

CURRICULUM VITAE

Shichen “Kevin” Shen, Ph.D.

(October 2022)

CURRENT ACADEMIC TITLE

Post-doctoral Research Associate

Department of Pharmaceutical Sciences,
School of Pharmacy and Pharmaceutical Sciences

Associate Director

Proteomics and Bioinformatics Core (PBC) Facility
University at Buffalo, State University of New York (SUNY)

OFFICE ADDRESS & CONTACT INFORMATION

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EDUCATION & TRAINING

◆ Fudan University, China	B.S.	2008-2012	Pharmaceutical Sciences
◆ Washington Univ. in St. Louis	Exchange Student	2011	Summer School
◆ University at Buffalo, SUNY	Ph.D.	2012-2017	Biochemistry

RESEARCH EXPERIENCES

◆ University at Buffalo, SUNY	Graduate Research Assistant	2013-2017	Biochemistry
◆ University at Buffalo, SUNY	Research Fellow	2017-2020	Pharmaceutical Sciences
◆ University at Buffalo, SUNY	Research Associate	2020-	Pharmaceutical Sciences

HONORS & AWARDS

- ◆ 2010 FDU Undergraduate Scholarships – First Class
- ◆ 2011 Fuhua Scholarships

- ◆ 2011 Haini Scholarships
- ◆ 2012 FDU Undergraduate Scholarships – First Class
- ◆ 2012 Excellent graduate of FDU

PROFESSIONAL SOCIETIES

- ◆ American Society for Mass Spectrometry (ASMS)
- ◆ American Association of Pharmaceutical Scientists (AAPS)
- ◆ Association of Biomolecular Resource Facilities (ABRF)
- ◆ US Human Proteome Organization (USHUPO)

PEER-REVIEWED PUBLICATIONS

1. Shen X, Nair B, Mahajan SD, Jiang X, Li J, **Shen S**, Tu C, Hsiao CB, Schwartz SA, Qu J*. New insights into the disease progression control mechanisms by comparing Long-term-non-progressors vs. Normal-progressors among HIV-1 positive patients using an ion current-based MS1 proteomics profiling. *J Proteome Res.* 14(12):5225-39 (2015) (IF = 4.074 in 2019)
2. **Shen S**, Li J, Hilchey S, Shen X, Tu C, Qiu X, Ng A, Ghaemmaghami S, Wu H, Zand M, Qu J*. An Ion-Current-Based Temporal Proteomic Profiling of Influenza A Virus Infected Mouse Lungs Revealed Underlying Mechanisms of Altered Integrity of the Lung Microvascular Barrier. *J Proteome Res.* 15(2):540-53. (2016) (IF = 4.074 in 2019)
3. Zhang T, **Shen S**, Qu J, Ghaemmaghami S*. Global analysis of cellular protein flux quantifies the selectivity of basal autophagy. *Cell Rep.* 14(10):2426-2439. (2016) (IF = 7.700 in 2020)
4. **Shen S**, Jiang X, Li J, Straubinger R, Suarez M, Tu C, Duan X, Thompson A*, Qu J*. Large-Scale, Ion-Current-Based Proteomic Investigation of the Rat Striatal Proteome in a Model of Short- and Long-Term Cocaine Withdrawal. *J Proteome Res.* 15(5):1702-16. (2016) (IF = 4.074 in 2019)
5. Tu C, Li J, **Shen S**, Sheng Q, Shyr Y, Qu J*. Performance Investigation of Proteomic Identification by HCD/CID Fragmentations in Combination with High/Low-Resolution Detectors on a Tribid, High-Field Orbitrap Instrument. *PLoS One.* 11(7):e0160160. (2016) (IF = 2.870 in 2020)
6. Tu C, Bu Y, Vujcic M, **Shen S**, Li J, Qu M, Hangauer DG, Clements JL*, Qu J*. Ion Current-based Proteomics Profiling in Understanding the Inhibitory Effect of Tumor Necrosis Factor Alpha on Myogenic Differentiation. *J Proteome Res.* 15(9):3147-57. (2016) (IF = 4.074 in 2019)
7. Welle K, Zhang T, Hrhorenko J, **Shen S**, Qu J, Ghaemmaghami S*. Time-resolved analysis of proteome dynamics by TMT-SILAC hyperplexing. *Mol Cell Proteomics.* 15(12):3551-3563. (2016) (IF = 4.830 in 2020)
8. Tu C, **Shen S**, Sheng Q, Shyr Y, Qu J*. A peptide-retrieval strategy enables significant improvement of quantitative performance without compromising confidence of identification. *J Proteomics.* 152:276-

