

Human Genome Variation

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[ABOUT THE JOURNAL](#)

Aims and Scope

Human Genome Variation is an online-only, full Open Access journal that contains articles and reports about variation and variability in human genomes and the consequences, implications and future impacts for the study of human genomics.

An important and innovative feature of the journal is the Data Report article; these are short reports about human genome variation and variability which describe disease-causing variation and/or their frequencies. In addition, Data Reports can describe and analyse human multifactorial disease associated variations and/or their frequencies.

A further feature of *Human Genome Variation* will be a curated database of the underlying data from Data Reports, which will grow into an important resource for the genomics community. *Human Genome Variation* also publishes Articles and Review Articles on the relevant topics in human genome studies. Full Articles will be accompanied by a professionally written Editorial Summary.

The intended audience for *Human Genome Variation* is researchers, scientists, clinicians, genetic counsellors and those interested in human genomics, from all sectors and from around the world.

Human Genome Variation is committed to providing an efficient service for both authors and readers. A streamlined peer review system, together with the support of an Editorial Board, allows a team of independent editors to make rapid and fair publication decisions. Prompt dissemination of accepted papers to Nature Publishing Group's wide readership and beyond is achieved through a programme of continuous online publication. Published manuscripts are enhanced by innovative web technologies, including interactive browsing and efficient data- and text-mining.

Journal Details

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ARTICLE TYPE SPECIFICATIONS

Article Description	Word Limit	Tables/ Figures	References
<p>Article Studies that are of high scientific quality and that are of interest to the diverse readership of the journal. Manuscripts should include an abstract and appropriate experimental details to support the conclusions. Articles should be no more than 5000 words excluding references and figure legends and should not normally include more than six display items (tables and/or figures). They should include title, abstract, introduction, materials and methods, results and discussion sections.</p>	<p>Article: 5,000 words max including abstract (150-200words) but excluding references and figure captions.</p>	<p>Max of 6</p>	<p>Max of 50. Please use as recent as possible.</p>
<p>Review Article Review Articles are normally solicited by the editors; however, we also welcome timely, unsolicited Review Articles. Authors with proposals for Review Articles should present information concerning the proposed content and authors to the editors prior to submission.</p>	<p>Article: 5,000 words max including abstract (150-200words) but excluding References and figure captions.</p>	<p>Max of 8</p>	<p>Max of 100</p>
<p>Data Report Data Reports are short reports about human genome variation and variability, which describe disease-causing variation and/or their frequencies. In addition, Data Reports can describe, and document human multifactorial disease-associated variations and their frequencies. Data Report authors are asked to check the mutation description information with the mutalyzer name checker (https://mutalyzer.nl) or relevant description checking system, and make sure that description follows the HGVS nomenclature in advance of submission. Please state in the manuscript cover letter that the checking process was undertaken. This format typically begin with a brief unreferenced abstract (not more than 70 words). The title is limited to 10 words (or 90 characters). The main text is typically no more than 1,500 words, including the abstract and contains no headings. Data Reports normally have no more than 2 display items, although this may be flexible at the discretion of the editor. References are limited to 20.</p>	<p>Article: 1,500 words max including abstract (70words) excluding references, figures and tables.</p>	<p>Max of 2</p>	<p>Max of 20</p>
<p>Editorial (by Editor invitation only) Proposals for Editorial may be submitted; however, authors should only send an outline of the proposed paper for initial consideration.</p>	<p>1,000 words</p>	<p>Max of 2</p>	<p>Max of 5</p>

PREPARATION OF ARTICLES

Please note that original articles must contain the following components. Please see below for further details.

- Title page
- Abstract
- Introduction
- Materials and Methods
- Results
- Discussion
- Acknowledgements

- Conflict of Interest
- References
- Figure legends
- Tables
- Figures

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- The title should be brief, informative, of 150 characters or less and should not make a statement or conclusion.
- The running title should consist of no more than 50 letters and spaces. It should be as brief as possible, convey the essential message of the paper and contain no abbreviations.
- Authors should disclose the sources of any support for the work, received in the form of grants and/or equipment and drugs.
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Introduction: This should give a short, clear account of the background and reasons for undertaking the study. It should not be a review of the literature. The Introduction should assume that the reader is knowledgeable in the field and should therefore be as brief as possible.

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Instruments used, as well as standard techniques and procedures applied throughout the work, should appear in a paragraph at the beginning of the Materials and Methods section. Novel experimental procedures should be described in detail, but published procedures should be referred to by literature citation of the original article and published modifications.

