Proteomics Facility

Service Request Form

University of Iowa, Carver College of Medicine

363 Eckstein Medical Research Building
Ph: 319-335-7956

>>>>

As the complexity of a sample increases, the risks of under-sampling are magnified. The risk rises faster for minor components, so the fidelity for trace level characterization tends to improve with affinity enrichment and often fractionation. Please raise the issue if you are concerned.

Last Name _____ First Name _____ MI _____

Lab Phone _____ Email _____ Your direct No. _____

Department _____ Advisor _____ Date _____

Note: Protein mixtures must be resolved in commercial Bis/TRIS or Tricine PAGE gels and stained with Coomassie (preferable) or "MS-compatible" Silver protocols. Please use; 1) *Coomassie*: Pierce Gel Code Blue or 2) *Silver*: Pierce Ag Stain kit for Mass Spectrometry (develop < 9 min.). Use "aseptic" precautions to avoid keratins and be advised that Ag staining increases the risks of keratin contamination. Beta mercaptoethanol (BME) in Laemmli buffer may be a source of keratin, use DTT instead. Keratin advise .

Sample Information	**User Input**		**Complete on the reverse side if necessary**	
Project Name	The Sample originates from		Taxonomy is	
❑**TAP** ❑imunoaffinity Other: ❑ Peptide Glycan	My Bait Protein is _____ ❑ Lipid ❑ Oligonucleotides	Expr'd in cell line**?** _____ Purified with?_____	Affinity support	
Buffer composition?	**Need mass of Intact oligomer?**❑ ❑**MALDI** ❑**nESI** ❑Conc_____	**Is the sample in a PAGE gel___ Manfact?_____**	Ladder Set _____ MW range_____	%T____ --_____
What do you know about the sample(s) now?				
What would you like to learn?				
Other Comments				

MFK

FUND	ORG	DEPT	SUBDEPT	GRANT/PRGM	INST ACCT	ORG ACCT	DEPT AQCCT	FN	CST CTR
XXX	**XX**	**XXXX**	**XXXXX**	**XXXXX XX**	**XXXX**	**XXX**	**XXXXX**	**XX**	**XXXX**

Analysis Method	**Core input**	**This section will be filled in during consultation or analysis**		
Enrichment? ❑C_{18} ❑TiO_2	❑IMAC ❑SCX	❑Other:	❑in gel digest(s)	❑Depletion:
❑**MALDI-TOF**	❑Require Sequence of m/z	_____	❑Identify Adducts?	_____
❑**ESI (infusion):**❑**pos** ❑**neg**	Require Sequence of:_____	_____	❑Identify Adducts?	
❑ Off Gel Protein Fract? ❑direct digest ❑ **Enzyme?** _____ ❑ **BioTyper?** _____	❑LC-ESI-MS/MS ❑LTQ XL ❑q/TOF ❑3Quad ❑ 1st Column_____ ❑ 2nd Column_____	❑gel-separated proteins ❑preferred ion list? ❑Exclude ❑ Gradient_____	❑Characterize PTM* Which PTM? _____ _____	❑3Q PreCur ❑3Q NI loss ❑3Q Product
Biomarker Discovery	❑MudPit*	❑LTQ XL ❑q/TOF ❑3Q	1st Dim._____	# Steps_____
❑**Targeted Quantification***	❑SILAC	❑Chemical Labeling:	❑diMethyl	❑Label-free
AQUA (long development)	AA label(s):_____	❑iTRAQ, ❑O_{18},		

***MudPit, PTM and quantification require advance consultation. **Extensive user projects may be charged for traps or columns.**

Analyst_____ Instrument _____ Filename_____ Comments_____