282. (2017) (IF = 3.660 in 2020)

9. Tu C, Mojica WD, Straubinger RM, Li J, **Shen S**, Nie L, Roberts R, An B, Qu J*. Quantitative proteomic profiling of paired cancerous and normal colon epithelial cells isolated freshly from colorectal cancer patients. *Proteomics Clin Appl*. 11(5-6). (2017) (RG Journal Impact = 1.75 in 2020)

10. **Shen S**, Ma JH, Wang JJ, He Z, Poon A, Li J, Qu J, Zhang SX*. Characterization of the Mitochondria-associated ER Membrane (MAM) Proteome in A Mouse Model of Type 2 Diabetes. *Sci Rep*. 7(1):2062. (2017) (IF = 4.120 in 2020)

11. Shen X, **Shen S**, Li J, Hu Q, Lie N, Tu C, Wang X, Orsburn BC*, Wang J*, Jun Qu*. An IonStar Experimental Strategy for MS1 Ion Current-Based Quantification Using Ultrahigh-Field Orbitrap: Reproducible, In-Depth, and Accurate Protein Measurement in Large Cohorts. *J Proteome Res*. 16(7):2445-2456. (2017) (IF = 4.074 in 2019)

12. Qu M, An B, **Shen S**, Zhang M, Shen X, Balthasar J, Qu J*. Qualitative and Quantitative Characterization of Protein Biotherapeutics by Liquid Chromatography Mass Spectrometry. *Mass Spectrom. Rev*. 36(6):734-754. (2017) (IF = 9.373 in 2016)

13. Zhang M, An B, Qu Y, **Shen S**, Fu W, Chen Y, Wang X, Young R, Canty JM Jr., Balthasar JP, Murphy K, Bhattacharyya D, Josephs J, Ferrari, L, Zhou S, Bansal S, Vazvaei F*, Qu J*. Sensitive, High-Throughput, and Robust Trapping-Micro-LC-MS Strategy for the Quantification of Biomarkers and Antibody Biotherapeutics. *Anal Chem*. 90(3):1870-1880. (2018) (IF = 6.986 in 2020)

14. Wang X, Niu J, Li J, Shen X, **Shen S**, Straubinger RM, Qu J*. Temporal Effects of Combined Birinapant and Paclitaxel on Pancreatic Cancer Cells Investigated via Large-Scale, Ion-Current-Based Quantitative proteomics (IonStar). *Mol Cell Proteomics*. 17(4):655-671. (2018) (IF = 4.830 in 2020)

15. **Shen S**, Shen X, Li J, Hu Q, Nie L, Tu C, Wang X, Poulsen DJ, Orsburn BC*, Wang J*, Qu J*. IonStar enables high-precision, low-missing-data proteomics quantification in large biological cohorts. *Proc Natl Acad Sci U S A*. 115(21):4767-4776. (2018) (IF = 9.350 in 2020)

16. **Shen S**, An B, Wang X, Hilchey SP, Li J, Cao J, Tian Y, Hu C, Jin L, Ng A, Tu C, Qu M*, Zand MS*, Qu J*. Surfactant Cocktail-Aided Extraction/Precipitation/On-Pellet Digestion Strategy Enables Efficient and Reproducible Sample Preparation for Large-Scale Quantitative Proteomics. *Anal Chem*. 90(17):10350-10359. (2018) (IF = 6.986 in 2020)

17. **Shen S**, Wang X, Orsburn BC*, Qu J*. How could IonStar challenge the current status quo of quantitative proteomics in large sample cohorts? *Expert Rev Proteomics*. 15(7):541-543. (2018) (IF = 1.500 in 2020)

