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EDUCATION AND EMPLOYMENT

2021-present: Associate Professor, Dept. of Integrative Biology and Dept. of Marine Science, UT Austin
2015-2021: Assistant Professor, Dept. of Marine Science, Univ. of Texas Austin, Marine Science Institute
2014-2015: Senior Research Fellow, Dept. Marine Science, Univ. of Texas Austin, Marine Science Institute
2010-2014: Ph.D. Student, Dept. of Earth and Environmental Sciences, Univ. of Michigan, Ann Arbor, MI
2002-2010: Research Associate IV, Dept. Earth and Planetary Sciences, Univ. of California Berkeley
1997-2000: M.S. Student, Dept. Biological Sciences, Univ. of Wisconsin Milwaukee, WI
1997: B.S. Student, Dept. of Biological Sciences, Univ. of Wisconsin-Milwaukee, WI

PUBLICATIONS (non-peer review articles are not numbered, members of my lab are in italics)

2026

- Baker BJ, Anda VA. (2026) Metabolism of our microbial ancestors. **Nature**, in press.
88. *Anda V, Aguilar-Pine E, Appler K, Halverson G, Baker BJ.* (2026) The archaeal roots of eukaryotic life. **Proc Natl Acad Sci** *In press.*
87. *Appler KE, Lingford JP, Gong X, Panagiotou K, Leao P, Langwig M, Greening C, Ettema TJG, Anda V, Baker BJ.* (2026) Oxygen metabolism in descendants of the archaeal-eukaryotic ancestor. **Nature** <https://doi.org/10.1038/s41586-026-10128-z>
86. Koestlbacher S, van Hooff JJE, Panagiotou K, Tamarit D, *Anda V, Appler KE, Baker BJ, Ettema TJG.* (2026) Prediction of eukaryotic cellular complexity in Asgard archaea using structural modelling. **Nature Microbiology** <https://doi.org/10.1038/s41564-026-02273-y>
85. Garcia PS, *Anda V, Baker BJ, Gribaldo S, Borrel G.* (2026) Evolution and diversity of oxidoreductases involved in redox balance and energy conservation. **Nature Ecology and Evolution** <https://doi.org/10.1038/s41559-025-02969-0>

2025

84. *Langwig MV, Anda VD, Sneed S, Seitz KW, Rasmussen A, Anantharaman K, Francis, CA, Baker BJ.* (2025) Metabolic capacity is maintained despite shifts in microbial diversity in estuary sediments. **ISME Comm.** Ycaf182 10.1093/ismeco/ycaf182
82. Acosta DJ, Daryl R. Barth, Bondy J, *Appler KE, Anda V, Ngo PHT, Alper HS, Baker BJ, Edward M. Marcotte, Ellington AD* (2025) Plastic degradation by enzymes from uncultured deep sea microorganisms. **ISME J.** 19, wraf068. <https://doi.org/10.1093/ismejo/wraf068>
81. *Rohwer RR, Kirkpatrick M, Sarcia SL, Kellom M, McMahon KD, Baker BJ.* (2025) Two decades of bacterial ecology and evolution in a freshwater lake. **Nature Microbiology** 10, 246-257. <https://doi.org/10.1038/s41564-024-01888-3>
80. Zhou Z, Tran PQ, Martin C, *Rohwer RR, Baker BJ, McMahon KD, Anantharaman K.* (2025) Unravelling viral ecology and evolution over 20 years in a freshwater lake. **Nature Microbiology** 10, 231-245. <https://doi.org/10.1038/s41564-024-01876-7>

2024

79. *Baker BJ, Sarno NO.* (2024) Small archaea may form intimate partnerships to maximize their metabolic potential. **mBio** 0:e00347-24 10.1128/mbio.00347-24
78. *Baker BJ, Hyde E, Leao P.* Nature should be the model for microbial sciences (2024) **J. Bacteriology** 0:e00228-24 10.1128/jb.00228-24
77. Valentin-Alvarado LE, Shi L-D, *Appler KE, Crits-Christoph A, Anda V, Leão P, Rohan Sachdeva, Schoelmerich MC, Roberts RJ, Baker BJ, Savage DF, and Banfield JF.* (2024) Complete genomes of Asgard

