

Zach Collester

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EXPERIENCE

STYLUS MEDICINE

Scientist I, Computational Biology

Cambridge, MA

Sep 2023 – Present

- Developed bioinformatics pipelines to identify engineered recombinase plasmid insertions in the human genome
- Conducted in-silico protein mutagenesis using advanced protein language models (ESM, AMPLIFY), generating a prioritized list of mutations for experimental validation
- Automated data workflows including sequencer-to-cloud integration and well-plate format processing, saving wet lab scientists approximately 5 hours per week
- Designed impactful data visualizations used in investor pitch decks to effectively communicate biological insights

KSQ THERAPEUTICS

Scientist, Computational Biology

Cambridge, MA

Aug 2021 – Sep 2023

- Led computational analysis for a novel engineered TIL therapy leveraging scRNA-seq and TCR repertoire data to characterize tumor-infiltrating T cells, resulting in a co-first author on a [peer-reviewed publication](#)
- Designed and analyzed genome-wide CRISPR screening experiments to discover novel autoimmune drug targets, contributing to intellectual property development

TREX BIO

Bioinformatics and Data Science Associate

San Francisco, CA (remote)

Jan 2021 – Aug 2021

- Conducted single-cell RNA-seq analysis on tissue Treg populations to identify key transcription factors and signaling pathways regulating Treg activity
- Collaborated effectively with cross-functional teams spanning multiple time zones in a fully remote environment

SEQUENTIA BIOTECH

Bioinformatics Intern

Barcelona, Spain

Apr 2020 – Jul 2021

- Developed pan-cancer classification models across 20+ tissue types using RNA-seq data (TCGA, GTEx) and machine learning algorithms (XGBoost, neural networks)

PROJECTS

scRegNetWrapper

Jan 2021 – Aug 2021

- Created [open-source R package](#) to streamline workflows for three single cell regulatory network analysis tools (DoRothEA, PROGENy, pySCENIC) with added functionality for downstream analysis

MACRO-COMPLEX MODELING OF BIOMOLECULES

Jan 2020 – Mar 2020

- Developed python-based application that utilizes pairwise interaction data from the Protein Data Bank (PDB) to generate models of biomolecules

EDUCATION

UNIVERSITAT POMPEU FABRA

Master of Science in Bioinformatics

Barcelona, Spain

Jul 2021

BATES COLLEGE

Bachelor of Science in Neuroscience

Cumulative GPA: 3.7/4.0

Lewiston, ME

May 2019

SKILLS

Programming: Advanced in R, Python, Bash; experience with workflow automation tools (Snakemake, Nextflow), and environment management (Anaconda)

Data Types: Extensive experience with scRNA-seq, bulk RNA-seq, TCR repertoire analysis, CRISPR screening, and amplicon sequencing

Cloud Computing: Proficient in AWS S3 and EC2