18. Ng AYH, Tu C, **Shen S**, Xu D, Oursler MJ. Qu J, Yang S*. Comparative characterization of osteoclasts derived from murine bone marrow macrophages and RAW 264.7 cells using quantitative proteomics. *JBMR Plus*. doi.org/10.1002/jbm4.10058. (2018)

19. An B, Zhang M, Pu J, **Shen S**, Qu Y, Chen YJ, Huo S, Wang X, Polli JR, Balthasar JP, Herzog D, Ferrari L, Staack RF, Richter WF, Otteneder MB, Benincosa LJ, Zhou S, Vazvaei F*, Qu J*. High-Throughput, Sensitive LC-MS Quantification of Biotherapeutics and Biomarkers Using Antibody-Free, Peptide-Level, Multiple-Mechanism Enrichment via Strategic Regulation of pH and Ionic and Solvent Strengths. *Anal Chem.* 91(5):3475-3483. (2019) (IF = 6.986 in 2020)
20. Singel KL, Emmons TR, Khan ANH, Mayor PC, **Shen S**, Wong JT, Morrell K, Eng KH, Mark J, Bankert RB, Matsuzaki J, Koya RC, Blom AM, McLeish KR, Qu J, Ram S, Moysich KB, Abrams SI, Odunsi K, Zsiros E, Segal BH*. Mature neutrophils suppress T cell immunity in ovarian cancer microenvironment. *JCI Insight.* 4(5):e122311. (2019) (IF = 6.205 in 2020)
21. Wang X, **Shen S**, Rasam SS, Qu J*. MS1 ion current-based quantitative proteomics: A promising solution for reliable analysis of large biological cohorts. *Mass Spectrom Rev.* 38(6):461-482. (2019) (IF = 9.373 in 2016)
22. Kumar A, Wilderman PR, Tu C, **Shen S**, Qu J, Estrada DF*. Evidence of Allosteric Coupling between Substrate Binding and Adx Recognition in the Vitamin D Carbon-24 Hydroxylase CYP24A1. *Biochemistry.* 59(15):1537-1548. (2020) (IF = 2.952 in 2018)
23. An B, Zhang M, Pu J, Qu Y, **Shen S**, Zhou S, Ferrari L, Vazvaei F, Qu J*. Toward Accurate and Robust Liquid Chromatography-Mass Spectrometry-Based Quantification of Antibody Biotherapeutics in Tissues. *Anal Chem.* 92(22):15152-15161. (2020) (IF = 6.986 in 2020)
24. Wang Y, Gao S, Zheng V, Chen L, Ma M, **Shen S**, Qu J, Zhang H, Gurney ME, O'Donnell JM, Xu Y*. A novel PDE4D inhibitor BPN14770 reverses scopolamine-induced cognitive deficits via cAMP/SIRT1/Akt/Bcl-2 pathway. *Front Cell Dev Biol.* 8:599389. doi: 10.3389/fcell.2020.599389. (2020) (IF = 5.201 in 2021)
25. Jin L, Bi Y, Hu Q, Qu J, **Shen S**, Wang X, Tian Y*. A comparative study of evaluating missing value imputation methods in label-free proteomics. *Sci Rep.* 11(1):1760. (2021) (IF = 4.120 in 2020)
26. **Shen S**, Zhang M, Ma M, Rasam M, Poulsen D, Qu J*. Potential Neuroprotective Mechanisms of Methamphetamine Treatment in Traumatic Brain Injury Defined by Large-Scale IonStar-Based Quantitative Proteomics. *Int J Mol Sci.* 22(5):2246. (2021) (IF = 4.556 in 2019)
27. Wang X, Jin L, Hu C, **Shen S**, Qian S, Ma M, Zhu X, Li F, Wang J, Tian Y*, Qu J*. Ultra-High-Resolution IonStar Strategy Enhancing Accuracy and Precision of MS1-Based Proteomics and an Extensive Comparison with State-of-the-Art SWATH-MS in Large-Cohort Quantification. *Anal Chem.* 93 (11), 4884-4893. (2021) (IF = 6.986 in 2020)
28. Pradhan A, Lu D, Parisi LR, **Shen S**, Berhane IA, Galster SL, Bynam K, Monje-Galvan V, Gokcumen O, Chelmer SR, Qu J, Kay JG, Atilla-Gokcumen GE*. Protein acylation by saturated very long chain fatty acids and endocytosis are involved in necroptosis. *Cell Chem Biol.* 28 (9), 1298-1309. e7. (2021) (IF = 7.739 in 2019)
29. Hayden ER, Chen M, Pasquariello KZ, Gibson AA, Petti JJ, **Shen S**, Qu J, Ong S, Chen T, Jin Y,

