

CURRICULUM VITAE**Si Wu**

Associate Professor
Department of Chemistry and Biochemistry
University of Oklahoma
101 Stephenson Parkway, Norman, Oklahoma 73072
Email: si.wu@ou.edu, Office Phone: (405) 325-6931

EDUCATION

- Ph.D.** Analytical Chemistry, Washington State University, Pullman, WA, 2006
Advisor: Professor James E. Bruce
Thesis "New techniques for proteomics study: instrumentation, separation, and application"
- B.S.** Chemistry, Anhui University, China, 1997

PROFESSIONAL POSITIONS

- 07/2020 to current **Associate Professor**, Department of Chemistry and Biochemistry, University of Oklahoma (*early tenure and promotion*)
- 01/2015 to 06/2020 **Assistant Professor**, Department of Chemistry and Biochemistry, University of Oklahoma
- 03/2010 to 12/2014 **Senior Research Scientist (III)**, Environmental Molecular Sciences Laboratory (EMSL), Pacific Northwestern National Laboratory (PNNL)
- 09/2008 to 02/2010 **Research Scientist**, Battelle Toxicology Northwest
- 10/2006 to 08/2008 **Postdoc**, Proteomics, Pacific Northwest National Laboratory (PNNL)
Advisors: Drs. Richard D. Smith and Ljiljana Pasa-Tolic

SELECTED HONORS AND AWARDS

- 2022-now Journal of Mass Spectrometry (JMS) Editor
- 2022 International Journal of Mass Spectrometry (IJMS) Young Scientist Feature
- 2021 Journal of American Society for Mass Spectrometry (JASMS) Outstanding Reviewers
- 2020 2020 US Human Proteome Organization (US HUPO) Robert J. Cotter New Investigator Award
- 2017 2017 American Society for Mass Spectrometry (ASMS) Emerging investigator
- 2011,2013,2014 Pacific Northwest National Laboratory Outstanding Performance Award
- 2012 Environmental Molecular Sciences Laboratory Director's Annual Award
- 2012,2013 Environmental Molecular Sciences Laboratory Outstanding Performance Award
- 2004 Gardner Stacey Research Scholarship, Washington State University
- 1997 Excellent Graduation Thesis Award, Anhui University

PROFESSIONAL ACTIVITIES***Professional Affiliations***

American Society for Mass Spectrometry (ASMS)
United States Human Proteome Organization (US HUPO)
Human Proteome Organization (HUPO)
American Chemistry Society (ACS)

Professional service (selected)

1. Editor, Journal of Mass Spectrometry (JMS) (**2022-now**)
2. ASMS Publications Committee (**2020-2022**)
3. Human Proteome Organization (HUPO) Nominations and Elections Committee, Co-chair (**2021-current**)
4. HUPO Council, Western Region Representative (**2020-current**)
5. Chinese American Society for Mass Spectrometry (CASMS), The Public Relation and Fund-Raising Committee, Co-chair (**2021-current**)
6. Guest Editor, "Themed issue: Cross-talk and integrated post-translational modifications", RSC MolOmics (**2021**)
7. ASMS Emerging talent program, Co-Organizer (**2020**)
8. HUPO ECR manuscript competition judge (**2020**)

Conference organization

1. ACS 2023 Spring, "Top-Down Proteomics and Native MS", Co-Organizer (**2023**)
2. US HUPO, "Top-Down Proteomics", Session Chair (**2023**)
3. 2st CASMS Virtual Conference, "PTMs and Proteoforms", Co-Session Chair (**2022**)
4. ASMS Annual Conference, Short course guest lecturer on "Top-down proteomics" (**2022**)
5. US HUPO, Workshop on "Top-down Proteomics", Co-Organizer (**2022**)
6. US HUPO, Short course guest lecturer on "Post-translational Modification" (**2022**)
7. HUPO Annual Conference, Hot topics on "Native MS and Top-down Proteomics", Session Chair (**2021**)
8. ASMS Annual Conference, Workshop on "Proteoform identification and quantification using TopPIC suite", Co-Organizer (**2021**)
9. 1st CASMS Virtual Conference, Workshop on "Females in Mass Spectrometry Workshop" (**2021**)
10. US HUPO, Workshop on "Top-down Proteomics", Co-Organizer (**2021**)
11. US HUPO, Short course guest lecturer on "Post-translational Modification" (**2021**)
12. ASMS Annual Conference, Workshop on "Proteoform identification and quantification using TopPIC suite", Co-Organizer (**2020**)
13. US HUPO, Section chair, "Post-translational Modification" (**2020**, canceled)
14. ASMS Annual Conference, Workshop on "Proteoform identification and quantification using TopPIC suite", Co-organizing with Drs. Xiaowen Liu and Liangliang Sun (**2019**)
15. ASMS Annual Conference, Section chair, Oral Session on "Top-down Proteomics" (**2018**)
16. ASMS Asilomar Conference, Section chair (**2018**)
17. ASMS Top-down Workshop, Section chair (**2017**)
18. ASMS Annual Conference, Section chair, Oral Session on "Top-down Proteomics" (**2016**)
19. American Society of Pharmacognosy (ASP) Conference, Co-Section chair (**2015**)

Grant Review Activities

1. Panel reviewer for NSF Chemistry of Life Process (CLP), **2022**
2. Panel reviewer for the Department of Defense Congressionally Directed Medical Research Programs (DOD-CDMRP), **2021**
3. *Ad hoc* reviewer for NIH Study Section (Shared Instrumentation S10 Special Emphasis Panel), **2021**
4. *Ad hoc* reviewer for NIH Study Section (Enabling Bioanalytical and Imaging Technologies), **2021**
5. Reviewer for Chemical Biology Call at the Vienna Science and Technology Fund (Austria), **2021**
6. *Ad hoc* proposal reviewer, Netherlands Organization of Scientific Research (NWO), **2019**

Journal Peer-Review Activities (10+ manuscripts per year)

Nucleic Acid Research, Genome Research, Talanta, Mass Spectrometry Reviews, Journal of Proteome Research, Proteomics, Analytical Chemistry, Analytica Chimica Acta, Journal of the American Society for Mass Spectrometry, Journal of Proteomics, Scientific Reports, Analyst, ACS omega, ACS Chemical

Biology, Biochemistry and Biophysics Reports, Analytical Methods, Journal of Agricultural and Food Chemistry, Microbial Biotechnology, Trends in Food Science and Technology, Journal of Natural Products, Mol Omics, International Journal of Mass Spectrometry, Journal of Pharmaceutical Analysis

RESEARCH ACTIVITIES

Selected oral presentations

1. Department Seminar (University of Texas-Taylor), "High-throughput quantitative top-down proteomics" (October 2022)
2. Department Seminar (University of Wisconsin-Madison), "High-throughput quantitative top-down proteomics" (October 2022)
3. 2022 ASMS Short course, "Quantitative top-down proteomics" (June 2022)
4. 2022 USHUPO Short course, "Post-translational Modification" (March 2022)
5. 2022 USHUPO Annual Conference, "High-throughput Quantitative Single-cell Proteomics Analysis Using Spray-Capillary-Based CE-MS" (March 2022)
6. 2021 iCMS Virtual Webinar, "High-throughput Quantitative Top-Down Proteomics" (November 2021)
7. 2021 ACS CE-MS symposium, "Spray-Capillary: A novel microsampling device for single cell sample collection and online CE-MS analysis" (August 2021)
8. 2021 1st CASMS Virtual Conference, "High-throughput Quantitative Top-Down Proteomics" (August 2021)
9. 2021 MSB conference, "Spray-capillary: A Novel Device for Microsampling and Online Capillary Electrophoresis Mass Spectrometry Analysis" (July 2021)
10. 2021 Top-down consortium webinar, "Advances in High-Throughput Quantitative Top-Down Proteomics" (May 2021)
11. 2021 USHUPO Short course, "Post-translational Modification" (March 2021)
12. 2020 ASMS Workshop, "Quantitative Top-Down MS with TopPIC" (June 2020)
13. 2020 ASMS annual conference, "Quantitative Top-down MS Analysis of Serum Autoantibody Repertoire in Systemic Lupus Erythematosus" (June 2020)
14. 2020 USHUPO Award Lecture, "High-throughput Quantitative Top-down Proteomics" (March 2020)
15. Department Seminar (Michigan State University), "High-throughput quantitative top-down proteomics" (September 2019)
16. 2019 Designing Molecular Workshop and Conference (Invited Speaker), "High-throughput quantitative top-down MS for functional proteome characterization" (August 2019)

17. 2019 ASMS Workshop, "Quantitative top-down proteomics in complex samples using protein-level tandem mass tag (TMT) labeling" (June 2019)
18. 2019 USHUPO Conference (Invited Speaker), "High-throughput quantitative top-down proteomics" (March 2019)
19. iConference on Mass Spectrometry (iCMS2018, Invited Speaker), "High-throughput quantitative top-down Proteomics" (December 2018)
20. 2018 SciX Conference (Invited Speaker), "Development and application of a novel function proteomics tool: Activity-Correlated Protein Profiling Platform (ACPP)" (October 2018)
21. 2018 SciX Conference (Invited Speaker), "High-throughput quantitative top-down proteomics" (October 2018)
22. Department Seminar (Kansas State University), "High-throughput top-down proteomics" (October 2018)
23. 256th ACS National Conference (Invited Speaker in Peter Derrick Memorial Symposium), "Two-dimensional separation using high-pH and low-pH reversed phase liquid chromatography for top-down proteomics" (August 2018)
24. 7th World Chinese Mass Spectrometry Conference (WCMSC) (Invited Speaker), "High-throughput quantitative top-down proteomics" (July 2018)
25. NIH Proteomics Interest Group (Invited Seminar), "High-throughput top-down proteomics" (May 2018)
26. 14th Uppsala Conference (UPPCON) (Invited talk in young investigator/rising star session), "Top-down MS and functional proteomics" (July 2017)
27. Department Seminar (Oklahoma State University), "Top-down MS and functional proteomics" (April 2017)
28. Invited Seminar (Oklahoma Medical Research Foundation), "High-throughput top-down proteomics" (January 2017)
29. Department Seminar (University of Oklahoma Health Science Center, OUHSC), "Top-down MS and functional proteomics" (October 2016)
30. Department Seminar (Wichita State University), "Top-down MS and functional proteomics" (March 2016)
31. NIH NIAID CSGADP annual plenary meeting (Invited talk), "Top-down proteomics on SLE autoantibodies" (October 2016)
32. HPLC2014 (Oral presentation). "Advanced top-down LC-MS platform for high-throughput characterization of histone modifications" (May 2014)
33. NIGMS PNNL Proteomics Resource Advisory Committee Meeting (invited presentation), "Advances in intact protein and top-down proteomics" (February 2014)

34. Department Seminar (Indiana University-Purdue University Indianapolis, IUPUI), "Advances in top-down proteomics" (June 2013)
35. EMSL integration: plants, microbials, and their interaction (Invited workshop), "Strengths of top-down proteomics" (July 2013)
36. ASMS intact protein workshop, "Comprehensive top-down characterization of microbial proteome" (June 2013)
37. EMSL user meeting (Invited talk), "Introduction of top-down proteomics" (July 2012)
38. HUPO 11th Annual World Congress, "High throughput top-down mass spectrometry for functional characterization of microbial Proteins" (September 2012)

