

Paul A. Rudnick, Ph.D.

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Guest Researcher, Mass Spectrometry Data Center, NIST, Gaithersburg, MD, USA
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SUMMARY

I am a partner in a small research and development firm located in the Seattle, Washington area. We produce reference data and provide advanced informatics services in the area of biological mass spectrometry to customers in industry, academia, and the federal government. I have been in the field of proteome informatics for more than thirteen years, seven of which were spent at the National Institute of Standards and Technology (NIST), where I co-developed the first ever set of QC metrics for monitoring variability in proteomics workflows. This work was done by interagency agreement between NIST and NCI and has continued by contract (2006-current.) As a part of this effort, I also designed and managed the Common Data Analysis Pipeline (CDAP) for the Clinical Proteomics Tumor Analysis Consortium (CPTAC) program. My personal research interests are in understanding how translated genetic mutations can be leveraged to target cancer and other inheritable diseases. I am also interested in how techniques like machine learning can be used to mine aggregated proteomics data resources.

PROFESSIONAL EXPERIENCE

08/2013-current

President / Co-founder
Spectragen Informatics LLC, Bainbridge Island, WA

- Advanced mass informatics research: search algorithms, pipelines, data integration
- Software and reference data development
- Consulting and contract work (NIH/National Cancer Institute, and private industry)

08/2013-current

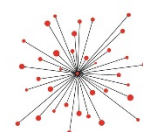
Guest Researcher
NIST, Mass Spectrometry Data Center, Gaithersburg, MD

- Collaborative interactions in the area of MS data analysis

07/2006-07/2013

Proteomics Team Leader, Biologist, ZP-IV (GS-14 equivalent)
NIST, Mass Spectrometry Data Center, Gaithersburg, MD

- Project lead: Development and distribution of peptide tandem mass spectral libraries (<http://peptide.nist.gov>)
- Project lead: NIH/NCI-CPTAC Common Data Analysis Pipeline for discovery cancer sample analyses, label-free and iTRAQ (<http://proteomics.cancer.gov/>)
- Project lead: Development of web-based reference data resources for NIST's Standard Reference Materials (SRM) program in complex biological materials (http://srm1950.nist.gov/srm_search.php)
- Studies on the analytical variability of LC-MS/MS-based proteomics; interagency agreement with NIH/NCI - Clinical Proteomics Technology Assessment for Cancer (CPTAC)



SPECTRAGEN
INFORMATICS



Paul A. Rudnick, Ph.D.

11/2003-07/2006

Director of Bioinformatics

Calibrant Biosystems, Inc., Gaithersburg, MD

- Proteome informatics group leader
- Maintained and extended company IT infrastructure
- Development of a custom LIMS
- Development of LC-MS/MS data analysis pipelines and storage systems
- Combining gene array data with spectral count LC-MS/MS data for surveying differential expression in tissues and fluids
- Principal investigator for awarded small business grants (SBIR/STTR)
- Established outside collaborations with academic and industry researchers
- Negotiated vendor contracts for all computer hardware and software

04/2002-9/2003

Bioinformatics Programmer Analyst II

National Cancer Institute (SAIC-Frederick), Frederick, MD

- *Ad hoc* bioinformatics consultant and programmer for NCI investigators and staff
- Developed and maintained DNA sequence analysis pipelines
- Programmed and extended genome browsers

12/2000-4/2002

Post-doctoral Research Associate

Department of Plant Pathology, The University of Arizona, Tucson, AZ

- Bacterial genome project: *Azotobacter vinelandii*
- Organized and led *Azotobacter* community-wide annotation meeting
- Dissection of signal transduction cascades involved in nitrogen-signaling using forward and reverse genetic strategies

EDUCATION

05/2001

Ph.D. The University of Arizona, Tucson, AZ

Thesis: Nitrogen Signaling in *Azotobacter vinelandii*

Advisor: Prof. Christina Kennedy

Major: Plant Pathology and Microbiology Minor: Molecular and Cellular Biology

07/1999

Cold Spring Harbor, Advanced Bacterial Genetics Course, Selected attendee

07/97-02/1998

Awarded Graduate Fellowship: Chateaubriand, French Mission for Science and Technology, "Molecular Biology of Nitrogen Signaling in Rhizobia", Toulouse, France