Uddin ME, Huang KM, Paz A, Sparreboom A, Hu S*, Sprowl JA*. Regulation of OATP1B1 function by tyrosine kinase-mediated phosphorylation. *Clinical Cancer Res.* 27 (15), 4301-4310. (2021) (IF = 10.107 in 2020)

30. Bryniarski MA, Zhao B, Chaves LD, Mikkelsen JH, Yee BM, Yacoub R, **Shen S**, Madsen M, Morris ME*. Immunoglobulin G is a Novel Substrate for the Endocytic Protein Megalin. *AAPS J.* 23(2):40. (2021) (IF = 3.737 in 2019)

31. Kumar A, Wilderman P, Tu C, **Shen S**, Qu J, Fernando D*. Deciphering allosteric coupling between substrate binding and redox partner recognition in rat CYP24A1, a Vitamin-D C-24 hydroxylase. *The FASEB Journal.* 35. (2021) (IF = 4.966 in 2019)

32. **Shen S**, Li J, Huo S, Ma M, Zhu X, Rasam S, Duan X*, Qu M*, Titus MA*, Qu J*. Parallel, High-quality Proteomic and Targeted Metabolomic Quantification Using Laser Capture Micro-Dissected Tissues. *Anal Chem.* 93 (25), 8711-8718. (2021). (IF = 6.986 in 2020)

33. Bianchi-Smiraglia A, Wolff DW, Marston DJ, Deng Z, Moparthy S, Wombacher RM, Mussel AL, **Shen S**, Yun DH, Cox AO, Furdue C, Hurley E, Feltri ML, Qu J, Hollis T, Nde Kengne J, Fongang B, Sousa RJ, Kandel ME, Kandel ES, Hahn KM, Nikiforov MA*. Regulation of local GTP availability controls RAC1 activity and cell invasion. *Nat Communications.* 12 (1), 1-15. (2021) (IF = 14.92 in 2020)

34. Wolff DW, Deng Z, Bianchi-Smiraglia A, Foley CE, Han Z, Wang X, **Shen S**, Rosenberg MM, Moparthy S, Yun DH, Chen J, Baker BK, Roll MV, Magiera AJ, Li J, Hurley E, Feltri ML, Cox AO, Lee J, Furdui CM, Liu L, Bshara W, LaConte LEW, Kandel ES, Pasquale EB, Qu J, Lizbeth H, Nikiforov MA*. Phosphorylation of guanosine monophosphate reductase triggers a GTP-dependent switch from pro- to anti-oncogenic function of EPHA4. *Cell Chem Biol.* 29 (6), 970-984. (2022) (IF = 9.039 in 2021)

35. Hove VN, Anderson K, Hayden ER, Pasquariello KZ, Gibson AA, **Shen S**, Qu J, Jin Y, Miecznikowski JC, Hu S, Sprowl JA*. Influence of Tyrosine Kinase Inhibition on Organic Anion Transporting Polypeptide 1B3-Mediated Uptake. *Mol Pharmacol.* 101 (6), 381-389. (2022) (IF = 4.883 in 2022)

36. Ebeling MC, Fisher CR, Kapphahn RJ, Stahl MR, **Shen S**, Qu J, Montezuma SR, Ferrington DA. Inflammasome Activation in Retinal Pigment Epithelium from Human Donors with Age-Related Macular Degeneration. *Cells.* 11 (13), 2075. (2022) (IF = 4.829 in 2022)

