

Resource Summary Report

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ARLEQUIN

RRID:SCR_009051

Type: Tool

Proper Citation

ARLEQUIN (RRID:SCR_009051)

Resource Information

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

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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 application, software resource

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: 20260805T044218+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 [RRID](#) .

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

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

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.

Du Z, et al. (2025) Global Invasion History and Genomic Signatures of Adaptation of the Highly Invasive Sycamore Lace Bug. *Genomics, proteomics & bioinformatics*, 22(6).

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

Tian X, et al. (2025) Genetic analysis of the Siberian flying squirrel population in the northern Changbai Mountains, Northeast China: Insights into population status and conservation. *Open life sciences*, 20(1), 20251128.

Saucedo-Montalvo MC, et al. (2025) First Report of the L925I kdr Mutation Associated with Pyrethroid Resistance in Genetically Distinct *Triatoma dimidiata*, Vector of Chagas Disease in Mexico. *Tropical medicine and infectious disease*, 10(7).

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.

Jeon JH, et al. (2025) Chloroplast genome and haplotype relationships unravel the genetic introgression and complex evolutionary history of East Asian *Rosa* section *Synstylae* roses (Rosaceae). *Botanical studies*, 66(1), 17.

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.

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.

Chilton NB, et al. (2025) Genetic diversity and phylogeographic relationships of *Dermacentor variabilis* (Acari: Ixodidae) within an established population in southern Manitoba (Canada), and the prevalence of *Rickettsia montanensis* and Francisella-like endosymbionts. *Journal of medical entomology*, 62(4), 840.

Banjoko AW, et al. (2025) High resolution class I HLA-A, -B, and -C diversity in Eastern and Southern African populations. *Scientific reports*, 15(1), 23667.

Kunishima T, et al. (2025) Genetic population structure of Japanese freshwater crab, *Geothelphusa dehaani* species complex using genome wide SNPs. *Scientific reports*, 15(1), 23781.

Henriques D, et al. (2025) Human-mediated introgression and *Varroa destructor* shaped the genetic structure of honey bee populations in the Azores. *Scientific reports*, 15(1), 25217.

Chen WG, et al. (2025) A new intermediate host of *Echinococcus shiquicus* in Qinghai-Tibet Plateau, China. *Parasitology research*, 124(6), 66.

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