

## Curriculum Vitae

# GAELEN D. GUZMAN, PhD

[GaelenGuzman.phd](#) · [gaelenguzman@gmail.com](mailto:gaelenguzman@gmail.com) · (208)-651-1748 · [Dissertation](#) · [ORCID](#)

### PERSONAL STATEMENT

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I am a molecular biologist who recently completed my doctoral and post-doctoral research at OHSU, where I studied host-pathogen interactions during *Mycobacterium tuberculosis* infection. I have experience in one-on-one mentorship, project management, experimental and study design, grant writing, and manuscript review. I am seeking a role in which I can leverage my extensive experience in multi-omics data analyses, data visualization, and scientific communication. Prior to my PhD work, I performed several proteomics analyses of uncharacterized IBD and colitis GWAS targets with the Proteomics Platform at the Broad Institute.

I subsequently received my PhD in 2024 from the Department of Molecular Microbiology and Immunology at Oregon Health & Science University. My dissertation project was focused on unraveling the manners in which host sphingolipids influence the progression of *Mycobacterium tuberculosis* infection. In this work with Dr. Fikadu Tefesse, I applied molecular cell biology techniques, fluorescence microscopy, lipidomics, and proteomics to explore the intersection of these understudied lipids and this understudied pathogen. As the antimicrobial capacity of host phagocytes plays an outsized role in the pathogenesis of an *Mtb* infection, I have a strong familiarity with the inflammatory and antimicrobial responses of macrophages, dendritic cells, and neutrophils. My dissertation can be viewed online [here](#).

During my postdoctoral research in Dr. Tefesse's lab and as a consulting analyst since my postdoc's completion, I performed data analysis as part of the Gates Foundation M72/AS10E tuberculosis vaccine study. I integrated lipidomics, metabolomics, and proteomics datasets for 53 subject participants and applied feature extraction methods including principal component analysis, balanced random forest analysis, and cross validation using R packages such as factextra, randomForest, and caret in order to identify a biosignature of vaccine response. The small cohort size of this phase of the trial precluded the use of foundation models in this analysis.

Additionally in my postdoc, I designed, developed, and maintained the [Lipid Interactome](#), an open-access data repository for proteomics analyses of utilizing R, adhering to reproducibility and interoperability standards in proteomics data. Our manuscript detailing this project is under review with *Bioinformatics*.

Among these experiences, I am also a new father and a proud husband. During my wife's pregnancy last spring, she was diagnosed with breast cancer – we are immensely relieved that she now has no evidence of disease and that our son is healthy. In between part-time data consulting and full-time dad-ing, I have been dedicating my time to building on my coding and informatics skills: I am currently learning C++ for projects using embedded microcontrollers and am working through the *Hands-On Machine Learning with Scikit-Learn and TensorFlow*. I am immensely grateful for the time I've been able to spend with my wife as she recovers and my son as he has gotten older, and I look forward to combining my old and new skills in a full time role in the coming months.

Thank you for considering my application!

### EDUCATION

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**Oregon Health & Science University**  
*PhD in Molecular Microbiology and Immunology*

Portland, OR  
Sept 2017 - Feb 2024

#### Relevant coursework:

- Structure and function of Biological Molecules
- Molecular Biophysics and Bioinformatics
- Bioregulation
- Genetic Mechanisms
- Molecular Cell Biology
- Introduction to Immunology
- Advanced Immunology
- Host-Pathogen Interactions
- Advanced Virology
- Molecular and Cellular Approaches to Disease
- Principles and Practices of Data Visualization
- Perspectives in Pulmonary Medicine

**Massachusetts Institute of Technology**  
*Bachelor of Science in Biology*

Cambridge, MA  
Sept 2010 - June 2014

#### Relevant coursework:

- Introductory biology
- Genetics
- Immunology
- Organic Chemistry
- General Biochemistry
- Molecular Cell Biology
- Human Physiology

- Molecular Basis of Infectious Disease
- Virus-Host Interactions
- Experimental Molecular Biology
- Development and Evolution
- Introductory Python
- Experimental Biology and Communication

## **LABORATORY AND PROFESSIONAL EXPERIENCE**

### **Carsten Schultz**

*Consulting Data Analyst*

Portland, OR (remote)

May 2025 – Present

- In this role, I am continuing the development of the [Lipid Interactome](#), an Open Science-driven repository for interaction proteomics data which utilize functionalize lipid analogs to identify lipid-protein interactions. I began this project during my postdoctoral work with Drs. Fikadu Tafesse and Carsten Schultz.
- I am continuing to add datasets to this repository and am developing new site features.

