CURRICULUM VITAE

Nathan C. VerBerkmoes
Staff Scientist

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Education:

Ph.D. in Life Science with focus on Genomic Sciences and Technology 2005.
University of Tennessee/Oak Ridge National Laboratory, Oak Ridge TN
Advisor: Dr. Robert L. Hettich and Dr. Frank Larimer
Ph.D. research emphasis: Proteomic analysis of microbes and microbial communities.

B.S. *cum laude*, Biochemistry and Cellular and Molecular Biology, 2001
University of Tennessee, Knoxville TN

Professional Experience:

1999-2000	Undergraduate research assistant, Yeast Genetics Lab of Dr. Jeffery Becker, University of Tennessee, Knoxville, TN
2000-2001	Undergraduate research assistant, Advisor: Dr. James L. Stephenson, Jr., Oak Ridge National Laboratory, Oak Ridge, TN
2001-2005	Graduate Student, Advisor: Dr. Robert L. Hettich and Dr. Frank Larimer, Oak Ridge National Laboratory, Oak Ridge, TN
2005-2006	Post-doctoral Associate, Dr. Robert L. Hettich, Oak Ridge National Laboratory, Oak Ridge, TN
2006-Present	Research Staff Member, Chemical Science Division, Oak Ridge National Laboratory, Oak Ridge, TN

Teaching Experience:

Spring 2003: Teaching Assistant for Life Sciences 521 Analytical Technologies in UT/ORNL GST graduate program.

Fall 2003: Teaching Assistant for Life Sciences 695 Introduction to Biological Mass Spectrometry in UT/ORNL GST graduate program.

Research Interest:

My research has focused on biological mass spectrometry and its applications in proteomics and structural biology. Specifically, I employ multi-dimensional liquid chromatography coupled with electrospray ion trap mass spectrometry for the analysis of purified proteins, protein complexes, and single/multi-species proteomes. The major focus of my research is the development and application of proteomics technologies to the understanding of microbial physiology through the analysis of whole proteomes or enriched protein complexes. The goal is to develop proteomic methodologies that allow for rapid data collection to gain greater insight into the physiology of the large number of microbes that are being sequenced and thus available for systems level studies. My research focus to date has been on those microbes that show promise for bioremediation and those involved in carbon sequestration. A recent goal is to develop proteome methodologies that will allow for the study of microbes and microbial communities directly from environmental samples.

Professional Memberships and Awards:

2001-Present: Member of the American Society for Mass Spectrometry

2001-Present: Member of the East Tennessee Mass Spectrometry Discussion Group

2003-Present: Member of the American Society for Microbiology

May 2004: Science Alliance Research Award, University of Tennessee, May 2004

August 2003: Awarded for travel and presentation at Sixth International Symposium on Mass Spectrometry in the Health and Life Sciences: Molecular and Cellular Proteomics. San Francisco, CA, Aug 24-28, 2003.

May 2002: Hollaender Fellowship, University of Tennessee, research fellowship for the 2002-2003 school year.

April 2002: Awarded for travel and presentation at Proteomics: The Next Grand Biological Challenge, Nashville, TN, May 19th-22nd, 2002.

January 2002: Selected for support by the Department of Energy Office of Science to attend the meeting of Nobel Laureates in Lindau, Germany, in July 2002.

January 2002: Received award from Cambridge Healthtech Institute for top poster presentation at Human Proteome Project Meeting 2002, San Diego, CA, January 9-11, 2002.

Publications:

1) Strader, M.B.; Smiley, R.D.; Stinnett, L.G.; **VerBerkmoes, N.C.;** and E.E. Howell. Role of S65, Q67, I68, Y69 residues in Homotetrameric R67 Dihydrofolate Reductase. *Biochemistry,* 2001; 40(38), 11344-11352.

2) Ding, F.A.; Schreiber, D.; **VerBerkmoes, N.C.;** Becker, J.M.; and F. Naider. The chain Length Dependence of Helix Formation of the Second Transmembrane Domain of the G Protein Coupled Receptor of Saccharomyces cerevisiae. *Journal of Biological Chemistry,* 2002, 277(17), 4483-92.

3) VerBerkmoes, N.C.; Strader, M.B.; Smiley, R.D.; Howell, E.E.; Hurst, G.B.; Hettich, R.L.; and J.L. Stephenson Jr. Intact protein analysis of Site Directed Mutagenesis Overexpression Products: Plasmid Encoded R67 Dihydrofolate Reductase. *Analytical Biochemistry,* 2002; 305(1), 68-81.

4) VerBerkmoes, N.C.; Bundy, J.L.; Hauser, L.; Asano, K.G.; Razumovskaya, J.; Larimer, F.W.; Hettich, R.L.; and J.L. Stephenson Jr. Integrating "Top-Down" and "Bottom-Up" Mass Spectrometric Approaches for Proteomic Analysis of *Shewanella oneidensis*. *Journal of Proteome Research,* 2002; 1(3), 239-252.

5) Naider, F.; Ding, F.A.; **VerBerkmoes, N.C.;** Arshava, B.; and J.M. Becker. Synthesis and Biophysical Characterization of a Multidomain Peptide from a *Saccharomyces cerevisiae* G Protein-coupled Receptor. *Journal of Biological Chemistry,* 2003, 278(52), 52537-52545.

6) Razumovskaya, J.; Olman, V.; Xu, D.; Uberbacher, E.; **VerBerkmoes, N.C.;** Hettich, R.L.; and Y. Xu. A computational method for assessing peptide-identification reliability in tandem mass spectrometry analysis with SEQUEST. *Proteomics,* 2004, 4, 961-969

7) VerBerkmoes, N.C.; Sharp, J.; and R.L. Hettich. Mass Spectrometry. Book Chapter in *Microbial Functional Genomics by J. Zhou, D.K. Thompson, Ying Xu, and James M. Tiedje,* 2004 John Wiley & Sons Inc.

