

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

- 2025 **Life Science Entrepreneurial Achievement Award**, Life Science Washington Institute (LSWI)
- 2024 **Rising Star Award**, Human Proteome Organization (HUPO)
- 2021 **Rising Stars in Proteomics and Metabolomics: 40 under 40**, Journal of Proteome Research (JPR)
- 2021 **Rising Stars in Analytical Chemistry**, Analytical Chemistry Diversity Colloquium
- 2020 **Postdoctoral Career Development Award**, American Society for Mass Spectrometry
- 2020–21 **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
- 2014–16 **NIH NHGRI T32 Interdisciplinary Training in Genome Sciences**
NIH T32HG000035, Predoctoral Trainee
- 2009–11 **US Fulbright Scholarship**, South Korea

Research Support

- 2023–25 Andy Hill CARE Fund, Life Science Start-Up and Development Cycle 1 (Pino/Federation), Role: Principal Investigator
\$298,973. Awarded for “Discovery of targeted small molecule MYCN therapeutics for neuroblastoma”
- 2023–25 Andy Hill CARE Fund, Life Science Start-Up and Development Cycle 1 (Federation/Pino), Role: Co-Investigator
\$1,995,337. Awarded for “Therapeutic disruption of the Rhabdomyosarcoma transcriptional core regulatory circuit”
- 2023–25 NIH/NCI, 4R44CA268146-02 (Federation/Pino), Role: Co-Investigator
\$1,000,000/year. Awarded for “Simultaneous pharmacological profiling of oncogenic gene fusion proteins in cancer (FastTrack Phase II)”
- 2022–23 NIH/NCI, 1R42CA268146-01 (Federation/Pino), Role: Co-Investigator
\$455,000. Awarded for “Simultaneous pharmacological profiling of oncogenic gene fusion proteins in cancer (FastTrack Phase I)”
- 2022–23 NIH/NCATS, 1R43TR004221-01 (Federation/Pino), Role: Co-Investigator
\$333,867. Awarded for “Illuminating the ‘dark’ kinases – effects on proteome translocation and chromatin binding”
- 2021–22 NSF, 2112191 (Federation/Pino), Role: Co-Investigator
\$255,831. Awarded for “SBIR Phase I: Simultaneous In situ Pharmacological Profiling of Gene Regulatory Proteins (GRPs) for Cancer Therapy”

Peer-Reviewed Publications

(21 total, 9 first author)

- (21) Sachsenberg T, **Pino LK**, Brunet M, Bludau I, Kohlbacher O, Vizcaino JA, Bittremieux W. (2025) Perspectives in computational mass spectrometry: recent developments and key challenges. *Bioinformatics Advances*. <https://doi.org/10.1093/bioadv/vbaf301>.
- (20) Gilbert MB, Glastad KM, Fioriti M, Sorek M, Scarpa T, Purnell FS, Xu D, **Pino LK**, Korotkov A, Biashad A, Baeza J, Lauman R, Filippova A, Kacsoh BZ, Bonasio R, Mathis MW, Garcia BA, Seluanov A, Gorbunova V, Berger SL. (2025) Neuropeptides specify and reprogram division of labor in the leafcutter ant *Atta cephalotes*. *Cell*. <https://doi.org/10.1016/j.cell.2025.05.023>.
- (19) Shortt RL, **Pino LK**, Chea EE, Ramirez CR, Polasky DA, Nesvizhskii AI, Jones LM. (2024) Covalent Labeling Automated Data Analysis Platform for High Throughput in R (coADAPTr): A Proteome-Wide Data Analysis Platform for Covalent Labeling Experiments. *J Am Soc Mass Spectrom*. <https://doi.org/10.1021/jasms.4c00196>.
- (18) **Pino LK**. (2024) The future role of mass spectrometry in proteomics: Embracing new technologies and building bridges for higher impact. *J Mass Spectrom*. <https://doi.org/10.1002/jms.5028>
- (17) Allen C, Meini R, Paez JS, Searle BC, Just S, **Pino LK**, WE Fondrie. (2023) nf-encyclopedia: A cloud-ready pipeline for chromatogram library data-independent acquisition proteomics workflows. *J Proteome Res*. <https://doi.org/10.1021/acs.jproteome.2c00613>

