Carson Broeker

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Research Interests

Cancer Biology, Immunology, Bioinformatics, Data Science, Machine Learning, Artificial Intelligence, and Data Engineering

Education

August 2019 – Present	**Michigan State University**
	East Lansing, MI
	PhD Candidate in Biochemistry and Molecular Biology
	GPA: 3.71
August 2015 – May 2019	**University of Missouri**
	Columbia, MO
	Bachelors of Science in Biochemistry, *Magna cum laude*
	Minor in Mathematics
	First Generation College Student
	GPA: 3.70

Honors, Scholarships, and Fellowships

2023 – Present	National Cancer Institute Ruth L. Kirschstein National Research Service Award (NRSA) Individual Predoctoral Fellowship (Parent F31) *Up to three year fellowship for thesis project worth $47,694 per year Fellowship award number: 1F31CA271689-01A1*
2022 – 2023	MSU Aitch Foundation Fellowship *One year fellowship for $30,000 in support of PhD thesis work*
2021 – 2022	MSU Museum Observation Research & Exhibition SEEK Fellowship *$3,000 fellowship to development a scientific communication exhibition at the MSU museum*
2021 – 2022	MSU Graduate School Writing in the Disciplines Fellowship *$2,000 fellowship to lead a weekly writing group for other biochemistry PhD students*
2018 – 2019	University of Missouri Alexander Research Scholarship *$2,000 scholarship to support independent undergraduate research project*
2015 – 2019	University of Missouri Excellence Award Scholarship *$1,000 scholarship each semester for academic performance*
2015 – 2019	University of Missouri Dean's List

Publications

2023   **Broeker, C.D.**, Ortiz, M.M.O., Murillo, M.S., Andrechek, E.R., 2023. *Integrative multi-omic sequencing reveals the MMTV-Myc mouse model mimics human breast cancer heterogeneity.* bioRxiv https://doi.org/10.1101/2023.03.28.534611

2022   Patterson, J.R., Cole-Strauss, A., Kuhn, N., Mercier, C., Kochmanski, J., Gerlach, J.A., LeVeque, R.M., Neugebauer, K.A., Conner, K.N., Gomez, J., Hennes, M.G., Thompson, K.E., Rytlewski, D.L., Bigwood, C.C., Scharmen, A., Simjanovski, G., Riley, C., Donaldson, J., Yasin, D., Kouja, N., Contejean, Z., Burnett, M., Aminova, S., Yawson, N.A., Singh, S.B., Alian, O.M., **Broeker, C.D.**, Zaluzec, E.K., ONeill, M., Puschner, B., Sousa, A., Bix, L., Jespersen, B., Holzman, C., Mitchell, J., Julien, R., Askin, Y., Barnes, D., Durshanpalli, P., Krum, D., Weber, R., Patterson, M., Anderson, B., Hunt, R., O'Brien, B., Umstead, A., Beck, J.S., Vega, I.E., Sortwell, C.E., Lipton, J.W., 2022. *Large-Scale SARS-CoV-2 Testing Utilizing Saliva and Transposition Sample Pooling.* JoVE (Journal of Visualized Experiments) e64008. https://doi.org/10.3791/64008

2022   **Broeker, C.D.**, Andrechek, E.R., 2022. *6.16 - E2F Transcription Factors in Cancer, More than the Cell Cycle*, in: Kenakin, T. (Ed.), Comprehensive Pharmacology. Elsevier, Oxford, pp. 277–311. https://doi.org/10.1016/B978-0-12-820472-6.00102-X

2021   To, B., **Broeker, C.**, Jhan, J.-R., Rempel, R., Rennhack, J.P., Hollern, D., Jackson, L., Judah, D., Swiatnicki, M., Bylett, E., Kubiak, R., Honeysett, J., Reaz, S., Nevins, J., Andrechek, E., 2021. *Insight into mammary gland development and tumor prevention in a newly developed metastatic mouse model of breast cancer.* bioRxiv https://doi.org/10.1101/2021.09.24.461727

