As a first approximation proteins can be assigned to one of three classes on the basis of shape and solubility. These are:

|  |  |  |
| --- | --- | --- |
|  |  | extracellular, cytoplasmic, nuclear |
|  |  | extracellular, globular, membrane |
|  |  | fibrous, cytoplasmic, membrane |
| http://owl.cengage.com/owlimages/check.GIF |  | fibrous, globular, membrane |

You have isolated a peptide, which you wish to sequence. First you treat the peptide with CNBr and isolate two fragments. With a separate portion of the peptide you cleave with trypsin and obtain 3 fragments. You sequence each of the five peptides and get the following data:  
  
Peptide 1: VALKTQAM  
Peptide 2: LDGKM  
Peptide 3: TQAM  
Peptide 4: LDGK  
Peptide 5: MVALK  
  
The sequence of the original peptide is:

|  |  |  |
| --- | --- | --- |
|  |  | MVALKTQAMLDGK |
|  |  | VALKTQAMLDGKM |
|  |  | VALKTQAMLDGKM |
| http://owl.cengage.com/owlimages/check.GIF |  | LDGKMVALKTQAM |

The effect of ionic strength on protein solubility is attributed to:

|  |  |  |
| --- | --- | --- |
|  |  | the decrease in electrostatic interactions between protein molecules |
|  |  | the increase in charge-counter ion interactions |
|  |  | competition between the protein and the salt ions for water of solution |
| http://owl.cengage.com/owlimages/check.GIF |  | all the above |

All proteins have a specific function (or functions) to perform in a cell or organism. Which of the following factors best explains the basis behind the ability of most proteins to perform correctly?

|  |  |  |
| --- | --- | --- |
|  |  | Every protein must be able to bind the high energy molecule ATP. |
| http://owl.cengage.com/owlimages/check.GIF |  | Many proteins function by having the ability to recognize specific target molecules and bind to them. |
|  |  | Every protein must have at least one disulfide bond. |
|  |  | All proteins must have a specific ratio of nonpolar to polar amino acid residues in order to perform a function. |

Through H-bond interactions between adjacent amino acids residues the polypeptide chain can arrange itself into characteristic helical or pleated segments. This is a definition of the

|  |  |  |
| --- | --- | --- |
|  |  | primary structure |
| http://owl.cengage.com/owlimages/check.GIF |  | secondary structure |
|  |  | tertiary structure |
|  |  | quaternary structure |

Two proteins are said to be homologous if they:  
  
A. Have the same function in different organisms  
B. Share a significant degree of sequence similarity  
C. Share a significant degree of sequence similarity but have completely different functions in different organisms  
D. Share a common tertiary structure fold but have little sequence homology  
E. Share a significant degree of structural similarity but have completely different functions in different organisms  
  
Which of the above statements are true?

|  |  |  |
| --- | --- | --- |
|  |  | A & B |
|  |  | A, B & C |
|  |  | All of the above |
| http://owl.cengage.com/owlimages/check.GIF |  | All except D |
|  |  | All except E |

You have a mixture of 4 proteins with the following characteristics:  
Protein a: pI = 6.2, Molecular Weight 43,000  
Protein b: pI = 7.1, Molecular Weight 61,000  
Protein c, pI = 5.5, Molecular Weight 60,000  
Protein d, pI = 5.1, Molecular Weight 79,000  
  
At pH = 8.0 you chromatograph them using an anion exchange column, with a gradient of NaCl to elute the proteins: what will be the order of elution?

|  |  |  |
| --- | --- | --- |
| http://owl.cengage.com/owlimages/check.GIF |  | b, a, c, then d |
|  |  | d, c, a, then b |
|  |  | a, c, b then d |
|  |  | d, b, c then a |

One of the common post-translational modifications found in proteins is phosphorylation of hydroxyl groups in some amino acid residues. Which of the following groups of amino acids may be present in phosphorylated form?

|  |  |  |
| --- | --- | --- |
|  |  | Ala, Gly, Phe |
| http://owl.cengage.com/owlimages/check.GIF |  | Ser, Thr, Tyr |
|  |  | Cys, Met |
|  |  | Trp, Lys, Asn |

Disulfide bonds, formed between cysteine residues, and other types of covalent cross-links in proteins are:

|  |  |  |
| --- | --- | --- |
|  |  | Primarily stabilizing quaternary structure |
|  |  | More common in intracellular proteins than intracellular proteins |
| http://owl.cengage.com/owlimages/check.GIF |  | Primarily stabilizing tertiary structure |
|  |  | More important than non-covalent forces in holding the tertiary structure of the protein together |

The secondary, tertiary and quaternary structures of proteins are stabilized principally by:  
a. covalent bonds  
b. H-bonds  
c. electrostatic interactions  
d. van der Waals forces  
e. hydrophobic interactions  
  
Choose the correct answer.

|  |  |  |
| --- | --- | --- |
|  |  | b, c, e |
|  |  | all the above |
|  |  | a, b, c, e |
| http://owl.cengage.com/owlimages/check.GIF |  | b, c, d, e |

The following table summarizes the purification scheme for the enzyme xanthine dehydrogenase (XDH):

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Fraction | Volume (mL) | Total Protein (mg) | Total Activity (nmoles/min) | Specific Activity | Percent Recovery |
| Crude Extract | 3,800 | 22,800 | 2,460 |  | 100 |
| Salt Precipitation | 165 | 2,800 | 1,190 |  | 48 |
| Ion Exchange Chromatography | 65 | 100 | 720 |  | 29 |
| Molecular Sieve Chromatography | 40 | 14.5 | 555 |  | 23 |
| Affinity Chromatography | 6 | 1.8 | 275 |  | 11 |

Which step is the most effective in terms of increased purity from the previous step?

|  |  |  |
| --- | --- | --- |
|  |  | Salt Precipitation |
|  |  | Molecular Sieve Chromatography |
| http://owl.cengage.com/owlimages/check.GIF |  | Ion Exchange Chromatography |
|  |  | Affinity Chromatography |