BIOSYNTHESIS
COMMITTED TO BIOMIC RESEARCH

PROTEIN/PEPTIDE SEQUENCE ANALYSIS SUBMISSION FORM

RESEARCHER INFORMATION

Date: _____

Principal Investigator: _____

Department/Company: _____

Phone: _____ Fax: _____

Email: _____

SHIPPING ADDRESS:

_____

_____

_____

BILLING INFORMATION

P.O./Credit Card #: _____

Exp. Date (if applicable): _____ CVV: _____

Department/Company: _____

Phone: _____ Fax: _____

Email: _____

BILLING ADDRESS:

_____

_____

_____

Sample Information:

Please provide as much information as possible:

1. SAMPLE AMOUNT: _____ 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. Number of cycles per sample: _____

3. Is sample in SOLUTION or DRY: _____
   A. If sample is in solution, what is the sample stored in? _____

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

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

5. 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

6. N-TERMINUS BLOCKED? Yes ☒ Do not know ☐ No ☐

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

7. DOES SAMPLE CONTAIN? 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

8. ARE THERE ANY KNOWN MODIFIED AMINO ACIDS? _____
   Phosphorylations: ☐ Conjugations: ☐ Cysteine Modified: ☐ If yes, what derivative?: _____

9. ENZYME TREATMENT: Yes ☐ No ☐ What enzyme? _____ Cleavage sites _____
   Phosphorylations: ☐ Conjugations: ☐ Cysteine Modified: ☐ If yes, what derivative?: _____

10. PROTEIN SEQUENCE KNOWN: Yes ☐ No ☐ (Please attach)

11. AMINO ACID ANALYSIS PERFORMED? Yes ☐ No ☐ (Please attach)

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. Customer samples will be discarded unless otherwise specified. Consult with our technical support at 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

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