Peer-reviewed journal publications

* corresponding author

After joining OU:

1. Cupp-Sutton, K.A., Welborn, T., Fang, M., Langford, J.B., Wang, Z., Smith, K., **Wu, S.* (2022)** The Deuterium Calculator: An open-source tool for hydrogen-deuterium exchange mass spectrometry analysis. *Journal of Proteome Research* (in revision)
2. Fang, M., Wu, O., Cupp-Sutton, K.A., Smith, K., **Wu, S.*(2022)** Elucidating Protein-Ligand Interactions In Cell Lysate Using High-Throughput Hydrogen Deuterium Exchange Mass Spectrometry With Integrated Protein Thermal Depletion. *Analytical Chemistry* (accepted)
3. Guo, Y., Chowdhury, T., Seshadri, M., Cupp-Sutton, K.A., Wang, Q., Yu, D., **Wu, S.* (2022)** Optimization of Higher-Energy Collisional Dissociation Fragmentation Energy for Intact Protein-level Tandem Mass Tag Labeling. *Journal of Proteome Research* (accepted)
4. Cupp-Sutton, K.A., Fang, M., **Wu, S.* (2022)** Separation methods in single-cell proteomics: RPLC or CE? *International Journal of Mass Spectrometry* 2022, 481, 116920, (Young Scientist Feature)
5. Guo, Y., Yu, D., Cupp-Sutton, K.A., Liu, X., **Wu, S. (2022)** A Benchmarking Protocol for Intact Protein-Level Tandem Mass Tag (TMT) Labeling for Quantitative Top-Down Proteomics. *MethodX*, Volume 9, 2022, 101873
6. Guo, Y., Yu, D., Cupp-Sutton, K.A., Liu, X., **Wu, S. (2022)** Optimization of Protein-Level Tandem Mass Tag (TMT) Labeling Conditions in Complex Samples with Top-Down Proteomics. *Analytica Chimica Acta*, 15 August 2022, 340037.
7. Fang, M., Wang, Z., Norris, K., James, J. A., **Wu, S.***, Smith, K.***(2022)** Hydrogen-Deuterium Exchange Mass Spectrometry Reveals a Novel Binding Region of a Neutralizing Fully Human Monoclonal Antibody to Anthrax Protective Antigen. *Toxins* 2022, 14 (2), 92.
8. Cupp-Sutton, K.A., Wang, Z., Yu, D., and **Wu, S.* (2022)** RPLC-RPLC-MS/MS for proteoform identification. on *Proteoform Identification: Methods and Protocols* in *Methods in Molecular Biology*, Page 31-42, 2022

9. Yang, W., Wang, L., Fang, M., Sheth, V., Zhang, Y., Holden, A. M., Donahue, N. D., Green, D. E., Frickenstein, A. N., Mettenbrink, E. M., Schwemley, T. A., Francek, E. R., Haddad, M., Hossen, M. N., Mukherjee, S., **Wu, S.**, DeAngelis, P. L., Wilhelm, S. (2022) Nanoparticle Surface Engineering with Heparosan Polysaccharide Reduces Serum Protein Adsorption and Enhances Cellular Uptake. *Nano Lett* 2022.
10. Huang, L., Fang, M., Cupp-Sutton, K.A., Wang, Z., Smith, K., and **Wu, S.*** (2021) Spray-capillary based capillary electrophoresis mass spectrometry for metabolite analysis in single live cells. *Analytical Chemistry*. 2021 Mar 16;93(10):4479-4487.
11. Yu, D., Wang, Z., Cupp-Sutton, K.A., Guo Y., Kou, Q., Smith, K., Liu, X., and **Wu, S.*** (2021) Quantitative top-down proteomics in complex samples using protein-level tandem mass tag (TMT) labeling. *Journal of the American Society for Mass Spectrometry*. 2021 Jun 2;32(6):1336-1344. (Supplementary journal cover)
12. Zeiner, C.A., Purvine, S.O., Zink, E., **Wu, S.**, Paša-Tolić, L., Chaput, D.P., Santelli, C.M., and Hansel, C.M. (2021) Mechanisms of manganese (II) oxidation by filamentous Ascomycete fungi vary with species and time as a function of secretome composition. *Front. Microbiol.* 2020. doi: 10.3389/fmicb.2021.610497
13. Fang, M., Wang, Z., Cupp-Sutton K.A., Welborn T., Smith, K., and **Wu, S.*** (2021) High-throughput hydrogen deuterium exchange mass spectrometry (HDX-MS) coupled with subzero temperature ultrahigh pressure liquid chromatography (UPLC) separation for complex sample analysis. *Analytica Chimica Acta*. 2021 Jan 25;1143:65-72.
14. Choi I.K., Jiang T., Kankara S.R., **Wu S.**, Liu X.* (2021) TopMSV: A Web-Based Tool for Top-Down Mass Spectrometry Data. *Journal of the American Society for Mass Spectrometry*. 2021 Jun 2;32(6):1312-1318.
15. Wang, Z., Yu, D., Liu, X., Cupp-Sutton, K.A., Smith, K., and **Wu, S.*** (2020) Development of an Online 2D Ultrahigh-Pressure Nano-LC System for High-pH and Low-pH Reversed Phase Separation in Top-Down Proteomics. *Analytical Chemistry*. 2020, Sep. 1.
16. Cupp-Sutton, K.A., and **Wu, S.*** (2020) High-throughput quantitative top-down proteomics. *Molecular Omics* 2020 Apr 1;16(2):91-99.
17. Huang, L., Wang, Z., Cupp-Sutton, K.A., Smith, K., and **Wu, S.*** (2020) Spray-capillary: an electrospray assisted device for quantitative ultra-low volume sample handling. *Analytical Chemistry*. 2020 Jan 7;92(1):640-646.
18. Rezinciuc S, Tian Z, **Wu S**, Hengel S, Pasa-Tolic L, Smallwood HS. (2020) Mapping Influenza-Induced Posttranslational Modifications on Histones from CD8+ T Cells. *Viruses*. 2020 Dec 8;12(12):1409.
19. Yu, D., Wang, Z., Kou, Q., Cupp-Sutton, K.A., Smith, K., Liu, X., and **Wu, S.*** (2019) Deep intact proteoform characterization in human cell lysate using high-PH and low-PH reversed phase liquid chromatography. *Journal of the American Society for Mass Spectrometry*. 2019 Dec; 30(12):2502-2513
20. Schaffer, L.V., Millikin, R.J., Miller, R.M., Anderson, L.C., Fellers, R.T., Ge, Y., Kelleher, N.L., LeDuc, R.D., Liu, X., Payne, S.H., Sun, L., Thomas, P.M., Tucholski, T., Wang, Z., **Wu, S.**, Wu, Z., Yu, D., Shortreed, M.R., and Smith, L.M.* (2019) Identification and quantification of proteoforms by mass spectrometry. *Proteomics*, 19(10)

21. Wang, Z., Liu, X., Muther, J., James, J. A., Smith, K., and **Wu, S.*** (2019). Top-down mass spectrometry analysis of human serum autoantibody antigen-binding fragments. *Scientific Reports*, 9(1), 2345.
22. Roberts, B. L., Severance, Z. C., Bensen, R. C., Le, A. T., Kothapalli, N. R., Nunez, J. I., Ma, H., **Wu, S.**, Standke, S. J., Yang, Z., Reddig, W. J., Blewett, E. L., and Burgett, A. W. G.* (2019) Transient compound treatment induces a multigenerational reduction of oxysterol-binding protein (osbp) levels and prophylactic antiviral activity. *ACS Chemical Biology*, 14(2), 276-287.
23. Kou, Q., Wang, Z., Lubeckyj, R. A., **Wu, S.**, Sun, L., and Liu, X.* (2019). A Markov chain Monte Carlo method for estimating the statistical significance of proteoform identifications by top-down mass spectrometry. *Journal of Proteome Research*, 18(3), 878-889.
24. Zhu, Z., Chen, H., Ren, J., Lu, J. J., Gu, C., Lynch, K. B., **Wu, S.**, Wang, Z., Cao, C., and Liu, S.* (2018) Two-dimensional chromatographic analysis using three second-dimension columns for continuous comprehensive analysis of intact proteins. *Talanta*, 179, 588-593.
25. Wang, Z., Ma, H., Smith, K., and **Wu, S.*** (2018) Two-dimensional separation using high-pH and low-pH reversed phase liquid chromatography for top-down proteomics. *International Journal of Mass Spectrometry*. 427, 43-51.
26. Li, Z., He, B., Kou, Q., Wang, Z., **Wu, S.**, Liu, Y., Feng, W., and Liu, X.* (2018) Evaluation of top-down mass spectral identification with homologous protein sequences. *BMC Bioinformatics*, 19(17), 494.
27. Kou, Q., **Wu, S.**, and Liu, X.* (2018) Systematic evaluation of protein sequence filtering algorithms for proteoform identification using top-down mass spectrometry. *Proteomics*, 18(3-4), 1700306.
28. Vyatkina, K., Dekker, L., **Wu, S.**, VanDuijn, M., Liu, X., Tolic, N., Luider, T., and Paša-Tolić, L.* (2018) De Novo sequencing of peptides from high-resolution bottom-up tandem mass spectra using top-down intended methods. *Proteomics*, 17(23-24), 1600321.
29. Ma, H., Delafield, D. G., Wang, Z., You, J., and **Wu, S.*** (2017) Finding biomass degrading enzymes through an activity-correlated quantitative proteomics platform (ACPP). *Journal of The American Society for Mass Spectrometry*, 28(4), 655-663.
30. Zhou, M., **Wu, S.**, Stenoién, D. L., Zhang, Z., Connolly, L., Freitag, M., and Paša-Tolić, L.* (2017) Profiling changes in histone post-translational modifications by top-down mass spectrometry. *Eukaryotic Transcriptional and Post-Transcriptional Gene Expression Regulation*. Humana Press, New York, NY, 2017: 153-168.
31. Yang, R., Zhu, D., Kou, Q., Bhat-Nakshatri, P., Nakshatri, H., **Wu, S.**, and Liu, X.* (2017) A spectrum graph-based protein sequence filtering algorithm for proteoform identification by top-down mass spectrometry. In *2017 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)* (222-229).
32. **Wu, S.**, Ma, H., Prytkova, I., Stenoién, D., and Paša-Tolić, L.* (2017) Proteomics, Top-Down. *Encyclopedia of Spectroscopy and Spectrometry*, 3rd Edition. UK: Oxford: Elsevier; p.774-778.

