AYAAN A. REZWAN

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Education

Bachelor of Applied Science (Co-op), Biomedical Engineering — 3.9/4.0 GPA Sep 2025 – Apr 2030
University of Waterloo • Specialization in Biomedical Artificial Intelligence Waterloo, ON
Relevant Coursework: Data Structures & Algorithms, Digital Computation, Linear Systems & Matrices, Engineering Design

Technical Skills

Machine Learning	PyTorch, scikit-learn, NumPy, pandas, SciPy, seaborn, matplotlib (classification, regression, feature engineering)
Bioinformatics	Biopython, NCBI/BLAST, UniProt, AlphaFold, Benchling, Addgene, Sequence analysis, Boltz-2
Programming	Python (primary), HPC, C++, C#, MATLAB, Arduino (Embedded C)
Tools	Git/GitHub, Docker, Claude Code, Linux/Zsh, Obsidian, LaTeX, SOLIDWORKS

Experience

Process Engineer (Co-op) May 2026 – Aug 2026
AstraZeneca Canada Hamilton, ON
- Installed, qualified, and maintained facility machines and equipment used for **clinical manufacturing** of radioconjugate drugs
- Obtained certification as a **Nuclear Energy Worker**, practicing proper handling of radioactive materials in **graded clean rooms**
- Incorporated **AI-Ops** for resource optimization within the facility to **increase output capacity** of drug manufacturing
- Researched applications of machine learning and bioinformatics for radioconjugate marker discovery during **initial molecule screening**

Machine Learning Technical Project Manager May 2026 – Sep 2026
WAT.ai Design Team, University of Waterloo Waterloo, ON (Hybrid)
- **Co-led and managed 10 members** to create "weatherloo", a **CNN post-processing layer** for weather forecasting models to improve prediction accuracy within the region of Waterloo
- Assigned and fulfilled **benchmarking and literature review** tasks to assess current strengths and weaknesses of industry NWP models
- Implemented **3 machine learning models** (U-Net, LSTM, CNN-LSTM) to evaluate which performs best within the problem space
- Determined that LSTM outperforms both models and industry NWP models (ECMWF AIFS), **roughly halving** the error on the **current top weather prediction model**

Undergraduate Research Assistant – Bioinformatics Sep 2026 – Present
Doxey Lab, University of Waterloo Waterloo, ON
- Conducting **computational analysis of S-layer proteins** and their encoding genes in prokaryotes under Dr. Andrew Doxey
- Built a **CNN classifier** separating S-layer from non-S-layer proteins of similar organisms using a lab-curated positive set
- Modeled **S-layer lattice assembly** with AlphaFold multimer runs of repeating units to visualize unit cells of lattice

Projects

earlySignal — Liquid Biopsy Cancer Classifier *Python, XGBoost, scikit-learn, pandas, NumPy, Streamlit, Git*
- Built an end-to-end **cfDNA methylation ML pipeline** on TCGA-LUAD data (132 samples, 413K CpG probes) for early lung cancer detection, **achieving 0.924 CV AUC and 1.0 holdout AUC**
- Implemented a **custom scikit-learn transformer** (`TopVarianceSelector`) for variance-based feature selection inside a leak-free cross-validation pipeline, reducing dimensionality from 413K to 5K probes
- Designed an **in-silico tumor fraction simulation modelling** plasma cfDNA dilution; quantified AUC degradation from **1.0 to 0.542 at 1% tumor fraction**, characterizing the core unsolved challenge in liquid biopsy diagnostics
- Deployed an interactive Streamlit app with live tumor fraction simulation; project discussed with **Dr. Fei Geng** (McMaster), whose lab researches plasma-based early cancer detection from cfDNA

Genomics Promoter Classification *Python, scikit-learn, Git*
- Developed a machine learning pipeline to **classify promoter DNA sequences** using real genomic datasets
- Engineered domain-specific features including **k-mer frequency encoding** and sequence composition metrics
- Trained classical models (logistic regression, SVM, random forest), **achieving >95% AUC**
- Conducted feature importance analysis to interpret the biological relevance of **high-yielding k-mers**

AI in Biotech Research *Python, AlphaFold, Benchling, Bindwell*
- Applied AlphaFold for protein **structure prediction** and Benchling for plasmid design within **drug discovery workflows**
- Designed a **genetically modified** yeast plasmid with an inserted **GFP promoter sequence** using Benchling and Addgene
- Performed comparative **molecular docking analysis**, observing $\sim$7% stronger binding affinity for naproxen vs. ibuprofen to COX-2