- archaea reveal diverse integrated and mobile genetic elements. **Genome Research** 34, 1-15. 10.1101/gr.279480.124
76. Valentin-Alvarado LE, *Appler KE, Anda VD, Schoelmerich MC, West-Roberts J, Kivenson V, Crists-Christoph A, Ly L, Sachdeva R, Savage DF, Baker BJ, Banfield JF.* (2024) Asgard archaea modulate potential methanogenesis substrates in wetland soil. **Nature Communications** 15, 6384. 10.1038/s41467-024-49872-z
 75. Gong X, Xu L, Langwig MV, Chen Z, Huang S, Zhao D, Su L, Zhang Y, Francis CA, Lui J, Li J, Baker BJ. (2024) Globally distributed marine Gemmatimonadota have unique genomic potentials. **Microbiome** 12, 14. 10.1186/s40168-024-01871-4
 74. Tamarit D, Köstlbacher S, *Appler KE, Panagiotou K, Anda V, Baker BJ, Ettema TJG.* (2024) Description of *Asgardarchaeum abyssi* gen. nov. spec. nov., a novel archaeal species within the class Asgardarchaeia and phylum Asgardarchaeota in accordance with the SeqCode. **System and Appl Microbiology** 47, 126525. <https://doi.org/10.1016/j.syapm.2024.126525>
 73. Sarno N, Hyde E, *Anda V, Baker BJ.* (2024) Beyond methane, new frontiers in microbial hydrocarbon utilizing pathways. **Microbial Biotechnology** 17, e14508 <https://doi.org/10.1111/1751-7915.14508>
 72. Leão P, Little ME, *Appler KE, Sahaya D, Aguilar-Pine E, Currie K, Finkelstein I, Anda VD, Baker BJ.* (2024) Extensive defense systems in Asgard archaea and their role in the origin of eukaryotic immunity. **Nature Communications** 15, 6386. <https://doi.org/10.1038/s41467-024-50195-2>
 71. Alvarado, LEV, Fakra SC, Giska JR, West-Roberts J, Jaffe A, Probst AJ, He C, Rowland J Al-Shayeb B, Manga M, Savage D, *Baker BJ, Banfield JF.* (2024) Autotrophic biofilms sustained by deeply-sourced groundwater host diverse CPR bacteria implicated in sulfur and hydrogen metabolism. **Microbiome** 15, 10.1186/s40168-023-01704-w
- 2023**
70. *Vázquez-Rosas-Landa M, Anda VD, Waldram G, Angelova A, Gutierrez T, Baker BJ.* (2023) Novel alkane degrading bacteria that contain unique hydrocarbon pathways in northeast Atlantic Ocean. **mSystems** 10.1128/msystems.00619-23.
 69. Bojanova DP, *Vázquez-Rosas-Landa M, Haghnegahdar MA, Anda VD, Baker BJ, Teske AP, Ash JL, Young ED, LaRowe DE, Amend JP.* (2023) Well-hidden methanogenesis in deep, organic-rich sediments of Guaymas Basin. **ISME J.** 10.1038/s41396-023-01485-y
 68. *Carlton JD, Langwig MV, Gong X, Aguilar-Pine EJ, Seitz KW, Baker BJ, Anda VD.* (2023) Expansion of Armatimonadota through marine sediment sequencing describes two classes with unique ecological roles. **ISME Comm.** 3, 64. <https://doi.org/10.1038/s43705-023-00269-x>
 67. Eme L, Tamarit, D, Caceres EF, Stairs CW, *Anda VD, Schon ME, Seitz KW, Dombrowski N, Lewis WH, Homa F, Saw JH, Lombard J, Nunoura T, Li W-J, Hua Z-S, Chen L-X, Banfield JF, St John E, Reysenbach A-L, Stott MB, Schramm A, Kjeldsen KU, Teske AP, Baker BJ, Ettema TJG.* (2023) Inference and reconstruction of the heimdallarchaeal ancestry of eukaryotes. **Nature.** 618, 992-999. <https://doi.org/10.1038/s41586-023-06186-2>
 66. Dichiera AM, *Anda V, Gilmour KM, Baker BJ, Esbaugh AJ.* (2023) Functional divergence of teleost carbonic anhydrase IV. **Comp Biochem Physiol Part A** 277, 111368. 10.1016/j.cbpa.2023.111368
- 2022**
65. Howe KL, *Seitz KW, Campbell LG, Baker BJ, Thrash JC, Rabalis NN, Rogener MK, Joye SB, Mason OU.* (2022) Metagenomic and metatranscriptomics reveal broadly distributed, active, novel methanotrophs in the Gulf of Mexico hypoxic zone and in the marine water column. **FEMS Microbial Ecology** 97, 1. 10.1093/femsec/fiac153
 64. *Gong X, Rodriguez A, Xu L, Langwig M, Su L, Sun L, Sun M, Huerta-Cepas, Anda VD, Baker BJ.* (2022) New globally distributed bacteria phyla with the FCB superphylum. **Nature Communications** 13, 7516. 10.1016/j.cbpa.2023.111368
 63. Fang Y, Lui J, Yang J, Wu G, Hua Z, Dong H, Hedlund BP, *Baker BJ, Jiang H.* (2022) Compositional and metabolic responses of autotrophic microbial community to salinity in lacustrine environments. **mSystems** 7, 4. 10.1128/msystems.00335-22
 62. Rambo I, *Anda VD, Langwig M, Baker BJ.* (2022) Genomes of six viruses that infect Asgard archaea from deep-sea sediments. **Nature Microbiology** 7, 953-961. 10.1038/s41564-022-01150-8