33. Vyatkina, K.*, Dekker, L. J., **Wu, S.**, VanDuijn, M. M., Liu, X., Tolić, N., Luider, T. M., and Paša-Tolić, L. (2017) De Novo sequencing of peptides from high-resolution bottom-up tandem mass spectra using top-down intended methods. *Proteomics*, 17(23-24), 1600321.
34. Zeiner, C. A., Purvine, S. O., Zink, E. M., Paša-Tolić, L., Chaput, D. L., **Wu, S.**, Santelli, C. M., and Hansel, C. M.* (2017) Quantitative iTRAQ-based secretome analysis reveals species-specific and temporal shifts in carbon utilization strategies among manganese (II)-oxidizing Ascomycete fungi. *Fungal Genetics and Biology*, 106, 61-75.
35. Kou, Q., **Wu, S.**, Tolic, N., Pasa-Tolic, L., Liu, Y., and Liu, X.* (2017) A mass graph-based approach for the identification of modified proteoforms using top-down tandem mass spectra. *Bioinformatics*, 33, 1309-1316
36. Cao, L., Qu, Y., Zhang, Z., Wang, Z., Prytkova, I., and **Wu, S.*** (2016) Intact glycopeptide characterization using mass spectrometry. *Expert Review of Proteomics*, 13, 513-522
37. Zeiner, C. A., Purvine, S. O., Zink, E. M., Paša-Tolić, L., Chaput, D. L., Haridas, S., **Wu, S.**, LaButti, K., Grigoriev, I. V., and Henrissat, B.* (2016) Comparative analysis of secretome profiles of manganese (II)-oxidizing ascomycete fungi. *PLoS one*, 11, e0157844
38. Vyatkina, K.*, **Wu, S.**, Dekker, L. J., VanDuijn, M. M., Liu, X., Tolić, N., Luider, T. M., Paša-Tolić, L., and Pevzner, P. A. (2016) Top-down analysis of protein samples by De Novo sequencing techniques. *Bioinformatics*, 32, 2753-2759
39. Srivastava, A., Amreddy, N., Babu, A., Panneerselvam, J., Mehta, M., Muralidharan, R., Chen, A., Zhao, Y. D., Razaq, M., Riedinger, N., Kim, H., Liu, S., **Wu, S.**, Abdel-Mageed, A. B., Munshi, A., and Ramesh, R.* (2016) Nanosomes carrying doxorubicin exhibit potent anticancer activity against human lung cancer cells. *Scientific Reports*, 6, 38541
40. Kou, Q., Zhu, B., **Wu, S.**, Ansong, C., Tolic, N., Paša-Tolić, L., and Liu, X.* (2016). Characterization of proteoforms with unknown post-translational modifications using the MIScore. *Journal of Proteome Research*, 15(8), 2422-2432.
41. Vyatkina, K.*, **Wu, S.**, Dekker, L. J., VanDuijn, M. M., Liu, X., Tolic, N., and Pevzner, P. A. (2015). De Novo sequencing of peptides from top-down tandem mass spectra. *Journal of Proteome Research*, 14(11), 4450-4462.
42. Aylward, F. O.*, Khadempour, L., Tremmel, D. M., McDonald, B. R., Nicora, C. D., **Wu, S.**, Moore, R. J., Orton, D. J., Monroe, M. E., and Piehowski, P. D. (2015) Enrichment and broad representation of plant biomass-degrading enzymes in the specialized hyphal swellings of *Leucoagaricus gongylophorus*, the fungal symbiont of leaf-cutter ants. *PLoS One*, 10(8), e0134752.

Before joining OU:

43. Qu, Y., Feng, J., Deng, S., Cao, L., Zhang, Q., Zhao, R., Zhang, Z., Jiang, Y., Zink, E. M., Baker, S. E., Lipton, M. S., Pasa-Tolic, L., Hu, J. Z., and **Wu, S.*** (2014) Structural analysis of N- and O-glycans using ZIC-HILIC/dialysis coupled to NMR detection. *Fungal Genetics and Biology*, 72, 207-215.
44. Zhang, Z., **Wu, S.**, Stenoien, D.L., and Paša-Tolić, L.* (2014). High-throughput proteomics. *Annual Review of Analytical Chemistry*, 7, 427-454. (**Co-first author**)

45. Cao, L., Tolic, N., Qu, Y., Meng, D., Zhao, R., Zhang, Q., Moore, R. J., Zink, E. M., Lipton, M. S., Pasa-Tolic, L., and **Wu, S.*** (2014) Characterization of intact N- and O-linked glycopeptides using higher energy collisional dissociation. *Analytical Biochemistry*, 452, 96-102.
46. **Wu, S.**, Brown, J. N., Tolic, N., Meng, D., Liu, X., Zhang, H., Zhao, R., Moore, R. J., Pevzner, P., Smith, R. D., and Pasa-Tolic, L.* (2014) Quantitative analysis of human salivary gland-derived intact proteome using top-down mass spectrometry. *Proteomics*, 14(10), 1211-1222.
47. Su, D., Gaffrey, M. J., Guo, J., Hatchell, K. E., Chu, R. K., Clauss, T. R., Aldrich, J. T., **Wu, S.**, Purvine, S., Camp, D. G., Smith, R. D., Thrall, B. D., and Qian, W. J.* (2014) Proteomic identification and quantification of S-glutathionylation in mouse macrophages using resin-assisted enrichment and isobaric labeling. *Free Radical Biology and Medicine*, 67, 460-470.
48. Nakayasu, E. S., **Wu, S.**, Sydor, M. A., Shukla, A. K., Weitz, K. K., Moore, R. J., Hixson, K. K., Kim, J. S., Petyuk, V. A., Monroe, M. E., Pasa-Tolic, L., Qian, W. J., Smith, R. D., Adkins, J. N., and Ansong, C.* (2014) A method to determine lysine acetylation stoichiometries. *International Journal of Proteomics*, 2014, 730725.
49. Mohimani, H., Kersten, R. D., Liu, W. T., Wang, M., Purvine, S. O., **Wu, S.**, Brewer, H. M., Pasa-Tolic, L., Bandeira, N., Moore, B. S., Pevzner, P. A., and Dorrestein, P. C.* (2014) Automated genome mining of ribosomal peptide natural products. *ACS Chemical Biology*, 9(7), 1545-1551.
50. Meng, D., Zhang, Q.*, Gao, X., **Wu, S.**, and Lin, G. (2014) LipidMiner: a software for automated identification and quantification of lipids from multiple liquid chromatography/mass spectrometry data files. *Rapid Communications in Mass Spectrometry: RCM*, 28(8), 981.
51. Liu, X., Dekker, L. J., **Wu, S.**, Vanduijn, M. M., Luider, T. M., Tolic, N., Kou, Q., Dvorkin, M., Alexandrova, S., Vyatkina, K., Pasa-Tolic, L., and Pevzner, P. A.* (2014) De novo protein sequencing by combining top-down and bottom-up tandem mass spectra. *Journal of Proteome Research*, 13(7), 3241-3248.
52. Kou, Q., **Wu, S.**, and Liu, X.* (2014) A new scoring function for top-down spectral deconvolution. *BMC Genomics*, 15(1), 1140.
53. Dekker, L., **Wu, S.**, Vanduijn, M., Tolic, N., Stingl, C., Zhao, R., Luider, T., and Paša-Tolić, L.* (2014) An integrated top-down and bottom-up proteomic approach to characterize the antigen-binding fragment of antibodies. *Proteomics*, 14(10), 1239-1248.
54. Dang, X., Scotcher, J., **Wu, S.**, Chu, R. K., Tolic, N., Ntai, I., Thomas, P. M., Fellers, R. T., Early, B. P., Zheng, Y., Durbin, K. R., Leduc, R. D., Wolff, J. J., Thompson, C. J., Pan, J., Han, J., Shaw, J. B., Salisbury, J. P., Easterling, M., Borchers, C. H., Brodbelt, J. S., Agar, J. N., Pasa-Tolic, L., Kelleher, N. L., and Young, N. L.* (2014) The first pilot project of the consortium for top-down proteomics: a status report. *Proteomics*, 14(10), 1130-1140.
55. **Wu, S.**, Brown, R. N., Payne, S. H., Meng, D., Zhao, R., Tolic, N., Cao, L., Shukla, A., Monroe, M. E., Moore, R. J., Lipton, M. S., and Paša-Tolić, L.* (2013) Top-down characterization of the post-translationally modified intact periplasmic proteome from the bacterium *Novosphingobium aromaticivorans*. *International Journal of Proteomics*, 2013, 279590.
56. Qu, Y., **Wu, S.**, Zhao, R., Zink, E., Orton, D. J., Moore, R. J., Meng, D., Clauss, T. R., Aldrich, J. T., Lipton, M. S., and Pasa-Tolic, L.* (2013) Automated immobilized metal affinity chromatography system

- for enrichment of *Escherichia coli* phosphoproteome. *Electrophoresis*, 34(11), 1619-1626. (**Co-first author**)
57. Liu, X., Hengel, S., **Wu, S.**, Tolic, N., Pasa-Tolic, L., and Pevzner, P. A.* (2013) Identification of ultramodified proteins using top-down tandem mass spectra. *Journal of Proteome Research*, 12(12), 5830-5838.
 58. Ansong, C., **Wu, S.**, Meng, D., Liu, X., Brewer, H. M., Deatherage Kaiser, B. L., Nakayasu, E. S., Cort, J. R., Pevzner, P., Smith, R. D., Heffron, F., Adkins, J. N.*, and Pasa-Tolic, L.* (2013) Top-down proteomics reveals a unique protein S-thiolation switch in *Salmonella Typhimurium* in response to infection-like conditions. *Proceedings of the National Academy of Sciences*, 110(25), 10153-10158. (**Co-first author**)
 59. Abdul Halim, M. F., Pfeiffer, F., Zou, J., Frisch, A., Haft, D., **Wu, S.**, Tolic, N., Brewer, H., Payne, S. H., Pasa-Tolic, L., and Pohlschroder, M.* (2013) *Haloferax volcanii* archaeosortase is required for motility, mating, and C-terminal processing of the S-layer glycoprotein. *Molecular Microbiology*, 88(6), 1164-1175.
 60. Tolmachev, A. V., Robinson, E. W., **Wu, S.**, Smith, R. D., Futrell, J. H., and Paša-Tolić, L.* (2012) Angular averaged profiling of the radial electric field in compensated FTICR Cells. *Journal of the American Society for Mass Spectrometry*, 23(7), 1169-1172.
 61. Tian, Z., Tolic, N., Zhao, R., Moore, R. J., Hengel, S. M., Robinson, E. W., Stenoien, D. L., **Wu, S.**, Smith, R. D., and Paša-Tolić, L.* (2012) Enhanced top-down characterization of histone post-translational modifications. *Genome Biology*, 13(10), R86.
 62. Shi, T., Fillmore, T. L., Sun, X., Zhao, R., Schepmoes, A. A., Hossain, M., Xie, F., **Wu, S.**, Kim, J. S., Jones, N., Moore, R. J., Pasa-Tolic, L., Kagan, J., Rodland, K. D., Liu, T., Tang, K., Camp, D. G., 2nd, Smith, R. D., and Qian, W. J.* (2012) Antibody-free, targeted mass-spectrometric approach for quantification of proteins at low picogram per milliliter levels in human plasma/serum. *Proceedings of the National Academy of Sciences*, 109(38), 15395-15400.
 63. Petrus, A. K., Swithers, K. S., Ranjit, C., **Wu, S.**, Brewer, H. M., Gogarten, J. P., Pasa-Tolic, L., and Noll, K. M.* (2012) Genes for the major structural components of Thermotogales species' togas revealed by proteomic and evolutionary analyses of OmpA and OmpB homologs. *PloS one*, 7(6), e40236.
 64. Payne, S. H., Bonissone, S., **Wu, S.**, Brown, R. N., Ivankov, D. N., Frishman, D., Pasa-Tolic, L., Smith, R. D., and Pevzner, P. A.* (2012) Unexpected diversity of signal peptides in prokaryotes. *MBio*, 3(6), e00339-12.
 65. Hengel, S. M., Floyd, E., Baker, E. S., Zhao, R., **Wu, S.***, and Pasa-Tolic, L.* (2012) Evaluation of SDS depletion using an affinity spin column and IMS-MS detection. *Proteomics*, 12(21), 3138-3142.
 66. **Wu, S.**, Tolic, N., Tian, Z., Robinson, E. W., and Paša-Tolić, L.* (2011) An integrated top-down and bottom-up strategy for characterization of protein isoforms and modifications. In *Bioinformatics for Comparative Proteomics* (pp. 291-304). Humana Press.
 67. Tolmachev, A. V., Robinson, E. W., **Wu, S.**, Smith, R. D., and Paša-Tolić, L.* (2011) Trapping radial electric field optimization in compensated FTICR cells. *Journal of the American Society for Mass Spectrometry*, 22(8), 1334-1342.

