Lindsay K Pino, PhD

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Education

2014–19	**PhD in Genome Sciences** University of Washington, Seattle Advisors: Michael J MacCoss, PhD and William S Noble, PhD
2005-09	**BS in Biochemistry and Molecular Biology** Pennsylvania State University Minor: Microbiology

Employment and Professional Appointments

2020–	**Co-founder, Chief Technology Officer**, Talus Bioscience, Inc.
2019–21	**Postdoctoral Researcher**, University of Pennsylvania Advisor: Benjamin A Garcia, PhD
2014–19	**Graduate Research Assistant**, University of Washington, Seattle Advisors: Michael J MacCoss, PhD and William S Noble, PhD
2011–14	**Research Associate I**, Broad Institute of MIT and Harvard 2012-14 Proteomics Platform: Steven A Carr, PhD and Susan Abbatiello, PhD 2011-12 Genomics Platform: Kristin Ardlie, PhD

Awards and Honors

2021	**Rising Stars in Proteomics and Metabolomics: 40 under 40**, *Journal of Proteome Research*
2021	**Rising Stars in Analytical Chemistry**, *Analytical Chemistry Diversity Colloquium*
2020	**Postdoctoral Career Development Award**, American Society for Mass Spectrometry
2020–	**NIH NCI T32 Training Program in Immunobiology of Normal and Neoplastic Lymphocytes** NIH T32CA009140, Postdoctoral Trainee
2017	**Graduate Research Award**, American Society for Mass Spectrometry
2016–19	**Ruth L Kirschstein Individual National Research Service Award** NIH F31AG055257, PI
2016	**NSF Graduate Research Fellowship Program** *Honorable Mention*
2014–16	**NIH NHGRI T32 Interdisciplinary Training in Genome Sciences** NIH T32HG000035, Predoctoral Trainee
2011	**US Student Fulbright Critical Language Enhancement Award**, South Korea
2009-11	**US Fulbright Scholarship**, South Korea

Peer-Reviewed Publications

(13) **Pino LK**, Schilling B. (2021) Proximity labeling and other novel mass spectrometric approaches for spatiotemporal protein dynamics. *Expert Rev Proteom*. https://doi.org/10.1080/14789450.2021.1976149

(12) Wang SY, Pollina EA, Wang IH, **Pino LK**, Bushnell HL, Takashima K, Fritsche C, Sabin G, Garcia BA, Greer PL, Greer EL. (2021) Role of epigenetics in unicellular to multicellular transition in Dictyostelium. *Genome Biol*. https://doi.org/10.1186/s13059-021-02360-9

(11) **Pino LK**, Baeza J, Lauman R, Schilling B, Garcia BA. (2021) Improved SILAC quantification with data independent acquisition to investigate bortezomib-induced protein degradation. *J Proteome Res*. https://doi.org/10.1021/acs.jproteome.0c00938

(10) **Pino LK**, Rose J, O'Broin A, Shah S, Schilling B. (2020) Biomedical applications of emerging mass spectrometry proteomics methodologies. *Biochem Soc Trans* https://doi.org/10.1042/BST20191091

(9) 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. (2020) Late-life restoration of mitochondrial function reverses cardiac dysfunction in old mice. *eLife* https://doi.org/10.7554/eLife.55513

(8) **Pino LK**, Just S, MacCoss MJ, Searle BC. (2020) Acquiring and analyzing data independent acquisition proteomics experiments without spectrum libraries. *Mol Cell Proteomics* https://doi.org/10.1074/mcp.P119.001913

(7) Federation AJ, Nandakumar V, Searle BC, Stergachis A, Wang H, **Pino LK**, Merrihew G, Ting YS, Howard N, Kutyavin T, MacCoss MJ, Stamatoyannopoulos JA. (2020) Highly parallel quantification and compartment localization of transcription factors and nuclear proteins. *Cell Reports* https://doi.org/10.1016/j.celrep.2020.01.096

(6) **Pino LK**, Searle BC, Yang HY, Hoofnagle AN, Noble WS, MacCoss MJ. (2020) Matrix-matched calibration curves for assessing analytical figures of merit in quantitative proteomics. *J Proteome Res* https://doi.org/10.1021/acs.jproteome.9b00666

(5) Searle BC, **Pino LK**, Egertson JD, Ting YS, Lawrence RL, MacLean BX, Villen J, MacCoss MJ. (2018) 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

(4) **Pino LK**, Searle BC, Huang E, Noble WS, Hoofnagle AN, MacCoss MJ. (2018) Calibration using a single-point external reference material harmonizes quantitative mass spectrometry proteomics data between platforms and laboratories. *Anal Chem* https://doi.org/10.1021/acs.analchem.8b04581

(3) Galitzine C, Egertson JD, Abbatiello S, Henderson CM, **Pino LK**, MacCoss M, Hoofnagle AN, Vitek O. (2018) Nonlinear regression improves accuracy of characterization of multiplexed mass spectrometric assays. *Mol Cell Prot* https://doi.org/10.1074/mcp.RA117.000322

(2) **Pino LK**, Searle BC, Bollinger JG, Nunn B, MacLean BX, MacCoss MJ. (2017) The Skyline Ecosystem: Informatics for Quantitative Mass Spectrometry Proteomics. *Mass Spectrom Rev* https://doi.org/10.1002/mas.21540

(1) 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. (2016) Reduced-representation Phosphosignatures Measured by Quantitative Targeted MS Capture Cellular States and Enable Large-scale Comparison of Drug-induced Phenotypes. *Mol Cell Proteomics* https://doi.org/10.1074/mcp.M116.058354

Additional Publications

(1) **Pino LK**. Methods for harmonizing and calibrating quantitative mass spectrometry experiments. PhD dissertation. University of Washington, Seattle. Aug, 2019. Advisors: Michael J MacCoss, PhD and William S Noble, PhD

Selected Talks

(6) **Pino LK**. Prospective system suitability and quality control design for large-scale and longitudinal quantitative mass spectrometry proteomics. (Mar 2022) *US HUPO Annual Conference*, Charleston, SC.

