

Willow Carretero Chavez

BIOLOGIST · SOFTWARE ENGINEER · NERD

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Education

Massachusetts Institute of Technology

Cambridge, MA

B.S. IN BIOLOGY — CUMULATIVE GPA: 4.6 / 5.0

Graduated Feb 2025

- Coursework: Fundamentals of Programming, Topics in Systems and Computational Biology, Molecular Basis of Infectious Disease, Molecular Biology, Microbial Physiology, Applied Molecular Biology Lab

Experience

Undergraduate Research Intern

Cambridge, MA

SINSKEY LAB — MIT DEPARTMENT OF BIOLOGY

Feb 2023 - May 2023, Sep 2024 - Dec 2024

- Characterized SARS-CoV2 virus-like particle (VLP) samples produced in HEK-293 cells using Western blot, nanoparticle tracking analysis, and ACE2 receiver cell assays
- Executed cell viability, nanodrop, ddPCR, qPCR, and ELISA assays for DNA and protein quantification of samples from adeno-associated virus (AAV) production in bioreactors

Software Engineering Intern

Seattle, WA

GOOGLE

May 2023 - Aug 2023, Jun 2024 - Aug 2024

- Implemented scaling of the Kubernetes (cluster management system) control plane gRPC proxy in Golang
- Extended the Kubernetes Addon Manager to accelerate cluster addon development and deployment in Golang

Undergraduate Research Intern

Cambridge, MA

JENSEN LAB — MIT DEPARTMENT OF CHEMICAL ENGINEERING

Sep 2022 - Dec 2022

- Expanded a method of chemo-enzymatic retrosynthesis in Python, poster presented at 2022 MLPDS Consortium

Software Engineering Co-Op

Boston, WA

WAYFAIR

Jan 2022 - Aug 2022

- Created microservice APIs for data processing pipelines using Java, Python, FastAPI, and PostgreSQL

Early College Intern

New York, NY (Remote)

D. E. SHAW RESEARCH

May 2021 - Aug 2021

- Optimized accuracy of free energy perturbation (FEP) molecular dynamics simulations of ligand:receptor systems
- Created novel method of FEP network generation in Python using integer linear programming

Staff Research Associate

Chula Vista, CA

KUFAREVA LAB — UC SAN DIEGO SKAGGS SCHOOL OF PHARMACY

Oct 2019 - Dec 2020

- Wrote toolkit to verify, validate, and visualize Boolean models of cell signaling networks in Python and R
- Analyzed mass spectrometry phosphoproteomic (TMT-MS²) data using R and linear modeling
- Implemented method of protein binding pocket similarity scoring using MolSoft ICMScript
- Trained in mammalian tissue culture (HEK-293 cell line) in a BSL-2 biosafety cabinet

Publications

1. **Carretero Chavez, W.**; Krantz, M.; Klipp, E.; Kufareva, I. *kboolnet*: a toolkit for the verification, validation, and visualization of reaction-contingency (rxncon) models. *BMC Bioinformatics* **24**, 246 (2023).

Skills

Coding Languages Golang · Python · R · Java · Bash

Technologies Kubernetes · Docker · Git · Numpy/Pandas · Linux · SQL · gRPC

Lab Techniques Western blot · ddPCR · ELISA · Mammalian cell culture · Biosafety cabinet (BSL-2)

Spoken Languages English (native) · Spanish (native) · French (conversational)

Soft Skills Knows when to ask for help · Driven by results and data · Fast learner · Curious