### **Fikadu Tafesse**

*Consulting Data Analyst*

Portland, OR (remote)

May 2025 – June 2025

- Collaborated on a multi-omics study of vaccine responsiveness for the Gates Foundation M72/AS01E clinical trial, continuing work initiated during my postdoctoral research.
- Analyzed >5,000 biomarkers across proteomics, lipidomics, and metabolomics platforms to identify candidate biosignatures of vaccine response. Applied machine learning techniques including PCA for dimensionality reduction, SMOTE-enhanced random forest modeling, and repeated cross-validation to assess feature importance and predictive power. (R packages I used included factoextra, randomForest, caret).
- Navigated challenges of low sample size (n=53) and class imbalance (42/11) by integrating ML outputs with biological insight, ultimately developing a robust semi-manual feature selection pipeline.
- Contributed to the design of our proposal for the next found of the M72/AS01E study to leverage a larger cohort and apply scalable ML workflows to refine biosignatures with improved statistical power and generalizability.

### **Robert Thibault**

*Open Science Consultant, Contract*

Portland, OR (remote)

April 2025 – Present

- In this consulting role, I am building data visualization and curation tools to allow for exploration and cleanup of the key resource tables of Open Science manuscripts; these data will be used to inform future funding and monitor grantee compliance with Open Science principles. These tools both accept user-submitted data and scrape key resource tables from these publications. Additionally, I am performing reviews to monitor grantee compliance with Open Science principles.

### **Oregon Health & Science University**

*Postdoctoral work with Dr. Fikadu Tafesse*

Portland, OR

May 2024 – April 2025

- Built and deployed the [Lipid Interactome data repository](#) for proteomics experiments utilizing trifunctional lipid analogs (an ongoing project).
- Data analysis for Round 1 of the Gates M72 *Mycobacterium tuberculosis* vaccine consortium. We performed coordinated lipidomics, proteomics, and metabolomics analyses on serum samples collected from vaccine-recipients and control volunteers. In this collaborative experience, I worked with the Multi-Omics core at the Pacific Northwest National Labs to prepare a data package; our research group is under consideration for Round 2 of the consortium.
- Published a manuscript reporting the identification and characterization of multiple sphingomyelin synthases in *C. elegans* (Accepted following peer review, publication pending editorial review).
- Mentored and advised a PhD student and a prospective lab member, performed and assisted in data analysis and data visualization projects in the lab.

### **Oregon Health & Science University**

*Dissertation work with Dr. Fikadu Tafesse*

Portland, OR

March 2018 – Feb 2024

- Under the mentorship of Dr. Tafesse, I designed a series of research goals that culminated in a dissertation focused on the identification and characterization of sphingolipid-mediated mechanisms of host-pathogen interaction in the context of the intracellular pathogen *Mycobacterium tuberculosis*.
- My research goals were designed both to answer novel questions regarding the roles of sphingolipids in pathogenic contexts, as well as to maximize my technical training. I employed and gained expertise in fluorescence microscopy, lipidomics and thin layer chromatography, and phenotypic assays and screens using novel biochemical tools.

- In this research experience, I received training in confocal microscopy (and subsequently, in image analysis), in CRISPR/Cas9 genomic editing, flow cytometry, Biosafety Level 3 laboratory practices, and bacterial and viral infections.
- As a member of this lab, I gained extensive experience in scientific writing through preparing two primary authorship research articles and three review/methods articles, performing peer reviews of several manuscripts, wrote and edited numerous grants (ranging from F31 to R01). I gained extensive expertise in data visualization using R. Additionally, I regularly presented my preliminary results to group meetings, as well as presented my work in poster form at several meetings and conferences (listed below).
- Among the most fulfilling and exciting components of this experience, I trained and mentored three graduate students and two research assistants – from direct guidance on experimental design and technique to project management to career advice.

