

**Joanne B. Emerson**

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**Education**

University of California, Berkeley, Ph.D. Earth and Planetary Science	2012
College of William and Mary, B.S. Biology	2003

**Professional Experience**

2017-present Assistant Professor, Department of Plant Pathology, University of California, Davis  
 2015-2017 Postdoctoral Researcher, University of Arizona and The Ohio State University  
 2012-2015 Postdoctoral Researcher, University of Colorado at Boulder  
 2003-2007 Research Associate, J. Craig Venter Institute/The Institute for Genomic Research

**Grants and Other External Support**

USDA NIFA AFRI Agricultural Microbiomes, “*Viruses in soil: untapped resources for understanding soil health and mitigating plant disease*” 2021-2024. #2021-67013-34815-0. (PI Emerson, Co-PI Amanda Hodson, \$749,960)

DOE EMSL Exploratory Research Program, “*Evaluating viral activity and infection dynamics during wet-up of dry grassland soils*” 2020-2021. #51641. (PI Emerson, Co-PI Christian Santos-Medellín, \$81,766)

DOE Early Career Award, “*Infective viruses and inert virions: illuminating abundant unknowns in terrestrial biogeochemical cycles*” 2020-2025. DE-SC0021198. (PI Emerson, \$750,957)

Tri-Institutional Partnership in Microbiome Research, “*Unraveling strain-level virus-host dynamics in diverse ecosystems*” 2020-2022. (PI Emerson, Co-PIs C. Titus Brown, Simon Roux, Peter Turnbaugh, \$174,795)

DOE BER Genomic Sciences, Systems Biology Enabled Research on Microbiomes in Nutrient Cycling Processes, “*Cross-Kingdom Interactions: the Foundation for Nutrient Cycling in Grassland Soils*” 2019-2022. DE-SC0020163. (PI Mary Firestone, \$643,423 to Co-PI Emerson)

DOE JGI New Investigator Community Sequencing Program, “*Elucidating Depth-Resolved Viral Links to Soil Carbon Chemistry and Crop Yields in Agricultural Systems*” 2018-2021. (PI Emerson, in-kind sequencing, ~\$50,000 equivalent)

Amway Grant, “*Evaluating the link between Cauliflower mosaic virus (CaMV) infection and false-positive GMO detection in organic farms*” 2018-2020. (PI Emerson, \$139,085)

**Teaching**

Instructor, <i>SAS 13: Disease and Society</i> , 250-350 undergraduates	W2019, W2020, W2021
Instructor, <i>GDB 187: Global Disease Biology Seminar</i> , 50 undergraduates	S2019, S2020, S2021

**Service (select examples)**

Senior Editor, <i>The ISME Journal</i>	2020-present
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- Editor, *mSystems* 2019-present  
 Review Editor, *Frontiers in Agronomy*, Plant-Soil Interactions section 2019-present  
 Review Editor, *Frontiers in Microbiology*, Aquatic Ecology section 2018-2019  
 Proposal reviewer for DOE BER, DOE PNNL (EMSL), NSF Polar Programs, NSF EpSCOR, NASA  
 Peer reviewer for *Applied and Environmental Microbiology*, *Atmospheric Environment*, *Biogeosciences*, *Biology and Fertility of Soils*, *BMC Evolutionary Biology*, *BMC Genomics*, *Boreal Environment Research*, *Communications Biology*, *Ecological Applications*, *Ecological Indicators*, *Environmental Microbiology*, *Environmental Science & Technology*, *FEMS Microbiology Ecology*, *Frontiers in Earth Science*, *Frontiers in Microbiology*, *Genome Biology and Evolution*, *Geophysical Research Letters*, *Indoor Air*, *Infection*, *Genetics*, and *Evolution*, *The ISME Journal*, *Life*, *Limnology & Oceanography*, *Microbial Ecology*, *Microbiome*, *mBio*, *mSphere*, *mSystems*, *Nature Biotechnology*, *Nature Microbiology*, *Pedosphere*, *PeerJ*, *Science of the Total Environment*, *Soil Biology and Biochemistry*, *Viruses*, and *Water Research*  
 Organizing Committee, Viral EcoGenomics and Applications (VEGA) 2017-2020  
 Symposium (part of the DOE JGI User meeting, <http://usermeeting.jgi.doe.gov>)

