

FY24 Molecular Bioinformatics Core (mBIO) Services and Fees Note: Prices will increase by 3% each fiscal year.

The pricing structure listed below is effective as of July 1, 2023. For all custom projects, please consult the mBIO core director for a quote.

Standard data analysis workflows:

Workflow	Cost	
ATAC-seq	\$100.56 per sample [includes QC (\$5.30), alignment (\$10.61), peak calling (\$35.95), peak annotation (\$24.35), and peak modeling (\$24.35)] Add \$34.90 if you need differential binding. Figures are extra.	
ChIP-seq	\$100.53 per sample ([includes QC (\$5.30), alignment (\$10.60), peak calling (\$35.95), peak annotation (\$24.35), and peak modeling (\$24.35)]. Add \$35.95 if you need differential binding. Figures are extra.	
DeNovo Assembly	\$1,194.06 per sample	
Differential Proteomics	\$272.90 (two conditions x three replicates/condition) [normalization (\$24.35), biostatistics (\$35.95), iPathway Guide (\$150), PCA (\$24.35), volcano Plot (\$12.75), Pearson's plot (\$12.75), and heatmap (\$12.75)]	
IP Proteomics	\$272.90 (two conditions x three replicates/condition) [normalization (\$24.35), biostatistics (\$35.95), iPathway Guide (\$150), PCA (\$24.35), and Pearson's plot (\$12.75)]	
Microarray Analysis	\$272.90 (two conditions x three replicates/condition) [normalization (\$24.35), biostatistics (\$35.95), iPathway Guide (\$150), PCA (\$24.35), volcano Plot (\$12.75), Pearson's plot (\$12.75), and heatmap (\$12.75)]	
RNA Sequencing	\$368.30 (two conditions x three replicates/condition) [includes QC (\$5.30 x 6), alignment (\$10.60 x 6), normalization (\$24.35), Biostatistics (\$35.95), iPathway Guide (\$150), PCA (\$24.35), Volcano Plot (\$12.75), Pearson's plot (\$12.75), and Heatmap (\$12.75)]	
scRNA Sequencing	\$450.55 (Per Comparison) [includes QC (\$5.30), alignment (\$10.60), normalization (\$24.35), biostatistics (\$35.95), PCA (\$24.35), Advance Clustering (\$75), pseudotime map (\$75) and 4 hours of customizing scripting to mine genes (\$200)]	
Targeted Sequencing	\$15.90 per sample [includes QC (\$5.30) and alignment (\$10.60)]	
Whole Genome Sequencing	\$105.16 per sample [includes QC (\$5.30), alignment (\$10.60), and variant calls (\$89.26)]	
Whole Exome Sequencing	\$105.16 per sample [includes QC (\$5.30), alignment (\$10.60), and variant calls (\$89.26)]	



Individual Tasks:

Service	Cost
Advanced Clustering	\$75 per experiment
Alignment	\$10.60 per sample
Biostatistics	\$35.95 per paired condition
Custom Scripting	\$50 per hour (1 hour min)
Data Mining	\$100 per hour (1 hour min)
David Pathway Analysis	\$59.12 per paired comparison
Gene Set Enrichment Analysis	\$89.26 per paired comparison
GEO Upload Support	\$275 per experiment
Hands-On Training	\$100 per hour
Heatmap	\$12.75 per image
iPathway Guide Analysis	\$150 per comparison
Pearson's correlation coefficient	\$12.75 per image
Principal Components Analysis (PCA)	\$24.35 per image
Quality Control Assurance	\$5.30 per sample
String Analysis	\$60 per comparison
Variant Calls	\$89.26 per sample
Venn Diagram	\$12.75 per image
Volcano Plot	\$12.75 per image
Experiment Design Assistance or Consultation	No charge for two hours; \$100/hr. afterward, unless allocation of at least 5% percent effort with salary coverage on a grant per year as key personnel in budget. Service fees are billed separately from the Director's effort.
Grant writing & manuscript writing assistance	Minimum of 5% effort salary coverage per year as key personnel in budget. Service fees are billed separately from the Director's effort. It is also expected that intellectual input of the Director will warrant authorship.

GraphPad Prism 9.0 software site license: \$120/copy/computer/year

(Mac or PC; Partial year use will be pro-rated; note: license is tied to a specific device address)

Local, long-term data storage: \$103/TB for 3-years of mirrored storage

Special projects: Priced by the director and approved by the

Office of Research

External customers rates:

External, academic: 20% surcharge

External, commercial: To be negotiated directly with the Office

of Research