

# Tenzin C Lhakang

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## Profile

Highly versatile bioinformatics professional who thrives working across the full stack of the bioinformatics space ranging from cloud based pipeline/tool development, dashboard development, to extracting downstream biological insights to move R&D and customer facing projects forward.

## Professional Experience

### Brucker Cellular Analysis,

03/2023 | Emeryville, California

#### *Manager of Bioinformatics | Team Lead*

- Team lead on the PrimeSeq Project, a customer facing software solution allowing users to perform T-Cell Profiling with recovery of cells of interest.
- Maintained and improved Terraform code base to automate the provisioning and management of GCP cloud resources.
- Assisted R&D with the data processing and analysis of NGS experiments to improve sc-BCR-sequencing assay.
- Conducted regular sprint planning, grooming, and review meetings, providing guidance and clarification to development teams, and ensuring that deliverables meet the defined acceptance criteria.

### IsoPlexis,

12/2020 – 03/2023 | Branford, CT

#### *Lead Bioinformatics Software Developer / Associate Manager*

- Led the software product development life cycle from research concept to commercialization for Duomics (a single cell multi omics chip), ensuring alignment with market needs and business objectives, while working closely with the wet lab R&D team to improve core technology and assay development.
- Built a cross functional team comprising of bioinformaticians and software engineers and consultants in order to create the MVP Software solutions for the product requiring a suite of software tools for processing image and NGS datasets for the duomics assay.
- Led and assisted the team in the analysis of high throughput transcriptomics, proteomics, and image datasets in order to improve the Duomics Assay.
- Worked with the IT group to build out the required Azure Infrastructure for data management, data processing, and data analysis in order to meet requirement needs for the R&D and Manufacturing departments.
- Sole developer on interactive web based data applications allowing internal lab users to execute data processing pipelines and visualize QC information related to duomic assay runs.
- Successfully led the cloud migration of our Nextflow pipelines utilizing Azure Batch for batch job processing, allowing us to scale to meet manufacturing needs for our duomic chips.
- Collaborative paper utilizing Duomic Chip: <https://www.nature.com/articles/s41467-023-37616-4>

### NYU School of Medicine | Applied Bioinformatics

06/2015 – 12/2020 | New York, New York

#### *Laboratories, Bioinformatician*

- Worked heavily with NGS datasets including: bulk RNA-seq, scRNA-seq, WGS, WES, 16s as well as metabolomics data.
- Developed, maintained, and improved bioinformatics pipelines for data processing, quality control, and analysis, ensuring accuracy, efficiency, and reproducibility on a HPC clusters utilizing SGE & SLURM job schedulers.
- Collaborated with researchers, scientists, and clinicians to provide bioinformatics support, guide experimental design, and integrate bioinformatics analyses with research activities.

- Developed web based application for dynamically creating custom metabolomic data processing nextflow pipelines for execution through interactive cytoscape based front end.

## **Education**

**Bsc. Biochemistry, Minor Statistics, *University of Vermont***

06/2014 | Burlington, VT

## **Skills**

### **Programming**

Python, R, Groovy ( Nextflow ), Bash, Docker, Azure DevOps, CICD, Terraform, HTML, CSS, PostgreSQL

### **Cloud**

Azure, GCP, AWS

### **Next Generation Sequencing**

Single Cell Omics, RNA-seq, TCR/BCR-seq, WGS, WES, ATAC-seq, 16s

### **Libraries**

Dash, Plotly, pandas, seaborn, jupyter, ggplot2, Bioconductor, etc.

## **Publications**

<https://www.researchgate.net/profile/Tenzin-Lhakang>

Coauthor on 19+ Publications