

1. Consider the following statement. “To produce one molecule of each possible kind of polypeptide chain, X amino acids in length, would require more atoms than exist in the universe.” Given the size of the universe, for what X do you suppose this statement could possibly be correct? Since counting atoms is a tricky business, consider the problem from the standpoint of mass. The number of atoms in the observable universe is estimated to be about 10^{80} , give or take an order of magnitude or so. Assuming that the average mass of an amino acid is 110 daltons, calculate approximately for which X the mass of one molecule of each possible kind of polypeptide chain X amino acids in length would be greater than the mass of the universe.

- a) The statement is true for X = 400, but false for X = 300;
- b) The statement is true for X = 300, but false for X = 200;
- c) The statement is true for X = 200, but false for X = 100;
- d) The statement is true for X = 100, but false for X = 50.

2. The so-called kelch motif consists of a four-stranded β sheet, which forms what is known as a β propeller. It is usually found to be repeated four to seven times, forming a kelch repeat domain in a multidomain protein. One such kelch repeat domain is shown in Figure 1 below. What would be the correct classification of this domain?

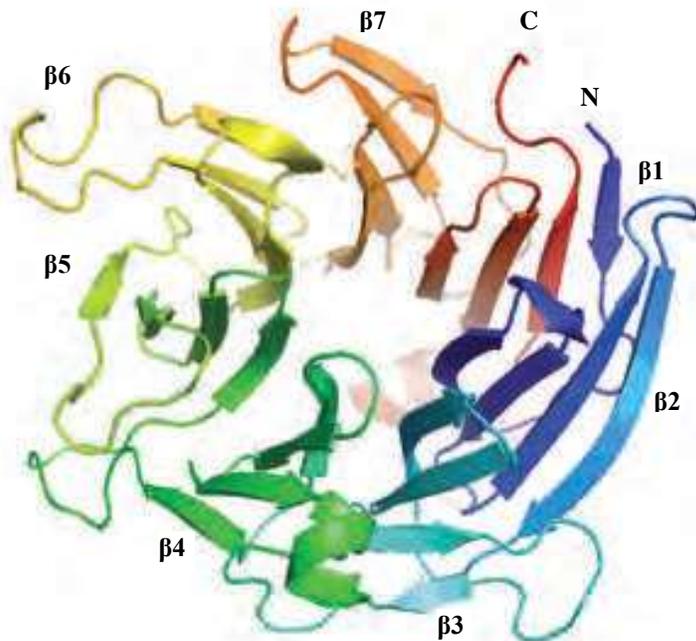


Fig. 1. The kelch repeat domain of galactose oxidase from D. dendroides. The seven individual β propellers are color coded and labeled. The N- and C-termini are indicated by N and C.

- a) A “in-line” type domain;
- b) A “plug-in” type domain;
- c) The protein includes both domain types;
- d) The protein includes neither domain type.

3. The arrangement of individual amino-acids in a protein polypeptide chain is:

- a) branched and formed of covalent bonds;
- b) unbranched and formed of covalent bonds;
- c) branched and formed of hydrogen bonds;
- d) unbranched and formed of hydrogen bonds.

4. The following interaction type **is not** a of weak noncovalent type bond commonly involved in protein folding:

- a) Electron paramagnetic resonance;
- b) Hydrogen bonds;
- c) Van der Waals attractions;
- d) Hydrophobic clustering force.

5. The backbone of a protein:

- a) Is outside the peptide bonds and has large hydrophobicity variations with the sequence;
- b) Is outside the peptide bonds and has a constant hydrophobicity;
- c) Includes the peptide bonds and has large hydrophobicity variations with the sequence;
- d) Includes the peptide bonds and has a constant hydrophobicity;

6. The optical activity of amino-acids:

- a) Is determined by the C carbonyl atoms and proteins consist exclusively of L-amino acids;
- b) Is determined by the C carbonyl atoms and proteins consist exclusively of D-amino acids;
- c) Is determined by the C α atoms and proteins consist exclusively of L-amino acids;
- d) Is determined by the C α atoms and proteins consist exclusively of D-amino acids.

7. The flexibility in the protein backbone is determined by the free dihedral rotations around:

- a) The C α -C bond and the C-N bond;
- b) The C-N bond and N-C α the bond;
- c) The N-C α bond and the C α -C bond;
- d) The C-N bond, the N-C α bond, the C α -C bond.

