

# Connor L. Brown, PhD

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## EDUCATION

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- Ph. D. Virginia Tech, Genetics, Bioinformatics, and Computational Biology (GBCB)  
Aug. 2019 – Dec. 2023 | GPA 3.84 | Advisor: Amy Pruden  
Dissertation title: *Bioinformatic Analysis of Wastewater Metagenomes Reveals Microbial Ecological and Evolutionary Phenomena Underlying Associations of Antibiotic Resistance with Antibiotic Use*
- M.S. Virginia Tech, Biochemistry  
May 2019 | GPA: 4.0 | Advisor: Biswarup Mukhopadhyay  
Thesis: *Secretion and environmental biochemistry of Legionella pneumophila in corrosive water*
- B.S. Virginia Tech, Biochemistry May 2018 | GPA: 3.54

## SELECTED HONORS AND AWARDS

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- 2022 Outstanding Doctoral Student in Interdisciplinary Programs | Virginia Tech  
2021 Outstanding Interdisciplinary Doctoral Student | GBCB  
2018 Commendation for excellence in undergraduate research  
2016 Inaugural Fralin Undergraduate Research Fellowship

## PROFESSIONAL SERVICE

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- 2021-2023 GBCB senator to the Graduate and Professional Student Senate  
2022 Co-chair of the Virginia Tech 38<sup>th</sup> Annual Graduate and Professional Student Senate Research Symposium  
2019-2020\* Ximbio | Campus representative for life science reagent non-profit  
2018-Present American Society for Biochemistry | Student member  
2016-Present American Society for Microbiology | Student member  
\*Position ended due to COVID-19

## RESEARCH APPOINTMENTS

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- Post-Doctoral Researcher** 2023-present. Virginia Tech Engineering Water Resources, Blacksburg, Virginia  
**Interdisciplinary Graduate Research Assistant** 2018 to Dec. 2023. Advisor: Amy Pruden. Virginia Tech Engineering Water Resources, Blacksburg, Virginia  
**Undergraduate Research Assistant** 2016 to 2018. Advisors: Amy Pruden, Marc Edwards. Virginia Tech Engineering Water Resources, Blacksburg, Virginia

## TEACHING SERVICE

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- Graduate Teaching Assistant** Aug-Dec 2019. Graduate teaching assistant for Virginia Tech BCHM4115 (First of two for-majors Biochemistry course).  
**Teaching Assistant** May 2022. Teaching assistant for a student-led metagenomics workshop.  
**Guest Lecturer** Jan 2024. Guest lecturer for Virginia Tech Transdisciplinary Research Seminar.

## CONTRIBUTIONS TO SPONSORED RESEARCH PROJECTS

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- 2024 **Quantifying Wastewater Sources of Antibiotic Resistance to Aquatic and Soil Environments and Associated Human Health Risks** \$2,000,000 (2024-2027 est.)  
Environmental Protection Agency (EPA); PI: Lola Olabode (Water Research Foundation)

Personal contribution: Contributed bioinformatics expertise and proposal of novel computational methods to address multivariate antibiotic susceptibility profiles of pathogens predicted solely from metagenomic data.

**2022                    Advancing Comprehensive Wastewater Surveillance of Endemic and Emerging Pathogens Across Multiple Microbial Domains through Strain-resolved Metagenomics \$584,968 (2022-2024)**

Centers for Disease Control (CDC); PI: Amy Pruden (VT), Co-PIs: Liqing Zhang (VT), Peter Vikesland (VT)

Personal contribution: Contribution to proposal development and project management as a PhD student/post-doc. Intellectual contribution to the development/evaluation of lab methods (nucleic acid extraction, target enrichment, ddPCR, short- and long-read sequencing) and software development (integration of standards for quantitative metagenomics and strain-resolved bioinformatics) to recommend a protocol to the CDC National Wastewater Surveillance System (NWSS) that captures multiple pathogens and ARGs, starting with sample collection all the way through metagenomic analysis.

**2020                    WRF 4961: The Use of Next Generation Sequencing (NGS) Technologies and Metagenomics Approaches to Evaluate Water and Wastewater Quality Monitoring and Treatment Technologies \$490,015 (2020-2023)**

Water Research Foundation, PI: Amy Pruden (VT), Co-PI: Emily Garner (WVU)

Personal contribution: Contributed to the development of an extensive guidance document for US water utilities on the use of NGS. Primary author of the chapter on methods and applications of metagenomic assembly algorithms. Co-authored the introduction to the report.

