

# Lindsay K. Pino

POSTDOCTORAL RESEARCHER

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## Summary

Postdoctoral researcher 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

Seattle, Washington

PHD, GENOME SCIENCES

Sep 2014 - Aug 2019

- Thesis: "Methods for harmonizing and calibrating quantitative mass spectrometry experiments"
- Selected coursework including Statistics for Genome Sciences, Introduction to Biomedical Data Science, Machine Learning for Biomedical and Public Health Big Data, Experimental Design

### Pennsylvania State University

University Park, Pennsylvania

BS, BIOCHEMISTRY AND MOLECULAR BIOLOGY

Sep 2005 - May 2009

- Minor in microbiology

## Research Experience

### Postdoctoral Researcher - Dr Benjamin A Garcia

Philadelphia, Pennsylvania

UNIVERSITY OF PENNSYLVANIA

Sep 2019 - present

- Characterizing the Stimulator of Interferon Gene (STING) protein's role in cellular senescence by describing STING post-translational modifications and protein-protein interactions, and STING regulation impacts on chromatin structure and gene transcription

### Graduate Research Assistant - Drs Michael J. MacCoss and William S. Noble

Seattle, Washington

UNIVERSITY OF WASHINGTON

Sep 2014 - Aug 2019

- 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.
- Constructed molecular phenotypes of the yeast replicative life span response to genetic and environmental modulators.

### Research Associate I

Cambridge, Massachusetts

THE BROAD INSTITUTE OF MIT AND HARVARD

Aug 2012 - Jul 2014

DR STEVEN 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.

DR KRISTIN ARDLIE (GENOMICS PLATFORM)

Sep 2011 - Aug 2012

- 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.

### Undergraduate Researcher

University Park, Pennsylvania

PENNSYLVANIA STATE UNIVERSITY

May 2008 - May 2009

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.

DR EMINE KOC

Jan 2006 - May 2008

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

### Intern Quality Control Bioanalyst II

Andover, Massachusetts

WYETH BIOPHARMA (NOW PFIZER)

May 2007 - Aug 2007

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

# Honors & Awards

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## 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**, South Korea
- 2009 **US Fulbright Scholarship**, South Korea

# Publications

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- **Pino LK**, Searle BC, Yang HY, Hoofnagle AN, Noble WS, MacCoss MJ. Matrix-matched calibration curves for assessing analytical figures of merit in quantitative proteomics. *bioRxiv* Jul 2019. <https://doi.org/10.1101/719179>
- Searle BC, **Pino LK**, Egertson JD, Ting YS, Lawrence RL, MacLean BX, Villen J, MacCoss MJ. Chromatogram libraries improve peptide detection and quantification by data independent acquisition mass spectrometry. *Nat Comm* Dec 2018. <https://doi.org/10.1038/s41467-018-07454-w>
- **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. *Anal Chem* Oct 2018. <https://doi.org/10.1021/acs.analchem.8b04581>
- Federation AJ, Nandakumar V, Wang H, Searle B, **Pino L**, Merrihew G, Ting YS, Howard N, Kutuyavin 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>
- 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>

# Teaching Experience

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## Quantitative Proteomics Workshops

### INSTRUCTOR

- Northeastern University (May 2017, 2018, 2019)
- Buck Institute (Mar 2018, 2019)
- University of Washington (Jul 2016, 2017, 2018)
- American Society for Mass Spectrometry short courses (Jun 2017, 2018)
- Duke University (Dec 2018)
- Center for Research in Energy and Materials, Brazil (Nov 2018)
- Mass Spectrometry: Applications to the Clinical Lab short courses (Jan 2018)

*various*  
*Jul 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*

# Presentations

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## SELECTED ORAL PRESENTATIONS

- **Pino LK**, Searle BC, Yang HY, Hoofnagle AN, Noble WS, MacCoss MJ. Using an external reference material to harmonize and calibrate quantitative mass spectrometry data at scale. *ASMS Annual Conference*, Jun 2019, Atlanta, GA.
- **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.

## SELECTED POSTER PRESENTATIONS

- **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**, Kaerberlein 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.

# Service

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## Digital Communications Committee

AMERICAN SOCIETY FOR MASS SPECTROMETRY

Aug 2019 - PRESENT

- Advise, review, and test the web site and custom software developed to enhance the management of ASMS membership, conference registration, abstracts, and program.

## Ad Hoc reviewer

VARIOUS

- Molecular & Cellular Proteomics, Analytical Chemistry, Scientific Reports.