Introduction
The Proteomics Research Group (PRG) of the AIBR® developed the 2009 study to assess approaches that individual laboratories would use to determine the relative abundance of target proteins in a complex mixture.

Objectives
The primary goals of this study are to document the breadth of approaches used by the proteomics community to determine the relative abundance of a target protein of interest.

Sample Preparation
Human plasma was obtained from Analytical Biological Services Inc. (Wilmington, DE). Human breast cancer antigen (PSA) was obtained from EUROPROF-Clonation GmbH (Glotting, Germany), chronic granulomatous disease (CGD), and glucogen phosphorylase (GYP) were obtained from Sigma-Aldrich (St. Louis, MO). Human apoB solutions were prepared as a concentration of 1 mg/mL in 50 mM Tris-HCl, pH 8. Study samples were prepared by spiking appropriate volumes of stock solutions to give target concentrations shown in Table 1 and aliquots were prepared with the volumes shown. The study samples were then lyophilized and shipped to the study participants for analysis. The participant key is shown in Table 2.

Lab methods used

Results and Conclusions

Discussion/Conclusions
Study samples were prepared as shown in Table 1 and distributed to 67 participants. The study participants were asked to determine the relative abundance of 4 proteins spiked into the samples and report their methods and results.

Acknowledgements
The primary authors would like to thank...

Table 2: Study participants