Research Experience

June 2023 – August 2023

Global non-regulated bioanalysis database for method sharing and prediction

PhD Internship

AbbVie (North Chicago, IL)

Mentor: Estelle Maes, PhD (Director of Non-Regulated Bioanalysis)

Legacy distributed databases and systems make it difficult to access historic LCMS/MS bioanalytical data and methods in a user friendly manner. Moreover, method development for novel compounds can be a difficult and slow based on compound structure, often relying on method developer qualitative insights to choose appropriate starting methods. To address these issues, I created an internal, global, production ready database and user friendly web application for users to examine all method information in the same centralized space. Additionally, I employed machine learning methods based on compound physicochemical properties to predict the best bioanalytical methods to use for novel compounds and informative visualizations for users. My completed project enables rapid bioanalytical method dissemination to global sites and quantitative predictions for appropriate bioanalytical methods to use for novel compound analysis.

May 2021 – Present

Ascertaining the mechanisms of metastasis of a comaplification event in HER2+ breast cancer

Thesis project

Michigan State University (East Lansing, MI)

Mentor: Eran Andrechek, PhD (Professor of Physiology)

An amplification event found to co-occur with the overexpression of *Erbb2* in the MMTV-Neu mouse model of human HER2+ breast cancer was also found to exist in 25% of human HER2+ breast cancers, where it was associated with worse distant metastasis free survival compared to patients without the coamplification event. CRISPR knockout and CRISPRi knockdown of candidate genes within this 40 gene coamplification event showed decreased migration *in vitro* for both human/mouse HER2/Neu+ cell lines. These knockout and knockdown cell lines also showed significantly reduced metastasis *in vivo* after orthotopic injection. My thesis project will elucidate which specific stage(s) of metastasis this coamplification event affects, through what signaling pathways it acts, and whether certain genes are necessary or sufficient for the increased metastatic phenotype to occur. These research questions will be evaluated *in vitro*, *in vivo*, and through bioinformatic methods.

February 2023 – May 2023	**Extractive summarizer for text using natural language processing**
	Michigan State University (East Lansing, MI)
	Mentor: Michael Murillo, PhD (Professor of Computational Mathematics, Science, and Engineering)
	This app accepts user text input and summarizes it to different proportions depending on user preference. The TextRank algorithm is employed on NLTK tokenized sentences to create meaningful summaries. Exploratory data analysis is performed, including sentiment analysis and word frequency distribution. This app is available on GitHub.
October 2022 – December 2022	**Supervised machine learning app for METABRIC breast cancer intrinsic subtype prediction**
	Michigan State University (East Lansing, MI)
	Mentor: Michael Murillo, PhD (Professor of Computational Mathematics, Science, and Engineering)
	This app explores the different categories for each breast cancer patient in the METABRIC breast cancer dataset and how they relate to intrinsic breast cancer subtypes. This app also explores different supervised learning classification algorithms for predicting breast cancer intrinsic subtype based on gene expression data. The app is available on GitHub.
August 2022 – October 2022	**Deployable web app of METABRIC breast cancer patient clinical data**
	Michigan State University (East Lansing, MI)
	Mentor: Michael Murillo, PhD (Professor of Computational Mathematics, Science, and Engineering)
	This project involved customizable, intuitive, and informative visualizations of the METABRIC breast cancer dataset in a deployable web app through Heroku. This app utilized various Python libraries such as Pandas, Seaborn, HiPlot, pySankey, and Streamlit. The app is available on GitHub.

