



Center for Computational Biology and Bioinformatics (CCBB) 2024

Pricing

Organization	CCBB Hourly Rate
Scripps Internal	\$125.00
External non-profit	\$250.00
External for-profit	\$312.50

CCBB services: **Epigenomics**

- ChIP-Seq/eCLIP-Seq/CUT&RUN/CUT&TAG/RIP-Seq, ATAC-Seq

ChIP-Seq/eCLIP-Seq/CUT&RUN/CUT&TAG/RIP-Seq

Requirements:

- 1) Read targets reached (e.g. ~ 10 million reads per sample; human genome) for each of your samples in the study
- 2) Number of sample submitted are less than 10
- 3) Sample metadata (description of ChIP and INPUT samples) shared with CCBB prior to sequencing
- 4) Biological replicates if any for your ChIP samples
- 5) Reference genomes considered as standard: human, mouse, rat

Standard analysis (CCBB effort level - 5 hours; 3-5 business days)

Standard analysis: Alignment to reference genome using BWA, peak calling (using protocol specific peak callers), BigWig files, HOMER to annotate peaks relative to gene features along with QC plots/tables.

Additional analysis (**consult CCBB** for effort level and timeline for completion)

Integration analysis (e.g. ChIP-Seq and RNA-Seq)

Contribution to writing a scientific paper including Methods section

Motif discovery

Help with visualization etc.

ATAC-Seq

Standard analysis (CCBB effort level - 5 hours; 3-5 business days)

Alignment to reference genome using BWA, MACS2 for peak-calling, bed and BigWig files, HOMER to annotate peaks relative to gene features.

Additional analysis (consult CCBB for effort level and timeline for completion)

Motif searching

ATAC_ChIP and RNA-Seq

TF Footprinting

DE analysis

Email to ccbb.at.scripps.edu to set up a consultation meeting for additional service(s)

Additional services: Consult CCBB to get a quote/estimation of effort in hours. CCBB service hourly charges apply.

- Software development, custom pipeline implementation
- Re-analysis of older dataset
- Analysis for public dataset
- Specific figures/tables for publications; writing methods section or contribution for scientific papers/grant proposals
- Functional Analysis using Advaita/GSEA/SetRank
- Letter of Support for grants
- GEO/SRA submissions