

CURRICULUM VITAE

Carol Smith Giometti

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Education: Knox College B.A. 1972 Biology
Rush Hospital MT 1973 Medical Technology*
University of Illinois Chicago Ph.D. 1978 Biochemistry

*Certified Medical Technologist; Internship at Rush Hospital, Chicago, 1972-73

Professional Experience:

6/2007-present Acting Division Director, Biosciences Division
Argonne National Laboratory

2001-present Senior Biochemist and Group Leader, Protein Mapping Group
Argonne National Laboratory

1987- 2000 Biochemist and Group Leader, Protein Mapping Group

3/1999-5/2000 Acting Division Director, Biosciences Division
Argonne National Laboratory

1985-1987 Assistant Biochemist, Protein Mapping Group
Argonne National Laboratory

1982-1985 Assistant Biochemist, Molecular Anatomy Program
Argonne National Laboratory

1981-1982 Assistant Biologist, Molecular Anatomy Program
Argonne National Laboratory

1978-1981 Postdoctoral Appointee, Molecular Anatomy Program
Argonne National Laboratory

1973-1978 Teaching Assistant
University of Illinois at the Medical Center, Chicago

1972-1973 Medical Laboratory Intern
Rush Hospital, Chicago

Awards

Young Investigator Award in Clinical Chemistry from the American Association of Clinical Chemists, 1984

Current Professional Society Memberships

American Society of Microbiology
Electrophoresis Society

Recent Invited Talks (Selected)

- 2008 Guest Lecturer, Valparaiso University, Chemistry Department Lecture
- 2007 Plenary Speaker, American Electrophoresis Society Annual Meeting
Multiplexed Analysis of Microbial Proteomes
Guest Lecturer, Dominican University, Bioinformatics Seminar Series
- 2006 Invited Speaker, BER Genomics:GtL Contractors Meeting Proteomics Breakout Session
The Shewanella oneidensis MR-1 Phosphoproteome
- Invited Speaker, BER Environmental Remediation Sciences Program PI Meeting
Shewanella MR-1 Membrane Proteins
Guest Lecturer, Northwestern University, Biochemistry Department First Year Graduate Program Seminar
- 2005 Invited Speaker, American Electrophoresis Society Annual Meeting
The Microbial Proteome Project: A database of Microbial Protein Expression in the Context of Genome Analysis
Guest Lecturer, University of Illinois at Chicago, School of Pharmacy Seminar

Community Activities (selected)

Argonne

- 2001-present Member, Laboratory Reduction in Force Committee
2002-2004 Member, Biosciences Division Promotions and Hiring Committee
2005-2007 Chair, Biosciences Division Promotions and Hiring Committee
2002-2007 Member, Biosciences Executive Committee
2006-2007 Chair, Directorate Promotions and Hiring Committee
2001-2005 Member, Directorate Promotions and Hiring Committee

External

- 2007-present Executive Board Member, Great Lakes Regional Center of Excellence for Biodefense and Emerging Infectious Disease Research
2006-2007: Advisory Board Member, University of Illinois BitMap Program
2004 Invited Participant, American Academy of Microbiology Colloquium
"Systems Microbiology: Beyond Microbial Genomes"
2004-2005 Member, Genomics:GtL Data Sharing Working Group
2004-2005: Co-Chair, Shewanella Federation Data Integration Working Group
1997-2000: Secretary, American Electrophoresis Society

Ongoing Journal Referee - Proteomics, Electrophoresis, BMC Bioinformatics, Journal of Chromatography, Archives of Microbiology, and Journal of Microbiology Methods
Peer Reviewer for DOE Office of Biological and Environmental Research
Ad Hoc Peer Reviewer for National Institutes of Health

Current Research Interests and Collaborations

My current research interests include (1) the detection and characterization of changes in protein expression within biological systems in response to environmental stimuli and disease processes, (2) the development of new approaches to the separation and characterization of proteins in complex mixtures that are compatible with high-throughput research applications with a particular interest in environmental samples, (3) the construction of databases for proteomics data, (4) the interfacing of the proteomics databases with gene expression and gene sequence databases.