March 2020 – Present	**Genomic and transcriptomic integration parses histological heterogeneity in MMTV-Myc mouse model of breast cancer** *Michigan State University (East Lansing, MI)* Mentor: Eran Andrechek, PhD (Professor of Physiology) The MMTV-Myc mouse model recapitulates the various heterogeneous aspects of human breast cancer such as diversity in histology, gene expression profiles, and metastatic rates. However, the differentiating genetic factors between these subtypes remain unknown. To this end, we performed whole genome sequencing (WGS) on the three dominant histological subtypes of this model: microacinar, squamous, and epithelial-mesenchymal transition (EMT)-like. After processing and somatic variant calling, we integrated the genomic and transcriptomic data to reveal genetically heterogeneous conservation of signaling pathways and conserved copy number variants (CNVs) in the microacinar subtype, with implications in human breast cancer. Many of the events identified are conserved in humans and Kaplan-meier analysis revealed considerably decreased overall survival for patients with these events.
March 2020 – February 2021	**Validation of long range enhancer-gene regulatory network predictions from collaborative transcription factor modules** *Michigan State University (East Lansing, MI)* Mentors: Eran Andrechek, PhD (Professor of Physiology) and Jianrong Wang, PhD (Assistant Professor of Computational Mathematics, Science, and Engineering) Cell type specific transcriptional programs have been found to be regulated in part by long range distal enhancers. However, regulation by long range enhancers is not well understood and current enhancer-promoter interaction prediction algorithms are lacking. To address this, the lab of Jianrong Wang developed a predictive model for cell type specific interactions between promoters and enhancers based on transcription factor and protein-protein interaction signatures. To this end, we ablated predicted promoter binding sites of varying length within enhancers using CRISPR and analyzed gene expression of predicted target and control genes using qRT-PCR. In the end, it was found that there are context dependent factors on whether these particular promoter-enhancer interactions can act as activators or repressors.

September 2019 – October 2022	**Insight into mammary gland development and tumor prevention in a newly developed metastatic mouse model of breast cancer by conditional ablastion of E2F5** *Michigan State University (East Lansing, MI)* Mentor: Eran Andrechek, PhD (Professor of Physiology) Mammary gland development processes going awry leading to tumorigenesis under selective pressures is the collective consensus of the breast cancer field at this point in time. The E2F transcription factor family has previously been implicated and confirmed to play varying roles in mammary gland development. However, of these, E2F5 has not been thoroughly analyzed, although single cell RNAseq data suggest an important role. To this extent, our lab developed a novel mouse model where E2F5 is conditionally ablated (floxed/floxed) specifically in the epithelium of the mammary gland under MMTV-Cre driven recombination around exons 2 and 3 of E2F5. Moderate mammary development changes were observed, but after a long latency period, multifocal and highly metastatic mammary tumors formed. We performed both whole genome sequencing and RNAseq to ascertain the specific development process(es) that have contributed to tumor development. Through multi-omic integration and other methods, we determined that cyclin D1 is dysregulated in both primary tumors and metastases in this novel mouse model, suggesting that cyclin D1 is critical to normal mammary gland formation and development.

June 2018 – May 2019	**Identification of microvesicle biogenesis mechanisms and cargo selection in _Drosophila melanogaster_**

University of Missouri (Columbia, MO)

Mentor: Chiswili Yves Chabu, PhD (Assistant Professor of Biological Sciences)

There are various mechanisms through which cell-cell interactions takes place, with increasing awareness placed on the roles of extracellular vesicles. One categories of extracellular vesicles, microvesicles, bleb directly from the cell membrane and have been found to contain bioactive molecules that facilitate cell-cell interactions in the tumor microenvironment. Tumor derived microvesicles have been shown to suppress immune cells in the tumor microenvironment. Along with knowing that microvesicles promote tumor overgrowth, metastasis, and tumor resistance to therapies, there is a concerted interest in identifying changes to microvesicle count and composition between normal and tumor tissues. However, the mechanisms which underlie microvesicle biogenesis and cargo selection remain unknown, with few tools available to allow manipulation or visualization of microvesicles *in vivo*. To this end, the Chabu lab identified a fluorescent reporter that specifically localizes to microvesicles. Coupled with proximity based chemical tagging of putative microvesicle interacting proteins and subsequent pull down and identification of these proteins via mass spectrometry, *in vivo* functional assays will be performed on candidate proteins to verify their effects on microvesicle biogenesis. A potential application of this technology is delivery of an inhibitor of microvesicle biogenesis to boost efficacy of immunotherapy.

