Matthew E. Monroe

Expertise

Dr. Monroe's research involves development of algorithms and software for custom and automated analysis of proteomics and bioinformatics data, including managing and summarizing the large volumes of data generated. His areas of expertise include microcolumn liquid chromatography, LC-MS/MS of peptides and proteins using Q-TOF mass spectrometry, and analytical instrumentation design and automation. Dr. Monroe has over 15 years of programming experience, specializing in software design using Visual Basic .NET, LabView, and relational databases including Microsoft SQL Server and Microsoft Access.

Education

Bachelor of Science in Chemistry, 1997
Doctorate of Philosophy in Analytical Chemistry, 2002

Positions and Honors

Positions and Employment

2003 – present	Sr. Research Scientist, PNNL, Richland, WA
2002 – 2003	Postdoctoral Associate, Pacific Northwest National Laboratory (PNNL), Richland, WA
1994 – 1997	Undergraduate Chemistry Research Assistant, University of Wyoming, Laramie, WY
1993 – 1997	Office Assistant, University of Wyoming, Laramie, WY

Honors and Awards

1997 – 1998	Francis P. Venable Fellowship
1996	R. Owen Asplund Award for Outstanding Academic Performance
1995 & 1996	Summer EPSCoR Fellowship Recipient
1994	College of A&S Independent Study Fellowship

Peer-reviewed publications

"Ultra-Sensitive, High Throughput and Quantitative Proteomics Measurements," J.M. Jacobs, **M.E. Monroe**, W. Qian, Y. Shen, G.A. Anderson, and R.D. Smith, *Intl. J. of Mass Spectrometry*, 240 (3), 195-212 (2005).

"Probability-Based Evaluation of Peptide and Protein Identifications from Tandem Mass Spectrometry and SEQUEST Analysis: The Human Proteome", W. Qian, T. Liu, **M. E. Monroe**, E. F. Strittmatter, J. M. Jacobs, L. J. Kangas, K. Petritis, D. G. Camp II, and R. D. Smith, *J. Proteome Research*, in press (2004).

"Comparative proteome analyses of human plasma following in vivo lipopolysaccharide administration using mass spectrometry," W. Qian, J. M. Jacobs, D. G. Camp II, **M. E. Monroe**,

R. J. Moore, M. A. Gritsenko, S. E. Calvano, S. F. Lowry, W. Xiao, L. L. Moldawer, R. W. Davis, R. G. Tompkins, and R. D. Smith, *Nat. Biotechnol.*, in press (2004).

"Identification of Proteins in Human Cytomegalovirus (HCMV) Particles: the HCMV Proteome", S.M. Varnum, D.N. Streblow, **M.E. Monroe**, P. Smith, K.J. Auberry, L. Pasa-Tolic, D. Wang, D.G Camp, K. Rodland, S. Wiley, W. Britt, T. Shenk, R.D. Smith, and J.A. Nelson. *Journal of Virology*, 78 (20), 10960-10966 (2004).

"Estimating Probabilities of Peptide Assignments to LC-FTICR-MS Observations.", K.K. Anderson, **M.E. Monroe**, and D.S. Daly. *Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'04)*, ed. Faramarz Valafar and Homayoun Valafar, pp. 151-156 (2004).

"Integrative analysis of the mitochondrial proteome in yeast," H. Prokisch, C. Scharfe, D. G. Camp II, W. Xiao, L. David, C. Andreoli, **M. E. Monroe**, R. J. Moore, M. A. Gritsenko, C. Kozany, K. K. Hixson, H. M. Mottaz, H. Zischka, M. Ueffing, Z. S. Herman, R. W. Davis, T. Meitinger, P. J. Oefner, R. D. Smith, and L. M. Steinmetz, *PLoS Biology*, 2 (6), 795-804 (2004).

"Multidimensional proteome analysis of human mammary epithelial cells," J. M. Jacobs, H. M. Mottaz, L. Yu, D. J. Anderson, R. J. Moore, W. U. Chen, K. J. Auberry, E. F. Strittmatter, **M. E. Monroe**, B. D. Thrall, D. G. Camp II, and R. D. Smith, *J. Proteome Res.*, 3 (1), 68-75 (2004).