BIOGRAPHICAL SKETCH

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NAME Zhang, Xiang	POSITION TITLE Professor of Chemistry
eRA COMMONS USER NAME (credential, e.g., agency login) ZHANGX	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
Lanzhou University, Lanzhou, CHINA	B.S.	07/89	Radiochemistry
Institute of Modern Physics, Lanzhou, CHINA	M.S.	07/94	Nuclear Physics
Purdue University, West Lafayette, IN	Ph.D.	05/01	Analytical Chemistry

A. Positions and Honors

Positions and Employment

1989-1991	Patent Assistant, Institute of Science and Technology Information of Gansu, Lanzhou, CHINA
1991-1996	Research Associate, Institute of Modern Physics, Lanzhou. CHINA
2001-2004	Senior Scientist, Beyond Genomics Inc, Waltham, MA
2004-2007	Research Assistant Professor, Director of Computational Life Sciences and Informatics, Bindley Bioscience Center, Purdue University, West Lafayette, IN
2008-2011	Associate Professor, Department of Chemistry, University of Louisville, Louisville, KY Member of Institute for Molecular Diversity and Drug Design (IMD3) Member of Center for Regulatory and Environmental Analytical Metabolomics (CREAM)
2011-	Professor, Department of Chemistry, University of Louisville, Louisville, KY Member of Institute for Molecular Diversity and Drug Design (IMD3) Member of Center for Regulatory and Environmental Analytical Metabolomics (CREAM)

Other Experience and Professional Memberships

2000-	Member, American Chemical Society
1999-	Member, American Society of Mass Spectrometry
2009	NSF *ad hoc* Reviewer
2011-	NIH *ad hoc* Reviewer, the Instrumentation and Systems Development (ISD) Study Section

Honors

2000	Jon and Ruthanna Amy Award, Purdue University
2004	Patent Agent, United States Patent and Trademark Office, US
2004	Seed for Success Award, Purdue University
2005	Professional Development Award, Purdue University
2007	Bioinformatics Platform Dissemination Award, Canary Foundation

B. Selected Peer-reviewed Publications (Selected from 82 peer-reviewed publications)

Most relevant to the current application (in chronological order)

1. Kim, S.; Fang, A.; Wang, B.; Jeong, J.; Zhang, X. An optimal peak alignment for comprehensive two-dimensional gas chromatography mass spectrometry using mixture similarity measure. *Bioinformatics.* **2011**, 27, 1660-1666.
2. Zhang, J.; Fang, A.; Wang, B.; Bogdanov, B.; Kim, S. H.; Zhou, Z.; McClain, C.; Zhang, X. iMatch, A retention index tool for analysis of gas chromatography mass spectrometry data. *J. Chromatogr. A* **2011**, 1218, 6522-6530.
3. Koo, I.; Zhang, X.; Kim, S. Wavelet- and Fourier-Transforms-based spectrum similarity approaches to compound identification in gas chromatography/mass spectrometry. *Anal. Chem.* **2011**, 83, 5631-5638.

4. Jeong, J.; Shi, X.; Zhang, X; Shen, C. An empirical Bayes model using a competition score for metabolite identification in gas chromatography mass spectrometry. *BMC Bioinformatics* **2011**, 12:392.
5. Wei, X.; Sun, W.; Shi, X.; Koo, I.; Wang, B.; Yin, X.; Tang, Y.; Bogdanov, B.; Kim, S. H.; Zhou, Z., McClain, C. J.; Zhang, X. MetSign: A computational platform for high-resolution mass spectrometry-based metabolomics. *Anal. Chem.* **2011**, 83, 7668-7675**.**
6. Zhao, Y.; Zhang, J.; Wang, B.; Kim, S.; Fang, A.; Bogdanov, B.; Zhou, Z.; McClain, C.; Zhang, X. A method of calculating the second dimension retention index in comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry. *J. Chromatogr. A* **2011**, 1218, 2577-2583.
7. Jeong, J.; Shi, X.; Zhang, X.; Kim, S.; Shen, C. Model-based peak alignment of metabolomics profiling from comprehensive two-dimensional gas chromatography mass spectrometry. *BMC Bioinformatics* **2012**, 13:27.
8. Kim, S.; Koo, I.; Wei, X.; Zhang, X. A method of finding optimal weight factors for compound identification in gas chromatography–mass spectrometry. *Bioinformatics* **2012**, 28(8), 1158-1163.
9. Zhong, W.; Zhao, Y.; Sun, X.; Wei, X.; Shi, X.; Sun, W.; Yin, X.; Sun, X.; Kim, S.; McClain, C. J.; Zhang, X.; Zhou, Z. Chronic alcohol exposure stimulates adipose tissue lipolysis in mice: Role of reverse triglyceride transport in the pathogenesis of alcoholic steatosis. *Am. J. Pathol.* **2012**, 180, 998-1007**.**

Additional recent publications of importance to the field (in chronological order)

