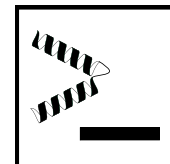


# Willow Ross Carretero Chavez

+1 (619) 832-5823 | [carreter@mit.edu](mailto:carreter@mit.edu)



## Education

- **Massachusetts Institute of Technology** — Expected Graduation: May 2024 — Cambridge, MA
  - Candidate for BS in Chemistry and Biology with Minor in Computer Science
  - Relevant Coursework: Fundamentals of Programming, Organic Chemistry I, Math for Computer Science, Principles of Chemical Science, Intro to Biology, Intro to Computer Science in Python
- **Mater Dei Catholic High School** — Graduated: May 2019 — Chula Vista, CA
  - GPA — 4.63 — Class Rank (10<sup>th</sup>-12<sup>th</sup>) — 1<sup>st</sup>
  - AP Coursework (Score for all exams: 5) — Environmental Science, Chemistry, Calculus AB & BC, Physics C: Mechanics, Biology, English Literature, US History, US Gov & Politics
  - SAT — 1590 (800 Math/790 EBRW, 99<sup>th</sup> Percentile) — Math II: 800 — Chemistry: 800
  - Awards — National AP Scholar, California Mathematics Council Award, National Hispanic Recognition Program Scholar, National Honor Society Member

## Work Experience

- **Sinskey Lab @ Massachusetts Institute of Technology** — Cambridge, MA  
*UROP Student Intern: February 2021–Present*
  - Independently carried out cell culture maintenance on several HEK 293 human cell lines
  - Performed cell counts and metabolite analysis from Erbi and miniBio bioreactors
  - Carried out nanodrop, ddPCR, qPCR, and ELISA assays for DNA and protein quantification
- **Mathnasium of Mission Gorge** — Santee, CA  
*Instructor: August 2019–Present*
  - Teaches students of all ages (2<sup>nd</sup>-12<sup>th</sup> grade) topics ranging from single-digit addition to single-variable calculus
  - Effectively leverages online teaching platforms to perform engaging remote instruction
- **Kufareva Lab @ UCSD Skaggs School of Pharmacy and Pharmaceutical Sciences** — La Jolla, CA  
*Staff Research Associate: October 2019–December 2020*  
*Volunteer: July 2018–August 2018, February 2019–October 2019*
  - Analyzed protein structure using the MolSoft ICM protein modeling suite, implementing a new method of protein binding pocket similarity scoring in ICMScript
  - Wrote toolkit to validate, process, and visualize Boolean models of cell signaling networks using Python and R; manuscript currently in preparation
  - Performed normalization, analysis, and visualization of tandem-mass-tag MS<sup>2</sup> phosphoproteomic data using R
  - Learned and performed tissue culture, PCR, and Gibson cloning methods

## Interests and Skills

- Bilingual — Native speaker of English and Spanish, elementary French knowledge
- Programming Languages — HTML5, CSS3, JavaScript (Node.js), Python (NumPy), ICMScript, R
  - Able to quickly adapt to new languages through hands-on experience
- Familiar with \*nix and bash environments (Arch, Ubuntu/Debian)
  - Multiple years of using Arch Linux as a daily driver
- Hobbies:
  - Hiking and Backpacking — The source of my appreciation for the natural world and its beauty
  - Travel — Have visited countries all over the world and can't wait to see more!