

# Daniel Marrama

marrama.me | [GitHub](#) | [Google Scholar](#) | [LinkedIn](#)

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## BIOINFORMATICIAN

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Leveraging a background in bioinformatics, I am dedicated to advancing research and developing solutions for human disease, particularly autoimmunity. My expertise is in building software tools and conducting analyses on immunological data.

## EXPERIENCE

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### Associate Bioinformatics Specialist

*La Jolla Institute for Immunology, Peters Lab*

Feb 2020 – Present

*La Jolla, CA*

- Developed PEPMatch for the Immune Epitope Database (IEDB), an efficient and precise peptide/epitope search tool capable of accounting for residue substitutions in large sets of proteins. Successfully designed an accompanying benchmarking framework, deployed a user-friendly Django application for IEDB curators, and authored the manuscript for the tool.
- Led in-depth conservation analyses to investigate potential immune cross-reactivity across infectious diseases, allergies, and autoimmune disorders, contributing to a better understanding of immune responses.
- Created a comprehensive pipeline for the exploration and analysis of features of autoimmune antigens sourced from the IEDB, enhancing research capabilities in the field of autoimmunity.
- Rewrote the IEDB protein tree codebase, accurately assigning IEDB antigens to their respective genes and epitopes to parent proteins utilizing alignment tools and PEPMatch. This overhaul resulted in a 10x reduction in codebase size and significantly improved speed and accuracy.

### Data Analyst

*Sony Electronics*

Mar 2018 – Aug 2018

*San Diego, CA*

- Developed an innovative data tracking system using Python to efficiently manage tens of thousands of electronic returns and exchanges.
- Formulated and executed a strategic plan to minimize financial losses for the company using the tracking system.
- Created automation of daily and weekly Excel reports with Python, enhancing overall efficiency and data accuracy.

### Biostatistics and Calculus Teaching Assistant

*Gordon College*

Jan 2015 – May 2016

*Wenham, MA*

- Led groups of students through weekly course material, addressing questions and clarifying concepts.
- Graded assignments and exams for 50+ students each semester.

## TECHNICAL SKILLS

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<b>Languages</b>	: Python, Rust, SQL, Javascript, HTML/CSS
<b>Libraries</b>	: pandas, numpy, Biopython, matplotlib, seaborn, scipy, Django
<b>Bioinformatics</b>	: Alignment (BLAST, MMseqs2, DIAMOND, MUSCLE)
<b>Databases</b>	: SQLite, MySQL, PostgreSQL
<b>Other</b>	: Linux (Bash), Git, Docker, NextFlow, expertise in UniProt

## EDUCATION

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### UCSD

*Premedical Studies (No Degree)*

San Diego, CA

Sep 2018 – Mar 2020

### Gordon College

*Bachelor of Science in Mathematics*

Wenham, MA

Aug 2012 – May 2016

- (Manuscript Under Review) Marrama, D. et al. (2023). PEPMatch: a tool to identify short peptide sequence matches in large sets of proteins
- Roy, P. et al. (2022). Immunodominant MHC-II (Major Histocompatibility Complex II) Restricted Epitopes in Human Apolipoprotein B. Circulation research, 131(3), 258–276. <https://doi.org/10.1161/CIRCRESAHA.122.321116>
- Frankel, A. et al. (2022). Bioinformatic Analysis Underpinning the Frequent Occurrence of Immune Thrombocytopenic Purpura in COVID-19 Patients. The Israel Medical Association journal : IMAJ, 24(5), 320–326.
- Marrama, D. et al. (2022). Lack of evidence of significant homology of SARS-CoV-2 spike sequences to myocarditis-associated antigens. EBioMedicine, 75, 103807. <https://doi.org/10.1016/j.ebiom.2021.103807>
- Grifoni, A. et al. (2020). Targets of T Cell Responses to SARS-CoV-2 Coronavirus in Humans with COVID-19 Disease and Unexposed Individuals. Cell, 181(7), 1489–1501.e15. <https://doi.org/10.1016/j.cell.2020.05.015>