

# William E Fondrie, PhD

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## Education

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- 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

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- 2019– **University of Washington Data Science Postdoctoral Fellow**
- 2018– **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

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- 2020 **Emerging Talent: Academia**, American Society for Mass Spectrometry
- 2019– **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**

## Preprints

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- (1) **Fondrie WE**, Noble WS. (2020) mokapot: Fast and flexible semi-supervised learning for peptide detection. *bioRxiv*. DOI: 10.1101/2020.12.01.407270.

## Peer-Reviewed Publications

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(\* indicates equal contributions)

- (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 Ca<sup>2+</sup> 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 TiO<sub>2</sub>. *J Am Chem Soc* 135(14):5250–5253. PMID: 23514453.

## Additional Publications

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- (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

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- (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

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- (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](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

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- (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 Seminar, August 12, 2020. University of Washington Department of Genome Sciences, Seattle, Washington.
- (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- $\beta$  signaling in the descending thoracic aorta. Molecular Medicine Research Retreat, October 6, 2016. Baltimore, MD.

## Posters

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- (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- $\beta$  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 Ru(II) and Os(II) chromophore separation. Southeastern Regional Meeting of the American Chemical Society, November 14–17, 2012. Raleigh, NC.

## Teaching

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### Training

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

### Experience

2021      UW Winter Quarter Software Carpentry Workshop Instructor  
<https://uwescience.github.io/2021-01-11-uw-online/>

## Mentoring

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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–      **Donovan See**, Undergraduate student  
University of Washington

2020–      **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

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### Editorial Boards

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

### Conference Organization

2020 Workshop on High Performance Computing, Big Data Analytics and Integration for Multi-Omics Biomedical Data (HPC-BOD 2020) *Program Committee Member*.

### Professional Memberships

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

### Departmental Service

2019– UW Genome Sciences Art Committee  
2018– 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:** Scientific Reports, Journal of Proteome Research

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

## Scientific Blog Posts

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- (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/>

## References

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**David Goodlett**

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