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Peptide Bonds & Levels of Protein Structure

Study Guide — Biochemistry

Pre-med/IB-style questions on peptide bond chemistry, polypeptide directionality, and how primary/secondary/tertiary/quaternary structure are formed, stabilized, disrupted, and tested experimentally.

50 items — Study Guide with Answers

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1 **Formation of a peptide bond between two amino acids is best described as a:**

A Hydrolysis reaction that consumes water

B **Condensation (dehydration) reaction that releases water** ✓

C Redox reaction that transfers electrons

D Phosphorylation reaction that adds a phosphate group

E Ionic bond formation between side chains

▶ **Explanation:** A peptide bond forms when the carboxyl group of one amino acid reacts with the amino group of another, releasing H2O (condensation). Hydrolysis is the reverse process, and phosphorylation/redox/ionic side-chain bonding are different reactions.

2 **A peptide bond forms specifically between which two functional groups?**

A Two amino groups (–NH2 and –NH2)

B Two carboxyl groups (–COOH and –COOH)

C Two R groups (side chains)

D **The carboxyl group of one amino acid and the amino group of another amino acid** ✓

E A phosphate group and a hydroxyl group

▶ **Explanation:** The peptide bond is the covalent C–N bond linking the carbonyl carbon of one amino acid's carboxyl group to the nitrogen of another's amino group. Side-chain bonds (like disulfides) are different.

3 **Which property of the peptide bond most strongly explains why protein backbones are relatively rigid in specific places?**

A The peptide bond is an ionic bond

B The peptide bond is nonpolar and repels water

C The peptide bond has partial double-bond character, restricting rotation around the C–N bond ✓

D The peptide bond is weaker than hydrogen bonds

E The peptide bond is always in the cis configuration in proteins

▶ **Explanation:** Resonance gives the peptide bond partial double-bond character, making the peptide group planar and limiting rotation around the C–N bond. It is covalent (not ionic), and most peptide bonds are trans (not cis).

4 A polypeptide chain is conventionally written from:

A N-terminus to C-terminus ✓

B C-terminus to N-terminus

C The most hydrophobic amino acid to the most hydrophilic amino acid

D The middle of the chain outward

E The chain has no directionality

▶ **Explanation:** Polypeptides have directionality: an N-terminus (free amino group) and a C-terminus (free carboxyl group). Sequences are written N $\rightarrow$ C by convention.

5 During translation, the polypeptide chain grows primarily by adding each new amino acid to the:

A N-terminus (amino end)

B C-terminus (carboxyl end) ✓

C Middle of the chain

D Side chain of the previous amino acid

E Phosphate group on mRNA

▶ **Explanation:** Ribosomes synthesize proteins from N → C. Each incoming amino acid is added to the carboxyl end, extending the chain at the C-terminus.

6 **Which statement about peptide bond hydrolysis is most accurate?**

A Peptide bonds break spontaneously at a high rate in water at neutral pH

B Peptide bond hydrolysis is the same as condensation and releases water

C **Peptide bond hydrolysis is favored by proteases in cells because it is slow without catalysis** ✓

D Peptide bonds can only be broken by breaking disulfide bonds first

E Hydrolysis of peptide bonds does not change primary structure

▶ **Explanation:** Hydrolysis uses water to break peptide bonds and is slow without enzymes under physiological conditions. Proteases catalyze this reaction. Breaking peptide bonds directly changes primary structure.

7 **How many peptide bonds are present in a peptide made of 9 amino acids?**

A 7

B **8** ✓

C 9

D 10

E 18

▶ **Explanation:** A chain of n amino acids has $n - 1$ peptide bonds because each bond links two amino acids. For 9 amino acids: $9 - 1 = 8$.

8 **Primary structure of a protein refers to:**

A The overall 3D shape of the protein

B The way multiple polypeptide chains assemble

C **The linear amino acid sequence (order of residues) in the polypeptide** ✓

D Hydrogen bonding between backbone groups in -helices and -sheets

E Only the covalent disulfide bonds between cysteines

▶ **Explanation:** Primary structure is the amino acid sequence. Secondary structure is local backbone folding (/) stabilized by backbone H-bonds; tertiary is overall 3D fold; quaternary is multi-subunit assembly.

