

UC San Diego Center for Computational Biology & Bioinformatics
Multiomic Analysis
2023

UCSD Internal rate: \$180/hour

Non-profit rate: \$261/hour

For-profit rate: \$522/hour

Estimates below are shown for the UCSD internal rate. All projects are subject to operational charges.

Single cell Multiome ATAC + Gene Expression

Primary Analysis

1. Alignment, peak calling, and quantification of raw data using Cell Ranger ARC (10X Genomics)

Estimate: \$180/sample

Secondary Analysis

Using the standard Seurat and Signac workflows:

1. Quality control
2. Initial clustering analysis
3. Peak calling using MACS2
4. Cell type predictions using SingleR or equivalent software
5. Cell type identification and relabeling with direction from customer
6. Differential expression and differential peak comparisons between conditions for all cell types
7. Linking peaks to genes to calculate correlation between peak accessibility and gene expression
8. Standard figures: Heatmaps, UMAP plots, feature plots, dot plots, coverage plots, etc.

Estimate: \$5,400-\$7,200 and a storage and compute charge of \$270. May be higher for complex experimental designs.

Follow-Up Analysis

Further analysis (such as inclusion of additional datasets, custom visualizations, and other downstream requests) will be scoped on a per-project basis.