

Foreword to the special issue on ALGORITHMIC METHODOLOGIES FOR PROCESSING
PROTEIN STRUCTURES, SEQUENCES AND NETWORKS

With rapid increase in the volume of data that is generated in relation to protein sequences, structures and networks, designing efficient algorithms to process these data and gain biological insight has become a significant challenge. This special issue is a natural followup of a DIMACS workshop on Information Processing by Protein Structures in Molecular Recognition (see <http://dimacs.rutgers.edu/Workshops/InformationProcessing/> for details) by two of the special issue editors. The call for paper submission was open to all interested authors. After a rigorous review process we selected eight papers for publication in this special issue.

We would like to thank all the authors that submitted papers to this special issue. Our special thanks go to all the reviewers who unselfishly devoted their professional time to assist us in our decision process.

Piotr Berman
Pennsylvania State University
University Park, PA 16802

Bhaskar DasGupta Jie Liang
University of Illinois at Chicago
Chicago, IL 60607