

Matthew R. Olm, Ph.D.

Assistant Professor

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EDUCATION

- 2014 – 2019 **The University of California, Berkeley**
Ph.D. in Microbiology (May 2019)
Advisor: Jillian F. Banfield
- 2010 – 2014 **The University of Pittsburgh**
B.Sc. in Microbiology; Minor in Computer Science
Department of Biological Sciences

RESEARCH EXPERIENCE

- 2024 - Present **University of Colorado, Boulder**
Assistant Professor
Department of Integrative Physiology
- 2020 - 2024 **Stanford University**
Postdoctoral Fellow
PI: Justin Sonnenburg; Department of Microbiology and Immunology
- 2019 - 2020 **The University of California, Berkeley**
Interim Postdoctoral Scholar
PI: Jillian Banfield; Earth and Planetary Science Department
- 2014 - 2019 **The University of California, Berkeley**
Graduate student
PI: Jillian Banfield; Department of Plant and Microbial Biology
- 2011 - 2014 **The University of Pittsburgh**
Undergraduate researcher
PI: Graham Hatful; Department of Biological Sciences

RESEARCH GRANTS & FELLOWSHIPS

- 2024 - 2028 NIH Common Fund; Human Virome Program U01 (1U01DE034198-01). “Establishing laboratory methods for quantitative recovery of diverse DNA and RNA viral sequences from human biosamples.” Joanne Emerson (PI); Matthew Olm (Subaward PI); Sean Adams (Collaborator). 09/20/24-06/30/28.
- 2024 - 2026 CU Anschutz Nutrition Obesity Research Center (NORC) Pilot & Feasibility Study Award. “Quantifying the Impact of First Foods on the Infant Gut Microbiota and Immune Health”. Matthew Olm (PI). 8/1/2024 - 7/31/2026
- 2021 - 2024 Ruth S. Kirschstein F32 National Research Service Award
Funding institution: National Institute of Diabetes and Digestive and Kidney Diseases
- 2020 - 2021 T32 NIH Postdoctoral Training Fellowship
- 2014 - 2019 National Science Foundation Graduate Research Fellowship
- 2012 Howard Hughes Medical Institute Undergraduate Research Fellowship

HONORS & AWARDS

2024	“InStrain”, a program for microbial population genomics, achieved 100,000 downloads
2021	First-author Research article highlighted as one of “5 Top Cited Papers” of <i>mSystems</i>
2021	“dRep”, a program for rapid genomic comparison, achieved 100,000 downloads
2019	Keystone National Institute of Allergy and Infectious Diseases Travel Scholarship
2017	First-author Research article selected as Cover Image of <i>Genome Research</i>
2017	First-author Research article selected as “Editor’s Pick” of <i>mBio</i>

PUBLICATIONS

(* = equal contribution, † = not peer-reviewed, <https://scholar.google.com/citations?user=BoDUkpMAAAAJ&hl=en>)

