

# Katie Dillon

katiecdillon@gmail.com | Katie.Dillon@uga.edu

## EDUCATION

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### University of Georgia (Athens, GA)

2021 – Present

- PhD Candidate – Institute of Bioinformatics
- Principal Investigator – Travis Glenn, PhD
- Tentative graduation date: Summer 2025

### Oklahoma State University (Stillwater, OK)

2012 – 2016

- Bachelor of Science - Agricultural Sciences and Natural Resources
  - Major - Food Science

## RESEARCH & SCIENTIFIC EXPERIENCE

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### University of Georgia, Institute of Bioinformatics (Athens, GA)

- **Graduate Research Assistant** (full-time)

2021 – Present

*Skills: writing and submitting shell scripts to a HPCC, analyzing sequence data from Illumina and Oxford Nanopore sequencers, project design, C++ (beginner/intermediate), RStudio (intermediate), training personnel, writing abstracts, grants, and manuscripts, giving oral and poster presentations at domestic and international conferences, manual TE identification, comparative genomics, high throughput Illumina library prep, PCR assay design, RNA transcription PCR (RT-PCR, RTqPCR), quantitative PCR (qPCR), gel electrophoresis and imaging, wastewater sampling, recombineering and cloning E. coli*

- Dissertation/Thesis

- Performing an in-depth literature review on the current state of tick genomics and noting improvements and endeavors that can be pursued in the tick genomics community
- Assembling, annotating, and characterizing transposable elements in the first reference genome assembly for the European tick, *Dermacentor reticulatus*
- Identifying the best practices to achieve high-quality tick genome assemblies for future tick genomics studies

- Additional Projects

- Designing and optimizing amplicon-based molecular assays to amplify and sequence the receptor binding domain (RBD) of the spike protein on the SARS-CoV-2 genome for local, clinical, and wastewater surveillance.
- Library prepping ~1,300 clinical and wastewater samples confirmed positive for SARS-CoV-2 for a phylogenetic and phylogeographic study.

- Laboratory Rotations

- Analyzed and compared AMR genes from sequences from six samples of chicken litter independently library prepped at two labs.
- Optimized SARS-CoV-2 quantitative PCR primers from GT Molecular on synthetic multi-variant SARS-CoV-2 RNA to demonstrate proof-of-concept before testing on real-life COVID-19-positive wastewater samples.
- Applied recombineering, transformation, and cloning methods to overexpress the elongasome complex in *E. coli* with the aim to increase peptidoglycan synthesis in an *E. coli* strain containing *mlaC*, *pldA*, and *pagP* mutations.

**Centers for Disease Control and Prevention, Enteric Diseases Laboratory Branch**  
(Atlanta, GA)

- **Oak Ridge Institute for Science and Education (ORISE) Research Fellow** (full-time)

2016 – 2021  
(4 yrs 11 mos)

*Skills: prepared and tested microbiological culture media, extracted Salmonella spp. and E. coli isolate DNA, handled primary specimens, extracted human stool DNA, performed RNA transcription PCR (RT-PCR, RTqPCR), performed quantitative PCR (qPCR), performed gel electrophoresis and imaging, library prepped for and sequenced on Illumina MiSeq, HiSeq, NovaSeq and Oxford Nanopore MinION sequences, operated liquid handling and library prep robots, counted colony forming units (CFUs), designed projects, trained personnel, wrote abstracts and manuscripts, gave oral and poster presentations at domestic conferences, performed a systematic review, provided recommendations to public health lab partners, and wrote, implemented, and taught quality management systems (QMS).*

- Affordable, Long, Highly Accurate Nanopore Sequencing for Public Health Subtyping
  - Minimized the error rates associated with the MinION for NGS workflows that produce long reads by implementing unique molecular identifiers (UMIs).
- Commensal *E. coli* Project
  - Recovered and sequenced 191 commensal *E. coli* isolates from healthy patient stool samples and managed the work among two other laboratorians.
  - Designed and executed a laboratory approach to provide a public resource of isolated commensal bacterial genomes from a diversity of human stool specimens using culture-based and next-generation sequencing techniques. Sequencing data to be available via BioProject (PRJNA600256).
- Intestinal Microbiome Review
  - Reviewed and extracted information from 124 abstracts and 68 full-text articles with the aim to systematically review the available data on performance characteristics for mammalian intestinal microbiome sampling and storage techniques for NGS analyses

