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Association of Biomolecular Resource Facilities
Proteome Informatics Research Group (iPRG)

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Re: iPRG-2011: Proteome Informatics Research Group Study:
Identification of Electron Transfer Dissociation (ETD) Mass Spectra

Dear Fellow ABRF Member,

The field of mass spectrometry based proteomics has seen several key innovations over the last several years, including novel experimental methods, new instruments, and unique fragmentation strategies. The latter, in the form of electron capture dissociation (ECD) and electron transfer dissociation (ETD) have captured the imaginations of many researchers, expanding their ability to identify and analyze peptides and proteins. However, since ECD/ETD spectra differ substantial from more traditional collision induced dissociation (CID) spectra in both their prominent ion series as well as their preferred bond-breaking characteristics, the (automatic) interpretation of ECD/ETD spectra requires novel algorithm optimizations. Efficient identification of ECD/ETD spectra thus remains an active and exciting field of proteomics informatics research.

The Proteome Informatics Research Group (iPRG) of the Association of Biomolecular Resource Facilities (ABRF) invites you to participate in a collaborative data analysis study focusing on the evaluation of proteomics laboratories in identifying electron transfer dissociation (ETD) spectra. In this study, an LC-MS/MS dataset from a yeast lysate digested with Lys-C and enriched for highly charged peptides using strong cation exchange fractionation will be provided. This study will enable participants to evaluate their data analysis capabilities and approaches relative to others in analyzing a common data set.

Laboratories that request permission to participate will receive detailed instructions and passwords to access the mass spectral data in several formats, a reference FASTA formatted protein sequence database, a suitable peptide mass spectral library, and a template for reporting study results. The iPRG also requests that along with a final list of identified spectra, participants complete a web-based questionnaire summarizing the methods they used. Importantly, the iPRG possesses data from additional LC-MS/MS runs of the study samples and neighboring SCX fractions that were collected using CID and HCD. These runs will be released to participants upon study completion as a resource for further algorithm development.

The iPRG anticipates distributing study materials in mid October 2010, and requests that the results be returned by **Friday, December 10, 2010**, to enable sufficient time to analyze the results for presentation at the 2011 ABRF Meeting (**February 19-22, 2011** in San Antonio, TX). This year's study is open to both ABRF members and non-members. However, we do strongly encourage non-members to join, and thus help support ABRF (for more information visit http://www.abrf.org).

Requests to participate must be submitted by e-mail to iPRG2011@gmail.com prior to **Friday, November 26, 2010**. Please include the words "**iPRG Study 2011 request**" in the subject line. As in previous ABRF studies, submissions will be coded to ensure anonymity of the participating laboratories. A summary of the results of this study will be presented orally and as a poster at the ABRF 2011

meeting, subsequently posted on the ABRF website, and published in a peer reviewed journal.

We thank you for your support of the ABRF and look forward to your participation in this year's study.

Sincerely,

The ABRF Proteome Informatics Research Group (iPRG)

Lennart Martens (Chair) - Ghent University and VIB
Manor Askenazi - Dana-Farber Cancer Institute
Nuno Bandeira - UCSD
Robert Chalkley - UCSF
Karl Clauser - Broad Institute of MIT and Harvard
Eric Deutsch - Institute for Systems Biology
W. Hayes McDonald - Vanderbilt University
Paul A Rudnick - NIST
Thomas Neubert (EB Liaison) - New York University