61. Wang Y, Li W, Baker BJ, Zhou Y, Lu R, He L, Danchin A, Li Q, Gao Z. (2022) Carbon metabolism and adaptation of hyperalkaliphilic microbes in serpentinizing spring of Manleluag, the Philippines. **Environmental Microbiology Reports**. 14, 308-319. 10.1111/1758-2229.13052
 60. Langwig M, De Anda V, Dombrowski N, Seitz KW, Rambo I, Teske AP, Baker BJ. (2022) Large scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. **ISME J**. 16, 307-320. 10.1038/s41396-021-01057-y
- 2021**
59. Castelle CJ, Meheust R, Jaffe AL, Seitz KW, Gong X, Baker BJ, Banfield JF. (2021) Protein family content uncovers lineage relationships and bacterial pathway maintenance mechanisms in DPANN archaea. **Frontiers in Microbiology** 12, 660052. 10.3389/fmicb.2021.660052
 58. Baker BJ, Appler KE, Gong X. (2021) New microbial biodiversity in marine sediments. **Annual Reviews in Marine Science** 13, 161-175. 10.1146/annurev-marine-032020-014552
 57. Anda VD, Chen L-X, Dombrowski N, Hua Z-S, Jiang H-C, Banfield JF, Li W-J, Baker BJ. (2021) Brockarchaeota, a new archaeal phylum with unique and versatile pathways for carbon cycling. **Nature Communications** 12, 2404. 10.1038/s41467-021-22736-6
- 2020**
56. Murray AE, et al. (2020) Roadmap for naming uncultivated Archaea and Bacteria. **Nature Microbiology** 5, 987-997. 10.1038/s41564-020-0733-x
 55. Baker BJ, Anda VD, Seitz KW, Dombrowski N, Santoro A, Lloyd KA. (2020) Diversity, ecology, and evolution of Archaea. **Nature Microbiology** 5, 887-900. 10.1038/s41564-020-0741-x
 54. Rambo I, Dombrowski N, Constant, L, Erdner DL, Baker BJ. (2020) Metabolic reconstruction elucidates symbiotic relationships between bacteria and ciguatoxin-producing microalgae. **Environmental Microbiology** 22, 1764-1783. 10.1111/jam.14095.
- 2019**
53. Mullis MM, Rambo IM, Baker BJ, Reese BK. (2019) Diversity, ecology, and prevalence of antimicrobials in nature. **Front. Microbiol**. 10, 2518. 10.3389/fmicb.2019.02518
 52. Huang J-M, Baker BJ, Li J-T, Wang Y. (2019) New microbial lineages capable of carbon fixation and nutrient cycling in deep-sea sediments of the Northern China Sea. **Appl. Environ. Microbiol.** 85, e00523-19. 10.1128/AEM.00523-19
 51. Steen AD, Kevorkin RT, Bird JT, Dombrowski N, Baker BJ, Hagen SM, Mulligan KH, Schmidt JM, Webber AT, Alperin MJ. (2019) Kinetics and identities of extracellular peptidases in subsurface sediments of the White Oak River Estuary, NC. **Appl. Environ. Microbiol.** 85, e00102-19. 10.1128/AEM.00102-19
 50. Seitz KW, Dombrowski N, Eme L, Spang A, Lombard J, Seiber J, Teske AP, Ettema TJG, Baker BJ. (2019) Asgard archaea capable of anaerobic hydrocarbon cycling. **Nature Communications** 10, 1822. 10.1038/s41467-019-09364-x
 49. Spang A, Stairs C, Dombrowski N, Eme L, Lombard J, Caceres EF, Greening C, Baker BJ, Ettema TJG. (2019) Proposal of the reverse flow model for the origin of the eukaryotic cell based on comparative analysis of Asgard archaeal metabolism. **Nature Microbiology** 4, 1138-1148. 10.1038/s41564-019-0406-9
- 2018**
48. Dombrowski N, Teske AP, Baker BJ. (2018) Expansive microbial metabolic versatility and biodiversity in dynamic Guaymas Basin hydrothermal sediments. **Nature Communications** 9, 4999. 10.1038/s41467-018-07418-0
 47. Thrash JC, Seitz KW, Baker BJ, Temperton B, Campbell LG, Rabalais NN, Henrissat B, Mason OU. (2018) Metagenomic assembly and prokaryotic MAGs from the northern Gulf of Mexico “Dead Zone”. **Microbiol. Res. Announcements** 7, e01033-18. 10.1128/MRA.01033-18
 46. Narro AB, Spang A, Stairs C, Caceres EF, Baker BJ, Miller CS, Ettema TJG. (2018) Complex evolutionary history of translation elongation factor 2 and diphthamide biosynthesis in Archaea and parabasalids. **Genome Biol Evol** 10, 2380-2393. 10.1093/gbe/evy154
 45. Bacos HP, Erdner DL, Rosenheim BE, Shetty P, Seitz KW, Baker BJ, Liu Z (2018) Hydrocarbon degradation and response of seafloor sediment bacterial community in the northern Gulf of Mexico to light Louisiana sweet crude oil. **ISME J**. 12, 2532-2543. 10.1038/s41396-018-0190-1

44. Liu Y, Zhou Z, Pan J, [Baker BJ](#), Gu J, Li M (2018) Comparative genomic inference reveals mixotrophic lifestyle of Thorarchaeota. **ISME J.** 12, 1021-1031. 10.1038/s41396-018-0060-x
43. Chen L, Mendez-Garcia C, Dombrowski N, Servin-Garciduenas LE, Eloë-Fadrosch EA, Fang Z-H, Zhi X-Y, Hua Z-S, Martinez-Romero E, Woyke T, Huang L-N, Sanchez J, Pelaez AI, Ferrer M, [Baker BJ](#), Shu W-S (2018) Metabolic versatility of small deep-branching archaea. **ISME J.** 12, 756-775. 10.1038/s41396-017-0002-z

2017

42. Thrash JC, [Seitz KW](#), [Baker BJ](#), Temperton B, Campbell LG, Rabalais NN, Henrissat B, Mason OU, (2017) Metabolic roles of uncultivated bacterioplankton lineages in the northern Gulf of Mexico "Dead Zone". **MBio** 8:e01017-17. 10.1042/ETLS20160028
41. Bowers RM, et al., [Baker BJ](#), Eren MA, Hedlund B, McMahon K, Fierer N, Eisen J, Knight R, Cochrane G, Finn R, Mizrahi I and Woyke T. (2017) Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. **Nature Biotechnology** 35, 725-731. 10.1038/nbt.3893
40. [Dombrowski N](#), [Seitz KW](#), Teske AP, [Baker BJ](#) (2017) New insights into microbial hydrocarbon cycling and metabolic interdependencies in hydrothermal sediments. **Microbiome**. 5:106. 10.1186/s40168-017-0322-2
39. Zaremba-Niedzwiedzka, K, Caceres EF, Saw JH, Bäckström D, Juzokaite L, Vancaester E, [Seitz KW](#), Anantharaman, Stott MB, Nunoura T, Banfield JF, Schramm A, [Baker BJ](#), Spang A, and Ettema TJG. (2017) Asgard archaea illuminates the origin of eukaryotic cellular complexity. **Nature** 541, 353-358. 10.1038/nature21031
38. Lazar CS, [Baker BJ](#), [Seitz KW](#), Hinrichs K-U, Teske AP (2017) Genomic reconstruction of multiple lineages of uncultured benthic archaea suggests distinct biogeochemical roles and ecological niches. **ISME J.** 11, 1119-1129. 10.1038/ismej.2016.189

