

William E Fondrie, PhD

Talus Bioscience

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Education

- 2013–18 **PhD in Molecular Medicine**
University of Maryland, Baltimore
Advisors: David Goodlett, PhD and Dudley Strickland, PhD
- 2009–13 **BS in Chemistry**
University of North Carolina at Chapel Hill

Employment and Professional Appointments

- 2021– **Senior Data Scientist**, Talus Bioscience
- 2019–21 **University of Washington Data Science Postdoctoral Fellow**
UW eScience Institute
- 2018–21 **Postdoctoral Fellow**, University of Washington
Advisor: William Noble, PhD
- 2013–18 **Graduate Research Assistant**, University of Maryland, Baltimore
Advisors: David Goodlett, PhD and Dudley Strickland, PhD
- 2012–13 **Undergraduate Research Assistant**, University of North Carolina at Chapel Hill
Advisor: John Papanikolas, PhD

Awards and Honors

- 2021 **UW eScience Postdoctoral Fellow Research Funds**
- 2021 **Rising Stars in Proteomics and Metabolomics: 40 under 40**,
Journal of Proteome Research
- 2020 **Emerging Talent: Academia**, American Society for Mass Spectrometry
- 2019–21 **Ruth L Kirschstein Institutional National Research Service Award**
NIH T32HG000035, Postdoctoral Trainee
- 2017 **Travel Fellowship to the May Institute on Computation and Statistics for Mass Spectrometry and Proteomics**
- 2017–18 **Ruth L Kirschstein Individual National Research Service Award**
NIH F31CA213815, PI
- 2016–17 **Ruth L Kirschstein Institutional National Research Service Award**
NIH T32HL007698, Predoctoral Trainee
- 2012 **Markham Summer Undergraduate Research Award**
- 2009 **Central Carolina's chapter of Phi Beta Kappa Scholarship**

Peer-Reviewed Publications

(* indicates equal contributions)

- (14) **Fondrie WE**, Bittreieux W, Noble WS. (2021) ppx: Programmatic Access to Proteomics Data Repositories. *J Proteome Res*. Online ahead of print. PMID: 34342226
- (13) Mudge MC, Nunn BL, Firth E, Ewert M, Hales K, **Fondrie WE**, Noble WS, Toner J, Light B, Junge KA. (2021) Subzero, saline incubations of *Colwellia psychrerythraea* reveal strategies and biomarkers for sustained life in extreme icy environments. *Environ Microbiol*. 23(7):3840-3866. PMID: 33760340
- (12) **Fondrie WE**, Noble WS. (2021) mokapot: Fast and flexible semisupervised learning for peptide detection. *J Proteome Res*. 2;20(4):1966-1971. PMID: 33596079.
- (11) **Fondrie WE**, Noble WS. (2020) Machine learning strategy that leverages large datasets to boost statistical power in small-scale experiments. *J Proteome Res* 6;19(3):1267–1274. PMID: 32009418.
- (10) Liang T, Leung LM, Opene B, **Fondrie WE**, Lee YI, Chandler CE, Yoon SH, Doi Y, Ernst RK, Goodlett DR. (2019) Rapid microbial identification and antibiotic resistance detection by mass spectrometric analysis of membrane lipids. *Anal Chem* 91(2):1286–1294. PMID: 30571097.
- (9) **Fondrie WE**, Liang T, Oyler BL, Leung LM, Ernst RK, Strickland DK, Goodlett DR. (2018) Pathogen Identification Direct From Polymicrobial Specimens Using Membrane Glycolipids. *Sci Rep* 8(1):15857. PMID: 30367087.
- (8) Liang T, Schneider T, Yoon SH, Oyler BL, Leung LM, **Fondrie WE**, Yen G, Huang Y, Ernst RK, Nilsson E, Goodlett DR. (2018) Optimized surface acoustic wave nebulization facilitates bacterial phenotyping. *Int J Mass Spectrom* 427:65–72.
- (7) Au DT, Arai AL, **Fondrie WE**, Muratoglu SC, Strickland DK. (2018) Role of the LDL Receptor-Related Protein 1 in Regulating Protease Activity and Signaling Pathways in the Vasculature. *Curr Drug Targets* 19(11):1276–1288. PMID: 29749311.
- (6) Au DT, Ying Z, Hernández-Ochoa EO, **Fondrie WE**, Hampton B, Migliorini M, Galisteo R, Schneider MF, Daugherty A, Rateri DL, Strickland DK, Muratoglu SC. (2018) LRP1 (Low-Density Lipoprotein Receptor-Related Protein 1) Regulates Smooth Muscle Contractility by Modulating Ca²⁺ Signaling and Expression of Cytoskeleton-Related Proteins. *Arterioscler Thromb Vasc Biol* 38(11):2651–2664. PMID: 30354243.
- (5) Khan MM, Tran BQ, Jang Y, Park S, **Fondrie WE**, Chowdhury K, Yoon SH, Goodlett DR, Chae S, Chae H, Seo S, Goo YA. (2017) Assessment of the therapeutic potential of persimmon leaf extract on prediabetic subjects. *Mol Cells* 40(7):466. PMID: 28743946.
- (4) Leung LM, **Fondrie WE**, Doi Y, Johnson JK, Strickland DK, Ernst RK, Goodlett DR. (2017) Identification of the ESKAPE pathogens by mass spectrometric analysis of microbial membrane glycolipids. *Sci Rep* 7(1):6403. PMID: 28743946.

