Jacob Mattingly, PhD

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PROFESSIONAL SUMMARY

Structural biologist and biochemist with 7 years of experience efficiently delivering end-to-end cryo-EM structures of challenging targets, developing protein expression and purification processes, advancing research workflow productivity, and uncovering mechanistic and drug design principles.

SELECTED IMPACTS

- **Cryo-EM:** led collaborative projects resulting in 3 first-author manuscripts and 12 first-author PDB entries
- **Platform and productivity advancement**: deployed new software/hardware tools and standardized automated data processing workflows, cutting time to final models from weeks to days
- **Leadership:** managed cryo-EM lab's sample preparation and data collection operations; mentored 10+ colleagues across all stages of cryo-EM structure determination

KEY TECHNICAL SKILLS

- **Cryo-EM:** grid prep/data collection (Vitrobot, Talos Arctica, EPU), single-particle data processing (cryoSPARC, RELION), molecular modeling (*Coot*, PHENIX, ChimeraX, ModelAngelo)
- **Protein/RNA biochemistry:** protein/RNA overexpression and purification (AKTA FPLC), *in vitro* transcription and translation, bacterial and mammalian cell culture, molecular cloning/mutagenesis
- **Computation/automation:** Protein design (RFDiffusion3, ProteinMPNN) and structure prediction (AlphaFold3, RoseTTAFold3), Linux admin, workflow automation

RESEARCH EXPERIENCE

Postdoctoral Research Fellow – Emory University — Jan 2025 – Present

- Led project determining mechanisms of oligomerization and substrate binding of bacterial 3'-to-5' exoribonuclease **YhaM** using single-particle cryo-EM (**2.4** – **3.4 Å** resolution)
- Interpreted single-stranded RNA-bound reconstructions to guide hypothesis-driven sample preparation refinement, enabling double-stranded RNA-bound structures that clarified substrate engagement

Graduate Researcher – Emory University — Aug 2018 – Dec 2024

- Led project using cryo-EM to determine mechanism for aminoglycoside antibiotic evasion of 16S rRNA methylation-associated resistance and principles for **improved drug design** (**2.2** – **2.6 Å** resolution)
- Drove cryo-EM study of IF2-dependent translation initiation quality control on rare start codons, defining how IF2 preserves mRNA reading frame during start-site selection (**2.6** – **2.8 Å** resolution)

Research Technician - University of Chicago — Oct 2016 – Aug 2018

- Managed cell culture, flow cytometry, and mouse colony operations supporting immuno-oncology research (STING/AML)

EDUCATION

Doctor of Philosophy, Biochemistry/Structural Biology – **Emory University** (Atlanta, GA) 2018 – 2024
Dissertation: *RNA and Protein Features Controlling Bacterial Translational Fidelity*

Bachelor of Science, Chemistry and Philosophy – **University of Kentucky** (Lexington, KY) 2012 – 2016

SELECTED PUBLICATIONS

Mattingly, JM*, Liposka, A*, Tanquary, JR*, et al (2025). Structural insights into RNA recognition by the Staphylococcus aureus exoribonuclease YhaM. Under review.

Dey D*, **Mattingly JM***, et al (2025). Basis for selective drug evasion of an aminoglycoside-resistance ribosomal RNA modification. *Nature Communications.* https://doi.org/10.1038/s41467-025-63278-5

Mattingly JM, et al (2024). Structural analysis of noncanonical translation initiation complexes. *J. Biol. Chem.* https://doi.org/10.1016/j.jbc.2024.107743