68. Du, X., Chowdhury, S. M., Manes, N. P., **Wu, S.**, Mayer, M. U., Adkins, J. N., Anderson, G. A., and Smith, R. D.* (2011) Xlink-identifier: an automated data analysis platform for confident identifications of chemically cross-linked peptides using tandem mass spectrometry. *Journal of Proteome Research*, 10(3), 923-931.
69. Lourette, N., Smallwood, H., **Wu, S.**, Robinson, E. W., Squier, T. C., Smith, R. D., and Paša-Tolić, L.* (2009) A top-down LC-FTICR MS-based strategy for characterizing oxidized calmodulin in activated macrophages. *Journal of The American Society for Mass Spectrometry*, 21(6), 930-939.
70. Yang, F., **Wu, S.**, Stenoien, D. L., Zhao, R., Monroe, M. E., Gritsenko, M. A., Purvine, S. O., Polpitiya, A. D., Tolic, N., Zhang, Q., Norbeck, A. D., Orton, D. J., Moore, R. J., Tang, K., Anderson, G. A., Pasa-Tolic, L., Camp, D. G., 2nd, and Smith, R. D.* (2009) Combined pulsed-Q dissociation and electron transfer dissociation for identification and quantification of iTRAQ-labeled phosphopeptides. *Analytical Chemistry*, 81(10), 4137-4143. (**Co-first author**)
71. **Wu, S.**, Yang, F., Zhao, R., Tolic, N., Robinson, E. W., Camp, D. G., 2nd, Smith, R. D., and Paša-Tolić, L.* (2009) Integrated workflow for characterizing intact phosphoproteins from complex mixtures. *Analytical Chemistry*, 81(11), 4210-4219.
72. **Wu, S.**, Lourette, N. M., Tolic, N., Zhao, R., Robinson, E. W., Tolmachev, A. V., Smith, R. D., and Paša-Tolić, L.* (2009) An integrated top-down and bottom-up strategy for broadly characterizing protein isoforms and modifications. *Journal of Proteome Research*, 8(3), 1347-1357.
73. Tolmachev, A. V., Robinson, E. W., **Wu, S.**, Pasa-Tolic, L., and Smith, R. D.* (2009) FT-ICR MS optimization for the analysis of intact proteins. *International Journal of Mass Spectrometry*, 287(1-3), 32-38.
74. Chowdhury, S. M., Du, X., Tolic, N., **Wu, S.**, Moore, R. J., Mayer, M. U., Smith, R. D., and Adkins, J. N.* (2009) Identification of cross-linked peptides after click-based enrichment using sequential collision-induced dissociation and electron transfer dissociation tandem mass spectrometry. *Analytical Chemistry*, 81(13), 5524-5532.
75. Zhang, Q., Schepmoes, A. A., Brock, J. W., **Wu, S.**, Moore, R. J., Purvine, S. O., Baynes, J. W., Smith, R. D., and Metz, T. O.* (2008) Improved methods for the enrichment and analysis of glycosylated peptides. *Analytical Chemistry*, 80(24), 9822-9829.
76. Tolmachev, A. V., Robinson, E. W., **Wu, S.**, Kang, H., Lourette, N. M., Pasa-Tolic, L., and Smith, R. D.* (2008) Trapped-ion cell with improved DC potential harmonicity for FT-ICR MS. *Journal of the American Society for Mass Spectrometry*, 19(4), 586-597.
77. Kaiser, N. K., Skulason, G. E., Weisbrod, C. R., **Wu, S.**, Zhang, K., Prior, D. C., Buschbach, M. A., Anderson, G. A., and Bruce, J. E.* (2008) Restrained ion population transfer: a novel ion transfer method for mass spectrometry. *Rapid Communications in Mass Spectrometry*, 22(12), 1955-1964.
78. Zhang, K., **Wu, S.**, Tang, X., Kaiser, N. K., and Bruce, J. E.* (2007) A bifunctional monolithic column for combined protein preconcentration and digestion for high throughput proteomics research. *Journal of Chromatography B*, 849(1-2), 223-230.
79. **Wu, S.**, Zhang, K., Kaiser, N. K., Bruce, J. E., Prior, D. C., and Anderson, G. A.* (2006) Incorporation of a flared inlet capillary tube on a fourier transform ion cyclotron resonance mass spectrometer. *Journal of the American Society for Mass Spectrometry*, 17(6), 772-779.

80. **Wu, S.**, Tang, X. T., Siems, W. F., and Bruce, J. E.* (2005) A hybrid LC–Gel-MS method for proteomics research and its application to protease functional pathway mapping. *Journal of Chromatography B*, 822(1-2), 98-111.
81. **Wu, S.**, Kaiser, N. K., Meng, D., Anderson, G. A., Zhang, K., and Bruce, J. E.* (2005) Increased protein identification capabilities through novel tandem MS calibration strategies. *Journal of Proteome Research*, 4(4), 1434-1441.
82. Park, H., **Wu, S.**, Dunker, A. K., and Kang, C.* (2003) Polymerization of calsequestrin implications for Ca²⁺ regulation. *Journal of Biological Chemistry*, 278(18), 16176-16182.

Patent

1. Electrospray assisted capillary device for processing ultra low-volume samples.(2022) Wu S., Wang, Z., Huang L. *US patent 11340200*

Research support

External grant support

1. NIH-NIAID 1R01AI154274-01A1
Collaborator: Si Wu (PI: Anthony Burgett) 8/1/21-7/31/26
Title: Determining the cellular role of oxysterol-binding protein (OSBP) in viral replication
Wu group total award amount: \$45,000 (Wu group direct cost: \$31,000)
2. NIH-NIAID 5U19AI062629
Co-Investigator (Subcontract and project lead): Si Wu (PI: Mark Coggeshall) 8/1/19-7/31/24
Title: Mechanisms of waning immunity after vaccination with anthrax vaccine adsorbed
Wu group total award amount: \$603,174 (Wu group direct cost: \$400,000)
3. NIH-NIAID 1R01AI141625
Contact PI: Si Wu (Co-PI: Ken Smith, collaborator: Xiaowen Liu) 11/15/18-11/14/23
Title: Quantitative analysis of serum autoantibody repertoires in systemic lupus erythematosus
Total award amount: \$2,079,172
Wu group total award amount: \$1,069,755 (Wu group direct cost: \$700,000)
4. Oklahoma Center for the Advancement of Science and Technology (OCAST) HR16-125
PI: Si Wu (Collaborator: Ken Smith) 8/1/16-7/31/19
Title: Characterization of serum autoantibody biomarkers through an antigen-targeted top-down mass spectrometry (ATT-MS) platform
Total award amount: \$135,000 (direct cost)
5. NIH-NIGMS 1R01GM118470
Co-Investigator: Si Wu (PI: Xiaowen Liu and Yunlong Liu, IUPUI) 6/1/16-8/31/21
Title: Identification of complex proteoforms by top-down mass spectrometry and proteogenomics
Total award amount: \$1,079,172
Wu group award amount: \$225,605 (Wu group direct cost: \$150,550)
6. NIH NIAID Cooperative Study Group for Autoimmune Disease Prevention (CSGADP) Pilot Project (NIH 5U01AI101990-04, BRI sub-award No. FY15109843)

- PI: Si Wu (Collaborator: Ken Smith) 10/1/15-9/30/16
Title: Sequencing serum autoantibodies through antigen-targeted top-down MS (ATT-MS)
Total award amount: \$112,000 (Wu group direct cost: \$75,000)
7. NSF national high magnetic field laboratory user proposal
PI: Si Wu 6/1/15-5/31/18
Title: Deciphering the secrets of fungal secreted proteins
Total award amount: \$3,500 (travel award, direct cost) +instrument time
8. NSF-RET 1542446
Key personal and Participating faculty: Si Wu (PI: Mark Nanny) 9/1/15-5/31/19
Title: Rural educators engaged in bioanalytical engineering research and teaching
Total award amount: \$599,997
Wu group award amount: N/A
9. NSF-MRI 1626372
Co-PI: Si Wu (PI: Robert Cichewicz) 9/1/16-8/31/19
Title: MRI: Acquisition of high resolution exact mass liquid chromatograph mass spectrometer (LCMS) to broaden and enhance chemical and biological education and research
Total award amount: \$416,500
Wu group award amount: N/A

Internal grant support

10. OU VPR Faculty Investment Program
PI: Si Wu 1/1/18-12/31/18
Title: A novel functional proteomics approach for the characterization of intact active proteins
Total award amount: \$15,000
11. OU College of Arts and Sciences Junior Faculty Summer Fellowship (JFSF)
PI: Si Wu 4/26/16-8/15/16
Title: Deciphering the secrets in fungal secretome
Total award amount: \$7,000
12. OU VPR Instrument Upgrade Grant 11/1/16
PI: Si Wu
Total award amount: \$143,000
13. OU Faculty Startup 1/1/15-1/1/20
PI: Si Wu
Total award amount: \$500,000

Grant support before joining OU

14. EMSL Intramural Research & Capability Development Program
PI: Si Wu 9/1/11-8/31/14
Title: Systematic characterization of protein glycosylation of cell surface proteins
Total award amount: \$450,000
15. EMSL Intramural Research & Capability Development Program
PI: Si Wu 7/1/11-6/30/12
Title: Next generation multidimensional HPLC system for bacterial PTM characterization
Total award amount: \$200,000

TEACHING ACTIVITIES**Course developed**

CHEM 4923 "Introduction to Proteomics": A new senior capstone class that introduces the students to the fundamental concepts of proteomics, the tools of proteomics, and the applications of proteomics to real life biochemistry research. I developed all the class teaching material with the incorporation of a laboratory section.

