

Ljiljana Paša-Tolić

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EDUCATION

- 1992 Ph.D. Chemistry, University of Zagreb, Zagreb, Croatia
1989 M.S. Theoretical and Physical-Organic Chemistry, University of Zagreb,
Zagreb, Croatia
1986 B.S. Chemistry, University of Zagreb, Zagreb, Croatia

RESEARCH INTERESTS AND EXPERTISE

Dr. Paša-Tolić is a Staff Scientist at the Pacific Northwest National Laboratory (PNNL) and the Capability Steward for Mass Spectrometry at the Environmental Molecular Sciences Laboratory (EMSL), a national scientific user facility operated by PNNL for the U.S. Department of Energy (DOE). Her research centers on developing sophisticated analytical methods with emphasis on Fourier transform (FT) mass spectrometry (MS) and micro-separations, as well as the application of these techniques to accurately quantify changes in protein abundance, identity and activity during cell development or in response to stimuli.

Prior to accepting a postdoctoral fellowship at PNNL in 1995, she served as a Visiting Associate in Research at the National High Magnetic Field Laboratory in Prof. Alan G. Marshall's laboratory, where she designed the world's first 9.4T FTICR spectrometer and developed techniques for characterizing large biopolymers with high sensitivity. As a result of this expertise, her first assignment at PNNL was to bring the 11.5T FTICR to fruition for the EMSL Project. Since that time, Dr. Paša-Tolić have continuously been involved in EMSL's user program, and over the years have worked with numerous collaborators and outside users of MS instrumentation, developed core instrumentation and methods to enable previously intractable MS applications, and managed the operation of FTICR mass spectrometers for proteomics-related research. Furthermore, she was a key contributor in the pioneering efforts of PNNL's high throughput accurate mass and time (AMT) tag strategy for ultra sensitive proteomics.

Dr. Paša-Tolić current work responsibilities include stewarding EMSL's Mass Spectrometry capability, which includes 30+ mass spectrometers and 30+ commercial and custom LC systems, and a large international user base. Additionally, she is technical lead for the development of an exciting new capability that supports research focused on characterizing protein post-translational modifications, their coordination and dynamics.

PROFESSIONAL EXPERIENCE AND RELEVANT RESEARCH

2007 – Present	Staff Scientist & EMSL Capability Steward for Mass Spectrometry, PNNL
1997 – 2007	Senior Research Scientist, PNNL
1995 – 1997	Postdoctoral Fellow, PNNL
1993 – 1995	Visiting Associate in Research, National High Magnetic Field Lab
1986 – 1992	Research Associate, Rudjer Bosković Institute

HONORS AND AWARDS, PROFESSIONAL AFFILIATIONS AND SERVICE

“The 1988 International Institute in Quantum Chemistry and Solid State Theory”
Attendance Award, University of Florida, Gainesville, 1988
PNNL Outstanding Performance Award (four), 1998-2000
PNNL Key Contributor Award (two), 2002, 2003
Member, American Chemical Society
Member, American Society for Mass Spectrometry
Member, ASMS Sanibel Committee, 2006
Treasurer, ASMS Sanibel Committee, 2007
Chair, ASMS Sanibel Committee, 2008
Member, PhD Thesis Committee, Ioana M. Barbu, Utrecht University, Netherlands, 2008
Reviewer, NCI: IMAT Program, 2007-2010
Reviewer, NCI: Innovations in Cancer Sample Preparation, 2006, and 2007
Reviewer, NCI: Cancer Detection and Cancer Sample Preparation applications, 2006
Reviewer, NSF, Analytical and Surface Chemistry Program, 2005
Reviewer, NIH-NCRR Shared and High End Instrumentation, 2004-2010
Reviewer, NIH Bioanalytical Engineering and Chemistry Study Section, 2004
Reviewer, NCI: SBIR Program, 2004
Conference co-organizer: Mass Spectrometry in Biology and Medicine, held during first week of July in Dubrovnik, Croatia, 2007-present.
Reviewer, *Journal of Separation Science*, *Proteomics*, *Journal of Proteome Research*, *Analytica Chemica Acta*, *Analytical Biochemistry*, *Electrophoresis*, *Rapid Communications in Mass Spectrometry*, *Analytical Chemistry*, *Journal of the American Society for Mass Spectrometry*, 1995 to present