- (16) Lauman R, Kim HJ, **Pino LK**, Scacchetti A, Xie Y, Robison F, Sidoli S, Bonasio R, Garcia BA. (2023) Expanding the Epitranscriptomic RNA Sequencing and Modification Mapping Mass Spectrometry Toolbox with Field Asymmetric Waveform Ion Mobility and Electrochemical Elution Liquid Chromatography. *Anal Chem*. <https://doi.org/10.1021/acs.analchem.2c04114>
- (15) Martinez TF, Lyons-Abbott S, Bookout AL, De Souza EV, Donaldson C, Vaughan JM, Lau C, Abramov A, Baquero AF, Baquero K, Friedrich D, Huard J, Davis R, Kim B, Koch T, Mercer AJ, Misquith A, Murray SA, Perry S, **Pino LK**, Sanford C, Simon A, Zhang Y, Zipp G, Bizarro CV, Shokhirev MN, Whittle AJ, Searle BC, MacCoss MJ, Saghatelian A, Barnes CA. (2023) Profiling mouse brown and white adipocytes to identify metabolically relevant small ORFs and functional microproteins. *Cell Metab*. <https://doi.org/10.1016/j.cmet.2022.12.004>
- (14) **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>
- (13) 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>
- (12) **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>
- (11) **Pino LK**, Rose J, O'Broin A, Shah S, Schilling B. (2020) Emerging mass spectrometry-based proteomics methodologies for novel biomedical applications. *Biochem Soc Trans* <https://doi.org/10.1042/BST20191091>
- (10) 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>
- (9) **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>
- (8) Federation AJ, Nandakumar V, Searle BC, Stergachis A, Wang H, **Pino LK**, Merrihew G, Ting YS, Howard N, Kutayin 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>
- (7) **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>
- (6) **Pino LK**, Lin A, Bittremieux W. (2019) 2018 YPIC Challenge: A Case Study in Characterizing an Unknown Protein Sample. *J Proteome Res* <https://doi.org/10.1021/acs.jproteome.9b00384>
- (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>

Preprints

- (3) Wu A, Kohler D, Navada PP, Robbins J, Boyle G, Boshart A, Karis K, Neefjes J, Konvalinka A, Sarthy JF, **Pino LK**, Gyori BM, Vitek O. (2026) MSstatsBioNet: Integrating Statistical Analyses with Prior Knowledge Biomolecular Networks for Quantitative Proteomics and Phosphoproteomics. *bioRxiv*. <https://doi.org/10.64898/2026.07.09.737605>.
- (2) Wen B, Paez JS, Hsu C, Canzani D, Chang A, Shulman N, MacLean BX, Berg MD, Villen J, Fondrie WE, **Pino LK**, MacCoss MJ, Noble WS. (2026) Carafe2 enables high quality *in silico* spectral library generation for timsTOF data-independent acquisition proteomics. *bioRxiv*. <https://doi.org/10.64898/2026.03.27.714846>.
- (1) **Pino LK***, Canzani D, Gutierrez A, Robbins J, McEllin B, Hubbard E, Broderick E, Prymolenna A, Tatka L, Paez JS, Mercenne G, Siebenthal K, Fondrie WE, Federation AJ*. [**co-corresponding*] (2025) Native, Spatiotemporal Profiling of the Global Human Regulome. *bioRxiv*. <https://doi.org/10.1101/2025.06.14.659727>.