Throughout my career, I have used two-dimensional gel electrophoresis (2DE) as a tool for protein separations; in the past decade I have added peptide and protein mass spectrometry together with bioinformatics tools for the identification and characterization of specific proteins. I am also working on the development of methods for separation of native proteins (classical 2DE is designed for the separation of denatured proteins) that will allow the detection and characterization of protein-protein interactions as well as protein function. In addition, I continue to direct development and maintenance of a World Wide Web database for the storage and interrogation of the proteomics data generated by my current research projects (<http://gelbank.anl.gov/>) and develop collaborations to facilitate the interfacing of this database with existing and developing gene expression and gene sequence databases.

A majority of my research funding has come from the Department of Energy Office of Biological and Environmental Research and my current interest in developing methods for the identification and characterization of proteins from environmental samples is rooted in that experience. I have active collaborations within the Subsurface Science program at Argonne as well as with DOE-funded biogeochemistry and microbiology projects led by colleagues at Pacific Northwest National Laboratory; my past collaborations with colleagues at Oak Ridge National Laboratory provide potential for new research associated with the DOE Field Research Center.

In addition to my interest in analysis of environmental samples for the characterization of microbial community activities pertinent to the DOE mission needs, I collaborate locally with colleagues engaged in health-related research projects. These collaborations include work on human embryonic stem cells as well as proteins of interest to the Midwest Center for Structural Genomics here at Argonne and work on the characterization of paxillin with colleagues at the University of Chicago.

Management Experience

I have directed the Protein Mapping Group for approximately two decades, successfully leading the migration from human health effects protein studies to microbial proteome analyses. I orchestrated addition of peptide mass spectrometry to the 2DE proteomics capabilities at Argonne, first through obtaining Argonne laboratory directed research and development (LDRD) funding, then through collaboration with several of the most active protein mass spectrometry laboratories in the United States (e.g., John Yates at the Scripps Research Institute, David Lubman at University of Michigan, Richard Smith at Pacific Northwest National Laboratory) and,

most recently, by adding protein mass spectrometry capability to the Argonne Biosciences instrumentation. I have directed a research group since 1985, with the size of that group ranging from 2 members up to 12.

I am currently serving my second term as Acting Division Director for the Argonne Biosciences Division. During the 1999-2000 term, I worked with A. Joachimiak to produce the first Argonne application to the NIH for a Protein Structure Initiative Center. This successful application led to the initiation of the Midwest Center for Structural Genomics which is now known as the most productive of all of the NIH PSI Structural Genomics Centers. I gained valuable experience during that period of my career in how to interact with Program Managers at NIH and DOE as well as learning how to work with Argonne upper management and University of Chicago management. Now, having been asked to step into this temporary position for the second time, I am enjoying the challenges of creating integrated research teams, competing for funding in an even more competitive climate, and working together with other Argonne managers to generate new research initiatives, maintain existing collaborative research with local universities as well as other National Laboratories, and exploring new collaborations. I have an excellent working relationship with the Program Managers within the DOE Office of Biological and Environmental Research and am working on developing similar relationships with the NIH program offices. In addition, I am working with Argonne managers to improve the visibility of Argonne's Biosciences capabilities in the defense funding arena. With the importance of computation to biological studies increasing, I am working on a closer association of the Biosciences Division with the Mathematics and Computer Science Division.

Representative Past Funding (PI in parentheses)

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| KP-11, 61304 (C.S. Giometti)
U.S. Department of Energy
<i>Analysis of S. oneidensis membrane protein expression in response to electron acceptor availability</i>
The goal of the project was to characterize the environmental regulation of the expression of <i>Shewanella oneidensis</i> membrane proteins involved in the reduction of metals relevant to bioremediation. | 10/01/03-09/30/06 |
| KP-11, 60444 (C.S. Giometti)
U.S. Department of Energy
<i>The Microbial Proteomics Project: A Database of Microbial Protein Expression in the Context of Genome Analysis</i>
The goal of the project was to explore whole genome sequence information for defining the functions of unknown genes and regulatory networks in dissimilatory metal reduction pathways. | 06/01/01-09/30/06 |
| KP-11, 60448 (C.S. Giometti)
U.S. Department of Energy
<i>Genomes to Life Center for Molecular and Cellular Systems: A Research Program for Identification and Characterization of Protein Complexes</i>
The goal of this project, a subtask within the Oak Ridge National Laboratory GTL project, was to identify the protein components in isolated protein complexes. | 08/1/02-07/31/06 |
| 3284, 2004-157-NO (C.S. Giometti)
Argonne Laboratory Directed Research and Development | 10/01/03-09/30/06 |

High-throughput Analysis of Low Abundance Protein Constituents in Complex Biological Mixtures

The goal of this project is to develop protein separation and analysis methods for the high-throughput analysis of proteins expressed in low abundance by a variety of biological systems.