## Publications

\*undergraduate, §graduate student, or †postdoc in our group

- †Sorensen, J.W., †Zinke, L.A., §ter Horst, A.M., †Santos-Medellín, C., \*Schroeder, A., **Emerson, J.B.** (2021). DNase treatment improves viral enrichment in agricultural soil viromes. *submitted*.  
 (*bioRxiv* preprint: <https://www.biorxiv.org/content/10.1101/2021.06.01.446688v1.full>)
- §ter Horst, A.M., †Santos-Medellín, C., †Sorensen, J.W., †Zinke, L.A., Wilson, R.M., Johnston, E.R., Trubl, G., Pett-Ridge, J., Blazewicz, S.J., Hanson, P.J., Chanton, J.P., Schadt, C.W., Kostka, J.E., **Emerson, J.B.** (2021). Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. *submitted*.  
 (*bioRxiv* preprint: <https://www.biorxiv.org/content/10.1101/2020.12.15.422944v1.full>)
40. **Emerson, J.B.**, Varner, R.K., Wik, M., Parks, D.H., Neumann, R.B., Johnson, J.E., Singleton, C.M., Woodcroft, B.J., Tollerson II, R., Owusu-Dommey, A., Binder, N., Freitas, N.L., Crill, P.M., Saleska, S.R., Tyson, G.W., Rich, V.I. Diverse sediment microbiota shape methane emission temperature sensitivity in Arctic lakes. *Nature Communications*, *in press*.  
 (*bioRxiv* preprint: <https://www.biorxiv.org/content/10.1101/2020.02.08.934661v1>)
39. †Santos-Medellín, C., †Zinke, L.A., §ter Horst, A.M., Gelardi, D.L., Parikh, S.J., **Emerson, J.B.** (2021). Viromes outperform total metagenomes in revealing the spatiotemporal patterns of agricultural soil viral communities. *The ISME Journal*.  
<https://www.nature.com/articles/s41396-021-00897-y>
38. †Zinke, L.A., Evans, P.N., †Santos-Medellín, C., \*Schroeder, A.L., Parks, D.H., Varner, R.K., Rich, V.I., Tyson, G.W., **Emerson, J.B.** (2021). Evidence for non-methanogenic metabolisms in globally distributed archaeal clades basal to the *Methanomassiliicoccales*. *Environmental Microbiology*. 23(1):340-357.
37. Trubl, G., Stedman, K., Bywaters, K., Boston, P.J., Kaelber, J.T., Roux, S., **Emerson, J.B.**, Breitbart, M., Yin, J., Janjic, A., Sommers, P., Rodriguez-Roman, E. (2021).

