



# HUMAN IMMUNOLOGY

Official Journal of the [American Society for Histocompatibility and Immunogenetics](#)

## AUTHOR INFORMATION PACK

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### DESCRIPTION

*Human Immunology* publishes full-length, original, hypothesis-driven basic and clinical research articles as well as brief communications, reviews and editorials covering immunogenetics, transplantation immunology, autoimmunity, and immunity to infectious diseases in humans. It also publishes short population reports, which are tied to the [allele frequencies.net](#) database, describing allele frequencies of HLA and KIR.

The journal's scope includes understanding the genetic and functional mechanisms that distinguish human individuals in their immune responses to allografts, pregnancy, infections or vaccines as well as the immune responses that lead to autoimmunity, allergy or drug hypersensitivity. It also includes examining the distribution of the genes controlling these responses in populations.

Research areas include:

Studies of the genetics, genomics, polymorphism, evolution, and population distribution of immune-related genes

Studies of the expression, structure and function of the products of immune-related genes

Immunogenetics of susceptibility to infectious and autoimmune disease, and allergy

The role of the immune-related genes in hematopoietic stem cell, solid organ, and vascularized composite allograft transplant

Histocompatibility studies including alloantibodies, epitope definition, and T cell alloreactivity

Studies of immunologic tolerance and pregnancy

T cell, B cell, NK and regulatory cell functions, particularly related to subjects within the journal's scope

Pharmacogenomics and vaccine development in the context of immune-related genes

*Human Immunology* considers immune-related genes to include those encoding classical and non-classical HLA, KIR, MIC, minor histocompatibility antigens (mHAgs), immunoglobulins, TCR, BCR, proteins involved in antigen processing and presentation, complement, Fc receptors, chemokines and cytokines. Other immune-related genes may be considered.

*Human Immunology* is also interested in bioinformatics of immune-related genes and organizational topics impacting laboratory processes, organ allocation, clinical strategies, and registries related to autoimmunity and transplantation.

Original papers with new data will be given preference over uninvited reviews and meta- analyses.

As the flagship scientific publication of the American Society for Histocompatibility and Immunogenetics (ASHI), *Human Immunology* is primarily directed to readers with an interest in histocompatibility, immunogenetics, transplantation, anthropology/population studies, HLA disease association and pharmacogenomics. These include basic and clinical scientists as well as histocompatibility laboratory professionals.

## AUDIENCE

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Immunologists, Geneticists, Pathologists, Biochemists, Histocompatibility Technologists.

## IMPACT FACTOR

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## ABSTRACTING AND INDEXING

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## GUIDE FOR AUTHORS

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### INTRODUCTION

*Human Immunology* publishes full-length, original, hypothesis-driven basic and clinical research articles as well as brief communications, reviews and editorials covering immunogenetics, transplantation immunology, autoimmunity, and immunity to infectious diseases in humans. It publishes short population reports, which are linked to the [allelefreqencies.net](http://allelefreqencies.net) database, describing the allele and haplotype frequencies of HLA and KIR.

A complete description of the journal's aims, scope and research areas can be found on the [home page](#).

### TYPES OF PAPERS

#### Research papers

A full-length report of original, hypothesis-driven basic or clinical research, with new data, investigated using the scientific method, may be submitted as a research paper.

Limit- 4000 words excluding references, tables, and figures

Abstract- 200 words maximum

References- up to 75

#### Brief communications

A short report of a distinct novel observation arising from hypothesis-driven basic or clinical research, investigated using the scientific method, may be submitted as a brief communication.

Limit- 2500 words

Abstract- 150 words maximum

References- up to 30

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#### Review Articles

Review articles should focus on areas in which there has been recent significant progress by a number of laboratories and investigators. No previously unpublished results should be included. Invited review articles will get priority over uninvited submissions.

Limit- 5000 words, excluding references, tables, and figures

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References- up to 80

Review articles should include the following sections: Title Page (including an abbreviated title of not more than 45 characters and spaces) Abstract (number of words specified above) Keywords (up to 5) Abbreviations (list of abbreviations used) Introduction Discussion Conclusions Acknowledgements References Tables, Figure Legends, and Figures.

