

**PROTEIN/PEPTIDE SEQUENCE ANALYSIS SUBMISSION FORM**

**RESEARCHER INFORMATION**

Date: \_\_\_\_\_  
 Principal Investigator: \_\_\_\_\_  
 Department/Company: \_\_\_\_\_  
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**SHIPPING ADDRESS:**  
 \_\_\_\_\_  
 \_\_\_\_\_  
 \_\_\_\_\_

**BILLING INFORMATION**

P.O./MC/VISA #: \_\_\_\_\_  
 Exp. Date (if applicable): \_\_\_\_\_  
 Department/Company: \_\_\_\_\_  
 Phone: \_\_\_\_\_ Fax: \_\_\_\_\_  
**BILLING ADDRESS:**  
 \_\_\_\_\_  
 \_\_\_\_\_  
 \_\_\_\_\_

**Sample Information:**

Please provide as much information as possible:

1. **SAMPLE AOUNT:** \_\_\_\_\_ moles; or \_\_\_\_\_ micrograms  
 A. Recommend minimum amount of samples is 100 pMoles.  
 Example: 100 pmoles of a protein (M.W. 10,000) would weigh 1.0 µg  
 B. If less than 100 pmoles of protein sample, there are **NO GUARANTEES** of adequate sequencing results.

2. **IS SAMPLE in SOLUTION or DRY** \_\_\_\_\_  
 A. If sample is in solution, what is the sample stored in? \_\_\_\_\_

3. **METHOD(s) USED TO OBTAIN THE SAMPLE:** \_\_\_\_\_  
 A. For samples electroblotted to PVDF: What membrane was used?  
     \_\_\_\_\_ Immobilon-P (.45 micron) (Millipore)                      \_\_\_\_\_ Problot (.1 micron) (ABI)  
     \_\_\_\_\_ Westran (.45 micron) (Schleicher & Schuell)                      \_\_\_\_\_ Trans-Blot (.1 micron) (Biorad)  
     \_\_\_\_\_ Immobilon-PSQ (.1 micron) (Millipore)                      \_\_\_\_\_ Fluoratrans (.1 micron) Pall Corp)

B. It is possible to sequence directly from a membrane: PVDF & Immobilon

4. **ESTIMATED PURITY OF THE SAMPLE:** \_\_\_\_\_  
 A. Method(s) used to obtain Purity: \_\_\_\_\_  
 B. If your sample was collected on a HPLC, please attach the chromatogram with gradient, solvents, column and wavelength

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 A. Method(s) used to obtain Purity: \_\_\_\_\_  
 B. If your sample was collected on a HPLC, please attach the chromatogram with gradient, solvents, column and wavelength
5. N-TERMINUS BLOCKED? No \_\_\_\_\_ Do not know \_\_\_\_\_ Yes \_\_\_\_\_  
 A. If the peptide/protein is blocked, it will NOT be able to be sequenced, unless cleaved by enzyme(s) first.  
 B. The only way to determine if the peptide/protein is blocked is to:  
 1. Conduct a tryptic digest apriori  
 2. Attempt to sequence, and see what happens
6. IS THE SAMPLE FREE OF? Tris Salts \_\_\_\_\_ Amino Containing Buffers \_\_\_\_\_  
 Tris-Glycine \_\_\_\_\_ Detergents \_\_\_\_\_  
 1. If yes, name of detergent: \_\_\_\_\_  
 2. % of detergent in the sample: \_\_\_\_\_  
 A. Sequencing is hindered by the presence of any salt. Amino containing buffers, and some detergents.  
 B. De-salting is best accomplished by double dialysis treatment
7. ARE THERE ANY KNOWN MODIFIED AMINO ACIDS? \_\_\_\_\_  
 Phosphorylations: \_\_\_\_\_ Conjugations: \_\_\_\_\_ Cysteine Modified: \_\_\_\_\_ If yes, what derivative?: \_\_\_\_\_
8. ENZYME TREATMENT: Yes \_\_\_\_\_ What enzyme? \_\_\_\_\_ Cleavage sites \_\_\_\_\_  
 Phosphorylations: \_\_\_\_\_ Conjugations: \_\_\_\_\_ Cysteine Modified: \_\_\_\_\_ If yes, what derivative?: \_\_\_\_\_
9. PROTEIN SEQUENCE KNOWN: Yes \_\_\_\_\_ No \_\_\_\_\_ (Please attached)
10. AMINO ACID ANALYSIS PERFORMED? Yes \_\_\_\_\_ No \_\_\_\_\_ (Please attached)

Note: Proper sample preparation is crucial for optimal results. Important parameters include concentration and volume of sample, as well as the presence and concentration of detergents, glycerol, buffers and other salts. Requirements vary depending on the analysis requested. Do not make any assumptions about sample preparation requirements. Consult with our technical support at [support@biosyn.com](mailto:support@biosyn.com) or call **800-227-0627** for detailed

**Label sample to be sequence properly and return to:**

**Bio-Synthesis Inc.**  
**Analytical Service Coordinator**  
**612 E. Main Street**  
**Lewisville, TX 75057**