

Kate Jamboretz

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EDUCATION:

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

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

Future skills: Django, MySQL, MongoDB, Node.js, Express, 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

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.