

Caltech Bioinformatics Resource Center

Price information for calendar year 2019

Genome analysis	
Basic <i>de novo</i> assembly	Hourly rates apply
Genome variant calling (SNP, INDEL)	Hourly rates apply
Genome variant annotation (SNP, INDEL)	Hourly rates apply

Transcriptome analysis	
Bulk RNA-seq gene quantification and differential expression analysis	Hourly rates apply (12-24 hours for two group analysis) depending on sample size and sequencing depth
Single-cell RNA-seq gene quantification, clustering, marker gene identification, differential analysis, pseudo-time analysis	Hourly rates apply (16-40 hours for two group analysis) depending on sample size and sequencing depth
Transcriptome <i>de novo</i> assembly, prediction of coding regions	Hourly rates apply (16-40 hours) depending on sample size and sequencing depth

Epigenome analysis	
DNA methylation	Hourly rates apply
ChIP-seq and ATAC-seq data alignment, signal trace generation, peak calling, peak annotation	Hourly rates apply (12-40 hours for two group analysis) depending on sample size and sequencing depth
3C-based (HiC, ChIA-PET and others) chromosomal interaction analysis	Hourly rates apply (80 hours-160 hours) depending on sample size and sequencing depth

Pipeline/workflow development	
Customized pipeline development	Hourly rates apply (typically 40 hours to 160 hours)

Statistical consulting	
Customized consulting services	Hourly rates apply (typically 40 hours to 160 hours)

Academic rate: \$125/hr

Industry rate: \$160/hr