

# Mahbuba Tasmin

*PhD Candidate in Computer Science (Computational Biology & Machine Learning), UMass Amherst  
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## EDUCATION

<b>University of Massachusetts Amherst</b>	Amherst, MA
<i>Ph.D. Candidate in Computer Science (Advisor: Prof. Anna Green)</i>	<i>Expected Graduation: May 2027</i>
<ul style="list-style-type: none"><li>Research Interests: Resistance Forecasting, Explainable ML, Protein Language Models, Structural Bioinformatics</li><li>CGPA: 3.9/4.0</li><li>Awards: Sudha and Rajesh Jha Scholarship, 2023</li><li>Relevant Coursework: Advanced Algorithms, Machine Learning, Neural Networks, Computational Biology, AI, Information Assurance, Computer Architecture; Teaching for Tomorrow's Faculty; ML for Biological Sequence Data</li></ul>	
<b>University of Massachusetts Amherst</b>	Amherst, MA
<i>M.S. in Computer Science</i>	<i>Sep. 2022 – May 2025</i>
<ul style="list-style-type: none"><li>Thesis aligned with Ph.D. research on antibiotic resistance modeling.</li><li>CGPA: 3.9/4.0</li></ul>	
<b>North South University</b>	Dhaka, Bangladesh
<i>B.S. in Computer Science and Engineering (Summa Cum Laude)</i>	<i>Jan. 2016 – Dec. 2019</i>
<ul style="list-style-type: none"><li>Concentration: Artificial Intelligence and Algorithms; CGPA: 3.89/4.0</li></ul>	

## RESEARCH EXPERIENCE

<b>Graduate Research Assistant</b>	Sep. 2022 – Present
<i>SAGE Lab, University of Massachusetts Amherst</i>	<i>Amherst, MA</i>
<ul style="list-style-type: none"><li>Lead researcher on <b>BIG-TB</b>: a multimodal benchmark dataset (~17K isolates) for <i>M. tuberculosis</i> antibiotic resistance prediction across 11 WHO-priority drugs.</li><li>Designed sequence- and structure-aware models: CNNs, Transformers, and fused-ridge baselines using DNA/protein features, and ESM embeddings.</li><li>Constructed multi-species augmentation pipelines (UniProt, InterPro) to enhance protein generalization via evolutionary data.</li><li>Performed explainability analyses with SHAP and causal variant recovery (recall@<i>k</i>) against WHO 2023 catalog.</li><li>Lead researcher on <b>Forecasting Antibiotic Resistance Using Biophysics and Machine Learning</b>, supporting integrative modeling of resistance-conferring variants using protein thermostability and machine learning.</li><li>Collaborated with cross-institutional researchers (Harvard DBMI, Farhat Lab) on multi-gene model reproducibility and benchmarking.</li><li>Formulated and optimized a <b>Fused Ridge Regression</b> framework with convex regularization, fusion penalty, and enhanced gradient descent (momentum, clipping, Nesterov) for protein structure-aware resistance modeling.</li></ul>	

## INDUSTRY EXPERIENCE

<b>AI Engineer</b>	Mar. 2022 – Jul. 2022
<i>NITEX Solutions Ltd.</i>	<i>Dhaka, Bangladesh</i>
<ul style="list-style-type: none"><li>Implemented Detectron2-based instance segmentation for product identification and OCR-based automation tools.</li><li>Built fashion trend moodboards combining NLP and computer vision pipelines for workflow automation.</li></ul>	
<b>Software Engineer (AI &amp; ML)</b>	Jul. 2020 – Feb. 2022
<i>M2SYS Technology</i>	<i>Dhaka, Bangladesh</i>
<ul style="list-style-type: none"><li>Developed image spoofing detection and contextual recommendation systems using ML and NLP techniques.</li><li>Automated backend workflows with Camunda and deployed production ML models across distributed systems.</li></ul>	

## SELECTED PUBLICATIONS

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**Green, A. G., Tasmin, M., Vargas, R., Farhat, M. R.**

*The structural context of mutations in proteins predicts their effect on antibiotic resistance.*

Submitted to *eLife*. Preprint: bioRxiv 2025.09.23.676583 (2025)

**Tasmin, M., Green, A.**

*Beyond Sequence-only Models: Leveraging Structural Constraints for Antibiotic Resistance Prediction in Sparse Genomic Datasets.*

*ICLR 2025 MLGenX Workshop* (2025)

Yang, Z., Yao, Z., **Tasmin, M.** et al.

*Unveiling GPT-4V's hidden challenges behind high accuracy on USMLE questions.*

*J Med Internet Res* (2025)

## TALKS AND PRESENTATIONS

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**BIG-TB: A Benchmark Dataset for Genomic Resistance Prediction and Interpretability in *Mycobacterium tuberculosis***

*Machine Learning for Computational Biology (MLCB) Workshop, 2025*

Spotlight talk presented highlighting dataset design and explainability analyses.

**Protein Structure-Informed Regularized Linear Model Outperforms ESM for Predicting Antibiotic Resistance**

*Program in Quantitative Genomics Conference (PQG), Harvard University, 2024*

Poster presentation demonstrating integration of 3D structural features with machine learning models.

## TEACHING EXPERIENCE

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**Head Teaching Assistant**

Fall 2025 – Spring 2025

UMass Amherst

*CompSci 520: Theory and Implementation of Advanced Software Engineering*

- Led 140+ students, managed teaching assistants, and coordinated course logistics.
- Maintained GitHub Classroom and Gradescope automation pipelines.

**Course Developer Assistant**

Summer 2023

UMass Amherst

*CompSci 520: Theory and Implementation of Advanced Software Engineering*

- Revamped course structure, labs, and assignments with automated grading.

## HONORS AND AWARDS

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**CRA-WP Grad Cohort for Women**

2023

*San Francisco, USA*

## TECHNICAL SKILLS

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**Tools & Languages:** Python, Bash, R, LaTeX, pandas, NumPy, matplotlib, Git, Docker, Linux, SLURM

**ML/AI:** PyTorch, scikit-learn, XGBoost, CNNs, Transformers, Random Forests, SHAP

**Bioinformatics:** UniProt, InterPro, Rosetta, AAIndex, Protein Structure, VEP/ANNOVAR

## LEADERSHIP & MENTORSHIP

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**PhD Graduate Representative**

Fall 2025

*Student Representative in Faculty Senate*

College of Computer & Information Sciences, UMass Amherst

**Shakir Sahibul**

Fall 2024

*M.S. Student, UMass Amherst*

*Supervised Transformer-based resistance prediction project.*

**Suqi Hong**

Fall 2025

*M.S. Student, UMass Amherst*

*Supervising EvoAug-based protein resistance prediction project.*