BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors. Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Christina R. Bourne

eRA COMMONS USER NAME (credential, e.g., agency login): christinabourne

POSITION TITLE: Associate Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Oklahoma, Norman OK	BS	05/1997	Biochemistry
Oklahoma Medical Research Foundation and OU Health Sciences Center, Oklahoma City OK	PhD	10/2003	Biochemistry, Mol Biol and Structural Biology
OU Health Sciences Center, Oklahoma City OK	Postdoctoral Fellow	10/2007	Structural Virology

A. Personal Statement

I am a biochemist and structural biologist, and my scientific interests focus on innovative new methods and novel targets to control cell growth. I have extensive experience with structure-guided inhibitor development spanning viral, bacterial, and eukaryotic systems. My formal training is in X-ray crystallography, and in 2022 I extended my expertise into cryo-EM single particle analysis with 8 weeks of embedded training at the NIH funded NCCAT center. I have followed this initial training with multiple visits to both the NCCAT and PNCC centers. Multiple projects in my research program have on-going cryo-EM SPA in progress, with our first reconstruction nearly complete. I also work with three collaborators (Mitra, Burgett, DeLeon) to generate cryo-EM reconstructions for macromolecules of interest to their research programs.

My research program is currently focused on studies of Toxin Antitoxin (TA) systems and the bacterially specific folate synthesis pathway. While the latter work builds from my previous experience, *I launched our TA systems work independent from previous positions. This is a challenging field with fast paced discoveries,* frequently resulting from focused institutes and programs outside of the US. I have remained fascinated by the properties of one specific type and family of TA system – the type II RelE/ParE superfamily. These are highly abundant and share a common fold with divergent function and varied sequences spanning degrees of homology from 6-80%. Relationships between family members are also intriguing because of their high rates of horizontal gene transfer combined with evolution during vertical transmission for integrated copies. *Overall, this field provides a rich source of research questions, and for those we have formulated including in the current proposal, they are overall well with our continued interest in anti-folate and multi-target antibacterial discovery*.

My team is comprised of graduate and undergraduate students. *In the previous five years (2020 to present), I have had 7 graduate students (5 PhD, 2 MS),* with 3 currently in my team and, of these, 2 planning a defense in Spring 2025. Three of these graduate students (2 PhD, 1 MS) are currently employed in the biotech industry in other states. In this time, I have *also had 13 undergraduate students* actively carrying out research with me, with 2 current and a new freshman joining Spring 2025. Outcomes for the 11 previous members are: one started graduate school at NYU in Fall 24 with a focus in structural biology, one earned an MS in Bioinformatics and is employed in clinical sciences, one works in the non-profit public health sector, one works in a local biotech company, one is a current MD/PhD student, 3 are in or starting medical school and 2 more are current applicants, and one is a current undergraduate at OU.

As a first-generation (Pell Grant) student, I was helped enormously by mentors, and this continues to inspire me. I am active on campus as a facilitator for workshops in mentorship through our Center for Faculty Excellence.

I was recently selected as a Faculty Fellow in our Graduate College Office of the Dean to add new Professional Development and Mentorship tools for campus enrichment.

My training in structural biology, biochemistry, and microbiology combined with my experience in leading research teams and training students, and with the supportive infrastructure and expertise available at OU, combine to ensure success with the proposed studies.

Relevant and Recently Completed Projects:

U.S. Army, Department of Defense W81XWH2010121 (PI: C. Bourne) 02/20 – 05/23

"Unlocking the potential of bacterial ParE toxins: developing a blueprint for co-opting molecular time bombs that impact bacterial cell survival"

This project examined the phenotypic outcomes for three human bacterial pathogens when their native chromosomal ParE toxins are over-expressed. This highlighted a complex relation between primary sequence and inhibitory motifs of ParE toxins. We established mutation frequencies are increased above that of current anti-gyrase antibiotics, resulting in excessive toxicity and bacterial cell death before accumulation of mutations to produce useful resistance.

NIH National Institute of General Medical Science R15-GM140412 (PI: M. O'Reilly) 03/21 – 2/23

"Development of allosteric dihydrofolate reductase inhibitors: Exploration of a novel inhibitory mechanism of a validated antibiotic target."