### **Broad Institute Proteomics Platform** *Research Associate II with Dr. Monica Schenone*

Cambridge, MA  
March 2014 – July 2017

- Performed proteomic experiments in collaboration with numerous Broad, MIT, Cambridge (UK), and Harvard laboratories, as well as Cambridge (MA)-based pharmaceutical companies including Pfizer, Bayer, and AstraZeneca.
- Applied quantitative proteomics and data-dependent mass spectrometry to elucidate the proteomic interaction partners of target proteins and small molecules in order to better understand the underlying mechanisms of and identify therapeutic options for diseases such as Alzheimer's Disease, Inflammatory Bowel Disease, Type 2 Diabetes, and Myocardial Infarction.
- Independently managed over eighty-five experiments through sample preparation, mass spectrometric analysis, and data interpretation. Also assisted in the training and education of numerous new members of the interaction proteomics team and collaborating industry partners.
- Presented experimental results at group meetings and collaborative meetings, as well as in poster form at the First and Second Annual Broad RA/TS poster sessions (2015 and 2016) and at the 2016 Broad Retreat (abstracts listed below).
- Techniques of specialty include: protein purification, isobaric labeling (Stable Incorporation of Labeled Amino acids in Cell culture, isobaric Tagging for Relative and Absolute Quantitation, and Tandem Mass Tagging), HPLC use and maintenance, Thermo Fisher Q Exactive+ use and maintenance, and statistical data analysis and interpretation.

### **Massachusetts Institute of Technology** *MIT Course 7.16 – Senior Project Lab*

Cambridge, MA  
Sept 2013 – Dec 2013

- Partnered with a peer to perform an independent study on the role of Ubiquitination in the activation of NEMO, a regulator of the NFκB immunological pathway. NEMO misregulation is responsible for numerous chronic immune diseases such as autoinflammation, dermatitis, Parkinson's disease, and large B-cell lymphoma.
- Independently designed experimental methodology, with particular focus on human tissue culture, transient transfection, fluorescence imaging, and immunodetection and immunoprecipitation.
- Compiled experimental results into figures and authored a formal manuscript and presentation.

### **Massachusetts Institute of Technology** *MIT Undergraduate Research Opportunity Project*

Cambridge, MA  
Feb 2012 – Aug 2013

- Through these semester-long internships, I worked in the laboratory of Dr. Hidde Ploegh, where I obtained hands-on experience in various research techniques involving molecular biology, immunology, virology, and biochemistry.
- Assisted post-doctorates and fellows in designing and executing numerous projects including:
  - Cloning and purifying orphan cytokines and chemokines in order to identify their relevant binding partners. Through this project, I gained experience in bacterial and yeast protein expression systems, as well as experience in protein purification through HPLC.
  - Producing a column-based flow-through method for Sortase mediated fluorophore-protein conjugation. In the course of this project, I gained experience performing and assessing the effectiveness of chemical and biochemical reactions.
  - Calculating the mutation rates (via cDNA sequencing) of influenza virus particles after passage through B-cells that produce antibodies against hemagglutinin. Using this method, studied immune evasion mechanisms of the influenza virus. This project afforded me experience in mammalian tissue culture, gene sequencing, and genetic analysis.

