

Resource Summary Report

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PyPop

RRID:SCR_013425

Type: Tool

Proper Citation

PyPop (RRID:SCR_013425)

Resource Information

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

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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/alexlancaaster/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 70 mentions in open access literature.

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

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.

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.

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.

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.

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.

Alnaqbi H, et al. (2022) Characterizing the diversity of MHC conserved extended haplotypes using families from the United Arab Emirates. *Scientific reports*, 12(1), 7165.

Almawi WY, et al. (2022) Distribution of HLA-A, -C, -B, -DRB1, and -DQB1 polymorphisms in the Korean minority in Kazakhstan, and relatedness to neighboring and distant populations. *Gene*, 823, 146386.

Sahin Tekin M, et al. (2022) A Novel Finding of an HLA Allele's and a Haplotype's Relationship with SARS-CoV-2 Vaccine-Associated Subacute Thyroiditis. *Vaccines*, 10(12).