MENTOREES:

Mentor technical staff, postdoctoral fellows and research scientists. Postdoctoral fellows have included: Pamela K. Jensen (Monsanto); Suzana Martinović; Christophe D. Masselon (CEO, Grenoble, France); Lingjun Li (University of Wisconsin); Sang-Won Lee (Korea University); Vsevolod Rakov; Andrey N. Vilkov (MassTech Inc.), Bogdan Bogdanov (University of Louisville), David C. Simpson (Virginia Commonwealth University), Seema Sharma (Thermo Fisher Scientific); Hyuk Kang (Ajou University); Natacha Lourette (DSM Research Campus Geleen), Si Wu (PNNL/EMSL), Zhixin Tian, Haizhen Zhang.

PATENTS AND LICENSES

PUBLICATIONS

1. K. Hixson, D. Lopez-Ferrer, E. Robinson, and **L. Paša-Tolić**, “Proteomics”, in Encyclopedia of Spectroscopy and Spectrometry, 2nd Edition. **2010**, in press.
2. N. Lourette, H. Smallwood, S. Wu, T. Squier, R.D. Smith, **L. Paša-Tolić**, “A top-down LC-FTICR MS-based strategy for detecting and identifying Oxidized Calmodulin in Activated Macrophages”, *J Am Soc Mass Spectrom.* 2010, 21(6), 930-9.
3. H. Zhang, R. Brown, W-J Qian, M. Monroe, S. Purvine, R. Moore, M. Gritsenko, L. Shi, M. Romine, J. Fredrickson, **L. Paša-Tolić**, R.D. Smith, M. Lipton, “Quantitative analysis of cell surface membrane proteins using membrane-impermeable chemical probe coupled with ¹⁸O labeling.” *J Proteome Res.* 2010, 9(5), 2160-9.
4. R. Mercer, S. Callister, M. Lipton, **L. Paša-Tolić**, H. Strnad, V. Paces, J. Beatty, A. Lang, “Loss of the response regulator CtrA causes pleiotropic effects on gene expression but does not affect growth phase regulation in *Rhodobacter capsulatus*”. *J Bacteriol.* 2010, 192(11), 2701-10.
5. F. Yang, S. Wu, D. Stenoen, R. Zhao, M. Monroe, M. Gritsenko, S. Purvine, A. Polpitiya, N. Tolić, Q. Zhang, A. Norbeck, D. Orton, R. Moore, K. Tang, G. Anderson, **L. Paša-Tolić**, D. Camp II, R.D. Smith, “Combined pulsed-Q dissociation and electron transfer dissociation for identification and quantification of iTRAQ-labeled phosphopeptides”. *Anal Chem.* 2009, 81(10), 4137-43.
6. D. Springer, J. Miller, S. Spinelli, **L. Paša-Tolić**, S. Purvine, D. Daly, R. Zangar, S. Jin, N. Blumberg, C. Francis, M. Taubman, A. Casey, S. Wittlin, R. Phipps, “Platelet proteome changes associated with diabetes and during platelet storage for transfusion”. *J Proteome Res.* 2009, 8(5), 2261-72.
7. M. Lipton, L. Paša-Tolić, “Mass spectrometry of proteins and peptides: methods and protocols”. Preface. *Methods Mol Biol.* 2009, 492.
8. S. Wu, F. Yang, R. Zhao, N. Tolić, E. Robinson, D. Camp II, R.D. Smith, **L. Paša-Tolić**, “An integrated workflow for characterizing intact phosphoproteins from complex mixtures.” *Anal Chem.* 2009, 81(11), 4210-9.
9. A. Umar, H. Kang, M. Meijer-van Gelder, A. Timmermans, N. Jaitly, T. Luider, J. Foekens, **L. Paša-Tolić**, “Identification of a protein-profile associating with tamoxifen therapy-resistance in breast cancer,” *Mol Cell Proteomics* 2009, 8(6), 278-94.
10. H. Mottaz, A. Norbeck, J. Adkins, N. Manes, C. Ansong, L. Shi, Y. Rikihisa, T. Kikuchi, S. Wong, R. Estep, F. Heffron, **L. Paša-Tolić**, and R.D. Smith. 2008. “Optimization of proteomic sample preparation procedures for comprehensive protein characterization of pathogenic systems.” *Journal of Biomolecular Techniques.* 2008, 19(5), 285-295.
11. T. Ream, J. Haag, A. Wierzbicki, C. Nicora, A. Norbeck; J.-K. Zhu, G. Hagen, T. Guilfoyle, **L. Paša-Tolić**, C. Pikaard, “Subunit compositions of the RNA silencing