I served as a co-Investigator on this project and completed crystallographic and docking analyses to complement the synthetic chemistry performed by Dr. O'Reilly's team.

NIH National Institute of General Medical Science P30-GM145423 (PI: A. West) 09/22 – 5/24

"Structure/function of oxysterol binding protein to guide therapeutic development"

This on-going active collaborative project with Dr. Anthony Burgett (U of Okla. Health Sciences campus) is deducing differences in ligand binding for members of the human oxysterol binding protein family with a goal of selectively manipulating these to effect anti-cancer, anti-aging, and anti-viral effects. My team leads structural investigations by generating reagents and crystallographic and cryo-EM studies with ligands produced by the collaborating medicinal chemistry team.

NIH NIGMS P30-GM145423 (Pilot, PI: K. DeLeon, co-I: C. Bourne) 06/24 – 5/26

"Structural characterization of two Desulfovibrio Lap-like biofilm proteins"

This study aims to characterize the structures of two proteins essential for biofilm formation of model sulfate-reducing bacteria using cryoEM approaches. Outcomes from these studies will enable further studies on mechanism of biofilm formation by these and other organisms.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2024 – *current* Graduate College Faculty Fellow, U. of Oklahoma, Norman, OK

2021 – *current* Associate Professor with tenure, U. of Oklahoma, Dept. of Chem Biochem, Norman, OK

2021 – (*2023)* U. of Oklahoma, Dept. of Chem Biochem, Executive Comm. Member (elected)

2021 – *current* Member, User Review Committee, National Center for CryoEM Access and Training (NCCAT)

2017 – *current* Member (Chair, effective 2021), Advisory Committee, OU Biomolecular Structure Core Facility

2015 – c*urrent* Member, OU Institutional Biosafety Committee

2014 – 2021 Assistant Professor, U. of Oklahoma, Dept. of Chem Biochem

2011 – 2013 Member, BEI Resources Focus Group for Biodefense and High Containment Bacteria

2007 – 2013 Associate Research Scientist, Oklahoma State U., Center for Veterinary Health Sciences

2005 – 2007 American Cancer Society Postdoctoral Fellow, U. of Oklahoma Health Sciences Center

Other Experience and Professional Memberships

2024 (- 2027) American Crystallographic Association Communications Committee Member *(elected)*

2023 American Crystallographic Association Session Chair, DEI: Expanding Access and Opportunities in Structural Science

2023 Representative User for the NY National Center from Cryo-EM Access and Training, NIH Common Fund CryoEM Centers Annual Meeting

2022 (- 2025) Secretary, American Microbiology Society Missouri Valley Branch *(elected)*

Member, American Crystallographic Association (2001-present), American Society for Biochemistry and Molecular Biology (2003-present), American Society for Microbiology (2008-present), American Association for the Advancement of Science (2017-present), The Biophysical Society (2024-present)

Ad Hoc manuscript reviewer (previous 5 years): *ACS Medicinal Chemistry, ACS Omega, Frontiers in Microbiology, Frontiers in Genetics, Genes, Journal of Biochemistry, mBio, Medicinal Research Reviews, Microorganisms, Molecular Microbiology, Nature Communications, Nature Reviews in Microbiology, Nucleic Acids Research, Protein Science, Spectrum, Structure, Toxins*

Proposal reviews (previous 5 years): BBSRC, US Army Research Office, NIH Special Emphasis Panel ZRG1 BST-M, European Research Council Starting Grants panel, Joint Canada-Israel Health Research Program Phase II

Previous activities include Editorial roles at *Journal of Molecular* Recognition, *Frontiers in* Microbiology; BioCAT Advanced SAXS training course (APS, 2015), RapiData X-ray Diffraction Data Collection and Structure Solving (NSLS 2000, 2014), Guest at Tech to Trek (SWOSU 2015), Mentor for OSU Women's Mentorship Program (2012-2013), Guest Scientist "Born To Do Science" (OSU, 2010), Modern Drug Target Crystallography and Structure Based Drug Discovery (MolSoft, San Diego CA, 2009)