- (3) Clark DJ, **Fondrie WE**, Liao Z, Yang AJ, Mao L. (2016) Triple SILAC quantitative proteomic analysis reveals differential abundance of cell signaling proteins between normal and lung cancer-derived exosomes. *J Proteomics* 133:161–169. PMID: 26739763.
- (2) Clark DJ*, **Fondrie WE***, Liao Z, Hanson PI, Fulton A, Mao L, Yang AJ. (2015) Redefining the breast cancer exosome proteome by tandem mass tag quantitative proteomics and multivariate cluster analysis. *Anal Chem* 87(20):10462–10469. PMID: 26378940.
- (1) Ma D, Bettis SE, Hanson K, Minakova M, Alibabaei L, **Fondrie W**, Ryan DM, Papoian GA, Meyer TJ, Waters ML, Papanikolas JM. (2013) Interfacial energy conversion in Ru(II) polypyridyl-derivatized oligoproline assemblies on TiO₂. *J Am Chem Soc* 135(14):5250–5253. PMID: 23514453.

Additional Publications

- (1) **Fondrie WE**. Biological Insight from Mass Spectrometry Through Novel Computational Approaches. Ph.D. dissertation. University of Maryland, Baltimore. June, 2018. Advisors: Dudley K. Strickland, Ph.D. and David R. Goodlett, Ph.D.

Patents

- (1) Goodlett DR, Ernst RK, Liang T, **Fondrie WE**, Nilsson E. (2018) Methods for Lipid Extraction and Identification of Microbes Using Same Via Mass Spectrometry. US Patent Application 2017066342. Filed 12/14/2017. *Patent Pending*.

Scientific Software Contributions

- (10) **mokapot**. A Python package that enables the fast and flexible application of semi-supervised learning to detect peptides in proteomics experiments.
Homepage: <https://github.com/wfondrie/mokapot>
Roles: creator and maintainer
- (9) **ppx**. A Python package to retrieve metadata and files for proteomics projects from public repositories through ProteomeXchange.
Homepage: <https://github.com/wfondrie/ppx>
Roles: creator and maintainer
- (8) **Crux**. A mass spectrometry toolkit for proteomics data.
Homepage: <http://crux.ms>
Roles: contributor
- (7) **Percolator**. Semi-supervised learning for peptide identification from shotgun proteomics datasets.
Homepage: <http://percolator.ms>
Roles: contributor

