








Shen, Xiaotao Ph.D.

Prof. Michael Snyder's Lab

Center for Genomics and Personalized Medicine, Department of Genetics,
School of Medicine, Stanford University

Information

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Research Interests

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- > 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.

Education & Research Experience

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| > 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 |

Honors & Awards

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| > 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 3 rd 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 Author 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 author)**, 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

- > M. Wei, L. Zhao, J. Lv, X. Li, G. Zhou, B. Fan, **X. Shen**, D. Zhao, F. Xue, J. Wang, T. Zhang, The Mediation Effect of Serum Metabolites On The Relationship Between Long-Term Smoking Exposure and Esophageal Squamous Cell Carcinoma, **BMC cancer**, 2021, **21**, 415. [↗](#)
- > J. Lv, J. Wang, **X. Shen**, J. Liu, D. Zhao, X. Li, B. Fan, Y. Sun, F. Xue, Z.-J. Zhu, T. Zhang, A Serum Metabolomics Analysis Reveals A Panel of Screening Metabolic Biomarkers for Esophageal Squamous Cell Carcinoma, **Clinical and Translational Medicine**, 2021, **11**, 5. [↗](#)
- > X. Li, L. Zhao, M. Wei, J. Lv, Y. Sun, **X. Shen**, D. Zhao, F. Xue, T. Zhang, J. Wang, Serum Metabolomics Analysis for The Progression of Esophageal Squamous Cell Carcinoma, **Journal of Cancer**, 2021, **12**, 3190–3197. [↗](#)

- > 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 Publications

- > S. Chen, **X. Shen (Co-first author)**, L. Liang, M. P. Snyder, Longitudinal Urine Metabolic Profiling and Gestational Age Prediction in Pregnancy. **Submitted**. [↗](#)
- > S. Chen, G. Wang, **X. Shen (Co-first author)**, D. Hornburg, S. Rego, R. Hoffman, S. Nevins, X. Cheng, M.P. Snyder, Integration and Comparison of Multi-omics Profiles of NGLY1 Deficiency Plasma and Cellular Models to Identify Clinically Relevant Molecular Phenotypes. **Submitted**. [↗](#)
- > **X. Shen**, R. Kellogg, D. Panyard, N. Bararpour, M.P. Snyder, Multi-omic microsampling captures health perturbations in a lifestyle context. **Under review in Nature Biomedical Engineering**.
- > 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. **Submitted**.
- > **X. Shen**, C. Wang, M.P. Snyder. Nonlinear changes of human plasma multi-omics profiles across the lifespan. **Submitted**.
- > **X. Shen**, L. Liang, S. Chen, M.P. Snyder, Multi-Omics Molecular Profiling During Human Pregnancy. **Submitted**.

Oral Presentations

- > TidyMass an Object-oriented Reproducible Analysis Framework for LC-MS Data. **ACS Fall 2022**, August 2022, Virtual meeting.
- > metlID: 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

- > Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine. **Stanford Genetics Retreat 2022**, September 2022, Monterey, USA.
- > Deep Learning-based Pseudo-Mass Spectrometry Imaging Analysis for Precision Medicine. **Bay Area Metabolism Meeting (BAMM) 2xs022**, September 2022, Palo Alto, USA.
- > 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.
- > TidyMass An Object-oriented Reproducible Analysis Framework for LC-MS Data. **Stanford Genetics Retreat 2021**, September 2021, Palo Alto, 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.

Teaching Experience

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| > LC-MS Data Processing and Analysis Using R language | 2022/9, Biotree Company
Responsibilities: Lecture |
| > R Language for Reproducible Data Analysis | 2020/4, SCPA
Responsibilities: Lecture |
| > Stanford School of Medicine Intern | 2019/8 – Present, Stanford University
Responsibilities: Mentor |
| > Mass Spectrometry Analysis | 2014/9 – 2014/12, Chinese Academy of Sciences
Responsibilities: Guest lecturer |








Volunteering

- > **Co-chair** 2021/7 – 2022/8, Stanford Chinese Postdoctoral Association
- > **Organizer** 2020/2–2021/12
Stanford Chinese Postdoctoral Oral Presentation Improvement
- > **Member** 2019/7 – 2021/7, Stanford Chinese Postdoctoral Association
- > **Member** 2013/9-2014/7, **Student Association of IRCBC Chinese Academy of Sciences**

Reviews For Peer-Reviewed Journals

- > Nature Communications
- > Briefing in Bioinformatics
- > Bioinformatics
- > GigaScience
- > PLOS One
- > Phytochemistry
- > Genomics, Proteomics&Bioinformatics
- > Communications Chemistry
- > Communications Biology
- > Frontiers Molecular Biosciences
- > iMeta

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 