Honors

2022	OU Ed Cline Faculty Fellowship
2020	Nancy L. Mergler Faculty Mentor Award for Undergraduate Research
2020	Peggy Cotter Branch Travel Award, American Society of Microbiology
2018	OK - Louis Stokes Alliance for Minority Participation (LSAMP) Outstanding Faculty Mentor Award (Norman campus)
2014, 2015	VPR Summer Faculty Fellowship, University of Oklahoma
2005 - 2007	Mary Horton Postdoctoral Fellowship, American Cancer Society

Previous honors of note: Travel Grant from US National Committee for Crystallography (2005), Pauling Poster Prize, American Crystallographic Association (2003), Ludo Frevel Crystallography Scholarship, International Centre for Diffraction Data (2001)

C. Contributions to Science

1. **Toxin Antitoxin systems as targets to control bacterial growth and limit resistance via mobile genetic elements:** TA systems encode bacterial toxins whose list of targets overlaps closely with known effect antibacterial targets, suggesting mimics of these toxins may afford new means to battle the antimicrobial resistance crisis. Our focus is on the DNA gyrase-inhibiting ParE toxin. We have analyzed the potency of toxicity in the context of the highly variable primary sequences to identify motifs driving gyrase inhibition. We have determined that mutational capacity scales directly with toxicity, driving cell death before clinical resistance can arise. TA systems serve as "addiction" modules when carried on mobile genetic elements, requiring the host to continually transcribe the neutralizing co-encoded antitoxin to maintain viability. We have identified an unexpected and pervasive mutation in DNA polymerase in response to ParE toxins that triggers a reduced plasmid copy number by almost 1,000-fold.

   Ruan, S., **Bourne C.R.** "*Escherichia coli* cells evade inducible ParE toxin expression by reducing plasmid copy number." 2024 *Microbiol Spectr*. 12(6):e0397323. PMID: 38700352; PMCID: PMC11237751.

   Ruan, S., Tu, C.-H., **Bourne C.R.** "Friend or Foe: Protein Inhibitors of DNA Gyrase." 2024 *Biology* (Basel) 13(2):84. PMID: 38392303; PMCID: PMC10886550.

   Ames, J.R., Muthuramalingam M, Murphy, T., Najar F.Z., **Bourne C.R.** "Expression of different ParE toxins results in conserved phenotypes with distinguishable classes of toxicity." 2019 *Microbiol. Open* 8(10):e902. PMID: 31309747; PMCID: PMC6813445.

   Muthuramalingam M, White JC, Murphy, T., Ames, J.R., **Bourne C.R.** "The toxin from a ParDE toxin-antitoxin system found in *Pseudomonas aeruginosa* offers protection to cells challenged with anti-gyrase antibiotics." 2019 *Mol. Microbiol.* 111(2):441. PMID: 30427086; PMCID: PMC6368863.

2. **Type II Toxin Antitoxin systems as models for cognate pairing and intrinsic disorder-to-order transitions:** Our recent review article examined published data for the specific pairing of cognate ParE toxins with ParD antitoxins, finding little evidence for the cross-interactions posited by others for an "anti-addiction" role. Through studies to date, we have found different strengths of ParE toxin-induced phenotypes for homologous (30-80%) sequences, consistent with different levels DNA gyrase inhibition. We also identified different *in vitro* IC_{50} values for inhibition of the gyrase enzyme from *E. coli* versus that from *P. aeruginosa* by the same ParE toxin protein, suggesting a complex structure-function relationship. Through our studies, we also characterized RNase-type toxins, a promiscuous nuclease activity, and species-specific toxicity for the YoeB type (structure 6n90).

   Snead, K.J., Moore, L.L., **Bourne, C.R.** "ParD antitoxin hotspot alters a disorder-to-order transition upon binding to its cognate ParE toxin, lessening its interaction affinity and increasing its protease degradation kinetics." 2022 *Biochemistry* 61(1):34. PMID: 34914387; PMCID: PMC9805813

   Snead, K.J., **Bourne, C.R.** "Intrinsic degradation of the Type-II antitoxin ParD from *Pseudomonas aeruginosa*." 2021 bioRxiv. 2021.03.29.437564.

