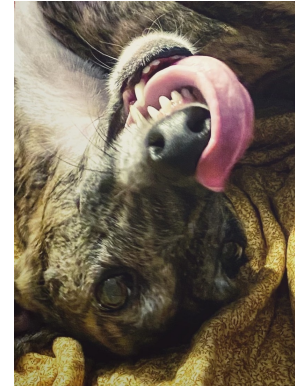


**CONTACT INFORMATION**

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**EDUCATION**

- 2007 **Ph.D., Environmental Engineering** (with minors in microbiology and bioengineering)  
University of California, Berkeley, CA, USA
- 2002 **M.S.E, Environmental Engineering**  
University of Michigan, Ann Arbor, MI, USA
- 2000 **B.S., Civil Engineering** (with environmental emphasis)  
Iowa State University, Ames, IA, USA

**PROFESSIONAL POSITIONS**

- 2014 – present **Senior Scientist / Group Leader**  
Swiss Federal Institute of Aquatic Science and Technology (Eawag), Dübendorf, Switzerland  
Department of Environmental Microbiology  
Microbial Community Assembly Group
- 2014 – present **Lecturer**  
Swiss Federal Institute of Technology (ETHZ), Zürich, Switzerland  
Department of Environmental Systems Science  
Institute of Biogeochemistry and Pollutant Dynamics
- 2016 – 2017 **Sabbatical Visiting Scientist**  
University of Michigan, Ann Arbor, MI, USA  
Department of Civil and Environmental Engineering  
Host: Prof. Dr. Lutgarde Raskin
- 2009 – 2014 **Junior Group Leader (Oberassistent)**  
Swiss Federal Institute of Technology (ETHZ), Zürich, Switzerland  
Department of Environmental Systems Science  
Institute of Biogeochemistry and Pollutant Dynamics  
Supervisor: Prof. Dr. Martin Ackermann
- 2007 – 2009 **Postdoctoral Researcher and Lecturer**  
University of Lausanne, Lausanne, Switzerland  
Department of Fundamental Microbiology  
Supervisor: Prof. Dr. Jan Roelof van der Meer

- 2004 – 2007 **Guest Researcher**  
Lawrence Berkeley National Laboratory, Berkeley, CA, USA  
Earth Sciences Division  
Ecology Department  
Host: Dr. Gary Andersen
- 2003 – 2007 **Research and Teaching Assistant,**  
University of California, Berkeley, CA, USA  
Department of Civil and Environmental Engineering  
Supervisor: Prof. Dr. Lisa Alvarez-Cohen
- 2001 – 2002 **Research Assistant**  
University of Michigan, Ann Arbor, MI, USA  
Department of Civil and Environmental Engineering  
Supervisor: Prof. Dr. Linda M. Abriola
- 1999 – 2000 **Laboratory Assistant**  
Iowa State University, Ames, IA, USA  
Department of Civil, Construction, and Environmental Engineering  
Supervisor: Prof. Dr. Say-Kee Ong

#### EDITORIAL POSITIONS

- 2021 – present **Current Opinion in Biotechnology**  
Editorial Board Member
- 2020 – present **The ISME Journal**  
Editorial Board Member

#### SCIENTIFIC BOARD/COMMISSION POSITIONS

- 2020 – present **European Federation of Biotechnology**  
Invited board member of the Environmental Biotechnology Division
- 2020 – present **Swiss Society for Microbiology**  
Member of the Lay Communication Section
- 2017 – present **Swiss Society for Microbiology**  
Elected head of the Environmental Microbiology Section
- 2014 – 2017 **IWA specialist group on Microbial Ecology in Water Engineering**  
Elected member of the management committee

#### AWARDS

1. Goldene Eule (Golden Owl), VSETH, ETH Zürich, 2020
2. Cover Image (Issue), *Philosophical Transactions of the Royal Society B*, 2020
3. Cover Image (Issue), *Communications Biology*, 2020
4. Cover Image (Volume), *The ISME Journal*, 2016

**TEACHING**

- Spring terms     **Environmental Microbiology Practical**  
 2010 – present    Department of Environmental Systems Science, ETHZ, Zürich, Switzerland  
 Co-led by Prof. Dr. Martin Ackermann, Dr. David R. Johnson, Dr. Frederik Hammes, and Dr. Tim Julian
- Autumn terms    **Eawag PhD Skills**  
 2014 – 2015      Department of Environmental Systems Science, ETHZ, Zürich, Switzerland  
 Led by Dr. David R. Johnson