8. The nonpolar side chains in a protein:

- a) Belong to such amino acids as phenylalanine, leucine, valine, and tryptophan and tend to cluster in the interior of the molecule;
- b) Belong to such amino acids as arginine, glutamine, and histidine and tend to arrange themselves near the outside of the molecule;
- c) Belong to such amino acids as phenylalanine, leucine, valine, and tryptophan and tend to arrange themselves near the outside of the molecule;
- d) Belong to such amino acids as arginine, glutamine, and histidine and tend to arrange themselves near the outside of the molecule.

9. The final folded structure of a polypeptide chain:

- a) Is named conformation and is generally the one that maximizes its free energy.
- b) Is named conformation and is generally the one that minimizes its free energy;
- c) Is named folding pattern and is generally the one that maximizes its free energy;
- d) Is named folding pattern and is generally the one that minimizes its free energy;

- c) Is named stereoisomer and is generally the one that maximizes its free energy;
- d) Is named stereoisomer and is generally the one that minimizes its free energy.

10. The amino-acid tyrosine:

- a) Has an acidic side chain;
- b) Has a basic side chain;
- c) Has an uncharged polar side chain;
- d) Has a nonpolar side chain.

11. The fact that the amino acid sequence contains all of the information needed for specifying the three-dimensional shape of a protein is proven by the:

- a) Formation of protein aggregates;
- b) Chaperone-assisted folding of newly synthesized proteins;
- c) Protein denaturation process;
- d) Protein renaturation process.

12. The protein folding pattern that consists of a polypeptide chain that twists around on itself to form a rigid cylinder is named:

- a) α helix;
- b) Coiled-coil;
- c) Parallel β sheet;
- d) Antiparallel β sheet.

13. The threshold of amino acid sequence identity above which two proteins usually share the same overall structure is:

- a) 5%

- b) 25%
- c) 50%
- d) 75%

14. The complete structure of a protein formed as a complex of more than one polypeptide chain is designated as the:

- a) Primary structure;
- b) Secondary structure;
- c) Tertiary structure;
- d) Quarternary structure.

15. The protein domain **is not**:

- a) A substructure produced by any contiguous part of a polypeptide chain that can fold independently of the rest of the protein into a compact, stable structure;
- b) Usually encompassing between 40 and 350 amino-acids;
- c) The modular unit from which many larger proteins are constructed;
- d) Change rapidly during evolution, with the majority of human protein domains being vertebrate-specific.

16. A protein domain formed almost completely of antiparallel β sheets is:

- a) The immunoglobuline domain;
- b) The cytochrome b562 domain;
- c) The NAD-binding domain;
- d) The hemoglobin domain.

17. The human Major Histocompatibility Complex (MHC) antigen-recognition protein domain is:

- a) An evolutionary conserved domain that has known orthologs in yeast, plants, worms and flies;
- b) An evolutionary conserved domain that has known paralogs in yeast, plants, worms and flies;
- c) A newly evolved domain that does not have known orthologs in yeast, plants, worms and flies;
- d) A newly evolved domain that does not have known paralogs in yeast, plants, worms and flies.

18. The human chromosomes contain about:

- a) 11,000 protein-coding genes;
- b) 21,000 protein-coding genes;
- c) 51,000 protein-coding genes;
- d) 101,000 protein-coding genes.

19. Any region of a protein's surface that can interact with another molecule through sets of noncovalent bonds is called:

- a) Protein subunit;
- b) Protein loop;
- c) Binding site;
- d) Ligand.

20. The intrinsically disordered regions of proteins:

- a) Form specific binding sites for other protein molecules that are of low specificity;
- b) Can be identified using bioinformatic methods to search genes for encoded amino acid sequences that possess high hydrophobicity and low net charge;
- c) Do not contain repeated sequences of amino acids;
- d) Can also serve as a "tether" to hold two protein domains in close proximity to facilitate their interaction.

21. The disulfide bonds in proteins:

- a) Form as cells prepare newly synthesized proteins for export outside the cell;
- b) Only form between two amino acids in the same protein;
- c) Induce large changes to the proteins' conformation;
- d) Are converted back to $-SH$ by the high concentration of reducing agents in the extracellular matrix.