   Bourne C.R. "Evaluating the potential for cross-interactions of antitoxins in Type II TA systems." 2020 Toxins (Basel). 12(6):422. PMID: 32604745; PMCID: PMC7354431.

3. **New inhibitors of bacterial dihydrofolate reductase:** Antibiotic resistance has challenged healthcare for decades, and those concerns were starkly amplified in the Anthrax attacks of 2001. The premise of our projects was to develop dihydrofolate reductase (DHFR) inhibitors that would be effective against bacteria of concern. In my previous position, I carried out extensive SAR studies to characterize a series of inhibitors derived from the structure of the antibiotic trimethoprim, including whole cell MIC measurements, *in vitro* enzyme activity inhibition, and three-dimensional structure determinations. I regularly interfaced with medicinal and synthetic organic chemists as well as microbiologists and became Select Agent certified to carry out screening work. *This work was continued in my independent research lab and forms the basis for our expanded anti-folate development interests*.

   Muddala NP, White JC, Nammalwar B, Pratt I, Thomas LM, Bunce RA, Berlin KD, **Bourne C.R.** "Inhibitor design to target a unique feature in the folate pocket of Staphylococcus aureus dihydrofolate reductase." 2020 *Eur J Med Chem.* 200:112412. PMID: 32502861; PMCID: PMC7932028.

   Bourne C.R., Wakeham N, Webb N, Nammalwar B, Bunce RA, Berlin KD, Barrow WW. "The structure and competitive substrate inhibition of dihydrofolate reductase from *Enterococcus faecalis* reveal restrictions to cofactor docking." 2014 *Biochemistry*. 53(7):1228. PMID: 24495113; PMCID: PMC3985486.

   Bourne C.R., Wakeham N, Nammalwar B, Tseitin V, Bourne PC, Barrow EW, Mylvaganam S, Ramnarayan K, Bunce RA, Berlin KD, Barrow WW. "Structure-activity relationship for enantiomers of potent inhibitors of *B. anthracis* dihydrofolate reductase." 2013 *Biochim Biophys Acta*. 1834(1):46. PMID: 22999981; PMCID: PMC3530638.

   Bourne, C.R., Barrow, E.W., Bunce, R.A., Bourne, P.C., Berlin, K.D., Barrow, W.W. "Inhibition of antibiotic-resistance *Staphylococcus aureus* by the broad-spectrum dihydrofolate reductase inhibitor RAB1." 2010 *Antimicrob Agents Chemother.* 54(9):3825. PMID 20606069; PMCID: PMC2934973.

4. **Collaborations in Structural Biology:** My research team is highly collegial and seeks to expand our scientific interests through sharing expertise, especially in overlaps with medicinal chemists (Burgett, O'Reilly). The collaboration with the Burgett team is on-going, and we are screening samples for cryo-EM SPA to characterize and test novel hypotheses on ORP family lipid transport and function. I have on-going collaborations in structure-function studies with other local colleagues Dr. Avishek Mitra (OSU) focused on heme-scavenging *Mycobacterial* PPE proteins and Dr. Kara DeLeon (OU) working with unique large adhesion proteins required for biofilm formation by *Desulfovibrio* species. Through these interactions I

provide co-mentorship to students beyond my department while expanding opportunities in research, networking, and publications for students in my own research program.

Our contributions to other research programs have resulted in the following co-authored publications:

Severance ZC, Nuñez JI, Le-McClain AT, Malinky CA, Bensen RC, Fogle RS, Manginelli GW, Sakers SH, Falcon EC, Bui RH, Snead KJ, **Bourne C.R.**, Burgett AWG. "Structure-activity relationships of ligand binding to Oxysterol-Binding Protein (OSBP) and OSBP-Related Protein 4." 2023 *J Med Chem.* 66(6):3866-3875. PMID: 36916802.

Boyer ZW, Kessler H, Brosman H, Ruud KJ, Falkowski AF, Viollet C, **Bourne C.R.**, O'Reilly MC. "Synthesis and characterization of functionalized amino dihydropyrimidines toward the analysis of their antibacterial structure-activity relationships and mechanism of action." 2022 *ACS Omega* 7(42):37907. PMID: 36312355; PMCID: PMC9607683.