**2020                    Frameworks: Developing Cyberinfrastructure for Waterborne Antibiotic Resistance Risk Surveillance (CI4-WARS) \$1,299,036 (2020-2024)**

National Science Foundation, PI: Liqing Zhang (VT), Co-PIs: Amy Pruden (VT), Peter Vikesland (VT), Ali Butt (VT)

Personal contribution: Led major sampling efforts for a prototype metagenomics based environmental monitoring program at three full scale wastewater treatment plants. Oversaw the collection of >1,000 wastewater samples and the generation of  $11 \times 10^{12}$  basepairs of Illumina and nanopore metagenomic sequences. Serving as lead analyst in a team of computer science PhD students and 6 undergraduate students. Worked with software developers to facilitate interdisciplinary communication and efficient completion of objectives for web interfaces with monitoring resources.

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## UNFUNDED RESEARCH PROPOSALS

**2023                    IntBio: A Predictive, Biologically Aware Framework for Horizontal Gene Transfer Dynamics in Wastewater (not funded) (2024-2027) \$1,742,708**

National Science Foundation, PIs: Allison Lopatkin (PI, U. Rochester), Amy Pruden (VT), Lenwood Heath (VT), Peter Vikesland (VT), Liqing Zhang (VT), Jillian Pope (FAMU).

Personal contribution: Lead author for the Pruden lab. Conducted experiments and provided data for preliminary results, brainstorming and development of research objectives, writing and literature review, and design of laboratory experiments. Collaboratively produced a novel intermediate-throughput experimental framework for hypothesis testing relating to the influence of selective agents on horizontal gene transfer in environmental organisms.

**2021                    NLM: Developing a comprehensive data and tool resource for identification of novel antibiotic resistance genes (not funded) (2022-2025) \$1,494,786**

National Institutes of Health, PIs: Liqing Zhang (PI, VT), Lifu Huang (VT), Amy Pruden (VT), Peter Vikesland (VT).

Personal contribution: Conducted the data analysis to demonstrate the proof-of-concept and participated in multiple rounds of editing and proof-reading.

**2021, 2023      Edge: ARGnet: Developing a comprehensive data and tool resource for identification of novel antibiotic resistance genes (not funded) (2022-2025/2023-2026)**  
\$1,300,000

National Science Foundation: PIs: Liqing Zhang (PI, VT), Anne Brown (VT), Lenwood Heath (VT), Amy Pruden (VT), Peter Vikesland (VT).

Personal contribution: Primary author of the proposal. Led the development of the prototype of the proposed online resource for the identification of putative antibiotic resistance genes (ARGs) including: (1) protein structural modeling and inhibitor design through molecular docking; (2) large-scale phylogenomics of ARGs and putative hosts; and (3) expansion of existing ARGminer, previously developed by the Zhang lab, and integration with updated deep learning models. Led development of Aims 1 and 2.

## PUBLICATIONS

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### Peer-Reviewed Journal Articles in Print (12)

