

Lindsay K. Pino

PHD CANDIDATE

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Summary

Graduate student with expertise in developing robust methods for the chemical analysis of proteins. Research and areas of experience includes mass spectrometry, statistical design of experiments, and analysis of big data.

Education

University of Washington

PHD, GENOME SCIENCES

Seattle, Washington

Sep 2014 - exp Jun 2019

Pennsylvania State University

BS, BIOCHEMISTRY AND MOLECULAR BIOLOGY

- Minor in microbiology

University Park, Pennsylvania

Sep 2005 - May 2009

Experience

University of Washington

GRADUATE RESEARCH ASSISTANT - DRs MICHAEL J. MACCOSS AND WILLIAM S. NOBLE

- Developed a data independent acquisition mass spectrometry (DIA-MS)-based system for quantification of proteomes using signal calibration principles.
- Described and demonstrated a straightforward approach for harmonizing MS quantification data across batches, instrument platforms, and laboratories.
- Modeled molecular phenotypes of the yeast replicative life span response to genetic and environmental modulators.

Seattle, Washington

Sep 2014 - Exp Jun 2019

The Broad Institute of MIT and Harvard

RESEARCH ASSOCIATE I - DR STEVEN A CARR (PROTEOMICS PLATFORM)

- Improved speed and selectivity of immuno-MRM targeted quantitative proteomics assay through hyphenation of high-field asymmetric waveform ion mobility spectrometry (FAIMS) to mass spectrometry.
- Evaluated prototype FAIMS electrode configurations for improved speed, selectivity, and sensitivity in targeted peptide quantitation.
- Developed and optimized a novel targeted quantitative assay for phosphopeptides implicated in cancer pathways.

Cambridge, Massachusetts

Aug 2012 - Jul 2014

RESEARCH ASSOCIATE I - DR KRISTIN ARDLIE (GENOMICS PLATFORM)

- Worked closely with collaborators and project managers to troubleshoot and ensure project successes, including large scale grants such as Genotype-Tissue Expression (GTEx) project and The Cancer Genome Atlas (TCGA) projects.

Sep 2011 - Aug 2012

Pennsylvania State University

UNDERGRADUATE RESEARCHER - DR MELISSA ROLLS

- Gathered in vivo data on polarity of microtubule growth through confocal microscopy of GFP-tagged tubulin proteins in live *Drosophila* larvae neurons.

University Park, Pennsylvania

May 2008 - May 2009

UNDERGRADUATE RESEARCHER - DR EMINE KOC

- Characterized mitochondrial ribosome protein L41 through chemical crosslinking assays, analysis by LC-MS, and database searches.

Jan 2006 - May 2008

Wyeth Biopharma (now Pfizer)

INTERN QUALITY CONTROL BIOANALYST II

- Performed daily monitoring and cGMP-regulation written reports of system status through assays for total organic carbon (TOC), lactate dehydrogenase (LDH), and pH.

Andover, Massachusetts

May 2007 - Aug 2007

Honors & Awards

PREDOCTORAL

- 2017 **Graduate Research Award** American Society for Mass Spectrometry
- 2016 **NIH F31 - Individual Predoctoral Fellowship** National Institute of Aging
- 2016 **NIH T32 - Genetic Approaches to Aging Training Grant** National Institute of Aging, *declined*
- 2016 **NSF Graduate Research Fellowship Program - Honorable Mention**
- 2014 **NIH T32 - Genome Training Grant** National Human Genome Research Institute

OTHER

- 2011 **US Student Fulbright Award Critical Language Enhancement Award**
- 2009 **US Fulbright Scholarship, South Korea**

