Harrison Specht

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EDUCATION

Northeastern University, Ph.D. Bioengineering, Graduate Student	March 2022
Cornell University, B.A. Chemistry, *magna cum laude*	2014

RESEARCH EXPERIENCE

Northeastern University

Slavov Lab, Bioengineering & Barnett Institute, Graduate Student	2016–2022

Merck, Sharpe & Dohme Corporation

Merck Exploratory Sciences Division, Coop	Spring 2020

Broad Institute of MIT and Harvard

Proteomics Platform, Research Associate	2014–2016

Cornell University, Ithaca, NY

Petersen Lab, Department of Chemistry, Research Assistant	2012–2014
Zinder Lab, Department of Microbiology, Research Assistant	2010–2011
The Triple Helix, magazine, Executive Editor-in-chief	2013 – 2014

Bermuda Institute for Ocean Sciences

National Science Foundation REU Fellow	2013

Vertex Pharmaceuticals, Boston, MA

Drug Metabolism and Pharmacokinetics, Internship	2013

FELLOWSHIPS AND AWARDS

2021 *NSF I-Corps Grant* $10,000 for development of single cell proteomics venture

2021 *Frequency Bio by Pillar VC & Petri* pillar.vc/frequency/

2020 *Rising Stars in Proteomics and Metabolomics*, Journal of Proteome Research.

https://pubs.acs.org/doi/full/10.1021/acs.jproteome.0c01026

2019 *2nd place in Chemical Biology*, Royal Society of Chemistry Twitter Poster Conference

2016– *College of Engineering Dean's Distinguished Fellowship*, Northeastern University

2013 *Best Oral Presentation*, Bermuda Institute for Ocean Science NSF REU Program

EXPERTISE

Computational: Proteomics data processing (DIA, DDA, phospho-, targeted-), transcriptomics and proteomics data integration, protein-set enrichment analysis (PSEA), gene-set enrichment analysis (GSEA), imputation, principal component analysis (PCA), created first computational single cell proteomics data processing pipeline (https://github.com/SlavovLab/SCoPE2/, replicated by 'scp' package: https://bioconductor.org/packages/release/bioc/html/scp.html)

Coding and Software: R, Shiny, MS-Fragger, DIA-NN, SpectroNaut, MaxQuant, Skyline

Experimental: Single-cell proteomics, triple-quad and orbitrap-based mass spectrometry proteomics, data dependent (DDA) and data independent (DIA) acquisition, protein and peptide N-terminomics, phosphoproteomics, antibody and chemical enrichment of proteins and peptides, reverse-phase and ERLIC liquid chromatography, robotic sample preparation, cell culture, flow cytometry

PUBLICATIONS

Derks, J., Leduc, A., Huffman, R.G., **Specht, H.**, Ralser, M., Demichev, V., Slavov, N. Increasing the throughput of sensitive proteomics by plexDIA. biorxiv. 2021. https://doi.org/10.1101/2021.11.03.467007

Petelski, A.A., Emmott, E., Leduc, A., Huffman, R.G., **Specht, H.**, Perlman, D.H., Slavov, N. Multiplexed single-cell proteomics using SCoPE2. Nature Protocols. doi: https://doi.org/10.1101/2021.03.12.435034

Specht, H., Emmott, E., Petelski, A.A. et al. Single-cell proteomic and transcriptomic analysis of macrophage heterogeneity using SCoPE2. Genome Biol 22, 50 (2021). https://doi.org/10.1186/s13059-021-02267-5

Specht, H., Slavov, N., 2021. Optimizing accuracy and depth of protein quantification in experiments using isobaric carriers. J. Proteome Res. 20, 880-887. https://doi.org/10.1021/acs.jproteome.0c00675

Keshishian et al. Highly multiplexed quantitative phosphosite assay for biology and preclinical studies. bioRxiv 2020.12.08.415281; doi: https://doi.org/10.1101/2020.12.08.415281 **In press at Molecular Systems Biology**

Huffman, R.G., Chen, A., **Specht, H.**, Slavov, N., 2019. DO-MS: Data-Driven Optimization of Mass Spectrometry Methods. J. Proteome Res. 18, 2493–2500. https://doi.org/10.1021/acs.jproteome.9b00039

Specht, H., Harmange, G., Perlman, D.H., Emmott, E., Niziolek, Z., Budnik, B., Slavov, N., 2018. Automated sample preparation for high-throughput single-cell proteomics. bioRxiv 399774. https://doi.org/10.1101/399774

Specht, H., Slavov, N., 2018. Transformative Opportunities for Single-Cell Proteomics. J. Proteome Res. 17, 2565–2571. https://doi.org/10.1021/acs.jproteome.8b00257