2016

37. Bird JT, [Baker BJ](#), Probst AJ, Podar M, Lloyd K (2016) Culture independent genomic comparisons reveal environmental adaptations for Altiarchaeales. **Frontiers in Microbiol.** 7, 1221. 10.3389/fmicb.2016.01221
36. Wasmund K, Cooper M, Schreiber L, Lloyd KG, [Baker BJ](#), Petersen DG, Schramm A, Stepanauskas R, Reinhardt R, Jørgensen BB, Loy A, Adrian L. (2016) Single Cell genome sequencing and targeted gene amplifications implicate members of the class *Dehalococcoidia* (phylum *Chloroflexi*) in sulfur cycling. **MBio**. 7, e00266-16. 10.1128/mBio.00266-16
35. [Dombrowski N](#), Donaho J, Teske AP, Gutierrez T, [Seitz KW](#), [Baker BJ](#). (2016) Reconstructing metabolic pathways of hydrocarbon-degrading bacteria from the Deepwater Horizon oil spill. **Nature Microbiology** 1, 16057. 10.1038/nmicrobiol.2016.57
34. Hug L, [Baker BJ](#), Anantharaman K, Brown CT, Probst AJ, Castelle C, Butterfield CN, Hernsdorf AW, Amano Y, Suzuki Y, Dudek N, Relman DA, Thomas BC, Banfield JF (2016) A new view of the tree of life. **Nature Microbiology** 1, 16048. 10.1038/nmicrobiol.2016.48
33. Lazar C*, [Baker BJ](#)*, [Seitz KW](#), Hyde AS, Dick GJ, Hinrich K-U, Teske A. (2016) Genomic evidence for distinct carbon substrate preferences and ecological niches of Bathyarchaeota in estuarine sediments. **Environmental Microbiology** 18, 1200-1211. 10.1111/1462-2920.13142 *Contributed equally
32. [Baker BJ](#), Saw J, Lind A, Lazar CS, Hinrichs K-U, Teske AP, Ettema T (2016) Genomic inference of the metabolism of cosmopolitan subsurface archaea, Hadesarchaea. **Nature Microbiology** 1, 16002. 10.1038/nmicrobiol.2016.2
31. [Seitz KW](#), Lazar CS, Hinrichs K-U, Teske A, [Baker BJ](#). (2016) Genomic reconstruction of a novel, deeply-branched sediment archaeal phylum with pathways for acetogenesis and sulfur reduction. **ISME J.** 10, 1696-1705. 10.1038/ismej.2015.233
30. Hu P, Tom LM, Singh A, Thomas BC, [Baker BJ](#), Piceno YM, Andersen GL, Banfield JF. (2016) Genome-resolve metagenomic analysis reveals roles for candidate phyla bacteria in biogeochemical transformations in hydrocarbon reservoirs. **MBio** 7, e01669-15. 10.1128/mBio.01669-15

2015

29. Li M, [Baker BJ](#), Anantharaman K, Breier J, Jain S, Dick GJ. (2015) Genomic and transcriptomic evidence for scavenging of diverse organic compounds by widespread deep-sea archaea. **Nature Communications** 6, 8933. 10.1038/ncomms9933