#### Short Population Reports

Structured descriptions of reference populations, populations of anthropological interest, and control populations for disease studies, with associated genetic data and minimal analysis, can be published in *Human Immunology* as peer-reviewed Short Population Reports.

*Human Immunology* has partnered with the Allele Frequencies Net Database (AFND) to archive and make publically accessible the primary genotype, allele frequency and haplotype frequency data for the HLA and KIR genes from these population studies, along with demographic data for each population. Both unambiguous and ambiguous genotype data, with information on how the ambiguities were resolved, are requested.

Details of the AFND data-submission process can be found at [www.allelefreqencies.net/submit](http://www.allelefreqencies.net/submit).

The subsequent instructions for submitting Short Population Reports must be followed exactly:

Demographic data must first be submitted to [AFND](#).

If the data is HLA, the type of each individual must be added to [AFND](#).

If the data is KIR, a file containing each individual type must be sent to [Derek.middleton@rlbuht.nhs.uk](mailto:Derek.middleton@rlbuht.nhs.uk)

Following checking and ratification of the data at AFND, authors will be informed that they may now submit the Short Population Report to *Human Immunology*.

The title of a Short Population Report should include the name of the population and its geographic region of origin in no more than 150 characters.

The body of a Short Population Report should include the following in no more than 1000 words: A description of the geographic origin of the population, indicating the general region where the samples were collected, and the region to which the population is indigenous if these locations differ. A brief anthropological and demographic overview of each population's history, including information regarding potential ancestral populations, the history of migrations and any changes in the historical range of the population, and the degree and extent of contact with neighbors or other populations. A summary of the languages spoken by the members of the population, along with any pertinent historical linguistic information. A summary of any relevant cultural or ethnographic information for the population (e.g., ethnic distinctions, marriage patterns, caste structures). A description of the methods employed in obtaining samples, including: the rationale for collecting the population sample, the rationale for selecting the sites from which the samples were obtained, information regarding the degree of relatedness among individuals, and information on whether or not data was collected in a disease study. A summary of the typing methods used to generate the genotype data for this population. Up to 10 citations of previous genetic studies on the population, for both immunogenetic and non-immunogenetic markers. The following three types of analyses of the genotype data: tests of deviation from Hardy-Weinberg expectations, calculation of allele frequencies, and when multi-locus data are presented, estimation of haplotype frequencies (or calculation of haplotype frequencies if phase is known).

Allele and haplotype frequency tables should be included as supplemental data.

The data and the name of the population in the Short Population Report MUST be identical to the data and name held on AFND. Any data not identical will be rejected. The number allocated by AFND must be included in the Short Population Report.

The AFND must be referenced as follows:

Dos Santos EJ, McCabe A, Gonzalez-Galarza FF, Jones AR, Middleton D.

Allele Frequencies Net Database: Improvements for storage of individual genotypes and analysis of existing data

*Human Immunology*, 77,(2016) 238-48

Authors are encouraged to submit reports that describe all commonly typed loci of a specific gene family (e.g. all commonly typed HLA genes, or all commonly typed KIR genes) for a population in a single report. Multiple short populations reports which add only incremental information for the same population will not be accepted. New short population report manuscript submissions should describe a population or gene family that the author(s) has not described before.

For example: Acceptable - descriptions of KIR loci in a population for which HLA genes have previously been described. Not acceptable - a new report describing HLA-B in a population for which an HLA-A report has been published. Not acceptable - a new report describing additional KIR genes for a population in which other KIR genes have already been described in a short population report.

Any additional work deemed insufficient to warrant publication as a new short population report can still be submitted to AFND.

#### *FOR ALL TYPES OF PAPERS*

The topics of all papers submitted to *Human Immunology* should fall within the [aims and scope](#) of the journal.

The title page should include the names and affiliations of the authors, the complete address, e-mail address, and telephone number of the corresponding author.

