MCB 102: Discussion 3 Problem Set Answers

1. The following reagents are often used in protein chemistry. Match the reagent with the purpose for which it is best suited. Some answers may be used more than once or not at all; more than one reagent may be suitable for a given purpose.

(a) CNBr (cyanogen bromide)
(b) Edman reagent (phenylisothiocyanate)
(c) FDNB
(d) dithiothreitol
(e) performic acid
(f) chymotrypsin
(g) trypsin

___ hydrolysis of peptide bonds on the carboxyl side of Lys and Arg
___ cleavage of peptide bonds on the carboxyl side of Met
___ breakage of disulfide (—S—S—) bonds
___ determination of the amino acid sequence of a peptide
___ determining the amino-terminal amino acid in a polypeptide

Ans: g; a; d and e; b; c
See pages: 98-100

2. In one or two sentences, describe the usefulness of each of the following reagents or reactions in the analysis of protein structure:
(a) Edman reagent (phenylisothiocyanate)
(b) Sanger reagent (1-fluoro-2,4-dinitrobenzene, FDNB)
(c) trypsin

Ans: (a) used in determination of the amino acid sequence of a peptide, starting at its amino terminus; (b) used in determination of amino-terminal amino acid of a polypeptide; (c) used to produce specific peptide fragments from a polypeptide.
See pages: 97-100

3. A biochemist wishes to determine the sequence of a protein that contains 123 amino acid residues. After breaking all of the disulfide bonds, the protein is treated with cyanogen bromide (CNBr), and it is determined that that this treatment breaks up the protein into seven conveniently sized peptides, which are separated from each other. It is your turn to take over. Outline the steps you would take to determine, unambiguously, the sequence of amino acid residues in the original protein.

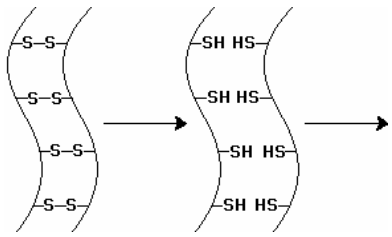
Ans: (1) Use Edman degradation to determine the sequence of each peptide. (2) Create a second set of peptides by treatment of the protein with a specific protease (e.g., trypsin), and determine the sequence of each of these. (3) Place the peptides in order by their overlaps. (4) Finally, by a similar analysis of the original protein without first breaking disulfide bonds, determine the number and location of —S—S— bridges.

4. A sequence of amino acids in a certain protein is found to be -Ser-Gly-Pro-Gly-. The sequence is most probably part of a(n):

A) antiparallel β sheet.
B) parallel β sheet.
C) α helix.
D) α sheet.
E) β turn.

Ans: E, See page: 124

5. The α--keratin chains indicated by the diagram below have undergone one chemical step. To alter the shape of the α--keratin chains—as in hair waving—what subsequent steps are required?



A) Chemical oxidation and then shape remodeling
B) Chemical reduction and then chemical oxidation
C) Chemical reduction and then shape remodeling
D) Shape remodeling and then chemical oxidation
E) Shape remodeling and then chemical reduction

Ans: D, See page: 127

6. Which of the following is *least* likely to result in protein denaturation?

A) Altering net charge by changing pH
B) Changing the salt concentration
C) Disruption of weak interactions by boiling
D) Exposure to detergents
E) Mixing with organic solvents such as acetone

Ans: B See page: 147