28. Baker BJ, Lazar C, Dick GJ, Teske A. (2015) Genomic resolution of linkages in carbon, nitrogen, and sulfur cycling among widespread estuary sediment bacteria. **Microbiome**, 3, 14. 10.1186/s40168-015-0077-6
- Baker BJ, Banfield JF. (2015) Metagenomics of acid mine drainage at Iron Mountain California: Expanding our view from individual genes and cultures to entire communities. *Chapter in "Acidophiles" book.*
27. Li M, Toner BM, Baker BJ, Myneni S, Dick GJ. (2014) Microbial iron uptake as a mechanism for dispersing iron from deep-sea hydrothermal vents. **Nature Communications** 5, 3192. 10.1038/ncomms4192
26. Li M, Jain S, Baker BJ, Taylor C, Dick GJ. (2014) Novel hydrocarbon monooxygenase genes in the metatranscriptome of a natural deep-sea hydrocarbon plume. **Environmental Microbiology** 16, 60-71. 10.1111/1462-2920.12182
- Baker BJ, Dick GJ. (2013) Omic approaches in microbial ecology; charting the unknown. **Microbe** 8, 353-359. 10.1128/microbe.8.353.1
- 2013**
25. Baker BJ, Taylor C, Jain S, Shiek CS, Bhasi A, Cavalcoli JD, Dick GJ. (2013) Community transcriptomic assembly reveals microbes contribute to carbon and nitrogen cycling in the deep sea. **ISME J.** 7, 1962-1973. 10.1038/ismej.2013.85
24. Dick GJ, Anantharaman K, Baker BJ, Li M, Reed DC, Sheik CS. (2013) The microbiology of deep-sea hydrothermal vent plumes: ecological and biogeographic linkages to seafloor and water column habitats. **Front Microbiol** 4, 1-16. 10.1126/science.1231707
23. Schönknecht G, Chen W-H, Ternes CM, Barbier GG, Shrestha RP, Stanke M, Bräutigam A, Baker BJ, Banfield JF, Garavito RM, Benning C, Carr K, Wilkerson C, Rensing SA, Gagneul D, Oesterhelt C, Lercher MJ, Weber APM. (2013) Gene Transfer from Bacteria and Archaea facilitated evolution of an extremophilic eukaryote. **Science** 339, 1207-1210. 10.1126/science.1231707
- 2012**
22. Baker BJ, Lesniewski R, Dick GJ (2012) Genome-enabled transcriptomics reveals archaeal populations that drive nitrification in a deep-sea hydrothermal plume. **ISME J.** 6, 2269-2279. 10.1038/ismej.2012.64
21. Fujishima K, Sugahara J, Miller CS, Baker BJ, Di Giulio M, Takesue K, Sato A, Tomita M, Banfield JF, Kanai A. (2011) A unique tRNA splicing endonuclease found in ultrasmall archaeon is a chimeric protein consisting of three domains. **Nucleic Acids Res** 39, 9695-9704. 10.1110/ps.37101
- 2011**
20. Miller CS, Baker BJ, Thomas BC, Singer S, Banfield JF (2011) EMIRGE: Reconstruction of full-length ribosomal genes from microbial community short read sequencing data. **Genome Biology** 12, R44. 10.1186/gb-2011-12-5-r44
- 2010**
19. Baker BJ, Comolli LR, Dick GJ, Hauser L., Land M, Hyatt, D, VerBerkmoes N, Hettich B, Banfield JF. (2010) Enigmatic, ultra-small uncultivated Archaea. **Proc. Natl. Acad. Sci.** 107, 8806-8811. 10.1073/pnas.0914470107
18. Denef VJ, Kalnejais LH, Mueller RS, Wilmes P, Baker BJ, Thomas BC, VerBerkmoes, NC, Hettich RL, Banfield, JF. (2010) Proteogenomic basis for ecological divergence of closely related bacteria in natural acidophilic microbial communities. **Proc. Natl. Acad. Sci** 107, 2383-2390. 10.1073/pnas.0907041107
- 2009**
17. Dick GJ, Andersson, A, Baker BJ, Yelton P, Sheri SS, Thomas BC, Banfield JF. (2009) Community-wide analysis of microbial genome sequence signatures. **Genome Biology** 10:R85. 10.1186/gb-2009-10-8-r85
16. Goltsman, DSA, Denef VJ, Singer SW, VerBerkmoes NC, Lefsrud M, Muller R, Dick GJ, Sun C, Wheeler K, Zemla A, Baker BJ, Hauser L, Land M, Shah M, Thelen MP, Hettich RL, Banfield JF (2009) Community genomics and proteomics of chemoautotrophic, iron-oxidizing "*Leptospirillum rubrum*" and *Leptospirillum ferrodiazotrophum* populations in acid mine drainage. **Appl. Environ. Microbiol.** 75, 4599-4615. 10.1128/AEM.02943-08
15. Baker BJ, Tyson GW, Goosherst L, Banfield JF (2009) Insights into the diversity eukaryotes in acid mine drainage biofilm communities. **Appl. Environ. Microbiol.** 75, 2192-2199. 10.1128/AEM.02500-08
14. Comolli LR, Baker BJ, Downing KH, Siegerist CE, Banfield JF (2009) Three-dimensional analysis of the structure and ecology of a novel, ultra-small archaeon. **ISME J.** 3, 159-1671. 10.1038/ismej.2008.99

2006

13. Baker BJ, Tyson, GW, Webb RI, Flanagan J, Hugenholtz P, Banfield JF (2006) Lineages of acidophilic Archaea revealed by community genomic analysis. **Science** 314, 1933-1935. 10.1126/science.1132690

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12. Moser DP, Gihring TM, Brockman FJ, Fredrickson JK, Balkwill DL, Dollhopf ME, Sherwood Lollar B, Pratt LM, Boice E, Southam G, Wanger G, Baker BJ, Pfiffner SM, L-H Lin, Onstott TC. (2005) *Desulfotomaculum* spp. and *Methanobacterium* spp. dominate a 4-5 km deep fault. **Appl. Environ. Microbiol.** 71, 8773-8783. 10.1128/AEM.71.12.8773-8783.2005
11. Tyson GW, Lo I, Baker BJ, Allen EE, Hugenholtz P, Banfield JF (2005) Genome-directed isolation of the key nitrogen fixer, *Leptospirillum ferroazotrophum* sp. nov., from an acidophilic microbial community. **Appl. Environ. Microbiol.** 71, 6319-6324. 10.1128/AEM.71.10.6319-6324.2005
10. Ram RJ, VerBerkmoes N, Thelen MP, Tyson GW, Baker BJ, Shah M, RC Blake II, Hettich R, Banfield JF (2005) Community proteomics of a natural microbial biofilm. **Science** 308, 1915-1920. 10.1126/science.110907