- (6) **dask-ml**. A library for distributed and parallel machine learning using dask.
Homepage: <https://ml.dask.org>
Roles: contributor
- (5) **Kojak**. A search engine for cross-linking proteomics.
Homepage: <http://www.kojak-ms.org>
Roles: contributor
- (4) **MSToolkit**. A library for interacting with proteomics data formats.
Homepage: <https://github.com/mhoopmann/mstoolkit>
Roles: contributor
- (3) **ANN-SoLo**. A spectral library search engine for fast and accurate open modification searching.
Homepage: <https://github.com/bittremieux/ANN-SoLo>
Roles: contributor
- (2) **spectrum_utils**. A Python package for efficient MS/MS spectrum processing and visualization.
Homepage: https://github.com/bittremieux/spectrum_utils
Roles: contributor.
- (1) **xComb**. A cross-linked peptide database approach to protein-protein interaction analysis.
Homepage: <https://github.com/GoodlettLab/xComb>
Roles: maintainer and contributor

Talks

- (5) **Fondrie WE**, Romero E, Noble WS. Learning Compact Representations of High-Resolution Tandem Mass Spectra Without Supervision. Intelligent Systems for Molecular Biology, July 25–30, 2021. Online.
- (4) **Fondrie WE**. Deep Learning to Enable Proteomics at Scale. American Society for Mass Spectrometry Emerging Talent: Academia webinar series, November 10–12, 2020. Online.
- (3) **Fondrie WE**. Learning from Mass Spectra. Genome Sciences Sciences, Seattle, Washington. Seminar, August 12, 2020. University of Washington Department of Genome
- (2) **Fondrie WE**, Leung LM, Strickland DK, Ernst RK, Goodlett DR. Detecting antibiotic resistance by MALDI-TOF analysis of bacterial membrane glycolipids. 65th American Society for Mass Spectrometry Annual Conference on Mass Spectrometry and Allied Topics, June 4–8, 2017. Indianapolis, IN.
- (1) **Fondrie WE**, Muratoglu SC, Hampton B, Migliorini M, Galisteo R, Strickland DK. LRP1 modulates TGF- β signaling in the descending thoracic aorta. Molecular Medicine Research Retreat, October 6, 2016. Baltimore, MD.

Posters

- (10) **Fondrie, WE**, Noble WS. Mokapot: Fast and Flexible Semi-Supervised Learning for Peptide Detection. US Human Proteome Organization 17th Annual Conference. March 4–12, 2021. Virtual.
- (9) **Fondrie, WE**, Noble WS. Mokapot: Fast and Flexible Semi-Supervised Learning for Peptide Detection. 28th Conference on Intelligent Systems for Molecular Biology, July 13–16, 2020. Montreal, QC, Canada. *Moved online due to COVID-19.*
- (8) **Fondrie, WE**, Noble WS. Boosting statistical power in small-scale experiments with Percolator. US Human Proteome Organization 16th Annual Conference. March 8–11, 2020. Seattle, WA *Moved online due to COVID-19.*
- (7) **Fondrie WE**, Noble WS. Robust Cross-Linked Peptide Detection Using Pretrained Neural Networks. 67th American Society for Mass Spectrometry Annual Conference on Mass Spectrometry and Allied Topics, June 1–6, 2019. Atlanta, GA.
- (6) **Fondrie WE**, Hampton B, Muratoglu SC, Goodlett DR, Strickland DK. Detecting LRP1B protein interactions in glioma. UMB Cancer Biology Research Retreat, June 13, 2017. Baltimore, MD.
- (5) **Fondrie WE**, Muratoglu SC, Hampton B, Migliorini M, Galisteo R, Strickland DK. LRP1 modulates TGF- β signaling in the descending thoracic aorta. GenTAC Thoracic Aortic Summit, September 22–23, 2016. Washington, DC.
- (4) **Fondrie WE**, Hampton B, Muratoglu SC, Goodlett DR, Strickland DK. Defining a mechanism of LRP1B tumor suppression in glioblastoma. UMB Cancer Biology Research Retreat, May 23, 2016. Baltimore, MD.
- (3) **Fondrie WE**, Clark DJ, Catania SM, Goo YA, Strickland DK, Goodlett DR. Investigating the regulated intramembrane proteolysis of LRP1B in glioblastoma progression through a proteogenomic approach. Mass Spectrometry in Biotechnology and Medicine, July 5–11, 2015. Dubrovnik, Croatia.
- (2) **Fondrie WE**, Clark DJ, Liao Z, Chen Y, Yang AJ. Novel identification of JAK1/STAT signaling proteins in breast cancer exosomes through shotgun proteomic analysis using multiple protein database search algorithms. UMB Cancer Biology Research Retreat, June 9, 2014. Baltimore, MD.
- (1) **Fondrie WE**, Bettis S, Ma D, Minakova M, Wilger D, Papoian G, Waters M, Papanikolas J. Flexibility matters: The role of scaffold tethers in the American Chemical Society, November 14–17, 2012. Raleigh, NC. Ru(II) and Os(II) chromophore separation. Southeastern Regional Meeting of