Course taught

Spring 2015, CHEM 4923, *Introduction to Proteomics*, Enrollment: 31. (3 CH)
 Spring 2016, CHEM 4933, *Introduction to Proteomics*, Enrollment: 41. (3 CH)
 Fall 2016, CHEM 4023, *Instrumental Analysis*, Enrollment: 24. (3 CH)
 Fall 2016, CHEM 5191, *Seminar in Analytical Chemistry*, Enrollment: 23. (1 CH)
 Spring 2017, CHEM 5191, *Seminar in Analytical Chemistry*, Enrollment: 22. (1 CH)
 Spring 2017, CHEM 5110, *Spectroscopic Chemical Analysis*, Enrollment: 11. (3 CH)
 Fall 2017, CHEM 4023, *Instrumental Analysis*, Enrollment: 28. (3 CH)
 Spring 2018, CHEM 5110, *Spectroscopic Chemical Analysis*, Enrollment: 6. (3 CH)
 Fall 2018, CHEM 4023, *Instrumental Analysis*, Enrollment: 17. (3 CH)
 Spring 2019, CHEM 5110, *Spectroscopic Chemical Analysis*, Enrollment: 12. (3 CH)
 Fall 2019, CHEM 4023, *Instrumental Analysis*, Enrollment: 32. (3 CH)
 Fall 2019, CHEM 5191, *Seminar in Analytical Chemistry*, Enrollment: 19. (1 CH)
 Spring 2020, CHEM1315, *General Chemistry*, Enrollment: 144. (3 CH)
 Spring 2020, CHEM 5191, *Seminar in Analytical Chemistry*, Enrollment: 19. (1 CH)
 Fall 2020, CHEM 4023, *Instrumental Analysis*, Enrollment: 19. (3 CH)
 Fall 2020, CHEM 5191, *Seminar in Analytical Chemistry*, Enrollment: 17. (1 CH)
 Spring 2021, CHEM1315, *General Chemistry*, Enrollment: 290. (3 CH)
 Spring 2021, CHEM 5191, 1 *Seminar in Analytical Chem*, Enrollment: 17. (1 CH)
 Spring 2022, CHEM 5110, *Spectroscopic Chemical Analysis*, Enrollment: 8. (3 CH)
 Fall 2022, CHEM 4023, *Instrumental Analysis*, Enrollment: 16. (3 CH)

MENTORING/SUPERVISING EXPERIENCE (AFTER JOINING OU)**Post doc**

Name	Dates
Kellye A. Sutton	01/2019-present

Graduate students (* current student)

Name	Dates	Notes
Zhe Wang	08/2015-12/2019	Graduated with Ph.D (currently senior scientist at Amgen)
Dahang Yu	08/2016-12/2021	Graduated with Ph.D (currently scientist at Sparks)
Lushuang Huang	08/2016-12/2021	Graduated with Ph.D (currently scientist at Regeneron)
Graham Delafield	08/2016-05/2018	MS student with thesis (Ph.D student at UW Maddison)
Yanting Guo*	08/2018-present	Ph.D student
Mulin Fang*	08/2018-present	Ph.D student
Ji Kang*	12/2020-12/2022	Master student with thesis
Jiaxue Li*	12/2020-12/2022	Master student
Trishika Chowdury*	05/2021-present	Ph.D student

Anju Sunny*	05/2021-present	Ph.D student
Zhitao Zhao*	05/2021-present	Ph.D student
Joe Langford*	12/2021-present	Ph.D student
Samin Anjum*	12/2021-present	Ph.D student
Tom Welborn	02/2019-07/2021	MS student, OU computer science

Undergraduate students (* current student)

Name	Dates	Notes
Iya Prytkova	05/2015-05/2016	Ph.D student, Icahn School of Medicine
Alex Wallace	05/2015-12/2015	Chemist at ARL Bio Pharma
Toni Woodard	05/2015-05/2017	MS student, Fairleigh Dickinson University
Graham Delafield	09/2015-05/2018	Ph.D student, University of Wisconsin Maddison
Monica Stevens	01/2016-01/2017	OU student
Richard Yang	01/2016-05/2016	FYRE student
Dominique Ropp	01/2016-05/2016	FYRE student
Jacob Klenke	01/2016-12/2020	FYRE student
Thi Lam	09/2016-01/2017	Undergraduate student assistant
Moria Rendon	08/2016-04/2017	UROP student
Morgan W. Mann	08/2017-08/2018	Ph.D student, University of Wisconsin Maddison
Alethia Li	10/2017-08/2019	Dental student, UPenn dental school
Anh-Thy Nguyen	01/2018-07/2018	PharmD student, OU medical school
Gavin Hetzler	01/2018-05/2018	FYRE student
Kathrin Thorisch	01/2018-05/2018	FYRE student
Paul White	01/2018-05/2018	FYRE student
Bo Zhao	04/2018-12/2018	Graduated from OU
Ji Kang	08/2018-05/2020	Exchange student from Korea
Caden Castelli	09/2018-12/2018	Chemist, FAST lab
Khanh Do	10/2018-08/2019	MD student, OU medical school
Russell Perkins*	02/2019-present	Current OU student
Nelson McEwen	05/2019-08/2020	FYRE student
Jarrold Casey	04/2019-12/2020	Current OU student
Zixiang Jiang	07/2019-01/2020	MS student, John Hopkins (expected in Spring 2021)
Siyu Wu	07/2019-05/2020	MS student, Boston College
Drew King	11/2019-05/2020	FYRE student
Manh Nguyen	07/2020-12/2021	Current OU student (applying for medical school)
An Nguyen	07/2020-12/2021	Current OU student (applying for medical school)
Eric Moore	04/2020-12/2021	Current OU student (Honors thesis)
Walter Galie*	10/2020-present	Current OU student
Alexandra Atchison*	08/2021-present	Current OU student (Honors research)
Elizabeth Ahmed*	11/2021-present	Current OU student
Vineet Madur*	01/2021-12/2021	FYRE student

Sam Pritchett*	10/2020-present	FYRE student
Oliver Wu *	10/2020-present	FYRE student

High school students

Name	Dates	Notes
Lily Taylor	05/2016-08/2016	Undergraduate, Stanford University
Willow Arana	05/2018-12/2018	Undergraduate
Ryan Clark	05/2018-08/2018	Undergraduate, OCU
Meena Seshadri	05/2021-now	OU REHSS student

High school teachers (NSF-RET)

Name	Dates	Notes
Joe Albrecht	Summer 2016	teacher at Liberty High School Science
James Hall	Summer 2016	teacher at Hooker high school
Patricia Hardre	Summer 2017	teacher at Geary High School
Robert Jones	Summer 2018	teacher at Cameron High School
Novah Klein	Summer 2019	teacher at Chickasha High School

College students (NSF-REU)

Name	Dates	Notes
Dale Conrad	Summer 2017	Undergraduate at Rose-Hulman Institute of Technology
Uriel Vasquez Rios	Summer 2017	Undergraduate at Hamline University

Student awards and scholarship

Name	Dates	Award/Fellowship
Zhe Wang	2017	Roland E. Lehr scholarship (OU chemistry)
Zhe Wang	2017	OU Provost's certificate of distinction for outstanding TA
Zhe Wang	2017	Travel stipend from USHUPO
Zhe Wang	2016, 2017	OU CAS student conference travel grant
Zhe Wang	2019	Department graduate student peer recognition awardee
Dahang Yu	2017	ASMS fall workshop student travel stipend
Dahang Yu	2017	OU CAS student conference travel grant
Lushuang Huang	2017	OU CAS student conference travel grant
Yanting Guo	2019	Outstanding graduate teaching assistant awardee
Kathrin Thorisch	2018	Best FYRE project awardee
Kathrin Thorisch	2018	Best FYRE poster awardee
Dale Conrad	2017	NSF-REU "Best Broader Impact Impresentation" awardee
Moria Rendon	2017	OU UROP grant recipient
Jacob Klenke	2016	Outstanding FYRE student of the year (finalist)
Graham Delafield	2016	OU UROP grant recipient
Graham Delafield	2016	John Laing award for outstanding undergraduate research
Siyu Wu	2020	Undergraduate research day oral presentation, an Honors

		College Award for Honorable Mention
Drew King	2020	Undergraduate research day oral presentation, an Honors College Award for Honorable Mention
Oliver Wu	2021	Undergraduate research day oral presentation, The First Prize Award
Yanting Guo	2021	Best poster award Chinese American Society for Mass Spectrometry 1st Virtual Conference
Yanting Guo	2021	Provost's Certificate of Distinction in Teaching
Walter Galie	2021	Dick Van der Helm Scholarship
Oliver Wu	2022	Undergraduate research day oral presentation, an Honors College Award for Honorable Mention
Oliver Wu	2022	Inaugural Provost's Undergraduate Research and Creative Activity Fellowship
Mulin Fang	2022	Dodge Family Finishing Fellowship
Oliver Wu	2022	Dick Van der Helm Scholarship
Yanting Guo	2022	Dodge Family Finishing Fellowship

Student conference presentations by students (presenter underlined, * undergraduate students)

Selected Oral Presentations at National and International Conferences:

1. *Hunting biomass degrading enzymes and their active proteoforms through an activity-correlated quantitative proteomics platform (ACPP)*. Hongyan Ma, Daniel Delafield*, Zhe Wang, and Si Wu. **2016 ASMS**, San Antonio, TX, June 5-9, 2016 (**oral presentation**)
2. *N-glycopeptide feature identification by revealing trends between analyte composition and compensation field through FAIMS-coupled MS Platform*. Daniel G. Delafield, Zhe Wang, Matthew Baird, Alexandre A. Shvartsburg, and Si Wu. **2018 US HUPO**, Minneapolis, MN, March 11-14, 2018 (**oral presentation**)
3. *Development of a novel drug target identification platform based on size (DTIPS)*. Yanting Guo, Zhe Wang, Dahang Yu, Kellye A Cupp-Sutton, and Si Wu. **2019 ASMS**, Georgia World Congress Center, Atlanta, GA, June 2-6, 2019 (**oral presentation**)
4. *Differential HDX-MS for characterizing protein-protein interaction*. Jiwon Kang*, Zhe Wang, Mulin Fang, Kellye A Cupp-Sutton, and Si Wu. **64th Annual Pentasectional Meeting of the American Chemical Society (ACS)**, the NCED Hotel and Conference Center. Norman, OK, April 13, 2019 (**oral presentation**)
5. *Spray-Capillary: an electrohydrodynamic spray assisted device for quantitative ultra-low volume extraction*. Lushuang Huang, Zhe Wang, and Si Wu. **2019 US HUPO**, Rockville, MD, March 3-6, 2019 (**selected for "tips and tricks" talk**)
6. *Quantification of Thermal Stability of Intact Proteoforms Using Quantitative Top-Down Proteomics*. Kellye A Cupp-Sutton, Thomas Welborn, Si Wu. **68th ASMS annual conference Reboot**. June 8-12, 2020 (**oral presentation**)
7. *Spray-capillary Based Capillary Electrophoresis Mass Spectrometry Analysis of Metabolites in Live Cells*. Lushuang Huang, Zhe Wang, Mulin Fang, Cupp-Sutton Kellye, and Si Wu. **68th ASMS Annual Conference Reboot**, May 31-June 4, 2020 (**Oral presentation**)
8. *Development and Application of Quantitative Top Down Mass Spectrometry Methods*. Kellye A. Cupp-Sutton, Si Wu. **69th ASMS Conference on Mass Spectrometry and Allied Topics**, Top-down workshop, October 31- November 4, 2021. (**Oral presentation**)
9. *Top-Down Proteomics of Complex Protein Samples using Online 2D High-pH/Low-pH Ultra High-Pressure Nano-RPLC-MS*. Dahang Yu, Zhe Wang, Yanting Guo, Kellye Cupp-Sutton, Xiaowen Liu, Kenneth Smith and Si Wu, **2021 37th Microscale separations conference (MSB)**, July12-July 15, 2021 (**Oral presentation**)