August 2016 – June 2018	**Genetic determinants of glutamate family amino acids in *Arabidopsis thaliana* seed development**
	Partially funded by an NSF EPSCoR fellowship
	University of Missouri (Columbia, MO)
	Mentor: Ruthie Angelovici, PhD (Assistant Professor of Biological Sciences)
	Plants have evolved many mechanisms to cope with both biotic and abiotic stresses during development. One of these mechanisms, is using free amino acids in the seeds of plants to aid in water transfer, metal chelation, and a rapidly usable energy source. Proline has emerged as a particularly important free amino acid and falls under the glutamate family of amino acids. Despite its importance in biological processes and defense, the mechanisms for determining free proline amino acid composition in seeds remains poorly understood. Through genome wide association studies (GWAS) of hundreds of *Arabidopsis thaliana* ecotypes, we identified many candidate genes affecting proline free amino acid composition. Of these genes, methylthioalkylmalate synthase 1 (MAM1), involved in methionine side chain elongation, was identified as the leading candidate. Several T-DNA insertion lines in different *A. thaliana* backgrounds were generated and characterized for knockout of MAM1 and protein composition of seeds via HPLC-MS. It was identified that knockout of MAM1 altered proline free amino acid composition in seeds within each background, but there was considerable variability between backgrounds.

Teaching Experience

August 2020 – December 2020	**Teaching assistant, BMB 470: Biochemistry Laboratory**
	Michigan State University (East Lansing, MI)
	Supervisor: Allan TerBush, PhD
	Penultimate biochemistry laboratory intended for senior biochemistry majors. Topics covered include methods of molecular biology and the underlying principles on which these methods are based. Responsibilities include holding office hours, proctoring exams, grading assignments, answering student emails, testing laboratory experiments and reagents prior to holding laboratories, creating rubric a rubric laboratory notebook from previous experiments, holding two 5 hours lab sections each week, and setup/teardown of biweekly lab sections.
	Nominated by faculty for the biochemistry TA award

August 2018 – December 2018	**Peer learning assistant, BIOCHM 4270: Biochemistry Lecture** *University of Missouri (Columbia, MO)* Supervisor: David Emerich, PhD First semester of comprehensive biochemistry course for juniors and seniors. Covers metabolic pathways, amino acids/proteins, carbohydrates, lipids, nucleic acids, kinetics, energy requirements, and metabolic regulation in living cells. Responsibilities included attending class to answer student questions, answering student emails, giving guest lectures, proctoring exams, and holding office hours.

Non-Research Experience

February 2023 – Present	**High Performance Computing Center (HPCC) ColdFront Project: Django Backend Web Developer** *Michigan State University (East Lansing, MI* Supervisor: Jim Leikert Django backend developer for the ColdFront web application for the Institute for Cyber Enabled Research (ICER) HPCC. Created and optimized relational databases using Django object relational mapping. Utilized Git for collaboration, codebase management, and version control.
January 2021 – May 2022	**Covid-19 Early Detection Laboratory Assistant** *Michigan State University (East Lansing, MI)* Supervisor: Amy Scharmen-Burgdolf Operated in a CLIA certified environment for processing of potentially positive Covid-19 saliva samples. I performed duties of intake, pre-processing, plating, and RNA extraction of saliva samples in a high throughput fashion. Followed good laboratory practices and standard operating procedures for the lab environment in addition to ensuring patient sample anonymity.

