# William E Fondrie, PhD

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https://willfondrie.com Updated September 29, 2020.

| Education | 1  |
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| 2013-18   | PhD in Molecular Medicine University of Maryland, Baltimore Advisors: Dudley Strickland, PhD and David Goodlett, PhD               |
| 2009-13   | BS in Chemistry University of North Carolina at Chapel Hill  |
| Employm   | ent and Professional Appointments  |
| 2019-     | University of Washington Data Science Postdoctoral Fellow  |
| 2018-     | Postdoctoral Fellow, University of Washington<br>Advisor: William Noble, PhD   |
| 2013-18   | <b>Graduate Research Assistant</b> , University of Maryland, Baltimore<br>Advisors: Dudley Strickland, PhD and David Goodlett, PhD |
| 2012-13   | <b>Undergraduate Research Assistant</b> , University of North Carolina at Chapel Hill Advisor: John Papanikolas, PhD               |
| Awards a  | nd Honors  |
| 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<br>Mass Spectrometry and Proteomics                       |
| 2017-18   | Ruth L Kirschstein Individual National Research Service Award<br>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-Revi | lewed Publications   |

(\* 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 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.

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| (1) Fondrie WE. Biological Insig | ht from Mass Spectrometry Through Novel Computational Approaches. |
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 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

(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

Additional Dublications

(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.

 $Homepage: \verb|https://github.com/bittremieux/spectrum_utils| \\$ 

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

- (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.
- 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.

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

# Mentoring

| 2020- | <b>Elena Romero</b> , PhD student<br>Department of Genome Sciences, University of Washington |
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| 2020- | <b>Donovan See</b> , Undergraduate student<br>University of Washington                       |
| 2020- | <b>Lilian Heil</b> , PhD student<br>Department of Genome Sciences, University of Washington  |
| 2019- | <b>Kianna Hales</b> , PhD student<br>Department of Genome Sciences, University of Washington |

### **Professional Service**

## **Departmental Service**

| 2019-   | UW Genome Sciences Art Committee                         |
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| 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                |

### **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)

Journal Referee: Scientific Reports

Conference Referee: Intelligent Systems for Molecular Biology 2020

# **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/

## References

#### William Noble

Department of Genome Sciences, University of Washington wnoble@uw.edu

## **Michael MacCoss**

Department of Genome Sciences, University of Washington maccoss@uw.edu

### **Dudley Strickland**

Center for Vascular and Inflammatory Diseases, University of Maryland Baltimore dstrickland@som.umaryland.edu

### **David Goodlett**

Genome BC Proteome Centre, University of Victoria goodlett@uvic.ca