06/1996

Ohio State University, Microbial Physiology Course, Selected attendee

05/1995

B.S. The University of Arizona, Tucson, AZ Major:

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Molecular and Cellular Biology Minor:
Math/Chemistry/Physics

SOCIETIES, ORGANIZATIONS AND WORKING GROUPS

AAAS
ASMS
ABRF Proteome Informatics Research Group (iPRG) (2008-2011)
 Chair ABRF iPRG (2010)
ABRF sPRG (2011-current)
CPTAC Bioinformatics WG
CPTAC Unbiased Discovery WG
HUPO
HUPO-PSI
NIST Building the Next Generation (leadership training 2010-2011)

PEER REVIEW

Journals

Analytical Chemistry
Analytical and Bioanalytical Chemistry Journal of
Proteome Research Molecular and Cellular
Proteomics Nature Methods
Nature Biotechnology
Nucleic Acids Research Proteomics
Rapid Communications in Mass Spectrometry

Grant Panels

07/2017 NIH/CSR Computational, Modeling, and Biodata Management (IMST 14)
06/2016 NIH/NCI/CPTAC Proteogenomic Data Analysis Centers
08/2011 NIH/CPTC Data Centers
06/2007 NIAID/NIH Bioinformatics, *ad hoc* grant review panelist 05/2005 NSF
Microbial Genomics, *ad hoc* grant review panelist
01/2004 NIAID/NIH Proteomics Data Center, *ad hoc* grant review panelist

INVITED TALKS

05/2017 (Sydney, Australia) "NCI's CPTAC Program: 10 years of Collaborative Investigations in Cancer Proteomics", Children's Medical Research Institute, ProCan, NSW
12/2012 (Ghent, Belgium) "Peptide Mass Spectral Libraries: Modern Application of an Old Technique"
06/2012 (Vienna, Austria) "SRM/D: A Qualitative and Quantitative Data Resource for Complex Biological SRMs at NIST"
06/2011 ASMS (Denver, CO) "Identification and Normalization of Systematic Biases Affecting Ion Current Measurements in 'Label-Free' Proteomics Data"
05/2011 NIH-MSIG (Bethesda, MD) "Identification and Normalization of Systematic Biases Affecting Ion Current Measurements in 'Label-Free' Proteomics Data"
03/2011 RECOMB-CP (San Diego, CA) "Systematic Biases Affecting Peptide Intensities in Shotgun Proteomics" (Flash talk)
6/2010 ASMS (Salt Lake City, UT) "ABRF iPRG2010: Informatic Evaluation of Phosphopeptide Identification and Phosphosite Localization Results From Multiple Proteomics Laboratories" (PTM workshop)
02/2009 USHUPO (San Diego, CA) "Building Performance Metrics Into a Proteomics Software Pipeline"

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10/2008 NERLSCD (Burlington, VT) " Using Mass Spectral Libraries for Proteomics: Old Method, New Application"

02/2008 ABRF (Salt Lake City, UT) "Combining MS/MS Sequence and Spectral Library Search Algorithms"

01/2008 Harvard Medical School, Department of Cell Biology, (Boston, MA) "Combining MS/MS Sequence and Spectral Library Search Algorithms"

09/2007 Mass Spectrometry Interest Group (NCI-Frederick, Frederick, MD) "NIST Reference Libraries of Peptide Tandem Mass Spectra: 2007"

SELECTED PUBLICATIONS ([Google Scholar](#))