Abstract Selected Talks

May 2023	**Gordon Research Seminar on Mammary Gland Biology** *West Dover, VT* Integrative multi-omic sequencing reveals the MMTV-Myc mouse model mimics human breast cancer heterogeneity

July 2022	**Origins of Cancer** *Grand Rapids, MI* Distinct Pathways Responsible for Histological and Metastatic Variance of Mmtv-Myc Tumors found by Genomic and Transcriptomic Integration *15 minute presentation given alongside other speakers such as Harold Varmus, Tony Hunter, Luis Parada, and Frank McCormick*
September 2021	**MSU Precision Health Symposium** *East Lansing, MI* Coamplification Event in HER2+ Breast Cancer Increases Metastasis

Elected Positions, Mentorship, Service, and Outreach

September 2022 – March 2023	**MSU Biochemistry and Molecular Biology Faculty Search Committee** Nominated to serve as the graduate student representative for the department of biochemistry and molecular biology teaching faculty search committee. I help to facilitate unbiased quantitative evaluations of candidate experience, participate in the interviewing process, and represent graduate student needs for the candidate.
June 2022	**Gordon Research Seminar on Mammary Gland Biology Co-Chair** Elected as co-chair for the 2024 Gordon Research Seminar (GRS) on Mammary Gland Biology in Barga, Italy through a competitive process during the 2022 GRS on Mammary Gland Biology. Responsibilities include finding donors, selecting abstracts for presentations among applicant pool, organizing talks and events, and facilitating productive scientific exchanges.
August 2021 – October 2022	**MSU Biochemistry and Molecular Biology Scientific Communications Co-Chair** Elected co-chair of scientific communication for MSU's BMB department. Responsibilities mainly pertained facilitating science communication events for low-income, minority 9-14 year old students in our long standing collaboration with the Carol J. Greer Community Learning Center of Lansing. The goals of this collaboration is to expose these students to enriching scientific experiences and spark scientific curiosity in students, ultimately leading to pursuing a STEM university education.
July 2021	**Fulbright English for Graduate Studies (EGSP) Student Forum** Led a group to onboard incoming Fulbright students and get them acquainted to studying at English speaking universities and providing mentorship.

June 2021 – May 2023	**Graduate Recruitment Initiative (GRIT) Application Feedback Coordinator** Graduate student led organization focused on recruiting, retaining, and mentoring students from marginalized and underrepresented backgrounds in the sciences. As the application feedback coordinator, I lead efforts to recruit a diverse population of would be graduate students to submit draft PhD application materials and facilitate reviews of these materials. The intention of this program is to level the gap between students with and without significant outside support in creating application materials.
August 2020 – May 2021	**Student Advisory Council Representative** As the graduate student representative of the biochemistry and molecular biology department, I informed the college dean on current department affairs, sentiment, and campus climate. I served on awards subcommittees and helped determine merit based scholarship recipients.
August 2018 – May 2019	**Undergraduate Research Ambassador – Outreach** The main purpose of this program was to instill a passion for undergraduate research to a diverse and interdisciplinary group of undergraduates. In this effort, I gave presentations to students interested in undergraduate research, staffed various events on campus and elsewhere representing the University of Missouri and the office of undergraduate research, and participated in workshops designed to inform students of various opportunities and how to get involved in undergraduate research.
January 2018 – May 2018	**Deaton Scholars Program Fellow** Interdisciplinary organization with a focus on alleviating poverty, food insecurity, and malnutrition both domestically and internationally. As part of a group effort, we created an evidence based and actionable plan to inform marginalized members of society on avoiding, lowering, and discharging medical related debts.

Poster Presentations

September 2023	The MMTV-Myc Mouse Model Recapitulates Human Breast Cancer Heterogeneity *Van Andel Institute Epigenetics Symposium (Grand Rapids, MI)*
May 2023	The MMTV-Myc Mouse Model Recapitulates Human Breast Cancer Heterogeneity *Gordon Research Conference and Seminar (West Dover, VT)*

