

October 31, 2007

Dear colleagues,

Please find enclosed the ABRF-2008 ESRG samples that you requested from the ABRF Edman Sequence Research Group. This is the 20th study in an annual series designed to aid laboratories in evaluating their abilities to obtain and interpret amino acid sequence data. This year, the test samples are three expressed proteins (named H, A, and C) blotted on PVDF membrane and stained with Coomassie Blue. For each protein you will receive two PVDF pieces containing approximately 25 pmol of protein. Depending on the sensitivity of your instrument you may load either one or two of the bands for one sequencing run. The ESRG recommends loading one band on the Procise cLc or 2 bands for the Procise HT.

The object of this year's study is to ascertain the difficulty of sequencing through an N-terminal His-tag and to still be able to determine a few amino acids of the protein sequence following the tag. The ESRG is asking all the participants to sequence a minimum of 17 residues for each sample. If it is not possible for you to sequence all three samples we ask that you give preference to samples H and A. Picomole amounts of each amino acid in each cycle are requested for this study. Preferably, all raw data should be submitted in electronic form as text files created directly from the sequencing software. On instruments connected to a Windows PC you can export the tabulated picomole raw data (open under "View", "Sequence Data") as text file (under "File", "Export"). On instruments connected to a Macintosh open the sequence data ("Analysis", "Show Sequence Data"), save the data as a text file ("File" menu select "Save As").

The ESRG is asking participants to return the raw data text files and the survey sheet by e-mail. You should have received an Excel file containing the survey sheet as attachment to the e-mailed confirmation of your sample request. If you did not receive the Excel file, or prefer a paper copy, please contact Brian Hampton (bhamp001@umaryland.edu) and he will resend it or fax you a paper copy. The files with the results should be e-mailed to Ms. Glenda Cowart (glenda.m.cowart@monsanto.com) as an attachment by December 1st, 2007. If you are returning paper copies of the survey sheet and/or raw data text files on a dos-formatted floppy disc, please mail to:

Glenda Cowart
Monsanto Co.
800 N. Lindbergh Blvd.
Mail Zone U4A
St. Louis, MO 63167, USA

In order to ensure anonymity, Glenda Cowart will remove all identifying marks prior to forwarding the data to the sequence committee for analysis. An e-mail will be sent to your facility with a three-digit code to allow you to evaluate your results as compared to others. The sequencing and survey results will be presented at ABRF 2008, February 09 - 12, 2008 in Salt Lake City, Utah, and will also help to guide future potential studies and tutorial sessions.

If your sample arrived damaged, if you have questions about the study or have problems saving the data please contact Brian Hampton at the above e-mail address. Equipment failures and "no data obtained" analyses are as important to us as data from "successful" runs. Please send us your results whatever happens. Thank you for your participation in this study!

The deadline for receiving data for inclusion in the study is December 1, 2007.

The Edman Sequencing Research Group:

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