- Astrovirology: Expanding the Search for Life. *Bulletin of the American Astronomical Society*. 53(4):516.
36. Wilson, R.M., Zayed, A., Krossen, K., Woodcroft, B.J., Tfaily, M., **Emerson, J.B.**, Raab, N., Hodgkins, S.B., Verbeke, B., Tyson, G.W., Crill, P.M., Saleska, S.R., Chanton, J.P., Rich, V.I. (2021). Functional capacities of microbial communities to carry out large scale geochemical processes are maintained during ex situ anaerobic incubation. *PLoS ONE*. 16(2):e0245857.
  35. †Bak, A. & **Emerson, J.B.** (2020). Cauliflower mosaic virus (CaMV) biology, management, and relevance to GM plant detection for sustainable organic agriculture. *Frontiers in Sustainable Food Systems*. 4:21.
  34. Bolduc, B., Hodgkins, S.B., Varner, R.K., Crill, P.M., McCalley, C.K., Chanton, J.P., Tyson, G.W., Riley, W.J., Palace, M., Duhaime, M.B., Hough, M.A., IsoGenie Project Coordinators, IsoGenie Project Team (including **Emerson, J.B.**), A2A Project Team, Saleska, S.R., Sullivan, M.B., Rich, V.I. (2020). The IsoGenie database: an interdisciplinary data management solution for ecosystems biology and environmental research. *PeerJ*. 8:e9467.
  33. Dundore-Arias, J.P., Eloë-Fadrosh, E., Schriml, L.M., Beattie, G.A., Brennan, F.P., Busby, P.E., Calderon, R.B., Castle, S.C., **Emerson, J.B.**, Everhart, S.E., Eversole, K., Frost, K.E., Herr, J.R., Huerta, A.I., Iyer-Pascuzzi, A.S., Kalil, A.K., Leach, J.E., Leonard, J., Maul, J.E., Prithiviraj, B., Potrykus, M., Redekar, N.R., Rojas, J.A., Silverstein, K.A.T., Tomso, D.J., Tringe, S.G., Vinatzer, B.A., Kinkel, L.L. (2020). Community-driven Metadata Standards for Agricultural Microbiome Research. *Phytobiomes Journal*. 4(2):115-121.
  32. †Bak, A.B. & **Emerson, J.B.** (2019). Multiplex quantitative PCR for single-reaction genetically modified (GM) plant detection and identification of false-positive GM plants linked to Cauliflower mosaic virus (CaMV) infection. *BMC Biotechnology*. 19(1):73.
  31. **Emerson, J.B.** (2019). Soil Viruses: A New Hope. *mSystems*. 4(3):e00120-19.
  30. Roux S., Adriaenssens, E.M., Dutilh, B.E., Koonin, E.V., Kropinski, A.M., Krupovic, M., Kuhn, J.H., Lavigne, R., Brister, J.R., Varsani, A., Amid, C., Aziz, R.K., Bordenstein, S.R., Bork, P., Breitbart, M., Cochrane, G.R., Daly, R.A., Desnues, C., Duhaime, M.B., **Emerson, J.B.**, Enault, F., Fuhrman, J.A., Hingamp, P., Hugenholtz, P., Hurwitz, B.L., Ivanova, N.N., Labonte, J.M., Lee, K.-B., Malmstrom, R.R., Martinez-Garcia, M., Mizrahi, I., Ogata, H., Paez-Espino, D., Petit, M.-A., Putonti, C., Rattei, T., Reyes, A., Rodriguez-Valera, F., Rosario, K., Schriml, L., Schulz, F., Steward, G.F., Sullivan, M.B., Sunagawa, S., Suttle, C.A., Temperton, B., Tringe, S.G., Thurber, R.V., Webster, N.S., Whiteson, K.L., Wilhelm, S.W., Wommack, K.E., Woyke, T., Wrighton, K.C., Yilmaz, P., Yoshida, T., Young, M.J., Yutin, N., Zeigler-Allen, L., Kyrpides, N.C., Eloë-Fadrosh, E.A. (2019). Minimum Information about an Uncultivated Virus Genome (MIUViG): a community consensus on standards and best practices for describing genome sequences from uncultivated viruses. *Nature Biotechnology*. 37(1):29.
  29. Trubl, G., Jang, H.B., Roux, S., **Emerson, J.B.**, Solonenko, N., Vik, D.R., Solden, L.M., Ellenbogen, J., Runyon, A.T., Bolduc, B.J., Woodcroft, B.J., Saleska, S.R., Tyson, G.W., Wrighton, K.C., Sullivan, M.B., Rich, V.I. (2018). Soil viruses are underexplored players in ecosystem carbon cycling. *mSystems*. 3(5):e00076-18.