1. **Olm, M.R.***, Spencer, S.P.*, Takeuchi, T., Silva, E.L., Sonnenburg, J.L., (2025). Metagenomic immunoglobulin sequencing reveals IgA coating of microbial strains in the healthy human gut. *Nature Microbiology* 10, 112–125. <https://doi.org/10.1038/s41564-024-01887-4>
2. †Qian, J., Yeo, E.N., **Olm, M.R.**, (2024). Hospitalization throws the preterm gut microbiome off-key. *Cell Host & Microbe* 32, 1651–1653. <https://doi.org/10.1016/j.chom.2024.09.009>
3. †**Olm, M. R.**, & Mueller, N. T. (2024). Milk to mucus: How *B. fragilis* colonizes the gut. *Cell Host & Microbe*, 32(2), 149–150. <https://doi.org/10.1016/j.chom.2024.01.007>
4. †Caffrey, E. B., **Olm, M. R.**, Kothe, C. I., Evans, J., & Sonnenburg, J. L. (2024). MiFoDB, a workflow for microbial food metagenomic characterization, enables high-resolution analysis of fermented food microbial dynamics. *bioRxiv* <https://doi.org/10.1101/2024.03.29.587370>
5. Gerrick, E. R., Zlitni, S., West, P. T., Carter, M. M., Mechler, C. M., **Olm, M. R.**, Caffrey, E. B., Li, J. A., Higginbottom, S. K., Severyn, C. J., Kracke, F., Spormann, A. M., Sonnenburg, J. L., Bhatt, A. S., & Howitt, M. R. (2024). Metabolic diversity in commensal protists regulates intestinal immunity and trans-kingdom competition. *Cell*, 187(1), 62-78.e20. <https://doi.org/10.1016/j.cell.2023.11.018>
6. Carter, M.M.*, **Olm, M.R.***, Merrill, B.D.*, Dahan, D., Tripathi, S., Spencer, S.P., Yu, F.B., Jain, S., Neff, N., Jha, A.R., Sonnenburg, E.D., Sonnenburg, J.L., (2023). Ultra-deep sequencing of Hadza hunter-gatherers recovers vanishing gut microbes. *Cell* 186, 3111-3124.e13. <https://doi.org/10.1016/j.cell.2023.05.046>
7. Gellman, R. H., **Olm, M. R.**, Terrapon, N., Enam, F., Higginbottom, S. K., Sonnenburg, J. L., & Sonnenburg, E. D. (2023). Hadza Prevotella require diet-derived microbiota-accessible carbohydrates to persist in mice. *Cell Reports*, 42(11), 113233. <https://doi.org/10.1016/j.celrep.2023.113233>
8. Lou, Y.C., Hoff, J., **Olm, M.R.**, West-Roberts, J., Diamond, S., Firek, B.A., Morowitz, M.J., Banfield, J.F., (2023). Using strain-resolved analysis to identify contamination in metagenomics data. *Microbiome* 11, 36. <https://doi.org/10.1186/s40168-023-01477-2>
9. **Olm M. R.***, Dahan, D.*, Carter M. M., Merrill B. D., Yu F. B., Jain S., Meng X., Tripathi S., Wastyk H., Neff N., Holmes S., Sonnenburg E. D., Jha A. R., Sonnenburg J. L. (2022). Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. *Science*, 376, 1220–1223. <https://doi.org/10.1126/science.abj2972>
10. Bouma-Gregson, K., Crits-Christoph, A., **Olm, M. R.**, Power, M. E., & Banfield, J. F. (2022). *Microcoleus* (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. *Molecular Ecology*, 31(1), 86–103. <https://doi.org/10.1111/mec.16208>
11. †Carter, M. M., **Olm, M. R.**, & Sonnenburg, E. D. (2022). Microbiome assembly in The Gambia. *Nature Microbiology*, 7(1), 18–19. <https://doi.org/10.1038/s41564-021-01036-1>

