

# Stanford

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## Matthew Raymond Olm

Postdoctoral Research Fellow, Microbiology and Immunology

### Bio

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#### BIO

I am a bioinformatician and microbiologist interested in studying the human microbiome and fine-scale microbial population genetics. See my personal website for more info- <https://mrolm.github.io/>

#### PROFESSIONAL EDUCATION

- Doctor of Philosophy, University of California Berkeley (2019)
- Bachelor of Science, University of Pittsburgh (2014)

#### STANFORD ADVISORS

- Justin Sonnenburg, Postdoctoral Faculty Sponsor

#### LINKS

- Personal website: <https://mrolm.github.io/>

### Publications

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#### PUBLICATIONS

- **Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries.** *mSystems*  
Olm, M. R., Crits-Christoph, A., Diamond, S., Lavy, A., Matheus Carnevali, P. B., Banfield, J. F.  
2020; 5 (1)
- **Necrotizing enterocolitis is preceded by increased gut bacterial replication, Klebsiella, and fimbriae-encoding bacteria** *SCIENCE ADVANCES*  
Olm, M. R., Bhattacharya, N., Crits-Christoph, A., Firek, B. A., Baker, R., Song, Y. S., Morowitz, M. J., Banfield, J. F.  
2019; 5 (12): eaax5727
- **Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms** *MICROBIOME*  
Olm, M. R., West, P. T., Brooks, B., Firek, B. A., Baker, R., Morowitz, M. J., Banfield, J. F.  
2019; 7: 26
- **dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication** *ISME JOURNAL*  
Olm, M. R., Brown, C. T., Brooks, B., Banfield, J. F.  
2017; 11 (12): 2864–68
- **Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates** *GENOME RESEARCH*  
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; 27 (4): 601–12

- **The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis** *MBIO*  
Olm, M. R., Butterfield, C. N., Copeland, A., Boles, T., Thomas, B. C., Banfield, J. F.  
2017; 8 (1)
- **Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity.** *Genome research*  
Crits-Christoph, A., Bhattacharya, N., Olm, M. R., Song, Y. S., Banfield, J. F.  
2020
- **Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow.** *The ISME journal*  
Crits-Christoph, A., Olm, M. R., Diamond, S., Bouma-Gregson, K., Banfield, J. F.  
2020
- **Clades of huge phages from across Earth's ecosystems.** *Nature*  
Al-Shayeb, B., Sachdeva, R., Chen, L., Ward, F., Munk, P., Devoto, A., Castelle, C. J., Olm, M. R., Bouma-Gregson, K., Amano, Y., He, C., Meheust, R., Brooks, et al  
2020
- **Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut.** *PloS one*  
Sher, Y., Olm, M. R., Raveh-Sadka, T., Brown, C. T., Sher, R., Firek, B., Baker, R., Morowitz, M. J., Banfield, J. F.  
2020; 15 (3): e0229537
- **Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network** *ISME JOURNAL*  
Bouma-Gregson, K., Olm, M. R., Probst, A. J., Anantharaman, K., Power, M. E., Banfield, J. F.  
2019; 13 (6): 1618–34
- **Megaphages infect Prevotella and variants are widespread in gut microbiomes** *NATURE MICROBIOLOGY*  
Devoto, A. E., Santini, J. M., Olm, M. R., Anantharaman, K., Munk, P., Tung, J., Archie, E. A., Turnbaugh, P., Seed, K. D., Blekhman, R., Aarestrup, F. M., Thomas, B. C., Banfield, et al  
2019; 4 (4): 693–700
- **Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria** *NATURE COMMUNICATIONS*  
Carnevali, P., 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, et al  
2019; 10: 463
- **The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms** *MICROBIOME*  
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., Bonfield, J. F.  
2018; 6: 112
- **Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles** *MBIO*  
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; 9 (2)
- **Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome.** *mSystems*  
Rahman, S. F., Olm, M. R., Morowitz, M. J., Banfield, J. F.  
2018; 3 (1)
- **Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome** *NATURE COMMUNICATIONS*  
Brooks, B., Olm, M. R., Firek, B. A., Baker, R., Thomas, B. C., Morowitz, M. J., Banfield, J. F.  
2017; 8: 1814
- **Measurement of bacterial replication rates in microbial communities** *NATURE BIOTECHNOLOGY*  
Brown, C. T., Olm, M. R., Thomas, B. C., Banfield, J. F.  
2016; 34 (12): 1256–63
- **Function, expression, specificity, diversity and incompatibility of actinobacteriophage parABS systems** *MOLECULAR MICROBIOLOGY*  
Dedrick, R. M., Mavrich, T. N., Ng, W. L., Reyes, J., Olm, M. R., Rush, R. E., Jacobs-Sera, D., Russell, D. A., Hatfull, G. F.

2016; 101 (4): 625–44

● **Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isoypes** *JOURNAL OF VIROLOGY*

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, et al

2014; 88 (5): 2461–80