**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.