- enzymes, Pol IV and Pol V reveal their origins as specialized forms of RNA Polymerase II”, Mol Cell. 2009, 33(2), 192-203.
12. A. Tolmachev, E. Robinson, S. Wu, **L. Paša-Tolić**, R.D. Smith, “FT-ICR MS optimization for the analysis of intact proteins”, Int. J. Mass Spectrometry, **2009**, 287, 32–38.
13. D. López-Ferrer, K. Petritis, N. Lourette, B. Clowers, K. Hixson, T. Heibeck, D. Prior, **L. Paša-Tolić**, D. Camp II, M. Belov, R.D. Smith, “On-line digestion system for protein characterization.” Anal Chem. 2008, 1; 80(23), 8930-6.
14. A. Umar, M. Jaremko, P. Burgers, T. Luider, J. Foekens, **L. Paša-Tolić**, “High-throughput proteomics of breast carcinoma cells: a focus on FTICR MS”, Expert Rev Proteomics, **2008**, 5(3), 445-55.
15. A.V. Tolmachev, E.W. Robinson, S. Wu, H. Kang, N.M. Lourette, **L. Paša-Tolić**, R.D. Smith, “Trapped-ion cell with improved DC potential harmonicity for FT-ICR MS”, J Am Soc Mass Spectrom., 2008, 19(4), 586-97.
16. Y. Shen, N. Tolić, K.K. Hixson, S.O. Purvine, **L. Paša-Tolić**, W. Qian, J.N. Adkins, R.J. Moore, R.D. Smith, “Proteome-wide identification of proteins and their modifications with decreased ambiguities and improved false discovery rates”, Anal. Chem., 2008, 80(6), 1871-82.
17. Y. Huang, G.C. Tseng, S. Yuan, **L. Paša-Tolić**, M.S. Lipton, R.D. Smith, V.H. Wysocki, "A Data-Mining Scheme for Identifying Peptide Structural Motifs Responsible for Different MS/MS Fragmentation Intensity Patterns ", J. Proteome Res., 2008, 7(1), 70-9.
18. **L. Paša-Tolić**, J.M. Jacobs, W. Qian, R.D. Smith "Quantitative Proteomics using NanoLC with High Accuracy Mass Spectrometry" in "Clinical Proteomics", 2008, pp. 89-100, eds. J. Van Eyk and M. Dunn, Wiley-VCH.
19. H.S. Smallwood, N.M. Lourette, C.B. Boschek, D.J. Bigelow, R.D. Smith, **L. Paša-Tolić**, T.C. Squier, “Identification of a Denitrase Activity Against Calmodulin in Activated Macrophages Using High-Field LC-FTICR Mass Spectrometry”, Biochemistry, 2007, 46(37), 10498-505.
20. H. Kang, **L. Paša-Tolić**, R.D. Smith, “Targeted Tandem Mass Spectrometry for High-Throughput Comparative Proteomics Employing NanoLC-FTICR MS with External Ion Dissociation”, 2007, J. Amer. Soc. Mass Spectrom., 2007, 18(7), 1332-43.
21. K.-J. Puan, C. Jin, H. Wang, G. Sarikonda, A.M. Raker, H.K. Lee, M.I. Samuelson, E. Märker-Hermann, **L. Paša-Tolić**, E. Kolas-Nieves, J.-L. Giner, T. Kuzuyama, C.T. Morita, “Preferential recognition of a microbial metabolite by human V γ 2V δ 2 T cells”, International Immunology, 2007, Int. Immunol. 2007 May; 19(5), 657-73.
22. S. Sharma, D.C. Simpson, N. Tolić, N. Jaitly, A.M. Mayampurath, R.D. Smith, **L. Paša-Tolić**, “Proteomic profiling of intact proteins using WAX-RPLC 2-D separations and FTICR mass spectrometry”, J. Proteome Res., 2007, 6, 602-10.
23. A. Umar, T.M. Luider, J.A. Foekens, **L. Paša-Tolić**, “NanoLC-FT-ICR MS improves proteome coverage attainable for 3000 laser-microdissected breast carcinoma cells.”, Proteomics, 2007, 7, 323-9.