1. Mertins P, Mani DR, Ruggles KV, Gillette MA, Clauser KR, Wang P, Wang X, Qiao JW, Cao S, Petralia F, Kawaler E, Mundt F, Krug K, Tu Z, Lei JT, Gatza ML, Wilkerson M, Perou CM, Yellapantula V, Huang KL, Lin C, McLellan MD, Yan P, Davies SR, Townsend RR, Skates SJ, Wang J, Zhang B, Kinsinger CR, Mesri M, Rodriguez H, Ding L, Paulovich AG, Fenyö D, Ellis MJ, Carr SA; NCI CPTAC. "Proteogenomics connects somatic mutations to signalling in breast cancer." *Nature*. 2016 Jun 2;534(7605):55-62.
2. Rudnick PA, Markey SP, Roth J, Mirokhin Y, Yan X, Tchekhovskoi DV, Edwards NJ, Thangudu RR, Ketchum KA, Kinsinger CR, Mesri M, Rodriguez H, Stein SE. "A Description of the Clinical Proteomic Tumor Analysis Consortium (CPTAC) Common Data Analysis Pipeline." *J Proteome Res*. 2016 Mar 4;15(3):1023-32
3. Abbatiello SE, Schilling B, Mani DR, Zimmerman LJ, Hall SC, MacLean B, Albertolle M, Allen S, Burgess M, Cusack MP, Gosh M, Hedrick V, Held JM, Inerowicz HD, Jackson A, Keshishian H, Kinsinger CR, Lyssand J, Makowski L, Mesri M, Rodriguez H, Rudnick P, Sadowski P, Sedransk N, Shaddox K, Skates SJ, Kuhn E, Smith D, Whiteaker JR, Whitwell C, Zhang S, Borchers CH, Fisher SJ, Gibson BW, Liebler DC, MacCoss MJ, Neubert TA, Paulovich AG, Regnier FE, Tempst P, Carr SA. Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. *Mol Cell Proteomics*. 2015 Sep;14(9):2357-74.
4. Zhang B, Wang J, Wang X, Zhu J, Liu Q, Shi Z, Chambers MC, Zimmerman LJ, Shaddox KF, Kim S, Davies SR, Wang S, Wang P, Kinsinger CR, Rivers RC, Rodriguez H, Townsend RR, Ellis MJ, Carr SA, Tabb DL, Coffey RJ, Slebos RJ, Liebler DC; NCI CPTAC. "Proteogenomic characterization of human colon and rectal cancer." *Nature*. 2014 Sep 18;513(7518):382-7.
5. Rudnick PA. "MRM as a discovery tool?" *Proteomics*. 2015 Apr;15(7):1194-5.
6. Dong Q, Yan X, Kilpatrick LE, Liang Y, Mirokhin YA, Roth JS, Rudnick PA, Stein SE. "Tandem mass spectral libraries of peptides in digests of individual proteins: Human Serum Albumin (HSA)." *Mol Cell Proteomics*. 2014 May;13(5):1341-51.
7. Rudnick PA, Wang X, Yan X, Sedransk N, Stein SE. "Improved normalization of systematic biases affecting ion current measurements in label-free proteomics data." *Mol Cell Proteomics*. 2014 May;13(5):1341-51.
8. Simón-Manso Y, Lowenthal MS, Kilpatrick LE, Sampson ML, Telu KH, Rudnick PA, Mallard WG, Bearden DW, Schock TB, Tchekhovskoi DV, Blonder N, Yan X, Liang Y, Zheng Y, Wallace WE, Neta P, Phinney KW, Remaley AT, Stein SE. Metabolite Profiling of a NIST Standard Reference Material for Human Plasma (SRM 1950): GC-MS, LC-MS, NMR, and Clinical Laboratory Analyses, Libraries, and Web-Based Resources. *Anal Chem*. 2013 Dec 17;85(24):11725-31. doi: 10.1021/ac402503m. Epub 2013 Dec 3. PubMed PMID: 24147600.
9. Rudnick PA. Refining spectral library searching. *Proteomics*. 2013 Nov;13(22):3247-50. doi: 10.1002/pmic.201300426. PubMed PMID: 24123856.
10. Walmsley SJ, Rudnick PA, Liang Y, Dong Q, Stein SE, Nesvizhskii AI. Comprehensive analysis of protein digestion using six trypsin reveals the origin of trypsin as a significant source of variability in proteomics. *J Proteome Res*. 2013 Dec 6;12(12):5666-80. doi: 10.1021/pr400611h. Epub 2013 Nov 14. PubMed PMID:24116745.
11. Ivanov AR, Colangelo CM, Dufresne CP, Friedman DB, Lilley KS, Mechtler K, Phinney BS, Rose KL, Rudnick PA, Searle BC, Shaffer SA, Weintraub ST. Interlaboratory studies and initiatives developing standards for proteomics. *Proteomics*. 2013 Mar;13(6):904-9.
12. Lowenthal MS, Phillips MM, Rimmer CA, Rudnick PA, Simón-Manso Y, Stein SE, Tchekhovskoi D, Phinney KW. Developing qualitative LC-MS methods for characterization of Vaccinium berry Standard Reference Materials. *Anal Bioanal Chem*. 2012 Sep 2.
13. Tu C, Rudnick PA, Martinez MY, Cheek KL, Stein SE, Slebos RJ, Liebler DC. Depletion of abundant plasma proteins and limitations of plasma proteomics. *J Proteome Res*. 2010 Oct 1;9(10):4982-91.
14. Johann DJ Jr, Wei BR, Prieto DA, Chan KC, Ye X, Valera VA, Simpson RM, Rudnick PA, Xiao Z, Issaq HJ, Linehan WM, Stein SE, Veenstra TD, Blonder J. "Combined blood/tissue analysis for cancer biomarker discovery: application to renal cell carcinoma." *Anal Chem*. 2010 Mar 1;82(5):1584-8.
15. Tabb DL, Vega-Montoto L, Rudnick PA, Variyath AM, Ham AJ, Bunk DM, Kilpatrick LE, Billheimer DD, Blackman RK, Cardasis HL, Carr SA, Clauser KR, Jaffe JD, Kowalski KA, Neubert TA, Regnier FE, Schilling B, Tegeler TJ, Wang M, Wang P, Whiteaker JR, Zimmerman LJ, Fisher SJ, Gibson BW, Kinsinger CR, Mesri M, Rodriguez H, Stein SE, Tempst P, Paulovich AG, Liebler DC, Spiegelman C. Repeatability and reproducibility in proteomic identifications by liquid chromatography-