- Screening abstracts and full texts with the aim to review the available data on performance characteristics for lower mammalian intestinal microbiome sampling and storage techniques for NGS analyses
- Salmonella & STEC Isolate Recovery Projects
  - Conducted over 700 experiments to support the development of recommendations for the efficient and cost-effective recovery of *Salmonella enterica* serotypes from patient stool samples for distribution to state public health lab partners.
  - Designed and executed a laboratory approach with the aim to compare the performance of commonly used transportation media, storage and transportation temperatures, and selective *Salmonella* and STEC enrichment media and plating agars among US public health laboratories with the intent to generate recommendations for the time and cost-effective recovery of *Salmonella* and STEC from CDT-positive human stool specimens.
- Emergency Operations Center – Laboratory Task Force – 2019 COVID-19 Response – Genome Sequencing Laboratory (Feb. 2021 – April 2021)
  - Implemented a cDNA synthesis workflow for the Genome Sequencing Laboratory housed within the Biotechnology Core Facility Branch at the Centers for Disease Control and Prevention
  - Performed cDNA synthesis on ~5,000 RNA and TNA extracted from COVID-19-positive specimens
  - Library prepped ~5,000 COVID-19-positive cDNA using the Swift Normalase Sars-CoV-2 Amplicon Panels on the SciClone NGS Workstation
- Emergency Operations Center – Laboratory Task Force – 2019 COVID-19 Response – Genome Sequencing Laboratory (May 2020 – July 2020)
  - Performed quality control of 2,000+ COVID-19 nucleic acids in preparation for NGS
  - Supported development of COVID-19-specific sequencing primers for NGS
  - Optimized Illumina and NEB NGS library preparation chemistries for bacterial NGS

## **IEH Laboratories & Consulting Group - FoodProtech (Stillwater, OK)**

- **Laboratory Technician/Analyst** (part-time 15-50hrs/wk)  
*Skills: prepared and quality tested microbiological culture media, handled food and environmental specimens, performed environmental testing, PCR, gel electrophoresis and imaging, counted colony forming units (CFUs), trained personnel, operated laboratory information management systems (LIMS), invoiced orders*
  - Executed the various functions of an ISO17025-certified food and environmental quality control laboratory from sample receipt to reporting quality results to food manufacturing clientele

2015 – 2016  
(1 yr 5 mos)

- performed multi- and single-plex PCR and gel electrophoresis and analyzed banding patterns; used other various laboratory equipment (pH meter, water activity meter) for sample quality control
- serially diluted and pour-plated large numbers of food and environmental samples and calculated CFU/mL; used autoclaves to sterilize media and laboratory equipment; prepared agars and enrichments
- trained new employees; prepared laboratory for audits; invoiced orders through Quickbooks; received and logged samples into a laboratory information management system; inventory control; general laboratory maintenance

## MANUSCRIPTS SUBMITTED

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1. Lott MEJ, Sullivan AH, Lariscy LM, Norfolk WA, **Dillon KC**, Beaudry MS, Glenn TC, Lipp EK. Comparison of three tiled amplicon sequencing approaches for SARS-CoV-2 variant detection from wastewater. *bioRxiv* (2024). <https://doi.org/10.1101/2024.06.16.599198>.
2. Ronai I, de Paula Baptista R, Paulat NS, Frederick JC, Azagi T, Bakker JW, **Dillon KC**, Sprong H, Ray DA, Glenn TC. The repetitive genome of the Ixodes ricinus tick reveals transposable elements have driven genome evolution in ticks. *bioRxiv* (2024). <https://doi.org/10.1101/2024.03.13.584159>.