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27. Y. Huang, J.M. Triscari, G.C. Tseng, **L. Paša-Tolić**, M.S. Lipton, R.D. Smith, V.H. Wysocki, "Statistical Characterization of the Charge State and Residue Dependence of Low Energy CID Peptide Dissociation Patterns", *Anal. Chem.*, 2005, 77, 5800-13.
28. F. Yang, B. Bogdanov, E.F. Strittmatter, A.N. Vilkov, M.A. Gritsenko, L. Shi, D.A. Elias, S. Ni, M.F. Romine, **L. Paša-Tolić**, M.S. Lipton, R.D. Smith, "Characterization of purified c-type heme-containing peptides and identification of c-type heme-attachment sites in *Shewanella oneidensis* cytochromes using mass spectrometry.", *J. Proteome Res.*, 2005, 4, 846-54.
29. E. Kolker, A.F. Picone, M.Y. Galperin, M.F. Romine, A. Osterman, K.S. Makarova, N. Kolker, G.A. Anderson, D. Anderson, K.J. Auberry, G. Babnigg, A.S. Beliaev, W.R. Cannon, T. Cherny, J. Cole, D.A. Elias, Y. Gorby, L.J. Hauser, R. Higdon, K. Hixson, T. Holzman, J. Klappenbach, K. Konstantinidis, M.L. Land, M.S. Lipton, L. McCue, M. Monroe, R. Moore, H. Mottaz, **L. Paša-Tolić**, G. Pinchuk, S. Purvine, X. Qiu, M. Serres, S. Tsapin, B.A. Zakrajsek, W. Zhu, J. Zhou, C. Lawrence, M. Riley, F.W. Larimer, R. Overbeek, F.R. Collart, J.R. Yates III, R.D. Smith, C. Giometti, K. Nealson, J.K. Fredrickson, J.M. Tiedje, "Global Profiling of *Shewanella oneidensis* MR-1: Expression of 'Hypothetical' Genes and Improved Functional Annotations," *Proc. Nat. Acad. Sci. USA*, 2005, 102, 2099-104.
30. C. Masselon, **L. Paša-Tolić**, N. Tolić, G.A. Anderson, B. Bogdanov, A.N. Vilkov, Y. Shen, R. Zhao, M.S. Lipton, D.G. Camp, R.D. Smith, "Targeted Comparative Proteomics by Combined Liquid Chromatography – Fourier Transform Mass Spectrometry", 2005, *Anal. Chem.*, 2005, 77, 400-6.
31. A.V. Tolmachev, A.N. Vilkov, B. Bogdanov, **L. Paša-Tolić**, C.D. Masselon and R.D. Smith, "Collisional activation of ions in RF ion traps and ion guides: the effective ion temperature treatment", *J. Am. Soc. Mass Spectrom.*, 2004, 15, 1616-28.
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33. S.M. Varnum, D.N. Streblow, M.E. Monroe, P. Smith, K.J. Auberry, **L. Paša-Tolić**, D. Wang, D.G. Camp II, K. Rodland, S. Wiley, W. Britt, T. Shenk, R.D. Smith, J.A. Nelson, "Identification of proteins in human cytomegalovirus (HCMV) particles: the HCMV proteome", *J Virol*, 2004, 78, 10960-6.

