LAUREN STOPFER

LESTOPFER@GMAIL.COM

EDUCATION

Massachusetts Institute of Technology September 2015 - February 2021

Ph.D., Department of Biological Engineering
Thesis: Quantitative mass spectrometry-based approaches for characterizing the immunopeptidome and tyrosine phosphoproteome in cancer

University of Wisconsin-Madison September 2011 -May 2015

Bachelor of Science, Department of Biomedical Engineering

EXPERIENCE

Scientist, Proteomics, BioNTech March 2021- present

- Protein sciences team member responsible for proteomics-based experiments (tryptic digestions, immunopeptidomics) leveraging DDA and targeted acquisition methods to identify and validate therapeutic targets across oncology and infectious disease project teams.
- Led methods development and optimization efforts to build quantitative ligandomics capabilities.
- Extensive experience presenting data and analyses, literature review, and competitive landscape analysis for projects related to target discovery.
- Proficiency in operating and maintaining Thermo Fisher Exploris 480 and Lumos mass spectrometers and Easy nLC 1200 HPLC systems.
- Management experience of one research associate direct report. Set project goals, met weekly to discuss project progress, provided training and mentorship for learning lab skills, data analysis, and presentations.

MIT, Department of Biological Engineering & Koch Institute October 2015- March 2021

Forest White and Douglas Lauffenburger Labs

SKILLS

- Extensive experience operating & maintaining Thermo Fisher hybrid quadrupole-orbitrap mass spectrometers (QE-plus, QE-HFX, Exploris 480) and HPLC systems (Easy nLC 1000, UltiMate 3000).
- Proficiency analyzing MS data using Proteome Discoverer & Skyline software.
- Experience designing experiments, building/optimizing acquisition methods, and acquiring/analyzing data across a range of proteomic applications including protein expression profiling, global phosphorylation, tyrosine phosphorylation (pTyr), ubiquitination, motif enrichments, & class I/II immunopeptidomics, in both discovery (DDA) and targeted (PRM, SureQuant IS-PRM) formats.
- Proficiency in quantitative MS strategies including Tandem Mass Tags, SILAC, and label free quantification.
- Competence with cell culture, MS sample preparation (ex. SPE, SP3, enzymatic digestions, immunoprecipitations), flow cytometry, sequencing, and other basic biology techniques.

RESEARCH AREAS

- Developed a multiplexed MS-based method to quantify changes in MHC class I peptide repertoires in response to targeted therapy using heavy isotope-coded pMHCs as internal standards. Data were used to identified peptides selectively upregulated in response to targeted therapy, which are currently being leveraged for peptide-MHC specific targeted immunotherapy.
- Created of a novel MS platform for absolute quantification of MHC antigen levels (copies per cell) using isotope-coded peptides to generate an internal isotopologue multipoint calibration curve using SureQuant-based Internal Standard triggered Parallel Reaction Monitoring (IS-PRM).
- Characterization of early pTyr signaling dynamics of NRAS mutant melanoma in response to Binimetinib (MEKi) to understand innate and adaptive resistance.
- Real-time, high density monitoring of 300+ tyrosine phosphorylation signaling targets in colorectal tumors using IS-PRM. Analysis of tumor specific signatures revealed druggable pathways and immune infiltration.
- Other areas of study include dendritic cell antigen cross presentation, characterizing impact of protein carrier channels (boosting) on pMHC/pTyr analyses, and small molecule target engagement of transcription factors.

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Thermo Fischer Scientific February 2019-current
Proteomics Vertical Marketing Group

Optimized and applied a new IS-PRM mass spectrometry method at the Thermo Fischer factory site to target hundreds of unique pTyr sites in colorectal cancer. Presented results at American Society of Mass Spectrometry 2019, International Human Proteome Organization 2019/2020. Webinar: *https://bit.ly/39p3NQ1*

RTW Investments June 2020- August 2020

Research analyst focused on biology deep dives on potential therapeutic targets and investment opportunities.

UW Madison, Department of Biomedical Engineering January 2013- May 2015
Pamela Kreeger Lab

Performed assays/blots, cell culture, imaging and analysis, and manufactured co-culture devices to study tumor-macrophage microenvironment interactions in ovarian cancer.

Mayo Clinic, Department of Physiology and Biomedical Engineering September 2014-May 2015
Daniel Tschumerperlin Lab

Developed cell-derived matrix protocols to study the relationship between fibroblast matrix deposition and transcriptional activator TAZ expression in the context of pulmonary fibrosis.

CONSULTING

Torque Therapeutics April 2019-present

Advise in experimental setup, methodology, and data analysis of immunopeptidomics experiments.