Current Funding (PI in parentheses)

859N2 (A. Joachimiak) 09/01/05-08/31/10

National Institutes of Health

The Midwest Center for Structural Genomics

The goal of this project, a subtask within the Midwest Center for Structural Genomics, is to characterize protein expression products that fail in crystallization trials as well as explore approaches to the identification and characterization of proteins expressed as components of protein complexes.

1 RO1 NS047719-01 (L. Chen) 12/1/04-11/30/09

National Institute of Neurological Disorders and Stroke

Nanotechnology for Systems Biology of Neural Stem Cells

The goal of this research is to develop methods for the analysis of the surface proteins of neural stem cells. C. Giometti supervises the separation and identification of proteins expressed on the outer surface of the cultured cells used for this project.

KP-1102010, 61318 (J. Fredrickson, PNNL) 09/01/06–09/30/08

U.S. Department of Energy

Shewanella oneidensis Ecophysiology

The overall goal of this project is to apply the tools of genomics, leveraging the availability of genome sequence for 18 additional strains of *Shewanella*, to better understand the ecophysiology and speciation of respiratory-versatile members of this important genus. This Argonne subtask, with C. Giometti as PI, is directed toward the characterization of proteome changes in cells with altered electron transport composition, including analysis of the phosphoproteome.

KP-1504010, 66288 (C. Giometti) 10/01/07–Open

U.S. Department of Energy

Argonne Subsurface Science Program

Argonne research efforts in the Subsurface Science Program focus around synchrotron-based biogeosciences relevant to the ERSD long-term measure to incorporate coupled physical, chemical, and biological processes into decision making for environmental remediation and long-term stewardship. As acting Argonne Biosciences Division Director, C. Giometti coordinates the Argonne program and also leads the environmental proteomics component of that program.

2008-124-N0, 03970 (K. Kemner) 10/01/07-09/30/08

Argonne Laboratory Directed Research and Development Program

Stabilization of Subsurface Contaminants Through Augmentation of Natural Biological and Geochemical Processes

Integration of Argonne's unique capabilities in high performance computing, synchrotron-based measurements, and high-throughput methods for analysis of biomolecules, together with the integration of novel Argonne scientific expertise, will be used for the study of

biogeochemical cycling, particularly as it relates to physical and chemical transformations of contaminants in lab- and field-based systems. C. Giometti leads the environmental proteomics component of this integrate program.

