

Alan Clay Richard

acr0116@auburn.edu | (615) 509-7766

1900 Samford Trace Court, Apt. 4408, Auburn, AL 36830 | U.S. Citizen

Education

Auburn University

August 2021 – Present

Ph.D. Candidate

Department of Chemical Engineering

GPA: 3.80/4

The University of Tennessee, Knoxville

August 2017 – May 2021

Degree Conferred: BSChE (*magna cum laude*)

Major: Chemical and Biomolecular Engineering

Minor: Mathematics

GPA: 3.66/4.00

Research Experience

Auburn University

November 2021 – Present

- Title: Ph.D. Candidate
- Advisor: Dr. Robert Pantazes | rjp0029@auburn.edu
- **Publications** ^[1,2,3]: “[Using Short Molecular Dynamics Simulations to Determine the Important Features of Interactions in Antibody–Protein Complexes](#)”
- Work: Developing engineering principles for computational design of binding proteins for applications in sensing and therapeutics

University of Tennessee, Knoxville

January 2020 – August 2021

- Title: Undergraduate Research Assistant (Computational Biomolecular Studies)
- Advisor: Dr. Steven Abel | abel@utk.edu
- Work: Investigating how cytoskeletal properties affect motion of transport proteins using Monte Carlo simulation.

Oak Ridge National Lab – Oak Ridge, TN

August 2018 – May 2019

- Job Title: ORISE Research Assistant in the Chemical Sciences Division (HERE Program)
- Supervisor: Dr. Xianhui Zhao | zhaox@ornl.gov
- **Publication** ^[4]: “[Bio-treatment of poplar via amino acid for interface control in biocomposites](#)”
- Work: Experimentally developing novel biopolymers for sustainable additive manufacturing workflows.

Work Experience

University of Tennessee Mathematics Department – Knoxville, TN

August 2018 – August 2021

- Job Title: Math Tutor
- Supervisor: Bob Guest | guest00@utk.edu

Technical Skills

- **Programming Languages:** C++, Python, MATLAB, GitHub for scientific software development and installation
- **Computational Protein Engineering Tools:** MD simulation, Machine Learning Techniques, MMPBSA/MMGBSA, Rosetta, CHARMM, Docking, Protein Language Models, RFDiffusion, ProteinMPNN
- **Data Analysis:** Proficient in analyzing biological data including for structural biology, computational chemistry, and dynamics data. Demonstrated ability to work with large datasets such as the Protein Data Bank for structures and Multiple Sequence Alignments.
- **Chemical Engineering Tools:** Excel, ASPEN, HYSYS

Presentations, Awards, and Fellowships

- National Society of Collegiate Scholars (2018-2019)
- Engineers in Medicine Society (University of Tennessee, 2019-2020)
- **Walt and Virginia Woltosz Fellow (Auburn University, 2021-Present)**
- **Keynote Speaker: "Designing Biosensor Recognition Elements", BIOSENS Annual Symposium, Auburn, AL, July 27, 2022**
- **"Computational Design of Proteins for Biosensor Applications", AIChE Annual Conference, Phoenix, AZ, November 14, 2022**
- Guest Lecture: "Computational Recognition Element Design", Senior Level Chemical Sensors Class, University of New Hampshire, April 11, 2023
- "Computational Analysis of Binding Proteins Using Molecular Dynamics", BIOSENS Annual Symposium, University of New England, Biddeford, ME, July 26, 2023
- "Computational Analysis of Binding Proteins Using Molecular Dynamics", Graduate Engineering Research Showcase, Auburn, AL, October 12, 2023
- **"Characterizing the Features of Protein-Protein Interfaces Over Time Using Molecular Dynamics", AIChE Annual Conference, Orlando, FL, November 8, 2023**
- "Using Pre- and Post-Binding Interaction Stabilization Features to Identify Non- Realistic Computationally Predicted Protein Interfaces", BIOSENS Annual Symposium, Laramie, WY, July 30, 2024
- **Invited Talk: "Towards On-Line Electrochemical Biosensors for Biomanufacturing", BIOSENS Annual Symposium, Laramie, WY, July 30, 2024**
- Sam J. Spiese, Lucas R. Girard, Jazmine A. Torres, A. Clay Richard, Robert J. Pantazes, Eva Rose M. Balog, High Throughput Screening of de Novo Protein Binding Affinities for Interleukin-6 with an *in Cellulo* Fluorescence-Based Assay. 3rd Annual BIO-SENS Industry-Academic Biotechnology Symposium, Laramie, WY, July 30, 2024.
- "Using Pre- and Post-Binding Interaction Stabilization Features to Identify Non- Realistic Computationally Predicted Protein Interfaces", 2024 Colorado Protein Stability Conference – 30th Anniversary, Breckenridge, CO, August 7th, 2024
- **"Using Pre- and Post-Binding Interaction Stabilization Features to Identify Non-Realistic Computationally Predicted Protein Interfaces", AIChE Annual Conference, San Diego, California, October 30, 2024**
- **"EPPI_ddg: Predicting Changes in Binding Free Energy from Point Mutations using a Structure Based Feature Space and Random Forest", PEGS (the Protein Engineering Summit) Boston, 2025**

Community Service and Outreach

- AIChE Annual Conference Undergraduate Recruiting
- AIChE Southern Regional Conference Car Team Judge
- AIChE Southern Regional Conference Jeopardy Judge
- Auburn University Chemical Engineering Graduate Organization (ChEGO) Ambassador, 2024
- Alabama State Science & Engineering Fair Judge, 2025

Publications

- [1] **Richard, A.C.** and Pantazes, R.J. (2025), Using Short Molecular Dynamics Simulations to Determine the Important Features of Interactions in Antibody–Protein Complexes. *Proteins*, 93: 812-830. <https://doi.org/10.1002/prot.26773>
- [2] **Richard, A.C.** and Pantazes, R.J. (2025), EPPI_ddg: Efficiently Predicting Point Mutation Effects Using a Structure-Based Feature Space, *in final preparation*.
- [3] Curley, C., Jovic Dold, K., Torres, J., **Richard, A.C.**, Sanders, E., Halpern, J., Pantazes, R., & Balog, E.R. (2025), Functional Design and Biophysical Characterization of Analyte-Responsive Polymers, *in revision*, *ACS Biomacromolecules*.
- [4] Zhao, X., Li, K., Wang, Y., Tekinalp, H., **Richard, A. C.**, Webb, E., & Ozcan, S. (2020). Bio-treatment of poplar via amino acid for interface control in biocomposites. *Composites Part B: Engineering*, 199, 108276. doi: [10.1016/j.compositesb.2020.108276](https://doi.org/10.1016/j.compositesb.2020.108276)