1. **Brown, C.L.**, Maile-Moskowitz, A., Xia, K., Logan, L., Zhang, L. Pruden, A., Vikesland, P. Selective agents and horizontal gene transfer underly microdiversity-level fate of resistance genes during biological wastewater treatment Available on Research Square <https://www.researchsquare.com/article/rs-3486488/v1>, Provisionally accepted by Nature Communications.
2. **Brown, C.L.**, Mullet, J., Hindi, F., Stoll, J., Gupta, S., Choi, M., Vikesland, P., Keenum, I., Pruden, A., Zhang, L. mobileOG-db: a manually curated reference database of proteins mediating the life cycle of bacterial mobile genetic elements. *Appl. Env. Micro.* <https://doi.org/10.1128/aem.00991-22>
3. **Brown, C.L.**, Keenum, I., Dai, D., Vikesland, P., Pruden, A., Zhang, L. (2021). Critical evaluation of short, long, and hybrid assembly for contextual analysis of antibiotic resistance genes in complex environmental metagenomes. *Scientific reports* 11.1 (2021): 3753. <https://doi.org/10.1038/s41598-021-83081-8>
4. **Brown, C.L.**, Garner, E., Jospin, G., Coil, D. A., Schwake, D. O., Eisen, J. A., Mukhopadhyay, B., & Pruden, A. J. (2020). Whole genome sequence analysis reveals the broad distribution of the RtxA type 1 secretion system and four novel putative type 1 secretion systems throughout the *Legionella* genus. *PLOS ONE*, 15 (1), e0223033. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0223033>
5. Kang, S., Maile-Moskowitz, A., **Brown, C.L.**, Pruden, A., Vikesland, P. (2024) Highly Multiplexed Reverse-Transcription Loop-Mediated Isothermal Amplification and Nanopore Sequencing (LAMPore) for Wastewater-Based Surveillance. *Environmental Science & Technology Water* <https://pubs.acs.org/doi/10.1021/acsestwater.3c00690>.
6. Cullom, A., Spencer, M. S., Williams, M. D., Falkinham III, J. O., **Brown, C.L.**, Edwards, M. A., & Pruden, A. (2023). Premise Plumbing Pipe Materials and In-Building Disinfectants Shape the Potential for Proliferation of Pathogens and Antibiotic Resistance Genes. *Environmental Science & Technology*. <https://doi.org/10.1021/acs.est.3c05905>
7. Davis, B., **Brown, C.L.**, Liguori, K., Milligan, E., Pruden, A., Keenum, I. Towards Standardization of Metagenomics for Monitoring Antibiotic Resistance in Wastewater and Impacted Aquatic Environments *Critical Reviews in Environmental Science and Technology*. 53:19, 1731-1756, DOI: 10.1080/10643389.2023.2181620.
8. Dai, D.; **Brown, C. L.**; Bürgmann, H.; Larsson, J; Nambi, I; Zhang, T; Flach, C-F; Pruden, A.; Vikesland, P. Long-read metagenomic sequencing reveals shifts in associations of antibiotic resistance genes with mobile genetic elements from sewage to activated sludge. *Microbiome* **10**, 20 (2022). <https://doi.org/10.1186/s40168-021-01216-5>
9. Marano, R. B. M., Fernandes, T., Manaia, C. M., Nunes, O., Morrison, D., Berendonk, T. U., Kreuzinger, N., Telson, T., Corno, G., Fatta-Kassinos, D., Merlin, C., Topp, E., Jurkevitch, E., Henn,

- L., Scott, A., Heß, S., Slipko, K., Laht, M., Kisand, V., [...] **Brown, C.L.**, Cytryn, E. (2020). A global multinational survey of cefotaxime-resistant coliforms in urban wastewater treatment plants. *Environment International*, 144, 106035. <https://doi.org/10.1016/j.envint.2020.106035>
10. Garner, E., **Brown, C. L.**, Schwake, D. O., Rhoads, W. J., Arango-Argoty, G., Zhang, L., Jospin, G., Coil, D. A., Eisen, J. A., Edwards, M. A., & Pruden, A. (2019). Comparison of Whole-Genome Sequences of *Legionella pneumophila* in Tap Water and in Clinical Strains, Flint, Michigan, USA, 2016. *Emerging Infectious Diseases*, 25 (11). [www.ncbi.nlm.nih.gov/pmc/articles/PMC6810188/](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC6810188/)
  11. Moumi, N., **Brown, C.L.**, Vikesland, P., Pruden, A., and Zhang, L, Protein-Protein Interaction Network Analysis Reveals Distinct Patterns of Antibiotic Resistance Genes at the IEEE BIBM 2022 conference, Las Vegas, Nevada, USA.
  12. Chandak, S.; Zhang, L.; **Brown, C. L.**, and Huang, L. 2022. Towards Automatic Curation of Antibiotic Resistance Genes via Statement Extraction from Scientific Papers: A Benchmark Dataset and Models. In Proceedings of the 21st Workshop on Biomedical Language Processing, pages 402–411, Dublin, Ireland. Association for Computational Linguistics.