**PEER-REVIEWED JOURNAL PUBLICATIONS**

1. Wang M, Chen X, Ma Y, Tang YQ, **Johnson DR**, Nie Y, Wu XL (2022) Type IV pilus shapes a ‘bubble-jet’ pattern opposing spatial intermixing of two interacting bacterial populations. *Microbiol Spectr.* *In press.*
2. Ciccacese D, Micali G, Borer B, Ruan C, Or D, **Johnson DR** (2022) Rare and localized events stabilize microbial community composition and patterns of spatial self-organization in a fluctuating environment. *ISME J.* *In press.*
3. Chen G, Hu Z, Ebrahimi A, **Johnson DR**, Wu F, Sun Y, Shen R, Liu L, Wang G (2022) Chemotactic movement and zeta potential dominate *Chlamydomonas microspheara* attachment and biocathode development. *Environ Technol.* *In press.*
4. Chen G, Hu Z, Ebrahimi A, **Johnson DR**, Wu F, Sun Y, Shen R, Liu L, Wang G (2022) Electrotaxis-mediated cell motility and nutrient availability determine *Chlamydomonas microspheara*-surface interactions in bioelectrochemical systems. *Bioelectrochem.* 143: 107989.
5. Ruan C, Ramoneda J, Chen G, **Johnson DR**, Wang G (2021) Evaporation-induced hydrodynamics promote conjugation-mediated plasmid transfer in microbial populations. *ISME Commun.* 1: 54.
6. Goldschmidt F, Caduff L, **Johnson DR** (2021) Causes and consequences of pattern diversification in a spatially self-organizing microbial community. *ISME J.* 15: 2415-2426.
7. Dubey M, Hadadi N, Pelet S, Carraro N, **Johnson DR**, van der Meer JR (2021) Environmental connectivity controls diversity in soil microbial communities. *Commun Biol.* 4: 492.
8. Borer B, Ciccacese D, **Johnson D**, Or D (2020) Spatial organization in microbial range expansion emerges from trophic dependencies and successful lineages. *Commun Biol.* 3: 685.
9. **Johnson DR**, Pomati F (2020) A brief guide for the measurement and interpretation of microbial functional diversity. *Environ Microbiol.* 22: 3039-3048.
10. Ciccacese D, Zuidema A, Merlo V, **Johnson DR** (2020) Interaction-dependent effects of surface structure on microbial spatial self-organization. *Philos Trans Royal Soc B.* 375: 20190246.
11. **Johnson DR**, Noack S (2020) Editorial overview: Causes and biotechnological application of microbial metabolic specialization. *Curr Opin Biotechnol.* 62: iii-vi.
12. Achermann S, Mansfeldt CB, Müller M, **Johnson DR**, Fenner K (2020) Relating metatranscriptomic profiles to the micropollutant biotransformation potential of complex microbial communities. *Environ Sci Technol.* 54: 235-244.
13. Wu L, Ning D, Zhang B, Li Y, Zhang P, Shan X, Zhang Q, Brown MR, Li Z, Van Nostrand JD, Ling F, Xiao N, Zhang Y, Vierheilig J, Wells GF, Yang Y, Deng Y, Tu Q, Wang A, **Global Water Microbiome Consortium**, Zhang T, He Z, Keller J, Nielsen PH, Alvarez PJJ, Criddle CS, Wagner M, Tiedje JM, He Q, Curtis TP, Stahl DA, Alvarez-Cohen L, Rittmann BE,