## MANUSCRIPTS IN PREP

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1. **Dillon KC**, Frederick JC, Ronai I, Glenn TC. The Current State of Tick Genomics.
2. **Dillon KC**, Sprong H, Baede VO, de Paula Baptista R, Ray DA, Glenn TC. Annotated Nanopore genome assemblies from the tick Dermacentor reticulatus illuminates intra- and inter-species differences in repetitive elements.
3. **Dillon KC**, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. The Recovery of Nontyphoidal Salmonella from CIDT-Positive Stool Specimens.
4. **Dillon KC**, Hensley JR, Aspinwall BA, Lucking ST, Carleton HA, Huang AD, Williams-Newkirk AJ. Isolation and Whole-genome Sequencing of Commensal Escherichia coli in Healthy Human Stool.
5. Gao Y, Aspinwall BA, **Dillon KC**, Thakur M, Trees E, Besser J, Carleton HA, Williams-Newkirk AJ, Huang AD. Targeted Enrichment of Enteric Pathogen DNA from Stool Samples for Metagenomic Subtyping Analysis.

## PUBLISHED PROTOCOLS

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1. **Dillon KC**, Hensley JR, Aspinwall BA, Lucking ST, Carleton H, Huang AD, Williams-Newkirk AJ. Small-Scale Stool Homogenization. *protocols.io* (2022). <https://dx.doi.org/10.17504/protocols.io.8epv5zn96v1b/v1>.
2. **Dillon KC**, Hensley JR, Aspinwall BA, Lucking ST, Carleton H, Huang AD, Williams-Newkirk AJ. Large-Scale Stool Homogenization. *protocols.io* (2022). <https://dx.doi.org/10.17504/protocols.io.yxmvmk3pbg3p/v1>.
3. **Dillon KC**, Hensley JR, Aspinwall BA, Lucking ST, Carleton H, Huang AD, Williams-Newkirk AJ. Isolation of Suspect Commensal Escherichia coli from Human Stool Specimens. *protocols.io* (2022). <https://dx.doi.org/10.17504/protocols.io.4r3l246nxg1y/v1>.

## OTHER PUBLICATIONS

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1. **Dillon KC**, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. 2019. The Recovery of Nontyphoidal *Salmonella* from CIDE-Positive Stool Specimens. Association for Public Health Laboratories: Lab Matters (2019). <https://view.joomag.com/lab-matters-fall-2019/0750638001574439750?short>. *Magazine Article*.

## ORAL PRESENTATIONS

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1. **Dillon KC**, Ronai I, de Paula Baptista R, Frederick JC, Sprong H, Ray DA, Glenn TC. Tick Genomics: Progress Towards Tick Genome Assembly and Annotation Best Practices. Nanopore Days – WYMM Tour – Atlanta. 2024 February 27. Atlanta, Georgia.
2. **Dillon KC**, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. The Recovery of Nontyphoidal *Salmonella* from CIDE-Positive Stool Specimens. Speed Dating Symposium, Association for Public Health Laboratories Annual Conference. 2019 June 3-6. St. Louis, Missouri.
3. **Dillon KC**, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. How to Grow Bad Cells from Human Number Two. Up Goer Five Plain Language Symposium, ASM Microbe. 2018 June 7-11. Atlanta, Georgia.

## POSTER PRESENTATIONS

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\*presenter

1. **Dillon KC**, Frederick JC, Glenn TC, Ronai I\*. The Current State of Tick Genomics. International Symposium on Ticks and Tick-borne Diseases. 2025 March 26-28. Weimar, Germany.
2. **Dillon KC\***, Ronai I, de Paula Baptista R, Frederick JC, Sprong H, Ray DA, Glenn TC. Tick Genomics: Progress Towards Tick Genome Assembly and Annotation Best Practices. Tick and Tick-borne Pathogens TTP11. 2024 Sept. 1-6. Havana/Varadero, Cuba.
3. Paradis RG\*, Vasquez M, Gao Y, **Dillon KC**, Lindsey R, Huang AD, Carleton HA, Williams-Newkirk AJ. Using Unique Molecular Identifiers to Increase the Accuracy of Oxford Nanopore Technology MinION Sequencing for Foodborne Enteric Surveillance. International Conference on Emerging Infectious Diseases; 2022 Aug 7-10; Atlanta, Georgia.
4. Sheth M\*, Burgin A, Burroughs M, Padilla J, Nobles S, Bentz ML, Madden J, Davis ML, **Dillon KC**, Le S, Rowe LA, Dhvani B, Knipe K, Howard D, Unoarumhi Y, Lacek K, Rambo M, Clint P, Strain Surveillance and Emerging Variants Working Group, Core Operations Outbreak Response and Support Laboratory, Sample Triage and Tracking Team, Lee J. National SARS-CoV-2 Strain Surveillance – High-Throughput NGS Wet Lab Processing. International Conference on Emerging Infectious Diseases; 2022 Aug 7-10; Atlanta, Georgia.
5. **Dillon KC\***, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. The Recovery of Nontyphoidal *Salmonella* from CIDE-Positive Stool Specimens. ASM Microbe; 2019 Jun 20-24; San Francisco, California.
6. Gao Y, **Dillon KC**, Hensley JR, Trees E, Besser J, Carleton HA, Williams-Newkirk AJ, Huang AD\*. Evaluation of Stool Nucleic Acid Preservation Methods for Culture-Independent Pathogen Subtyping. ASM Microbe; 2019 Jun 20-24; San Francisco, California.