Publications

- **Pino LK**, Searle BC, Huang E, Noble WS, Hoofnagle AN, MacCoss MJ. Calibration using a single-point external reference material harmonizes quantitative mass spectrometry proteomics data between platforms and laboratories. *under review with Anal Chem* Jul 2018
- Federation AJ, Nandakumar V, Wang H, Searle B, **Pino L**, Merrihew G, Ting YS, Howard N, Kuttyavin T, MacCoss MJ, Stamatoyannopoulos J. Quantification of nuclear protein dynamics reveals chromatin remodeling during acute protein degradation. *bioRxiv* Jun 2018. <https://doi.org/10.1101/345686>
- Searle BC, **Pino LK**, Egertson JD, Ting YS, Lawrence RL, Villen J, MacCoss MJ. Comprehensive peptide quantification for data independent acquisition mass spectrometry using chromatogram libraries. *bioRxiv* Mar 2018. <https://doi.org/10.1101/277822>
- Galitzine C, Egertson JD, Abbatiello S, Henderson CM, **Pino LK**, MacCoss M, Hoofnagle AN, Vitek O. Nonlinear regression improves accuracy of characterization of multiplexed mass spectrometric assays. *Mol Cell Prot* Jan 2018. <https://doi.org/10.1074/mcp.RA117.000322>
- **Pino LK**, Searle BC, Bollinger JG, Nunn B, MacLean BX, MacCoss MJ. The Skyline Ecosystem: Informatics for Quantitative Mass Spectrometry Proteomics. *Mass Spectrom Rev* Jul 2017. doi: <https://doi.org/10.1002/mas.21540>
- Abelin JG, Patel J, Lu X, Feeney CM, Fagbami L, Creech AL, Hu R, Lam D, Davison D, **Pino L**, Qiao JW, Kuhn E, Officer A, Li J, Abbatiello S, Subramanian A, Sidman R, Snyder E, Carr SA, Jaffe JD. Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. *Mol Cell Proteomics* May 2016. <https://doi.org/10.1074/mcp.M116.058354>

Presentations

ORAL

- **Pino LK**, Searle BC, Hoofnagle AN, Noble WS, MacCoss MJ. Signal calibration for quantitative proteomics. *Skyline User Group Meeting*, Jun 2018, San Diego, CA.
- **Pino LK**, Searle BC, Egertson JD, Yang HY, Noble WS, MacCoss MJ. Reproducible quantification of the yeast proteome using DIA mass spectrometry. *Cascadia Proteomics Symposium*, Jul 2016, Seattle, WA.
- **Pino LK**, Searle BC, Egertson JD, Yang HY, Noble WS, MacCoss MJ. Applying lessons learned from targeted mass spectrometry to data-independent acquisition (DIA) assays. *Skyline User Group Meeting*, Jun 2016, San Antonio, TX.

POSTER

- **Pino LK**, Searle BC, Hoofnagle AN, Noble WS, MacCoss MJ. Development and validation of a multiplex quantitative protein assay for human cerebrospinal fluid. *ASMS Annual Conference*, Jun 2018, San Diego, CA.
- **Pino LK**, Kaeberlein M, Noble WS, MacCoss MJ. Systematic proteome profiling by DIA-MS to characterize calorie restriction-induced life span extension in yeast. *ASMS Annual Conference*, Jun 2017, Indianapolis, IN.
- **Pino LK**, Merrihew G, Noble WS, MacCoss MJ. Reproducible quantification of the yeast proteome using data independent acquisition (DIA) mass spectrometry. *ASMS Annual Conference*, Jun 2016, San Antonio, TX.
- **Pino LK**, Abbatiello SE, Fagbami L, Greulich H, Kuhn E, Jaffe J, Carr SA. New Challenges in Targeted Peptide Quantitation: Phosphopeptides. *ASMS Annual Conference*, Jun 2014, Baltimore, MD.
- **Pino LK**, Abbatiello SE, Belford M, Kuhn E, Yates N, Carr SA. Improving Speed and Selectivity of Targeted Peptide Quantification using FAIMS. *ASMS Annual Conference*, Jun 2013, Minneapolis, MN.

Teaching

Skyline Workshop Courses

INSTRUCTOR

various locations

2016 - present

Introduction to Statistical and Computational Genomics (graduate)

TEACHING ASSISTANT

University of Washington

Winter 2018

Fundamentals of Genetics and Genomics (undergraduate)

TEACHING ASSISTANT

University of Washington

Spring 2017