28. **Emerson, J.B.**, Roux, S., Brum, J.R., Bolduc, B., Woodcroft, B.J., Jang, H.B., Singleton, C.M., Solden, L.M., Naas, A.E., Boyd, J.A., Hodgkins, S.B., Wilson, R.M., Trubl, G., Li, C., Frolking, S., Pope, P.B., Wrighton, K.C., Crill, P.M., Chanton, J.P., Saleska, S.R., Tyson, G.W., Rich, V.I., Sullivan, M.B. (2018). Host-linked soil viral ecology along a permafrost thaw gradient. *Nature Microbiology*. 3(8):870.
27. Woodcroft, B.J., Singleton, C.M., Boyd, J.A., Evans, P.N., **Emerson, J.B.**, Zayed, A.A.F., Hoelzle, R.D., Lambertson, T.O., McCalley, C.K., Hodgkins, S.B., Wilson, R.M., Purvine, S.O., Nicora, C.D., Li, C., Frolking, S., Chanton, J.P., Crill, P.M., Saleska, S.R., Rich, V.I., Tyson, G.W. (2018). Genome-centric view of carbon processing in thawing permafrost. *Nature*. 560(7716):49.
26. Clements, N., Keady, P., **Emerson, J.B.**, Fierer, N., Miller, S.L. (2018). Seasonal variability of airborne particulate matter and bacterial concentrations in Colorado homes. *Atmosphere*. 9(4):133.
25. Probst, A.J., Ladd, B., Jarett, J.K., Geller-McGrath, D.E., Sieber, C.M.K., **Emerson, J.B.**, Anantharaman, K., Thomas, B.C., Malmstrom, R.R., Stieglmeier, M., Klingl, A., Woyke, T., Ryan, C.M., Banfield, J.F. (2018). Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. *Nature Microbiology*. 3:328-336.
24. Roux, S., **Emerson, J.B.**, Eloie-Fadrosh, E.A., Sullivan, M.B. (2017). Benchmarking viromics: An *in silico* evaluation of metagenome-enabled estimates of viral community composition and diversity. *PeerJ*. 5:e3817.
23. **Emerson, J.B.**, Adams, R.I., Betancourt Roman, C.M., Brooks, B.B., Coil, D.A., Dahlhausen, K., Ganz, H.H., Hartmann, E.M., Hsu, T., Justice, N.B., Paulino Lima, I.G., Luongo, J.C., Lymperopoulou, D., Gomez Silvan, C., Rothschild-Mancinelli, B., Balk, M., Huttenhower, C., Nocker, A., Vaishampayan, P., Rothschild, L.J. (2017). Schrödinger's microbes: Tools for distinguishing the living from the dead in microbial ecosystems. *Microbiome*. 5:86.
22. **Emerson, J.B.**, Keady, P.B., Clements, N., Morgan, E.E., Awerbuch, J., Miller, S.L., Fierer, N. (2017). High temporal variability in airborne bacterial diversity and abundance inside single-family residences. *Indoor Air*. 27(3):576-586.
21. Vik, D.R., Roux, S., Brum, J.R., Bolduc, B., **Emerson, J.B.**, Padilla, C.C., Stewart, F.J., Sullivan, M.B. (2017). Putative archaeal viruses from the mesopelagic ocean. *PeerJ*. 5:e3428.
20. Probst, A.J., Castelle, C.J., Singh, A., Brown, C.T., Anantharaman, K., Sharon, I., Hug, L.A., Burstein, D., **Emerson, J.B.**, Thomas, B.C., Banfield, J.F. (2017). Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO<sub>2</sub> concentrations. *Environmental Microbiology*. 19(2):459-474.
19. **Emerson, J.B.**, Thomas, B.C., Alvarez, W., Banfield, J.F. (2016). Metagenomic analysis of a high carbon dioxide subsurface microbial community populated by chemolithoautotrophs and bacteria and archaea from candidate phyla. *Environmental Microbiology*. 18(6):1686-1703.
18. Andrade, K., Logemann, J., Heidelberg, K.B., **Emerson, J.B.**, Comolli, L.R., Hug, L.A., Probst, A.J., Keillor, A., Thomas, B.C., Miller, C.S., Allen, E.E., Moreau, J.W., Brocks, J.J., Banfield, J.F. (2015). Metagenomic and lipid analyses reveal a diel cycle in a