Khajuria, R.K., Munschauer, M., Ulirsch, J.C., Fiorini, C., Ludwig, L.S., McFarland, S.K., Abdulhay, N.J., **Specht, H.**, Keshishian, H., Mani, D.R., Jovanovic, M., Ellis, S.R., Fulco, C.P., Engreitz, J.M., Schütz, S., Lian, J., Gripp, K.W., Weinberg, O.K., Pinkus, G.S., Gehrke, L., Regev, A., Lander, E.S., Gazda, H.T., Lee, W.Y., Panse, V.G., Carr, S.A., Sankaran, V.G., 2018. Ribosome Levels

Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. Cell 173, 90-103.e19. https://doi.org/10.1016/j.cell.2018.02.036

Keshishian, H., Burgess, M.W., **Specht, H.**, Wallace, L., Clauser, K.R., Gillette, M.A., Carr, S.A., 2017. Quantitative, multiplexed workflow for deep analysis of human blood plasma and biomarker discovery by mass spectrometry. Nat Protoc 12, 1683–1701. https://doi.org/10.1038/nprot.2017.054

TALKS

2020. **Harrison Specht**, Edward Emmott, Aleksandra A. Petelski, R. Gray Huffman, David H. Perlman, Marco Serra, Peter Kharchenko, Antonius Koller, Nikolai Slavov. "How to perform quantitative single cell proteomics with SCoPE2." GenomeWeb Webinar Series. ***Invited***

2020. **Harrison Specht**, Edward Emmott, Aleksandra A. Petelski, R. Gray Huffman, David H. Perlman, Marco Serra, Peter Kharchenko, Antonius Koller, Nikolai Slavov. "How to perform quantitative single cell proteomics with SCoPE2." Association of Biomolecular Resource Facilities (ABRF) 2020 Annual Meeting. ***Invited***

2019. **Harrison Specht**, Edward Emmott, Aleksandra A. Petelski, R. Gray Huffman, David H. Perlman, Antonius Koller, Nikolai Slavov. "Design of single cell proteomics experiments." Single Cell Proteomics Conference. Boston, MA. 2019.

2019. **Harrison Specht**, Nikolai Slavov. Quantifying proteins by mass spectrometry. Models, Inference, and Algorithms Seminar. Broad Institutde of MIT and Harvard. ***Chalk-talk***

2018. **Harrison Specht**, Guillaume Harmange, David H Perlman, Edward Emmott, Zachary Niziolek, Bogdan Budnik, Nikolai Slavov. "Automated sample preparation for high-throughput single-cell proteomics." HUPO 2018.

2018. **Harrison Specht**, Guillaume Harmange, David H Perlman, Edward Emmott, Zachary Niziolek, Bogdan Budnik, Nikolai Slavov. "Automated sample preparation for high-throughput single-cell proteomics." Single Cell Proteomics Conference. Boston, MA. 2018.

POSTERS

2019. **Harrison Specht**. "Automated sample preparation for high-throughput single-cell proteomics." Royal Society of Chemistry Twitter Poster Conference. ***Twitter poster presenter*** Awarded 2nd place in Chemical Biology category.

2018. Hasmik Keshishian, Luke Wallace, **Harrison Specht**, Judit Jan-Valbuena, Rob McDonald, Dale Petterson, Eric Kuhn, Michael Burgess, D. R. Mani, Tomas Rejtar, Javad Golji, Karen Wang, William Sellers, Steven A. Carr. "SigPath300: A high throughput MS-based assay to quantify over 300 phosphosites of known biological relevance in cells and tissues." American Society for Mass Spectrometry Annual Meeting. ***Contributor***

2017. Bogdan Budnik, Ezra Levy, **Harrison Specht**, Nikolai Slavov. "Exploring cell division dynamics across single cell proteomes." Cold Spring Harbor Laboratories: Single Cell Analyses. ***Poster Presenter***

2017. **Harrison Specht**, Ezra Levy, Bogdan Budnik, Nikolai Slavov. "Mass-spectrometry of single mammalian cells quantifies proteome heterogeneity during cell differentiation." American Society for Mass Spectrometry Annual Meeting. ***Poster Presenter***

2015. **Harrison Specht**, Hasmik Keshishian, Rajiv K. Khajuria, et al. "Addressing the challenge of ribosomal protein stoichiometry by proteomics." Broad Institute of MIT and Harvard Retreat. ***Poster Presenter***

2013. **Harrison Specht** and Andrew Peters "Investigating North Atlantic Tar in Bermuda: the hydrocarbon composition of North Atlantic pelagic tar and their hydrocarbon leaching into seawater." BIOS NEF REU Program. ***Presenter***

PROFESSIONAL AFFILIATIONS, TRAINING & SERVICE

- Volunteer for Single Cell Proteomics Conference 2018, 2019, 2021
- Volunteer moderator for Single Cell Proteomics Conference (Zoom) 2020
- Northeastern University Graduate Student Liason, 2018-2019
- Member of Northeastern University Fencing Club
- Member of Barnett Institute for Chemical and Biological Analysis
- eLife Ambassador, 2018
- ASAPbio Ambassador, 2018
- American Society for Mass Spectrometry
- May Institute on computation and statistics for mass spectrometry and proteomics, 2016
- Lab preprint journal club founder

REFERENCES

Available upon request