The native folded structure of a protein is dictated by several factors. Which is the most important?

|  |  |  |
| --- | --- | --- |
|  |  | disulfide bonds |
|  |  | interactions with solvent |
|  |  | pH and ionic strength of solvent |
| http://owl.cengage.com/owlimages/check.GIF |  | the sequence of the protein |

Proteins that form stable quaternary structure do so because:  
  
A] There are enhanced polar interactions between the subunits relative to polar interactions with the solvent.  
B] There are increased van der Waals interactions at the subunit interfaces favoring quaternary structure formation.  
C] There is a considerable increase in entropy as a result of water molecules being excluded from the subunit interface.  
D] Each individual subunit becomes more flexible in the quaternary structure overcoming the entropy loss resulting from combining subunits.  
  
Which is the correct answer:

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

What are the major factors that favor the formation of quaternary structure?

|  |  |  |
| --- | --- | --- |
|  |  | ΔS solvent and ΔS subunits |
|  |  | ΔH solvent and ΔS subunits |
|  |  | ΔH solvent and ΔH subunits |
| http://owl.cengage.com/owlimages/check.GIF |  | ΔS solvent and ΔH subunits |

Which of the following non-covalent forces or interactions plays the dominant role in protein folding?

|  |  |  |
| --- | --- | --- |
|  |  | Hydrogen Bonds |
|  |  | Van der Waals Interactions |
| http://owl.cengage.com/owlimages/check.GIF |  | Hydrophobic Interactions |
|  |  | Electrostatic Interactions |

Which of the following is a benefit of intrinsically unstructured proteins?

|  |  |  |
| --- | --- | --- |
|  |  | A. Compared with compact, folded proteins, disordered segments in proteins appear to be able to form larger intermolecular interfaces to which ligands could bind. |
|  |  | B. The flexibility of disordered proteins may reduce protein, genome and cell sizes. |
| http://owl.cengage.com/owlimages/xmark.GIF |  | C. Disordered proteins cannot adapt their structures to bind to multiple ligands, which increases their specificity. |
|  |  | D. All of the above |
| http://owl.cengage.com/owlimages/GreenRightArrow.GIF |  | E. Answers A and B. |

The primary sequence of a protein governs:  
  
A] The final folded structure of the protein  
B] The localization of the protein  
C] The position of disulphide bonds in the protein  
D] The position of post translational modifications of the protein  
  
Which is the correct answer?

|  |  |  |
| --- | --- | --- |
|  |  | A, C, and D |
|  |  | A and C |
|  |  | A and D |
|  |  | A |
| http://owl.cengage.com/owlimages/check.GIF |  | All of the Above |

What are the advantages of forming a quaternary structure?  
  
a. stability: a decrease in the surface to volume ratio and shielding of hydrophobic residues from the solvent.  
b. genomic economy: less DNA required to code for a monomer that forms a homodimer.  
c. catalytic site: the monomer may not constitute a complete enzyme active site. The active site may only form in the oligomer using side chains from two-or-more monomers.  
d. substrate channeling: oligomeric enzymes may carry out different but related reactions on different subunits with the product from one active site on one subunit passing directly to the next active site on an adjacent subunit.  
e. cooperativity: many enzymes are controlled by means of conformational changes involving movement of one subunit relative to the others in the oligomer.  
  
Choose the correct answer.

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

Negatively charged ligands (e.g. phosphates) frequently bind to proteins near the N-terminus of an α-helix. This is because:

|  |  |  |
| --- | --- | --- |
|  |  | positively charged residues are found at the N-terminus |
|  |  | the helix cap provides H-bond partners for phosphate |
| http://owl.cengage.com/owlimages/check.GIF |  | the dipole moment of the α-helix is positive at the N-terminus |
|  |  | negatively charged residues are never found at the N-terminus |