34. L. Paša-Tolić, M.S. Lipton, "Advanced Mass Spectrometry for Proteomics", 2004, Business Briefing: LabTech, 2004, 53-6.
35. A.N. Vilkov, B. Bogdanov, L. Paša-Tolić, D.C. Prior, G.A. Anderson, C.D. Masselon, R.J. Moore and R.D. Smith, "Tailored Noise Waveform - Collision-Induced Dissociation of Ions Stored in a Linear Ion Trap Combined with Liquid Chromatography-Fourier Transform Ion Cyclotron Resonance Mass Spectrometry," Rapid Commun. Mass Spectrom., 2004, 18, 2682-90.
36. Y. Shen, N. Tolić, C. Masselon, L. Paša-Tolić, D.G. Camp II, K.K. Hixson, R. Zhao, G.A. Anderson, R.D. Smith, "Ultrasensitive proteomics using high-efficiency on-line micro-SPE-nanoLC-nanoESI MS and MS/MS", Anal. Chem., 2004, 76, 144-54.
37. Y. Huang, J.M. Triscari, L. Paša-Tolić, G.A. Anderson, M.S. Lipton, R.D. Smith, V.H. Wysocki, "Dissociation behavior of doubly-charged tryptic peptides: correlation of gas-phase cleavage abundance with ramachandran plots", J. Am. Chem. Soc., 2004, 126, 3034-5.
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39. Y. Shen, N. Tolić, C. Masselon, L. Paša-Tolić, D.G. Camp DG II, M.S. Lipton, G.A. Anderson, R.D. Smith, "Nanoscale proteomics", Anal. Bioanal. Chem., 2004, 378, 1037-45.
40. M.V. Gorshkov, C.D. Masselon, E.N. Nikolaev, H.R. Udseth, L. Paša-Tolić, R.D. Smith, "Considerations for electron capture dissociation efficiency in FTICR mass spectrometry", Int. J. Mass Spectrom., 2004, 243, 131-6.
41. Y. Shen, N. Tolić, C. Masselon, L. Paša-Tolić, D.G. Camp II, K.K. Hixson, R. Zhao, G.A. Anderson, R.D. Smith, "Ultra-sensitive nano-scale proteomics using high-efficiency on-line microSPE-nanoLC-nanoESI MS and MS/MS", Anal. Chem., 2004, 76, 144-54.
42. A.V. Tolmachev, A.N. Vilkov, L. Paša-Tolić, H.R. Udseth and R.D. Smith, "Suppression of the Lower Charge State ions in the External Accumulation RF Multipole with a Reduced Trapping DC Potential", J. Amer. Soc. Mass Spectrom., 2003, 14, 1229-35.
43. Y. Shen, R. J. Moore, R. Zhao, J. Blonder, D. L. Auberry, C. Masselon, L. Paša-Tolić, K. K. Hixson, K. J. Auberry and R. D. Smith, "High-Efficiency On-Line SPE Coupling to 15-150 µm I.D. Column LC for Proteomic Analysis", Anal. Chem., 2003, 75, 3596-605.
44. M. Ćurić, D. Babić, Z. Marinić, L. Paša-Tolić, V. Butković, J. Plavec, L. Tušek-Božić, "Synthesis and characterisation of Pd(II) complexes with a derivative of aminoazobenzene - Dynamic H-1-NMR study of cyclopalladation reactions in DMF", J. Organometallic Chem., 2003, 687, 85-99.
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- Mass Tags” in: Advances in Protein Chemistry, R. D. Smith and T. D. Veenstra, Eds., Elsevier Science, San Diego, CA, 2003, 65, 85-131.
46. D. Mohan, **L. Paša-Tolić**, C. D. Masselon, N. Tolić, B. Bogdanov, K. K. Hixson, R. D. Smith, and C. S. Lee, “Integration of electrokinetic-based multidimensional separation/concentratoin platform with ESI-FTICR-MS for proteome analysis of *Shewanella oneidensis*”, *Anal. Chem.*, 2003, 75, 4432-40.
47. C. Masselon, **L.Paša-Tolić**, S.-W. Lee, L. Li, G. A. Anderson, R. Harkewicz and R. D. Smith, “Identification of Tryptic Peptides from Large Databases using Multiplexed MS/MS: Simulations and Experimental Results”, *Proteomics*, 2003, 3(7), 1279-86.
48. K. Petritis, L.J. Kangas, P.L. Ferguson, G.A. Anderson, **L. Paša-Tolić**, M.S. Lipton, K.J. Auberry, E.F. Strittmatter, Y. Shen, R. Zhao, R.D. Smith, “Use of Artificial Neural Networks for the Accurate Prediction of Peptide Liquid Chromatography Elution Times in Proteome Analyses”, *Anal. Chem.*, 2003, 75, 1039-48.
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PRESENTATIONS

