## 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	
Genome assembly (NCBI WGS) No annotation	\$268.56	hourly rates apply	hourly rates apply	hourburgton opply
Transcriptome assembly (NCBI TSA) No annotation	\$268.56	\$358.08	\$447.60	hourly rates apply
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	nouny rates apply

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 $^{igtarrow}$	11-20 libraries $^{igtarrow}$	21-30 libraries $^{igtarrow}$	>31 libraries
Available reference(mRNA)	\$2,095.75	\$3,143.63	\$4,191.51	\$1,047.88 /10lib
Non-coding RNA	\$2,494.94	\$3,742.41	\$4,989.89	\$1,247.48 /10lib
No Reference (building reference <i>de novo <u>first</u> - each library assembled independently)</i>	\$4,191.50	\$6,287.24	\$9,787.14	\$3499.90/10lib
de novo Reference annotation		hourly rate	es apply	

Hourly rate = 82.93  $\nabla$ : 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: Sept 2019