# **Daniel Marrama**

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## **BIOINFORMATICIAN**

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

### **Associate Bioinformatics Specialist**

La Jolla Institute for Immunology, Peters Lab

Feb 2020 – Present La Jolla, CA

Location: San Diego, 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 AnalystMar 2018 – Aug 2018Sony ElectronicsSan 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**

Languages : Python, Rust, SQL, Javascript, HTML/CSS

**Libraries** : pandas, numpy, Biopython, matplotlib, seaborn, scipy, Django

**Bioinformatics** : Alignment (BLAST, MMseqs2, DIAMOND, MUSCLE)

**Databases** : SQLite, MySQL, PostgreSQL

Other : Git, Docker, NextFlow, expertise in UniProt

## **EDUCATION**

**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

#### **PUBLICATIONS**

- (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