Publication List

Journal Articles

1. The influence of cultivation methods on *Shewanella oneidensis* physiology and proteome expression. Elias DA, Tollaksen SL, Kennedy DW, Mottaz HM, **Giometti CS**, McLean JS, Hill EA, Pinchuk GE, Lipton MS, Fredrickson JK, Gorby YA. Arch Microbiol. 189:313-24, 2008.
2. A combinatorial approach to studying protein complex composition by employing size-exclusion chromatography and proteome analysis. Li SS, **Giometti CS**. J Sep Sci. 30:1549-55, 2007.
3. Differential Protein Expression in the Metal-Reducing Bacterium *Geobacter metallireducens* Grown with Fe(III) Citrate or Nitrate. Ahrendt AJ, Tollaksen SL, Lindberg C, Zhu W, Yates JR 3rd, Nevin KP, Babnigg G, Lovley DR, **Giometti CS**. Proteomics, 22: 4148-4157, 2007.
4. Detection of In-Situ Derivatized Peptides in Microbial Biofilms by Laser Desorption 7.87 eV Postionizaton Mass Spectrometry. Edirisinghe PD, Moore JF, Skinner-Nemec KA, Lindberg C, **Giometti CS**, Veryovkin IV, Hunt JE, Pellin MJ, Hanley L. Anal Chem. 79:508-514, 2007.
5. Proteomic Analysis of *Psychrobacter cryohalolentis* K5 During Growth at SubzeroTemperatures. Bakermans C, Tollaksen SL, **Giometti CS**, Wilkerson C, Tiedje JM, Thomashow MF. Extremophiles. 11:343-54, 2007.
6. A database of unique protein sequence identifiers for proteome studies. Babnigg G., **Giometti CS**. Proteomics 6:4514-4522, 2006.
7. The proteome of dissimilatory metal-reducing microorganism *Geobacter sulfurreducens* under various growth conditions. Ding YH, Hixson KK, **Giometti CS**, Stanley A, Esteve-Núñez A, Khare T, Tollaksen SL, Zhu W, Adkins JN, Lipton MS, Smith RD, Mester T, Lovley DR. Biochim Biophys Acta. 1764:1198-206, 2006.
8. DNA Microarray and Proteomic Analyses of the RpoS Regulon in *Geobacter sulfurreducens*. Nunez C., Esteve-Nunez A, **Giometti CS**, Tollaksen S, Khare T, Lin W, Lovley DR, Methe BA J. Bacte. 188:2792–2800, 2006.
9. Differential recovery of biotinylated microbial proteins using monomeric or polymeric avidin. Khare T and **Giometti CS**. BioTechniques 40:584-588, 2006.
10. Knock-out of a prohibitin-like protein results in alteration of iron metabolism, increased spontaneous mutation and hydrogen peroxide sensitivity in bacterium *Shewanella oneidensis*. Gao W, Liu Y, **Giometti CS**, Tollaksen S, Khare T, Wu L, Fields MW and Zhou J. BMC Genomics 7:76, 2006.

11. Differential protein expression in the metal-reducing bacterium *Geobacter sulfurreducens* PCA grown with fumarate or ferric citrate. Khare T, **Giometti CS**, Esteve-Núñez A, Nevin KP, Zhu W, Yates III JR, and Lovley DR. *Proteomics* 6: 632-40, 2006.
12. Large-scale muLC-MS/MS for silver and Coomassie blue-stained polyacrylamide gels. Zhu, W, Venable, J, **Giometti, CS**, Khare, T, Tollaksen, S, Ahrendt, AJ, and Yates, JR 3rd. *Electrophoresis* 26: 4495-4507, 2005.
13. XRF and XAFS analysis of electrophoretically isolated nondenatured proteins. Kemner KM, Kelly SD, O'Loughlin EJ, Khare T, Moe LA, Fox BG, Donnelly MI, Londer Y, Schiffer M, and **Giometti CS**. *Physica Scripta*, T115: 940-942, 2005.
14. Global profiling of *Shewanella oneidensis* MR-1: Expression of 'hypothetical' genes and improved annotations. Kolker E, Purvine, S, Picone AF, Kolker N, Holzman T, Cherny T, ... **Giometti CS et al.** *Proc. Natl. Acad. Sci.*, 102: 2099-2104, 2005.
15. Differentiation of prostate cancer PC-3 Cells induced by inosine-5'-monophosphate dehydrogenase inhibitors. Floryk D, Tollaksen S, **Giometti CS**, and Huberman E. *Cancer Res.* 64: 9049-9056. 2005.
16. Low temperature growth of *Shewanella oneidensis* MR-1. Abboud R, Popa R, Souza-Egipsy V, **Giometti CS**, Tollaksen SL, Mosher JJ, Findlay RH, and Nealson KH. *Appl. Env. Microbiol* 71: 811-816, 2005.
17. Shotgun proteomics of *Methanococcus jannaschii* and insights into methanogenesis. Zhu W, Reich CI, Olsen GJ, **Giometti CS**, Yates JR 3rd. *J Proteome Research* 3: 538-48, 2004.
18. GELBANK: a database of annotated two-dimensional gel electrophoresis patterns of biological systems with completed genomes. Babnigg G and **Giometti CS**. *Nucleic Acids Res.* 32: D582-585, 2004.
19. Identification of 2D-gel Proteins: A Comparison of MALDI/TOF Peptide Mass Mapping to μ LC-ESI Tandem Mass Spectrometry. Lim H, Hays LG, Eng J, Tollaksen SL, **Giometti CS**, Holden JF, Adams MWW, Reich CI, Olsen GJ, and Yates III JR, *J. Am. Soc. Mass. Spectrom.* 14: 957-970, 2003.
20. Analysis of the *Shewanella oneidensis* Proteome by Two-Dimensional Gel electrophoresis under Non-denaturing Conditions. **Giometti CS**, Khare T, Tollaksen SL, Tsapin A, Zhu W, Yates III JR, and Nealson KH, *Proteomics* 3: 777-785, 2003.
21. ProteomeWeb: A Web-Based Interface for the Display and Interrogation of Proteomes. Babnigg G and **Giometti CS**. *Proteomics* 3: 584-600, 2003.
22. Global Analysis of a "Simple" Proteome: *Methanococcus jannaschii*. **Giometti CS**, Reich CI, Tollaksen SL, Babnigg G, Lim H, Zhu W, Yates III JR, and Olsen GJ. *J. Chrom. B*, 782: 227-243, 2003.

