



Charles W. Gehrke Proteomics Center

University of Missouri

External Academic Fee Schedule

Please contact Brian at 573-884-7374 to discuss sample submission. July 2022

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
	96-well plate	per plate	\$2,879
silver	band or spots	1 to 10	\$204
		>10	\$184
In-Solution Trypsin Digestion + C18 SPE peptide purification		(1 to 10)	\$171
other proteases are available, e.g. GluC, LysC		(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

\$102	163
\$92	171
\$76	141
\$50	93
\$45	84
\$38	71
\$25	46
\$25	46
\$117	217
\$144	267
\$172	319
\$84	156
\$42	78
\$97	180
\$48	89
\$106	197
\$96	178
\$1,550	2879
\$110	204
\$99	184
\$92	171
\$83	154
\$69	128
\$46	85
\$96	178
\$766	1423
\$3,829	7111
\$29	54
\$19	35
\$10	19
\$6	11
\$26	48
\$52	97
\$433	804
\$2,164	4019
\$85	158
\$76	141
\$43	80
\$82	152
\$73	136
\$61	113
\$41	76
\$21	39
\$45	84
\$41	76
\$22	41