

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: 20260829T183104+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 [NIF](#) .

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.

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 chosonicus*) and its phylogenetic context within the genus *Pelophylax*. *Scientific reports*, 16(1), 4470.

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.

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.

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

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 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).

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).

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.

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.

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.

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.

Derouiche L, et al. (2026) Genetic evidence for the rediscovery in the wild of the critically endangered Sahara killifish *Apricaphanius saourensis* (Cyprinodontiformes: Aphaniidae). *Die Naturwissenschaften*, 113(1), 21.

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).

Mapua SA, et al. (2026) Microsatellite analysis of genetic differentiation among populations of the malaria vector *Anopheles funestus* across mainland Tanzania reveals contrasted patterns of geographic isolation and gene flow. *Parasites & vectors*, 19(1), 76.

Lessios HA, et al. (2026) Phylogeography of *Heteropriacanthus*, a circumtropical reef fish with very little morphological variation. *Scientific reports*, 16(1).