- Wen X, Zhou J (2019) Global diversity and biogeography of bacterial communities in wastewater treatment plants. *Nat Microbiol.* 4: 1183-1195.
14. Mansfeldt C, Achermann S, Men Y, Walser JC, Villez K, Joss A, **Johnson DR**, Fenner K (2019) Microbial residence time is a controlling parameter of the taxonomic composition and functional profile of microbial communities. *ISME J.* 13: 1589-1601.
  15. Ju F, Beck K, Yin X, Maccagnan A, McArdell CS, Singer H, **Johnson DR**, Zhang T, Bürgmann H (2019) Wastewater treatment plant resistomes are shaped by bacterial composition, genetic exchange, and upregulated expression in the effluent microbiomes. *ISME J.* 13: 346-360.
  16. Lilja EE, **Johnson DR** (2019) Substrate cross-feeding affects the speed and trajectory of molecular evolution within a synthetic microbial assemblage. *BMC Evol Biol.* 19: 129.
  17. Tecon R, Mitri S, Ciccarese D, Or D, van der Meer JR, **Johnson DR** (2019) Bridging the holistic-reductionist divide in microbial ecology. *mSystems.* 4: e00265-18.
  18. Patsch D, van Vliet S, Marcantini LG, **Johnson DR** (2018) Generality of associations between biological richness and the rates of metabolic processes across microbial communities. *Environ Microbiol.* 20: 4356-4368.
  19. Goldschmidt F, Regoes R, **Johnson DR** (2018) Metabolite toxicity slows local diversity loss during expansion of a microbial cross-feeding community. *ISME J.* 12: 136-144.
  20. Wells GF, Shi YJ, Lauren M, Weissbrodt DG, Joss A, Bürgmann H, **Johnson DR**, Morgenroth E (2017) Comparing the resistance, resilience, and stability of replicate moving bed biofilm and suspended growth combined nitrification-anammox reactors. *Environ Sci Technol.* 51: 5108-5117.
  21. Goldschmidt F, Regoes R, **Johnson DR** (2017) Successive range expansion promotes diversity and accelerates evolution in spatially structured microbial populations. *ISME J.* 11: 2112-2123.
  22. Marchal M, Selina Derksen, Sven Panke, Ackermann M, **Johnson DR** (2017) A passive mutualistic interaction promotes the evolution of spatial structure within microbial populations. *BMC Evol Biol.* 17: 106.
  23. Lilja EE, **Johnson DR** (2017) Metabolite toxicity determines the pace of molecular evolution within microbial populations. *BMC Evol Biol.* 17: 52.
  24. Men Y, Achermann S, Helbling DE, **Johnson DR**, Fenner K (2017) Relative contribution of ammonia oxidizing bacteria and other members of nitrifying activated sludge communities to micropollutant biotransformation. *Water Res.* 109: 217-226.
  25. Men Y, Han P, Helbling DE, Jehmlich N, Herbold C, Guide R, Onnis-Hayden A, Gu AZ, **Johnson DR**, Wagner M, Fenner K. (2016) Biotransformation of two pharmaceuticals by the ammonia-oxidizing archaeon *Nitrososphaera gargensis*. *Environ Sci Technol.* 50: 4682-4692.
  26. Filippidou S, Bueche M, Wunderlin T, Junier T, Roussel-Delif L, Jeanneret N, Dorador C, Molina V, Ioannidou A, Vargemezis G, **Johnson DR**, Junier P (2016) A combination of extreme environmental conditions favor the prevalence of endospore-forming firmicutes. *Front Microbiol.* 7: 1707.
  27. Dolinšek J, Goldschmidt F, **Johnson DR** (2016) Synthetic microbial ecology and the dynamic interplay between microbial genotypes. *FEMS Microbiol Rev.* 40: 961-979.
  28. Kinnunen M, Dechesne A, Proctor C, Hammes F, **Johnson DR**, Quintela-Baluja M, Graham D, Daffonchio D, Fodelianakis S, Hahn N, Boon N, Smets BF (2016) A conceptual framework for invasion in microbial communities. *ISME J.* 10: 2773-2775.