Teaching

Training

2020 The Carpentries Instructor Training
<https://carpentries.org/>

Experience

- 2021 UW Spring Quarter Software Carpentry Workshop Instructor
<https://uwescience.github.io/2021-05-10-uw-online/>
- 2021 Lecture for the “Statistics for Proteomics” video series
<https://slavovlab.net/stats>
- 2021 UW Winter Quarter Software Carpentry Workshop Instructor
<https://uwescience.github.io/2021-01-11-uw-online/>

Mentoring

- 2021– **Lincoln Harris**, PhD student
Department of Genome Sciences, University of Washington
- 2020 **Elena Romero**, PhD student
Department of Genome Sciences, University of Washington
- 2020–21 **Donovan See**, Undergraduate student
University of Washington
- 2020–21 **Lilian Heil**, PhD student
Department of Genome Sciences, University of Washington
- 2019– **Kianna Hales**, PhD student
Department of Genome Sciences, University of Washington

Professional Service

Editorial Boards

- 2021–23 *Journal of Proteome Research*. Editorial Advisory Board.

Conference Organization

- 2021 Intelligent Systems for Molecular Biology CompMS COSI. *Program Committee Member*.
- 2020 Workshop on High Performance Computing, Big Data Analytics and Integration for Multi-Omics Biomedical Data (HPC-BOD 2020). *Program Committee Member*.

Professional Memberships

- 2021– American Chemical Society (ACS)
- 2021– Human Proteome Organization (HUPO)
- 2020– United States Human Proteome Organization (US HUPO)
- 2013– American Society for Mass Spectrometry (ASMS)

Departmental Service

- 2019–21 UW Genome Sciences Art Committee
- 2018–21 Postdoctoral representative in UW Genome Sciences
- 2015–17 UMB Molecular Medicine Event Planning Committee
- 2017 UMB Cancer Biology Research Retreat Organizing Committee
- 2016 UMB Grollman Lecture Organizing Committee

Journal Referee: *Bioinformatics*, *Journal of Proteome Research*, *Scientific Reports*

Conference Referee: Intelligent Systems for Molecular Biology 2020, 2021; Research in Computational Molecular Biology 2021

Scientific Blog Posts

- (2) **Fondrie WE.** (2019) Using Static Models in Percolator.
<https://willfondrie.com/2019/11/using-static-models-in-percolator/>
- (1) **Fondrie WE.** (2019) An Intuitive Look at the xcorr Score Function in Proteomics.
[https://willfondrie.com/2019/02/
an-intuitive-look-at-the-xcorr-score-function-in-proteomics/](https://willfondrie.com/2019/02/an-intuitive-look-at-the-xcorr-score-function-in-proteomics/)

References

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David Goodlett

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