

September 25, 2006

Dear Fellow ABRF Member,

Phosphorylation of proteins on serine, threonine, and tyrosine residues is among the most important of the posttranslational modifications, playing a critical role in regulating many cellular processes. Proteomics laboratories that are called upon to determine the sites of phosphorylation have numerous strategies available to carry out phosphoprotein analysis, yet may still find such analyses a formidable challenge. Successful analysis requires that techniques in the laboratory be optimized with phosphorylated protein standards resembling as closely as possible the samples to be analyzed. A clear need exists for a reasonably complex phosphorylated protein mixture to serve as a reference standard.

The Proteomics Standards Research Group (sPRG) of the Association of Biomolecular Resource Facilities (ABRF) would like you to participate in a collaborative study focusing on the ability of core facilities to determine the identities and phosphorylation sites of multiple proteins present in a single sample.

The primary goals of this study are to provide each participating laboratory with an opportunity to evaluate its capabilities and approaches with regard to:

- Methods used to identify proteins
- Methods used for phosphoprotein and phosphopeptide enrichment
- Methods used for phosphorylation site identification

Most importantly, this study represents the first step in developing a phosphoprotein standard more closely resembling a real life sample. Laboratories requesting samples will receive a mixture containing up to 10 proteins, some of which will contain one or more phosphorylated residues. The proteins will be present in sufficient amounts, at a minimum of 5 pmoles each, to utilize a wide variety of strategies. Participants will be asked to complete an on-line survey and submit data supporting identification of phosphorylation sites.

This year's study is again open to both ABRF members and non-members. However, the total number of samples is limited, and priority will be given to ABRF members. All labs, including vendor-sponsors, should only request one sample per lab. Non-members are encouraged to join the ABRF (for more information, go to <http://www.abrf.org>).

The sPRG anticipates distributing the samples on November 15, 2006 and requests the resulting data to be returned by December 31, 2006 so that sufficient time will be available to tabulate the results and present them at the 2007 ABRF Meeting (March 31-April 3, Tampa, FL).

Requests for samples must be submitted by e-mail to mag4@columbia.edu **prior to Oct. 31**. Please include the words "sample request" in the subject line and provide contact name, affiliation, and complete mailing address in the body of the message. To reiterate, because of limited availability and the significant effort that goes into the preparation of the samples by the sPRG, the research group asks that samples only be requested if there is a reasonable probability

you will be able to return data by the deadline. As in the past, result 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 '06 meeting, subsequently posted on the ABRF website, and ultimately published in the Journal of Biomolecular Techniques.

We thank you for your support of the ABRF. We look forward to your participation in this study and your help in producing a community standard.

Sincerely,

The ABRF Proteomics Standards Research Group

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