12. †**Olm, M. R.**, & Sonnenburg, J. L. (2021). Ancient human faeces reveal gut microbes of the past. *Nature*. <https://doi.org/10.1038/d41586-021-01266-7>
13. **Olm, M. R.**, Crits-Christoph, A., Bouma-Gregson, K., Firek, B. A., Morowitz, M. J., & Banfield, J. F. (2021). inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. *Nature Biotechnology*, 39(6), 727–736. <https://doi.org/10.1038/s41587-020-00797-0>
14. Mirzayi, C., Renson, A., Furlanello, C., Sansone, S.-A., Zohra, F., Elsafoury, S., Geistlinger, L., Kasselmann, L.J., Eckenrode, K., van de Wijgert, J., Loughman, A., Marques, F.Z., MacIntyre, D.A., Arumugam, M., Azhar, R., Beghini, F., Bergstrom, K., Bhatt, A., Bisanz, J.E., Braun, J., Bravo, H.C., Buck, G.A., Bushman, F., Casero, D., Clarke, G., Collado, M.C., Cotter, P.D., Cryan, J.F., Demmer, R.T., Devkota, S., Elinav, E., Escobar, J.S., Fettweis, J., Finn, R.D., Fodor, A.A., Forslund, S., Franke, A., Furlanello, C., Gilbert, J., Grice, E., Haibe-Kains, B., Handley, S., Herd, P., Holmes, S., Jacobs, J.P., Karstens, L., Knight, R., Knights, D., Koren, O., Kwon, D.S., Langille, M., Lindsay, B., McGovern, D., McHardy, A.C., McWeeney, S., Mueller, N.T., Nezi, L., **Olm, M. R.**, Palm, N., Pasolli, E., Raes, J., Redinbo, M.R., Rühlemann, M., Balfour Sartor, R., Schloss, P.D., Schriml, L., Segal, E., Shardell, M., Sharpton, T., Smirnova, E., Sokol, H., Sonnenburg, J.L., Srinivasan, S., Thingholm, L.B., Turnbaugh, P.J., Upadhyay, V., Walls, R.L., Wilmes, P., Yamada, T., Zeller, G., Zhang, M., Zhao, N., Zhao, L., Bao, W., Culhane, A., Devanarayan, V., Dopazo, J., Fan, X., Fischer, M., Jones, W., Kusko, R., Mason, C.E., Mercer, T.R., Sansone, S.-A., Scherer, A., Shi, L., Thakkar, S., Tong, W., Wolfinger, R., Hunter, C., Segata, N., Huttenhower, C., Dowd, J.B., Jones, H.E., Waldron, L. (2021). Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine*, 27(11), 1885–1892. <https://doi.org/10.1038/s41591-021-01552-x>
15. Lou, Y. C., **Olm, M. R.**, Diamond, S., Crits-Christoph, A., Firek, B. A., Baker, R., Morowitz, M. J., & Banfield, J. F. (2021). Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. *Cell Reports Medicine*, 2(9), 100393. <https://doi.org/10.1016/j.xcrm.2021.100393>
16. West, P. T., Peters, S. L., **Olm, M. R.**, Yu, F. B., Gause, H., Lou, Y. C., Firek, B. A., Baker, R., Johnson, A. D., Morowitz, M. J., Hettich, R. L., & Banfield, J. F. (2021). Genetic and behavioral adaptation of *Candida parapsilosis* to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics, and proteomics. *Microbiome*, 9(1), 142. <https://doi.org/10.1186/s40168-021-01085-y>
17. Carnevali, P. B. M., Lavy, A., Thomas, A. D., Crits-Christoph, A., Diamond, S., Méheust, R., **Olm, M. R.**, Sharrar, A., Lei, S., & Dong, W. (2021). Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. *Microbiome*, 9(1), 1–23. <https://doi.org/10.1186/s40168-020-00957-z>
18. Crits-Christoph, A., Kantor, R. S., **Olm, M. R.**, Whitney, O. N., Al-Shayeb, B., Lou, Y. C., Flamholz, A., Kennedy, L. C., Greenwald, H., Hinkle, A., Hetzel, J., Spitzer, S., Koble, J., Tan, A., Hyde, F., Schroth, G., Kuersten, S., Banfield, J. F., & Nelson, K. L. (2021). Genome Sequencing of Sewage Detects Regionally Prevalent SARS-CoV-2 Variants. *MBio*, 12(1), e02703-20. <https://doi.org/10.1128/mBio.02703-20>
19. Crits-Christoph, A., Bhattacharya, N., **Olm, M. R.**, Song, Y. S., & Banfield, J. F. (2021). Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. *Genome Research*, 31(2), 239–250. <https://doi.org/10.1101/gr.268169.120>
20. Crits-Christoph, A., **Olm, M. R.**, Diamond, S., Bouma-Gregson, K., & Banfield, J. F. (2020). Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. *The ISME Journal*, 1–13. <https://doi.org/10.1038/s41396-020-0655-x>
21. Sher, Y., **Olm, M. R.**, Raveh-Sadka, T., Brown, C. T., Sher, R., Firek, B., Baker, R., Morowitz, M. J., & Banfield, J. F. (2020). Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut. *Plos One*, 15(3), e0229537. <https://doi.org/10.1371/journal.pone.0229537>
22. **Olm, M. R.**, Crits-Christoph, A., Diamond, S., Lavy, A., Carnevali, P. B. M., & Banfield, J. F. (2020). Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. *mSystems*, 5(1). <https://doi.org/10.1128/mSystems.00731-19>
23. Al-Shayeb, B., Sachdeva, R., Chen, L.-X., Ward, F., Munk, P., Devoto, A., Castelle, C. J., **Olm, M. R.**, Bouma-Gregson, K., Amano, Y., He, C., Méheust, R., Brooks, B., Thomas, A., Lavy, A., Matheus-Carnevali, P., Sun, C., Goltsman, D. S. A., Borton, M. A., ... Banfield, J. F. (2020). Clades of huge phages from across Earth's ecosystems. *Nature*, 578(7795), 425–431. <https://doi.org/10.1038/s41586-020-2007-4>

