Harrison Specht

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EDUCATION

Northeastern Universiy, Ph.D. Bioengineering, Graduate Student   expected 2021

Cornell University, B.A. Chemistry, *magna cum laude*   2014

RESEARCH EXPERIENCE

Northeastern University

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

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

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

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

2013 *National Science Foundation REU Fellowship*, Bermuda Institute for Ocean Sciences

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

PUBLICATIONS

Specht, H., Emmott, E., Petelski, A.A., Huffman, R.G., Perlman, D.H., Serra, M., Kharchenko, P., Koller, A., Slavov, N., 2019. Single-cell mass-spectrometry quantifies the emergence of macrophage heterogeneity. bioRxiv 665307. https://doi.org/10.1101/665307

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." 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

- Barnett Institute for Chemical and Biological Analysis
- Northeastern Univeristy Graduate Student Liason, 2018-2019
- eLife Ambassador, Class of 2018
- American Society for Mass Spectrometry
- May Institute on computation and statistics for mass spectrometry and proteomics, 2016
- Lab preprint journal club founder

TECHNIQUES

Coding and Software: R, perl, MaxQuant, Skyline, MatLab

Experimental: Single-cell proteomics, triple-quad and orbitrap-based mass spectrometry proteomics, antibody and chemical enrichment of proteins and peptides, liquid chromatography, robotic sample preparation, cell culture, flow cytometry and FACS

REFERENCES

Available upon request