## **AWARDS, HONORS, AND GRANT APPOINTMENTS**

- **Award for Best Question @ Sphingolipid Biology FEBS Special Meeting; October 2023**
- **Rittenberg Meritorious Travel Award; September 2023** – A departmental travel award supporting travel to the 2024 FEBS Special Meeting on Sphingolipid Biology

- **Award for Excellent Talk by a Trainee – International Ceramide Conference; April 2023**
- **Sears Microbiology Fellowship Award; April 2023** – Departmental travel award supporting my travel to the International Ceramide Conference in Charleston, NC, USA.
- **Pulmonary and Critical Care Medicine (T32 Graduate Fellow); July 2022** – An NIH-sponsored training grant supporting graduate students and postdocs studying fields relevant to pulmonary or critical care medicine. This program provides in-depth didactic sessions on the mechanisms of pulmonary function and care in addition to career-driven training opportunities. This award grants stipend and tuition support.
- **Program in Enhanced Research Training (T32 Graduate Fellow); August 2018** – An NIH-sponsored training grant available to 2nd year students in the OHSU PMCB program. This one-year fellowship provides a unique curriculum and mentorship experience that is designed to give career-driven students opportunities for scientific and professional development. In the years following the fellowship, students act as mentors in support of incoming awardees. This award grants stipend and tuition support independent of the OHSU School of Medicine and faculty grants.
- **Henry Collins Foundational Fellowship; July 2018** – An OHSU Department of Molecular Microbiology and Immunology-funded award that provides stipend and tuition support and allows students to participate in the departmental T32 training activities.
- **Early Independence Fellowship Award; July 2017** – A unique opportunity at OHSU, designed to give promising graduate students enhanced flexibility both in research scope and access to cross-disciplinary mentorship. This award provides stipend and tuition support independent of faculty grants, and is annually renewable up to four years.
- **Promising Scholars Award; March 2017** – Awarded by the OHSU School of Medicine and Center for Diversity and Inclusion, directed towards scholars who show great potential to contribute to the intellectual richness and diversity of the OHSU student community.

## COMPUTATIONAL AND DATA ANALYSIS SKILLS

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**Programming:** Proficiency in R: Applied Tidyverse for data wrangling and transformation of multi-omics datasets; developed Shiny apps for interactive explorations of proteomics and lipidomics data. Familiarity with Python: Undergraduate coursework, hobbyist Advent of Code (Pandas, NumPy, Matplotlib); working through the *Hands-On Machine Learning* guide to the Scikit-Learn and TensorFlow libraries. Learning C++: microcontroller programming for ESP32-based hobbyist projects. Significant experience with version control via Git.

**Data Visualization:** Expertise in creating publication-ready graphics and interactive dashboards using Shiny, Plotly, and Quarto Markdown. Extensive experience in figure preparation in Adobe Illustrator.

**Bioinformatics and data pipelines:** Extensive experience in automating workflows to analyze proteomics and lipidomics datasets via R and Python.

**Repository Development:** Lead the design and deployment of a centralized data repository and presentation tool for affinity proteomics to enhance storage, access, and collaborative capabilities of studies utilizing functionalized lipid probes. Ongoing work seeks to improve site functionality, such as multi-user data upload, scalability, and efficiency.

## LABORATORY TECHNIQUES

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**Bio Safety Level 3 (BSL3):** Expertise in high-containment laboratory protocols, requiring meticulous planning, precise execution, and strict adherence to safety standards for infectious disease research.

**Fluorescence Microscopy:** Skilled in advanced imaging techniques for studying cellular processes, including live-cell imaging and quantitative analysis.

**Affinity Proteomics:** Extensive experience in designing and executing workflows for proteomic profiling, including mass spectrometry-based methods.

**Flow Cytometry:** Proficient in multi-parameter flow cytometry for cell population analysis, data acquisition, and interpretation.

**Experimental Design:** Demonstrated expertise in planning and optimizing complex experiments to ensure reproducible, high-quality data, including integration of computational analysis pipelines for downstream insights.

## PRIMARY AUTHORSHIP PUBLICATIONS

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Guzman, G., Tafesse, F. G. (2023) Systematic analysis of the sphingomyelin synthase family in *C. elegans*. Preprint on BioRxiv <https://doi.org/10.1101/2023.07.25.550547>.

Guzman, G., Farley, S. E., Creek, C., Tafesse, F. G. (2023) Genetic tools for studying the roles of sphingolipids in viral infections. *Methods in Molecular Biology*, ISBN 9781071628942 (Book chapter). [https://doi.org/10.1007/978-1-0716-2895-9\\_1](https://doi.org/10.1007/978-1-0716-2895-9_1).