7. **Dillon KC\***, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. The Recovery of Nontyphoidal *Salmonella* from CIDT-Positive Stool Specimens. APHL Annual Conference; 2019 Jun 3-6; St. Louis, Missouri. *Awarded best poster*.
8. Aspinwall BA\*, Hensley JR, **Dillon KC**, Lucking ST, Carleton HA, Huang AD, Williams-Newkirk AJ. Isolation and Whole-Genome Sequencing of Commensal *Escherichia coli* in Healthy Human Stool. SFAF Meeting; 2019 May 21-23; Santa Fe, New Mexico.
9. Rowell JL\*, Zhang S, Rodriguez-R LM, Suttner B, Caban-Figueroa KT, Kostantinidis, Hensley JR, **Dillon KC**, Aspinwall BA, Gao Y, Kanwar N, Weltmer KL, Harrison CJ, Selvarangan R, Besser J, Carleton HA, Trees E, Huang AD, Williams-Newkirk AJ. ROcker for Improved Antimicrobial Resistance Determinant Detection in Stool and Isolate Samples. SFAF Meeting; 2019 May 21-23; Santa Fe, New Mexico.
10. Aspinwall BA\*, Hensley JR, **Dillon KC**, Lucking ST, Carleton HA, Huang AD, Williams-Newkirk AJ. Isolation and Whole-Genome Sequencing of Commensal *Escherichia coli* from Healthy Human Stool. ASM Southeast Regional Meeting; 2018 Nov 30-Dec 2; Atlanta, Georgia.
11. **Dillon KC\***, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. The Recovery of Nontyphoidal *Salmonella* from CIDT-Positive Stool Specimens. International Conference on Emerging Infectious Diseases; 2018 Aug 26-29; Atlanta, Georgia.
12. Gao Y\*, **Dillon KC**, Hensley JR, Aspinwall BA, Trees E, Besser J, Carleton HA, Williams-Newkirk AJ, Huang AD. Evaluation of Fecal Nucleic Acid Preservatives for Culture-Independent Pathogen Subtyping Using Metagenomics. International Conference on Emerging Infectious Diseases; 2018 Aug 26-29; Atlanta, Georgia.
13. Hensley JR\*, Chen JC, **Dillon KC**, Aspinwall BA, Huang AD, Besser J, Carleton HA, Trees E, Williams-Newkirk AJ. Development of a Targeted Sequencing Panel to Detect Antimicrobial Resistance Determinants in Human Stool. International Conference on Emerging Infectious Diseases; 2018 Aug 26-29; Atlanta, Georgia.
14. Rowell JL\*, Hensley JR, **Dillon KC**, Gao Y, Shay JA, Chen JC, Aspinwall BA, Kanwar N, Weltmer KL, Harrison CJ, Selvarangan R, Wikswo ME, Payne DC, Friedman CR, Plumb ID, Besser J, Carleton HA, Trees E, Williams-Newkirk AJ, Huang AD. Comparison of Shotgun and Amplicon Sequencing for Antimicrobial Resistance Determinant Detection in Stool and Isolate Samples. International Conference on Emerging Infectious Diseases; 2018 Aug 26-29; Atlanta, Georgia.
15. **Dillon KC\***, Hensley JR, Blackstock E, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. The Recovery of Nontyphoidal *Salmonella* from CIDT-Positive Stool Specimens. ASM Microbe; 2018 Jun 7-11; Atlanta, Georgia.
16. Gao Y\*, **Dillon KC**, Hensley JR, Aspinwall BA, Trees E, Besser J, Carleton HA, Williams-Newkirk AJ, Huang AD. Evaluation of Fecal Nucleic Acid Preservatives for Culture-Independent Pathogen Subtyping Using Metagenomics. ASM Microbe; 2018 Jun 7-11; Atlanta, Georgia.
17. Hensley JR\*, **Dillon KC**, Gao Y, Aspinwall BA, Chen JC, Rowell JL, Lucking ST, Kanwar N, Weltmer KL, Harrison CJ, Selvarangan R, Wikswo ME, Payne DC, Friedman CR, Plumb ID, Huang AD, Besser J, Carleton HA, Trees E, Huang AD, Williams-Newkirk AJ. Antimicrobial Resistance Gene Detection by Targeted Sequencing Panel in Clinically Healthy Human Stool. ASM Microbe; 2018 Jun 7-11; Atlanta, Georgia.
18. Gao Y\*, **Dillon KC**, Hensley JR, Aspinwall BA, Trees E, Besser J, Carleton HA, Williams-Newkirk AJ, Huang AD. Evaluation of Fecal Nucleic Acid Preservation Methods for Culture-Independent Metagenomic Analyses of Foodborne Pathogens. SFAF Meeting; 2018 May 22-24; Santa Fe, New Mexico.
19. Rowell JL\*, Hensley JR, **Dillon KC**, Gao Y, Shay JA, Chen JC, Aspinwall BA, Kanwar N, Weltmer KL, Harrison CJ, Selvarangan R, Wikswo ME, Payne DC, Friedman CR, Plumb ID, Besser J, Carleton HA, Trees E, Huang AD, Williams-Newkirk AJ. Comparison of Shotgun and Amplicon Sequencing for Antimicrobial

