



**Association of Biomolecular
Resource Facilities**
Proteomic Standards Research Group
<http://www.abrf.org/sPRG>

October 21, 2008

Dear Colleague:

An emerging request of proteomics laboratories is relative or absolute quantification of known proteins. Because laboratories that do not have experience in quantification of proteins have no objective way of ascertaining their level of performance, especially relative to laboratories with extensive experience, a clear need exists for a well-defined mixture of proteins to serve as a reference standard. To address this need, the Proteomics Standards Research Group (sPRG) of the Association of Biomolecular Resource Facilities (ABRF) has developed a prototype standard consisting of a digest of a mixture of known proteins and selected stable isotope labeled synthetic peptides that will serve as internal standards.

The sPRG invites you to participate in this collaborative study that focuses on evaluating the ability of proteomics laboratories to determine the quantities of several proteins in a digest. Participation in this study will provide each laboratory with an opportunity to assess its capabilities with regard to:

- Methodologies for protein quantification by mass spectrometry
- Bioinformatics for data analysis

An additional goal of this study is to evaluate this protein mixture as the first step in the development of a quantitative analysis protein standard that can be used by the proteomics community.

A Laboratory requesting a study sample will receive a mixture of 3–6 proteins that have been digested with Trypsin and a mixture of known quantities of 3–5 stable isotope labeled, synthetic peptide analogs corresponding to each protein. Participants will be asked to determine the quantity of each protein present in the mixture based on comparison to the corresponding peptides. There will be sufficient material to perform multiple analyses.

The sPRG requests that along with the final list of quantities of identified proteins, participants complete a web-based questionnaire that summarizes the results obtained and the methods used. The sPRG also encourages submission of raw data files so that they can be available for future bioinformatics studies.

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. Non-members are encouraged to join the ABRF. For more information, go to <http://www.abrf.org>

The sPRG anticipates distributing the samples in the second week of November 2008 and requests that the results be returned by December 12, 2008 so that sufficient time will be available for presentation at the 2009 ABRF Meeting (February 7 – 10, 2009, Memphis, Tennessee).

Please submit your request for samples by e-mail to Dr. Jim Farmar at jfarmar@aecom.yu.edu (note the spelling) and include the following:

Subject line: "Sample request"
Message: Contact name
Affiliation
Complete mailing address

Because of the significant effort that goes into the preparation of the samples by the sPRG, we ask 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 '09 meeting and will be 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
David Arnott
Jim Farmar, Chair
Alexander Ivanov
Jeffrey Kowalak, ABRF Executive Board Liaison
William Lane
Karl Mechtler
Brett Phinney
Manfred Raida
Susan Weintraub