

Protein Analysis Sample Submission Form

University of Virginia Biomolecular Research Facility

<i>Person supplying sample</i>	<i>Phone No.</i>	
<i>Principal investigator of lab</i>	<i>Fax no</i>	
<i>Charge code</i>	<i>email</i>	
<i>Investigator address</i>		
<i>billing address</i>		
<i>Sample name</i>		
<i>species</i>	<i>tissue</i>	
<i>molecular weight</i>	<i>isoelectric point</i>	
<i>Date submitted</i>		
<i>Desired analysis; sequencing by mass spectrometry</i>	<i>Edman sequencing</i>	<i>mass mapping</i>
<i>mass determination, reverse phase chromatography</i>		
<i>Reason for analysis ;</i>		
<i>sequence for probe design</i>	<i>comparison with another protein</i>	<i>identification of protein</i>
<i>identification of a particular amino acid</i>	<i>sequence confirmation</i>	<i>identification of proteolysis site</i>
<i>other</i>		
<i>Amount of sample supplied:</i>	<i>(μg)</i>	<i>means of estimation</i>
<i>pmole of protein</i>		
<i>Form in which sample is supplied</i>		
<i>in gel</i>		<i>blotted on PVDF</i>
<i>in solution – (solvent</i>	<i>)</i>	<i>volume</i>
<i>dried – (previous solvent</i>	<i>)</i>	
<i>other :</i>		
<i>Solvents to re-dissolve sample</i>		
<i>For samples in gels or on PVDF, please supply a picture with the protein of interest</i>		

See next page

Do you know what type of data you expect? If so, please provide information about the expected results. If your expected sequence is not in publicly available databanks, please include the name of the databank where it might be found.

Edman sequencing only

If the sequence we obtain is not what you expect, should we sequence further to try to obtain sufficient data to identify the protein? Yes No

Type of data that is useful:

- unambiguous data without gaps
- data with unknowns or gaps
- sequences of more than one protein.
- Other

Number of amino acids

The number of amino acids that can be obtained is sample dependent. Low amounts of sample will limit the amount of data obtainable. Provided that there is sufficient sample, the limiting factor in the length of sequence obtainable is the amount of amino acid background, which is commonly increased by; length of the protein; composition, where serine, proline and aspartate in particular decrease the signal to noise ratio. With a adequate amounts of clean sample, 20 or more amino acids are typically obtainable.

What were the last two or more steps in the preparation?

Has cysteine been alkylated or modified to protect it during sequencing? Yes No

Describe any modifications

Do you want the sample alkylated to aid identification of cysteine (standard cost of \$90)? Yes No

Describe any evidence that this sample does not have a blocked N-terminal amino acid: e.g. production from a digestion, similarity to unblocked samples, expression system

Chromatography

Is there a particular column that should be used for this sample?

Should the gradient be chosen to better separate small or large molecules?

What needs to be collected?