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Charles W. Gehrke Proteomics Center University of Missouri

University of Misso	uri		
On-Campus Fee Sc	hedule		
Rates are for MU users. For off-campus rates please contact	Brian at 573-884-7374. J	luly 2022	
PROTEIN PREPARATION		1 OR 2	\$104
phenol extraction (useful for plants and other recalcitrant tissues)	3 to 5	\$94	
		>5	\$78
acetone/TCA precipitation (human cells, lysates, etc.)		1 to 10	\$51
		11 to 25	\$46
		26 to 50	\$39
		>50	\$26
resuspension & quantitation of user-supplied acetone pellet (per sam	unle)		\$26
SDS-PAGE	ipic)		φ20
Pour gel, run, stain with coomassie blue	MiniVE	10 lanes	\$119
	SE600	25 lanes	\$147
	DALT6	35 lanes	\$200
ELECTROPHORETIC TRANSFER			+=++
set up, transfer, staining with Ponceau	MiniVE	1st gel	\$86
choice of nitrocellulose or PVDF		extra gel(s)	\$43
	SE600	1st gel	\$99
		extra gel(s)	\$49
In-Gel Trypsin Digestion			
coomassie	band or spots	1 to 10	\$108
		>10	\$98
	96-well plate	per plate	\$1,550
silver	band or spots	1 to 10	\$112
		>10	\$101
In-Solution Trypsin Digestion + C18 SPE peptide purification		(1 to 10)	\$94
other proteases are available, e.g. GluC, LysC		(11 to 20)	\$85
		(21 to 40)	\$70
		(>40)	\$47
Bruker timsTOF-PRO High Proteome Coverage LCMS+MSMS			
	(per hour, 70min :	= 1 sample)	\$98
Reversed phase separation of protein digests, MS & MS/MS data	(per day, ∼16 sam	nples)	\$781
acquisition using the PASEF method.	(per week, ~110 samples)		\$3,906
DB search & Quantitative Data analysis (per sample)		$(1 t_0, 10)$	¢20
DD search & Quantitative Data analysis (per sample)		(1 to 10)	\$30
		(11 to 20)	\$20
		(>20)	\$12
CLIENT use of in-house PEAKS software for results analysis		per hour	\$7
Targeted Protein Quantitation using LC-MRM (multiple reaction me	onitoring)		
Method development (generate peptide list unique to protein of interes using recombinant protein or 1-2 samples, method refinement)	per hour	\$27	
LC-MRM (using optimized methods)	per hour	~2 samples	\$55
	per day	~48 samples	\$441
	per week	~330 samples	\$2,207
Intact Mass analysis of proteins and DNA	permeent	000 04	<i>\\\\\\\\\\\\\</i>
C8 reversed-phase separation of purified/enriched samples, deconvo	(1 to 5)	\$75	
vield intact mass	(5 to 15)	\$67	
		(>15)	\$37
LTQ Orbitrap LC-MS+MSMS		(/	701
Reversed phase separation of protein digests, data acquisition, and	digests, data acquisition, and (samples 1 throug		\$84
database search	(samples 6 throug	. ,	\$75
	(samples 16 throu		\$62
	(samples 10 throu	• /	
		igii 100)	\$42 \$21
LTQ Orbitrap Accurate/Exact mass MS and MSMS (pure compoun	(samples >100)		\$21
		(1 + c E)	¢.27
ESI direct infusion MS (high resolution, <5ppm mass accuracy, negati modes)	ve- or positive-ion	(1 to 5)	\$35
modoj		(6 to 10)	\$31
		(>10)	\$18