# Rates for the Bioinformatics Services Offered through CBC

Computational Biology Core

| NCBI/Ensembl Data Submission | | | | |
|---|---|---|---|---|
| | <10 libraries* | 11-30 libraries* | 31-40 libraries* | >41 libraries* |
| RAW reads (NCBI SRA) | $179.05 | $223.80 | $268.56 | hourly rates apply |
| Genome assembly (NCBI WGS) No annotation | $268.56 | hourly rates apply | hourly rates apply | |
| Transcriptome assembly (NCBI TSA) No annotation | $268.56 | $358.08 | $447.60 | |
| SNP(NCBI dbSNP or Ensembl) | $895.21 | hourly rates apply | hourly rates apply | |

Hourly rate = $82.93

| Web or Application Hosting Configuration at UCH | |
|---|---|
| Configuration of web host including DNS | $1,342.81 |

| Data Acquisition/Storage (cost per library) from CGI, MARs, or External Source (with or without quality control of Illumina data) | | | | |
|---|---|---|---|---|
| | <10 libraries* | 11-30 libraries* | 31-40 libraries* | >41 libraries* |
| Including quality control (fastqc/multiqc) | $134.28 | $179.05 | $223.80 | hourly rates apply |
| Not including quality control | $89.52 | $134.28 | $179.05 | |

Hourly rate = $82.93

## Genome Assembly

| | <10 libraries* |
|---|---|
| Eukaryotic (without gene annotation) (per genome) | $6,399.96 |
| Eukaryotic with gene annnotation (per genome) | hourly rates appy |
| Assemblies without annotation | $1,129.40 |
| Assemblies with basic annotation (RAST) | $1,505.87 |
| Assemblies with advanced annotation (Prokka) | $3,011.75 |
| Assemblies with comparative annotation | hourly rates apply |

Hourly rate = $82.93

## RNA-seq analysis

| Number of libraries | <10 libraries ▽ | 11-20 libraries ▽ | 21-30 libraries ▽ | >31 libraries |
|---|---|---|---|---|
| Available reference(mRNA) | $2,095.75 | $3,143.63 | $4,889.45 | $2,369.40 /10lib |
| Non-coding RNA | $2,494.94 | $3,742.41 | $6,111.81 | |
| No Reference (building reference *de novo* <u>first</u> - each library assembled independently) | $4,191.50 | $6,287.24 | $9,787.14 | $3499.90/10lib |
| *de novo* Reference annotation | hourly rates apply | | | |

Hourly rate = $82.93    ▽: 2-condition comparisons ; Please enquire for multi-conditions (ANOVA kind of stiudy), Timecourse or other designs

## ChIP-Seq Analysis

| Number of libraries | <10 libraries * | 11-20 libraries * | 21-30 libraries* | >31 libraries* |
|---|---|---|---|---|
| Reference available | $4,517.61 | $6,023.48 | $9,035.23 | hourly rates apply |

Hourly rate = $82.93

| **Other Services Available: (Hourly rates apply )** | |
|---|---|
| *Estimates will be provided in advance based upon experimental design, scale, and complexity* | |
| | per hour |
| RAD-Seq analysis | $82.93 |
| SNP detection and annotation (GBS and Genotyping Arrays) | $82.93 |
| Microarray Analysis | $82.93 |
| Association Genetics | $82.93 |
| Pathway Analysis | $82.93 |
| Single-Cell Transcriptomics | $82.93 |
| Proteomics | $82.93 |
| Data Visualization | $82.93 |

*Library: A library is defined as a single or paired-end run originating from NGS (Illumina, Ion Torrent, PacBio).

Updated: July 2019