10. Application of Top-Down Thermal Proteome Profiling to the analysis of Staurosporine Treated HeLa proteome stability. Kellye A. Cupp-Sutton, Yanting Guo, Trishika Chowdhury, Ji Kang, Si Wu. **US HUPO 2022 One World**, February 26 – March 2, 2022 (**Oral presentation**)
11. Top-down Proteomics for PTM Characterization. Yanting Guo, Kellye A. Cupp-Sutton, Si Wu. **US HUPO 2022 One World**, February 26 – March 2, 2022 (**Short course oral presentation**)
12. Investigation of the Effect of Staurosporine Induced Kinase Inhibition on HeLa using Top-down Proteome Profiling and Thermal Proteome Profiling. Kellye A. Cupp-Sutton, Yanting Guo, Trishika Chowdhury, Walter Galie, Si Wu. **HUPO Cancun**, December 4-8, 2022 (**Oral presentation**)
13. High-throughput Quantitative Single-cell Proteomics Analysis Using Spray-Capillary-Based Capillary Electrophoresis Mass Spectrometry. Jiaxue Li, Yanting Guo, Kellye Cupp-Sutton, Si Wu. **70th ASMS Conference on Mass Spectrometry and Allied Topics**, June 5-9, 2022 (**Oral presentation**)
14. Development and Application of High-Throughput Top-down Thermal Proteome Profiling to Probe Proteoform Functionality. Kellye A Cupp-Sutton, Yanting Guo, Trishika Chowdhury, and Si Wu. **CASMS**, October 17 – 21, 2022 (**Oral Presentation**)

Poster Presentations

15. *Developing a liquid chromatography assisted functional proteomics platform for characterizing biomass degrading enzymes from *Aspergillus niger* secretome.* Hongyan Ma, Zhe Wang, Jianlan You, and Si Wu. 2015 Annual American Society of Pharmacognosy Conference, Copper Mountain, CO, July 25-29, 2015
16. *Applying a tangential flow filtration approach for low concentration proteomics sample preparation.* Toni Woodard*, Zhe Wang, Ma Hongyan, Saurav Malla, and Si Wu. 2016 ASMS, San Antonio, TX, June 5-9, 2016
17. *Magnetic resin microreactor for affinity-capture top-down mass spectrometry.* Daniel Delafield*, Zhe Wang, Toni Woodard*, and Si Wu. 2016 ASMS, San Antonio, TX, June 5-9, 2016
18. *Separation and characterization of intact IgG fabs using ultra performance liquid chromatography coupled with top-down mass spectrometry.* Zhe Wang, Kenneth Smith, and Si Wu. 2016 ASMS, San Antonio, TX, June 5-9, 2016
19. *Two-dimensional separation using high pH and low pH reversed phase liquid Chromatography for top-down proteomics.* Zhe Wang, Hongyan Ma, Kenneth Smith, and Si Wu. 2017 US HUPO, San Diego, CA, March 20-22, 2017(**selected for "tips and tricks" talk**)
20. *Two-dimensional separation using high pH and low pH reversed phase liquid Chromatography for top-down proteomics.* Zhe Wang, Hongyan Ma, Kenneth Smith, and Si Wu. 2017 ISCC, Fort Worth, TX, May 8-12, 2017
21. *Active enzyme characterization using two-dimensional activity-correlated quantitative proteomics platform (2D-ACPP).* Hongyan Ma, Toni Woodard*, Morgan W. Mann*, and Si Wu. 2017 ISCC, Fort Worth, TX, May 8-12, 2017
22. *Bioactive fungal screening to find efficient biomass-degrading enzymes.* Dale Conrad*, Uriel A. Vasquez Rios*, Hongyan Ma, Toni Woodard*, and Si Wu. 2017 OU 2nd Annual C2C Summer Symposium, University of Oklahoma, Norman, OK, July 16, 2017
23. *Serum antibody characterization using a novel on-bead digestion approach and top-down proteomics.* Jacob Klenke*, Zhe Wang, and Si Wu. 2017 OU FYRE Presentation, University of Oklahoma, Norman, OK, April 6, 2017
24. *Characterization of N-linked isomeric glycans using LC and field asymmetric waveform ion mobility spectrometry (FAIMS).* Daniel Delafield, Zhe Wang, Matthew Baird, Kenneth Smith, Alexandre A. Shvartsburg, and Si Wu. 2017ASMS, Indianapolis, IN, June 4-8, 2017
25. *Coupling reversed phase liquid chromatography and capillary zone electrophoresis for top-down mass spectrometry.* Lushuang Huang, Zhe Wang, and Si Wu. 2017ASMS, Indianapolis, IN, June 4-8, 2017
26. *Autoantibody biomarker discovery by top-down proteomics of serum from patients with Systemic Lupus Erythematosus.* Zhe Wang, Xiaowen Liu, Kenneth Smith, and Si Wu. 2017ASMS, Indianapolis, IN, June 4-8, 2017

27. *Active enzyme characterization using two-dimensional activity-correlated quantitative proteomics platform (2D-ACPP)*. Morgan Mann*, Hongyan Ma, Toni Woodward*, and Si Wu. 2017 OU Research Day, University of Oklahoma, Norman, OK, April 15, 2017 (**oral presentation**)
28. *Detection of protein-protein interactions using a 2-dimensional chemical crosslinking activity correlated proteomics platform (2D-XL-ACPP)*. Morgan Mann*, Hongyan Ma, Toni Woodward*, and Si Wu. 2018 OU Research Day, University of Oklahoma, Norman, OK, April 15, 2018 (**oral presentation**)
29. *Target identification using activity correlated protein profiling*. Kathrin Thorisch*, Hongyan Ma, and Si Wu. 2018 OU Research Day, University of Oklahoma, Norman, OK, April 15, 2018 (**oral presentation**)
30. *Active" fungal classification utilizing top-down proteomics*. Toni Woodard*, Zhe Wang, Hongyan Ma, Monica Stevenson, and Si Wu. 2017ASMS, Indianapolis, IN, June 4-8, 2019
31. *Quantitative profiling of snake venom using TMT protein labeling and top-down mass spectrometry*. Dahang Yu, Zhe Wang, Hongyan Ma, and Si Wu. 2017ASMS, Indianapolis, IN, June 4-8, 2017
32. *Active enzyme characterization using an isobaric labeling activity-correlated quantitative proteomics platform (TMT-ACPP)*. Hongyan Ma, Morgan W. Mann*, Toni Woodard*, and Si Wu. 2017ASMS, Indianapolis, IN, June 4-8, 2017
33. *Intact protein quantitation in complex samples using protein-level TMT labeling and top-down mass spectrometry*. Dahang Yu, Zhe Wang, Qiang Kou, Xiaowen Liu, and Si Wu. 2018 US HUPO, Minneapolis, MN, March 11-14, 2018
34. *Development of a high-performance sheathless CZE-MS Interface for top-down proteomics*. Lushuang Huang, Zhe Wang, and Si Wu. 2018 US HUPO, Minneapolis, MN, March 11-14, 2018
35. *Finding a needle in a haystack: novel top-down proteomics tools for serum antibody analysis*. Zhe Wang, Kenneth Smith, and Si Wu. 2018 US HUPO, Minneapolis, MN, March 11-14, 2018
36. *Antibody-antigen interaction characterization using stopped flow assisted hydrogen deuterium exchange mass spectrometry*. Zhe Wang, Kellye Sutton, Michael Ashby, Kenneth Smith, and Si Wu. 2018 US HUPO, Minneapolis, MN, March 11-14, 2018
37. *Novel top-down proteomics tools for the quantitative analysis of serum autoantibody repertoires in patient samples*. Zhe Wang, Xiaowen Liu, Jennifer Muther, Judith A. James, Kenneth Smith, and Si Wu. 2018 ASMS, San Diego Convention Center, San Diego, CA, June 3-7, 2018
38. *Active kinase characterization in cancer cell line using an isobaric labeling activity-correlated protein profiling platform (TMT-ACPP)*. Hongyan Ma, Morgan Mann, Paul Sims, Alethia Li, Katie Thorisch, Willow Arana, and Si Wu. 2018 ASMS, San Diego Convention Center, San Diego, CA, June 3-7, 2018
39. *Characterization analysis of glycopeptides through arrival time correlation using concurrent RPLC fraction monitoring and FAIMS filtering*. Daniel G. Delafield, Matthew A. Baird, Zhe Wang, Alexandre A. Shvartsburg, and Si Wu. 2018 ASMS, San Diego Convention Center, San Diego, CA, June 3-7, 2018
40. *Detection of protein-protein interactions using a 2-dimensional chemical crosslinking activity correlated proteomics platform (2D-XL-ACPP)*. Morgan W Mann*, Hongyan Ma, Zhe Wang, and Si Wu. 2018 ASMS, San Diego Convention Center, San Diego, CA, June 3-7, 2018
41. *Development of a sensitive 2d RPLC-CZE top-down approach for sub-microgram sample analysis*. Lushuang Huang, Zhe Wang, and Si Wu. 2018 ASMS, San Diego Convention Center, San Diego, CA, June 3-7, 2018
42. *Intact protein quantitation in complex samples using protein-level TMT labeling and top-down mass spectrometry*. Dahang Yu, Zhe Wang, Hongyan Ma, Qiang Kou, Xiaowen Liu, and Si Wu. 2018 ASMS, San Diego Convention Center, San Diego, CA, June 3-7, 2018
43. *Two-dimensional separation using high-pH and low-pH reversed phase liquid chromatography for top-down proteomics*. Zhe Wang, Dahang Yu, Kenneth Smith, and Si Wu. 2018 ACS nation meeting at Boston, Boston, MA, August 19-23, 2018
44. *Differential hydrogen/deuterium exchange mass spectrometry analysis of antibody-antigen interaction*. Zhe Wang, Kellye Sutton, Michael Ashby, Kenneth Smith, and Si Wu. 2018 OU Symposium on Structural Biology, University of Oklahoma, Norman, OK, June 14, 2018
45. *Protein characterization using a novel on-bead digestion approach*. Paul White*, Dahang Yu, Zhe Wang, and Si Wu. 2018 FYRE, University of Oklahoma, Norman, OK, April 4, 2018

