



Association of Biomolecular Resource Facilities

Business Office:

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Re: iPRG-2010: Proteome Informatics Research Group Study - Phosphopeptide Identification

Dear Fellow ABRF Member,

Many LC-MS/MS based phosphoproteomic studies are entering the literature which report thousands of phosphopeptide identifications accompanied by both precisely and ambiguously localized phosphorylation sites. Since each peptide is often the only peptide observed for a particular protein, both confident identification of the peptide and accurate localization of the site(s) of phosphorylation to particular Ser, Thr, Tyr, or His residues is one of the major challenges in proteome informatics.

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 phosphopeptides and localizing the phosphorylation sites. In this study, an LC-MS/MS dataset from a lysate digested with trypsin and enriched for phosphopeptides using strong cation exchange fractionation followed by immobilized metal affinity chromatography (SCX/IMAC) 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, and a template for reporting study results. The iPRG also requests that along with a final list of identified peptides and localized phosphorylation sites, participants complete a web-based questionnaire summarizing the methods they used.

The iPRG anticipates distributing study materials in mid November 2009, and requests that the results be returned by **Monday, January 11, 2010**, to enable sufficient time to analyze the results for presentation at the 2010 ABRF Meeting (**March 20-23, 2010** in Sacramento, CA). This year's study is open to both ABRF members and non-members. However, the total number of participants may be limited, and priority will be given to ABRF members. Non-members are encouraged to join the ABRF (For more information visit <http://www.abrf.org>).

Requests to participate must be submitted by e-mail to iPRG2010@gmail.com prior to **Monday, November 30, 2009**. Please include the words "iPRG Study 2010 request" in the subject line and provide contact name and affiliation in the body of the message. Because of the significant effort that goes into the analyses conducted by the iPRG, the research group asks that requests to participate only be sent if there is a reasonable probability you will be able to complete the study by the deadline. As in previous ABRF studies, submissions will be coded to insure anonymity of the participating laboratories. A summary of the results of this study will be presented orally and as a poster at the ABRF 2010 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)

Paul A Rudnick (Chair) - NIST
Manor Askenazi - Dana-Farber Cancer Institute
Conrad Bessant - Cranfield University
Karl Clauser - Broad Institute of MIT and Harvard
Jayson Falkner – Single Organism Software, Inc.
William S. Lane - Harvard University

Lennart Martens - EMBL-EBI
W. Hayes McDonald - Vanderbilt University
Karen Meyer-Arendt - University of Colorado, Boulder
Brian C. Searle - Proteome Software Inc.
Jeffrey A Kowalak (EB Liaison) - NIMH