29. Widder S, Allen R, Pfeiffer T, Curtis TP, Wiuf C, Sloan WT, Cordero OX, Brown SP, Momeni B, Shou W, Kettle H, Flint HJ, Haas AF, Laroche B, Kreft JU, Rainey PB, Freilich S, Schuster S, Milferstedt K, van der Meer JR, Grosskopf T, Huisman J, Free A, Picioreanu C, Quince C, Klapper I, Labarthe S, Smets BF, Wang H, **Isaac Newton Institute Fellows**, Soyer OS (2016) Challenges in microbial ecology: building predictive understanding of community function and dynamics. *ISME J.* 10: 2557-2568.
30. Lindemann SR, Bernstein HC, Song HS, Fredrickson JK, Fields MW, Shou W, **Johnson DR**, Beliaev AS (2016) Engineering microbial consortia for controllable outputs. *ISME J.* 10: 2077-2084.
31. Lilja EE, **Johnson DR** (2016) Segregating metabolic processes into different microbial cells accelerates the consumption of inhibitory substrates. *ISME J.* 10: 1568-1578.
32. **Johnson DR**, Lee TK, Park J, Fenner K, Helbling DE (2015) The functional and taxonomic richness of wastewater treatment plant microbial communities are associated with each other and with ambient nitrogen and carbon availability. *Environ Microbiol.* 17: 4851-4860.
33. **Johnson DR**, Helbling DE, Men Y, Fenner K (2015) Can meta-omics help to establish causality between contaminant biotransformations and genes or gene products? *Environ Sci: Water Res Technol.* 1: 272-278.
34. **Johnson DR**, Helbling DE, Lee TK, Park J, Fenner K, Kohler HPE, Ackermann M (2015) Association of biodiversity with the rates of micropollutant biotransformations among full-scale wastewater treatment plant communities. *Appl Environ Microbiol.* 81: 666-675.
35. Helbling DE, **Johnson DR**, Lee TK, Scheidegger A, Fenner K (2015) A framework for establishing predictive relationships between specific bacterial 16S rRNA sequence abundances and biotransformation rates. *Water Res.* 70: 471-484.
36. West KA, Lee PKH, **Johnson DR**, Zinder SH, Alvarez-Cohen L (2013) Global gene expression of *Dehalococcoides* within a robust dynamic TCE-dechlorinating community under conditions of periodic substrate supply. *Biotechnol Bioeng.* 110: 1333-1341.
37. Coronado E, Roggo C, **Johnson DR**, van der Meer JR (2012) Genome-wide analysis of salicylate and dibenzofuran metabolism in *Sphingomonas wittichii* RW1. *Front Microbiol.* 3: 300.
38. Fida TT, Breugelmans P, Lavigne R, Coronado E, **Johnson DR**, van der Meer JR, Mayer AP, Heipieper HJ, Hofkens J, Springael D (2012) Exposure to solute stress affects genome-wide expression but not the polycyclic aromatic hydrocarbon-degrading activity of *Sphingomonas* sp. LH128 in biofilms. *Appl Environ Microbiol.* 78: 8311-8320.
39. Helbling DE, Ackermann M, Fenner K, Kohler HPE, **Johnson DR** (2012) The activity level of a microbial community function can be predicted from its metatranscriptome. *ISME J.* 6: 902-904.
40. Helbling DE, **Johnson DR**, Honti M, Fenner K (2012) Micropollutant biotransformation kinetics associate with WWTP process parameters and microbial community characteristics. *Environ Sci Technol.* 46: 10579-10588.
41. **Johnson DR**, Goldschmidt F, Lilja EE, Ackermann M (2012) Metabolic specialization and the assembly of microbial communities. *ISME J.* 6: 1985-1991.
42. Men Y, Feil H, VerBerkmoes NC, Shah MB, **Johnson DR**, Lee PK, West KA, Zinder SH, Andersen GL, Alvarez-Cohen L (2012) Sustainable syntrophic growth of *Dehalococcoides ethenogenes* strain 195 with *Desulfovibrio vulgaris* Hildenborough and *Methanobacterium congolense*: global transcriptomic and proteomic analysis. *ISME J.* 6: 410-421.
43. **Johnson DR**, Coronado E, Moreno-Forero SK, Heipieper HJ, van der Meer JR (2011) Transcriptome and membrane fatty acid analyses reveal different strategies for responding to permeating and non-permeating solutes in the bacterium *Sphingomonas wittichii*. *BMC Microbiol.* 11: 250.

44. Gaillard M, Pradervand N, Minoia M, Sentchilo V, **Johnson DR**, van der Meer JR (2010) Transcriptome analysis of the mobile genome ICE<sub>clc</sub> in *Pseudomonas knackmussii* B13. *BMC Microbiol.* 10: 153.
45. **Johnson DR**, Czechowska K, Chèvre N, van der Meer JR (2009) Toxicity of triclosan, penconazole, and metalaxyl on *Caulobacter crescentus* and a freshwater microbial community as assessed by flow cytometry. *Environ Microbiol.* 11: 1682-1691.
46. **Johnson DR**, Nemir A, Andersen GL, Zinder SH, Alvarez-Cohen L (2009) Transcriptomic microarray analysis of corrinoid responsive genes in *Dehalococcoides ethenogenes* strain 195. *FEMS Microbiol Lett.* 294: 198-206.
47. Czechowska K, **Johnson DR**, van der Meer JR (2008) Use of flow cytometric methods for single-cell analysis in environmental microbiology. *Curr Opin Microbiol.* 11: 205-212.
48. **Johnson DR**, Brodie EL, Hubbard AE, Andersen GL, Zinder SH, Alvarez-Cohen L (2008) Temporal transcriptomic microarray analysis of “*Dehalococcoides ethenogenes*” strain 195 during the transition into stationary phase. *Appl Environ Microbiol.* 74: 2864-2872.
49. West KA, **Johnson DR**, Hu P, DeSantis TZ, Brodie EL, Lee PKH, Feil H, Andersen GL, Zinder SH, Alvarez-Cohen L (2008) Comparative genomics of “*Dehalococcoides ethenogenes*” 195 and an enrichment culture containing unsequenced “*Dehalococcoides*” strains. *Appl Environ Microbiol.* 74: 3490-3496.
50. **Johnson DR**, Park J, Kukor JJ, Abriola LM (2006) Effect of carbon starvation on toluene degradation activity by toluene monooxygenase-expressing bacteria. *Biodegradation.* 17: 437-445.
51. Lee PKH, **Johnson DR**, Holmes VF, He J, Alvarez-Cohen L (2006) Reductive dehalogenase gene expression as a biomarker for physiological activity of *Dehalococcoides* spp. *Appl Environ Microbiol.* 72: 6161-6168.
52. Pecson BM, Barrios JA, **Johnson DR**, Nelson KL (2006) A real-time PCR method for quantifying viable *Ascaris* eggs using the first internally-transcribed spacer region of rRNA. *Appl Environ Microbiol.* 72: 7864-7872.
53. **Johnson DR**, Lee PKH, Holmes VF, Alvarez-Cohen L (2005) An internal reference technique for accurately quantifying specific mRNAs by real-time PCR with application to the *tceA* reductive dehalogenase gene. *Appl Environ Microbiol.* 71: 3866-3871.
54. **Johnson DR**, Lee PKH, Holmes VF, Fortin AC, Alvarez-Cohen L (2005) Transcriptional expression of the *tceA* gene in a *Dehalococcoides*-containing microbial enrichment. *Appl Environ Microbiol.* 71: 7145-7151.

