

Editor  
ProteoMonitor

February 24, 2005

Re: 2/11/05 ProteoMonitor article on ABRF/PRG *de novo* peptide sequencing study

Dear Sir/Madam:

We, the authors of the Association of Biomolecular Resource Facilities Proteomics Research Group *de novo* peptide sequencing study presented at this year's ABRF meeting in Savannah, Georgia, consider the headline and sections of your article about our study in the February 11, 2005 issue of ProteoMonitor to be misleading as to the purpose and conclusions of the study. As we stated in our poster describing the study, "The purpose of this study was to evaluate the capabilities of core laboratories to determine the sequences of peptides not found in any published database." The main findings of our study relate to the difficulty of *de novo* peptide sequencing, the importance of high mass accuracy for obtaining good results, the benefit of using multiple approaches, and the shortcomings of current software. The study was not designed to compare different types of instruments as the headline of your article suggests. While our results showed some differences in the *de novo* sequencing results for different instrument types, we clearly noted that the number of each type of instrument was too small to draw conclusions and that we did not control for operator expertise. We respectfully request that you publish this letter in ProteoMonitor to provide your readers a more balanced view of our study.

Sincerely,

The ABRF Proteomics Research Group

Tom Neubert (Chair)

Arnie Falick

Jeff Kowalak

Bill Lane (EB Liaison)

Brett Phinney

Christoph Turck

Susan Weintraub

Karen West