37. Hilchey SP, Palshikar MG, Mendelson ES, **Shen S**, Rasam S, Emo JA, Qu J, Thakar J, Zand MS*. Cyclosporine A Modulates LSP1 Protein Levels in Human B Cells to Attenuate B Cell Migration at Low O₂ Levels. *Life.* 12 (8), 1284. (2022) (IF = 3.251 in 2021)

38. Pajic P, **Shen S**, Qu J, May AJ, Knox S, Ruhl S, Gokcumen O*. A mechanism of gene evolution generating mucin function. *Sci Adv.* 8 (34), eabm8757. (2022) (IF = 14.14 in 2021)

39. Wang JJ, Park KS, Dhimal N, **Shen S**, Tang X, Qu J, Zhang SX*. Proteomic Analysis of Retinal

Mitochondria-associated ER Membranes Identified Novel Proteins of Retinal Degeneration in Long-term Diabetes. *Cells*. 11 (18), 2819. (2022) (IF = 4.829 in 2022)

40. Zhao B, Tu C, **Shen S**, Qu J, Morris ME*. Identification of Potential Megalin/Cubilin Substrates Using Extensive Proteomics Quantification from Kidney Megalin-Knockdown Mice. *AAPS J*. 24 (6), 109 (2022). (IF = 4.009 in 2020)

MANUSCRIPTS ACCEPTED & IN PREPRINT

1. **Shen S**, Wang X, Rasam S, Ma M, Huo S, Qian S, Zhu X, Zhang M, Qu M, Hu C, Jin L, Tian Y, Sethi S, Poulsen D, Wang J, Qu J*. An IonStar quantitative proteomics protocol for reproducible and robust large-cohort investigation and enables high-quality clinical investigation. Accepted by *Nat Protocol*.

2. Kalem MC, Subbiah H, **Shen S**, Chen R, Terry L, Sun Y, Qu J, Panepinto JC*. The interactome of *Cryptococcus neoformans* Rmt5 reveals multiple regulatory points in fungal cell biology and pathogenesis. *bioRxiv*. (2022)

3. Kalem MC, Duffy SR, **Shen S**, Kaur JN, Qu J, Panepinto JC*. Arginine methylation of Puf4 drive diverse protein functions. *bioRxiv*. (2022)

4. Ma M, Huo S, Zhang M, Qian S, Zhu X, Pu J, Rasam S, Xue C, **Shen S**, An B, Jianmin W, Qu J*. Whole-tissue Mapping of > 5000 proteins by Micro-scaffold Assisted Spatial Proteomics (MASP). *ResearchSquare*. (2022)

5. Sahoo A, Zollo RA, **Shen S**, Ashraf M, Nelson S, Koudelka G, Qu J, Barbi J, Walker SE*. Dynamic Phosphorylation Regulates Eukaryotic Translation Initiation Factor 4A Activity During the Cell Cycle. *bioRxiv*. (2022)

INVITED BOOK CHAPTERS

1. Shen X, **Shen S**, Qu J*. Labeling and label-free shotgun proteomics quantification in the research of cardiovascular diseases. *Manual of Cardiac Proteomics*. Wiley. (2016)

2. **Shen S**, An B, Qu J*. Sample Preparation Methods for Targeted Biomarker Quantification by LC-MS. *Targeted biomarker quantitation by LC-MS*. Wiley. (2017)

CONFERENCE ABSTRACTS & PUBLICATIONS

1. Li J, Poitelon Y, **Shen S**, Shen X, Feltri ML, Qu J*. An ion-current-based, sensitive and reproducible proteomic investigation of Schwann cells radial sorting revealed new insights into directional cell migration and neural developments. 2014 ASMS Annual Meeting, Baltimore, MD.