Resistance Determinant Detection in Stool and Isolate Samples. SFAF Meeting; 2018 May 22-24; Santa Fe, New Mexico.

20. **Dillon KC\***, Hensley JR, Patel M, Trees E, Besser J, Carleton HA, Huang AD, Williams-Newkirk AJ. Hensley. Progress Towards an Optimized *Salmonella* Isolate Recovery Protocol. Integrated Foodborne Outbreak Response and Management Conference; 2017 Nov 6-9; Garden Grove, California.
21. Williams-Newkirk AJ, Hensley JR, Chen JC, **Dillon KC**, Patel M, Huang AD, Besser J, E. Trees, H.A. Carleton\*. Development of Sequencing Methods for Direct-from-Specimen Surveillance and Subtyping. Integrated Foodborne Outbreak Response and Management Conference; 2017 Nov 6-9; Garden Grove, California.
22. Gao Y\*, **Dillon KC**, Hensley JR, Patel M, Besser J, Trees E, Carleton HA, Williams-Newkirk AJ, Huang AD. Stool Nucleic Acid Preservation and Recovery at Times and Temperatures of Public Health Relevance. ASM Conference on Rapid Applied Microbial NGS and Bioinformatic Pipelines; 2017 Oct 8-11; Washington, District of Columbia.
23. Williams-Newkirk AJ\*, Hensley JR, Chen JC, **Dillon KC**, Patel M, Huang AD, Besser J, Carleton HA, Trees E. Highly Multiplexed Amplicon Sequencing: A Wet to Dry Lab Proof of Concept Using Antimicrobial Resistance Targets in *Salmonella* and Human Stool. ASM Conference on Rapid Applied Microbial NGS and Bioinformatic Pipelines; 2017 Oct 8-11; Washington, District of Columbia.
24. **Dillon KC\***, Hensley JR, Gao Y, Patel M, Carleton HC, Trees E, Besser J, Huang AD, Williams-Newkirk AJ. Garbage In, Garbage Out: Optimization of Stool Handling Protocols for Culture Independent Subtyping of PulseNet Pathogens. Advanced Molecular Detection Day; 2017 Sep 25-26; Atlanta, Georgia.
25. Hensley JR\*, **Dillon KC**, Patel M, Carleton HC, Trees E, Besser J, Huang AD, Williams-Newkirk AJ. Highly Multiplexed Amplicon Panels for the Subtyping of PulseNet Pathogens. Advanced Molecular Detection Day; 2017 Sep 25-26; Atlanta, Georgia.
26. Williams-Newkirk AJ, Hensley JR\*, Im SB, Chen JC, **Dillon KC\***, Patel M, Espitia H, Rishishwar L, Jordan K, Huang AD, Besser J, Carleton HA, Trees D. Targeted Sequencing Detects Antimicrobial Resistance in *Salmonella* Isolates and Human Stool. ASM Microbe; 2017 Jun 1-5; New Orleans, Louisiana.
27. Williams-Newkirk AJ\*, Hensley JR, Chen JC, **Dillon KC**, Patel M, Huang AD, Besser J, E. Trees, H.A. Carleton. Analysis of Highly Multiplexed Amplicon Sequencing Data: A Proof of Concept Using Antimicrobial Resistance Targets in *Salmonella* and Human Stool. SFAF; 2017 May 16-18; Santa Fe, New Mexico.

