







Xiaotao Shen Ph.D.

Prof. Michael Snyder's Lab

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Information

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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.

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**

Honors & 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)

- > L. Liang, M. Rasmussen, B. Piening, **X. Shen**, S. Chen, H. Rost, J. Snyder, R. Tibshirani, L. Skotte, N. Lee, K. Contrepolis, 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

- > **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.**
- > 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**, 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) 2022**, 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**, June 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

- > **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**

Journal Referee

- > *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 