23. Gene Expression and Protein Profiles of *Shewanella oneidensis* during anaerobic growth with different electron acceptors. Beliaev AS, Thompson DK, Khare T, Lim H, Brandt CC, Li G, Murray AE, Heidelberg JF, **Giometti CS**, Yates III JR, Nealson KH, Tiedje JM, and Zhou J. *Omics* 6: 39-60, 2002.
24. Transcriptional and Proteomic Analysis of a Ferric Uptake Regulator (Fur) Mutant of *Shewanella oneidensis*: Possible Involvement of Fur in Energy Metabolism, Transcriptional Regulation, and Oxidative Stress. Thompson DK, Beliaev AS, **Giometti CS**, Tollaksen SL, Khare T, Lies DP, Nealson KH, Lim H, Yates J 3rd, Brandt CC, Tiedje JM, Zhou J. *Appl Environ Microbiol.* 68:881-892, 2002.
25. Structural modifications of *Methanococcus jannaschii* flagellin proteins revealed by proteome analysis. **Giometti CS**, Reich CI, Tollaksen SL, Babnigg G, Lim H, Yates III JR, and Olsen GJ. *Proteomics* 1:1033-1042, 2001.
26. Methanol toxicity and formate oxidation in NEUT2 mice. CookRJ, Champion KM, and **Giometti CS**. *Arch. Biochem. Biophys.* 393:192-198, 2001.
27. Identification of membrane proteins in the hyperthermophilic archaeon *Pyrococcus furiosus* using proteomics and prediction programs. Holden JF, Poole II FL, Tollaksen SL, **Giometti CS**, Lim H, Yates III JR, and Adams MWW. *Comp. and Funct. Genomics* 2: 275-288, 2001.
28. Improved expression of a highly toxic protein, Bax, in *Escherichia coli* by attachment of a leader peptide derived from the GroES cochaperone. Donnelly MI, Stols L, Wilkins-Stevens P, Cai X, Tollaksen SL, **Giometti CS**, and Joachimiak A. *Protein Expression and Purification* 22: 422-429, 2001.
29. Structural modifications of *Methanococcus jannaschii* flagellin proteins revealed by proteome analysis. **Giometti CS**, Reich CI, Tollaksen SL, Babnigg G, Lim H, Yates III JR, and Olsen GJ. *European J. Mass Spectrometry* 7: 207-217, 2001.
30. Mouse liver selenium-binding protein decreased in abundance by peroxisome proliferators. **Giometti CS**, Liang X, Tollaksen SL, Wall DB, Lubman DM, Subbarao V, and Rao MS. *Electrophoresis* 21: 2162-2169, 2000.
31. The fat liver dystrophy mutant mouse: Microvesicular steatosis associated with altered expression of levels of peroxisome proliferator-regulated proteins. Rehnmark S, **Giometti CS**, Slavin BG, Doolittle MH, and Reue K. *J. Lipid Res.*, 39, 2209-2217, 1998.
32. A comparison of liver protein changes in mice and hamsters treated with the peroxisome proliferator Wy-14, 643. **Giometti CS**, Tollaksen SL, Liang X, and Cunningham ML. *Electrophoresis*, 19: 2498-2505, 1998.
33. Gel electrophoresis for studying biological function. Barany M, Barany K, and **Giometti CS**. *Analyt. Chim. Acta* 372: 1-34, 1998.
34. Analysis of differential protein expression in normal and neoplastic human breast epithelial cell lines. Williams K, Chubb C, Huberman E, and **Giometti CS**. *Electrophoresis* 19: 333-343, 1998.

