

SERVICES	COST	EXPLANATION	OUTPUT
<u>Protein Electrophoresis</u>			
SDS-PAGE gel, small	75	either a minigel or a criterion gel. Includes running and staining with coo blue, silver, or sypro ruby	gel and image
<b>SDS-PAGE gel, small (non UofAZ user)</b>	<b>112</b>		
SDS-PAGE gel, large	150	18 x 18 cm gel for enhanced resolution gel. Includes running and staining with coo blue,	gel and image
<b>SDS-PAGE gel, large (non UofAZ user)</b>	<b>225</b>		
2D-PAGE gel, small	90	11cm strip, criterion gel, Includes running and staining with coo blue, silver, or sypro ruby	gel and image
<b>2D-PAGE gel, small (non UofAZ user)</b>	<b>135</b>		
2D-PAGE gel, large	340	17cm strip, 18cm gel, Includes running and staining with coo blue, silver, or sypro ruby	gel and image
<b>2D-PAGE gel, large (non UofAZ user)</b>	<b>510</b>		
2D-DIGE	600	25cm strip, 18cm gel, includes cleanup, quantitation and CyDye labelling of two samples, and extensive image analysis. This is more expensive because of the dyes, but is very good for accurate quantitation of subtle changes	gel and image, plus detailed quantitative image analysis of differentially expressed proteins
<b>2D-DIGE (non UofAZ user)</b>	<b>900</b>		
<u>Mass Spectrometry</u>			
protein molecular weight determination	30	MS only. may be done via MALDI, FTMS, infusion into ion-trap, or micro-bore LC-MS	spectra and calculated molecular weight
<b>protein molecular weight determination (non UofAZ user)</b>	<b>45</b>		
MALDI-Tof peptide fingerprinting of a digested protein	60	high resolution MALDI-Tof, plus database search and interpretation of results (includes digestion)	spectra plus database search results
<b>MALDI-Tof peptide fingerprinting of a digested protein (non UofAZ user)</b>	<b>90</b>		
MALDI-Tof peptide fingerprinting of a digested protein	45	high resolution MALDI-Tof, plus database search and interpretation of results (no digestion; sample already digested by user)	spectra plus database search results
<b>MALDI-Tof peptide fingerprinting of a digested protein (non UofAZ user)</b>	<b>67</b>		
HPLC-MS/MS non protein sample	@ \$15/hr	Development of HPLC-MS/MS method for non protein samples using column/solvents/source variations	spectra and interpretation of data
<b>HPLC-MS/MS non protein sample (non UofAZ user)</b>	<b>@ \$22/hr</b>		
HPLC-MS/MS non protein sample	60	HPLC method already developed, plug and play with user or pre-existing developed methods	spectra and interpretation of data
<b>HPLC-MS/MS non protein sample (non UofAZ user)</b>	<b>90</b>		
nanoLC-MS/MS of a sample in solution	60	C18 reverse phase chromatography on a 75u ID column coupled to an LCQ ion trap Mass Spec	chromatogram and selected spectra
<b>nanoLC-MS/MS of a sample in solution (non UofAZ user)</b>	<b>110</b>		
nanoLC-MS/MS of a protein sample in solution	75	C18 reverse phase chromatography on a 75u ID column coupled to an LCQ ion trap Mass Spec, and SEQUEST database searching and analysis of results (no digestion; sample already digested by user)	chromatogram and selected spectra, and protein identification report
<b>nanoLC-MS/MS of a protein sample in solution (non UofAZ user)</b>	<b>125</b>		
nanoLC-MS/MS of a sample in solution for protein identification	90	C18 reverse phase chromatography on a 75u ID column coupled to an LCQ ion trap Mass Spec, and SEQUEST database searching and analysis of results (includes digestion)	chromatogram and selected spectra, and protein identification report

<b>nanoLC-MS/MS of a sample in solution for protein identification (non UofAZ user)</b> 140			
nanoLC-MS/MS of a sample in gel for protein identification	120	C18 reverse phase chromatography on a 75u ID column coupled to an LCQ ion trap Mass Spec, and SEQUEST database searching and analysis of results (includes digestion)	chromatogram, selected spectra, and protein identification report
<b>nanoLC-MS/MS of a sample in gel for protein identification (non UofAZ user)</b> 170			
<b>Proteomics Analysis</b>			
proteomics 2D gel package	900	includes mini format 2D gel, staining, in-gel digestion, nanoLC-MS/MS and SEQUEST database searching for up to 12 spots	annotated gel image and protein identification report
<b>proteomics 2D gel package (non UofAZ user)</b> 1,350			
2D-DIGE proteomics package	1500	includes 2D DIGE gel, image analysis, post-staining with coomassie blue or silver or second separate gel stained, in-gel digestion, nanoLC-MS/MS and SEQUEST database searching for up to 12 spots	annotated gel image, quantitative image analysis, and protein identification report
<b>2D-DIGE proteomics package (non UofAZ user)</b> 2,250			
LC-LC-MS/MS of a complex protein mixture (aka Mudpit Analysis)	500	includes digestion, cleanup, 10 salt step gradient and SEQUEST database searching	large scale protein identification report
<b>LC-LC-MS/MS of a complex protein mixture (aka Mudpit Analysis) (non UofAZ user)</b> 750			
Gel-based LC-LC/MS/MS (Mudpit of a whole 1D gel lane)	650	includes digestion of individual gel slices cut from gel lane, pool of extracts and 10 salt step gradient and SEQUEST database searching	
<b>Gel-based LC-LC/MS/MS (Mudpit of a whole 1D gel lane) (non UofAZ user)</b> 975			
<b>Other</b>			
Albumin Depletion	300		Call for consultation
<b>Albumin Depletion (non UofAZ user)</b> 450			
Cy Dyes	\$50/μL		
Typhoon multi-wavelength fluorescent scanner usage	40/hour		
additional sample preparation or cleanup time	30/hour	for example: microdialysis, ziptip purification, acetone precipitation	
****PRICES ARE SUBJECT TO CHANGE			
*** SAMPLE LOAD CAPACITY IS IMPORTANT. PLEASE CONSULT WITH US FOR LARGE SAMPLE SET BEING SUBMITTED			