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Microbiology and Immunology, Stanford University
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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

- 2020 - Present **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

- 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

- 2021 First-author Research article highlighted as one of “5 Top Cited Papers” of *mSystems*
- 2019 Keystone National Institute of Allergy and Infectious Diseases Travel Scholarship
- 2017 First-author Research article selected as Cover Image of *Genome Research*
- 2017 First-author Research article selected as “Editor’s Pick” of *mBio*

<https://scholar.google.com/citations?user=BoDUkpMAAAAJ&hl=en>

1. **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>
2. Merrill, B. D.*, Carter, M. M.*, **Olm, M. R.***, Dahan, D., Tripathi, S., Spencer, S. P., Yu, B., Jain, S., Neff, N., Jha, A. R., Sonnenburg, E. D., & Sonnenburg, J. L. (2022). Ultra-deep Sequencing of Hadza Hunter-Gatherers Recovers Vanishing Microbes. *BioRxiv*, 2022.03.30.486478. <https://doi.org/10.1101/2022.03.30.486478>
3. Lou, Y. C., Hoff, J., **Olm, M. R.**, West-Roberts, J., Diamond, S., Firek, B. A., Morowitz, M. J., & Banfield, J. F. (2022). Using strain-resolved analysis to identify contamination in metagenomics data. *BioRxiv*, 2022.01.16.476537. <https://doi.org/10.1101/2022.01.16.476537>
4. 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>
5. Carter, M. M., **Olm, M. R.**, & Sonnenburg, E. D. (2022). Microbiome assembly in The Gambia. *Nature Microbiology News & Views*, 7(1), 18–19. <https://doi.org/10.1038/s41564-021-01036-1>
6. **Olm, M. R.**, & Sonnenburg, J. L. (2021). Ancient human faeces reveal gut microbes of the past. *Nature News & Views*. <https://doi.org/10.1038/d41586-021-01266-7>
7. **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>
8. Mirzayi, C., Renson, A., Furlanello, C., Sansone, S.-A., Zohra, F., Elsafoury, S., Geistlinger, L., Kasselmann, L.J., Eckenrode, K., van de Wiggert, 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>
9. 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>
10. 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>
11. 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>
12. 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>
13. 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>
 14. 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>
 15. 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>
 16. **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>
 17. 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>
 18. **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>
 19. Devoto, A. E., Santini, J. M., **Olm, M. R.**, Anantharaman, K., Munk, P., Tung, J., Archie, E. A., Turnbaugh, P. J., Seed, K. D., Blekhan, 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>
 20. 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>
 21. **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>
 22. 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>
 23. 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>
 24. 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>
 25. 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>

26. 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>
27. 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>
28. 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>
29. **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>
30. **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>
31. **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>
32. 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>
33. 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., Krukonis, 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>

* Denotes authors contributed equally to this work

INVITED PRESENTATIONS

- | | |
|------|---|
| 2022 | 7th EBAME Workshop on Computational Microbial Ecogenomics
<i>Hands-on genome dereplication and population genomics</i>
European Institute for Marine Sciences at Western Brittany University, France
(Accepted; will take place in person October 2022) |
| 2022 | Biotecmar Bioinformatics Tools and Applications Workshop
<i>Genome-resolved population genomics and strain-level comparisons</i>
All-Atlantic Joint Pilot Action AA-BIOTECMAR workshop (online presentation) |
| 2022 | Virginia Tech's Life Science Seminar Series
<i>Metagenomics of modern hunter-gatherers to understand the human microbiome</i>
Virginia Tech, Blacksburg, VA |
| 2021 | Molecular and Bioinformatic Methods in Ecology and Evolution Seminar Series
<i>Tracking microbial strains and quantifying in situ evolution with genome-resolved metagenomics</i>
University of Duisburg-Essen, Germany (online presentation) |
| 2021 | Applied Bioinformatics & Public Health Microbiology 2021
<i>Tracing the spread and evolution of microbial populations in hospital rooms and sewage with metagenomics</i>
Wellcome Genome Campus, UK (online presentation) |

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

PROFESSIONAL ACTIVITIES AND OUTREACH

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>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>

SOFTWARE DEVELOPMENT

inStrain: Population genomics analyses from metagenomic data Source Code: https://github.com/MrOlm/instrain Documentation: https://instrain.readthedocs.io 15,000+ total downloads
dRep: Rapid comparison and dereplication of genomes Source Code: https://github.com/MrOlm/drep Documentation: https://drep.readthedocs.io 20,000+ total downloads

TEACHING EXPERIENCE

2022	Guest Lecturer, Stanford University <i>MI 215: Principles of Biological Technologies</i> with Dr. Peter Sarnow
2021	Guest Lecturer, Stanford University <i>MI 221: Gut Microbiota in Health and Disease</i> with Drs. Bhatt and Sonnenburg
2021	Guest Lecturer, Stanford University <i>MI 215: Principles of Biological Technologies</i> 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

REFERENCES

Dr. Justin Sonnenburg, Postdoctoral Advisor

Professor of Microbiology and Immunology, Stanford University.

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