

# Eric Au

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## EXPERIENCE

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### Mammoth Biosciences, Inc.

Software Engineer

Mar 2022 – Present

- Design, build, and implement full stack applications to support diagnostics CRISPR gene editing platform
- Improves cloud infrastructure for submitting cloud batch jobs by optimizing cost and resource allocation
- Support laboratory scientists with analysis of internal experiments as a part of cross functional team efforts

### Berkeley Lights, Inc.

Software Engineer

Jun 2021 – Mar 2022

- Build scalable automation testing infrastructure for continuous integration and deployment using cloud compute engines, storage buckets and data lakes to advance cutting-edge bioinformatics software
- Develop cloud computing pipelines for T-Cell-Receptor-SEQ and scRNA-SEQ to assist R&D Life Sciences
- Engineer high quality genomic software workflows to optimize automated data wrangling

### Invitae Corporation

Research Associate

Jan 2021 – Apr 2021

- Designed validation strategies for library prep and sequencing of SARS-CoV-2 samples as public health surveillance to identify new variants which included the novel strain variant CAL.20C
- Supports clinical sample management, develops scaling assays with laboratory automation, data analysis, software and leads end-to-end pipeline development for exploratory projects

### Duke University

Research Analyst, Molecular Genetics and Microbiology

Jul 2018 – Dec 2020

- Programed a framework which computed Illumina, Pacific Biosciences, Oxford Nanopore sequencing that produced a full 22 chromosome genome assembly that identified candidate genes and genomic changes
- Developed graph data structure that incorporated genome diversity within populations which captured more detailed and accurate variant analyses of haplotype-resolved genes or genomic regions
- Identified allele specific enhancers from regions of open chromatin that overlap differentially expressed genes to pinpoint biological discovery of functional enhancers in the developing brain

### Stanford University

Life Science Research Professional, Genetics

Oct 2013 – Jul 2018

- Managed mRNA-Seq analysis on responses to physical activity from a cohort resulted in a comprehensive molecular map that accelerated the development of therapeutics and exercise recommendations
- Designed DNA/RNA isolation assays at production scale which optimized workflow and reduced cost

## COMPUTATIONAL SKILLS

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- **Programing Languages:** Go (Lang), Bash/Linux, Python, HTML/CSS/JS, Java, C/C++, R, Php
- **Cluster & Cloud Computing:** Aws, Google Cloud Platform, Slurm, Sun Grid Engine (SGE)
- **APIs & Frameworks:** Apache, Docker, DevOps, Prefect, React, TensorFlow

## MOLECULAR BIOLOGY

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- **NGS Library Preparation & High-throughput Sequencing:** Illumina, Oxford Nanopore Technologies, Pacific Bioscience, RNA-Seq, ATAC-Seq, Whole Genome, Hi-C, Target Enrichment
- **Liquid Handling and Automation:** Beckman Coulter Biomek, Agilent Bravo
- **Quality Control & Quantification:** Nanodrop, Qubit, Tape Station, qPCR, DNA/RNA extraction

## EDUCATION

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San Jose State University

Bachelor of Science in Applied & Computational Mathematics

- **Relevant Coursework:** Bioinformatics Numerical Analysis, Scientific Computing, Mathematical Modeling, Statistics, Data Structures and Algorithms, Differential Equations and Dynamical Systems