



For cell proliferate FY19 Proteomics & Metabolomics Core (PMC) Services and Fees

*Prices will increase by 3% per each fiscal year
Revised August 31, 2018*

The pricing structure listed below is effective as of August 28, 2018. Standard services are listed; minutes refer to gradient time. Unless otherwise noted, pricing includes acquisition of raw LC/MS/MS data, post-acquisition basic database (DB) search, and quantification (where applicable). Services have been expanded for FY19 to include targeted metabolomics via the Metabolic Phenotyping Mass Spectrometry (MPMS) unit. For custom projects, please consult the PMC Director for a quote.

Proteomics and Untargeted Metabolomics:

Protein iTRAQ (isobaric tags for relative and absolute quantification)/TMT (tandem mass tags) labeling:

4-plex:	\$721.00
6-plex:	\$1,030.00
8-plex:	\$1,287.50
10-plex:	\$1,390.50

Protein identification:

LC/MS/MS, DB search, note: does not include sample digestion/preparation)

RP LC/MS/MS (30 min):	\$72.10/run
RP LC/MS/MS (60 min):	\$113.30/run
RP LC/MS/MS (120 min):	\$185.40/run
RP LC/MS/MS (2400 min):	\$309.00/run

Protein identification and mapping of specified post-translational modifications (PTM):

LC/MS/MS, DB/PTM search, note: does not include sample digestion/preparation

RP LC/MS/MS (60 min):	\$113.30/sample
RP LC/MS/MS (120 min):	\$185.40/sample
RP LC/MS/MS (240 min):	\$309.00/sample
Search for specified PTMs:	\$30.90/PTM

Differential protein expression analysis by iTRAQ/PMT (reporter ion quantification):

LC/MS/MS, DB search/quantification, note: does not include sample labeling/preparation

Unfractionated mixture of labeled peptides, 2hr RP-LC/MS/MS:	\$206.00/run
Unfractionated mixture of labeled Peptides, 4hr RP-LC/MS/MS:	\$339.90/run

Differential protein expression analysis by SILAC analysis (precursor ion quantification):

LC/MS/MS, DB search/quantification, note: does not include sample labeling/preparation

Unfractionated mixture of labeled peptides, 2hr RP-LC/MS/MS:	\$206.00/run
Unfractionated mixture of labeled Peptides, 4hr RP-LC/MS/MS:	\$339.90/run

Protein differential expression analysis, MudPIT:

MudPit, DB search, note: does not include sample digestion/preparation;
2hr RP-LC/MS/MS/fraction:

6 (SCX or HpHRP) step fractions	\$154.50
7-12 (SCX or HpHRP) step fractions:	\$149.35
>12 (SCX or HpHRP) step fractions:	\$144.20

Absolute quantification of specified (targeted) proteins (parallel reaction monitoring):

PRM analysis for peptide quantification, note: does not include sample digestion/preparation

LC/MC/MS (30 min)	\$82.40/run
LC/MS/MS (60 min)	\$128.75/run
LC/MS/MS (120 min)	\$206.00/run

Absolute quantification of specified metabolites/small molecules:

LC/MS/MS, post-acquisition analysis, calibration Curve, internal standard, AUC quantification

LC/MS/MS (15 min):	\$17.51/run
LC/MS/MS (30 min):	\$30.90/run

Differential quantification of metabolites – untargeted analysis

LC/HRAM-MS/MS, post-acquisition analysis, HRAM AUC Quantification, MS/MS identification

LC/MS/MS (15 min):	\$30.90/run
LC/MS/MS (30 min):	\$51.50/run

NEW! Volume Discount for PMC Bulk MS runs:

The volume MS “run” discount rate does not include reagents or kits, such as the TMT kit for isobaric labeling, or labor-intensive steps, such as sample processing, but will be applied to MS “runs” – to Mass Spectrometry Services, Proteomics, service codes 300-533, as will be detailed in a custom quote for discounted services by the Core Director.

The below volume discount rate will be applied if samples are submitted simultaneously for processing in bulk*, or after the volume threshold has been met for the current FY.

30-49 MS runs, for a single project:	10% discount, all MS runs
50-99 MS runs, for a single project:	15% discount, all MS runs
100+ MS runs, for a single project:	20% discount, all MS runs

*If samples are submitted piecemeal, then the volume discount will be applied only for those MS runs that exceed the discount threshold. For example, if a PI submits three sets of samples requiring 15, then 10, then 20 MS runs, for a total of 45 MS runs completed at different times on separate iLab service requests, then the discount would be applied at MS run #31 onwards.

NEW FOR FY19: The Metabolic Phenotyping Mass Spectrometry (MPMS) Unit:

Directed by Michelle Puchowicz, Ph.D., Department of Pediatrics

For unique projects, please request a consultation

Citric Acid Cycle- related intermediates

Metabolite concentrations:	\$100/run
Metabolite enrichments -MPE (2h, 13C):	\$75/run
Both concentration/MPE:	\$150/run
Search for specified PTMs:	\$30.90/PTM

Total Protein / Protein Turnover

Via D20 water method:	\$50/run
Tracer infusion method:	\$150/run

Glucose or Glycerol

Concentrations:	\$50/run
Enrichments -MPE (2H, 13C):	\$35/run
Both concentration/MPE:	\$75/run
Glucose and Glycerol:	\$100/run

Lipids:

Total fatty acid profile (C10-C18/sat./unsat.):	\$125/run
Fatty acid /Cholesterol:	\$100/run
Isotopomer analysis (MPE):	\$100/run
Synthesis- fractional rates (D20 method):	\$150/run

Use of GC-MS/MS by Trained Users (at discretion of the MPMS Director):

Standard-EI mode (60 min):	\$110
Extended-CI mode (60 min):	\$150
Duplicate runs:	\$70

High volume discounts, MPMS:

High-volume discounts will be provided to core users as negotiated with the MPMS Core Director and as approved by the Associate Vice Chancellor for Research-Cores (typically >100 samples).

All Services:

External rates:

Academic:	50% markup
Commercial:	Negotiated with Office of Research