

Instructions to Authors

Genes & Genetic Systems (GGS) is the official journal of the Genetics Society of Japan, which has been published bimonthly since 1918. *GGS*, one of the most time-honored scientific journals in the world, is now an international peer-reviewed Open Access journal.

AIMS & SCOPE

Genes & Genetic Systems is an international peer-reviewed Open Access journal. It publishes important original papers and review articles bimonthly that address a wide range of fields in genetics. These include general genetics, molecular genetics, cell genetics, developmental genetics, behavioral genetics, ecological genetics, chemical genetics, epigenetics, cytogenetics, population genetics, evolutionary genetics, and molecular evolution. *GGS* also welcomes papers in the following fields, if they are related to genetics: genome-wide research, bioinformatics, systems biology, database, genetic bioresources, and technical advances (in both experimental and *in silico* methods). *GGS* maintains the highest standards of scientific and publication ethics. Articles are available freely online to a diverse global audience.

MANUSCRIPT TYPES

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Full Papers are full-length research articles on important and comprehensive original research. There is no minimum or maximum length.

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Short Communications are short reports of the results of studies that are of sufficient interest to justify publication. They must be no longer than 15,000 characters (including spaces but excluding the title page and references) and 4 display items (i.e., figures or tables). Figure legends must be included in the character count. The text of Short Communications should not be divided into sections, such as Introduction, Results and Discussion.

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GGS welcomes manuscripts that describe genetic or analytic methods, tools or resources that are likely to have broad impact. They can be full-length research articles or Short Communications. The method or resource needs to be novel or be a significant advance to an existing method or resource. The necessary reagents or resources need to be available upon request. All Methods, Technology and Resources are peer reviewed in the same way as Full Papers and Short Communications.

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Meeting Reports summarize a meeting on a genetics-related topic. Interested authors should contact one of the Editors in the related field before submission. All Meeting Reports are peer reviewed to the same rigorous standard as Full Papers and Short Communications.

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MANUSCRIPT PREPARATION

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Style and format

Full papers should be arranged in the following order: (i) Title page, (ii) Abstract, (iii) Main body, (iv) References, (v) Tables, (vi) Legends to Figures, and (vii) Figures. The main body should be divided into sections: Introduction, Results, Discus-

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There is no specific style for **Reviews, Minireviews** or **Meeting Reports**. Please refer to previously published articles for further guidance.

Title page

The title page should comprise: (i) the title of the manuscript, (ii) name(s) of the author(s), (iii) academic or professional affiliation(s), (iv) address(es) including city, prefecture/state, zip code, country, (v) any footnotes referring to the above items, (vi) a running title (not exceeding 50 letters including spaces), (vii) up to five keywords (do not capitalize words unless they are proper names), and (viii) the name of the corresponding author, his/her telephone and E-mail address.

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Acknowledgments

This section should be brief. All authors should list all funding sources for their work in the Acknowledgments section.

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Journal articles

Tajima, F. (1989) Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* **123**, 585–595.

Saitou, N., and Nei, M. (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* **4**, 406–425.

Sarojam, R., Sappl, P. G., Goldshmidt, A., Efroni, I., Floyd, S. K., Eshed, Y., and Bowman, J. L. (2010) Differentiating *Arabidopsis* shoots from leaves by combined YABBY activities. *Plant Cell* **22**, 2113–2130.

Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T., Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y., et al. (2002) The genome sequence and structure of rice chromosome 1. *Nature* **420**, 312–316.

Books

Steeves, T. A., and Sussex, I. M. (1989) *Patterns in Plant Development*. Cambridge University Press, Cambridge, UK.

Nakazaki, T., Naito, K., Okumoto, Y., and Tanisaka, T. (2008) Active transposons in rice. *In Rice Biology in the Genomics Era*. (eds.: Hirano, H.-Y., Hirai, A., Sano, Y., and Sasaki, T.), pp. 69–79. Springer, Heidelberg.

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Tables should be placed after the References. Tables should be provided with their descriptions on the same sheet.

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New nucleotide sequence data must be submitted and deposited in the DDBJ/EMBL/GenBank databases, and an accession number must be obtained before the 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: "Note: Nucleotide sequence data reported are available in the DDBJ/EMBL/GenBank databases under the accession number(s)---." If requested by the author, the database will withhold release of data until publication.

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