1. Pasa-Tolic L, L Brechenmacher, TH Nguyen, M Libault, KK Hixson, MA Gritsenko, TRW Clauss, F Yang, and G Stacey. 2010. "Soybean Root Hairs:

Proteomics and Beyond." Presented by L Paša-Tolić at **58th ASMS Conference on Mass Spectrometry and Allied Topics**, Salt Lake City, UT, on May 26, 2010

2. L. Paša-Tolić, E. Robinson, Z. Tian, N. Tolić, D. Lopez-Ferrer, H. Zhang, S. Wu, and R.D. Smith. 2009. "Integrated Top-Down And Bottom-Up Mass Spectrometry For Characterization Of Intact Proteins." Presented by L Paša-Tolić (Invited Speaker) at the Proteomic Technology Development Symposium of **HUPO 2009**, September 27, 2009; Toronto, ON, Canada.
3. Paša-Tolić, E. Robinson, Z. Tian, N. Tolić, D. Lopez-Ferrer, K. Petritis, S. Wu, and R.D. Smith. 2009. "Combined Top-Down And Bottom-Up Proteomics For Characterization Of Protein Isoforms." Presented by L. Paša-Tolić (Invited Speaker) at **7th North American FT-ICR MS Conference**, April 19-23, 2009, Key West, Florida.
4. L. Paša-Tolić, 2009. "Proteomics Using Accurate Mass and Time Tags." Presented by L. Paša-Tolić (Invited Speaker) at **Pittcon 2009**, Chicago, IL, 08 - 13 March 2009.
5. L. Paša-Tolić. 2009. "Accurate Mass and Time Tags for Quantitative Proteomics." Presented by L. Paša-Tolić (Invited Speaker) at Mass Spectrometry in Biotechnology and Medicine (**MSBM III**), Dubrovnik, Croatia.
6. L. Paša-Tolić. 2009. "Integrated Top-Down and Bottom-up Proteomics." Presented by L Paša-Tolić (Invited Speaker) at Mass Spectrometry in Biotechnology and Medicine (**MSBM III**), Dubrovnik, Croatia
7. L. Paša-Tolić, S. Wu, F. Yang, R. Zhao, N. Lourette, N. Tolić, K. Hixson, S. Callister, S. Kaplan, and R.D. Smith. 2008. "An integrated workflow for identification and quantitation of intact phosphoproteins." Presented by L Paša-Tolić at **56th ASMS Conference on Mass Spectrometry and Allied Topics**, Denver, CO on June 2, 2008.
8. L. Paša-Tolić, 2008. "Advanced LC-MS strategies for protein profiling and biomarker discovery", Presented by L. Paša-Tolić (Invited Speaker) at **FOM-Institute for Atomic and Molecular Physics**, Amsterdam, Netherlands, April 10, 2008
9. L. Paša-Tolić, 2008. "FT-ICR for Proteomics" Presented by L. Paša-Tolić (Invited Speaker) at **Science Challenges and Design Concepts for Deploying a High Magnetic Field High Performance FT-ICR Mass Spectrometer System**, National High Magnetic Field Lab, Tallahassee, FL, January 16, 2008.
10. L. Paša-Tolić, 2007. "Integrated Top-Down And Bottom-Up Strategy For Characterizing Intact Proteins And Their Modifications", Presented by L. Paša-Tolić (Invited Speaker) at **2007 AIChE (The American Institute of Chemical Engineers) Annual Meeting**, Salt Lake City, Utah, November 4 -9, 2007.
11. L. Paša-Tolić, 2007. "Probing oxidative stress using intact protein LC-MS" Presented by L. Paša-Tolić (Invited Speaker) at the 2nd Summer Course on Mass Spectrometry in Biotechnology and Medicine (**II MSBM**), Dubrovnik, Croatia, July 6, 2007.

