

# 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:** 20260912T200239+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 5656 mentions in open access literature.

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

Fan PZ, et al. (2026) Genetic origins and climate-induced erosion in economically important Asian walnuts. *Conservation biology : the journal of the Society for Conservation Biology*, 40(1), e70125.

Schulz EJ, et al. (2026) Genetic diversity of US Rambouillet in the National Sheep Improvement Program compared to other sheep breeds. *The Journal of heredity*, 117(2), 211.

Lan X, et al. (2026) Mixed-source introductions successfully enhance the genetic diversity of captive forest musk deer (*Moschus berezovskii*). *Scientific reports*, 16(1).

Wang W, et al. (2026) Paternal genetic structure and Y-chromosomal haplogroup prediction in the Tujia and Bai ethnic groups of Guizhou, Western China. *BMC genomics*, 27(1).

Wan WJ, et al. (2026) Population genetics and ecological niche modeling of *Diglyphus albiscapus* (Hymenoptera: Eulophidae) in China. *Journal of economic entomology*, 119(2), 1389.

Meheret F, et al. (2026) Genetic diversity and population structure in Ethiopian *Urochloa brizantha* genotypes uncovered using inter simple sequence repeat (ISSR) markers. *PloS one*, 21(1), e0340368.

Jeong D, et al. (2026) Population genetic structure of the gold-spotted pond frog (*Pelophylax chosenicus*) and its phylogenetic context within the genus *Pelophylax*. *Scientific reports*, 16(1), 4470.

Turganbekova A, et al. (2026) NGS identifies novel HLA-DQA1 and DPB1 associations with aplastic anemia in the Kazakhstani population. *Frontiers in immunology*, 17, 1752687.

Wang M, et al. (2026) Multiple southward migrations of Neolithic Chinese farmers into Southeast Asia revealed from large-scale Y-chromosome sequences. *Science advances*, 12(8), eady1597.

Wernström JV, et al. (2026) Recent postglacial population expansions may explain a surprising lack of lineage splitting in Arctic meiobenthic flatworms. *BMC ecology and evolution*, 26(1).

Godinez CJP, et al. (2026) Phylogeny and Genetic Diversity of Philippine Mallard Ducks Based on the Mitochondrial DNA D-loop Region. *The journal of poultry science*, 63, 2026012.

Haider MZ, et al. (2026) Phylogeography of the Black Kite (*Milvus migrans*) in Punjab Wetlands: Assessing genetic connectivity and lineage admixture at a migratory crossroads. *PloS one*, 21(6), e0351642.

Rosario YV, et al. (2026) Full-Length Next-Generation Sequencing of 11 HLA Loci of More Than 1000 Individuals From Clinical Cohorts in East and West Africa. *HLA*, 108(1), e70814.

Froehlich CYM, et al. (2026) Population Genomics Highlight the Vulnerability of Coral-Dwelling Gobies to Ecological Losses due to Climatic Disturbances. *Molecular ecology*, 35(13), e70455.

Guzmán K, et al. (2026) Genetic association of IL-1B-511 (C/T), TNF-A-308 (G/A) and IL-10-1082 (G/A) with gastric cancer risk in Colombian populations. *Ecancermedicalscience*, 20, 2107.

Dai Q, et al. (2026) Comparative Population Genetics of Two Alvinocaridid Shrimp Species in Chemosynthetic Ecosystems of the Western Pacific. *Integrative zoology*, 21(2), 291.

Ekerette E, et al. (2026) Divergent ancestry of Korean native and Thai chickens with independent gene pool retention by Korean commercial chickens. *Animal bioscience*, 39(3), 250315.

Adnan A, et al. (2026) Unveiling the genetic tapestry of Kohistan: a population genetic analysis of autosomal STRs in a South Asian population. *BMC genomics*, 27(1).

Jiang X, et al. (2026) Maternal genetic structure and population affinities of the Sichuan Han Chinese based on whole mitochondrial genomes. *BMC genomics*, 27(1).

Olaoluwa FD, et al. (2026) Dataset on MatK chloroplast gene sequences of five underutilized nigerian native legume species. *Data in brief*, 65, 112609.