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

RELEVANT RESEARCH EXPERIENCE

Northeastern University

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

Broad Institute of MIT and Harvard

Proteomics Platform, Research Associate — 2014–2016

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., Schutz, 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.

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