

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

PyPop

RRID:SCR_013425

Type: Tool

Proper Citation

PyPop (RRID:SCR_013425)

Resource Information

URL: <http://www.pypop.org/>

Proper Citation: PyPop (RRID:SCR_013425)

Description: Open-source software pipeline for population genomics. Designed for processing genotype and allele data and running population genetic analyses, including conformity to Hardy-Weinberg expectations; tests for balancing or directional selection; estimates of haplotype frequencies and measures and tests of significance for linkage disequilibrium.

Abbreviations: PyPop

Synonyms: , Python for Population Genomics, PYthon for POPulation genetics

Resource Type: software application, software resource

Defining Citation: [DOI:10.3389/fimmu.2024.1378512](https://doi.org/10.3389/fimmu.2024.1378512)

Keywords: gene, genetic, genomic, python, ms-windows, (98/2000/xp), linux, macos

Availability: Free, Available for download, Freely available

Resource Name: PyPop

Resource ID: SCR_013425

Alternate IDs: nlx_154559

Alternate URLs: <https://github.com/alexlanaster/pypop>,
<https://zenodo.org/records/19170148>

License: GNU GPL v2

Record Creation Time: 20220129T080316+0000

Ratings and Alerts

No rating or validation information has been found for PyPop.

No alerts have been found for PyPop.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 74 mentions in open access literature.

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

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.

Leong SL, et al. (2025) Lack of immunogenicity for an influenza-derived peptide across the HLA-B44 supertype molecules. *Clinical & translational immunology*, 14(9), e70051.

Hof LJV, et al. (2025) Maternal-Foetal HLA-DQB1 Incompatibility Is Associated With Pregnancy-Induced Hypertensive Disorders in a Genetically Isolated Population. *HLA*, 106(2), e70374.

Jean-Baptiste E, et al. (2025) Etiologic Determinants and Characteristics of Diabetes in Haitian Youth (EDDHY Study). *Pediatric diabetes*, 2025, 9974561.

Olieslagers TI, et al. (2025) Full-length gene polymorphism of the non-classical HLA-E in Estonian individuals. *Immunogenetics*, 77(1), 24.

Tran L, et al. (2025) HLAtools, Searching Shared HLA Amino Acid Residue Prevalence, and the Global Frequency Browsers: New Computational Resources for Working With HLA Data and Visualizing Global Patterns of HLA Variation. *International journal of immunogenetics*, 52(6), 358.

Rosario YV, et al. (2025) Full-length next-generation sequencing of 11 HLA loci of more than 1000 individuals from clinical cohorts in East and West Africa. *bioRxiv : the preprint server for biology*.

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.

Liu Y, et al. (2025) Uncovering genetic diversity and admixture of British Africans with HLA alleles inferred from whole genome sequencing. *European journal of human genetics : EJHG*, 33(8), 1057.

Schaschl H, et al. (2025) HLA diversity and signatures of selection in the Maniq, a nomadic hunter-gatherer population in Southern Thailand. *Immunogenetics*, 77(1), 23.

Leong SL, et al. (2024) Fighting flu: novel CD8+ T-cell targets are required for future influenza vaccines. *Clinical & translational immunology*, 13(2), e1491.

Marzouka NAD, et al. (2024) Investigating the genetic makeup of the major histocompatibility complex (MHC) in the United Arab Emirates population through next-generation sequencing. *Scientific reports*, 14(1), 3392.

Lancaster AK, et al. (2024) PyPop: a mature open-source software pipeline for population genomics. *Frontiers in immunology*, 15, 1378512.

Banjoko AW, et al. (2024) High Resolution Class I HLA -A, -B, and -C Diversity in Eastern and Southern African Populations. *bioRxiv : the preprint server for biology*.

Mukisa J, et al. (2024) High KIR diversity in Uganda and Botswana children living with HIV. *bioRxiv : the preprint server for biology*.

Yant??r E, et al. (2023) HLA Alleles, Genotype and Haplotype Analyzes from Central Anatolia Region of Turkey. *Balkan medical journal*, 40(5), 358.

Mashayekhi P, et al. (2023) Influence of HLA-A, -B, -DR Polymorphisms on the Severity of COVID-19: A Case-Control Study in the Iranian Population. *Archives of Iranian medicine*, 26(5), 261.

Al Yafei Z, et al. (2023) Analysis of the Origin of Emiratis as Inferred from a Family Study Based on HLA-A, -C, -B, -DRB1, and -DQB1 Genes. *Genes*, 14(6).

Nanjala R, et al. (2023) Assessing HLA imputation accuracy in a West African population. *bioRxiv : the preprint server for biology*.

Nanjala R, et al. (2023) Assessing HLA imputation accuracy in a West African population. *PloS one*, 18(9), e0291437.