

Resource Summary Report

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Allele Frequencies in Worldwide Populations

RRID:SCR_007259

Type: Tool

Proper Citation

Allele Frequencies in Worldwide Populations (RRID:SCR_007259)

Resource Information

URL: <http://www.allelefrequencies.net>

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Description: The main purpose of the allelefrequencies.net website is to provide one central source, freely available to all. For the storage of allele frequencies from different polymorphic areas in the HUMAN genome. Users can contribute the results of their work into one common database, and can perform database searches on information already available. They have currently collected data in allele, haplotype and genotype format. The success of this website will depend on you to contribute your data. Sponsors: This resource is supported Royal Liverpool University. Keywords: Allele, Polymorphic, Genome, Database, Data, Haplotype, Genotype,

Synonyms: Allele Frequencies

Resource Type: database, data or information resource

Keywords: bio.tools, FASEB list

Funding:

Resource Name: Allele Frequencies in Worldwide Populations

Resource ID: SCR_007259

Alternate IDs: biotools:allele_frequency_net, nif-0000-30079

Alternate URLs: https://bio.tools/allele_frequency_net

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250412T055150+0000

Ratings and Alerts

No rating or validation information has been found for Allele Frequencies in Worldwide Populations.

No alerts have been found for Allele Frequencies in Worldwide Populations.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 382 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Petito E, et al. (2025) Association of human leucocyte antigen loci with vaccine-induced immune thrombotic thrombocytopenia: Potential role of the interaction between platelet factor 4-derived peptides and MHC-II. British journal of haematology, 206(1), 290.

Raghavan R, et al. (2025) Rational engineering of minimally immunogenic nucleases for gene therapy. Nature communications, 16(1), 105.

Briercheck EL, et al. (2024) Geographic EBV variants confound disease-specific variant interpretation and predict variable immune therapy responses. Blood advances, 8(14), 3731.

Claeys A, et al. (2024) MHC class II genotypes are independent predictors of anti-PD1 immunotherapy response in melanoma. Communications medicine, 4(1), 184.

Gurung HR, et al. (2024) Systematic discovery of neoepitope-HLA pairs for neoantigens shared among patients and tumor types. Nature biotechnology, 42(7), 1107.

Lobos CA, et al. (2024) Molecular insights into the HLA-B35 molecules' classification associated with HIV control. Immunology and cell biology, 102(1), 34.

Kirk AM, et al. (2024) DNAJB1-PRKACA fusion neoantigens elicit rare endogenous T cell responses that potentiate cell therapy for fibrolamellar carcinoma. Cell reports. Medicine, 5(3), 101469.

Shkuri O, et al. (2024) Efficient test for deviation from Hardy-Weinberg equilibrium with known or ambiguous typing in highly polymorphic loci. *Briefings in bioinformatics*, 25(5).

Vargas-Montes M, et al. (2024) In silico identification and ex vivo evaluation of *Toxoplasma gondii* peptides restricted to HLA-A*02, HLA-A*24 and HLA-B*35 alleles in human PBMC from a Colombian population. *Medical microbiology and immunology*, 214(1), 5.

Beelen NA, et al. (2024) HLA class I NK-epitopes and KIR diversities in patients with multiple myeloma. *Immunogenetics*, 76(3), 155.

Thrift WJ, et al. (2024) Towards designing improved cancer immunotherapy targets with a peptide-MHC-I presentation model, HLApollo. *Nature communications*, 15(1), 10752.

Slieker RC, et al. (2024) Reassessing human MHC-I genetic diversity in T cell studies. *Scientific reports*, 14(1), 7966.

Vichara-Anont I, et al. (2024) HLA variants and their association with IgE-Mediated banana allergy: A cross-sectional study. *Heliyon*, 10(12), e32787.

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.

Barquera R, et al. (2024) Ancient genomes reveal insights into ritual life at Chichén Itzá. *Nature*, 630(8018), 912.

Weisbrod L, et al. (2024) FASTMAP-a flexible and scalable immunopeptidomics pipeline for HLA- and antigen-specific T-cell epitope mapping based on artificial antigen-presenting cells. *Frontiers in immunology*, 15, 1386160.

Menon T, et al. (2024) CD8+ T-cell responses towards conserved influenza B virus epitopes across anatomical sites and age. *Nature communications*, 15(1), 3387.

Guo N, et al. (2024) Immunoinformatics Design and In Vivo Immunogenicity Evaluation of a Conserved CTL Multi-Epitope Vaccine Targeting HPV16 E5, E6, and E7 Proteins. *Vaccines*, 12(4).

Matern BM, et al. (2024) Quantifying uncertainty of molecular mismatch introduced by mislabeled ancestry using haplotype-based HLA genotype imputation. *Frontiers in genetics*, 15, 1444554.

Obispo D, et al. (2024) New Associations with the HIV Predisposing and Protective Alleles of the Human Leukocyte Antigen System in a Peruvian Population. *Viruses*, 16(11).