Authors should use approved nomenclature for gene symbols, and use symbols rather than italicized full names (TTN, not titin). Please consult the appropriate nomenclature databases for correct gene names and symbols. A useful resource is LocusLink. Approved human gene symbols are provided by HUGO Gene Nomenclature Committee (HGNC), e-mail: nome@galton.ucl.ac.uk; see also www.gene.ucl.ac.uk/nomenclature. Approved mouse symbols are provided by The Jackson Laboratory, e-mail: nomen@informatics.jax.org; see also www.informatics.jax.org/mgihome/nomen.

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Results: The description of results should not simply reiterate data that appear in tables and figures and, likewise, the same data should not be displayed in both tables and figures. The results section should be concise and follow a logical sequence. If the paper describes a complex series of experiments, it is permissible to explain the protocol/experimental design before presenting the results. Do not discuss the results or draw any conclusions in this section. This section may be divided into subheadings to assist the reader. Large datasets or other cumbersome data pertinent to the manuscript may be submitted as supplementary information.

Discussion: Do not recapitulate the results, but discuss their significance against the background of existing knowledge, and identify clearly those aspects that are novel. The final paragraph should highlight the main conclusion(s), and provide some indication of the direction future research should take. This section may be divided into subheadings to assist the reader. Results and Discussion may be combined.

Acknowledgements: These should be brief, and should include sources of financial support, material (e.g. novel compounds, strains, etc.) not available commercially, personal assistance, advice from colleagues and gifts.

Conflict of Interest: Authors must declare whether or not there are any competing financial interests in relation to the work described. This information must be included at this stage and will be published as part of the paper. Conflict of Interest should be noted in the cover letter and in the paper. Please see the Conflict of Interest documentation in the [Editorial Policy](#) section for detailed information.

References: Authors are responsible for the accuracy of the references. Only papers directly related to the article should be cited; exhaustive lists of related reading should be avoided. References should be numbered in order of appearance, cited in text using superscript numbers (if the citation falls next to punctuation, the number should be inserted after, not before, the punctuation).

The reference list should be double-spaced, and there should be only one reference per number. Include only published references or those accepted and waiting for publication (listed as 'in press' following digital object identifier number) - not personal communications, "submitted" papers, or text notes. ("Personal communication" and "Unpublished data" references should be inserted in the text in parentheses, e.g., "(J. Smith, personal communication)."

Similarly, references to a general website instead of a specific page or document should not be included in the reference list, but instead inserted in the text in parentheses, e.g., "(http://who.org)".

If there are references that are cited only in a figure or table, place them at the end of the list. In other words, number all references in the main text first, then any that appear only in figures, followed by any that appear only in tables.

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Online publication. In general, the order is author (or authoring entity, e.g., "US Food and Drug Administration"), title of page or document, date (at least the year), URL (always include "http://"), access date (if relevant).

Examples:

Journal article, up to six authors:

Belkaid Y, Rouse BT. Natural regulatory T cells in infectious disease. *Nat Immunol* 2005; **6**: 353–360.

Journal article, more than six authors:

Miller W, Flynn P, McCullough J, Balfour HH Jr., Goldman A, Haake R *et al*. Cytomegalovirus infection after bone marrow transplantation: an association with acute graft-v-host disease. *Blood* 1986; **67**: 1162–1167.

Journal article, e-pub ahead of print:

Bonin M III, Pursche S, Bergeman T, Leopold T, Illmer T, Ehninger G *et al*. F-ara-A pharmacokinetics during reduced-intensity conditioning therapy with fludarabine and busulfan. *Bone Marrow Transplant* 2007; e-pub ahead of print 8 January 2007; doi:10.1038/sj.bmt.1705565.

Journal article, in press [note that the year is not included for "in press" references]:

Gallardo RL, Juneja HS, Gardner FH. Normal human marrow stromal cells induce clonal growth of human malignant T-lymphoblasts. *Int J Cell Cloning* (in press).

Abstract/supplement:

Syrjala KL, Abrams JR, Storer B, Heiman JR. Prospective risk factors for five-year sexuality late effects in men and women after haematopoietic cell transplantation. *Bone Marrow Transplant* 2006; **37**(Suppl 1): S4 (abstract 107).

Letter:

Caocci G, Pisu S. Overcoming scientific barriers and human prudence [letter]. *Bone Marrow Transplant* 2006; **38**: 829–830.

Book (complete):

Atkinson K, Champlin R, Ritz J, Fibbe W, Ljungman P, Brenner MK (eds). *Clinical Bone Marrow and Blood Stem Cell Transplantation*. Cambridge University Press: Cambridge, UK, 2004.

Book (chapter in book):

Coccia PF. Hematopoietic cell transplantation for osteopetrosis. In: Blume KG, Forman SJ, Appelbaum FR (eds). *Thomas' Hematopoietic Cell Transplantation*, 3rd edn. Blackwell Publishing: Malden, MA, USA, 2004: 1443–1454.

