

Lindsay K. Pino

POSTDOCTORAL RESEARCHER

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Summary

Postdoctoral researcher developing mass spectrometry-based proteomics technologies to study the basic biology of aging. Research and areas of expertise includes quantitative proteomics, statistical design of experiments, and analysis of big data.

Education

University of Washington

PHD, GENOME SCIENCES

Seattle, WA

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

BS, BIOCHEMISTRY AND MOLECULAR BIOLOGY

University Park, PA

Sep 2005 - May 2009

- Minor in microbiology

Research Experience

Postdoctoral Researcher - Dr Benjamin A Garcia

UNIVERSITY OF PENNSYLVANIA

Philadelphia, PA

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

UNIVERSITY OF WASHINGTON

Seattle, WA

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

THE BROAD INSTITUTE OF MIT AND HARVARD

Cambridge, MA

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.
- 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

PENNSYLVANIA STATE UNIVERSITY

University Park, PA

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.

Honors & Awards

POSTDOCTORAL

- 2020 **NIH T32 - Immunology of Normal and Neoplastic Lymphocytes**, National Cancer Institute
- 2020 **Postdoctoral Career Development Award**, American Society for Mass Spectrometry

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

- **Pino LK**, Baeza J, Lauman R, Schilling B, Garcia BA. Improved SILAC quantification with data independent acquisition to investigate bortezomib-induced protein degradation. *bioRxiv*. Dec 2020. <https://doi.org/10.1101/2020.11.23.394304>
- **Pino LK**, Rose J, O'Broin A, Shah S, Schilling B. Biomedical applications of emerging mass spectrometry proteomics methodologies. *Biochem Soc Trans* Oct 2020. <https://doi.org/10.1042/BST20191091>
- Chiao YA, Zhang H, Mariya Sweetwyne M, Jeremy Whitson J, Ting YS, Nathan Basisty N, **Pino LK**, Ellen Quarles E, Nguyen NH, Campbell MD, Zhang T, Gaffrey MJ, Merrihew G, Wang L, Yue Y, Duan D, Granzier HL, Szeto HH, Qian WJ, Marcinek D, MacCoss MJ, Rabinovitch P. Late-life restoration of mitochondrial function reverses cardiac dysfunction in old mice. *eLife* Jul 2020. <https://doi.org/10.7554/eLife.55513>
- **Pino LK**, Just S, MacCoss MJ, Searle BC. Acquiring and analyzing data independent acquisition proteomics experiments without spectrum libraries. *Mol Cell Proteomics* Apr 2020. <https://doi.org/10.1074/mcp.P119.001913>
- Federation AJ, Nandakumar V, Searle BC, Stergachis A, Wang H, **Pino LK**, Merrihew G, Ting YS, Howard N, Kutayin T, MacCoss MJ, Stamatoyannopoulos JA. Highly parallel quantification and compartment localization of transcription factors and nuclear proteins. *Cell Reports* Feb 2020. <https://doi.org/10.1016/j.celrep.2020.01.096>
- **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. *J Proteome Res* Feb 2020. <https://doi.org/10.1021/acs.jproteome.9b00666>
- 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>
- 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

Quantitative Proteomics Workshops

INSTRUCTOR

various

Jul 2016 - present

- Human Proteome Organization Pre-Congress Training, "Introduction to Proteomics", (Oct 2020*)
- University of Washington (Jul 2016, 2017, 2018, 2020*)
- Northeastern University (May 2017, 2018, 2019, 2020*)
- Buck Institute (Mar 2018, 2019, 2020*)
- Targeted Quantitative Proteomics Course, South Africa (Nov 2019)
- Duke University (Dec 2018)
- Center for Research in Energy and Materials, Brazil (Nov 2018)
- American Society for Mass Spectrometry short courses (Jun 2017, 2018)
- Mass Spectrometry: Applications to the Clinical Lab short courses (Jan 2018)

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

Mentoring Experience

Michael Gilbert, PhD candidate

THESIS: TBD

Jan 2020 - PRESENT

Gabriela Witek, PhD candidate

THESIS: TBD

Jan 2020 - PRESENT

Adetola Alonge, undergraduate

PROJECT: *Metaanalysis of Patient Cerebrospinal Fluid by Mass Spectrometry Proteomics Discovers Known and Novel Biomarkers of Parkinson's Disease*

Jul 2020 - PRESENT

- ePoster Award for Biochemistry and Molecular Biology, Annual Biomedical Research Conference for Minority Students (ABRCMS) (Nov 2020*)

Presentations

SELECTED ORAL PRESENTATIONS

- **Pino LK.** Introduction to Proteomics. *Pre-Congress Training at HUPO Connect 2020*, Oct 2020, virtual.
- **Pino LK**, Baeza J, Lauman RA, Garcia BA. Opportunities and challenges for improving quantitative accuracy and precision in SILAC with DIA-MS. *ASMS Annual Conference*, Jun 2020, virtual.
- **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**, 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.

- **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.

Service

Co-organizer

INTELLIGENT SYSTEMS FOR MOLECULAR BIOLOGY CONFERENCE (ISMB), MASS SPECTROMETRY AND PROTEOMICS TRACK

Jan 2021 - PRESENT

Editorial Advisory Board

JOURNAL OF PROTEOME RESEARCH

Jan 2021 - Dec 2023

Organizer, Early Career Research Group

US HUMAN PROTEOME ORGANIZATION (US HUPO)

Sep 2020 - PRESENT

- Contribute to organizing committee for 2021 US HUPO conference.

Co-coordinator for Data Independent Acquisition Interest Group

AMERICAN SOCIETY FOR MASS SPECTROMETRY

Aug 2020 - PRESENT

- Organize and facilitate interest group meetings and workshops during the annual conference.

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.

Guest editor

MOLECULAR OMICS JOURNAL

2020

- Securing and reviewing articles for a special issue titled "Cross-talk and Integrative Post-translational Modifications."
- Securing and reviewing articles for a special issue in combination with US HUPO.

Ad Hoc reviewer

VARIOUS

2019 - PRESENT

- Nature Communications, Molecular & Cellular Proteomics, Journal of Proteome Research, Analytical Chemistry, Scientific Reports, Proteomics, Frontiers in Molecular Neuroscience, Journal of the American Society for Mass Spectrometry