2. **Shen S**, Li J, Shen X, Ng A, Nouri E, Zand M, Wu H, Ghaemmaghmi S, Qu J*. A Large-Scale, Ion-Current-Based Proteomic Investigation of the Temporal Profiles of Influenza A Virus Infected Mouse Lungs Revealed Underlying Mechanisms of Altered Permeability of the Lung Endothelial Microvascular Barrier. 2014 ASMS Annual Meeting, Baltimore, MD.
3. **Shen S**, Li J, Shen X, Ng A, Ghaemmaghmi S, Wu H, Zand M*, Qu J*. A Ion-Current-Based, 44-Plex Investigation of Influenza A Virus Infected Mouse Lungs Revealed Altered Integrity of Lung Microvascular Barriers. 2015 ASMS Annual Meeting, St. Louis, MO.
4. **Shen S**, Li J, Shen X, Tu C, Qu J*. Rapid, efficient and reproducible sample preparation for bottom-up proteomics by a surfactant-aided precipitation/on-pellet digestion strategy. 2015 ASMS Annual Meeting, St. Louis, MO.
5. Miao X, **Shen S**, Li J, Shen X, Straubinger RM, Qu J, Jusko WJ*. Dynamic proteomic responses of pancreatic cancer cells during combination exposures to gemcitabine and Et 743. 2015 AAPS Annual Meeting, Orlando, FL.
6. **Shen S**, Duan X, Wang J, An B, Qu Y, Balthasar JP, Qu J*. A Novel Blue Native PAGE and Targeted Mass Spectrometry Strategy Enable Quantitative Characterization of the Kinetics of Protein-Ligand Interactions *In Vivo*. 2016 ASMS Annual Meeting, San Antonio, TX.
7. **Shen S**, Miao X, Li J, Shen X, Wang X, Jusko WJ, Qu J*. MS1-based quantitative proteomics investigation of mechanisms underlying Gemcitabine and Trabectedin synergism with high multiplexing capacity and extremely low missing value. 2016 ASMS Annual Meeting, San Antonio, TX.
8. **Shen S**, An B, Li J, Shen X, Tu C, Qu J*. Rapid, efficient and reproducible sample preparation for quantitative proteomics by a surfactant-aided precipitation/on-pellet digestion strategy. 2016 ASMS Annual Meeting, San Antonio, TX.
9. Miao X, **Shen S**, Li J, Shen X, Wang X, Koch G, Ait-Oudhia S, Straubinger RM, Qu J, Jusko WJ*. Mathematical models of temporal proteomic profiles of pancreatic cancer cells in response to gemcitabine and trabectedin combinations. 2016 AAPS Annual Meeting, Denver, CO.
10. Miao X, Koch G, **Shen S**, Li J, Shen X, Wang X, Ait-Oudhia S, Straubinger RM, Qu J, Jusko WJ*. Mathematical modeling of temporal proteomic profiles in response to gemcitabine on pancreatic cancer cells. ACoP7, Bellevue, WA.
11. **Shen S**, Li J, Straubinger NL, Wang X, Green MK, Scott CJ, Ma W, Straubinger RM, Qu J*. Unambiguously and comprehensively resolving adenocarcinoma and stromal proteomes and their interactive signaling without cell sorting in patient-derived xenograft models. US HUPO 13th Annual Conference, San Diego, CA.
12. **Shen S**, Li J, Shen X, Qu J*. IonStar-Mine: reproducible, fractionation-free measurement of 8000+ unique proteins in 100 biological samples with high accuracy, precision and <1% missing data. 2017

ASMS Annual Meeting, Indianapolis, IN.

13. **Shen S**, Li J, Straubinger NL, Wang X, Green MK, Scott CJ, Ma W, Straubinger RM, Qu J*. Unambiguously and comprehensively resolving adenocarcinoma and stromal proteomes and their interactive signaling without cell sorting in patient-derived xenograft models. 2017 ASMS Annual Meeting, Indianapolis, IN.

14. **Shen S**, An B, Wang X, Li J, Cao J, Ng A, Tu C, Zand M*, Qu J*. A surfactant-aided extraction/precipitation/on-pellet digestion strategy (SEPOD) enables rapid, efficient and reproducible sample preparation for large-scale quantitative proteomics. 2018 ASMS Annual Meeting, San Diego, CA.