#### In Review (8)

1. Maile-Moskowitz, A., **Brown, C.L.**, Rumi, M.A., Sein, J., Choi, M., Hindi, F., Mullet, J., Emon, M., Moumi, N.A., Blair, M.F., Rao, J., Baffoe-Bonnie, A., Zhang, L A., Pruden, A., Vikesland, P.; Can Wastewater-Based Surveillance Relate Antimicrobial Use to Resistance Patterns? Metagenomic Analysis of Two Neighboring Treatment Plants. *In review at Nature Water*.
2. **Brown, C.L.**, Huang, E., Garcia, J. Brown, A. National correspondence test reveals distinct patterns of transfer student perceptions by researchers of differing seniority at R1 universities. In revision, *CC Journal of Research and Practice*.
3. **Brown, C.L.**, Feng, Y.C., Song, H., Maile-Moskowitz, A., Snead, Xia, K., D., Logan, Vikesland, P., L., Zhang, L. Pruden, A. Kairos enables sensitive detection of mobile element-associated microdiversity and in situ horizontal gene transfer in complex microbiomes *Available on BioRxiv* [<https://doi.org/10.1101/2023.10.24.563791>], *pending submission to Microbiome*.
4. Talat, A., Bashir, Y., **Brown, C.L.**, Gupta, D., Khaleel, N., Khan, A., Advancing AMR Surveillance: Metagenomic Insights from Traditional and UV-enabled Advanced Wastewater Treatment Plants. *Submitted to Environmental Pollution*.
5. Rumi, M.A., Oh, M., Davis, B.C., Juvekar, A., **Brown, C.L.**, Vikesland, P.J., Pruden, A., Zhang, L. MetaCompare 2.0: Differential ranking of ecological and human health resistome risks. *In review at FEMs*.
6. Choi, JM.; Manthapuri, V.; Keenum, I.; **Brown, C.L.**; Xia, K.; Vikesland, P.; Blair, M.; Bott, C.; Pruden, A.; Zhang, L. A machine learning approach to predicting PPCP removal through various water reuse treatment processes. *Submitted to ES&T WR*.
7. Aguilar, D., Song, Y., **Brown, C.L.**, Pruden, A., Helm, R.F. Multiomic profiling of copper resistant outbreak strains of *Legionella pneumophila*. *In review at Appl. Env. Micro*.
8. Song, Y., Aguilar, D., **Brown, C.L.**, Pruden, A., & Edwards, M. Copper induced viable-but-not-culturable *Legionella pneumophila* retain infectivity and undergo metabolic shutdown. *In revision. Microorganisms*.

#### In Preparation (6)

1. **Brown, C.L.**, Afrin, MR., McDaniel, L., Maile-Moskowitz, A., Sein, J., Choi, M., Hindi, F., Mullet, J., Emon, M., Moumi, N.A., Blair, M.F., Rao, J., Baffoe-Bonnie, A., Vikesland, P., Pruden, A., Zhang, L. Resistance in sewage-associated microbiota mirror patterns of clinical bacteria and reflect a variable lagging association with antibiotic usage
2. **Brown, C.L.**, Vikesland, P.V., Pruden, A., Zhang, L.; Sewage metagenomics traces regionally prevalent variants of CTX-M extended spectrum beta-lactamases
3. Maile-Moskowitz, Ayella, **Brown, C.L.**, Latania Logan, Kang Xia, Amy Pruden, P. V. Impact of hospital wastewater on simulated activated sludge treatment and antibiotic resistome. in 47–85 (2023).

4. Kulkarni, R., Arango, G., Gupta, S., Pruden, A., Zhang, L. DeepARG+: A Computational Tool for Predicting Antibiotic Resistance Genes Leveraging Amino Acid Sequences and Physiochemical Properties
5. Keenum, I. **Brown, C.L.**, Gupta, S., Calarco, J., Harwood, J., Pruden, A. Applications and limitations of genome resolved metagenomics for monitoring of antibiotic resistance at recycled water treatment plants
6. Khoi, D., **Brown, C.L.**, Pruden, A., Zhang, L. Bioinformatic recovery of putatively dual-function antibiotic resistance genes with homology to disparate resistance classes.

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## PEER REVIEW SERVICE

Peer Reviewer for *Genes (1)*, *Frontiers in Water (1)*, *Briefings in Bioinformatics (2)*, *Environmental Science: Nano (4)*, *Bioinformatics (1)*, *ISME (3)*, *PNAS (1)*, *Microbiology Spectrum (1)*; *Water Research (1)*; *Env. Science and Pollution Research (1)*. *npj Clean Water (1)*; *Microbiome (2)*; *Environmental Science & Technology (1)*. Trusted reviewer for *Microbiome*.

