

**FY24-25 PROTEOMICS & METABOLOMICS CORE (PMC)  
SERVICES AND FEES**

<b>SERVICES</b>	<b>SERVICE CODE</b>	<b>UNIT</b>	<b>INTERNAL USERS, \$\$/Unit</b>
<b>Sample Preparation Services</b>			
Agilent QC test - up to 10 amples per chip	100	per chip	61.50
In-gel trypsin digestion	101	per band	49.19
In-solution trypsin digestion	102	per sample	49.19
In-solution LysC/trypsin digestion	102a	per sample	73.80
Reduction/alkylation	103	per sample	24.62
Desalting of peptide mixtures - ZipTip	104	per sample	12.31
Detergent removal/clean-up through acetone precipitation of proteins	105	per sample	24.62
Protein concentration - BCA assay in triplicates - at least 3 samples	106	per sample	24.62
Peptide (mixture) concentration - BCA assay in triplicates - at least 3 samples	107	per sample	24.62
High pH Reversed-Phase (HpHRP) Fractionation - 8 step fractions	110	per sample	196.76
Complete sample processing starting from cleared cell lysate, membrane pellets, or cell pellets			
Processing for following LC/MS/MS analysis	111	set-up	245.98
	111a	per sample	61.50
Processing for following label-free differential protein expression analysis	112	set-up	245.98
	112a	per sample	61.50
Processing for following TMT/iTRAQ labeling	113	set-up	245.98
	113a	per sample	61.50
TMT/iTRAQ labeling/preparation for LC and MS analysis, 4-plex (set of 4 samples)	114	per set	860.93
TMT/iTRAQ labeling/preparation for LC and MS analysis, 6-plex (set of 6 samples)	116	per set	1229.88
TMT/iTRAQ labeling/preparation for LC and MS analysis, 8-plex (set of 8 samples)	118	per set	1537.35
TMT/iTRAQ labeling/preparation for LC and MS analysis, 10-plex (set of 10 samples)	119	per set	1660.34

TMT/iTRAQ labeling, 11-plex (set of 11 samples)	120	per set	1744.54
TMT/iTRAQ labeling, 16-plex (set of 16 samples)	120a	per set	2021.55
TMT/iTRAQ labeling, 18-plex (set of 18 samples)	120b	per set	2200.00
TiO2 enrichment of phospho-peptides	121a	per run	196.97
Fe-NTA enrichment of phospho-peptides	121b	per run	196.97
SMOAC (TiO2+Fe-NTA) enrichment of phospho-peptides	121c	per run	337.65

## Mass Spectrometry Services - Direct Infusion

### Determination of the Molecular Mass

Infusion ESI-HRAM MS analysis - small analyte	201	61.5013	59.71
Intact protein	202	98.3856	95.52

## Mass Spectrometry Services - Proteomics

### Protein Identification

#### LC/MS/MS, DB search (does not include sample digestion/preparation)

RP LC/MS/MS - 30 min gradient	300	per sample	86.08
RP LC/MS/MS - 60 min gradient	301	per sample	135.29
RP LC/MS/MS - 120 min gradient	302	per sample	221.38
RP LC/MS/MS - 240 min gradient	304	per sample	368.96

#### MudPIT, DB search (does not include sample digestion/preparation)

6 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	310	per fraction	172.20
7-12 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	311	per fraction	166.05
>12 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	312	per fraction	159.89

### Protein Identification and Mapping of Specified PTMs

#### LC/MS/MS, DB/PTM search (does not include sample digestion/preparation)

RP LC/MS/MS - 60 min gradient	401	per sample	135.29
RP LC/MS/MS - 120 min gradient	402	per sample	221.38
RP LC/MS/MS - 240 min gradient	403	per sample	368.96
Search for specified PTMs	404	per PTM	36.88

### Differential Protein Expression Analysis - iTRAQ/TMT Based Analysis (Reporter Ion quantification)

#### LC/MS/MS, DB search/quantification (does not include sample labeling/preparation)

Unfractionated mixture of labeled peptides - 2 hr RP-LC/MS/MS	500	per run	245.98
Unfractionated mixture of labeled peptides - 4 hr RP-LC/MS/MS	500a	per run	405.86

MudPIT, DB search/quantification (does not include sample labeling/preparation)

6 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	501	per fraction	184.48
7-12 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	502	per fraction	178.32
>12 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	503	per fraction	172.20

**Differential Protein Expression Analysis - SILAC Analysis (Precursor Ion Quantification)**

LC/MS/MS, DB search/quantification (does not include sample labeling/preparation)

Unfractionated mixture of labeled peptides - 2 hr RP-LC/MS/MS	510	per run	245.98
Unfractionated mixture of labeled peptides - 4 hr RP-LC/MS/MS	510a	per run	405.86

MudPIT, DB search/quantification (does not include sample labeling/preparation)

6 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	511	per fraction	184.48
7-12 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	512	per fraction	178.32
>12 (SCX or HpHRP) step fractions - 2 hr RP-LC/MS/MS per fraction	513	per fraction	172.20

**Differential Protein Expression Analysis - Label Free Analysis (Precursor ion Peak Area Detection)**

RP-LC/HRAM-MS/MS, post-acquisition analysis (does not include sample digestion/preparation)

RP-LC/HRAM-MS/MS - 60 min gradient	520	per run	159.88
RP-LC/HRAM-MS/MS - 120 min gradient	521	per run	245.98
RP-LC/HRAM-MS/MS - 240 min gradient	522	per run	405.86

**Absolute Quantification of Specified (Target) Proteins - Parallel Reaction Monitoring (PRM)**

PRM analysis for peptide quantification (does not include sample digestion/preparation)

RP LC/MS/MS, post-acquisition analysis, Peptide Internal Standard, AUC quantification

RP LC/MS/MS - peptide quantification, 30 min gradient	531	per run	98.39
RP LC/MS/MS - peptide quantification, 60 min gradient	532	per run	153.74
RP LC/MS/MS - peptide quantification, 120 min gradient	533	per run	245.98

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