: this software is about the study of genetic polymorphism.), a character of the Italian Commedia dell'Arte. He has many aspects, but can switch among them very easily according to needs and necessities. Similarly, (French translation of Arlecchino

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ms-windows, (95/98/nt/2000/xp)

Resource Name: ARLEQUIN

Resource ID: SCR_009051

Alternate IDs: nlx_154029

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260801T191052+0000

Ratings and Alerts

No rating or validation information has been found for ARLEQUIN.

No alerts have been found for ARLEQUIN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5536 mentions in open access literature.

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

Ten S, et al. (2025) Phylogeography of Pennella (Copepoda: Siphonostomatoida: Pennellidae) indicates interoceanic dispersal mediated by cetacean and fish hosts. Parasitology, 152(2), 195.

Xia X, et al. (2025) Orogeny and High Pollen Flow as Driving Forces for High Genetic Diversity of Endangered Acer griseum (Franch.) Pax Endemic to China. International journal of molecular sciences, 26(2).

Dong J, et al. (2025) Natural variation in CTF1 conferring cold tolerance at the flowering stage in rice. Plant biotechnology journal, 23(5), 1491.

Hecker AS, et al. (2025) Population genetic analysis of the liver fluke Fasciola hepatica in German dairy cattle reveals high genetic diversity and associations with fluke size. Parasites & vectors, 18(1), 51.

Long J, et al. (2025) Population genetic diversity of Schistosoma japonicum arises from the host switching in the life cycle. PLoS neglected tropical diseases, 19(3), e0012931.

Ebbs ET, et al. (2025) Legacy parasite collections reveal species-specific population genetic patterns among three species of zoonotic schistosomes. Scientific reports, 15(1), 9410.

Wambulwa MC, et al. (2025) Incorporating Genetic Diversity to Optimize the Plant Conservation Network in the Third Pole. Global change biology, 31(3), e70122.

Anyango VO, et al. (2025) Genetic diversity of Aedes aegypti populations from Kisumu and Busia counties, western Kenya, and their vector competence for chikungunya virus. PLoS one, 20(3), e0289191.

Hirai J, et al. (2025) Population panmixia of the pelagic shrimp Lucensosergia lucens between Japanese and Taiwanese waters in the western North Pacific. Scientific reports, 15(1), 7040.

Ralf A, et al. (2025) UYSD: a novel data repository accessible via public website for worldwide population frequencies of Y-SNP haplogroups. European journal of human genetics : EJHG, 33(7), 904.

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.

McKeown NJ, et al. (2025) Low genetic variation and strong genetic structure across a range of geographical scales in European smelt (*Osmerus eperlanus* L.). *Journal of fish biology*, 107(3), 918.

Rucińska A, et al. (2025) Halfway Through Ex Situ Population Genetic Lifespan: The Case of *Cochlearia polonica*. *Biology*, 14(6).

de Souza ATB, et al. (2025) Comparison of IL-10 gene promoter polymorphisms and haplotypes between high-grade squamous intraepithelial lesions or cervical cancer and negative cervical cytology. *Scientific reports*, 15(1), 28330.

Zhang Y, et al. (2025) Genetic diversity analysis of IVM resistant *Haemonchus contortus* in sheep in inner Mongolia of China. *Scientific reports*, 15(1), 29344.

Naczek AM, et al. (2025) Climate change-driven northward expansion of the mediterranean orchid *Ophrys apifera* from genetic and ecological perspectives. *Scientific reports*, 15(1), 29634.

McElwee-Adame A, et al. (2025) Evolutionary History and Rhizosphere Microbial Community Composition in Domesticated Hops (*Humulus lupulus* L.). *Molecular ecology*, 34(24), e17769.

Chen T, et al. (2025) Deciphering the evolutionary imprints of *Camellia oleifera* Abel.: delineating its distinct phylogeographic structure and demographic history through microsatellite and plastid fragment. *BMC plant biology*, 25(1), 526.

Zhunossova A, et al. (2025) Genetic genealogy of Y-chromosome in the Zhetiru tribe of the Kazakh population from Kazakhstan. *Frontiers in genetics*, 16, 1516130.

Kutanan W, et al. (2025) Maternal genetic origin of Chao Lay coastal maritime populations from Thailand. *BMC biology*, 23(1), 146.