Full Paper LaTeX2ε Template for Genome Informatics 2003

FirstName1 MiddleName LastName1[1] **FirstName2 LastName2**[2]
lastname1@disorder.chem.wsu.edu lastname2@jaist.ac.jp

FirstName3 LastName3[3]
lastname3@ims.u-tokyo.ac.jp

[1] School of Molecular Biosciences, Washington State University, Pullman, WA 99164, U.S.A.
[2] Japan Advanced Institute of Science and Technology, 1-1 Asahidai, Tatsunokuchi, Ishikawa 923-1292, Japan
[3] Human Genome Center, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan

Abstract

This document is a LaTeX2ε template file for preparing a full paper. Please read the instructions carefully and prepare your manuscript.

Keywords: aberrant splicing, database, point mutation, scanning model

1 Introduction

The page limit for full paper is TEN. In case the number of pages still exceeds this limit after your efforts, please contact the Editor-in-Chief (Satoru Miyano: giw@ims.u-tokyo.ac.jp) for advice.

Do not change the text width, text height, baseline, font size, etc., specified in LaTeX2e/LaTeX/MS Word templates.

2 Method and Results

Of course you can create more sections with any section titles.

2.1 Tables

Table 1 is an example of a table.

Table 1: Bioinformatics conferences in 2003.

Conference	Date	Site
PSB	January 3-7	Hawaii
RECOMB	April 10-13	Berlin
ISMB	August 3-7	Edmonton
GIW	December 16-18	Tokyo

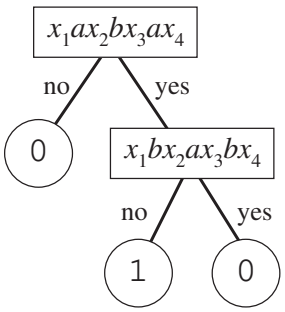

Figure 1: This is a sample figure.

Figure 2: This is a color sample figure.

2.2 Figures

When you use figures (Fig. 1, Fig. 2) with a special style file, please provide it.

Printed version of "Genome Informatics" is monochromatic and has a page limit. But, electronic version (PDF, then HTML, XML) does not have such restrictions. Therefore, we encourage the author(s) to send any hypermedia files which can be attached to your paper. The electronic version will be open to public at JSBi Home Page (http://www.jsbi.org/journal.html).

2.3 Citation and References

Here are examples of citation [1, 2, 3, 4, 5, 6]. Reference style and citation should strictly follow this template.

1. References should be arranged in the alphabetical order of authors and all references should be cited in the paper.
2. Style (see examples in **References** below).
   (a) Journal: author(s), title, journal name, vol(issue):startpage-endpage, year.
   (b) Proceedigns: author(s), title, Proc. conference name, publisher (if possible), startpage-endpage, year.
   (c) Book: author(s), title, publisher, year.
   (d) Other: author(s), title, any helpful information, year.
   (e) URL: http://(URL site). URLs should be listed in the last.

3 Discussions

Authors are recommended to use spell checker program and grammar check program for improving your final version.

References

[1] Akutsu, T., Kuhara, S., Maruyama, O., and Miyano, S. Identification of gene regulatory networks by strategic gene disruptions and gene overexpressions, *Proc. 9th ACM-SIAM Symp. Discrete Algorithms*, 695–702, 1998.

[2] Chen, T., He, H.L., and Church, G.M., Modeling gene expression with differential equations, *Proc. Pacific Symp. Biocomputing '99*, World Scientific, 29–40, 1999.

[3] Doi, K. and Imai, H., A greedy algorithm for minimizing the number of primers in multiple PCR experiments, *Genome Informatics*, 10:73–82, 1999.

[4] Motowani, R. and Raghavan, P. *Randomized Algorithms*, Cambridge University Press, 1994.

[5] Smith, T.F. and Waterman, M.S., Identification of common molecular subsequences, *J. Mol. Biol.*, 147(1):195–197, 1981.

[6] http://www.jsbi.org/