Johnson BP, Kumar V, Scull EM, Thomas LM, **Bourne C.R.**, Singh S. "Molecular basis for the substrate promiscuity of isopentenyl phosphate kinase from *Candidatus methanomethylophilus* alvus." 2022 *ACS Chem Biol.* 17(1):85-102. PMID: 34905349; PMCID: PMC9745668.

5. **A new strategy for antiviral therapy using misdirection of capsid assembly:** As a *post-doc* I contributed to a novel approach in anti-viral therapies by altering the assembly pathway of the Hepatitis B virus capsid. Using biophysical measurements and biochemical assays, we determined this compound mis-directed HBV assembly and, using a structure-guided approach, I identified point mutants that could mimic these mis-directing effects. I was awarded a fellowship from the American Cancer Society to pursue structural studies, leading to my identification of the binding pocket for these compounds.

Bourne C.R., Finn MG, Zlotnick A. "Global structural changes in hepatitis B virus capsids induced by the assembly effector HAP1." 2006 *J Virol.* 80(22):11055. PMID: 16943288; PMCID: PMC1642186.

Stray SJ, **Bourne C.R.**, Punna S, Lewis WG, Finn MG, Zlotnick A. "A heteroaryldihydropyrimidine activates and can misdirect hepatitis B virus capsid assembly." 2005 *Proc Natl Acad Sci U S A.* 102(23):8138. PMID: 15928089; PMCID: PMC1149411.

Bourne C., Lee S, Venkataiah B, Lee A, Korba B, Finn MG, Zlotnick A. "Small-molecule effectors of hepatitis B virus capsid assembly give insight into virus life cycle." 2008 *J Virol.* 82(20):10262. PMID: 18684823; PMCID: PMC2566253.

9 publications (including two review articles) from 2020 – current
senior corresponding author on 6; first authors: one undergraduate, remaining five graduate

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/10usXwuC15FAk/bibliography/47974641/public/?sort=date&direction=descending

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. DO NOT EXCEED FIVE PAGES.

NAME: De Leon, Kara

eRA COMMONS USER NAME (credential, e.g., agency login): deleonkb

POSITION TITLE: Assistant Professor of Microbiology

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
Northwest Nazarene University, Nampa, Idaho	BS	05/2006	Biology and Chemistry
Montana State University, Bozeman, Montana	PHD	05/2013	Microbiology
University of Missouri, Columbia, Missouri	Postdoctoral Fellow	08/2019	Microbial Genetics and Environmental Microbiology

A. Personal Statement

My interdisciplinary research combines computational biology, genomics, high-throughput and targeted mutant generation, and biochemical and molecular methods to determine the genetic requirements for microbial functions of interest. I am particularly interested in the community structure and function of anaerobic microbes when attached to surfaces as biofilms because on or near an abiotic or biotic surface tends to be where the most active microbes are found. My lab has generated over 30 mutants in our model sulfate-reducing bacterium, Desulfovibrio vulgaris Hildenborough and generated a transposon mutant pool comprised of approximately 300,000 transposon mutants. We grow robust, steady-state biofilms in anaerobic bioreactors and have all the equipment needed to perform the anaerobic culturing for this project. Recently, we differentiated the role of two adhesins in cell-cell and cell-surface attachment. Through a collaboration with Dr. Christina Bourne at OU, we have recently added structural biology to our tools to study biofilms. My research contributions have also been published under my former name Kara B. Bowen.

