

Poster/Software Demonstration Abstract LaTeX2 ϵ Template

FirstName1 MiddleName LastName1¹

lastname1@ims.u-tokyo.ac.jp

FirstName2 LastName2²

lastname2@ims.u-tokyo.ac.jp

FirstName4 LastName4³

lastname4@jsbi.org

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

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

1 Introduction

This section title is recommended for the first section.

The number of pages for poster/software demonstration abstract is **exactly TWO**. In case the number of pages still exceeds this limit after your efforts, please contact giw2009@edelweiss.ims.u-tokyo.ac.jp for advice.

Do not change the text width, text height, baseline, font size, etc., specified in LaTeX2 ϵ /LaTeX/MS Word templates.

2 Method and Results

Of course you can create more sections if you want, within the page limit.

2.1 Tables

Table 1 is an example of a table.

Table 1: Bioinformatics conferences in 2009.

Conference	Date	Site
RECOMB	May 18-21	Arizona
ISMB	June 27-July 2	Stockholm
GIW	December 14-16	Yokohama

2.2 Figures

When you use a figure (Figure 1) with a special style file, please provide it.

Printed version of the abstract is monochromatic. The poster and software demonstration abstracts are compiled as “The 20th International Conference on Genome Informatics, Poster and Software Demonstration Abstracts” and will be delivered at the conference. The electronic version (PDF) will be published at JSBi Home Page (<http://www.jsbi.org/modules/journal1/index.php/index.html>).

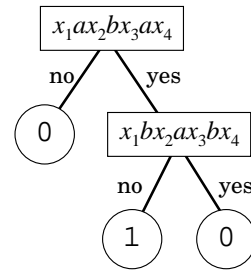


Figure 1: This is a sample figure.

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) Proceedings: 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/>