

<b>Arizona Proteomics Consortium Prices</b>				
<b>Service</b>	<b>Description</b>	<b>Output</b>	<b>Cost UA</b>	<b>Cost non-UA</b>
<b>Protein electrophoresis</b>				
SDS-PAGE gel, small	BioRad Minigel or Criterion gel. Includes staining with Coomassie blue or silver	gel and image	60	112
2D-PAGE gel, small	IEF with 11cm strip, BioRad Criterion gel. Includes staining with Coomassie blue or silver	gel and image	190	241
<b>Mass Spectrometry</b>				
Protein molecular weight determination	MS by MALDI-TOF or ESI-MS	spectrum and calculated molecular weight	40	45
HPLC- or infusion MS/MS	Method development for non-protein or protein identification or quantification	best method to find or quantitate molecule of interest	1100	1300
HPLC- or infusion MS/MS	Method already developed	spectrum, calculated molecular weight and peak area or intensity	50	90
Infusion MS, SIM or MRM MS	MS by ESI-MS	spectrum or quantitative trace, done by requestor after training by Core staff member OR when sample requires excessive instrument cleaning time by Core personnel	\$40/hr	UA only
nano LC-MS/MS of a peptide digest in solution*	Nano-HPLC-MS/MS by C18 reverse phase chromatography, SEQUEST database searching and analysis or results (sample digested by user)	protein and peptide identification report	40	88
nano LC-MS/MS of a protein sample in solution for protein identification*	Protease digestion of solution protein(s), nano-HPLC-MS/MS by C18 reverse phase chromatography, SEQUEST database searching and analysis of results	protein and peptide identification report	143	193

nano LC-MS/MS of a gel band for protein identification*	Protease digestion of in-gel protein(s), nano-HPLC-MS/MS by C18 reverse phase chromatography, SEQUEST database searching and analysis of results	protein and peptide identification report	178	228
Orbitrap Mass Analysis*	Static infusion by syringe or using Nanomate source	high resolution spectrum	65	91
Orbitrap LC-MS/MS of a peptide digest in solution*	Nano-HPLC-MS/MS by C18 reverse phase chromatography, SEQUEST or DISCOVERER database searching and analysis of results (sample digested by user)	protein and peptide identification report	45	100
Orbitrap LC-MS/MS of a protein sample in solution for protein identification*	Protease digestion of solution protein(s), nano-HPLC-MS/MS by C18 reverse phase chromatography, SEQUEST or DISCOVERER database searching and analysis of results	protein and peptide identification report	130	205
Orbitrap LC-MS/MS of a gel band for protein identification*	Protease digestion of in-gel protein(s), nano-HPLC-MS/MS by C18 reverse phase chromatography, SEQUEST or DISCOVERER database searching and analysis of results	protein and peptide identification report	150	240
LCLC MS/MS of a complex protein mixture (aka MudPIT Analysis)	Protease digestion of solution proteins, 10-step salt gradient, C18 reverse phase chromatography, MS/MS and SEQUEST database searching	large scale protein and peptide identification report	330	750
Gel-based LC LC/MS/MS (MudPIT of a 1D gel lane)	Protease digestion of individual gel slices, extracts pooled, 10-step salt gradient, C18 reverse phase chromatography, MS/MS, and SEQUEST database searching	large scale protein and peptide identification report	560	975
<b>Protein characterization</b>				
Chromatography	Ion exchange, affinity, gel filtration, hydrophobic interaction	chromatogram and fractions	415	1000
Molecular Interactions	Biacore T100 SPR method development, kinetics, affinity, concentration:protein:protein, protein:small molecule, nucleic acid:protein, nucleic acid:small molecule. Price includes 1 CM5 chip, more chips or specialty chips to be purchased by the service requestor.	report including kinetic or equilibrium constants	900	1000

<b>Sample preparation</b>				
Depletion of 12 abundant proteins from human serum or plasma	Removes albumin, IgG, transferrin, fibrinogen, $\alpha$ 1-antitrypsin, IgA, IgM, $\alpha$ 2-macroglobulin, haptoglobin, apolipoproteins A-I and A-II, and orosomuroid	chromatogram and fractions	420	600
Protein assay	Bradford, BCA, micro BCA, BioRad RC/DC	report	55	60
Sample cleanup/enrichment	Dialysis, acetone precipitation, ultrafiltration, SPE		50	60
<b>Prices are set by the University of Arizona Financial Services Office and are subject to change without notice.</b>				
<b>Please consult with Proteomics personnel when bringing new projects or large/complex projects as above descriptions cannot include all details</b>				
<b>*SAMPLE CLEAN-UP BY SOLID PHASE EXTRACTION (SPE) IS MANDATORY FOR ORBITRAP and LTQ SAMPLES AT A COST OF \$49/SAMPLE</b>				
<b>USERS MAY CLEAN-UP THEIR OWN SAMPLES - FAILURE TO CLEAN UP WILL RESULT IN A CHARGE FOR PRECOLUMN OR COLUMN IF IT BLOCKS DURING INJECTION</b>				
<b>This price list supercedes any previous pricing on UA Proteomics mirror websites as of July 1 2014.</b>				