

Willow Carretero Chavez

COMPUTATIONAL BIOLOGIST · SOFTWARE ENGINEER · LABORATORY SCIENTIST

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Education

Massachusetts Institute of Technology

Cambridge, MA

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

Aug 2020 - Feb 2025

- Coursework: Fundamentals of Programming, Math for CS, Topics in Systems and Computational Biology, Molecular Basis of Infectious Disease, Microbial Physiology, Molecular Biology, Cell Biology

Software Engineering Experience

Software Engineer (L3)

Seattle, WA

GOOGLE

May 2025 - Present

- Active contributor to JobSet, a Kubernetes-native API for deploying HPC and AI/ML workloads at scale
- Integrate and meticulously test new GPU/TPU accelerator models for Google Kubernetes Engine (GKE)
- Collaborate with team of 20+ engineers to provide direct support to customers running AI/ML workloads

Software Engineering Intern

Seattle, WA

GOOGLE

May 2023 - Aug 2023, Jun 2024 - Aug 2024

- Implemented horizontal scaling of the Kubernetes (cluster management system) control plane proxy in Golang, demonstrating ability to troubleshoot and improve complex data-intensive systems at scale
- Extended internal cluster developer tooling, deploying changes to world's largest fleet of Kubernetes clusters

Software Engineering Co-Op

Boston, MA

WAYFAIR

Jan 2022 - Aug 2022

- Implemented and deployed microservice APIs for data pipelines using Java, Python, PostgreSQL, and Kubernetes

Research Experience

Undergraduate Research Intern

Cambridge, MA

SINSKEY LAB — MIT DEPARTMENT OF BIOLOGY

Feb 2023 - May 2023, Sep 2024 - Dec 2024

- Conducted molecular (ddPCR), biochemical (Western blot, nanoparticle tracking analysis), and cell-based (ACE2⁺ cell transduction) assays to verify proper assembly of SARS-CoV2 structural proteins into virus-like particles (VLPs)
- Quantified viral DNA, RNA, and capsid protein levels from a bioreactor-based adeno-associated virus (AAV) production platform using nanodrop, qPCR, and ELISA
- Performed routine laboratory tasks while following best practices: sterile buffer/media preparation, aseptic mammalian cell culture (HEK-293 cell line), data collection, and sample management

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 to enable greener synthesis pathways
- Presented poster at the 2022 MIT Machine Learning for Pharmaceutical Discovery and Synthesis Consortium

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

- Trained in mammalian tissue culture in a BSL-2 biosafety cabinet, performing cell viability assays and routine passaging of HEK-293 cells for protein expression studies
- Wrote toolkit to verify, validate, and visualize Boolean models of cell signaling networks in R and Python
- Explored literature on immune cell signaling pathways to create computational model and perturbation-response database of CCR2⁺ monocyte chemotaxis
- Analyzed proteome-wide phosphorylation responses of CCR2⁺ immune cells in response to CCL2 and inhibitor analogue treatment through linear modeling on mass spectrometry data

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 · Rust · Julia

Developer Skills Kubernetes · **Distributed computing** · Git · CI/CD pipelines · Linux · Docker

Lab Techniques **Mammalian cell culture (BSL-2)** · **Western blot** · qPCR/ddPCR · ELISA

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