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## PRESENTATIONS

### Major Oral Presentations (presenter)

1. **Brown, C.L.**, Afrin, MR., McDaniel, L., Maile-Moskowitz, A., Sein, J., Choi, M., Hindi, F., Mullet, J., Emon, M., Moumi, N.A., Blair, M.F., Rao, J., Baffoe-Bonnie, A., Vikesland, P., Pruden, A., Zhang, L. (2024). Resistance in sewage associated microbiota mirror patterns of clinical isolates and reflect a variable lagging association with antibiotic usage. AMR, Genomes, Big Data, and Emerging Technologies, Hinxton, U.K., March 14-17.
2. **Brown, C.L.**, Afrin, MR., McDaniel, L., Maile-Moskowitz, A., Sein, J., Choi, M., Hindi, F., Mullet, J., Emon, M., Moumi, N.A., Blair, M.F., Rao, J., Baffoe-Bonnie, A., Vikesland, P., Pruden, A., Zhang, L. (2024). Resistance in sewage associated microbiota mirror patterns of clinical isolates and reflect a variable lagging association with antibiotic usage. Environmental Dimensions of Antibiotic Resistance (EDAR) 7, Montreal, Canada, May 25-28.
3. **Brown, C.L.**, Maile-Moskowitz, A., Vikesland, P., Zhang, L., Pruden, A. (2023). Longitudinal metagenomics of wastewater relays signals of community and environmental health that are sensitive to seasonal weather patterns. Microbial Ecology and Water Engineering Special Section Conference, Brisbane, Australia, September 20-23.
4. **Brown, C.L.**, Mullet, J., Maile-Moskowitz, A., Vikesland, P., Zhang, L., Pruden, A. (2022). Development and application of mobileOG-db: a unified database and ontology of MGE protein families leveraged for tracking the fate of hospital sewage-derived resistance genes. Environmental Dimensions of Antibiotic Resistance (EDAR) 6. Gothenburg, Switzerland. Sep 15-18.
5. **Brown, C.L.**, Maile-Moskowitz, A., Vikesland, P., Pruden, A., Zhang, L. (2022). Metagenomics based environmental monitoring for community and environmental health: preliminary results of a pilot system at three full scale wastewater treatment plants, Gen. Bio. Comp. Bio Departmental Seminar. September 2022.
6. **Brown, C.L.** (2022). Harnessing massive biological data to protect natural resources and human health through surveillance, monitoring, and impact assessment. Invited talk at Oakwood University Graduate Research Seminar. September 2022.

### All Other Posters and Presentations

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| 2023 | Evaluating a metagenomic workflow for nontargeted detection and typing of disease agents in wastewater (AEESP)<br>Katie Scott, <b>Connor Brown</b> , Haoqiu Song, Matthew Blair, Benjamin Davis, Clayton Markham, Liqing Zhang, Amy Pruden, and Peter Vikesland |
| 2022 | CIWARS: harnessing massive biological data for monitoring antibiotic resistance and pathogens through shotgun metagenomics of wastewater, CIP-CAR NRT, opening workshop<br><b>Connor Brown</b> , Monjura Rumi, Peter Vikesland, Amy Pruden, Liqing Zhang        |
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- 2022 Assessing the impact of the COVID-19 pandemic on antibiotic resistance and the microbial community of wastewater  
Ayella Maile-Moskowitz, Raul Gonzalez, Carla Finkelstein, **Connor Brown**, Peter Vikesland, Amy Pruden
- 2022 Proteomic profiling of a copper resistant *Legionella pneumophila* strain.  
Didier Aguilar, Yang Song, **Connor Brown**, Marc Edwards, Amy Pruden, Rich Helm
- 2022 Effect of hospital sewage on antibiotic resistance in treated wastewater effluent (2022, AEESP)  
Ayella Maile-Moskowitz, **Connor Brown**, Latania Logan, Amy Pruden, Peter Vikesland
- 2022 Loop-mediated isothermal amplification (LAMP) and nanopore sequencing for SARS-CoV-2 wastewater surveillance, (2022, AEESP)  
Seju Kang, **Connor Brown**, Ayella Maile-Moskowitz, Amy Pruden, Peter Vikesland
- 2021 Metagenomics-enabled surveillance of the environmental mobilome: towards predictive public health insights (Virginia Tech GBCB department seminar)  
**Connor Brown**
- 2021 Evaluation and quantification of high molecular weight DNA from wastewater across different DNA extraction kits  
Fadi Hindi, James Mullet, Minyoung Choi, Krista Liguori, Benjamin Davis, **Connor Brown**, Amy Pruden (2021 Summer REU Symposium)
- 2021 Influence of *Acanthamoeba castellanii* on the copper inactivation of environmental strains of *Legionella pneumophila* in simulated premise plumbing  
Minyoung Choi, Didier Mena Aguilar, James Mullet, Fadi Hindi, Marc Edwards, **Connor Brown**, Amy Pruden (2021 Summer REU Symposium)
- 2021 mobileOGs.pl-kyanite: a tool for classifying bacterial mobile genetic elements using the colocalization pattern of mobile orthologous groups (2021 Summer REU Symposium)  
James Mullet, **Connor Brown**, Fadi Hindi, Minyoung Choi, Amy Pruden, Liqing Zhang
- 2021 Assessing Microbial Wastewater Community Composition and Antibiotic Resistance in the Presence of Hospital Sewage  
Delaney Snead, **Connor Brown**, Ayella Maile-Moskowitz, Latania Logan, Peter Vikesland, Amy Pruden
- 2021 Persistence of hospital-derived multidrug resistant bacteria in nitrifying sequencing batch reactors (poster; Wellcome Genome Conference, Online)  
**Connor Brown &** Ayella Maile-Moskowitz, Delaney Snead, Latania Logan, Peter Vikesland, Amy Pruden
- 2020 Impact of hospital effluent on levels and fate of antibiotic resistant organisms in sequencing batch reactors (oral presentation; Microbial Systems Symposium, Virginia Tech)  
Ayella Maile-Moskowitz, **Connor Brown**, Peter Vikesland, Amy Pruden
- 2020 Mass spectrometry methods to study the opportunistic pathogen *Legionella pneumophila* in premise plumbing.  
Didier Aguilar, Rebekah Martin, **Connor Brown**, Marc Edwards, Rich Helm, Amy Pruden
- 2019 Secretion and environmental biochemistry of *Legionella pneumophila* in corrosive water (Virginia Tech Biochemistry department seminar)  
Connor Brown
- 2018 Whole genome sequence comparison of clinical and drinking water *Legionella pneumophila* isolates associated with the Flint Water Crisis (2018 Microbiology of the Built Environment Gordon Research Conference, poster);  
Emily Garner, **Connor Brown**, Otto Schwake, William Rhoads, Gustavo Arango-Argoty, Liqing Zhang, Guillaume Jospin, David Coil, Jonathan Eisen, Marc Edwards, Amy Pruden