## PROFESSIONAL SERVICE

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### CDC Enteric Diseases Laboratory Branch (EDLB)

2019 – 2021

- Professional Development Workgroup Leader – developed a welcome packet for new EDLB members.

(1 yr 10 mos)

### CDC Division of Foodborne, Waterborne, and Enteric Diseases (DFWED)

2018 – 2021

- Division Safety Volunteer – supported site-specific safety efforts for division level laboratories.

(3 yrs 4 mos)

## COMMUNITY SERVICE

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### Upper Oconee Watershed Network (UOWN)

2022 – Present

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- Science and Monitoring Committee Member – monitoring of Upper Oconee watershed every quarter by performing river water sampling and/or filtering for *E. coli*. <http://uown.org/UOWN-Wordpress/>

#### Athens Science Café (ASC)

- Director – managing a team of six who are responsible for inviting and hosting monthly speakers at each café event, interacting with café attendees, and managing the café's online presence. 2024 – Present  
<https://athenssciencecafe.wordpress.com/>  
<https://www.instagram.com/athscialli/> 2021 – 2024
- Member – managed the ASC website via HTML coding, served as a core board member, attended monthly cafés, and managed invited speakers. (2 yrs 7 mos)

#### Scientific Research and Education Network (SciREN) Georgia

- Director – managing a team of five people responsible for engaging with the UGA graduate student body and local educators, hosting a virtual lesson planning workshop of ~30 attendees, and hosting an in-person networking event of ~30 attendees. <https://sciren.org/networking-events/sciren-georgia/> 2023 – 2024  
(1 yr)
- Member – engaged with the UGA graduate student body and local educators, hosted two virtual lesson planning workshops of 15-30 attendees, and hosted two in-person networking events of 15-30 attendees. 2021 – 2023  
(2 yrs)

## GRANTS & SCHOLARSHIPS

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Summer Research Grant, University of Georgia	2022
Provost's Tuition Scholarship, Fort Lewis College	2012 – 2013
Don Whalen Foundation Scholarship, Fort Lewis College	2012 – 2013

## AWARDS

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National Center for Emerging and Zoonotic Infectious Diseases Director's Recognition Award, Enteric Diseases Laboratory Branch Awarded	2019
CDC Fellows Professional Development Collective Second Annual 2019 Fellow Day, Award Nominee, Fellows Day, Centers for Disease Control and Prevention	2019
Best Poster Award, Association for Public Health Laboratories Conference	2019

## PROFESSIONAL CERTIFICATIONS

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HACCP Certification, Oklahoma State University	2015
CRLA Certified Tutor Level I, Fort Lewis College	2012
College Algebra Outstanding Student Award, Fort Lewis College	2012



## 10-YEAR EMPLOYMENT HISTORY

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Organization	Job Title	Location	Dates
University of Georgia	Graduate Research Assistant	Athens, GA	<i>2021 – Present</i>
Oak Ridge Institute for Science and Education + Centers for Disease Control and Prevention	ORISE Research Fellow	Atlanta, GA	<i>2016 - 2021</i> (4 yrs 11 mos)
Fort Lewis College - Admissions	Office Receptionist	Durango, CO	<i>2016 - 2016</i> (2 mos)
IEH Laboratories - FoodProtech	Laboratory Technician	Stillwater, OK	<i>2015 - 2016</i> (1 yr 5 mos)