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9. Baker BJ, Lutz MA, Dawson SC, Bond PL, Banfield JF (2004) Metabolically active eukaryotic communities in extremely acidic mine drainage. **Appl. Environ. Microbiol.** 70, 6264-6271. 10.1128/AEM.70.10.6264-6271.2004
8. Druschel GK*, Baker BJ*, Gihring TH, Banfield JF (2004) Acid mine drainage biogeochemistry at Iron Mountain, California. **Geochem. Trans.** 5, 13-32. 10.1186/1467-4866-5-13 *contributed equally
7. Moser DP, Onstott TC, Fredrickson JK, Brockman FJ, Takai K, Balkwill DL, Drake, G, Pfiffner, S, White DC, Baker BJ, Pratt LM, Fong J, Lollar BS, Slater G, Phelps TJ, Spoelstra N, DeFlaun M, Southam G, Welty AT, Hoek J (2003) Evolution of microbial community structure and geochemistry in an ultradeep South African gold mine borehole. **Geomicrobiology J.** 20, 517-548. 10.1080/713851170

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6. Baker BJ, Hugenholtz, P, Dawson, SC, Banfield, JF (2003) Extremely acidophilic protists host *Rickettsiales*-lineage endosymbionts with an intervening sequence in their 16S rRNA genes. **Appl Environ. Microbiol.** 69, 5512-5518. 10.1128/AEM.69.9.5512-5518.2003.
5. Baker BJ, Banfield JF (2003) Microbial communities in acid mine drainage. **FEMS Microbial Ecol.** 44, 139-152. 10.1016/S0168-6496(03)00028-X.
4. Baker BJ, Moser DP, MacGregor BJ, Fishbain S, Wagner M, Fry N, Jackson B, Spoelstra N, Loos S, Takai K, Fredrickson J, Balkwill D, Onstott TC, Wimpsee CF, Stahl DA (2003) Related assemblages of sulfate-reducing bacteria associated with ultradeep gold mines of South Africa and deep basalt aquifers of Washington State. **Environ. Microbiol.** 5, 267-277. 10.1046/j.1462-2920.2003.00408.x.

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3. Stahl DA, Fishbain S, Klein M, Baker BJ, Wagner M (2002) Origins and diversification of sulfate-respiring microorganisms. **Antonie van Leeuwenhoek** 81, 189-195. 10.1023/a:1020506415921.

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2. MacGregor BJ, Van Mooy B, Baker BJ, Mellon M, Moisaner PH, Pearl HW, Zehr, J, Hollander, D, Stahl DA (2001) Microbiological, molecular biological and stable isotopic evidence for nitrogen fixation in the open waters of Lake Michigan. **Environ. Microbiol.** 3, 205-209. 10.1046/j.1462-2920.2001.00180.x.
1. MacGregor BJ, Moser DP, Baker BJ, Alm EW, Maurer M, Nealson KH, Stahl DA (2001) Seasonal and spatial variability in Lake Michigan sediment small-subunit rRNA concentrations. **Appl Environ. Microbiol.** 67, 3908-3922. 10.1128/AEM.67.9.3908-3922.2001.

PRESENTATIONS SINCE JOINING UT

Keynote speaker at Luxembourg Microbiology Day, May 12-13, 2026
 Invited speaker at Texas State University Dept. of Biology, October 10, 2025
 Keynote speaker at Northeastern Geobiology Symposium, McGill University, April 2025
 Keynote speaker at GRC Archaea, July 2025, Switzerland
 Seminar speaker at Virginia Tech, April 2025
 Invite speaker at ASM Microbe Conference, Los Angeles, CA June 2025 "Is microbial diversity infinite?"
 Invited speaker at BSE International Symposium on "Microbiomes: Exploring Invisible Frontiers"

in Health, Habitat, Space, and Beyond, India
 Invited speaker at GRC Geobiology, January 2024, Galveston, TX
 Invited speaker at GRC Archaea, July 2023 Mt Snow, Vermont
 Speaker at the Texas Science Festival, March 22, 2021
 Chair of a session entitled, “The expanding archaeal tree of life”
 Chairing a session at ASM-FEMS World Microbe Forum, June 2021
 February 2025, Indian Institute of Technology Madras, Chennai, India
 Virginia Polytechnic Institute and State University, April 4, 2025
 Purdue University, Dept. of Biological Sciences, November 18, 2024
 University of Texas Austin, Dept of Molecular Biosciences, October 2022
 Oceanography Dept. October 2021 University of Hawaii
 Biology Dept., April 1, 2021, Duke University
 Dept of Bacteriology Dept. March 25, 2021, Univ. of Wisconsin
 Biology Department, March 27, 2019, University of Montreal Canada
 Marine and Environmental Biology, February 26, 2019, USC
 Ecology, Evolution and Marine Biology Department, April 2019, UC Santa Barbara
 Earth Sciences Dept, November 7. 2018, Stanford University
 Integrative Biology January 2018, UT Austin
 Biochemistry Department, December 2017, Montana State University
 Darwin Day invited speaker, Feb, 2017 University of Minnesota Duluth
 Texas A&M Univ., Feb 2017
 Oklahoma State Univ., March 2017
 Cal State San Bernardino, October 2016
 JAMSTEC Yokohama Japan, Sept 2016
 Portland State Univ, Biology Dept, May 2016
 Oregon Health and Science Univ, May 2016
 Uppsala University, Sweden in June 2016
 Biology Dept seminar series, Texas A&M Corpus Christi, May 2016
 University of Colorado Denver Integrative Biology Seminar, March 2015
 Public seminar at University of Texas OLLI program for adults 50 and better, October 27, 2020 “Exploring new branches on the tree of life”
 Invited Speaker Harvard Microbial Science Initiative annual symposium, April 18, 2020, Harvard University
 “Leveraging metagenomics to explore marine sediments”, Texas Branch of the American Society for Microbiology fall meeting, November 10, 2018
 “Physiological capacity of archaea in anoxic sediments” EMBO Molecular biology of archaea: From mechanisms to ecology, Sept 5, Vienna, Austria
 Gordon Research Conference – Marine Microbes, July 2, 2018, Lucca Italy
 Invited speaker at Global Soil Biodiversity Conference GSBC2, October 2017, Nanjing, China
 Keynote speaker at Goldschmidt Conference August 2017, Paris, France
 Speaker at ASM Microbe conference, New Orleans, LA, June 2017
 Presenter at Explore UT, a research presentation for the public Texas community
 Invited seminar at Cal State San Bernardino, October 2016
 Keynote speaker at Extremophiles 2016 conference Kyoto Japan, Sept 2016
 Convenor of session at AGU general meeting, San Francisco, December 2015
 Speaker at Gulf of Mexico Research Initiative Conference 2015, Houston, TX
 Invited speaker American Chemical Society General Meeting, 2015, Denver CO
 Speaker at ASM general meeting 2015, New Orleans, LA.