24. **Olm, M. R.**, Bhattacharya, N., Crits-Christoph, A., Firek, B. A., Baker, R., Song, Y. S., Morowitz, M. J., & Banfield, J. F. (2019). Necrotizing enterocolitis is preceded by increased gut bacterial replication, *Klebsiella*, and fimbriae-encoding bacteria. *Science Advances*, 5(12), eaax5727. <https://doi.org/10.1126/sciadv.aax5727>
25. Devoto, A. E., Santini, J. M., **Olm, M. R.**, Anantharaman, K., Munk, P., Tung, J., Archie, E. A., Turnbaugh, P. J., Seed, K. D., Blekhnman, R., Aarestrup, F. M., Thomas, B. C., & Banfield, J. F. (2019). Megaphages infect *Prevotella* and variants are widespread in gut microbiomes. *Nature Microbiology*, 4(4) 693. <https://doi.org/10.1038/s41564-018-0338-9>
26. Bouma-Gregson, K., **Olm, M. R.**, Probst, A. J., Anantharaman, K., Power, M. E., & Banfield, J. F. (2019). Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. *The ISME Journal*, 13(6), 1618. <https://doi.org/10.1038/s41396-019-0374-3>
27. **Olm, M. R.***, West, P. T.*, Brooks, B., Firek, B. A., Baker, R., Morowitz, M. J., & Banfield, J. F. (2019). Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. *Microbiome*, 7(1), 26. <https://doi.org/10.1186/s40168-019-0638-1>
28. Carnevali, P. B. M., Schulz, F., Castelle, C. J., Kantor, R. S., Shih, P. M., Sharon, I., Santini, J. M., **Olm, M. R.**, Amano, Y., Thomas, B. C., Anantharaman, K., Burstein, D., Becraft, E. D., Stepanauskas, R., Woyke, T., & Banfield, J. F. (2019). Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. *Nature Communications*, 10(1), 463. <https://doi.org/10.1038/s41467-018-08246-y>
29. †Rahman, S. F., **Olm, M. R.**, Morowitz, M. J., & Banfield, J. F. (2019). Functional potential of bacterial strains in the premature infant gut microbiome is associated with gestational age. *BioRxiv*, 530139. <https://doi.org/10.1101/530139>
30. Brooks, B., **Olm, M. R.**, Firek, B. A., Baker, R., Geller-McGrath, D., Reimer, S. R., Soenjoyo, K. R., Yip, J. S., Dahan, D., Thomas, B. C., Morowitz, M. J., & Banfield, J. F. (2018). The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. *Microbiome*, 6(1), 112. <https://doi.org/10.1186/s40168-018-0493-5>
31. Brown, C. T., Xiong, W., **Olm, M. R.**, Thomas, B. C., Baker, R., Firek, B., Morowitz, M. J., Hettich, R. L., & Banfield, J. F. (2018). Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. *MBio*, 9(2), e00441-18. <https://doi.org/10.1128/mBio.00441-18>
32. Rahman, S. F., **Olm, M. R.**, Morowitz, M. J., & Banfield, J. F. (2018). Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. *mSystems*, 3(1), e00123-17. <https://doi.org/10.1128/mSystems.00123-17>
33. Brooks, B., **Olm, M. R.**, Firek, B. A., Baker, R., Thomas, B. C., Morowitz, M. J., & Banfield, J. F. (2017). Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. *Nature Communications*, 8(1), 1814. <https://doi.org/10.1038/s41467-017-02018-w>
34. Brown, C. T., **Olm, M. R.**, Thomas, B. C., & Banfield, J. F. (2017). Measurement of bacterial replication rates in microbial communities. *Nature Biotechnology*, 34(12), 1256–1263. <https://doi.org/10.1038/nbt.3704>
35. **Olm, M. R.**, Brown, C. T., Brooks, B., & Banfield, J. F. (2017). dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication. *The ISME Journal*, 11(12), 2864–2868. <https://doi.org/10.1038/ismej.2017.126>
36. **Olm, M. R.**, Brown, C. T., Brooks, B., Firek, B., Baker, R., Burstein, D., Soenjoyo, K., Thomas, B. C., Morowitz, M., & Banfield, J. F. (2017). Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. *Genome Research*, 27(4), 601–612. <https://doi.org/10.1101/gr.213256.116>
37. **Olm, M. R.**, Butterfield, C. N., Copeland, A., Boles, T. C., Thomas, B. C., & Banfield, J. F. (2017). The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. *MBio*, 8(1), e01969-16. <https://doi.org/10.1128/mBio.01969-16>
38. Dedrick, R. M., Mavrich, T. N., Ng, W. L., Reyes, J. C. C., **Olm, M. R.**, Rush, R. E., Jacobs-Sera, D., Russell, D. A., & Hatfull, G. F. (2016). Function, expression, specificity, diversity and incompatibility of actinobacteriophage parABS systems. *Molecular Microbiology*, 101(4), 625–644. <https://doi.org/10.1111/mmi.13414>