15. **Shen S**, Zhang M, Osei J, Rasam SS, Poulsen DJ, Qu J*. Large-scale IonStar-based quantification of cortex and hippocampus proteomes revealed novel neuroprotective mechanisms of two drug candidates against traumatic brain injury. 2018 ASMS Annual Meeting, San Diego, CA.

16. **Shen S**, Qian S, Ma M, Zhang M, Qu J*. IonStar.Mine: Extending Quantitative Depth of IonStar by High-Resolution MS1-Based Feature Matching. 2019 ASMS Annual Meeting, Atlanta, GA.

17. **Shen S**, Li J, Ma M, Rasam SS, Mohler JL, Duan X, Qu J*. Parallelizable Quantitative Characterization of Proteome and Targeted Metabolome from Laser Capture Microdissected Tissue Cells. 2019 ASMS Annual Meeting, Atlanta, GA.

18. **Shen S**, Ma M, Zhang M, Poulsen DJ, Qu J*. Spatially-Resolved Neuroproteomics with IonStar Reveals Differential Landscapes of Signal Transduction Dysregulation in a Rat Ischemic Stroke Model. 2019 ASMS Annual Meeting, Atlanta, GA.

19. Niu J, Wang X, **Shen S**, Qu J, Mager D, Straubinger RM*. Pharmacodynamic and proteomic analysis of combined gemcitabine/nab-paclitaxel in patient-derived pancreatic cancer xenograft models. AACR Annual Meeting 2019, Atlanta, GA.

20. Wang JJ, Dhimal N, **Shen S**, Tang X, Verhoski A, Qu J, Zhang SX*. Proteomic Analysis of Mitochondria-associated ER Membranes Identified Novel Proteins of Retinal Degeneration in Diabetes. ARVO Annual Meeting 2019, Vancouver, Canada.

21. Yu X, Cheng K, Pawlowski G, Kelkar A, Friedman A, **Shen S**, Qu J, Neelamegham S*. Synglycan: A Glycomics Reporter Toolkit for Multiple Cell Types and In Vivo Application. 2019 AlchE Annual Meeting, Orlando, FL.

22. Ma M, **Shen S**, Huo S, Zhang M, Qu J*. A Comprehensive Evaluation of Variabilities Arising from Experimental Factors on LC-MS-based Proteomics Biomarker Discovery. ASMS Reboot 2020.

23. Rasam S, **Shen S**, Qian S, Qu J*. Enhancement on IonStar Using Off-line Fractionation to Increase Protein Quantitative Depth. ASMS Reboot 2020.

24. Ma M, **Shen S**, Huo S, Zhang m, Qu Y, Zhu X, Xue C, Vu A, Yang X, Qian S, Shen Q, Qu J*. Development of a reliable protein marker panel for evaluation of intracellular contamination in

interstitial fluid extraction using high-resolution LC-MS. ASMS Reboot 2020.

25. Wang X, Jin L, Hu C, **Shen S**, Qian S, Tian Y, Qu J*. An ultra-high-resolution IonStar proteomics strategy enables accurate and reproducible large-cohort quantification and outperforms the state-of-the-art SWATH-MS. ASMS Reboot 2020.

26. **Shen S**, Hilchey SP, Rasam S, Palshikar MG, Emo J, Thakar J, Zang M, Qu J*. Investigation of hypoxia and calcineurin inhibition-induced global phosphoproteome changes in human RAMOS B cells. ASMS Reboot 2020.

27. **Shen S**, Tu C, Shen H, Zhang J*, Qu J*. Comparative Proteomics Analysis of Exosomes Identifies Key Pathways and Protein Markers Related to Breast Cancer Metastasis. 2021 ASMS Annual Meeting, Philadelphia, PA.

28. Ma M, Huo S, Zhang M, Qian S, Zhu X, Pu J, **Shen S**, Qu J*. Spatially-Resolved Proteomics to Reliably Map Whole-Tissue Distribution of >5000 Proteins Using a Novel, Precise 3D-Fabricated Micro-Sampling Device and IonStar. 2021 ASMS Annual Meeting, Philadelphia, PA.

