



## Center for Computational Biology and Bioinformatics (CCBB) 2022

### CCBB services: **Epigenomics**

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

**ChIP-Seq/eCLIP-Seq/CUT&RUN/RIP-Seq** (standard Level 1 services: ~3 to 5 business days)

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

**Level 1 services:** CCBB effort level - 2 hours

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.

**Level 2 services:** CCBB effort level - 5 hours

- Level 1 services + Motif discovery
- Help with visualization

**Level 3 services:** Consult CCBB first! CCBB effort level no more than 8 hours - short term collaboration less than one month

- Large datasets with more than 20 samples
- Multiple sets of standard analysis
- Integration analysis (e.g. ChIP-Seq and RNA-Seq)
- Contribution to writing a scientific paper including Methods section

**ATAC-Seq** (standard level 1 service: ~3 to 5 business days)

**Level 1 services:** CCBB effort level - 2 hours

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

[Email to ccbb@scripps.edu](mailto:ccbb@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