8) Strader, M.B.; **VerBerkmoes, N.C.**; Tabb, D.L.; Connelly, H.M.; Barton, J.W.; Bruce, B.D.; Pelletier, D.A.; Davison, B.H.; Hettich, R.L.; Larimer, F.W.; and G.B. Hurst. Characterization of the 70S Ribosome from *Rhodopseudomonas palustris* using an Integrated "Top-Down" and "Bottom-Up" Mass Spectrometric Approach. *Journal of Proteome Research,* 2004, 3, 965-978.

9) Wan, X.; **VerBerkmoes, N.C.;** McCue, L.A.; Stanek, D.; Connelly, H.M.; Hauser, L.; Wu, L.; Liu, X.; Yan, T.; Leaphart, A.; Hettich, R.L.; Zhou, J.; Thompson D.K. Transcriptomic and Proteomic

Characterization of the Fur Modulon in the Metal-Reducing Bacterium *Shewanella oneidensis*. *Journal of Bacteriology*, 2004, 186, 8385-8400.

10) VerBerkmoes, N.C.; Connelly, H.M.; Pan, C. and R.L. Hettich, R.L. Mass Spectrometric Approaches to Characterizing Bacterial Proteomes. *Expert Review in Proteomics*, 1, 433-445.

11) Fridman, T.; Razumovskaya, J.; **VerBerkmoes, N.C.;** Hurst, G.B.; and Y. Xu. HyLa fast and accurate scoring algorithm for tandem spectra identification through database search. *Journal of bioinformatics and computational biology*, 2005, 3, 455-476.

12) VerBerkmoes, N.C.; Hervey, W.J.; Land, M.; Hauser, L.; Larimer, F.W.; Van Berkel, G.J.; and D.E. Goeringer. Evaluation of Shotgun Proteomics for Identification of Biological Threat Agents in Complex Environmental Matrices: Experimental Simulations. *Analytical Chemistry*, 2005, 77, 923-932.

13) Ram, R.J.; **VerBerkmoes, N.C.;** Thelen, M.P.; Tyson, G.W.; Shah, M.; Baker B.J.; Blake II, R.C.; Hettich, R.L.; and J.F. Banfield. Community proteomics of a natural microbial biofilm. *Science*, 2005, 308, 1915-1920.

14) Tabb, D.L.; Thompson M.R.; Khalsa-Moyers G.K.; **VerBerkmoes N.C**.; and W.H. McDonald. MS2Grouper: group assessment and synthetic replacement of duplicate proteomic tandem mass spectra. *Journal of Mass Spectrometry*, 2005, 16, 1250-1261.

15) Narasimhan C.; Tabb D.L.; **VerBerkmoes N.C**.; Thompson M.R.; Hettich R.L.; and Uberbacher E.C. MASPIC: intensity-based tandem mass spectrometry scoring scheme that improves peptide identification at high confidence. Anal Chem. 2005, 77(23), 7581-93.

16) Banfield, J.F.; **VerBerkmoes, N.C.;** Hettich R.L.; and M.P. Thelen. Proteogenomic approaches for the molecular characterization of natural microbial communities. *OMICS*. 2005, 9, 301-333.

17) VerBerkmoes, N.C.; Pelletier, D.; Lankford, P.; Tabb, D.L.; Shah, M.; Strader, M.B.; Hauser, L.; Fejes, A.P.; Davison, B.H.; Hurst, G. B.; Beatty, J.T.; Harwood, C.S.; Tabita, R.F; Hettich, R.L.; and F.W. Larimer. Determination and comparison of the baseline proteomes of the versatile microbe *Rhodopseudomonas palustris* under its major metabolic states. *Journal of Proteome Research.* 2006, 5, 287-298.

Selected Oral Presentations:

1) VerBerkmoes, N.C.; Larimer, F.W.; and R.L. Hettich. *LC-MS/MS methodologies for automated analysis of protein complexes and proteomes from bacteria.* MCF symposium and University of Minnesota Dept. Seminar, Minneapolis, MN, May 13th and 14th 2004, (Invited lectures)

2) VerBerkmoes, N.C.; Hervey, J.W.; Razumovskaya, J.; Land, M.K.; Hauser, L.; Larimer, F.W.; Van Berkel, G.J.; and D.E. Goeringer. *Experimental Simulations for Mass Spectrometry-Based Identification of Biological Threat Agents Within a Complex Mixture Via Shotgun Proteomic*. Mass Spectrometry in Homeland Security, September, 2003.

3) VerBerkmoes, N.C.; Larimer, F.W.; and R.L. Hettich. *Bacterial and plant proteome analysis by 1D and 2D LC-MS.* Bioanalysis Seminar, Los Angeles and San Diego, CA, December 12th and 13th, 2002. (Invited lecture)

4) VerBerkmoes, N.C.; Bundy, J.L.; Hauser, L.; Asano, K.G.; Razumovskaya, J.; Larimer, F.W.; Hettich, R.L.; and J.L. Stephenson Jr. *Proteome analysis of the metal reducing microbe Shewanella oneidensis MR-1.* Biovalley proteomics symposium, Basel, Switzerland, June 14th, 2002. (Invited lecture)

5) VerBerkmoes, N.C.; Bundy, J.L.; Hauser, L.; Asano, K.G.; Razumovskaya, J.; Larimer, F.W.; Hettich, R.L.; and J.L. Stephenson Jr. *Proteome analysis of the metal reducing microbe Shewanella oneidensis MR-1.* 50th ASMS Conference on Mass Spectrometry and Allied Topics, Orlando, FL, June 2-6, 2002.