Evan Beatty
M. Sc., MB(ASCP)CM
Medical Technologist

Location   Houston, TX 77021

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evan.cgl.bio

Objective

Admission to a PhD program that allows me to advance my career as a bioinformatics programmer while contributing to innovative research in the multiomic (specifically genomic) and data-driven biology space.

Work Experience

Medical Technologist
John Welsh Genetics Lab
Texas Children's Hospital
Houston, TX
September 2022 - Current
Paid Position

- Well-established within the division with a strong history of work in all three of our core laboratories (Welsh, Clinical Genomics, Molecular Oncology). Exposure to their differences has helped shape the way I think about the operation of molecular labs.
- Directly involved in the development, validation and successful launch of multiple new laboratory developed genomic assays (CMA, NGS), including assays developed as collaborations between multiple entities within the division.
- Developed resources to aid in the classification and characterization of clinically relevant copy number variants. This task required an ability to implement ideas in several languages (VBA, Python) as well as a focus on health informatic datasets and reverse engineering. Currently responsible for the analysis of germline CNV's.
- Participated in the smooth transition of the John Welsh lab from BCM to TCH.
- Played a critical role in both in-person CAP inspections that the Welsh lab has taken part in since the transition to TCH. This included being directly responsible for the implementation of on-site protocol adjustments suggested during a recent inspection (2023).
- Involved in the training of students, fellows and technologists on the genomic assays that we develop and their context both on and off the bench. For the technologists that have shown interest, I've also offered informal training in Python (and programming concepts in general) and troubleshooting assistance.

Medical Genetics Technologist II
John Welsh Cardio. Diagnostic Lab
Baylor College of Medicine
Houston, TX
December 2019 - September 2022
Paid Position

- Responsible for the identification of viral nucelotides in human tissue, blood and bodily fluid via an rtPCR & nested PCR-based assay.
- Performed total nucleotide extraction, rtPCR, nested PCR and gel electrophoresis.
- Gained experience working in a clinical and CAP-accredited laboratory.
- Remained flexible to adapt to a drastically changing post-COVID workplace. We were never able to shift entirely to remote working as a diagnostic lab, so I've had to focus on the adoption of habits that support the minimization of risk.

Graduate Research Assistant
Xiang Lab
Illinois Institute of Technology
Chicago, IL
September 2017 - June 2019
Paid Position

- Conducted research on the tumor supressor protein BAXΔ2.
- Performed PCR (normal, nested & single cell), DNA mini- and large-prep, IHC, IVTT, western blot and luciferase and dual luciferase reporter assays.
- Wrote scripts to comb through the NCBI database, generate statistics, and predict (typical and atypical) mRNA folding motifs.
- Designed a dual luciferase assay to either disprove or provide evidence for a novel biosynthesis pathway.

Undergraduate Research Assistant
Trivedi Lab
Oakland University
Rochester, MI
September 2015 - April 2016
Unpaid Position

- Provided cell culture support to a synthetic chemistry lab with a focus on treating cancer with light reactive molecules.
- Worked primarily with cancer cells as a biologist/biochemist for the lab, testing the efficacy of molecules synthesized by the chemists.

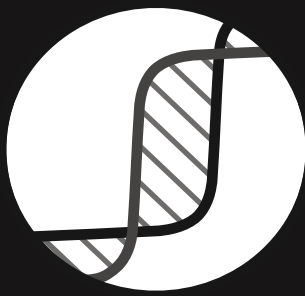## Education

M.Sc. Biology
Illinois Institute of Technology
Chicago, IL
August 2017 - May 2019

B.Sc. Biochemistry and Mol. Bio.
Michigan State University
East Lansing, MI
August 2012 - May 2016

High School
Utica Center for Math, Science and Tech.
Sterling Heights, MI
August 2008 - June 2012

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Publications

Academic
E. Beatty, Detection Of BAXΔ2 Reading Frame Shift Using A Dual Luciferase Reporter System, thesis, 2019.

Peer Reviewed
A. Mañas, Q. Yao, A. Davis, S. Basheer, E. Beatty, H. Zhang, et al., Immunohistochemical detection of the pro-apoptotic BaxΔ2 protein in human tissues, Histochemistry and Cell Biology. 154 (2020) 41–53. doi:10.1007/s00418-020-01874-w.

Q. Yao, A. Mañas, E. Beatty, A. C. dos Santos, Y. Zhou, O. Juárez, H. Chen, and J. Xiang, Alternative production of pro-death BAXΔ2 protein via ribosomal frameshift in alzheimer's disease, Scientific Reports. 14 (2024). doi:10.1038/s41598-024-76061-1.

Under Review
T. Horvath, S. Haidacher, S. Thapa, N. Oezguen, A. Harpavat, A. Horvath, M. P. Murugesan, E. Beatty, Z. Keihani, S. Yadav, V. Orlovsky, J. Isoe, P. Scaraffia, Protocol for arginine-polyamine pathway metabolite quantitation in mosquito whole body sample extracts, STAR Protocols (Submitted Nov. 2025)

Relevant Skills, Experience & Certifications

NGS and Bioinformatics

Python	5+ Years	Fluent
Perl	5+ Years	Fluent
C++	3 Years	Comfortable
VBA	3 Years	Comfortable
PS	3 Year	Comfortable
Bash	5+ Year	Comfortable

	Library Prep.	Pipeline Dev.	Data Analysis
Illumina	✓	✓	✓
Nanopore	✓	✓	✓

Software & Tools

Genome Assembly	Ray, canu, Unicycler
Annotation	Prokka, DFAST
Quality Control	FastQC, quast, Artemis
Misc.	BLAST, SSH, (s)FTP, SQL, MS Access, GNU Screen, tmux

General

Linux	10+ Years	Comfortable
Windows	15+ Years	Native

Molecular Biology
- NGS library prep. for both DNA and RNA sequencing
- PCR, rtPCR, nested PCR, single cell & low template PCR and primer design
- DNA and RNA purification
- DNA fragment digestion, electrophoresis, mutation, mini- and large-prep
- Tissue, blood, FFPE, bodily fluid handling
- Mammalian cell culture, plating, transfection, sterile handling
- In vitro transcription and translation
- UV-Vis, IR & NMR spectroscopy, fluorescence and light microscopy

Certifications
MB(ASCP)CM, Certification #7666

Bonus
Experienced Dataminer
Reverse Engineer
Server Administrator
Novice Network Administrator
Matrix Synapse Host (>5 years)
Arctic Code Vault Contributor
OSS & OA Advocate