- Niekamp, P\*, Guzman, G.\*, Leier, H. C., Rashidfarrokhi, A., Richina, V., Pott, F., Barisch, C., Holthuis, J. C. M. M., and Tafesse, F.G. (2021). Sphingomyelin Biosynthesis Is Essential for Phagocytic Signaling during Mycobacterium tuberculosis Host Cell Entry. *MBio*, 12(1), 1–19. <https://doi.org/10.1128/mBio.03141-20> (\*co-first authorship)
- Guzman, G., Niekamp, P., and Tafesse, F. G. (2020). The Squeaky Yeast Gets Greased: The Roles of Host Lipids in the Clearance of Pathogenic Fungi. *Journal of Fungi*, 6(1), 19. <https://doi.org/10.3390/jof6010019>.
- Guzman, G., and Tafesse, F. G. (2020). Visualization and Quantification of Phagocytosis by Neutrophils (pp. 141–148). [https://doi.org/10.1007/978-1-0716-0154-9\\_11](https://doi.org/10.1007/978-1-0716-0154-9_11).

## NON-PRIMARY AUTHORSHIP PUBLICATIONS

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- Zhu, Q.M., Hsu, Y.H., Lassen, F.H., MacDonald, B., Stead, S., Malolepsza, E., Kim, A., Li, T., Mizoguchi, T., Schenone, M., Guzman, G., Tanenbaum, B., ... Lage, K. (2024) Protein interaction networks in the vasculature prioritize genes and pathways underlying coronary artery disease. *Communications Biology*, 7, 87. <https://doi.org/10.1038/s42003-023-05705-1>.
- Bates T, McBride S., Leier H., Guzman, G., Lyski Z., Schoen D., Winders B., Lee J., Lee D., Messer W., Curlin M., Tafesse F.G. (2022). Vaccination before or after SARS-CoV-2 infection leads to robust humoral response and antibodies that effectively neutralize variants. *Science Immunology*, 7(68). <https://doi.org/10.1126/sciimmunol.abn8014>.
- Mohanan, V., Nakata, T., Desch, A. N., Lévesque, C., Boroughs, A., Guzman, G., ... Xavier, R. J. (2018). C1orf106 is a colitis risk gene that regulates stability of epithelial adherens junctions. *Science*, 359(6380), 1161–1166. <https://doi.org/10.1126/science.aan0814>.
- Hung, V., Lam, S. S., Udeshi, N. D., Svinkina, T., Guzman, G., Mootha, V. K., ... Ting, A. Y. (2017). Proteomic mapping of cytosol-facing outer mitochondrial and ER membranes in living human cells by proximity biotinylation. *eLife*, 6. <https://doi.org/10.7554/eLife.24463>.
- Rusu, V., Hoch, E., Mercader, J. M., Florez, J. C., Jacobs, S. B. R., Guzman, G., ... Lander, E. S. (2017). Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. *Cell*, 170(1), 199–212.e20. <https://doi.org/10.1016/j.cell.2017.06.011>.
- Graham, D. B., Lefkovith, A., Deelen, P., de Klein, N., Varma, M., Boroughs, A., Guzman, G., ... Xavier, R. J. (2016). TMEM258 Is a Component of the Oligosaccharyltransferase Complex Controlling ER Stress and Intestinal Inflammation. *Cell Reports*, 17(11), 2955–2965. <https://doi.org/10.1016/j.celrep.2016.11.042>.

