








SHEN, XIAOTAO Ph.D.

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INFORMATION

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EDUCATION & RESEARCH EXPERIENCE

- > **Postdoctoral Research Fellow** 2019/4 – present, **Stanford University**
(Advisor: [Prof. Michael Snyder](#))
- > **Research Scientist** 2019/1 – 2019/3, **Chinese Academy of Sciences**
(Advisor: [Prof. Zheng-Jiang Zhu](#))
- > **Ph.D.** 2013/8 – 2018/12, **Chinese Academy of Sciences**
(Advisor: [Prof. Zheng-Jiang Zhu](#))
- > **B.S.** 2009/9 – 2013/6, **Inner Mongolia University**

RESEARCH INTERESTS

- > Mass Spectrometry Data Processing Algorithms and Software Development.
- > Multi-omics Data Integration Methods Development.
- > Precision Exposome and Multi-omics Integration for Healthcare.
- > Multi-omics Profiling for Human Pregnancy Related Disease Diagnosis and Mechanism Research.
- > Aging and Neurodegenerative Diseases.
- > Microbiome Data Processing.
- > Wearable Data and Precision Medicine.

HONORS AND AWARDS

- > Winner Selected by the Event Committee Exposome Data Challenge Event (2021)
- > Student Travel Award for Oral Presentation The International Metabolomics Society (2018)
- > International Conference Travel Award The Metabolites Journal (2018)
- > China National Scholarship Ministry of Education of the People's Republic of China (2017)
- > Award for Outstanding Youth Report The 3rd China MS Analysis Conference (2017)
- > Merit Student University of Chinese Academy of Sciences (2016)

- > Award for Outstanding Youth Report The 34th China MS Society Conference (2016)
- > Inner Mongolia Outstanding Graduate Inner Mongolia Autonomous Region (2013)
- > National Encouragement Scholarship Inner Mongolia University (2011)

FIRST/CO-FIRST PUBLICATIONS

- > **X. Shen**, C. Wang, M.P. Snyder, massDatabase: Utilities for the Operation of the Public Compound and Pathway Database, **Bioinformatics**, 2022, btac546. [↗](#)
- > **X. Shen**, W. Shao, C. Wang, L. Liang, S. Chen, S. Zhang, M. Rusu, M.P. Snyder, Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine, **Briefing in Bioinformatics**, 2022, bbac331. [↗](#)
- > **X. Shen**, H. Yan, C. Wang, P. Gao, C.H. Johnson, M.P. Snyder, TidyMass an Object-oriented Reproducible Analysis Framework for LC-MS Data, **Nature Communications**, 2022, 4365. [↗](#)
- > P. Gao, **X. Shen (Co-first)**, X. Zhang, C. Jiang, M. P. Snyder, Precision Environmental Health Monitoring by Longitudinal Exposome and Multi-omics Profiling, **Genome Research**, 2022, **32**, 1199-1214. [↗](#)
- > **X. Shen**, S. Wu, L. Liang, S. Chen, K. Contrepois, Z.-J. Zhu and M.J. Snyder, metID: an R Package for Automatable Compound Annotation for LC-MS-based Data, **Bioinformatics**, 2021, 1, 1-2. [↗](#)
- > **X. Shen**, R. Wang, X. Xiong, Y. Yin, Y. Cai, J. Ma, N. Liu, Z.-J. Zhu, Large-scale Metabolite Identification for Untargeted Metabolomics Using Metabolic Reaction Network, **Nature Communications**, 2019, 10:1516. [↗](#)
- > **X. Shen** and Z.-J. Zhu, MetFlow: An Interactive and Integrated Workflow For Metabolomics Data Cleaning and Differential Metabolite Discovery, **Bioinformatics**, 2019, 35, 16. [↗](#)
- > H. Jia, **X. Shen (Co-first author)**, Y. Guan, M. Xu, M. Mo, J. Zhu and Z.-J. Zhu, Assessment of The Response to Neoadjuvant Chemo-Radiation in Rectal Cancer Patients based on A Metabolomics Approach, **Radiotherapy and Oncology**, 2018, 128, 548-556. [↗](#)
- > J. Wang, T. Zhang, **X. Shen (Co-first author)**, J. Liu, D. Zhao, Y. Sun, L. Wang, Y. Liu, X. Gong, Y. Liu, Z.-J. Zhu, F. Xue, Serum Metabolomics for Early Diagnosis of Esophageal Squamous Cell Carcinoma by UHPLC-QTOF/MS, **Metabolomics**, 2016, 12: 116. [↗](#)
- > **X. Shen**, X. Gong, Y. Cai, Y. Guo, J. Tu, T. Zhang, J. Wang, F. Xue, Z.-J. Zhu, Normalization and Integration of Large-Scale Metabolomics Data Using Support Vector Regression, **Metabolomics**, 2016, 12: 89. [↗](#)

