

# Full Paper LaTeX2 $\epsilon$ Template for Genome Informatics 2006

**FirstName1 MiddleName LastName1<sup>1</sup>**      **FirstName2 LastName2<sup>2</sup>**  
lastname1@ims.u-tokyo.ac.jp      lastname2@ims.u-tokyo.ac.jp

**FirstName3 LastName3<sup>3</sup>**  
lastname3@jsbi.org

- <sup>1</sup> Human Genome Center, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
- <sup>2</sup> San Diego Supercomputer Center, University of California at San Diego, 9500 Gilman Dr., La Jolla, CA 92093, USA
- <sup>3</sup> Institute for Infocomm Research, 21 Hen Mui Keng, Terrace, Singapore 119613

## Abstract

This document is a LaTeX2 $\epsilon$  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 giw2004@ims.u-tokyo.ac.jp for advice.

Do not change the text width, text height, baseline, font size, etc., specified in LaTeX2 $\epsilon$ /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      |
|------------|----------------|-----------|
| RECOMB     | April 2-5      | Venice    |
| ISMB       | August 6-10    | Fortaleza |
| GIW        | December 18-20 | Yokohama  |

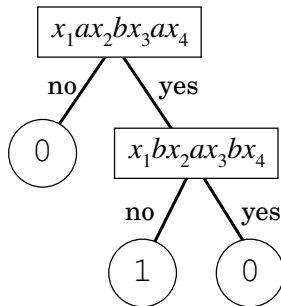


Figure 1: This is a sample figure.



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 Vol. 17, No. 2” is monochromatic and has a page limit. But, the electronic version (PDF, HTML) 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 also published at JSBi Home Page ([http://www.jsbi.org/jsbi\\_new/gioinfo.html](http://www.jsbi.org/jsbi_new/gioinfo.html)).

## 2.3 Citation and References

Reference style and citation should strictly follow this template [1, 2, 3, 4, 5].

1. References should be arranged in the alphabetical order of authors and all references SHOULD be cited.
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://\(URLsite\)](http://(URLsite)). URLs should be listed in the last.
3. Provide all author names. If the number of authors is too large, you may reduce appropriately (such as Venter, J.C., Adams, M.D., Myers, E.W., Li, P.W., *et al.*, The sequence of the human genome, *Science*, 291(5507):1304–1351, 2001.)

## 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] Doi, K. and Imai, H., A greedy algorithm for minimizing the number of primers in multiple PCR experiments, *Genome Informatics*, 10:73–82, 1999.
- [3] Motowani, R. and Raghavan, P., *Randomized Algorithms*, Cambridge University Press, 1994.
- [4] Smith, T.F. and Waterman, M.S., Identification of common molecular subsequences, *J. Mol. Biol.*, 147(1):195–197, 1981.
- [5] <http://www.jsbi.org/>