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- tandem mass spectrometry. *J Proteome Res.* 2010 Feb 5;9(2):761-76.
16. Paulovich AG, Billheimer D, Ham AJ, Vega-Montoto L, Rudnick PA, Tabb DL, Wang P, Blackman RK, Bunk DM, Cardasis HL, Clauser KR, Kinsinger CR, Schilling B, Tegeler TJ, Variyath AM, Wang M, Whiteaker JR, Zimmerman LJ, Fenyo D, Carr SA, Fisher SJ, Gibson BW, Mesri M, Neubert TA, Regnier FE, Rodriguez H, Spiegelman C, Stein SE, Tempst P, Liebler DC. Interlaboratory study characterizing a yeast performance standard for benchmarking LC-MS platform performance. *Mol Cell Proteomics.* 2010 Feb;9(2):242-54.
 17. Rudnick PA, Clauser KR, Kilpatrick LE, Tchekhovskoi DV, Neta P, Blonder N, Billheimer DD, Blackman RK, Bunk DM, Cardasis HL, Ham AJ, Jaffe JD, Kinsinger CR, Mesri M, Neubert TA, Schilling B, Tabb DL, Tegeler TJ, Vega-Montoto L, Variyath AM, Wang M, Wang P, Whiteaker JR, Zimmerman LJ, Carr SA, Fisher SJ, Gibson BW, Paulovich AG, Regnier FE, Rodriguez H, Spiegelman C, Tempst P, Liebler DC, Stein SE. Performance metrics for liquid chromatography-tandem mass spectrometry systems in proteomics analyses. *Mol Cell Proteomics.* 2010 Feb;9(2):225-41.
 18. Addona TA, Abbatiello SE, Schilling B, Skates SJ, Mani DR, Bunk DM, Spiegelman CH, Zimmerman LJ, Ham AJ, Keshishian H, Hall SC, Allen S, Blackman RK, Borchers CH, Buck C, Cardasis HL, Cusack MP, Dodder NG, Gibson BW, Held JM, Hiltke T, Jackson A, Johansen EB, Kinsinger CR, Li J, Mesri M, Neubert TA, Niles RK, Pulsipher TC, Ransohoff D, Rodriguez H, Rudnick PA, Smith D, Tabb DL, Tegeler TJ, Variyath AM, Vega-Montoto LJ, Wahlander A, Waldemarson S, Wang M, Whiteaker JR, Zhao L, Anderson NL, Fisher SJ, Liebler DC, Paulovich AG, Regnier FE, Tempst P, Carr SA. Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. *Nat Biotechnol.* 2009 Jul;27(7):633-41.
 19. Guo T, Wang W, Rudnick PA, Song T, Li J, Zhuang Z, Weil RJ, DeVoe DL, Lee CS, Balgley BM. Proteome analysis of microdissected formalin-fixed and paraffin-embedded tissue specimens. *J Histochem Cytochem.* 2007 Jul;55(7):763-72.
 20. Wang W, Guo T, Rudnick PA, Song T, Li J, Zhuang Z, Zheng W, DeVoe DL, Lee CS, Balgley BM. Membrane proteome analysis of microdissected ovarian tumor tissues using capillary isoelectric focusing/reversed-phase liquid chromatography-tandem MS. *Anal Chem.* 2007 Feb 1;79(3):1002-9.
 21. Martin DN, Balgley B, Dutta S, Chen J, Rudnick P, Cranford J, Kantartzis S, DeVoe DL, Lee C, Baehrecke EH. Proteomic analysis of steroid-triggered autophagic programmed cell death during *Drosophila* development. *Cell Death Differ.* 2007 May;14(5):916-23.