1. Pickens CP, Wang D, Pan C, De León KB. Absence of biofilm adhesin proteins changes surface attachment and cell strategy for Desulfovibrio vulgaris Hildenborough. J Bacteriol. 2025 Jan 31;207(1):e0037924. PubMed Central ID: PMC11784015.
2. De León KB. mSphere of Influence: Surface Sensing in Biofilm Formation. mSphere. 2021 May 12;6(3) PubMed Central ID: PMC8125057.
3. Wall JD, Zane GM, Juba TR, Kuehl JV, Ray J, Chhabra SR, Trotter VV, Shatsky M, De León KB, Keller KL, Bender KS, Butland G, Arkin AP, Deutschbauer AM. Deletion Mutants, Archived Transposon Library, and Tagged Protein Constructs of the Model Sulfate-Reducing Bacterium Desulfovibrio vulgaris Hildenborough. Microbiol Resour Announc. 2021 Mar 18;10(11) PubMed Central ID: PMC7975874.
4. De León KB, Zane GM, Trotter VV, Krantz GP, Arkin AP, Butland GP, Walian PJ, Fields MW, Wall JD. Unintended Laboratory-Driven Evolution Reveals Genetic Requirements for Biofilm Formation by Desulfovibrio vulgaris Hildenborough. mBio. 2017 Oct 17;8(5) PubMed Central ID: PMC5646257.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2022 - Affiliate Faculty, Institute for Environmental Genomics, University of Oklahoma, Norman, Oklahoma

2019 - Assistant Professor of Microbiology, University of Oklahoma, Norman, Oklahoma

2019 - 2019	Research Scientist, University of Missouri, Columbia, MO
2013 - 2018	Post-doctoral Research Fellow, University of Missouri, Columbia, MO
2008 - 2013	Graduate Research Fellow, Montana State University, Bozeman, MT
2007 - 2008	Research Technician, Northwest Nazarene University, Nama, ID

Honors

2008 - 2013	NSF-IGERT Fellowship, Montana State University
2007 - 2013	Molecular Biosciences Program Fellowship, Montana State University
2022	Vice President for Research & Partnerships Award for Excellence in Transdisciplinary Convergent Research, University of Oklahoma
2020	University of Oklahoma Junior Faculty Fellowship, University of Oklahoma
2019	Peggy Cotter Travel Award, Missouri Branch American Society for Microbiology

C. Contribution to Science

1. Physiological Characterization of Sulfate-Reducing Bacteria (SRB). I have worked on linking genes to function in SRB for over 13 years and this has been a focus of my research since beginning my own lab in 2019. The references here and those highlighted in my Personal Statement above are examples of these contributions to the field which include: the discovery of 5 genes required for biofilm formation and 2 for isethionate transport by my lab (De Leon and Day), fitness changes during hydrogen oxidation and uranium tolerance as part of a large collaborative effort to characterize the fitness effects of mutants in over 400 conditions to date (Trotter et al). We have also shown that molybdate inhibition of SRB via ATP depletion is not only due to futile cycling of by SRB-specific enzyme sulfate adenylyl transferase, but a YcaO-like enzyme also contributes to the depletion (Zane et al; I led this work as a research scientist and completed it at OU). I generated 52 mutants of the model sulfate-reducing bacterium, Desulfovibrio vulgaris Hildenborough, during my post-doctoral research (some of which were deposited into a mutant culture collection described in Wall et al 2021) and my lab at OU has generated over 30 mutants and a transposon mutant library that we use to assess the fitness of nearly every gene in the genome. My current research is on surface-sensing (commentary in De Leon 2021) and the mechanism of biofilm formation by SRB.
    a. Trotter V, Shatsky M, Price M, Juba T, Zane G, De León K, Majumder E, Gui Q, Ali R, Wetmore K, Kuehl J, Arkin A, Wall J, Deutschbauer A, Chandonia J, Butland G. Large-scale genetic characterization of the model sulfate-reducing bacterium, Desulfovibrio vulgaris Hildenborough. Frontiers in Microbiology. 2023; 14:-. Available from: https://www.frontiersin.org/articles/10.3389/fmicb.2023.1095191/full DOI: 10.3389/fmicb.2023.1095191
    b. Zane G, Wall J, De León K. Novel Mode of Molybdate Inhibition of Desulfovibrio vulgaris Hildenborough. Frontiers in Microbiology. 2020 December 8; 11:-. Available from: https://www.frontiersin.org/articles/10.3389/fmicb.2020.610455/full DOI: 10.3389/fmicb.2020.610455
    c. Day LA, De León KB, Kempher ML, Zhou J, Wall JD. Complete Genome Sequence of Desulfovibrio desulfuricans IC1, a Sulfonate-Respiring Anaerobe. Microbiol Resour Announc. 2019 Aug 1;8(31) PubMed Central PMCID: PMC6675984.
2. Structure and Function of Biofilms in Different Environments. My graduate training was focused on the ecology of different environmental biofilms. I have analyzed the microbial community by sequencing biofilms from hot springs and have contributed reviews on on subsurface and oil and gas system biofilms where I consolidated the literature and proposed strategies for microbial cell attachment strategies, microbial community activities, and mechanisms of survival within these environments.
    a. Jenneman G, De León K. Environmental stressors alter the susceptibility of microorganisms to biocides in upstream oil and gas systems. International Biodeterioration & Biodegradation. 2022 April; 169:105385-. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0964830522000130 DOI: 10.1016/j.ibiod.2022.105385
    b. Smith H, Zelaya A, De León K, Chakraborty R, Elias D, Hazen T, Arkin A, Cunningham A, Fields M. Impact of hydrologic boundaries on microbial planktonic and biofilm communities in shallow terrestrial subsurface environments. FEMS Microbiology Ecology. 2018 September 27; 94(12):-. Available from: https://academic.oup.com/femsec/article/doi/10.1093/femsec/fiy191/5107865 DOI: 10.1093/femsec/fiy191