39. Pope, W.H., Anders, K.R., Baird, M., Bowman, C.A., Boyle, M.M., Broussard, G.W., Chow, T., Clase, K.L., Cooper, S., Cornely, K.A., DeJong, R.J., Delesalle, V.A., Deng, L., Dunbar, D., Edgington, N.P., Ferreira, C.M., Hafer, K.W., Hartzog, G.A., Hatherill, J.R., Hughes, L.E., Ipapo, K., Krukoni, G.P., Meier, C.G., Monti, D.L., **Olm, M. R.**, Page, S.T., Peebles, C.L., Rinehart, C.A., Rubin, M.R., Russell, D.A., Sanders, E.R., Schoer, M., Shaffer, C.D., Wherley, J., Vazquez, E., Yuan, H., Zhang, D., Cresawn, S.G., Jacobs-Sera, D., Hendrix, R.W., Hatfull, G.F. (2014). Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isotypes. *Journal of Virology*, 88(5), 2461–2480. <https://doi.org/10.1128/JVI.03363-13>

INVITED PRESENTATIONS

- 2024 **Quantitative Biosciences and Engineering (QBE) Seminar Invited Speaker**
Deciphering the impact of industrialization on the human gut microbiome
Colorado School of Mines, Golden, CO
- 2024 **Rust Belt Microbiome Conference**
Infant Microbiome Development Through Maternal Influence
University of Pittsburgh, PA
- 2024 **Colorado Nutrition and Obesity Center Retreat**
Quantifying the impact of first foods on the infant gut microbiota and immune health
CU Anschutz Medical Campus, Aurora, CO
- 2024 **American Chemical Society Fall 2024 Meeting**
Metagenomic immunoglobulin sequencing (MIg-seq) exposes patterns of IgA antibody binding in the healthy human gut microbiome
Colorado Convention Center, Denver, CO
- 2024 **“Emerging Leader” Invited Speaker – Front Range Microbiome Symposium**
Deciphering the impact of industrialization on the human gut microbiome with metagenomic sequencing
CSU Microbiome Initiative, Fort Collins, CO
- 2023 **American Chemical Society Fall 2023 Meeting**
Applying metagenomic sequencing to decipher the human gut microbiome
Moscone Center, San Francisco, CA
- 2022 **Department of Microbiology and Immunology Wednesday Seminar Series**
Deciphering the human gut microbiome with ultra-deep sequencing
Stanford University, Stanford, CA
- 2022 **7th EBAME Workshop on Computational Microbial Ecogenomics**
Hands-on genome dereplication and population genomics
European Institute for Marine Sciences at Western Brittany University, France
- 2022 **Biotecmar Bioinformatics Tools and Applications Workshop**
Genome-resolved population genomics and strain-level comparisons
All-Atlantic Joint Pilot Action AA-BIOTECMAR workshop (virtual)
- 2022 **Virginia Tech's Life Science Seminar Series**
Metagenomics of modern hunter-gatherers to understand the human microbiome
Virginia Tech, Blacksburg, VA
- 2021 **Molecular and Bioinformatic Methods in Ecology and Evolution Seminar Series**
Tracking microbial strains and quantifying in situ evolution with genome-resolved metagenomics
University of Duisburg-Essen, Germany (virtual)
- 2021 **Applied Bioinformatics & Public Health Microbiology 2021**
Tracing the spread and evolution of microbial populations in hospital rooms and sewage with metagenomics
Wellcome Genome Campus, UK (virtual)

