

# Poster Abstract LaTeX2 $\epsilon$ Template

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

## 1 Introduction

The number of pages for a poster abstract is **exactly One for CBI session** and **exactly TWO for JSBi session**. Do not change the text width, text height, baseline, font size, etc., specified in this template file.

The poster abstracts are compiled as “ The 2011 Joint Conference on CBI & JSBi: Poster Abstracts ”and will be delivered at the conference in an electric form (e.g., USB memory).

If you are submitting a poster abstract to a CBI session, it is not required to divide the abstract into sections.

## 2 Method and Results

You can create more sections with any section titles, within the page limit.

### 2.1 Figures

A sample figure is given in Fig. 1.

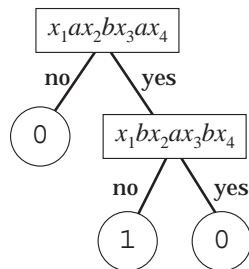


Figure 1: This is a sample figure.

### 2.2 Tables

Table 1 is an example of a table.

Table 1: Bioinformatics conferences in 2011.

Conference	Date	Site
RECOMB	March 28-31	Vancouver
ISMB/ECCB	July17-19	Vienna
GIW	December 5-7	Busan

## 2.3 Citation and References

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

- References should be arranged in the alphabetical order of authors and all references SHOULD be cited.
- Style (see examples in **References** below).
  - Journal: author(s), title, journal name, vol:startpage–endpage, year.
  - Proceedings: author(s), title, Proc. conference name, publisher (if possible), startpage–endpage, year.
  - Book: author(s), title, publisher, year.
  - Other: author(s), title, any helpful information, year.
  - URL: `http://(URLsite)`. URLs should be listed in the last.
- Provide all author names. If the number of authors is too large, you may reduce appropriately (such as Venter, J.C., *et al.*, The sequence of the human genome, *Science*, 291:1304–1351, 2001).

## 3 Discussions

Authors are recommended to use spell checker program and grammar check program for improving English presentation.

## References

- [1] Alon, U., *An Introduction to Systems Biology: Design Principles of Biological Circuits*, CRC Press, 2006.
- [2] Altschul, S. F., Gish, W., Miller, W., Myers, E.W., and Lipman, D.J., Basic local alignment search tool, *Journal of Molecular Biology*, 215:403–410, 1990.
- [3] Friedman, N., Linial, M., Nachman, I., and Pe’er, D., Using Bayesian networks to analyze expression data, *Proc. 4th Annual International Conference on Computational Molecular Biology*, ACM, 127–135, 2000.
- [4] Smith, T.F. and Waterman, M.S., Identification of common molecular subsequences, *Journal of Molecular Biology*, 147:195-197, 1981.
- [5] Venter, J.C., *et al.*, The sequence of the human genome, *Science*, 291:1304–1351, 2001.
- [6] [http://cbi-society.org/cbi/taikai/taikai11/index\\_e.html](http://cbi-society.org/cbi/taikai/taikai11/index_e.html)