29. Qian S, Ma M, **Shen S**, Qu J*. A novel quantitative deconvolution proteomics strategy enables accurate in situ quantification of cancer and stroma proteins from patient-derived xenograft models. 2021 ASMS Annual Meeting, Philadelphia, PA.

30. Ma M, Huo S, **Shen S**, Zhang M, Qu Y, Zhu X, Pu J, Xue C, Vu A, Yang X, Qian S, Shen Q, Qu J*. A Well-characterized and Stringently Controlled Strategy to Procure High-quality Interstitial Fluid from Tissues with Minimal Intracellular Contamination. 2021 ASMS Annual Meeting, Philadelphia, PA.

31. Zhu X, **Shen S**, Qian S, Sethi S, Broderick G, Morris M, Mammen M, Qu J*. Large-Scale Proteomics Analysis by UHR-IonStar Enables Identification of Novel Biomarkers for Chronic Obstructive Pulmonary Disease (COPD). 2021 ASMS Annual Meeting, Philadelphia, PA.

32. Rasam S, **Shen S**, Lin Q, Straubinger RM, Qu J*. A highly-robust, reproducible, quantitative proteomics pipeline reveals metabolic, apoptotic, and immunological responses of pancreatic cancer cells to novel drug combinations. 2021 ASMS Annual Meeting, Philadelphia, PA.

33. **Shen S**, Kappahn B, Zhang M, Ferrington DA, Qu J*. Large-Scale IonStar Quantitative Proteomics of Human Retinal Mitochondrial Fractions Reveals Key Regulators for Early Pathogenesis of Age-Related Macular Degeneration (AMD). 2022 ASMS Annual Meeting, Minneapolis, MN.

34. **Shen S**, Medella M, Qian S, Zhu X, McCann R, Zeldich E, Xin H, Buller B, Moore T, Qu J*.

Multi-Compartment Quantitative Proteomics Revealing Potential Mechanisms Underlying the Treatment Effects of Mesenchymal-Derived Exosomes in a Monkey Model of Cortical Injury. 2022 ASMS Annual Meeting, Minneapolis, MN.

35. Ma M, Huo S, Zhang M, Qian S, Zhu X, Pu J, Xue C, **Shen S**, An B, Qu J*. Whole-Tissue Mapping of > 5000 Proteins by Micro-scaffold Assisted Spatial Proteomics (MASP). 2022 ASMS Annual Meeting, Minneapolis, MN.

INVITED SEMINARS & CONFERENCE PRESENTATION

1. An B, Zhang M, Qu Y, **Shen S**, Qu J*. A Trapping micro-LC/MS strategy for ultra-sensitive, robust and high-throughput quantification of biotherapeutics and biomarkers in complex matrices. 2016 ASMS Annual Meeting, San Antonio, TX.
2. Shen S. IonStar: Solution to the Dilemma of Reliable Proteomics Investigation in Large Biological Cohorts. Center for Hearing and Deafness, University at Buffalo. Jun 2019.
3. Shen S. Enhancing clinical and pharmaceutical investigation with novel quantitative proteomics techniques. Department of Pharmaceutical Sciences, University at Buffalo. Sep 2021.

PROFESSIONAL SERVICES

a. Invited journal peer-review activities

Journal of Agriculture and Food Chemistry, Proteomics, PLoS One, Drug Discovery Today, International Journal of Molecular Sciences, RSC Advances, Journal of Biomedical Materials Research: Part B – Applied Biomaterials, Molecules, Pathogens, Diagnostics, Science Progress, etc.

b. Non-credit journal peer-review activities

Molecular and Cellular Proteomics, Journal of Proteome Research, Proteomics Clinical Applications, Analytical Chemistry, Nature Communications, Scientific Reports, Early Career Research Initiative (ECR) – Human Proteome Organization (HUPO)

TEACHING

a. Tutor

PHC510 (Lab)	Pharmaceutical Analysis	2019-present	Mandatory graduate course, Five 3-hr lab sessions.
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