35. Purification of chaperonins from thermophilic bacteria and archaea. Joachimiak A, Quaiter-Randall E, Tollaksen SL, Mai X, Adams MWW, Josephs R, and **Giometti CS**. *J. Chromatogr. A* 773: 131-138, 1997.
36. A two-dimensional electrophoresis database of human breast epithelial cell proteins. **Giometti CS**, Williams K, and S. L. Tollaksen. *Electrophoresis* 18: 573-581, 1997.
37. Sequential muscle biopsy changes in a case of congenital myopathy. Danon MJ, **Giometti CS**, Manaligod JR, and Swisher C. *Muscle Nerve* 20: 561-569, 1997.
38. Regulation of thymus PCNA expression is altered in radiation-sensitive wasted mice. Woloschak GE, Paunesku T, Libertin CR, Chang-Liu C-M, Churchill C, Panozzo J, Grdina DJ, Gemmell MA, and **Giometti CS**. *Carcinogenesis* 17: 2357-2365, 1996.
39. Two-dimensional gel electrophoresis mapping of proteins isolated from the hyperthermophile *Pyrococcus furiosus*. **Giometti CS**, Tollaksen SL, Mukund S, Zhou Z-H, Ma K, Mai X, and Adams MWW. *J. Chromatogr. A* 698: 341-349, 1995.
40. Polyacrylamide gel electrophoretic methods in the separation of structural muscle proteins. Barany K, Barany M, **Giometti CS**. *J. Chromatogr.* 698: 301-332, 1995.
41. Analysis of proteins from human breast epithelial cells using two-dimensional gel electrophoresis. **Giometti CS**, Tollaksen SL, Chubb C, Williams C, Huberman E. *Electrophoresis* 16: 1215-1224, 1995.
42. Identification of a heritable deficiency of the folate-dependent enzyme 10-formyltetrahydrofolate dehydrogenase in mice. Champion KM, Cook RJ, Tollaksen SL, and **Giometti CS**. *Proc. Natl. Acad. Sci. USA* 91: 11338-11342, 1994.
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45. Differentiation induction in human breast tumor cells by okadaic acid and related inhibitors of protein phosphatases 1 and 2A. Kiguchi K, **Giometti CS**, Chubb CH, Fujiki H, and Huberman E. *Biochemical and Biophysical Research Communications* 189: 1261-1267, 1992.
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53. A comparative study of the effects of clofibrate, ciprofibrate, WY-14, 643, and di-(2-ethylhexyl)-phthalate on liver protein expression in mice. **Giometti CS**, Taylor J, Gemmell MA, Tollaksen SL, Lalwani ND, and Reddy JK. Appl. Theor. Electrophoresis 2: 101-107, 1991.
54. Characterization of a protein that appears in the nervous system of the moth *Manduca sexta* coincident with neuronal death. Montemayor ME, Fahrbach SE, Giometti CS, and Roy EJ. FEBS Letters 276: 219-222, 1990.
55. The expression of myosin light chains and tropomyosin in human muscle biopsies with histochemical type 1 and type 2 fiber deficiency. **Giometti CS** and Danon MJ. Muscle and Nerve 13: 209-214, 1990.
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58. Mixture decomposition applied to the analysis of two-dimensional electrophoretic preparation of protein samples. Taylor J and **Giometti CS**. Appl. Theor. Electrophoresis 1: 47-51, 1988.
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65. Protein changes occurring during storage of platelet concentrates: A two-dimensional gel electrophoretic analysis. Snyder EL, Dunn BE, **Giometti CS**, Napychank PA, Ferri PM, Tandon NN, and Hofmann J-P. *Transfusion* 27: 335-341, 1987.
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