July 2022	Distinct Pathways Responsible for Histological and Metastatic Variance of Mmtv-Myc Tumors found by Genomic and Transcriptomic Integration *Origins of Cancer (Grand Rapids, Michigan)*
June 2022	Integration of Transcriptomic and Genomic Mouse Data to Parse the Heterogeneity of Myc Induced Breast Cancer *Normal Breast Biology and Its Relationship to Breast Cancer Initiation and Progression – Gordon Research Conference and Seminar (Barga, Italy)*
September 2021	Coamplification Event in HER2+ Breast Cancer Increases Metastasis *MSU Precision Health Symposium (East Lansing, Michigan)*
May 2019	Mechanisms of Tumor Microvesicle Signaling *Undergraduate Research and Creative Achievements Spring Forum (Columbia, Missouri)*
April 2018	Determining the Genetic Mechanism Responsible for Specific Amino Acid Levels in Seeds *Missouri State Capitol Rotunda (Jefferson City, Missouri)*
July 2017 – August 2018	Genetic Control of Glutamate Family Amino Acids in *Arabidopsis thaliana* Seed Development *Undergraduate Research and Creative Achievement Forum (Columbia, Missouri)* *Missouri Transect Annual Meeting (St. Louis, Missouri)* *Science Teachers of Missouri Conference (Columbia, Missouri)* *University of Missouri Extension Summit (Columbia, Missouri)*

Professional Memberships

2021 – Present	American Society of Biochemistry and Molecular Biology (ASBMB)
2020 – Present	American Association for Cancer Research (AACR)
2020 – Present	American Association for the Advancement of Science (AAAS)

Technical Skills

Programming languages

Python (Pandas, NumPy, SciKitLearn, Seaborn, Matplotlib, Plotnine, SciPy, TensorFlow, PyTorch, Apache Spark, NLTK)

R (Tidyverse, Limma, DESeq, Dplyr, ggplot2, Shiny)

SQL (MySQL, PostgreSQL, Oracle)

NoSQL (MongoDB)

Linux/Unix systems, Bash

Software

LaTeX, Git, BLAST, Clustal Omega, NCBI Suite, Galaxy Suite, Circos, IGV, UCSC Genome Browser, cBioPortal, STAR, Salmon, GSEA, Delly, Lumpy, GATK, VarScan, BWA, SAMtools, Imaris, interfacing with high performance computing (HPC) systems and remote databases, object oriented programming, and Slurm task scheduling

Lab Techniques

PCR, qRT-PCR, western blotting, molecular cloning, plasmid transformation, primer and sgRNA design, CRISPR/CRISPRi/CRISPRa, lentiviral transduction, aseptic eukaryotic cell culture and antibiotic or flow cytometry selection, GLP, CLIA operations, mouse handling/survival, mouse oral gavage, mouse total necropsy, fly larval microscope assisted dissection, Leica confocal microscopy, and selective breeding for desired genotypes/phentoypes (*Mus musculus, Drosophila melanogaster, and Arabidopsis thaliana*)

Soft Skills

Interpersonal communication; scientific communication to both advanced and lay audiences; interdisciplinary; punctual; adaptable; integrity; quick learner; evidence-based teaching; amicable; scientific and critical thinking; breaking down complex problems into simpler tasks and solutions; detail and big picture oriented; crafting intuitive and informative visualizations for publishing or internal presentations; ability to work in a team and independently; and outcome driven

Relevant Knowledge Base

Biology

Molecular Biology, Cancer Biology, Cell Biology, and Genetics

Biochemistry

Advanced Biochemistry, Protein Structure Design and Mechanisms, Methods of Macromolecular Analysis and Synthesis, Metabolism and Signal Transduction, and Cell Structure and Function

Chemistry

General Chemistry (I & II), Organic Chemistry (I & II), and Physical Chemistry (I & II)

Machin Learning

Linear Algebra, Singular Value Decomposition, Classification, Regression, Regularization, Hyperparameter Optimization

Math

Calculus (I, II, & III), Differential Equations, Linear Algebra, Discrete Mathematical Structures, and Math for Physical Chemistry

Physics

Calculus Based University Physics (I & II), Modern Physics

Statistics

Mathematical Statistics, Biostatistics, Linear Regression, and Statistical Analysis