

Kate Jamboretz

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I am hoping to break into full stack development, focused in the bioinformatics space.

EDUCATION:

UC Berkeley Extension

Full Stack Coding Bootcamp, 6 month, Part-Time, Online

Jan.2020-present

Current skills: HTML, CSS, Javascript, JQuery, Firebase, Bootstrap, Responsive Design, Local & Session Storage, Git, Commandline, Node.js, Express, MySQL

Future skills: Django, User Authentication, MERN stack, Quality Assurance

General Assembly, San Francisco, California

Courses and Bootcamps

2018-2019

Python and Machine Learning Bootcamp, SQL Bootcamp, Intro to Coding (HTML, CSS), Introduction to Adobe Photoshop, Intro to Data Analytics, Mastering Negotiations

University of San Francisco, California

Professional Masters, Biotechnology, Bioinformatics focus

2015-2017

Merit-based Scholarship 2015-7

Relevant Coursework: Bioinformatics, Statistical Computing for Biomedical Data Analytics, Molecular Genetics & Biotechnology Lab, Molecular Biology

Bachelors of Science, Biology, Minor Biochemistry

2011-2015

University Scholar, Deans Honor Roll Fall 2011, 2013; Spring 2012, 2014, 2015

NCAA D1 All Academic 2015, All Region 2013, Team Captain 2014-6

Dante Benedetti Award 2015: awarded to one female and male USF athlete each year for commitment, work ethic, positive attitude, self-sacrifice and team loyalty

EXPERIENCE:

Nkarta, South San Francisco, CA: Sr. Research Associate II, Binder & Platform Development (prev. RA, SRA I) Aug. 2017-present

- Contribute to development of genetically modified immune cell therapy in a team-oriented environment through oncology target and antibody discovery and enhancing the overall platform.
 - Assist with management of several antibody campaigns outsourced to contract research organizations
 - Run lab experiments individually and in teams involving NK isolation, expansion, cryopreservation, virus generation, transduction, cytotoxicity assays, multicolor flow cytometry for surface protein expression, hybridoma secondary screens.
 - Analyse RNA expression data available through the OmicSoft platform and in-house data through Nanostring.

Amgen, South San Francisco, CA: Grad Co-Op Student, Protein Expression and Purification, Prot. Technologies June 2016-April 2017

- Accelerate therapeutic discovery by optimizing production of difficult proteins, including scFvs of antibodies and target proteins for downstream crystallography, assay development, immunization.
 - Small-scale optimization by testing transfection conditions, induction concentration, time and temperature.
 - Large-scale expression in bacterial cell cultures and intracellular/secreted proteins from mammalian cell cultures.
 - Purification of soluble protein by centrifugation, lysis and affinity, size exclusion and/or ion exchange chromatography, and additional inclusion body preparation and refolding for insoluble proteins.
 - Produce ECD successfully crystallized downstream and enzymatically active tool enzyme TEV Protease.
 - Complete three projects by delivering milligrams of pure protein, with three more projects near completion.

Distributed Bio, South San Francisco, CA: Graduate Student Researcher, Industry Collaboration with USF Aug. 2016-May 2017

- Promote immuno-therapeutic discovery by contributing to phage display libraries and predictive structural modeling of single chain variable fragments (scFvs) of antibodies.
 - Attempt construction of six phage display libraries from pooled cDNA to transformable scFv constructs.
 - Improve antibody single chain variable fragment homology modeling package of Perl and Python scripts.
 - High throughput antibody single chain variable fragment modeling for molecular dynamics and stability analysis.

Blood Systems Research Institute (BSRI), San Francisco, CA: Research Intern

Sept. 2015-May 2016

- Assess whether there is a correlation between differences in phyla and families of bacteriophages from fecal samples and disease state in patients as part of a larger collaboration to reproduce data published in other cities.
 - Self taught basic R skills for statistical analysis of cleaned deep sequencing data sorted by count in various families.
 - Visualize results with Prism and produce slides for mentor and UCSF collaborators.
 - Exposure to wet lab techniques for processing samples for deep sequencing analysis and BLASTing resulting data.