

# JUSTIN Z. TAM

(917) 892-9765 • jzt320@lehigh.edu • linkedin.com/in/justin-z-tam • jtam97.github.io

## SUMMARY

Ph.D. student in Computer Science at Lehigh University specializing in bioinformatics, with experience as a Bioinformatics research co-op at Moderna. Skilled in machine learning, 3D modeling, full-stack development, and software engineering tools. Developed novel LLM and graph-based deep learning models to enhance Moderna's computational mRNA pipeline, driving innovation in the field. Expert in applying graph-based machine learning methods to structural protein and mRNA research, with a strong focus on biochemical-driven solutions.

## EDUCATION

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|---|---------------------|
| <b>Ph.D. Candidate in Computer Science/Bioinformatics</b><br>Lehigh University, P.C. Rossin College of Engineering, Bethlehem, PA<br>Advisor: Brian Y. Chen | Aug 2020 - Dec 2025 |
| <b>B.A. in Mathematics, Minor in Computer Science and Chemistry</b><br>Skidmore College, Saratoga Springs, NY   | Aug 2015 - May 2019 |

## TECHNICAL SKILLS

**Machine Learning:** (*proficient*) Tensorflow, PyTorch, transformer and deep learning models, GPT Prompt Engineering, (*familiar*) Scala

**Programming:** (*proficient*) Python, C, C++, JavaScript (*familiar*) Java

**Full Stack Web Development:** NodeJS, ReactJS, MongoDB

**Other Technical Skills:** Git, Matlab, Unix, Docker, Google Cloud, AWS, 3D visualization

**Other Relevant Skills:** Presentation, Project Planning, Independent Research Development and Proposal, Team Management, Wet Lab Protein Research, Biochemistry

## EXPERIENCE

|   |                      |
|---|----------------------|
| <b>Moderna Therapeutics, Cambridge, MA: Bioinformatics Research Co-op</b>   | Jan 2024 - June 2024 |
| <ul style="list-style-type: none"><li>Developed a PyTorch-based transformer model and graph neural network model for mRNA analysis</li><li>Discovered a novel method for altering normally inflexible mRNA structural properties using graph features.</li><li>Engineered several production-level features and improvements to the current Moderna computational pipeline.</li><li>Presented comprehensive reviews and project insights to executive leadership at Moderna, including the VP and directors of computational science.</li></ul> |                      |
| <b>New York City College of Technology, Brooklyn, NY: Adjunct Professor in Mathematics</b>  | Aug 2019 - June 2020 |
| <ul style="list-style-type: none"><li>Aided in the development of a web-based interactive homework assignment and grading system, used in all math classes throughout the college.</li><li>Taught several college level mathematics courses including pre-calculus, calculus 1, and calculus 2.</li><li>Utilized a mix of lecture-style and activity-style teaching strategies to maximize participation and understanding of difficult topics.</li></ul>   |                      |

## PUBLICATIONS

**Tam, J.Z. et al. A Containerization Framework for Bioinformatics Software to Advance Scalability, Portability, and Maintainability**

*Proceedings of the 14th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, Sept 3–6, 2023*

- Independent full-stack development project to build a container framework with reusable templates, streamlining the dissemination and deployment of Bioinformatics software.
- Awarded best paper finalist of CSBW at ACM-BCB 2023

Liu, Y., Armstrong, G., **Tam, J.Z.**, & Chen, B. Y. **MechPPI: Binding Mechanism-based Machine-Learning tool for Predicting Protein-Protein Binding Affinity Changes Upon Mutations**

*bioRxiv*, Oct 31, 2023

- Presented a state-of-the-art ML method leveraging gradient boosted trees and shapley values to curated mechanistic features for analyzing protein-protein binding affinity changes.

**Tam, J. Z. et al. HBcompare: Classifying Ligand Binding Preferences with Hydrogen Bond Topology**

*Biomolecules*, MDPI, Oct 28, 2022

- Presented a graph neural network pipeline for analyzing hydrogen bond topology in proteins
- Performed a benchmark study using various machine learning methods like graph neighborhood aggregation strategies, graph kernels, principal component analysis, and convolutional neural networks.

**Tam, J. Z.**, Palumbo, T., Miwa, J. M., & Chen, B. Y. **Analysis of Protein-Protein Interactions for Intermolecular Bond Prediction**

*Molecules*, MDPI, Sep 21, 2022

- Designed a novel graph network representation of protein-protein interactions, accurately representing intermolecular bonds with efficient representations using networkx.

**Tam, J. Z.**, Palumbo, T., Miwa, J. M., & Chen, B. Y. **DiffBond: A Method for Predicting Intermolecular Bond Formation**

*2021 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, IEEE, Dec 9, 2021

## LANGUAGES

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English (Native)

Mandarin (Fluent)

Cantonese (Limited Working)