- 2017 Influence of climate on *Legionella* contamination in automobile washer fluid (9th International conference on Legionella, poster); Otto Schwake, **Connor Brown**, Linsey Marr
- 2017 Geographical Distribution of *Legionella pneumophila* in automobile washer fluid in the continental United States (ASM Microbe, poster)  
Otto Schwake, **Connor Brown**, Amy Pruden, Linsey Marr
- 2017 Is climate fate? *Legionella* in washer fluid may be a bigger problem in some states than in others (Fralin Undergraduate Research Fellowship Symposium, poster)  
**Connor Brown**, Otto Schwake, Amy Pruden, Linsey Marr
- 2016 Examining the effects of the Flint water crisis on Endemic Legionella populations: An ongoing investigation (Virginia State ASM, oral presentation)  
**Connor Brown**, Emily Garner, Otto Schwake, Amy Pruden, Marc Edwards
- 2016 Survey of science and health profession utilities of Virginia Western Community College for Legionella spp. (Shenandoah Valley Regional ASM, Poster)  
**Connor Brown**, Justin Magda, Kari Stanley

#### **STUDENTS MENTORED, DEGREE PROGRAM, & POST-GRADUATE PLACEMENT/ACCOMPLISHMENTS**

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Yat Fei Cheung, Virginia Tech, Computer Modeling and Data Analytics (Virginia Tech, M.S. Program)  
Chad Kelly, Virginia Tech, Computer Modeling and Data Analytics; (Virginia Tech, GBCB Ph. D. Program)  
Loc Nguyen, Virginia Tech, GBCB Ph. D. Program  
Haoqiu Song, Virginia Tech, Computer Science Ph. D. Program  
Nazifa Mouni Ahmed, Virginia Tech, Computer Science Ph. D. Program  
Justin Sein, Virginia Tech, GBCB Ph. D. Program  
Minyoung Choi, Virginia Tech, Biology  
Fadi Hindi, Virginia Tech, Biology  
James Mullet\*, Virginia Tech, Biology and Biochemistry, (MIT, [*Biology Senior of the Year 2023*])  
Monica Gurung, Virginia Tech, Civil and Env. Engineering (UCLA Berkeley, M.S. Program)  
Callen Barlik, Virginia Tech, Microbiology (Johnson & Johnson)  
Ana Haines, Virginia Tech, Civil and Env. Engineering  
Delaney Snead\*\*, Virginia Tech, Civil and Env. Engineering (University of Michigan, Ph.D. Program [*CEE Senior of the Year, 2021*])