LEADERSHIP & INVOLVEMENT

MIT Communications Lab – Writing Fellow & Advisor — April 2016-January 2020
MIT Graduate Admissions Blog – Founding Student Editor and Writer — January 2016-January 2019
MIT Graduate Resident Advisor – East Campus 2E — October 2018-June 2020
BE Application Assistance Program – Co-founder — November 2016-September 2018
MIT Teaching Assistant – Biomolecular Systems & Cellular Dynamics (20.320) — September-December 2017
MIT UROP – Undergraduate Research Mentor — September 2017-present

SELECTED AWARDS & HONORS

2020: Margaret A. Cunningham Immune Mechanisms of Cancer Research Fellowship,
Koch Institute Director's Fund Travel Award
2019: 2020 Biological Engineering Siebel Scholar, runner-up in Wishnok prize for department seminar
2018: 3rd Place in Center for Environmental Health Sciences Annual Poster session,
Travel Award from Greater Boston Mass Spectrometry Discussion Group
2017: MIT BE Teaching Assistant of the Year
2016-present: Toxicology Training Grant Fellow
2016: Honorable Mention, NSF Graduate Research Fellowship

PUBLICATIONS

1. **LE Stopfer***, NJ Rettko*, O Leddy, JM Mesfin, E Brown, S Winski, B Bryson, JA Wells, and FM White. MEK inhibition enhances presentation of targetable MHC-I tumor antigens in mutant melanomas. *In review, 2022. bioRxiv 475285. *Co-first authors.*
2. AM Jaeger, **LE Stopfer**, EA Sanders, DA Sandel, WA Freed-Pastor, WM Rideout III, S Naranjo, T Fessenden, PS Winter, RE Kohn, J Schenkel, S Shanahan, AK Shalek, S Spranger, FM White, and T Jacks. Deciphering the tumor-specific immunopeptidome in vivo with genetically engineered mouse models. *In review, 2021. bioRxiv 450516.*
3. **LE Stopfer**, AD D'Souza, and FM White. 1,2,3, MHC: a review of mass-spectrometry-based immunopeptidomics methods for relative and absolute quantification of pMHCs. *Immuno-Oncology Technol.* Oct. 2021.

4. **LE Stopfer**, AS Gajadhar, B Patel, S Gallien, DT Frederick, GM Boland, RJ Sullivan, and FM White. Absolute quantification of tumor antigens using embedded MHC-I isotopologue calibrants. *Proc. Natl. Acad. Sci. U.S.A.*, Aug. 2021.
5. **LE Stopfer,** CT Flower, AS Gajadhar, B Patel, S Gallien, D Lopez-Ferrer, and FM White. High-density, targeted monitoring of tyrosine phosphorylation reveals activated signaling networks in human tumors. *Cancer Research*, May 2021.
6. **LE Stopfer**, JE Conage-Pough, and FM White. Quantitative Consequences of Protein Carriers in Immunopeptidomics and Tyrosine Phosphorylation MS^2 Analyses. *Mol. Cell. Proteomics,* May 2021.
7. **LE Stopfer**, JM Mesfin, BA Joughin, DL Lauggenburger, and FM White. Multiplexed relative and absolute quantitative Immunopeptidomics reveals MHC I repertoire alterations induced by CDK4/6 inhibition. *Nat. Commun.,* 11, 1–14, Jun 2020.
8. A Jaeger, **L Stopfer**, SL Giorgio Gaglia, S Santagata, NU Lin, J Trepel, F White, T Jacks, L Whitesell, and S Lindquist. Rebalancing protein homeostasis enhances tumor antigen presentation, *Clin. Cancer Res.*, 2019.
9. LS Prahl, PF Bangasser, **LE Stopfer**, M Hemmat, FM White, SS Rosenfeld, and DJ Odde. Microtubule-based control of motor-clutch system mechanics in glioma cell migration, *Cell Reports*, Nov 2018.
10. J Wilson, E Kefaloyianni, **L Stopfer**, C Harrison, V Sabbisetti, E Fraenkel, D Lauffenburger and A Herrlich. Functional Genomics Approach Identifies Novel Signaling Regulators of TGF**a** Ectodomain Shedding, *MCR,* Nov. 2017
11. F Liu, D Lagares, K. Choi, **L Stopfer**, A Marinkovic, V Vrbanac, C Probst, S Hiemer, T Sisson, J Horowitz, I Rosas, L Fredenburgh, C Feghali-Bostwick, X Varelas, A Tager, and D Tschumperlin. Mechanosignaling through YAP and TAZ drive fibroblast activation and fibrosis. *AM J PHYSIOL-LUNG C*, Dec. 2014.
12. MJ Carroll, **LE Stopfer**, PK Kreeger. A simplified culture system to examine soluble factor interactions between mammalian cells, *Chem Commun*, 2013.

Connect with me
laurenstopfer.com Twitter: @lstops Linked in: /in/laurenstopfer ORCID: 0000-0001-6984-3004