12. L. Paša-Tolić, 2007. "Advanced LC-MS strategies for protein profiling and biomarker discovery." Presented by L. Paša-Tolić (Invited Speaker) at the 2nd Summer Course on Mass Spectrometry in Biotechnology and Medicine (**II MSBM**), Dubrovnik, Croatia, July 4, 2007.
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16. L. Paša-Tolić, R.D. Smith. 2006. "Quantitative proteomics using nanoLC with high accuracy mass spectrometry" Presented by L. Paša-Tolić (Invited Speaker) at the **Symposium Biomarker Discovery by Mass Spectrometry** on May 19, 2006 in Amsterdam, The Netherlands
17. L. Paša-Tolić. 2006. "Advanced strategies for protein profiling using liquid chromatography coupled with Fourier transform ion cyclotron resonance mass spectrometry (LC-FTICR/MS)." Presented by L. Paša-Tolić (Invited Speaker) at **Washington State University Molecular Plant Sciences Seminar**, WSU Tri-Cities, Richland, WA, on April 11, 2006.
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19. L. Paša-Tolić, DC Simpson, S Sharma, AN Vilkov, CD Masselon, and RD Smith. 2005. "Global Proteomics for Intact Proteins." Presented by L. Paša-Tolić (Invited Speaker) at **5th North American FT-ICR MS Conference**, Key West, FL on April 19, 2005.
20. L. Paša-Tolić, Seema Sharma, David C. Simpson, Heather M. Mottaz, and Richard D. Smith. 2005. "Probing proteomes at the intact protein level." Presented by L. Paša-Tolić at **18th International Symposium on MicroScale Bioseparations**, New Orleans, LA on February 16, 2005.
21. L. Paša-Tolić, S Ahn, HM Mottaz, S Sharma, DC Simpson, MS Lipton, B Bogdanov, GA Anderson, and RD Smith. 2004. "Mass spectrometric analysis of intact proteins." Presented by L. Paša-Tolić at the **Annual Conference of Japanese Society of Biochemistry**, Yokohama, Japan on October 13, 2004.
22. L. Paša-Tolić, GA Anderson, MS Lipton, DG Camp, II, Y Shen, CD Masselon, and RD Smith. 2004. "Advanced strategies for profiling protein abundances using LC-FTICR/MS." Presented by L. Paša-Tolić at the **Netherlands Proteomics Platform**, Amsterdam, on October 3, 2004.

23. L. Paša-Tolić, CD Masselon, AN Vilkov, GA Anderson, Y Shen, MS Lipton, N Tolić, and RD Smith. 2004. "Profiling protein abundances using advanced mass spectrometry." Presented by L. Paša-Tolić at **PittCon2004**, Chicago, IL on March 9, 2004.
24. L. Paša-Tolić, CD Masselon, N Tolić, GA Anderson, AN Vilkov, Y Shen, MS Lipton and RD Smith. 2004. "Profiling protein abundances using LC-FTICR MS" Presented by L. Paša-Tolić at **5th International Symposium on the Interface between Analytical Chemistry and Microbiology**, Richland, WA on April 21, 2004.
25. L. Paša-Tolić, Y Shen, CD Masselon, N Tolić, DG Camp, II, W Qian, GA Anderson, K Williams, M Pallavicini, and RD Smith. 2003. "Nano-scale proteomics by LC-FTICR MS." Presented by L. Paša-Tolić at **4th North American FT-ICR MS Conference**, Marshall, CA on April 4, 2003.
26. L. Paša-Tolić, GA Anderson, MS Lipton, Y Shen, N Tolić, CD. Masselon, and RD. Smith 2002. "Gene Expression Profiling Using Advanced Mass Spectrometry" Presented by L. Paša-Tolić (Invited Speaker) at the **1st Croatian Congress on Molecular Life Sciences**, Opatija, Croatia on June 10, 2002.
27. Paša-Tolić L. 2002. "Advanced Mass Spectrometric Approaches for Quantitative Proteomics." Presented by Ljiljana Paša-Tolić (Invited Speaker) at **223rd ACS National Meeting** (Alan G. Marshall's ACS Award in Analytical Chemistry), Orlando, FL on April 8, 2002.
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29. L. Paša-Tolić, GA Anderson, MS Lipton, Y Shen, N Tolić, CD Masselon, BD Thrall, and RD Smith. 2002. "Protein Abundance Measurements using Advanced Mass Spectrometric Proteomics Approaches." Presented by L. Paša-Tolić at **50th American Society for Mass Spectrometry**, Orlando, FL on June 3, 2002.
30. L. Paša-Tolić, PK Jensen, S Martinović, KK Peden, MS Lipton, GA Anderson, N Tolić, and RD Smith. 1999. "Proteome Analysis: Comparison of Gene Expression Via CIEF FTICR-MS." Presented by L. Paša-Tolić at **47th Annual American Society for Mass Spectrometry**, Dallas, TX on June 13, 1999.

