

# Eric Au

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(408)-786-4934 | San Francisco, CA

## EXPERIENCE

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### Mammoth Biosciences, Inc.

Software Engineer, Full-Stack

Mar 2022 – Present

- Manages cloud infrastructure using Cloud Formation and Terraform stacks to deploy load balancers, batch jobs, and serverless AWS Lambda functions to ensure consistency and efficiency across our platforms
- Leads development of cost-optimized Kubernetes cluster in AWS Cloud (EKS) to scale Jupyter Hub Notebooks to streamline and enhance accessibility for end-users
- Develops full-stack applications, leveraging Django, MySQL, and ReactJS that innovate creative solutions to improve the accuracy and efficiency of the CRISPR diagnostics platform and drive business value
- Communicates effectively to explain technical concepts in a concise manor, as well as proactively listen and collaborate with others to foster an environment of open communication and teamwork

### Berkeley Lights, Inc.

Software Engineer, Bioinformatics

Jun 2021 – Mar 2022

- Designed architecture of testing processes and automation infrastructure to scale continuous integration and deployment of software applications, which positively impacted cross-functional teams
- Supported clinical sample management and developed computing pipelines for scaling assays in laboratory automation and leaded end-to-end pipeline development for exploratory research and development projects
- Formulated library prep and sequencing strategies for SARS-CoV-2 samples as part of public health surveillance, which led to the identification of the novel strain variant CAL.20C
- Displayed exceptional time management skills, prioritizing tasks effectively, managing multiple projects simultaneously, and consistently delivering high-quality work on or ahead of schedule

### Duke University

Research Analyst, Molecular Genetics and Microbiology

Jul 2018 – Dec 2020

- Implemented a computational graph framework and incorporated bioinformatic algorithms, which leveraged problem-solving skills at the intersection of computer science and biomedical research
- Programmed frameworks to compute Illumina, Pacific Biosciences, and Oxford Nanopore sequencing to assemble a full 22-chromosome genome, which leads to identified candidate genes and genomic changes
- Identified allele-specific enhancers from regions of open chromatin that overlap differentially expressed genes to pinpoint the biological discovery of functional enhancers in the developing brain

### Stanford University

Senior Research Associate, Developmental Biology

Oct 2013 – Jul 2018

- Managed RNA-Seq analysis on responses to physical activity from a cohort and produced a comprehensive molecular map that accelerated the development of therapeutics and exercise recommendations
- Designed DNA/RNA isolation assays at the production scale which optimized workflow and reduced cost
- Responsible for replenishing stock supplies, and facilitated stickleback fish feeding & health monitoring, which increased the efficiency and quality of all laboratory experiments

## COMPUTATIONAL SKILLS

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- **Programming Languages:** Go, Bash/Linux, Python, HTML/CSS/JS/TS, C/C++, MySQL/Postgre, R
- **Cluster & Cloud Computing:** Amazon Web Services, Google Cloud Platform, Dask, Kubernetes, Slurm
- **APIs & Frameworks:** Docker, Django, Flask, Prefect, NodeJS, ReactJS, Redux, Terraform
- **Business Solutions:** Adobe Illustrator, Confluence, Google Docs, Github, Jira, Lucid, Microsoft Office

## EDUCATION

San Jose State University

Bachelor of Science in Applied & Computational Mathematics

- **Relevant Coursework:** Bioinformatics, Differential Equations, Dynamical Systems, Numerical Analysis, Scientific Computing, Mathematical Modeling, Statistics, Object-Oriented, Data Structures and Algorithms
- **Undergraduate Research:** A Gap-Oriented Genetic Algorithm for aligning multiple protein sequences based on computational biology concepts and principles

## PUBLICATIONS

- Au EH, Fauci, C, Luo Y, Mangan RJ, Snellings DA, Shoben CR, Weaver S, Simpson S, Lowe CB. Gonomics: Uniting high performance and readability for genomics with Go. <https://github.com/vertgenlab/gonomics>. **Journal to be determined** (In Preparation)
- Mangan RJ, Alsina FC, Mosti F, Sotelo-Fonseca JE, Snellings DA, **Au EH**, Carvalho J, Sathyan L, Johnson GD, Reddy TE, Silver DL, Lowe CB. Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. DOI: [10.1016/j.cell.2022.10.016](https://doi.org/10.1016/j.cell.2022.10.016). **Cell Press 2022**.
- Wucherpennig JI, Howes TR, Au JN, **Au EH**, Roberts Kingman GA, Brady SD, Herbert AL, Reimchen TE, Bell MA, Lowe CB, Dalziel AC, Kingsley DM. Evolution of stickleback spines through independent cis-regulatory changes at HOXD. DOI: [10.1038/s41559-022-01855-3](https://doi.org/10.1038/s41559-022-01855-3). **Nature Ecol. Evol. 2022**.