FUNDING

Quantifying Hydrogen Storage Risks to Potable Groundwater and Climate Change

Role: PI Alexandra Clara Saracho, coI's - Baker, Charles Werth

Source: National Science Foundation Environmental Engineering

Award Amount: \$419,890

Start/End Date: 1/1/2025-12/31/2028

Searching for our microbial ancestors

Role: PI Baker, co-PI Alyson Santoro (UCSB)

Source: Gordon and Betty Moore Foundation Award 13546 (<https://doi.org/10.37807/GBMF13546>)

Award: \$1,053,785 to UT (\$1,729,116 in total)

Start/End Date: 6/1/2025-5/31/2027

A holistic survey of ecological roles of microbes in marine sediments

Role: sole PI Baker

Source: Simons Foundation (Award LI-SIAME-00002001)

Award Amount: \$1,749,450 to Baker

Start/End Date: 7/1/2023-4/31/2028

Texas-ECE

Role: PI Baker

Source: Marine Science Institute

Award: \$150,000 to Baker

Start/End Date: 09/1/2025-08/31/2027

The role of protein interactions in the origin of complex cellular life

Role: PI Baker

Source: University of Texas, College of Natural Sciences, Spark Award

Award Amount: \$200,000

Start/End Date: 3/1/2023-8/31/2028

Pending awards

NSF Engineering Research Center for Mechanisms for Engineering Technologies and Harnessing Advance Networked Ecosystems (METHANE)

Role: co-PI Baker (leads at Colorado State Kelly Wrighton and Jason Quinn)

Source: National Science Foundation

Award: \$3,970,454 (UT Bio team)

Start/End Date: 9/1/2026-7/31/2031

Prior awards

Searching for our microbial ancestors

Role: Chief Scientist – Baker

Source: Schmidt Oceanographic Institute

Award: In-kind use of R/V Falkor (too)

Start/End Date: 11/1/2025-11/23/2025

Mining the Texas coast for novel plastic degrading enzymes

Role: PI Baker, CoIs Andrew Ellington and Edward Marcotte

Source: University of Texas, Texas Gulf Coast Research Center

Award Amount: \$100,000

Start/End Date: 3/1/2024-8/31/2025

Diversity, genomic, physiology, and ultrastructure of Asgard archaea and implications for eukaryogenesis

Role: lead PI (other PIs: Mark Ellisman, Thijs Ettema, and Roland Hatzenpichler)

Source: Simons and Moore Foundations (Award 735925LPI)

Award Amount: \$1,920,000 (\$480,000 to Baker)

Start/End Date: 9/1/2020-8/31/2023

Simons Early Career Investigator in Marine Microbial Ecology and Evolution Award

Role: sole PI

Source: Simons Foundation (Award number 687165)

Award Amount: \$666,000

Start/End Date: 4/1/2020-3/31/2023

Project title: Sloan Foundation Fellowship in Ocean Sciences

Role: sole PI

Source: Alfred P. Sloan Foundation

Award Amount: \$55,000

Start/End Date: 09/01/2016-08/31/2018

Conference: Participation of early-career and diverse scientists in the International Conference on Geo-Omics of Archaea II

Role: PI Brian Hedlund, coPI's Baker, Anna-Louise Reysenbach, Jose R de lo Torre

Source: National Science Foundation DEB

Award Amount: \$25,000

Start/End Date: 8/1/2024-7/31/2026

Resolving the ecological biodiversity of Asgard archaea and their role in the evolution of eukaryotes

Role: sole PI

Source: NSF DEB SBS – Biodiversity: Discovery and Analysis (Award number 1753661)

Award Amount: \$288,928

Start/End Date: 02/01/2018-1/31/2020

Linking nutrient cycling to microbial communities in San Francisco Bay using paired 'omics, 16S rRNA libraries, and functional gene analyses, and biogeochemical rate measurements

Role: Co-PI (PI: Christopher Francis)

Source: DOE Joint Genome Institute Community Science Program

Award Amount: instrument time only

Start/End Date: 01/01/2017-12/31/2019

Collaborative research: Next generation physiology: a systems-level understanding of microbes driving carbon cycling in marine sediments

Role: co-PI (other PIs: Roland Hatzenpichler, Andreas Teske)

Source: NSF MCB - Systems and Synthetic Biology (Award number 1817354)

Award Amount: \$1,062,283 (\$374,675 to Baker)

Start/End Date: 06/01/2018-11/30/2020

ADVISORY ACTIVITIES**Current team members**

Benamin Jelen, Research fellow (2025-present)

Emily Aguilar-Pine, currently Lab manager (Undergraduate Researcher/Lab Technician 2022-present)

Dr. Robin Rohwer, Postdoctoral fellow/Research associate (2022-present)

Lara Codignola, M.S. Student (2024-present)