Current Research Support:

Active:

Campbell (PI) 10/01/95 – 09/30/10
 6.0 Cal. Months effort \$32M annual funding
 DOE OBER: Environmental Molecular Sciences Laboratory Operations
 This project supports the Environmental Molecular Sciences laboratory facility operation and efforts in support of DOE users to the facility.
 Role: Research Scientist (Capability Lead for Mass Spectrometry)

Paša-Tolić (PI) 10/01/08 – 09/30/10
 1.2 Cal. Months effort \$150K annual funding

DOE OBER: Environmental Molecular Sciences Laboratory Operations

An Integrated workflow for identification and quantitation of intact phosphoproteins
The main goals of this proposal are to develop a technology platform to quantitatively map multiple posttranslational modifications (with emphasis on phosphorylation) occurring within protein complexes with high sensitivity and throughput and test the hypothesis that this system can be used to identify protein signatures associated with specific biological responses, such as DNA damage repair.

Role: Principal Investigator

Smith (PI) 10/01/99 – 09/30/10
1.2 Cal. Months effort \$2M annual funding

DOE OBER

Development of High-Throughput Proteomics Production Operations

The goal of this project is to develop and apply a capability for detecting and identifying large numbers of proteins from microbial proteomes, and for improving the understanding of complex microbial communities.

Role: Research Scientist

P41 RR018522 Smith (PI) 09/15/03 – 06/30/13
1.2 Cal. Months effort \$3.3M annual funding

NIH NCRR

A Proteomics Research Resource for Integrative Biology

Research Resource focused on serving the NIH-supported biomedical research community by developing and integrating new proteomic technologies for collaborative and service studies, disseminating the new technologies, and training scientists in their use.

Role: Research Scientist

Stenoien (PI) 10/01/09 – 09/30/11
1.2 Cal. Months effort \$450K annual funding

DTRA JSTO CBS. MEDRAD.01-10.PN.PP.017

Biosignatures of acute radiation exposure

The main objectives of this proposal are to identify novel molecular targets of acute radiation exposure and to elucidate the molecular mechanisms associated with acute radiation syndrome. Specifically, we Appendix 2 – page 5 will test the hypothesis that alterations in protein levels, post-translational modifications, and metabolic factors and products can serve as molecular fingerprints of radiation exposures that can accurately assess radiation doses received and highlight signaling pathways associated with acute radiation syndrome.

Role: Co-Principal Investigator

Thomas (PI) 04/30/10 – 09/01/10
0.12 Cal. Months effort \$30K total funding

NIH

Immunodominance hierarchies and compensation in influenza

Develop and apply mass spectrometry based techniques to measure the variables necessary for a thorough assessment and the refinement of the influenza infection model

in BL/6 mice. Research will be done in collaboration with St. Jude Children's Research Hospital.

Role: Research Scientist

Pending:

Stacey (PI)

9/15/10 – 09/14/13

0.3 Cal months effort

DOE OBER

Systems View of Root Hair Nutrient Uptake Focus on defining the transcriptional and proteomic response of the soybean root hair cell to variations in temperature and water availability. These data allow the development of computational models to examine regulatory networks controlling the response to environmental change, which should have relevance to issues of climate change.

Role: Co-Principal Investigator