## BOOK CHAPTERS

55. Ciccarese D, **Johnson DR** (2019) Functional microbial landscapes. In *Comprehensive Biotechnology 3<sup>rd</sup> ed.* Ed. Moo-Young M. Elsevier: Pergamon.
56. Müller S, **Johnson DR** (2011) Application of cytomics to separate natural microbial communities by their physiological properties. In *Handbook of Molecular Microbial Ecology Vol I: Metagenomics and Complementary Approaches.* Ed. de Bruijn FJ. Wiley-Blackwell.
57. **Johnson DR** (2009) Transcriptome analysis using high-density oligonucleotide microarrays. In *Handbook of Hydrocarbon and Lipid Microbiology Vol 5: Experimental Protocols and Appendices.* Eds. Timmis KN, McGenity T, van der Meer JR, de Lorenzo V. Springer.

**REVIEWING ACTIVITIES**Peer-Reviewed Scientific Journals

Over thirty scientific journals, including *Science*, *Proceedings of the National Academy of Sciences USA*, *Nature Communications*, *Nature Microbiology*, *Nature Ecology & Evolution*, *Current Biology*, *The ISME Journal*, and *Environmental Science & Technology*.

**CONFERENCE ORGANIZING**

1. Member of the local organizing committee for the 18<sup>th</sup> International Symposium on Microbial Ecology (ISME), Lausanne, Switzerland (2022)
2. President of the organizing committee for the Annual Assembly of the Swiss Society for Microbiology, Virtual (2021)
3. Member of the International Scientific Committee for the 11<sup>th</sup> International Conference on Environmental Engineering and Management, Muttenz, Switzerland (2021)
4. Member of the organizing committee for the Annual Assembly of the Swiss Society for Microbiology, Zürich, Switzerland (2019)
5. Member of the organizing committee for the Annual Assembly of the Swiss Society for Microbiology, Lausanne, Switzerland (2018)
6. Member of the organizing committee for the Eawag Symposium, Dübendorf, Switzerland (2017)
7. Member of the organizing committee for the Eawag Symposium, Dübendorf, Switzerland (2016)
8. Member of the organizing committee for the Eawag Symposium, Dübendorf, Switzerland (2015)
9. Member of the organizing committee for the 6<sup>th</sup> Swiss Microbial Ecology Meeting, Ascona, Switzerland (2015)
10. Member of the organizing committee for the Eawag Symposium, Dübendorf, Switzerland (2014)
11. Member of the organizing committee for the Eawag Symposium, Dübendorf, Switzerland (2013)
12. Member of the organizing committee for the 5<sup>th</sup> Swiss Microbial Ecology Meeting, Neuchatel, Switzerland (2013)
13. Member of the organizing committee for the Eawag Symposium, Dübendorf, Switzerland (2012)

**PROFESSIONAL MEMBERSHIPS AND AFFILIATIONS**

1. American Society for Microbiology (ASM)
2. Federation of European Microbiological Societies (FEMS)
3. International Society for Microbial Ecology (ISME)
4. Swiss Society for Microbiology (SSM)
5. Global Water Microbiome Consortium