c. Bowen De León K, Gerlach R, Peyton BM, Fields MW. Archaeal and bacterial communities in three alkaline hot springs in Heart Lake Geyser Basin, Yellowstone National Park. Front Microbiol. 2013;4:330. PubMed Central PMCID: PMC3824361.

3. Wastewater-Based Epidemiology for Pathogen Detection in Oklahoma. From January 2022-August 2023 I led the microbiology and molecular labs for monitoring pathogens in wastewater across the state of Oklahoma. This is part of a large collaborative effort that includes microbiologists, engineers, epidemiologist, and an architect. This was funded through contracts with the state and 2 county health departments and started with SARS-CoV-2 monitoring during the pandemic. As part of this effort, I expanded our monitoring capabilities to 13 different pathogens. My contributions to the field have been in methods development for new pathogen targets, particularly for bacterial targets that cause gastrointestinal disease and identification of novel SARS-CoV-2 lineages within wastewaters of Oklahoma. I was an invited panelist on methods for bacterial targets and my contributions were recently highlighted in a commentary written by the post doc that moderated the panel discussion (Philo et al) and my methods for Campylobacter and Salmonella are described in Kuhn et al. In recognition of our impactful contributions to the field and the citizens of Oklahoma, the I and the 4 other PIs on this project were awarded the OU Vice President for Research & Partnerships Award for Excellence in Transdisciplinary Convergent Research in 2022.
   a. Shelton K, Deshpande GN, Sanchez GJ, Vogel JR, Miller AC, Florea G, Jeffries ER, De León KB, Stevenson B, Kuhn KG. Real-Time Monitoring of SARS-CoV-2 Variants in Oklahoma Wastewater through Allele-Specific RT-qPCR. Microorganisms. 2024 Sep 30;12(10) PubMed Central PMCID: PMC11509313.
   b. Philo S, De León K, Noble R, Zhou N, Alghafri R, Bar-Or I, Darling A, D'Souza N, Hachimi O, Kaya D, Kim S, Gaardbo Kuhn K, Layton B, Mansfeldt C, Oceguera B, Radniecki T, Ram J, Saunders L, Shrestha A, Stadler L, Steele J, Stevenson B, Vogel J, Bibby K, Boehm A, Halden R, Delgado Vela J. Wastewater surveillance for bacterial targets: current challenges and future goals. Applied and Environmental Microbiology. 2024 January 24; 90(1):-. Available from: https://journals.asm.org/doi/10.1128/aem.01428-23 DOI: 10.1128/aem.01428-23
   c. Kuhn K, Shukla R, Mannell M, Graves G, Miller A, Vogel J, Malloy K, Deshpande G, Florea G, Shelton K, Jeffries E, De León K, Stevenson B. Using Wastewater Surveillance to Monitor Gastrointestinal Pathogen Infections in the State of Oklahoma. Microorganisms. 2023 August 30; 11(9):2193-. Available from: https://www.mdpi.com/2076-2607/11/9/2193 DOI: 10.3390/microorganisms11092193