46. *Characterizing intact phosphoproteins from human cancer cells.* Gavin Hetzler*, Dahang Yu, and Si Wu. 2018 FYRE, University of Oklahoma, Norman, OK, April 4, 2018
47. *Target identification using activity correlated protein profiling.* Kathrin Thorisch*, Hongyang Ma, and Si Wu. 2018 FYRE, University of Oklahoma, Norman, OK, April 4, 2018
48. *Protein-protein interaction characterization using differential HDX-MS.* Jiwon Kang*, Zhe Wang, Mulin Fang, Kellye A Cupp-Sutton, and Si Wu. 2019 OU Undergraduate Research Day, University of Oklahoma, Norman, OK, April 6, 2019 (**oral presentation**)
49. *1400 proteoforms identified from five micrograms of Escherichia coli proteins using online 2D pH RP/RPLC top-down mass spectrometry.* Zhe Wang, Dahang Yu, Xiaowen Liu, Kenneth Smith, and Si Wu. 2019 ASMS, Georgia World Congress Center, Atlanta, GA, June 2-6, 2019
50. *Deep intact proteome quantification using protein-level tandem mass tag (TMT) labeling and online 2d liquid chromatography.* Dahang Yu, Zhe Wang, Kellye A Cupp-Sutton, Kenneth Smith, Xiaowen Liu, and Si Wu. 2019 ASMS, Georgia World Congress Center, Atlanta, GA, June 2-6, 2019
51. *Direct thermal proteome profiling using quantitative top-down proteomics.* Kellye A Cupp-Sutton, Zhe Wang, and Si Wu. 2019 ASMS, Georgia World Congress Center, Atlanta, GA, June 2-6, 2019
52. *Optimization of a low-temperature LC-MS system for hydrogen/deuterium exchange mass spectrometry.* Mulin Fang, Zhe Wang, Jiwon Kang, Kellye A Cupp-Sutton, Christina Bourne, and Si Wu. 2019 ASMS, Georgia World Congress Center, Atlanta, GA, June 2-6, 2019
53. *Spray-Capillary: an electrohydrodynamic spray assisted device for quantitative ultra-low volume extraction.* Lushuang Huang, Zhe Wang, and Si Wu. 2019 ASMS, Georgia World Congress Center, Atlanta, GA, June 2-6, 2019
54. *Quantitative top-down proteomics in complex samples using protein-level tandem mass tag (TMT) labeling.* Dahang Yu, Zhe Wang, Qiang Kou, Kenneth Smith, Xiaowen Liu, and Si Wu. 2019 US-HUPO, Rockville, MD, March 3-6, 2019
55. *Spray-Capillary: an electrohydrodynamic spray assisted device for quantitative ultra-low volume extraction.* Lushuang Huang, Zhe Wang, and Si Wu. 2019 US-HUPO, Rockville, MD, March 3-6, 2019 (**selected for "tips and tricks" talk**)
56. *Top-Down proteogenomics analysis of serum autoantibody repertoire for the discovery of biomarker of Systemic Lupus Erythematosus.* Zhe Wang, Xiaowen Liu, Kenneth Smith, and Si Wu. 2019 US-HUPO, Rockville, MD, March 3-6, 2019
57. *High-throughput quantitative top-down proteomics in complex samples using protein-level tandem mass tag (TMT) labeling.* Dahang Yu, Zhe Wang, Kellye A. Cupp-Sutton, Qiang Kou, Kenneth Smith, Xiaowen Liu, Si Wu. 31st ASMS Sanibel Conference, St. Petersburg, FL, January 24-27, 2019
58. *Top-Down Thermal Proteome Profiling of the E. Coli Proteome for Drug Target Identification.* Kellye A Cupp-Sutton, Zhe Wang, Si Wu. 2019 Designing Molecules and Workshop Conference. Kansas State University. Manhattan, KS, August 15-17, 2019
59. *Drug Target Identification Platform based on Size (DTIPS).* Yanting Guo, Zhe Wang, Dahang Yu, Kellye A Cupp-Sutton, and Si Wu. 2019 Designing Molecules and Workshop Conference. Kansas State University, Manhattan, KS, August 15-17, 2019
60. *Hydrogen/deuterium exchange mass spectrometry (HDX-MS) for complex sample analysis.* Mulin Fang, Zhe Wang, Thomas Welborn, Kellye A. Cupp-Sutton, Kenneth Smiths, and Si Wu. 68th ASMS Annual Conference Reboot, June 8-12, 2020
61. *The deuterium calculator: software for hydrogen-deuterium exchange mass spectrometry analysis to produce standard output.* Thomas Welborn, Kellye A. Cupp-Suttona, Mulin Fang, Zhe Wang, Kenneth Smith, and Si Wu. 68th ASMS Annual Conference Reboot, June 8-12, 2020
62. *Optimization of Quantitative Top-Down Proteomics in Complex Samples using Protein-Level Tandem Mass Tag (TMT) Labeling.* Dahang Yu, Yanting Guo, Kellye A Cupp-Sutton, Zhe Wang, Mulin Fang, Xiaowen Liu, and Si Wu. 68th ASMS Annual Conference Reboot, June 8-12, 2020
63. *Optimization of Gel Elution Liquid Fraction Entrapment Electrophoresis Fractionation Coupled with Reversed Phase Liquid Chromatography Separation for Deep Proteome Analysis.* Siyu Wu, Ji Won Kang,

- Kellye Cupp-Sutton, Si Wu. 32nd Annual Undergraduate Research Day 2020, The Honors College at the University of Oklahoma, April 25-26, 2020.
64. Implementing a Neutral Chemical Coating to Spray-Capillary Device for Ultra Low Volume Sample Analysis. Drew King, Lushuang Huang, Si Wu. 32nd Annual Undergraduate Research Day 2020, The Honors College at the University of Oklahoma, April 25-26, 2020.
 65. Spray-capillary based capillary electrophoresis mass spectrometry analysis of metabolites in live cells. Lushuang Huang, Mulin Fang, Kellye Cupp-Sutton, Zhe Wang, Kenneth Smith, Si Wu. 17th USHUPO Virtual Annual Conference, March 3-8, 2020
 66. Construction of a Reusable GELFrEE Cartridge using 3D-printing. Walter Galie, Si Wu. Undergraduate Research Day 2021, April 9-10, 2021. (Oral Presentation)
 67. Optimization of Quantitation of Sodium Dodecyl Sulfate (SDS) by Visible Light Spectroscopy following Pierce Detergent Removal. Oliver Wu, Si Wu. Undergraduate Research Day 2021, April 9-10, 2021. (Oral Presentation)
 68. Optimization of Size Exclusion Chromatography to Increase Mass Spectrometry Sensitivity in Top Down Thermal Proteome Profiling. Eric Moore, Si Wu. Undergraduate Research Day 2021, April 9-10, 2021. (Oral Presentation)
 69. Optimization of Parameters for Recycled and 3D Printed Gel Elution Liquid Fraction Entrapment Electrophoresis (GELFrEE) Cartridges for Size-based Separation of Proteins. Joseph Pritchett, Si Wu. Undergraduate Research Day 2021, April 9-10, 2021. (Oral Presentation)
 70. Size Exclusion Chromatography Fractionation for Enrichment of Low Molecular Weight Plasma Proteins for Top-down Plasma Proteome Profiling. An Nguyen, Si Wu. Undergraduate Research Day 2021, April 9-10, 2021. (Oral Presentation)
 71. Low Molecular Weight Plasma Proteins Enrichment using Gel Elution Liquid Fraction Entrapment Electrophoresis (GELFrEE) for In-depth Analysis of Plasma Proteomes using Top-down Proteomics. Manh Nguyen, Si Wu. Undergraduate Research Day 2021, April 9-10, 2021. (Oral Presentation)
 72. Construction of a reusable Gel-Eluted Liquid Fraction Entrapment Electrophoresis (GELFrEE) using 3D printing. Walter Galie, Yanting Guo, Kellye Cupp-Sutton, Si Wu. OK-LSAMP 27th Annual Research Symposium, October 8, 2021. (Poster Presentation)
 73. Quantitative Top-down Thermal Proteome Profiling of E. coli lysate and Standard Proteins. Kellye Cupp-Sutton, Thomas Welborn, Ji Won Kang, Si Wu. US HUPPO 2021, March 4-12, 2021. (Poster and Lightning talk)
 74. Optimization of Protein-Level Tandem Mass Tag (TMT) Labeling in Complex Sample with Top-Down Proteomics. Yanting Guo, Dahang Yu, Kellye A. Cupp-Sutton, Xiaowen Liu, Si Wu. US HUPPO 2021, March 4-12, 2021. (Poster and Lightning talk)
 75. Optimization of a long-gradient ultrahigh pressure liquid chromatography (UPLC) separation for HDX-MS. Mulin Fang, Zhe Wang, Kellye A. Cupp-Sutton, Thomas Welborn, Kenneth Smith, Si Wu. US HUPPO 2021, March 4-12, 2021. (Poster and Lightning talk)
 76. Top-down Tandem Mass Tag (TMT) Labeling on the Intact Plasma Proteome for Biomarker Discovery in Systematic Lupus Erythematosus (SLE). Yanting Guo, Kellye A. Cupp-Sutton, Dahang Yu, Walter P. Galie, Kenneth Smith, Xiaowen Liu, Si Wu. 69th ASMS Conference on Mass Spectrometry and Allied Topics, October 31- November 4, 2021. (Poster and lightning talk)
 77. Development of a high-throughput and automated spray-capillary platform for the microsampling and CE-MS analysis of picoliter and nanoliter volume samples. Jiaxue Li, Lushuang Huang, Kellye A. Cupp-Sutton, Si Wu. 69th ASMS Conference on Mass Spectrometry and Allied Topics, October 31- November 4, 2021. (Poster presentation)
 78. Direct antigen epitope-mapping in vaccine-elicited serum samples using high-throughput HDX-MS. Mulin Fang, Kenneth Smith Zhe Wang, Kellye A. Cupp-Sutton, Kathleen Haley, Judith A. James, Si Wu. 69th ASMS Conference on Mass Spectrometry and Allied Topics, October 31- November 4, 2021. (Poster presentation and lightning talk)
 79. Adaptation of Top-down Thermal Proteome Profiling for the Analysis of the Thermal Stability of the Human Proteome. Kellye A Cupp-Sutton, Yanting Guo, Trishika Chowdhury, Ji Kang, Si Wu. 69th