## CONTRIBUTED PRESENTATIONS

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- Guzman, G., Griffith, A., Garcia, M., Trank-Greene, M., Tafesse, F.G. “Exploring the role of sphingolipids during *emphMycobacterium tuberculosis* infection.” Short talk at the 2023 FEBS Special Meeting: Sphingolipid Biology, the Dawn of a New Era. Funchal, Portugal. Oct 8, 2023.
- Guzman, G., Griffith, A., Garcia, M., Trank-Greene, M., Tafesse, F.G. “Sphingolipids: A double-edged sword in the defense against *emphMycobacterium tuberculosis*.” Poster presentation at the 2023 International Ceramide Conference. Charleston, NC. Apr 16, 2023.
- Guzman, G., Niekamp, P., Tafesse, F.G. “Sphingolipids: A double-edged sword in the defense against *emphMycobacterium tuberculosis*.” Poster presentation at the following two meetings: American Association of Immunologists IMMUNOL-OGY2022. Portland, OR. May 6-10, 2022; Microbiology and Immunology Departmental Retreat. Welches, OR. Oct 13-15, 2022.
- Guzman, G., Niekamp, P., Tafesse, F.G. “Sphingomyelin biosynthesis is critical during the phagocytic uptake of *emphMycobacterium tuberculosis*.” OHSU Research Week 2019. Portland, OR. May 13, 2019.
- Guzman, G., Niekamp, P., Tafesse, F.G. “Host sphingolipids in the phagocytic uptake of *Mycobacterium tuberculosis*.” Poster presented at the 3rd Annual PacTB Symposium. Portland, OR. Mar. 21, 2019.
- Guzman, G., Niekamp, P., Tafesse, F.G. “Investigating the dependencies of intracellular bacteria on host sphingolipids.” Sept. 2018. Abstract selected for presentation at the following three meetings: the American Society for Microbiology Northwest Conference, at the OHSU campus in Portland, OR on Oct. 6, 2018; the 4th Annual International Workshop on the Molecular Medicine of Sphingolipids, at the Weizmann Institute of Science in Ein Gedi, Israel on Oct. 16, 2018; and the OHSU Molecular Microbiology and Immunology Departmental Retreat in Portland, OR on Nov. 11, 2018.
- Guzman, G., Schenone, M., Rillahan, C., Bradshaw, B., Carr, S., de Jager, P. “Identifying the interactors of Alzheimer’s Disease factor CD33 using quantitative proteomics.” Nov. 2016. Poster presentation given at: the 2nd Annual Broad

RA/TS Poster Session, at the Broad Institute of MIT and Harvard, Nov. 29, 2016; and the Broad Retreat, Dec. 12, 2016.

Guzman, G., Schenone, M., Graham, D., Carr, S. "Identifying a novel role of Protein Tmem258 through Quantitative Mass Spectrometry." Nov. 2015. Poster presentation given at: the 1st Annual Broad RA/TS Poster Session, at the Broad Institute of MIT and Harvard, Nov. 14, 2015.

## **COMMUNITY ENGAGEMENT AND LEADERSHIP**

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### **Graduate Researchers United**

*Contract Action Team, member*

*Union Steward*

Portland, OR

*Dec 2019 – June 2022*

*Jan 2020 – Jan 2022*

- Assisted in labor organizing for card signing, rallies, and contract ratification.
- Served as union steward for two years, wherein I submitted several grievances on behalf of Graduate Researchers suffering from contract violations.
- Collaborated with other graduate students at OHSU to draft contract language which will codify and expand student benefits, protect students from abuse by departmental and advisory faculty, and represent students with grievances in cases of abuse and harassment.

### **FSILG, Theta Xi**

*Vice President of Theta Xi Fraternity*

Boston, MA

*Sept 2012 – May 2013*

- Organized, co-facilitated, and kept minutes at all chapter meetings in a fraternity of 44 members. Lead numerous committees, including the chapter Judicial Committee and By-Laws Revision Committee. Organized two chapter retreats and facilitated numerous communication-promoting activities.
- Regularly organized volunteering opportunities with Red Cross donation centers, and coordinated fraternity volunteer days with Habitat for Humanity.

## **HOBBIES**

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In addition to my work at OHSU, I am a new father and husband. In my (now scant) free time, I enjoy cycling, rock climbing, and running. I recently discovered a new interest in hobby electronics, through which I've built several ESP32-driven devices – [several are highlighted on my personal site](#); please feel free to take a look and see some of my works in progress!