



Charles W. Gehrke Proteomics Center

University of Missouri

External Academic Fee Schedule

Please contact Brian at 573-884-7374 to discuss sample submission. July 2021

PROTEIN PREPARATION

phenol extraction (useful for plants and other recalcitrant tissues)	1 OR 2	\$189
	3 to 5	\$171
	>5	\$141
acetone/TCA precipitation (human cells, lysates, etc.)	1 to 10	\$93
	11 to 25	\$84
	26 to 50	\$71
	>50	\$46
resuspension & quantitation of user-supplied acetone pellet (per sample)		\$46

SDS-PAGE

Pour gel, run, stain with coomassie blue	MiniVE	10 lanes	\$217
	SE600	25 lanes	\$267
	DALT6	35 lanes	\$319

ELECTROPHORETIC TRANSFER

set up, transfer, staining with Ponceau choice of nitrocellulose or PVDF	MiniVE	1st gel	\$156
		extra gel(s)	\$78
	SE600	1st gel	\$180
		extra gel(s)	\$89

In-Gel Trypsin Digestion

coomassie	band or spots	1 to 10	\$197
		>10	\$178
silver	96-well plate	per plate	\$2,879
	band or spots	1 to 10	\$204
		>10	\$184

In-Solution Trypsin Digestion + C18 SPE peptide purification

other proteases are available, e.g. GluC, LysC	(1 to 10)	\$171
	(10 to 20)	\$154
	(20 to 50)	\$128
	(>50)	\$85

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)	\$178
	(per day, ~16 samples)	\$1,423
	(per week, ~110 samples)	\$7,111
DB search & Quantitative Data analysis (per sample)	(1 to 10)	\$54
	(11 to 20)	\$35
	(>20)	\$19
CLIENT use of in-house PEAKS software for results analysis	per hour	\$11

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	\$48
LC-MRM (using optimized methods)	per hour	~2 samples \$97
	per day	~48 samples \$804
	per week	~330 samples \$4,019

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)	\$158
	(5 to 15)	\$141
	(>15)	\$80

LTQ Orbitrap LC-MS+MSMS

Reversed phase separation of protein digests, data acquisition, and database search	(samples 1 through 5)	\$152
	(samples 6 through 15)	\$136
	(samples 16 through 50)	\$113
	(samples 51 through 100)	\$76
	(samples >100)	\$39

LTQ 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 10)	\$84
	(11 to 15)	\$76
	(>15)	\$41