

# David B. Friedman, Ph.D.

## **ABRF functions**

member since 2006

Executive Board, term ending 2014

Proteomics Satellite Workshop co-organizer (ABRF2009, 2010)

Annual meeting co-Organizer ABRF2011, 2012

Proteomics Research Group, 2007 – 2010 (chair 2009 – 2010)

Membership Committee, 2009 - present

Corporate Relations Committee, 2010-present

Proteomics Standards Research Group, 2010-present

Webpage facelift subcommittee, 2010-2011



## **Affiliations**

Research Associate Professor of Biochemistry, Mass Spectrometry Research Center, Vanderbilt University  
co-Associate Director, Proteomics Laboratory, Mass Spectrometry Research Center, Vanderbilt University.

Vanderbilt Ingram Cancer Center

Association of Biomolecular Resource Facilities

American Society for Mass Spectrometry

## **A Brief History of David's Research**

I studied genetics and aging in nematode worms while working towards my B.S. degree at the University of California, Irvine, in 1987. I received my Ph.D. in yeast genetics at the University of Washington, Seattle, in 1993 (during which I also met my wife; we now have three beautiful children ages 15, 12 and 6). I continued in Seattle studying cell-cycle regulation of a centrosome phosphoprotein, which led me to lc/ms-based and 2Dgel/ms-based proteomic strategies in Boulder, Colorado. In early 2000 I joined the faculty at University of Colorado Health Sciences Center, and then moved to Vanderbilt in 2001 to help establish the Proteomics Laboratory with Richard Caprioli in the Mass Spectrometry Research Center at Vanderbilt University. Over the past 10 years this facility has grown to provide the complementary technologies of lc/ms-based and gel-based proteomics, as well as characterization and mapping of sites of post-translational modification and targeted proteomics strategies.

I am privileged to be working with an outstanding staff of fellow Associate Directors, Senior Scientists, Research Assistants and my other colleagues in the Mass Spectrometry Research Center to bring these technical resources to the Vanderbilt community. These include sensitive and rapid protein identification technologies using single- and multi-dimensional HPLC peptide separations coupled directly to tandem mass spectrometry (ESI-LTQ, LTQ-Orbitrap, Velos Orbitrap ETD, Thermo Scientific), as well as MALDI-TOF/TOF mass spectrometry (Applied Biosystems). These instruments are also used to characterize and map sites of post-translational modification, as well as mapping of stable domains of proteins for subsequent structural analysis (NMR, X-ray crystallography). Targeted proteomics using multiple reaction monitoring is performed on a UPLC-equipped triple quadrupole mass spectrometer (NanoAcquity, Waters; Vantage, Thermo Scientific). For 2Dgel-based proteomics we specialize in the multiplexing Difference Gel Electrophoresis (DIGE) platform which allows for independent (biological) replicates from multiple conditions to be quantitatively analyzed across a series of gels that are all coordinated by a sample-based internal standard.

## **Selected Publications**

- Friedman, Andacht, Bunger, Chien, Hawke, Krijgsveld, Lane, Lilley, Maccoss, Moritz, Settlage, Sherman, Weintraub, Witkowska, Yates, Turck, 2011 "The ABRF Proteomics Research Group Studies: Educational exercises for qualitative and quantitative proteomic analyses." *Proteomics*. 2011 Mar 3. doi: 10.1002/pmic.201000736. PMID:21394914.
- Franco, Friedman, Krishna, Kendall, Israel, Backert, and Peek, 2009 "Delineation of a Carcinogenic *Helicobacter pylori* Proteome" *Mol Cell Proteomics*, 8(8):1947-1958.
- Friedman DB, Hoving S, Westermeier R, 2009 "Isoelectric focusing and two-dimensional gel electrophoresis". 2009 *Methods Enzymol*. 463:515-40. Review. PMID: 19892190
- Friedman DB and KS Lilley, 2009 "Difference Gel Electrophoresis (DIGE)". In: *The Protein Protocols Handbook 3rd edition* (J. Walker, ed), The Humana Press/Springer.
- Friedman, Wang, Whitwell, Caprioli, Arteaga, 2007 "Multi-variable Difference Gel Electrophoresis and Mass Spectrometry: A Case Study on TGF-beta and ErbB2 signaling". *Mol Cell Proteomics*, 6(1):150-169.
- Friedman, Hill, Keller, Merchant, Levy, Coffey, and Caprioli, 2004 "Proteome Analysis of Human Colon Cancer by 2 Dimensional Difference Gel Electrophoresis and Mass Spectrometry", *Proteomics* 4(3), 793-811.
- Friedman, Kern, Huneycutt, Vinh, Crawford, Steiner, Scheiltz, Yates III, Resing, Ahn, Winey, and Davis, 2001. "Yeast Mps1p Phosphorylates the Spindle Pole Component Spc110p in the N-Terminal Domain." *J Biol. Chem.* 276(21): 17958-17967.