

# Lindsay K. Pino

PHD CANDIDATE

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## Summary

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

## Education

### University of Washington

Seattle, Washington

PHD, GENOME SCIENCES

Sep 2014 - exp Jun 2019

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

## Experience

### University of Washington

Seattle, Washington

GRADUATE RESEARCH ASSISTANT - DEPT OF GENOME SCIENCES, DRs MICHAEL J MACCOSS AND WILLIAM STAFFORD NOBLE

Sep 2014 - Exp Jun 2019

Developed and characterized a high-throughput method for commutable quantification of proteomes using data independent acquisition mass spectrometry (DIA-MS)

Modeled molecular phenotypes of the yeast replicative life span response to genetic and environmental modulators

### The Broad Institute of MIT and Harvard

Cambridge, Massachusetts

RESEARCH ASSOCIATE I - PROTEOMICS PLATFORM, DR STEVEN A CARR

Aug 2012 - Jul 2014

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

RESEARCH ASSOCIATE I - GENOMICS PLATFORM, DR KRISTIN ARDLIE

Sep 2011 - Aug 2012

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

### Pennsylvania State University

University Park, Pennsylvania

UNDERGRADUATE RESEARCHER - DEPT OF BIOCHEMISTRY AND MOLECULAR BIOLOGY, DR MELISSA ROLLS

May 2008 - May 2009

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

UNDERGRADUATE RESEARCHER - DEPT OF BIOCHEMISTRY AND MOLECULAR BIOLOGY, DR EMINE KOC

Jan 2006 - May 2008

Characterized mitochondrial ribosome protein L41 through chemical crosslinking assays, analysis by HPLCMS, and database searches

### Wyeth Biopharma (now Pfizer)

Andover, Massachusetts

INTERN QUALITY CONTROL BIOANALYST II

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

### PREDOCTORAL

- 2017 **Graduate Research Award** American Society for Mass Spectrometry
- 2016 **NIH F31/NRSA - 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 NHGRI T32 - Genome Training Grant**

### OTHER

## Publications

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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.

**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.

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.

## Presentations

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### ORAL

**Pino LK**, Searle BC, Egertson J, Yang HY, Noble WS, MacCoss MJ. Reproducible quantification of the yeast proteome using DIA mass spectrometry. *Cascadia Proteomics Symposium*, Jul 2016, Seattle, WA. Oral presentation.

### POSTER

**Pino LK**, Kaeberlein M, Hoofnagle AN, Noble WS, MacCoss MJ. Lessons learned in high-dimensional analysis of quantitative DIA-MS proteome profiling. *Cascadia Proteomics Symposium*, Aug 2017, Seattle, WA. Poster presentation.

**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. Poster presentation.

**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. Poster presentation.

**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. Poster presentation.

**Pino LK**, Abbatiello SE, Belford M, Kuhn E, Yates N, Carr SA. New Challenges in Targeted Peptide Quantitation: Phosphopeptides. *ASMS Annual Conference*, Jun 2013, Minneapolis, MN. Poster presentation.