1. Shen, C.; Wang, Z.; Shankar, G.; Zhang, X.; Li, L. A hierarchical statistical model to assess the confidence of peptide and protein identifications made by tandem mass spectrometry. *Bioinformatics* **2008**, 24, 202-208.
2. Wang, B.; Fang, A.; Heim, J.; Bogdanov, B.; Pugh, S.; Libardoni, M.; Zhang, X. DISCO: distance and spectrum correlation optimization alignment for two-dimensional gas chromatography time-of-flight mass spectrometry - based metabolomics. *Anal. Chem*. **2010**, 82, 5069-5081.
3. Zhang, X.; Fang, A.; Riley, C. P.; Wang, M.; Regnier, F. E. Buck, C. Multi-dimensional liquid chromatography in quantitative proteomics. *Anal. Chimica Acta* **2010**, 664, 101-113.
4. Kim, S.; Koo, I.; Fang, A.; Zhang, X. Smith-Waterman peak alignment for comprehensive two-dimensional gas chromatography mass spectrometry. *BMC Bioinformatics* **2011**, 12, 235
5. Zhao, Y.; Tan, Y.; Dai, J.; Li, B.; Guo, L.; Cui, J.; Wang, G.; Shi, X.; Zhang, X.; Mellen, N.; Li, W.; Cai, L. Exacerbation of diabetes-induced testicular apoptosis by zinc deficiency is most likely associated with oxidative stress; p38 MAPK activation; and p53 activation in mice. *Toxicol. Lett.* **2011**, 200, 100-106.
6. Zhao, Y.; Zhang, J.; Wang, B.; Kim, S.; Fang, A.; Bogdanov, B.; Zhou, Z.; McClain, C.; Zhang, X. A method of calculating the second dimension retention index in comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry. *J. Chromatogr. A* **2011**, 1218, 2577-2583.

C. Research Support

Ongoing Research Support

1. NIH M. Cave (PI) 08/01/12 - 08/31/17
PCBs Worsen Obesity/metabolic Syndrome Through ‘Toxic Metabolic Endotoxemia’
This project will examine how PCBs affect the gut:liver:adipose axis and lead to toxic-metabolic endotoxemia.
Role: Consultant

2. NIH W. Watson (PI) 04/01/12 - 03/30/14
Effect of Dietary Fat on the Hepatotoxicity of Environmental Arsenic
In this proposal we will test the hypothesis that arsenic exposure facilitates the progression from simple steatosis to steatohepatitis by altering metabolic pathways related to inflammation. We will use a combination of metabolomics and proteomics to identify pathways that are dysregulated in our novel animal model of environment-diet interactions.
Role: Co-I

3. NIH/NIGMS RO1GM087735 X. Zhang (PI) 05/01/09 - 04/30/13
Mass Informatics of Two Dimensional Gas Chromatography Time-of-flight Mass Spectrometry

This project will develop informatics tools to analyze metabolomics data generated from gas chromatography / gas chromatography / time-of-flight mass spectrometry experiments to enable comparative metabolite profiling with high precision and high volume.
Role: PI

4. NIH/NIAAA 1RC2AA019385 C. McClain (PI) 10/01/09 - 09/30/12
   Biomarkers of Steatohepatitis
   This project uses a large number of serum/plasma specimens from well-characterized patients with severe alcoholic hepatitis, non-alcoholic steatohepatitis, and a highly-novel patient population of well-characterized environmental toxicants and both a proteomics and metabolomics approaches for discovery of biomarkers for alcoholic liver disease and specifically alcoholic steatohepatitis.
   Role: Co-I

5. Industry Research Gift X. Zhang (PI) 01/01/08 -
   Mass Informatics of Differential Metabolomics
   The goal of this project is to support the bioinformatics projects to study metabolite regulation.
   Role: PI

Completed Research Support

1. UofL/MRG M. Yu (PI) 06/01/11 - 05/31/12
   Quantum Mechanics Simulation-based Metabolite Identification
   This project will create an in-silico MS/MS database based on quantum mechanics simulation. A bioinformatics system will be further developed for metabolite identification using the in-silico MS/MS database.
   Role: co-PI

2. The Multiple Myeloma Research Foundation M. Wang (PI) 08/01/08 - 07/30/11
   Biomarker Discovery and Validation in Multiple Myeloma Cells Using Multiple Proteomics Platforms
   The study employs cutting-edge proteomic technologies to analyze myeloma patient tissue samples and identify biomarkers that are responsible for the disease's onset and progression, as well as patients' response to treatments.
   Role: Co-I

3. NIH/NCI U24CA126480 F. Regnier (PI) 10/01/06 - 09/30/11
   APT: the Analytical Proteomics Team
   The major goal of this project is to develop robust protocols and standards for biomarker discovery in MS based proteomics. High specificity immunologic reagents will be developed for precise detection and quantification of biomarkers of relevance for breast and prostate cancer.
   Role: Co-PI

4. University of Louisville X. Zhang (PI) 02/01/09 - 01/31/10
   Development of Two Dimensional Gas Chromatography Time-of-flight Mass Spectrometry for Differential Metabolomics
   This one year project will assess the technical capability of two dimensional gas chromatography time-of-flight mass spectrometry for differential metabolomics.
   Role: PI

5. NIH R41RR024306 Zhang (PI) 02/01/08 - 01/31/09
   Accurate Protein Identification Using Peptide Separation Information and Tandem MS Algorithms
   This project will develop algorithms aimed at predicting peptide separation profiles for two-dimensional ion mobility spectrometry. The developed algorithms will be used to assist protein identification.
   Role: PI

6. Canary Foundation X. Zhang/J. Chen (co-PIs) 06/01/07 - 05/30/08
   CAPS Bioinformatics Platform Dissemination
   The major goal of this project is to develop bioinformatics system for meta data management for the computational proteomics analysis system.
   Role: Co-PI

7. NIH DK070290 F. Regnier (PI) 10/01/04 - 09/30/07
   Tools for Differential Metabolics
   The major goal of this project is to develop a new set of tools for characterizing and recognizing temporal changes in the metabolome of model organisms.
   Role: Co-PI
8. Showalter Trust SPS 0IK44 M. Mohammed (PI) 07/01/06 - 06/30/07
   The Use of Proteomics to Determine Pathways of Metastasis
   This study identifies biomarkers that distinguish metastatic mammary tumors in lymph and also evaluate the predictive value of the biomarkers.
   Role: Co-I