Papers should be divided into clearly defined, labeled and numbered sections.

Writing should be clear and concise. English should be easily understandable with proper grammar and spelling.

All submissions should include a cover letter including the following: A statement that the manuscript is being submitted to *Human Immunology*. Those aspects of the journal's aims and scope to which the manuscript pertains. That the manuscript has not been published and is not currently under consideration by any other journal. That all authors have contributed to the submitted work, and approve the manuscript and its submission to the journal. That any novel HLA sequences have already been checked and named at [IPD-IMGT/HLA](#).

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As applicable, manuscripts must be in compliance with the following guidelines for reporting: Strengthening the Reporting of Observational Studies in Epidemiology ([STROBE](#)), Strengthening the Reporting of Genetic Association studies ([STREGA](#)), Strengthening the Reporting of Immunogenomic Studies ([STREIS](#)), Preferred Reporting Items for Systematic Reviews and Meta-Analyses ([PRISMA](#)), Meta-analysis Of Observational Studies in Epidemiology ([MOOSE](#))

A statement that the authors have followed the applicable reporting guidelines and their associated checklists (specify which guidelines were followed) should be included in the methods section of the manuscript.

**GUIDELINES FOR CANDIDATE GENE ASSOCIATION STUDIES** Carefully describe the cohort's characteristics and the patient recruitment criteria. Describe in detail the rationale for gene selection - it will be carefully evaluated by the editors. Report power calculations for the known effect sizes and allele frequencies. (studies of multifactorial diseases with <500 samples are rarely accepted for publication) Include only unrelated subjects or control for any relatedness. Include genotyping quality control information. Provide sequences of primers or details of kits used for genotyping. Carefully describe the typing methods used and their accuracy. Perform high-resolution HLA analysis where appropriate. Check genotype data for Hardy-Weinberg equilibrium. Describe the statistical methods used and their appropriateness. Present the results clearly and thoroughly and avoid excess tables (no more than 3) Correct for any multiple testing. Control for population stratification. Control for any significant HLA associations. Describe the haplotypic structure of the association. Studies showing replication of results in a second cohort are strongly favored. Studies showing experimental evidence for functional relevance are strongly favored. Association studies focusing on a single gene or a single polymorphism have limited relevance and will likely be rejected. Cite previous papers that demonstrate associations with the same gene(s) and provide possible explanations for any inconsistencies. Use WHO gene/allele nomenclature. Please also refer to the STREGA guidelines for the reporting of genetic association studies. Gene association studies not following these guidelines will likely be rejected without review.

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State the objectives of the work and provide an adequate background, avoiding a detailed literature survey or a summary of the results.

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### *Results*

Results should be clear and concise.

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This should explore the significance of the results of the work, not repeat them. A combined Results and Discussion section is often appropriate. Avoid extensive citations and discussion of published literature.

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## Abstract

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[2] Van der Geer, J., Hanraads, J.A.J., Lupton, R.A., 2018. The art of writing a scientific article. *Heliyon.* 19, e00205. <https://doi.org/10.1016/j.heliyon.2018.e00205>.

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[3] W. Strunk Jr., E.B. White, *The Elements of Style*, fourth ed., Longman, New York, 2000.

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[4] G.R. Mettam, L.B. Adams, How to prepare an electronic version of your article, in: B.S. Jones, R.Z. Smith (Eds.), *Introduction to the Electronic Age*, E-Publishing Inc., New York, 2009, pp. 281–304.

Reference to a website:

[5] Cancer Research UK, Cancer statistics reports for the UK. <http://www.cancerresearchuk.org/aboutcancer/statistics/cancerstatsreport/>, 2003 (accessed 13 March 2003).

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[dataset] [6] M. Oguro, S. Imahiro, S. Saito, T. Nakashizuka, Mortality data for Japanese oak wilt disease and surrounding forest compositions, *Mendeley Data*, v1, 2015. <https://doi.org/10.17632/xwj98nb39r.1>.

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