- ASMS Conference on Mass Spectrometry and Allied Topics, October 31- November 4, 2021. (Poster presentation)
80. Optimization of Quantitative Top-Down Proteomics in Complex Samples using Protein-Level Tandem Mass Tag (TMT) Labeling. Yanting Guo, Dahang Yu, Kellye A. Cupp-Sutton, Xiaowen Liu, Si Wu. 2021 Chinese American Society for Mass Spectrometry, August 9-13, 2021. (Poster and Lightning talk)
 81. Optimization of a long-gradient ultrahigh pressure liquid chromatography (UPLC) separation for complex sample analysis using HDX-MS. Mulin Fang, Zhe Wang, Thomas Welborn, Kellye A. Cupp-Sutton, Kenneth Smiths, and Si Wu. 2021 Chinese American Society for Mass Spectrometry, August 9-13, 2021. (Poster and Lightning talk)
 82. The development of a high-throughput and automated spray-capillary based CE-MS platform for microsampling analysis of picoliter and nanoliter volume samples. Jiaxue Li, Lushuang Huang, Kellye A. Cupp-Sutton, and Si Wu. 2021 Chinese American Society for Mass Spectrometry, August 9-13, 2021. (Poster)
 83. Quantitative Top-down Thermal Proteome Profiling of *E. coli* lysate and Standard Proteins. Ji Kang, Kellye Cupp-Sutton, Thomas Welborn, Si Wu. 2021 Chinese American Society for Mass Spectrometry, August 9-13, 2021. (Poster)
 84. Optimization and Evaluation of Size Exclusion Chromatography Protein Enrichment Top-Down Thermal Proteome Profiling. Eric A. Moore, Kellye A. Cupp-Sutton, Yanting Guo, Ji Kang, Si Wu. Senior Thesis Poster Session, December 8, 2021. (Poster presentation)
 85. Direct antigen epitopes mapping in human serum samples against AVA vaccine-elicited polyclonal antibodies. Mulin Fang, Kenneth Smith, Zhe Wang, Kellye A. Cupp-Sutton, Kathleen Haley, Judith A. James, and Si Wu. US HUPO 2022 One World, February 26 – March 2, 2022 (Poster presentation and lightning talk).
 86. Quantitative analysis of Intact Plasma Proteome in Systematic Lupus Erythematosus (SLE) using Protein-Level TMT Labeling and Top-Down Proteomics. Yanting Guo, Walter P. Galie, Kellye A. Cupp-Sutton, Dahang Yu, Ken Smith, Xiaowen Liu, Si Wu. US HUPO 2022 One World, February 26 – March 2, 2022 (Poster presentation and lightning talk).
 87. Elucidating protein-ligand interactions in cell lysates using high throughput hydrogen deuterium exchange mass spectrometry with integrated protein thermal depletion. Mulin Fang, Oliver Wu, Kellye A. Cupp-Sutton, Kenneth Smith, Si Wu. 33rd Sanibel Conference on Mass Spectrometry, January 19 - 22, 2023 (Poster presentation)
 88. High throughput quantitative single-cell proteomics analysis using spray-capillary-based CE-MS. Jiaxue Li, Yanting Guo, Lushuang Huang, Mulin Fang, Zhitao Zhao, Kellye A. Cupp-Sutton, Si Wu. US HUPO 2022 One World, February 26 – March 2, 2022 (Oral presentation)
 89. Thermo proteome profiling (TPP) coupled with high throughput HDX-MS for functional characterizations of drug targets in cell lysate. Oliver Wu, Mulin Fang, Kellye A. Cupp-Sutton, and Si Wu. OU undergraduate research day, April 9, 2022 (Oral presentation)
 90. Characterization of human polyclonal antibody-mediated neutralizing responses in AVA vaccine-elicited serum samples using high-throughput HDX-MS. Mulin Fang, Kenneth Smith, Kellye A. Cupp-Sutton, Joel B. Langford, Kathleen Haley, Judith A. James, Si Wu. ASMS 2022, June 5 - 9, 2022 (Poster presentation)
 91. Thermo proteome profiling (TPP) coupled with high throughput HDX-MS for functional characterizations of drug targets in cell lysate. Oliver Wu, Mulin Fang, Kellye A. Cupp-Sutton, and Si Wu. ASMS 2022, June 5 - 9, 2022 (Poster presentation)
 92. Investigation of Systematic Lupus Erythematosus (SLE) Biomarkers using Top-down TMT Labeling and Two-Dimensional High-pH/Low-pH Reversed Phase Liquid Chromatography Separation. Yanting Guo, Kellye A. Cupp-Sutton, Dahang Yu, Walter P. Galie, Ken Smith, Xiaowen Liu, Si Wu. 70th ASMS Conference on Mass Spectrometry and Allied Topics, June 5-9, 2022 (Poster presentation)
 93. Quantitative top-down proteomics for understanding the mechanism of action of Staurosporine in cancer cells. Trishika Chowdhury, Kellye Cupp-Sutton, Yanting Guo, Si Wu. 70th ASMS Conference on Mass Spectrometry and Allied Topics, June 5-9, 2022 (Poster presentation)

94. Construction of a Reusable Gel-Eluted Liquid Fraction Entrapment Electrophoresis (GELFrEE) Using 3D Printing. Walter Galie, Kellye Cupp-Sutton, Yanting Guo, Si Wu. 70th ASMS Conference on Mass Spectrometry and Allied Topics, June 5-9, 2022 (Poster presentation)
95. Isobaric Labeling Based Top-Down Thermal Proteome Profiling (TD-TPP) for Proteome Scale Drug Target Characterization. Kellye Cupp-Sutton, Yanting Guo, Trishika Chowdhury, Walter Galie, Si Wu. 70th ASMS Conference on Mass Spectrometry and Allied Topics, June 5-9, 2022 (Poster presentation)
96. Development and Optimization of a Top-down SPROX Platform for Complex Protein Mixtures. Anju Teresa Sunny, Kellye A. Cupp-Sutton, Yanting Guo, and Si Wu. 2nd CASMS, October 17-October 21, 2022 (Poster presentation)
97. Development and Optimization of a Top-down SPROX Platform for Complex Protein Mixtures. Anju Teresa Sunny, Kellye A. Cupp-Sutton, Yanting Guo, and Si Wu. 10th Annual Structural Biology Symposium, June 16, 2022 (Poster presentation)
98. Proteoform-level Quantitative Analysis of the HeLa proteome as a Result of Staurosporine Treatment. Trishika Chowdhury, Kellye Cupp-Sutton, Yanting Guo, Si Wu. 2nd CASMS, October 17-October 21, 2022 (Poster presentation)
99. Thermo proteome profiling (TPP) coupled with high throughput HDX-MS for functional characterizations of drug targets in cell lysate. Oliver Wu, Mulin Fang, Kellye A. Cupp-Sutton, and Si Wu. 2nd CASMS, October 17-October 21, 2022 (Poster presentation)
100. Direct antigen epitope-mapping in vaccine-elicited serum samples using HDX-MS. Mulin Fang, Kenneth Smith, Kellye A. Cupp-Sutton, Joel B. Langford, Si Wu. 2nd CASMS, October 17-October 21, 2022 (Poster presentation)

DEPARTMENT SERVICE

Service	Time	Notes
Graduate student recruiting and admissions committee	2021-now	Chair , organize recruiting activities such as virtual open house and conference exhibition booths, arrange graduate student application evaluation, interviews, and visits
Committee A	2022-2024	Department Committee A member (elected) , the faculty evaluation committee
Seminar Committee	2016-2022	Member , help committee chair select seminar speakers
Department library liaison	2018-present	Communications between department faculty and the university library
Graduate student recruiting and admissions committee	2018-2021	Member and co-chair , participate in graduate student application evaluation, interview, and visit arrangement
Graduate student committee	2016-2018	Member , participate in meetings and related discussions, prepare annual evaluation for students in analytical division
FYRE program mentor	2016-now	mentored 10 FYRE students
Graduate student advisory committee member	2015-present	Serve on 40+ committees (students not from my group)
OU CBA symposium	2015	Help organize the symposium

Graduate student committee member (students not from my group)

Name	Dates	Group
------	-------	-------

Matt Atteberry	2022-present	Dong
Andrew Chesney	2022-present	Hansmann
Mithila Farjana	2022-present	Zgurskaya
Ke Zhang	2021-present	Outside department
Melvynn Mangione	2021-present	Cichewicz (master)
Jeff Tu	2020-present	Bourne
Shengfeng Ruan	2020-present	Bourne
Chaoyi Wu	2019-2020	McCall
Heidi Noneman	2019-present	White
Michael McCoy	2019-2020	Mao
Neda Heydarian	2019-present	Rice
Shannon Fulton	2019-present	outside department
Xuxin Chen	2019-present	outside department
Zhitao Zhao	2019-2020	Liu
Alan Ray	2018-present	Hansmann
Jaspreet Singh	2018-2021	White
Liwei Zhang	2018-present	Mao
Xingxiu Chen	2018-present	Yang
Anh Lam	2017-2021	Rice
Josh Garton	2016-2020	Bourne
Piliang Xiang	2016-2021	Liu
Songyuan Yao	2016-2020	Mao
Songyuan Yao	2020-present	Shao
Wenhua Wang	2016-2021	Hansmann
Victoria Anderson	2016-2021	Cichewicz
Laurence Niadj	2016-2018	Cichewicz
Matt Beckner	2016-2018	Liu
Megan Ayala	2016-2017	Richter-Addo
Melissa Foxley	2015-present	Rice
Mengmeng Zhai	2015-present	Mao
Ningyun Zhou	2015-present	Mao
Xiang Tian	2015-present	Yang
Yang Yu	2015-present	Liu
Mei Sun	2015-2019	Yang
Shawna Dtrandke	2015-2019	Yang
Wentao Dai	2015-2019	Cichewicz
Morgan Harris	2021	McCall (replacement for GE)
Shubhangi Singh	2021	Rice (master)
Kyle Lynch	2018	Liu
Rachael Kim	2018	West

OUTREACH ACTIVITIES

1. OU 3MT® Competition judge (**February 2022**)
2. VPR Blavatnik National Awards for Young Scientists Internal Review (**October 2021**)
3. Research Experience for High School Students (REHSS) Program here at OU, mentor, **2021**
4. Course developer and lecturer, OU Mini college for K-12 students "What is protein?" (**August 2021**)
5. Panelist, USHUPO workshop, "Interactive career planning and development" (**March 2021**)
6. OU undergraduate research day, judge (**April 2021**)
7. Panelist, ASMS Emerging Talent Special Meeting for "Career planning and development" (**November 2020**)
8. Meeting with "Woman in Chemistry" student group, Department of Chemistry, Michigan State University (MSU) (**September 2019**)
9. Panelist, ASMS workshop (Young Mass Spectrometrists Interest Group), "How to kick start your career" (**June 2019**)
10. Invited to present a research presentation for Norman High School (**December 2017**)
11. Faculty mentor, OU FYRE program, **2016-now** (mentored 10 students)
12. Faculty mentor, NSF REU program "Program in Structural Biology at the University of Oklahoma", **2017** (mentored 2 students)
13. Faculty mentor, NSF RET program "Rural Educators Engaging in Bioanalytical Engineering Research and Teaching", **2016-2019** (mentored 5 high school teachers)
14. FYRE program poster judge, **2015**
15. Mentor, Honors Research Assistant Program (HRAP), **2016-2017**