- 2020 **Innovative Genomic Institute “Shelter in Place” Seminar Series**
Beyond strain-level: tracking identical microbial populations and intra-specific variation in the human microbiome
 Innovative Genomics Institute, Berkeley, CA (virtual)
- 2019 **Keystone Symposia: Microbiome: Therapeutic Implications**
Metagenomic identification of fecal microbial signatures preceding acute intestinal inflammation in premature infants
 Killarney, Co. Kerry, Ireland
- 2017 **Microbiology & Molecular Genetics Seminar Series**
Using genome-resolved metagenomics to study the developing infant microbiome
 University of Pittsburgh, Pittsburgh, PA
- 2016 **Lake Arrowhead Microbial Genomics Conference**
Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates
 Lake Arrowhead, CA

TEACHING EXPERIENCE

- 2024 **Instructor, University of Colorado, Boulder**
IPHY 5800: Advanced Statistics and Research Methods
- 2023 **Guest Lecturer, Stanford University**
BIOS 264: Answering biological questions with Metagenomic Data with Dr. Alexander Jaffe
- 2022 **Guest Lecturer, Stanford University**
MI 215: Principles of Biological Technologies with Dr. Peter Sarnow
- 2021 **Guest Lecturer, Stanford University**
MI 221: Gut Microbiota in Health and Disease with Drs. Bhatt and Sonnenburg
- 2021 **Guest Lecturer, Stanford University**
MI 215: Principles of Biological Technologies with Dr. Peter Sarnow
- 2016 **Course Co-founder and Graduate Student Instructor, University of California, Berkeley**
ESPM 112L: Metagenomics Computer Lab with Professor Jillian Banfield
- 2016 **Graduate Student Instructor, University of California, Berkeley**
ESPM 112: Microbial Ecology with Professors Rodrigo Almeida and Jillian Banfield
- 2015 **Graduate Student Instructor, University of California, Berkeley**
Biology 1A: Introduction to Biology
- 2013 **Teaching Assistant, University of Pittsburgh**
NROSCI 1250: Human Physiology with Dr. Alan Sved
- 2012 **Lab Instructor, University of Pittsburgh**
CHEM 0113-0114: General Chemistry Lab 1 and 2

PROFESSIONAL ACTIVITIES AND OUTREACH

- 2024 - 2025 Member of the steering committee for the 2025 Front Range Microbiome Symposium
- 2024 Speaker at the 2024 Northern Colorado Breastfeeding Coalition Annual Meeting
- 2024 Grant Reviewer for the University of Delaware Center of Biomedical Research Excellence
- 2023 - Present Member of the Mountain West Microbiome Alliance

2023	Thesis Examiner for the University of Pretoria, South Africa
2023	Presenter at Chan Zuckerberg Initiative Faculty Application Bootcamp
2021 - 2022	Founding member of Sonnenburg Lab DEI Committee
2021	Referee for UK Research and Innovation Career Development Award
2015 - 2019	Presenter at California Academy of Sciences NightLife events
2016 – 2017	Contributing author to science dissemination website microBE.net
2011 – 2014	Mentor to high school students in the HHMI Phagehunting program
Continuous	Invited Peer reviewer for <i>Nature</i> , <i>Science</i> , <i>Cell</i> , <i>Nature Microbiology</i> , <i>Nature Biotechnology</i> , <i>Bioinformatics</i> , <i>Genome Research</i> , <i>BMC Biology</i> , <i>Microbiome</i> , <i>ISME Journal</i> , <i>Nature Protocols</i> , <i>Molecular Systems Biology</i> , <i>mSystems</i> , <i>BMC Genomics</i> , and <i>Frontiers in Bioinformatics</i>