



Charles W. Gehrke Proteomics Center
University of Missouri
On-Campus Fee Schedule

Rates are for MU users. For off-campus rates please contact Brian at 573-884-7374. July 2021

PROTEIN PREPARATION			
phenol extraction (useful for plants and other recalcitrant tissues)		1 OR 2	\$102
		3 to 5	\$92
		>5	\$76
acetone/TCA precipitation (human cells, lysates, etc.)		1 to 10	\$50
		11 to 25	\$45
		26 to 50	\$38
		>50	\$25
resuspension & quantitation of user-supplied acetone pellet (per sample)			\$25
SDS-PAGE			
Pour gel, run, stain with coomassie blue	MiniVE	10 lanes	\$117
	SE600	25 lanes	\$144
	DALT6	35 lanes	\$172
ELECTROPHORETIC TRANSFER			
set up, transfer, staining with Ponceau choice of nitrocellulose or PVDF	MiniVE	1st gel	\$84
		extra gel(s)	\$42
	SE600	1st gel	\$97
		extra gel(s)	\$48
In-Gel Trypsin Digestion			
coomassie	band or spots	1 to 10	\$106
		>10	\$96
	96-well plate	per plate	\$1,550
silver	band or spots	1 to 10	\$110
		>10	\$99
In-Solution Trypsin Digestion + C18 SPE peptide purification			
other proteases are available, e.g. GluC, LysC		(1 to 10)	\$92
		(11 to 20)	\$83
		(21 to 40)	\$69
		(>40)	\$46
Bruker timsTOF-PRO High Proteome Coverage LCMS+MSMS			
Reversed phase separation of protein digests, MS & MS/MS data acquisition using the PASEF method.		(per hour, 70min = 1 sample)	\$96
		(per day, ~16 samples)	\$766
		(per week, ~110 samples)	\$3,829
DB search & Quantitative Data analysis (per sample)		(1 to 10)	\$29
		(11 to 20)	\$19
		(>20)	\$10
CLIENT use of in-house PEAKS software for results analysis		per hour	\$6
Targeted Protein Quantitation using LC-MRM (multiple reaction monitoring)			
Method development (generate peptide list unique to protein of interest, check signal using recombinant protein or 1-2 samples, method refinement)		per hour	\$26
LC-MRM (using optimized methods)	per hour	~2 samples	\$52
	per day	~48 samples	\$433
	per week	~330 samples	\$2,164
Agilent 6520 Intact Mass analysis of proteins and DNA			
C8 reversed-phase separation of purified/enriched samples, deconvolution of data to yield intact mass		(1 to 5)	\$85
		(5 to 15)	\$76
		(>15)	\$43
LITQ Orbitrap LC-MS+MSMS			
Reversed phase separation of protein digests, data acquisition, and database search		(samples 1 through 5)	\$82
		(samples 6 through 15)	\$73
		(samples 16 through 50)	\$61
		(samples 51 through 100)	\$41
		(samples >100)	\$21
LITQ Orbitrap Accurate/Exact mass MS and MSMS (pure compounds)			
ESI direct infusion MS (high resolution, <5ppm mass accuracy, negative- or positive-ion modes)		(1 to 5)	\$45
		(6 to 10)	\$41
		(>10)	\$22