Arvin Zaker

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1 Educational Background

Honours Bachelor of Science - Translational and Molecular Medicine | (September 2019 - April 2023)

University of Ottawa, Ottawa, ON

- CGPA: 9.98/10
- Major Research Project Supervisor: Dr. Arvind Mer
- Major Research Project Title: Comparative analysis of drug response metrics in patient-derived xenografts

2 Honours, Scholarships and Awards

NSERC - Undergraduate Student Research Awards (USRA) | (May 2023)

University of Ottawa, Ottawa, ON

- Competitive merit-based award. Selection based on academic performance, quality of the research proposal, and the research's potential impact.
- One of 88 awards available at the University of Ottawa.
- Valued at $7500 for 3 months

Work in Biomedical Research Scholarship | (May 2022)

University of Ottawa, Ottawa, ON

- Competitive merit-based award. Selection based on academic performance and the quality of the research proposal.
- Under 50% success rate.
- Valued at $3500 for 3 months

TMM Summer Training program | (May 2022)

University of Ottawa, Ottawa, ON

- Competitive merit-based award. Selection based on based on academic performance and the quality of the research proposal.
- Valued at $8900 for 3 months.

Undergraduate Research Opportunities (UROP) | (December 2020)

University of Ottawa, Ottawa, ON

- Competitive merit-based award. Selection based on academic performance and the quality of the research proposal.
- Valued at $1000 for 4 months.

Dean's Honour List & Merit Scholarship | (September 2019 - April 2023)

University of Ottawa, Ottawa, ON

- Merit-based award. Selection based on grade point average (GPA) in post-secondary studies.
- Valued at $1000 per term (awarded every term).

3 Skills

- Experienced in bioinformatics data analysis using R and Python programming languages
- Proficiency in developing reproducible bioinformatics pipelines in Unix systems with a set of languages such as Bash, Nextflow and Nix.
- Expertise in Multi-omics data analysis, including genomics, epigenomics, and transcriptomics data.
- Proficient in bioinformatics programming using R and Python programming languages
- Expert in developing reproducible bioinformatics workflows across Unix and high-performance computing environments, utilizing pipeline frameworks like Nextflow, and Nix.
- Advanced machine learning model development in cancer genomics and precision medicine.
- Proficient in data visualization and statistical interpretation of complex biological datasets.

4 Research Experience

Research Assistant - Epigenomics   **March 2024 - Present**

Supervisor: Dr. Arvind Mer (Primary Supervisor) and

Contribution:

- Collaborators: Dr. Ben Tsang, Dr. Gilda Stefanelli, and Dr. Jean-Francois Couture
- Perform epigenomic analysis of clinical exosomal DNA samples to identify differentially methylated regions and pathways.
- Created and optimized Cut&Run epigenomic analysis pipeline to explore the developmental impacts of neurological conditions in mice.
- Integrated and aggregated multi-omics data from 44 studies and databases.
- Performing external validation of the results on public datasets.

Research Assistant - Machine learning   **May 2023 - February 2024**

Supervisor: Dr. Arvind Mer

Contribution:

- Developed machine-learning-based drug response metrics to predict the probability of response to anti-cancer medication.
- Compared multiple feature selection methods for drug-response prediction machine-learning models to identify the most suitable methods for translatable clinical models.
- Applied the machine learning model to predict drug response to chemotherapies.
- Visualized the performance differential between machine learning models.

Undergraduate Thesis   **September 2022 - April 2023**

Supervisor: Dr. Arvind Mer

Title: Comparative Analysis of Drug Response Metrics for Patient-Derived Xenograft

Contribution:

- Performed literature review to identify common methods of quantifying drug response in patient-derived xenografts (PDX)
- Developed xeMetron package to calculate 250 existing and novel metrics for measuring the drug response in PDX.
- Performed biomarker discovery to identify transcriptional markers of drug sensitivity in chemotherapies.
- Created machine learning algorithms to predict drug response in clinical datasets.

Summary Research Assistant   **January 2022 - August 2022**

Supervisor: Dr. Arvind Mer (Primary Supervisor) and Dr. Damien D'Amours

Title: Large-scale phenogenomic analysis of human cancers uncovers frequent alterations affecting SMC5/6 complex components in breast cancer

Contribution:

- Aggregated and combined data from 199 cancer studies to analyze the mutational effects of SMC5/6 DNA repair complex in a pan-cancer cohort.
- Utilized R programming language to analyze the functional impact of SMC5/6 mutation using transcriptomic data.
- Performed cancer phenotype and survival analysis to study the clinical implication of SMC5/6.

Student Research Assistant   **September 2021 - April 2022**

Supervisor: Dr. Adam Rudner

Title: Discovery and Characterization of Phage Arzan and Khorshid

Contribution:

- Performed environmental sampling, phage extraction, and phage amplification assays
- Conducted DNA extraction and restriction digest analysis via gel electrophoresis.
- Discovered and annotated the genome of two novel phages, Arzan and Khorshid

UROP Research Assistant   **November 2020 - July 2022**

Supervisor: Dr. Jean-Marc Renaud

Title: Role of Adenosine Receptors on Mice Skeletal Muscle Fatigue Kinetics.

Contribution:

- Designed experiments and set up research equipment for data collection
- Performed experiments on mouse muscles using electrophysiological equipment
- Performed antibody staining, fluorescent imaging, and analysis of muscle tissue in the Imiris program

5   Publications, Presentations, and Abstracts

Publications

Asare-Werehene, M., **Zaker, A.**, Tripathi, S., Communal, L., Carmona, E., Mes-Masson, A., Tsang, B., and Mer, A. (2024). Spotlight on Nuclear PD-L1 in Ovarian Cancer Chemoresistance: Hidden but Mighty. Cancer Research (Submitted manuscript in December 2024, currently under review).