Book (with volume and edition information):

Shadwell, J. The common vampire fish. In: Howlett R, Thomas, A (eds). *Proc 4th Int Symp Transylvanian Fish Soc*, 2nd edn, vol 2. Springer: Berlin, Germany, 2012: 21–29.

Meeting:

Brentjens, R, Riviere, I, Frattini, M, Wang, X, Taylor, C, Olszewska, M *et al*. Marked regression of adenopathy following infusion of autologous T cells. Presented at the 13th annual meeting of the American Society of Gene and Cell Therapy, Washington, DC, 17–22 May 2010.

Online (journal):

Huynen MMTE, Martens P, Hilderink HBM. The health impacts of globalisation: a conceptual framework. *Global Health* **1**: 14. <http://www.globalizationandhealth.com/content/1/1/14>.

Online (dated report):

Centers for Disease Control and Prevention. Smallpox vaccine and monkeypox. <http://www.cdc.gov/ncidod/monkeypox/pdf/vaccineqa.pdf>. 9 July 2003.

Online (dynamic Web page):

National Institutes of Health. Genome-Wide Association Studies (GWAS) (2006). <http://grants.nih.gov/grants/gwas/index.htm>. Accessed 4 January 2007.

Thesis:

Gee H. Trends in Infant Growth Rates. Thesis, Princeton University, 1978.

Package inserts and prescribing information:

Lamasil [package insert]. Sandoz Pharmaceuticals, 1993.
Kaletra [prescribing information]. Abbott, 2005.

Newspaper:

FDA strengthens warnings on stimulants. *New York Times*, 22 August 2006.

Press release:

US Food and Drug Administration. FDA approves updated warfarin (Coumadin) prescribing information. Press release, 16 August 2007.

Patent:

Wilson ST, Oak S, Flanigen EM. US patent 4567029 (1986).
Kuznicki SM, Thrush AK. European patent 0405978A1 (1990).

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New nucleotide data must be deposited in the DDBJ/EMBL/GenBank databases and an accession number obtained before a paper can be accepted for publication. Submission to any one of the three collaborating databanks is sufficient to ensure data entry in all. The accession number should be included in the manuscript, e.g. as a footnote on the title page: The nucleotide sequence data reported are available in the DDBJ/EMBL/GenBank databases under the accession number(s) ----. If requested, the database will withhold release of data until publication. The most convenient method for submitting sequence data is by using the following URLs:

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HGV Database

Human Genome Variation hosts a fully searchable database of genomic variation as documented in the published Data Reports. These will be linked to the journal content and provide an important step towards giving the research community a verified and accessible place to publish, share and further utilize human genomics articles, data and analysis. For this purpose authors of Data Reports are required to fill in the form to register information on the reported genome variation and submit it together with the manuscript. For further information please see [Database FAQ](#) page on the journal's site.

Data Report authors are asked to check the mutation description information with the mutalyzer name checker (<https://mutalyzer.nl>) or relevant description checking system, and make sure that description follows the HGVS nomenclature in advance of submission. Please state in the manuscript cover letter that the checking process was undertaken.

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- be publicly available, searchable, and open to all prospective registrants
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Human Genome Variation requires authors of all submitted original research papers to declare any Conflict of Interest (COI) in relation to the submitted work, following the guidelines and detailed regulations set by the Japan Society of Human Genetics (JSHG) in 2012.

Authors submitting their manuscripts using the journal's online manuscript tracking system are required to make their declaration as part of this process and to specify the competing interests in cases where they exist.

Criteria for COI disclosure

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4. Received patent royalties or licensing fees of 1,000,000yen or more (in one year)
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Dr Caron's work has been funded by the NIH. He has received compensation as a member of the scientific advisory board of Acadia Pharmaceutical and owns stock in the company. He also has consulted for Lundbeck and received compensation. Dr Rothman and Dr Jensen declare no potential conflict of interest.

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A condition of publication is that authors are required to make materials, data and associated protocols promptly available to others without preconditions. Data sets must be made freely available to readers from the date of publication, and must be provided to editors and peer reviewers at submission, for the purposes of evaluating the manuscript.

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We encourage authors to deposit data from genome-wide association studies in *Human Genome Variation Database*, dbGap, or EGA (European Genome-phenome Archive) upon submission to the journal.

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Authors are welcome to post pre-submission versions or the original submitted version of the manuscript on a personal blog, a collaborative wiki or an institution-hosted repository at any time (but not subsequent pre-accept versions that evolve due to the Editorial process).

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