 22. Guo T, Rudnick PA, Wang W, Lee CS, DeVoe DL, Balgley BM. Characterization of the human salivary proteome by capillary isoelectric focusing/nanoreversed-phase liquid chromatography coupled with ESI-tandem MS. *J Proteome Res.* 2006 Jun;5(6):1469-78.
 23. Wang Y, Rudnick PA, Evans EL, Li J, Zhuang Z, DeVoe DL, Lee CS, Balgley BM. Proteome analysis of microdissected tumor tissue using a capillary isoelectric focusing-based multidimensional separation platform coupled with ESI-tandem MS. *Anal Chem.* 2005 Oct 15;77(20):6549-56.
 24. Rudnick PA, Wang Y, Evans E, Lee CS, Balgley BM. Large scale analysis of MASCOT results using a mass accuracy-based threshold effectively improves data interpretation. *J Proteome Res.* 2005 Jul-Aug;4(4):1353-60.
 25. Wang Y, Balgley BM, Rudnick PA, Lee CS. Effects of chromatography conditions on intact protein separations for top-down proteomics. *J Chromatogr A.* 2005 May 6;1073(1-2):35-41.
 26. Wang Y, Balgley BM, Rudnick PA, Evans EL, DeVoe DL, Lee CS. Integrated capillary isoelectric focusing/nano-reversed phase liquid chromatography coupled with ESI-MS for characterization of intact yeast proteins. *J Proteome Res.* 2005 Jan-Feb;4(1):36-42.
 27. Stewart C., Lum N., Stephens R., Rudnick P., Rasmussen L., Munroe D. High Throughput Primer Walking of cDNA Clones. *JALA.* April 2003. Vol. 8, no. 2, pp. 64-65.
 28. Kennedy C, Rudnick P., MacDonald M, and Melton T. Genus III. *Azotobacter*. In *Bergey's Manual of Determinative Bacteriology* 2nd Ed. Vol. 2 *The Proteobacteria*, Ed. George M. Garrity (2004).
 29. Rudnick P and Kennedy C. Regulation of Mo Nitrogenases. In *Nitrogen Fixation at the Millennium*. Ed. G. Jeffery Leigh. Pp. 155-164. Elsevier Science B.V. (2002).
 30. Rudnick P, Kunz C, Gunatilaka MK, Hines ER and Kennedy C. Role of GlnK in NifL-mediated regulation of NifA activity in *Azotobacter vinelandii*. *J. Bacteriol.* 2002 Feb;184(3):812-20.
 31. Rudnick PA, Arondeguy T, Kennedy CK, and Kahn D. *glnD* and *mviN* Are Genes of an Essential Operon in *Sinorhizobium meliloti*. *J. Bacteriol.* Vol. 183, No. 8. p. 2682-2685.

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32. Colnaghi, R, Rudnick P, He L, Green A, Yan D, Larson E and Kennedy C. Characterization of *glnD* null mutations in *Azotobacter vinelandii*: lethality is suppressible by prevention of glutamine synthetase adenylylation. Microbiology May 2001, Vol. 147, 1267-1276.
33. Meletzus D, Rudnick P, Doetsch N, Green A and Kennedy C. Characterization of the *glnK-amtB* Operon of *Azotobacter vinelandii*. J. Bacteriol. June 1998, p. 3260-3264
34. Rudnick P, Meletzus D, Green A, He L and Kennedy C. Regulation of Nitrogen Fixation by Ammonium in Diazotrophic Species of Proteobacteria. Soil Biol. Biochem. Vol. 29, No. 5/6, pp. 831-841, 1997.