- hypersaline microbial ecosystem. *The ISME Journal*. 9:2697-2711.
17. **Emerson, J.B.**, Keady, P.B., Brewer, T.E., Clements, N., Morgan, E.E., Awerbuch, J., Miller, S.L., Fierer, N. (2015). Impacts of flood damage on airborne bacteria and fungi in homes after the 2013 Colorado Front Range flood. *Environmental Science & Technology*. 49(5):2675-2684.
  16. Tully, B., **Emerson, J.B.**, Andrade, K., Brocks, J.J., Allen, E.E., Banfield, J.F., Heidelberg, K.B. (2014). De novo sequences of *Haloquadratum walsbyi* from Lake Tyrrell, Australia reveal a variable genomic landscape. *Archaea*. 2014:875784.
  15. Probst, A.J., Weinmaier, T., Raymann, K., Perras, A., **Emerson, J.B.**, Rattei, T., Wanner, G., Klingl, A., Berg, I., Yoshinaga, M., Viehweger, B., Hinrichs, K., Thomas, B.C., Meck, S., Auerbach, A.K., Heise, M., Schintlmeister, A., Schmid, M., Wagner, M., Gribaldo, S., Banfield, J.F., Moissl-Eichinger, C. (2014). Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. *Nature Communications*. 5:5497.
  14. Podell, S., **Emerson, J.B.**, Jones, C.M., Ugalde, J.A., Welch, S., Heidelberg, K.B., Banfield, J.F., Allen, E.E. (2014). Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. *The ISME Journal*. 8(5):979-990.
  13. Bowers, R.M., Clements, N., **Emerson, J.B.**, Wiedinmyer, C., Hannigan, M.P., Fierer, N. (2013). Seasonal variability in the bacterial and fungal diversity of the near-surface atmosphere. *Environmental Science & Technology*. 47(21):12097-12106.
  12. Doll, H.M., Armitage, D.W., Daly, R.A., **Emerson, J.B.**, Goltsman, D.A., Yelton, A.P., Kerekes, J., Firestone, M.K., Potts, M.D. (2013). Utilizing novel diversity estimators to quantify multiple dimensions of microbial biodiversity across domains. *BMC Microbiology*. 13:259.
  11. **Emerson, J.B.**, Thomas, B.C., Andrade, K., Heidelberg, K.B., Banfield, J.F. (2013). New approaches indicate constant viral diversity despite shifts in assemblage structure in an Australian hypersaline lake. *Applied and Environmental Microbiology*. 79(21):6755-6764.
  10. **Emerson, J.B.**, Andrade, K., Thomas, B.C., Norman, A., Allen, E.E., Heidelberg, K.B., Banfield, J.F. (2013). Virus-host and CRISPR dynamics in archaea-dominated hypersaline Lake Tyrrell, Victoria, Australia. *Archaea*. 2013:370871.
  9. Heidelberg, K.B., Nelson, W.C., Holm, J.B., Eisenkolb, N., Andrade, K., **Emerson, J.B.** (2013). Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. *Frontiers in Microbiology*. 13(4):115.
  8. **Emerson, J.B.**, Thomas, B.C., Andrade, K., Allen, E.E., Heidelberg, K.B., Banfield, J.F. (2012). Dynamic viral populations in hypersaline systems as revealed by metagenomic assembly. *Applied and Environmental Microbiology*. 78(17):6309-6320.
  7. Narasingarao, P., Podell, S., Ugalde, J.A., Brochier-Armanet, C., **Emerson, J.B.**, Brocks, J.J., Heidelberg, K.B., Banfield, J.F., Allen, E.E. (2012). *De novo* metagenomic assembly reveals abundant, novel major lineage of Archaea in hypersaline microbial communities. *The ISME Journal*. 6(1):81-93.
  6. Bik, E.M., Long, C.D., Armitage, G.C., Loomer, P., **Emerson, J.**, Mongodin, E.F., Nelson, K.E., Gill, S.R., Fraser-Liggett, C.M., and Relman, D.A. (2010). Bacterial diversity in the oral cavity of 10 healthy individuals. *The ISME Journal*. 4(8):962-974.

5. Brulc, J.M., Antonopoulos, D.A., Berg Miller, M.E., Wilson, M.K., Yannarell, A.C., Dinsdale, E.A., Edwards, R.E., Frank, E.D., **Emerson, J.B.**, Wacklin, P., Coutinho, P.M., Henrissat, B., Nelson, K.E., White, B.A. (2009). Gene-centric metagenomics of the fiber adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. *Proceedings of the National Academy of Sciences*. 106(6):1948-1953.
4. DeBoy, R.T., Mongodin, E.F., Fouts, D., Tailford, L., Khouri, H., **Emerson, J.B.**, Mohamoud, Y., Watkins, K., Henrissat, B., Gilbert, H.J., Nelson, K.E. (2008). Insights into plant cell wall degradation from the genome sequence of the soil bacterium *Cellvibrio japonicus*. *Journal of Bacteriology*. 190(15):5455-5463.
3. Mongodin, E.F., Shapir, N., Daugherty, S.C., DeBoy, R.T., **Emerson, J.B.**, Shvartzbeyn, A., Radune, D., Vamathevan, J., Riggs, F., Grinberg, V., Khouri, H., Wackett, L.P., Nelson, K.E., Sadowsky, M.J. (2006). Secrets of soil survival revealed by the genome sequence of *Arthrobacter aurescens* TC1. *PLoS Genetics*. 2(12):e214.
2. DeBoy, R.T., Mongodin, E.F., **Emerson, J.B.**, Nelson, K.E. (2006). Chromosome evolution in the Thermotogales: large-scale inversions and strain diversification of CRISPR sequences. *Journal of Bacteriology*. 188(7):2364-2374.
1. Mongodin, E.F., **Emerson, J.B.**, Nelson, K.E. (2005). Microbial metagenomics. *Genome Biology*. 6(10):347.1-347.3.