Journal of Proteomics & Bioinformatics - Open Access

www.omicsonline.com *Editorial* JPB/Vol.1/April 2008

Editorial

This issue marks the launch of the Journal of Proteomics and Bioinformatics (JPB) as the first *open access* journal in the field of proteomics and bioinformatics. The aim of JPB is to be the premier open source of information in all biological fields related to proteomics and bioinformatics. Open access affords the opportunity of an international audience larger than that of any subscription based journal. This is largely due to its provision of barrier-free access to peer-reviewed literature, cutting-edge reviews of the field, without the constraints of library budgets and access privileges.

Biological macromolecules are the main actors in the makeup of life. To understand biology and medicine at a molecular level, we need to visualize the activity and interplay of large macromolecules such as proteins, as well as small physiological peptides. To study protein and peptide molecules, principles of their separation, quantitation, determination of their individual characteristics and interacting partners had to be developed. One of the most important disciplines for performing these tasks is proteomics. More and more, as researchers from different disciplines delve into intricate biological questions that require protein chemistry input, they are confronted with the pressing need to learn fundamental protein separation methods and techniques. In the case of systems-level analysis of biological processes there is a pressing need for an integrative approach that encompasses proteomics, genomics and bioinformatics. For these reasons, JPB will cover, but not be limited to, these multidisciplinary themes. In addition to monthly publications, JPB is planning to release 'special issues' and conference proceedings. The first of these Special Issue, to be published May 2008, will be devoted to the 95th Indian science Congress-Bioinformatics section; Guest Editor- Prof. Allam Appa Rao-Chair of Bioinformatics Section and Principal/President of Andhra University College of Engineering). Fellow Members of the JPB Executive Editorial Board include Helmut Meyer (Bochum, Germany), Sudhir Srivastava (NCI, Bethesda, USA), Kazuyuki Nakamura (Yamaguchi Univ., Japan) Ruth van Bogelen (Pfizer) and we are joined by the following Board Members – Judit Nagy (Imperial College of London, UK), Terence Poon (Chinese Univ. of Hong Kong, Hong Kong), Roman Zubarev (Uppsala Univ., Sweden), Richard Smith (Pacific Northwest National Laboratory, Washington, USA), Ho Jeong Kwon (Yonsei University, Korea), Mario Genero (Austral Univ. Argentina), Denong Wang (Stanford Uni., USA), Cathy Wu (Georgetown Univ. Washington, USA), Anil Kimar (Devi Ahilya Univ., Madhya Pradesh, India), Thomas Conrads (Univ. Pittsburgh, USA), Young Mok Park (KBRI, Korea), Babu Purkayastha (Applied Biosystems, Framingham, USA) Mark S. Baker (Australian Proteome Analysis Facility, Macquarie University), David Fenyo (The Rockefeller University, New York), Veera V R Bandaru, (Johns Hopkins University), Phan Van Chi (Protein Biochemistry Laboratory and Proteomics Unit, Hanoi), Laura Beretta (Fred Hutchinson Cancer Research Center) and Srinubabu Gedela (Andhra University)

I hope that you will enjoy the first issue of our new journal. The first paper by Christian Stephan etal, briefly describes about HUPO (Human proteome organization) focusing on HUPO brain proteome project. Next paper a review of the HUPO Proteomics Standards Initiative by Sandra Orchard and Henning Hermjakob, describes the activities of this group over the past 6 years that have culminated in the design and implementation of common data reporting and exchange of standards that enable the transfer of proteomics data from originator to collaborator to a final public repository. A paper by Michael Kohl and colleagues present a software solution for calculating unique peptide sequences for the unambiguous MS-based identification of highly homologous proteins. Implementing a bioinformatics analysis of Alzheimer's disease, Allam Rao and colleagues describe the use of functional protein sequences to study the underlying molecular mechanisms of this disease. Interestingly, their study suggests the possibility that genetic components are more important in Alzheimer's disease compared to environmental, metabolic, and age-related factors. Historically, blood has been considered the 'window of disease'. In a short communication, Tran Thanh and colleagues report the use of proteomics strategy based on ConA affinity capture / 2-DE/ nanoLC-MS/MS to compare serum glycoproteins between healthy and lung cancer patients. Their findings demonstrate the usefulness of proteomics for discovering potential biomarkers for lung cancer. Although 2-DE has been one of the stalwart techniques in proteomics, historically it has been very difficult to compare 2-DE gels. To this end, the first issue of JPB describes a webserver for the analysis and comparison of 2-DE gels (Amit Kush and G. Raghava); this webserver allows searching of gels from their database (3,500 well-annotated 2-DE gel images obtained from public databases and literature) by keywords.

We hope that those working in the area of proteomics and bioinformatics will now choose the Journal of Proteomics and Bioinformatics as the premier open access place in which to publish the results of their research and for keeping abreast of developments in the field. We look forward to receiving your manuscripts on-line at http://www.omicsonline.com

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