Xinhao Shao

Ph.D. candidate at
University of Illinois at
Chicago

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Summary

- Proteomic scientist with extensive experiences 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 *Omics* 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

Omics data/statistical analysis

- Proficient in multiple proteomics software workflow (SEQUEST, FragPipe, Skyline, DIA-NN, etc.)
- Advanced *Python* programming (quantitative analysis such as extraction of peptide intensity, custom DB handling, 3D structure 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*: http://matrisomedb.org/, http://scv.lab.gy/, https://pypi.org/project/extPep-identifier-blackjack/, https://github.com/blackjack-uic/MatrisomeDB2
- Also proficient in *R, HTML, MySQL,* comfortable working under *Windows/Linux* system
- Personal git page: http://pepchem.org:35091/blackjack

Continuing to the back

Skills

Wet lab experiments

- Shot-gun proteomics sample preparation, including eukaryotic/bacterial cell lysis, protein precipitation, protein quantification assay, enzymatic digestion, peptide de-salting and quantification, peptide fractionation, phospho-peptide enrichment, TMT-labelling.
- Operation of LC-MS/MS (Q-Exactive HF) instrument for proteomics 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

• Matsumoto, C., **Shao, X.**, Bogosavljevic, M., Chen, L., & Gao, Y. (2022). Automated container-less cell processing method for single-cell proteomics. *bioRxiv.*

• 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, *JPR, https://doi.org/10.1021/acs.jproteome.2c00358*

• **Shao, X.**[#], Lee, F.[#], 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*.

• 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.

• **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.

Podium/Poster presentations

07/2022   **Shao, X.;** Narayanan, R.; Grams, C.; Gao, Y. (<u>Oral talk</u>) 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. (<u>Poster</u>) 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. (<u>Poster)</u> Protein structure validation by limited proteolysis. *MIKIW-2022*, University of Iowa, Iowa city, IA, USA

11/2021   **Shao, X.**; Grams, C.; Gao, Y. (<u>Poster</u>) 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. (<u>Poster</u>) 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	Research Assistant	IIT, IL, USA
01/2015 – 03/2015	QA intern	LIBP Co., Ltd. Lanzhou, China