

# Third IAPR International Conference on Pattern Recognition in Bioinformatics

15 -17 October 2008, Melbourne

## Special Session: SS5 Proteins: structure, function and interaction

Bioinformatics plays a major role in large scale computations on analysis and prediction of protein structure, function and their interactions. The three-dimensional structures of proteins dictate their functions and the amino acid sequence carries the necessary information for encoding the 3D structure. Hence, prediction of protein structure and function from their amino acid sequences remains a major challenge in Bioinformatics. The sequence and structural analysis reveal deep insights to understand the structure and functions of proteins as well as to derive the numerical values for different parameters. The sequence and structure based parameters have wide range of applications in predicting protein secondary and tertiary structures, solvent accessibility, folding rates, disorder, binding sites in protein complexes, fold recognition and so on

### Topics include, but are not limited to:

In this special session, we invite papers from all areas of protein structure and function using computational techniques. The areas of interest (but not limited to) are as follows:

Sequence and structural analysis of proteins and complexes, Prediction of protein secondary and tertiary structures, solvent accessibility and other residue wise parameters, Analysis and prediction of binding sites in protein-protein, protein-nucleic acid, protein-carbohydrate and protein-ligand complexes, Functional prediction of proteins, Machine learning techniques, Database analysis, Protein stability, Patterns in protein structures and their complexes

### Important dates:

- Paper Submission: 15 April 2008
- Decision Notification: 15 May 2008
- Camera-Ready Submission: 15 Jun 2008

### Paper Submission:

Submission of papers will be electronic and through the conference website at <http://callforpapers.com.au/prib2008/submitpaper.php>. Instructions to authors are available at <http://www.infotech.monash.edu.au/about/news/conferences/prib08/>. Submissions must be formatted using the Springer LNCS style and must not exceed 12 pages in length. Simultaneous submission to journals or other conferences with published proceedings is not allowed. All submitted papers will be peer reviewed and the accepted papers will be published in the conference proceedings as an edited volume in *Lecture Notes in Bioinformatics* by Springer or supplementary proceedings.

### Special Session Organizers:

**Name: Dr. Michael Gromiha**  
Address: Computational Biology  
Research Center, AIST, Japan

**Name: Dr. Shandar Ahmad**  
Address: National Institute of  
Biomedical Innovation, Japan

Name: Y. H. Taguchi  
Address: Chuo University, Tokyo