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 Invited Research Lectures

- (19) **Pino LK.** Small-molecule modulation of chromatin-associated protein function in native cells. (Jan 2026) *University of Washington Department of Chemistry*, Seattle, WA.
- (18) **Pino LK.** Profiling the regulome with high-throughput proteomics to enable small-molecule therapeutics. (Dec 2025) *Northwestern University Department of Biochemistry and Molecular Genetics*, Chicago, IL.
- (17) **Pino LK.** Spatiotemporal Dynamics of the Transcriptional Regulome Across Cell State and Drug Response Landscapes. (Nov 2025) *24th Human Proteome Organization World Congress*, Toronto, Canada.
- (16) **Pino LK.** Integrating AI throughout a Mass Spectrometry-driven Drug Discovery Approach. (Oct 2024) *23rd Human Proteome Organization World Congress*, Dresden, Germany.
- (15) **Pino LK.** Developing and optimizing mass spectrometry methods to improve detection of covalently modified peptides in complex lysates. (Jun 2024) *American Society for Mass Spectrometry 2024 Annual Conference*, Anaheim, CA.
- (14) **Pino LK.** Profiling oncogenic transcription factors using mass spectrometry proteomics. (Jun 2024) *Bruker eXceed Symposia 2024*, Anaheim, CA.
- (13) **Pino LK.** Embracing Disruption and New Opportunities in the Evolution of Proteomics Technologies. (Apr 2024) *Association of Biomolecular Resource Facilities*, Minneapolis, MN.
- (12) **Pino LK.** From Lab to Launch: Navigating the Entrepreneurial Path in Start-up Biotech. (Mar 2024) *Ohio State University Biochemistry Department*, virtual.
- (11) **Pino LK.** Transcription Factor Profiling by Mass Spectrometry to Discover and Develop Cancer Therapeutics. (Mar 2024) *US HUPO Parallel Session 14: Transcription Factors*, Portland, OR.
- (10) **Pino LK.** Automating proteomics for scale: Chasing asymptotic efficiency. (Mar 2024) *US HUPO Bruker Sponsored Lunch*, Portland, OR.
- (9) **Pino LK.** Mass Spectrometry-Based Approaches for Chemoproteomics and Activity-Based Protein Profiling. (Jan 2024) *Annual BCPM Network Symposium*, Simon Fraser University, Canada.
- (8) **Pino LK.** Mass Spectrometry-Based Approaches for Chemoproteomics and Activity-Based Protein Profiling. (Jan 2024) *Bruker eXceed Event: UC Berkeley Mass Spec Seminar*, Berkeley CA.
- (7) **Pino LK.** Profiling the DNA Regulome to Discover Direct Inhibitors of the Brachyury Transcription Factor. (Nov 2023) *Ohio State University Biochemistry Seminar*, Columbus OH.
- (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.

Entrepreneurship

Accelerator Programs

- 2025 *Founder To Leader*. Femme Fellowship.
- 2022 *Creative Destruction Laboratories (CDL)*. Computational Health (Seattle) graduate.
- 2022 *Project W*. Women Entrepreneurs Boot Camp.
- 2021 *Y Combinator (YC), S21 Batch*. Group partners: Surbhi Sarna, Jared Friedman, Brad Flora.
- 2020–24 *Life Sciences Washington Institute*. Washington Innovation Network (WIN) graduate.

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

Committee and Research Group Membership

- 2023–24 Member-at-Large, US Human Proteome Organization (US HUPO). *Board of Directors*.
- 2021–24 Proteomics Standards Research Group (sPRG), Association of Biomolecular Resources Facilities (ABRF). *Committee member*.
- 2021– Intelligent Systems for Molecular Biology Conference (ISMB), Mass Spectrometry and Proteomics Track. *Co-coordinator*.
- 2020–22 Early Career Research Group, US Human Proteome Organization (US HUPO). *Committee member*.
- 2020–23 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*.

Professional Memberships

- 2021–24 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)

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

- 2024 Ubuntu Proteomics Summer School
Cradle of Humankind, South Africa
- 2023–25 Proteomics (label-free quantification section)
Cold Spring Harbor Laboratory Courses, New York
- 2020–25 Skyline Online
virtual
- 2020 Human Proteome Organization Pre-Congress Training
virtual
- 2019 Quantitative Targeted Proteomics and Metabolomics Course
University of Cape Town, Cape Town, South Africa
- 2017–25 Computation and statistics for mass spectrometry and proteomics
Northeastern University, Boston; 2020–21 virtual
- 2017–19 Bay-area Targeted Proteomics Course
Buck Institute for Research on Aging, Novato
- 2016–25 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

Audio/Video Features

- (6) Life Science Washington Institute WIN Mentoring Program (2024)
<https://vimeo.com/873842986?fl=pl&fe=sh>
- (5) Genetic Engineering & Biotechnology News (GEN) LIVE: Is Proteomics the Next Big “Ome”?

(2024)

<https://www.genengnews.com/multimedia/is-proteomics-the-next-big-ome/>

- (4) S02E12: THE proteomics BATTLE ROYALE. (2023) The Proteomics Show podcast and US HUPO.

<https://open.spotify.com/episode/1rGJGYeTIdqQICKBqPoUKA?si=0d6eb195498b4f03>

<https://www.youtube.com/watch?v=OybDot4U7uc>

- (3) Talk is Biotech! with Lindsay Pino. (2022)

<https://www.scispot.com/blog/talk-is-biotech-with-lindsay-pino>

- (2) Holiday Special - Dr. Lindsay Pino. (2022) The Proteomics Show podcast

<https://open.spotify.com/episode/73MEMk6hMGCgfpjIQVqRwh?si=3wni6oXnTAST7zIE-XWV1g>

- (1) Proteomics calibration with Lindsay Pino. (2021) The Bioinformatics Chat podcast.

<https://bioinformatics.chat/proteomics-calibration>