

# Bioinformatics Services

UB Genomics and Bioinformatics

## CHIP-SEQ PACKAGES

### ChIP-Seq standard analysis

- Bowtie/BWA Alignment
- UCSC Links
- MACS2 Peak Calling
- FASTQC

(per sample-control pair) \$75.00

## RNA-SEQ PACKAGES

### RNA-Seq standard analysis

- Tophat Alignment
- UCSC Links
- Cufflinks Quantification
- FASTQC
- Cuffdiff Group Comparison

(max 5x5 case-control) \$300.00

## SMALL RNA-SEQ PACKAGES

### Small-RNA Analysis

- Adapter Trimming
- Sequence Quantification
- MiRBASE Alignment

(per sample) \$35.00

## CUSTOM REQUESTS

Many biological questions persist after initial data analysis. For specific requests, an in-person meeting at the Center for Bioinformatics and Life Sciences with the UB GBC staff members is encouraged. Typically we require at least a two- week lead-time for in-person meetings, with experimental information provided prior to meeting with us.

Please note, we do not take analysis requests for data generated outside of our facility due to limited resources.

## À LA CARTE

Alignments (per sample) \$30.00

Data sequenced at our facility can be taken from raw fastq to aligned BAM files via Bowtie/Bowtie2/BWA

Peak Calling (per sample-control pair) \$25.00

ChIP-Seq samples can be processed for peak calling through the MACS2 algorithm.

RNA-Seq Expression (per sample) \$25.00

Profile RNA-Seq expression using the cufflinks algorithm to generate FPKM metrics.

RNA-Seq Group (max 5x5 comparison) \$100.00

Case-control RNA-Seq expression comparison via the Cuffdiff algorithm, calculates log2ratio and probabilities.

Bacterial Variant Calling (per sample) \$25.00

CLC Genomics based probabilistic variant calling for bacterial samples. Includes SNP and Small Indel calling.

## CONTACT US

The most convenient way to contact the core Bioinformatics team is through shared-email:

 [cbi-ubgbc@buffalo.edu](mailto:cbi-ubgbc@buffalo.edu)

Contacting specific staff members through direct email is discouraged due to the large volume of requests that we receive, and for the most prompt service we recommended contacting the above email.