

## Editorial

This special issue contains the papers accepted for presentation at the Sixteenth ISMB Conference (<http://www.iscb.org/ismb2008/>). The 'Intelligent Systems for Molecular Biology' conference took place in Toronto, Canada from July 19–July 23, 2008.

The papers contained in this volume are a selection of the 287 papers submitted to the conference. The papers were organized in 10 areas edited by two scientists. Half of Area Chairs were new as ISMB editors (see Table 1). In contrast with the previous years we decided to join the 'Protein Structure' and 'Protein Function' areas.

The Area Chairs were responsible for selecting the member of the Program Committee that comprised of more than 300 reviewers who were assisted by a sizeable number of sub-reviewers.

Most papers received three reviews and many of them four or more reports. There was an intense discussion between referees fostered by the area chairs. In a first round of evaluation, 224 papers were selected for rejection, 32 for acceptance and 31 as undecided. The papers classified for potential acceptance and those classified as undecided were revised by the Conference Chairs and by the Area Chairs, and most of them were referred again to the referees, with additional Area Editors' comments. The phone conference confirmed the selection of 34 papers and reserved another 15 for additional discussion, in most cases by obtaining new reports or additional editorial advice in light of previous comments. For all the papers in which the referee comments might have confused the authors, editorial comments explaining the basic reasons for the rejection of the papers were introduced. In total, 45 papers were finally accepted, and four more accepted after compulsory revision. Unfortunately, one of these 49 accepted papers was withdrawn by the authors during

the production phase. We are happy to say that we have received a single rebuttal letter from the 224 submissions.

We truly believe that Area Editors and Referees made a consistent effort to increase the quality of the referee process by selecting only papers of scientific excellence in their area. The selected papers have a balance between the novelty of the methods and the significance of their contribution to the corresponding areas of biology, as well as being of general interest for the conference. After such a large evaluation effort it is difficult to imagine that the quality of the conference can be further improved by additional evaluation efforts. In our opinion the only way to produce this desired quality transition, would be to introduce a second round of evaluation, a topic that is being discussed for ISMB09.

The final acceptance rate was 17.1%, a ratio similar to previous year's (15.8% in 2007). The corresponding authors of submitted papers came from 26 countries, 244 authors were from North America, 104 from Europe and Israel, 51 from Asia, 2 from South America and 5 from Australia.

We expect the conference to be a scientific success and a solid contribution to the role of ISCB and its contribution to Molecular Biology and Biomedicine.

We would like to thank the Area Chairs and reviewers for their effort, dedication and quality of their professional work; to Thomas Lengauer and Mario Albrecht for sharing their invaluable experience in ISMB-ECCB07, Andrei Voronkov for technical support with the EasyChair system, the team at Oxford Journals for proof-setting the papers; the Conference Chairs, Burkhard Rost, Michal Linial, Jill Mesirov for their continuous support, and Steven Leard for helping us to deal with the all kind of issues.

Alfonso Valencia (ISMB Paper Selection Chair)  
Idefonso Cases (Co-Chair)

**Table 1.**

	Area	Area Chairs	Submissions	Accepted
1	Sequence analysis and alignment	Serafim Batzoglou <sup>a</sup> , Des Higgins	39	8
2	Evolution and phylogeny	Junhyong Kim <sup>a</sup> , Tandy Warnow	23	3
3	Comparative genomics	Roderic Guigo <sup>a</sup> , David Sankoff <sup>a</sup>	16	5
4	Protein structure and function	Nir Ben-Tal, Ora Schueler-Furman <sup>a</sup>	27	5
5	Gene regulation and transcriptomics	Olga Troyanskaya, Zhaolei Zhang	35	5
6	Protein interactions and molecular networks	Joel Bader, Edward Marcotte <sup>a</sup>	43	3
7	Databases and ontologies	Helen Parkinson, Robert Stevens	11	4
8	Text mining	Mark Craven <sup>a</sup> , Hagit Shatkay <sup>a</sup>	19	4
9	Bioinformatics of disease	Igor Jurisica <sup>a</sup> , Anna Tramontano <sup>a</sup>	38	3
10	Other	Janice Glasgow, Richard H. Lathrop	36	8

<sup>a</sup>New Area Chair this year.