COLLABORATIVE PUBLICATIONS

- > L. Liang, M. Rasmussen, B. Piening, **X. Shen**, S. Chen, H. Rost, J. Snyder, R. Tibshirani, L. Skotte, N. Lee, K. Contrepois, B. Feenstra, H. Zackriah, M.J. Snyder, M. Melbye, Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women, **Cell**, 2020, 181, 7, 1680-1692. [↗](#)
- > Z. Wang, B. Cui, F. Zhang, Y. Yang, **X. Shen**, Z. Li, W. Zhao, Y. Zhang, K. Deng, Z. Rong, K. Yang, X. Yu, K. Li, P. Han, and Z.-J. Zhu, Development of A Correlative Strategy to Discover Colorectal Tumor Tissue Derived Metabolite Biomarkers in Plasma Using Untargeted Metabolomics, **Analytical Chemistry**, 2019, 91, 3, 2401-2408. [↗](#)

- > Z. Zhou, **X. Shen**, X. Chen, J. Tu, X. Xiong, and Z.-J. Zhu, LipidIMMS Analyzer: Integrating Multi-dimensional Information to Support Lipid Identification in Ion Mobility–Mass Spectrometry based Lipidomics, *Bioinformatics*, 2018, 35, 4, 698-700. [↗](#)
- > Z. Zhou, J. Tu, X. Xiong, **X. Shen**, and Z.-J. Zhu, LipidCCS: Prediction of Collision Cross-Section Values for Lipids with High Precision to Support Ion Mobility-Mass Spectrometry based Lipidomics, *Analytical Chemistry*, 2017, 89, 9559–9566. [↗](#)
- > Z. Zhou, **X. Shen**, J. Tu, and Z.-J. Zhu, Large-Scale Prediction of Collision Cross-Section Values for Metabolites in Ion Mobility-Mass Spectrometry, *Analytical Chemistry*, 2016, 88, 11084-11091. [↗](#)

SUBMITTED/PREPARED PUBLICATIONS

- > S. Chen, **X. Shen (Co-first author)**, L. Liang, M. P. Snyder, Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. **Submitted.** [↗](#)
- > **X. Shen**, R. Kellogg, D. Hornburg, N. Bararpour, D.J. Panyard, M.P. Snyder, Multi-omic microsampling captures health perturbations in a lifestyle context. **Submitted.**
- > X. Zhou, **X. Shen (Co-first author)**, G.M. Weinstock, M.P. Snyder. Longitudinal profiling of the microbiome at four body sites reveals core stability and individualized dynamics during health and disease. **Submitted.**
- > **X. Shen**, C. Wang, M.P. Snyder. Extracting Alerted Metabolic Modules Across Human Aging. **In Preparation.**
- > **X. Shen**, L. Liang, S. Chen, M.P. Snyder, Multi-Omics Molecular Profiling During Human Pregnancy. **In Preparation.**








ORAL PRESENTATIONS

- > TidyMass an Object-oriented Reproducible Analysis Framework for LC-MS Data. ACS Fall 2022, August 2022, Virtual meeting.
- > metlD: an R Package for Automatable Compound Annotation for LC–MS-based Data. The 69th American Society for Mass Spectrometry Conference, November 2021, Philadelphia, USA.
- > Decoding Links Between the Exposome and Health Outcomes by Multi-omics Analysis. Exposome Data Challenge Event, April 2021, Virtual meeting.
- > Metabolic Reaction Network-based Recursive Metabolite Identification for Untargeted Metabolomics. The 14th International Conference of the Metabolomics Society, June 2018, Seattle, USA.
- > Assessment of the Response to Neoadjuvant Chemo-Radiation in Rectal Cancer Patients based on a Metabolomics Approach. The 3rd China Mass Spectrometry Analysis Conference, December 2017, Xiamen, China. [↗](#)
- > Normalization and Integration of Large-Scale Mass Spectrometry-based Metabolomics Data Using Support Vector Regression. The 34th China Mass Spectrometry Society Conference, September 2016, Xining, China.
- > Normalization and Integration of Large-Scale Mass Spectrometry-based Metabolomics Data Using Support Vector Regression. The 64th American Society for Mass Spectrometry Conference, June 2016, San Antonio, USA. [↗](#)

POSTER PRESENTATIONS

- > TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. The 70th American Society for Mass Spectrometry Conference, June 2022, Minneapolis, USA.
- > Longitudinal Interactions Between Levels of Serum Cytokine and the Microbiome from Four Body Sites. IMMUNOLOGY2022, May 2022, Portland, USA.
- > Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. The 17th International Conference of the Metabolomics Society, 2020, Virtual meeting.
- > Metabolic Reaction Network based Metabolite Annotation in Untargeted Metabolomics. The 13th International Conference of the Metabolomics Society, June 2017, Brisbane, Austria.

TECHNICAL STRENGTH

-  Languages: Mandarin (Very fluent), English (Fluent).
-  Programming Languages: R , Python , HTML.
-  Bioinformatic Tools: RNA-seq, Proteomics.
-  Other Skills: Markdown, Photoshop, Illustrator, Linux, GitHub , Shiny 