(5) **Pino LK**, Baeza J, Lauman RA, Garcia BA. (Jun 2020) Opportunities and challenges for improving quantitative accuracy and precision in SILAC with DIA-MS. *ASMS Annual Conference*, virtual.

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

(3) **Pino LK**, Searle BC, Hoofnagle AN, Noble WS, MacCoss MJ. (Jun 2018) Signal calibration for quantitative proteomics. *Skyline User Group Meeting*, San Diego, CA.

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

(1) **Pino LK**, Searle BC, Egertson JD, Yang HY, Noble WS, MacCoss MJ. (Jun 2016) Applying lessons learned from targeted mass spectrometry to data-independent acquisition (DIA) assays. *Skyline User Group Meeting*, San Antonio, TX.

Selected Posters

(6) **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.

(5) **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.

(4) **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.

(3) **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.

(2) **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.

(1) **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.

Mentoring

2020– **Adetola Alonge**, undergraduate, University of Florida
Project: Metaanalysis of Patient Cerebrospinal Fluid by Mass Spectrometry Proteomics Discovers Known and Novel Biomarkers of Parkinson's Disease
ePoster Award for Biochemistry and Molecular Biology, Annual Biomedical Research Conference for Minority Students (ABRCMS) (Nov 2020)

2020– **Gabriela Witek**, PhD student, University of Pennsylvania
Thesis: Proteomics of ALK mutation in neuroblastoma

2019– **Michael Gilbert**, PhD student, University of Pennsylvania
Thesis: Investigating Caste Differences in *Atta cephalotes*

Teaching

Teaching Assistance

2018 Introduction to Statistical and Computational Genomics (graduate)
University of Washington, Seattle

2017 Fundamentals of Genetics and Genomics (undergraduate)
University of Washington, Seattle

Quantitative Mass Spectrometry Proteomics Workshop Instructor and Organizer

2-5 day workshops held for academic and industry scientists of all backgrounds covering topics including introductory proteomics and mass spectrometry, LC-MS method development, LC-MS data quality control, analysis of quantitative proteomics data

2020–22	Skyline Online virtual
2017–21	Computation and statistics for mass spectrometry and proteomics Northeastern University, Boston; 2020-21 virtual
2020	Human Proteome Organization Pre-Congress Training virtual
2017–19	Bay-area Targeted Proteomics Course Buck Institute for Research on Aging, Novato
2019	Quantitative Targeted Proteomics and Metabolomics Course University of Cape Town, Cape Town, South Africa
2016–19	Quantitative Targeted Mass Spectrometry Course University of Washington, Seattle
2018	Skyline@Duke Short Course Duke University, North Carolina
2018	VIII Proteomics Workshop Skyline Center for Research in Energy and Materials, Campinas, Brazil
2017–18	Case Studies in Quantitative Proteomics Course American Society for Mass Spectrometry
2018	Proteomics 202 Short Course Mass Spectrometry: Applications to the Clinical Lab

Professional Service

Editorial Boards

2021–23	*Journal of Proteome Research*. Editorial Advisory Board.
2021	*Molecular Omics*. Guest editor, special issue covering the 2021 Annual US HUPO Conference.
2021	*Molecular Omics*. Guest editor, special issue titled "Cross-talk and Integrative Post-translational Modifications".

Journal Referee: 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, Clinical Proteomics

Conference Organization

2021–	Intelligent Systems for Molecular Biology Conference (ISMB), Mass Spectrometry and Proteomics Track. *Co-coordinator*.
2020–	Early Career Research Group, US Human Proteome Organization (US HUPO). *Committee member*.
2020–	Data Independent Acquisition Interest Group, American Society for Mass Spectrometry (ASMS). *Co-coordinator*.
2019–21	Digital Communications Committee, American Society for Mass Spectrometry (ASMS). *Committee member*.

Committees

2021–	Proteomics Standards Research Group (sPRG), Association of Biomolecular Resources Facilities (ABRF). *Committee member*.

Professional Memberships

2021–	Association of Biomolecular Resources Facilities (ABRF)
2020–	International Society for Computational Biology (ISCB)
2020–	Human Proteome Organization (HUPO)
2020–	United States Human Proteome Organization (US HUPO)
2020–	American Aging Association (AGE)
2013–	American Society for Mass Spectrometry (ASMS)

Audio/Video Features

(3) **Pino LK**. Proteomics calibration with Lindsay Pino. (2021) The Bioinformatics Chat podcast. https://bioinformatics.chat/proteomics-calibration

(2) **Pino LK**. Data independent acquisition mass spectrometry for dynamic spatiotemporal proteomics. (2021) Proteome Software ScaffoldDIA Virtual Brunch featured presentation. https://youtu.be/HFDJthoq6hs

(1) **Pino LK**. Basics of targeted mass spectrometry with Skyline. (2020) Scientific blog post. https://lindsaykpino.com/2020/04/29/basics-of-targeted-mass-spectrometry-with-skyline/

References

William Noble
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Michael MacCoss
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Susan Abbatiello
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