Aerial Bellatin, M.S. Student (2024-present)
Georgina Aitolo, Ph.D. student (2024-present)
Ericka Meitzen, Ph.D. student (2025-present)
Emily Hyde, Ph.D. student (2023-present)
Natalie Sarno, Ph.D. student (2022-present)
Nathalie Scott, Undergraduate Researcher (2024-present)
Caroline Cole, Undergraduate Researcher (2024-present)
Trenton Turpin, Undergraduate Researcher (2025-present)

Past team members

Kathryn Appler, Ph.D. student (2019-2024) currently Postdoctoral Fellow Pasteur Institute
Dr. Valerie de Anda, Postdoctoral fellow (2018-2024) currently Assistant Professor University of Florida
Dr. Pedro Lopes Leao, Postdoctoral fellow (2021-2024) Faculty member at Radboud University
Dr. Mirna Vázquez Rosas Landa (2020-2022) now faculty member UNAM Mexico City
Dr. Xianzhe Gong, Postdoctoral fellow (2018-2022) now faculty in China
J.D. Carlton, lab technician and M.S. student (2020-2024) now PMF Fellow at USGS
Ian Rambo, Ph.D. student (2016-2021) now Postdoctoral research USDA
Dr. Nina Dombrowski, Postdoctoral fellow (2015-2018)
Maggie Langwig, M.S. student (2017-2020) now PhD student UW Madison
Kiley Seitz, Ph.D. student (2015-2019) now Researcher at EMBO
Kathryn Currie (Undergraduate Researcher/Lab Technician 2022-2024)
John Donaho, NSF REU student (summer 2015)
Roy Rodriguez Carrero, NSF REU student (summer 2016)
Lauren Constant, UT Semester by the Sea undergraduate student (spring 2017)
Tara Johnson, UT Semester by the Sea undergraduate student (spring 2018)
Addison Denton, UT Semester by the Sea undergraduate student (spring 2018)
Lacie Levy (Undergraduate Researcher 2022-2023)
Sophie Hoefner (Undergraduate Researcher 2021-2024)
Sunny Sneed, lab technician (2020) now PhD student
Brennan Martinez (Undergraduate Researcher 2023-2024)
Kathleen Leever, Undergraduate Researcher (2020-2023)
Francisco Elohim Cardenas Gonzalez, NSF REU student (summer 2023)
Jennifer Hunt, LSAMP student (summer 2023)
Jasmine Koh (Undergraduate Researcher 2023-2025)

TEACHING EXPERIENCE

MBL Microbial Diversity course 2024
Microbial Ecology, UT 2022-present
Aquatic microbiology, UT 2016-2022-present
Scientific communications, UT 2017-2020
Genomics in ocean science, UT 2017-2021

AWARDS

Rackham Pre-Doctoral Graduate Fellowship – 2013 competition, University of Michigan
Funding for summer and fall 2013 through summer 2014
University of Texas College of Natural Science, Visualizing Science Contest 2015 – 1st place
Sloan Research Fellowship in Ocean Sciences – 2016
Simons Early Career Investigator in Marine Microbial Ecology and Evolution Award – 2020
Elected to the American Academy of Microbiology - 2024

OTHER SCIENTIFIC ACTIVITIES

- Led the organization of an international workshop on the origin of eukaryotes (Nov 7-8, Montevideo, Uruguay).
- Chief Scientist on a Falkor (too) expedition (Schmidt Ocean Institute) to sample the South Atlantic (November 2025)
- Co-director of the University of Texas Center for Planetary Systems Habitability (CPSH) (2023-present)
- Instructing faculty Marine Biological Laboratory, Woods Hole, MA Microbial Diversity course (2024 and 2025)
- UT Faculty Development Leave (FDL) Committee representative for Integrative Biology (2023-present)
- UT Department of Integrative Biology Search Committee member for Mentoring faculty position 2023
- Panel review committee for University of Texas Stengl-Wyer Scholars and Fellows (2022-2024)
- Led a University of Texas Summer Science program for 3-4th graders (2017-2019)
- Panel reviewer for NASA Exobiology and International Ocean Discovery Program (IODP)
- External reviewer for several NSF competitions and panelist for DEB SBS Sept. 2020.
- Ad hoc reviewer for *Nature*, *Science*, *PNAS*, *Nature Microbiology*, *Nature Biotechnology*, *PLoS Genetics*, *ISME Journal*, and others.
- Editor for several topics in *Frontiers in Microbiology*, including “Diversity, ecology, and evolution of archaeal viruses”, “Recent insights into the essential roles of archaea in the marine carbon cycle”, “Rising stars in hydrothermal vents and cold seeps: 2021”, and “Metagenomics, genomic and single-cell approaches advancing the microbial physiology and ecology of extreme environments.”
- Ad hoc reviewer for UT College of Natural Sciences Dean’s Honors graduates 2025, member of the CNS Dean’s emerging leader’s faculty group 2023-2024, Marine Science Dean’s select admissions committee

LEADERSHIP ACTIVITIES

As co-director of the University of Texas Center for Planetary Systems Habitability (CPSH)

- The Center engages 43 faculty across the College of Natural Sciences, Cockrell School of Engineering, and the Jackson School of Geoscience
- Oversee an annual budget of ~\$200,000 from the university
- Lead the executive committee which oversees, budget, seminars, student funding, funding raising, and initiate grants among center participants
- Organize workshops and social events among faculty, postdoctoral researchers, and graduate students involved in the center
- Lead monthly meetings that engage faculty across several departments on campus, this has led to several interdisciplinary grants to federal agencies