

Xinhao Shao

Ph.D. candidate at
University of Illinois at
Chicago

Address: 833 S. Wood St, Room 590, Chicago, IL

Phone: (312) 358-1502

Email: xshao8@uic.edu

Linkedin: [linkedin.com/in/xinhao-shao-870118127](https://www.linkedin.com/in/xinhao-shao-870118127)



Summary

- Proteomic scientist with extensive experience from LC-MS/MS based sample preparation to data analysis, particularly passionate in *Omics* data analysis/mining.
- Great publication records (7 manuscripts published, in total 10 manuscripts are expected to be submitted upon graduation), excellent programming skills in Python.
- Expect to graduate as a Ph.D. in 05/2023, actively looking for positions as proteomics scientist or data scientist in industry (Will be legal to work in US after graduate as OPT).

Education

2018 – 2023	Ph.D. in Pharmaceutical Science at University of Illinois at Chicago, Chicago, IL
2016 – 2018	M.S. in Bioengineering at Illinois Institute of Technology, Chicago, IL
2012 – 2016	B.eng. in Pharmaceutical engineering at Heilongjiang University, Harbin, China

Awards

10/2022	Dean's Fund for Excellence Scholarship, PSCI, UIC, Chicago, IL, USA
02/2022	Travel Award for PhD Students (TAPS) from the Office of the Dean of the College of Pharmacy, UIC, Chicago, IL, USA
11/2020	Oscar Robert Oldberg Prize in Pharmaceutical Chemistry from the College of Pharmacy, UIC, Chicago, IL, USA

Skills

Data analysis

- Proficient in multiple proteomics software workflow (SEQUEST, FragPipe, Skyline, MaxQuant, etc.)
- Advanced *Python* programming (quantitative analysis such as extraction of peptide intensity, custom DB handling, 3D coverage visualization, scoring of peptide spectra with predictions, etc.)
- Statistical modelling and visualization with Python packages (supervised/unsupervised learning, CNN, LSTM, UMAP, HDBSCAN, etc.)
- Completed projects based on *Python*: <https://matrisomedb.org/>, <http://scv.lab.gy/>, <https://pypi.org/project/extPep-identifier-blackjack/>, <https://github.com/blackjack-uic/MatrisomeDB2>
- Also proficient in *R*, *HTML*, *Bash*, *MySQL*
- Personal git page: <http://pepchem.org:35091/blackjack>

Continuing to the back

Skills

Wet lab experiments

- Proteomics sample preparation, including eukaryotic/bacterial cell lysis, protein precipitation, protein quantification assay, enzymatic digestion, peptide salting and quantification.
- Operation of Liquid chromatography–mass spectrometry (Q Exactive HF) for proteomic sample running.

Publication

- **Shao, X.**, Gomez, C., Kapoor, N., Considine, J., Gao, Y., and Naba, A., 2022. MatrisomeDB 2.0: 2023 updates to the ECM protein knowledge database. *Nucleic Acids Research* <https://doi.org/10.1093/nar/gkac1009>
- Laczkovich, I., Mangano, K., **Shao, X.**, Hockenberry, A., Gao, Y., Mankin, A., Vazquez-Laslop, N., and Federle, M., 2022. Discovery of unannotated sORFs in *Streptococcus pneumoniae* D39 involved in quorum sensing and virulence using ribosome profiling. *Mbio*, 13.4 (2022): e01247-22..
- **Shao, X.**, Grams, C., and Gao, Y., 2022. Sequence Coverage Visualizer: A web application for protein sequence coverage 3D visualization. Accepted by *Journal of Proteome Research*
- Lee, F.[#], **Shao, X.**[#], Gao, Y., and Naba, A., 2022. Time-lapsed proteomics reveals a role for the novel protein, SNED1, in modulating ECM composition and protein folding. *bioRxiv*, #: co-first authors
- Mangano, K.[#], Florin, T.[#], **Shao, X.**, Klepacki, D., Chelysheva, I., Ignatova, Z., Gao, Y., Mankin, A.S. and Vázquez-Laslop, N., 2020. Genome-wide effects of the antimicrobial peptide apidaecin on translation termination in bacteria. *eLife*, 9, p.e62655. #:co-first authors
- **Shao, X.**, Taha, I.N., Clauser, K.R., Gao, Y. and Naba, A., 2020. MatrisomeDB: the ECM-protein knowledge database. *Nucleic Acids Research*, 48(D1), pp.D1136-D1144
- **Shao, X.**[#], Fang, K.[#], Medina, D., Wan, J., Lee, J.L. and Hong, S.H., 2020. The probiotic, *Leuconostoc mesenteroides*, inhibits *Listeria monocytogenes* biofilm formation. *Journal of Food Safety*, 40(2), p.e12750. #:co-first authors

Podium/Poster presentations

- 07/2022** **Shao, X.**; Narayanan, R.; Grams, C.; Gao, Y. (Oral talk) Protein structure validation by limited proteolysis. *Chicago Mass Spec Day 2022*, UIC, Chicago, IL, USA
- 06/2022** **Shao, X.**; Narayanan, R.; Grams, C.; Gao, Y. (Poster) Protein structure validation by limited proteolysis. *American society for Mass Spectrometry 2022 conference*, Minneapolis Convention Center, Minneapolis, MN, USA
- 04/2022** **Shao, X.**; Narayanan, R.; Grams, C.; Gao, Y. (Poster) Protein structure validation by limited proteolysis. *MIKIW-2022*, University of Iowa, Iowa city, IA, USA
- 11/2021** **Shao, X.**; Grams, C.; Gao, Y. (Poster) Native digestion combined with 3D Proco assists cross-validation of AlphaFold predictions. *COP research day-2021*, University of Illinois at Chicago, Chicago, IL, USA
- 11/2020** **Shao, X.**; Gao, Y. (Poster) The Dark Side of Proteome. *COP research day-2020*, University of Illinois at Chicago, Chicago, IL, USA

Professional experience

2018 – present	Research/Teaching Assistant	UIC, IL, USA
2017 – 2018	Teaching Assistant	IIT, IL, USA
01/2015 – 03/2015	QA intern	LIBP Co., Ltd. Lanzhou, China
