



ACADEMIC COST-RECOVERY FEES

CORE OMICS SERVICES

General omics sample processing

Standard processing (QC, alignment/quantification, output object) for RNA-seq, WGS, or proteomics; assumes clean input

\$275–\$300/sample

Large dataset (>100K cells) surcharge

Only if large memory/runtime required

\$450/dataset

Custom reference creation

e.g., mixed species, custom GTF

\$300

DATA QUALITY AND RESCUE

Metadata rescue

Includes fixing sample sheets, file renaming, structure standardization

\$450

Missing data imputation

Price varies based on complexity of missing data

\$225–\$725

Data triage/QC review only

Review of raw or intermediate data to assess usability before full analysis

\$175

GENERAL STATISTICAL SERVICES

Statistical analysis (standard)

Includes services such as correlation analysis, contingency table analysis, power calculations, ANOVAs, and basic linear or mixed-effects models. Deliverables include summary outputs and brief interpretation

\$225–\$375

Experimental design consultation

Guidance on structuring experiments for statistical validity, including selecting controls, determining sample sizes, defining replicates, and planning for downstream analysis

\$300–\$575

Bucket of time

General data analysis services, charged in 10-hour increments; valid for two years

\$150/hour



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COMMUNICATION AND OUTPUT

Figure generation for grant or manuscript

Custom UMAPs, heatmaps, diagrams, or summary figures for funding applications or publications

\$375/figure

Methods support for grant or manuscript

Annotated scripts, written methods, and/or GitHub support

\$300–\$725

ADVANCED ANALYSES

Differential expression

Price varies based on study design complexity and number of contrasts

\$300–\$575/dataset

Variant annotation & prioritization

Annotated VCF, gene impact summary, risk variant filtering (e.g., ClinVar, gnomAD)

\$450

Post-imputation downstream integration

Using imputed data in DE, correlation, clustering, or modeling workflows

\$375

scRNA-seq follow-up analyses

Advanced downstream analysis using tools such as SCENIC, CellChat, or NicheNet; pseudotime trajectory inference; or latent factor modeling. Includes tailored visual outputs and summary interpretation

\$875/dataset

Multimomics exploratory summary

Correlations, PCA, shared feature plots across blocks (e.g. RNA–protein)

\$875/dataset

Bayesian mixed effects modeling

Hierarchical modeling using brms or Stan to account for donor effects, repeated measures, or complex experimental designs. Includes model fitting, diagnostics, and summary plots

\$575/model

- Clients will be billed in CAD or USD, depending on their location. All items are tax-exempt.
- Prices reflect cost-recovery fees and include 30% for indirect costs of research.
- Well-structured input data is assumed; extra time may be billed for troubleshooting.
- This list is not exhaustive; custom quotes available for multimomics or collaborative projects.
- Additional charges apply for more complex data types.