

**UC San Diego Center for Computational Biology & Bioinformatics**  
**ChIP-Seq/ATAC-Seq Analysis**  
**2022**

*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.

**Primary Analysis**

1. Raw data quality control (method: FASTQC)
2. Alignment of raw data to genome (method: Bowtie or STAR)
3. Quality control of aligned data (method: RSeQC)
4. Peak calling (method: HOMER/MACS)

*Estimate:*

*ChIP-seq: \$90/sample for  $\leq 20$  samples ; \$45/sample for any additional samples above 20 (bulk rate)*

*ATAC-seq: \$360/sample*

**Secondary Analysis**

1. Assessment of experimental design and analysis design
2. Differential peak calling (method: Homer, DESeq2, limma, DiffBind)
3. Functional enrichment analysis & pathway analysis

*Estimate: \$3,240-\$7,560. 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.