Grégoire, S., Grégoire, J., Yang, Y., Capitani, S., Joshi, M., Sarvan, S., **Zaker, A.**, Ning, Z., Figeys, D., Ulrich, K., Brunzelle, J. S., Mer, A., & Couture, J.-F. (2024). Structural insights into an atypical histone binding mechanism by a PHD finger. Structure, 32(9), 1498-1506.e4. DOI: 10.1016/J.STR.2024.06.017

Wu, G., **Zaker, A.**, Ebrahimi, A., Tripathi, S., & Mer, A. S. (2024). Text-mining-based feature selection for anticancer drug response prediction. Bioinformatics Advances, 4(1), vbae047. DOI: 10.1093/BIOADV/VBAE047

Nasser, F., Gaudreau, A., Lubega, S., **Zaker, A.**, Xia, X., Mer, A. S., & D'Costa, V. M. (2024). Characterization of the diversity of type IV secretion system-encoding plasmids in Acinetobacter. Emerging Microbes & Infections, 13(1), 2320929. DOI: 10.1080/22221751.2024.2320929

Roy, S., **Zaker, A.**, Mer, A., & D'Amours, D. (2023). Large-scale phenogenomic analysis of human cancers uncovers frequent alterations affecting SMC5/6 complex components in breast cancer. NAR Cancer, 5(3), zcad047. DOI: 10.1093/NARCAN/ZCAD047

Posters and presentations at scientific meetings

Roy, S., **Zaker, A.**, Mer, A., D'Amours, D. (2023). Large-scale phenogenomic analysis of human cancers uncovers frequent alterations affecting SMC5/6 complex components in breast cancer. *Canadian Society for Molecular Biosciences (CSMB) International Conference.* Ottawa, ON. (poster and presentation)

Zaker, A., Mer, A. (2022). Comparative analysis of drug response metrics in patient-derived xenografts. *4th Annual University of Ottawa Faculty of Medicine Research Day.* Ottawa, ON. (oral presentation)

Friesen, R., Algharbi S., **Zaker, A.**, Mahdi, O., Gao, R., Ferri, O., Li, J., Wang, SY., HeffernanC., Featherstone, A., Radar, A., Gandelman, M., Chander N., Bancud, SE., Rege, I., Shriraam, R., Jung, D., Karunakaran, G., Sarakbi, R., Znamenski, E., Ristovski, M., Freitas, JD., McCarthy, L., Williams, EC., D'Ambrosio, L., Chan, K., Wheaton, K., Rudner, AD. (2022). Investigating Nucleotide-binding Proteins in Bacteriophage JohnDoe. *SEA Symposium.* Pittsburgh, PA. (abstract & presentation).

Featherstone, A., Radar, A., Salama, A., Tiukuvaara, S., Ferri, O., **Zaker, A.**, Algharbi, S., Mahdi, O., Setia, G., Friesen, R., Wang, GY., Li, J., Gao, R., Jung, D., Karunakaran, G., Znamenski, E., Ristovski, M., Sarakbi, R., Freitas, JD., McCarthy, L., Williams, EC., D'Ambrosio, L., Wheaton, K., Rudner AD. (2022). Give Us a Millet of Your Time: Dehusking the Singleton Bacteriophage Arzan. *SEA Symposium.* Pittsburgh, PA. (abstract & presentation)

Zaker, A., McCarthy, L., Jung, D., Karunakaran, G., Rudner, A. (2022). Discovery and characterization of bacteriophage Arzan. *Ottawa, ON.* (poster and presentation)

Zaker, A., McRae, C., Renaud, J.M. (2021). Role of Adenosine Receptors on mice skeletal muscle fatigue kinetics. *University of Ottawa UROP symposium.* Ottawa, ON. (abstract and poster).

6 Software Projects and Repositories

cut_run_pipeline_nix ⍥   **September 2024**

- Collaborative project with Dr. Stefanelli lab.
- Developed a pipeline for performing Cut&Run analysis and annotating the analysis outcomes.
- Successfully stacked multiple technologies to create a user-friendly pipeline
- Created a user-friendly guide for improving the utility of the pipeline for our collaborators.
- Improved the reproducibility of existing pipelines by utilizing Nix programming language.

text_features ⍥   **March 2024**

- Compared and analyzed the impact of various feature selection methods in influencing
- Created scripts to be used in high-performance computing environment
- Created large-scale visualizations to communicate abstract findings to a wide audience

SMC5-6_complex ⍥   **September, 2023**

- Collaborative project with Dr. D'Amours lab.
- Aggregated pan-cancer dataset of over 65,000 patients from across 144 studies.
- Analyzed the mutational effect of the SMC5/6 protein complex and its subunits.
- Performed survival analysis to identify the SMC5/6-related risk factors to cancer prognosis.
- Identified large-scale genomic instability associated with SMC5/6 mutation in patient transcriptome and phenome.

vian-clin-sci ⍵   **March 2023**

- Reproduced the bioinformatics analysis performed by Viñas et al. (2020) <u>PMID: 32662516</u>
- Created a formatted report to present the re-analysis.
- Enhanced the analysis outcomes by utilizing newer and more cutting-edge tools.

ATG16L1-MYPT1 ⍵   **November 2022**

- Collaborative project with Dr. Ryan Russel lab
- Performed a differential expression analysis of VHL and RB knockout mice samples
- Identified the differentially expressed genes and pathways associated with knockouts
- Verified findings using literature text mining tools.