9 **Which interaction is most directly responsible for stabilizing -helices and -sheets?**

A Covalent disulfide bonds between cysteines

B Hydrogen bonds between side chains (R groups) only

C Ionic bonds between charged side chains only

D **Hydrogen bonds between backbone C=O and N–H groups** ✓

E Van der Waals forces between peptide bonds only

▶ **Explanation:** Secondary structure is stabilized mainly by hydrogen bonding between backbone carbonyl oxygens and backbone amide hydrogens. Side chains influence which structures form, but they are not the main stabilizing H-bonds for / .

10 **Which statement correctly compares an -helix and a -sheet?**

A Both require disulfide bonds as their main stabilizing force

B **-helices are stabilized by H-bonds within one segment of a chain; -sheets are stabilized by H-bonds between neighboring strands** ✓

C -sheets are always made from different proteins, never from one protein chain

D -helices have side chains pointing inward to the helix axis

E -sheets cannot occur in globular proteins

▶ **Explanation:** -helices use intra-chain backbone H-bonds (local). -sheets use backbone H-bonds between adjacent strands, which can be from the same chain folded back or from different chains. Side chains generally project outward in both structures.

11 **Proline is often called a "helix breaker" because it:**

A **Has a rigid ring that disrupts helix geometry and lacks a backbone N–H for helix H-bonding** ✓

B Always forms disulfide bonds in helices

C Is strongly positively charged and repels other amino acids

D Is the only amino acid that is hydrophobic

E Forces all peptide bonds into the cis configuration

▶ **Explanation:** Proline's cyclic structure restricts backbone angles and it lacks a backbone hydrogen on the amide nitrogen, making it difficult to maintain the regular H-bond pattern of an -helix. It does not "always" force cis bonds.

12 **Glycine is frequently found in turns and flexible regions of proteins mainly because:**

A It forms disulfide bonds easily

B It has a bulky aromatic side chain that packs tightly

C **It has a very small side chain (H), allowing unusual backbone angles and flexibility** ✓

D It is always positively charged at pH 7.4

E It is the only amino acid that can form peptide bonds

▶ **Explanation:** Glycine's minimal side chain reduces steric hindrance, allowing flexible conformations and tight turns. It does not form disulfide bonds (cysteine does).

13 **A disulfide bond in a protein is best described as:**

A A hydrogen bond between two peptide backbones

B An ionic bond between Lys and Asp side chains

C A peptide bond between two cysteines

D **A covalent bond between the sulfur atoms of two cysteine side chains** ✓

E A bond that exists only in DNA, not proteins

▶ **Explanation:** Disulfide bonds are covalent S–S bonds formed by oxidation of two cysteine thiols. They are not peptide bonds and not hydrogen/ionic interactions.

14 **Which statement about denaturation is MOST accurate?**

A **Denaturation usually disrupts secondary/tertiary/quaternary structure but leaves most peptide bonds (primary structure) intact** ✓

B Denaturation always breaks peptide bonds into free amino acids

C Denaturation increases enzyme specificity by improving the active site

D Denaturation refers only to breaking disulfide bonds

E Denaturation cannot be caused by pH changes

▶ **Explanation:** Denaturation disrupts folding interactions (H-bonds, ionic interactions, hydrophobic packing). Primary structure generally remains unless conditions are harsh enough to hydrolyze peptide bonds. It usually reduces or abolishes function.

15 A protein is treated with SDS and a reducing agent (like -mercaptoethanol). What is the most direct effect of adding the reducing agent?

A It breaks peptide bonds into amino acids

B It removes phosphate groups from serine residues

C It stabilizes hydrogen bonds in -helices

D It causes the protein to fold into its native conformation

E **It breaks disulfide bonds, separating chains or domains linked by S–S bonds** ✓

▶ **Explanation:** Reducing agents convert disulfide bonds back to two thiols, breaking S–S links. SDS mainly disrupts noncovalent interactions and gives a uniform negative charge, but it does not reduce disulfides.

16 For a typical globular protein in water, the primary driving force that makes it fold into a compact shape is the:

A Formation of peptide bonds

B **Hydrophobic effect (burying nonpolar side chains away from water)** ✓

C Formation of glycosidic bonds

D Formation of phosphodiester bonds

E Repulsion between water molecules

▶ **Explanation:** Nonpolar side chains cluster away from water, driving folding (hydrophobic effect). Peptide bonds form the chain but do not explain folding into a specific 3D shape; glycosidic/phosphodiester bonds are not protein bonds.

17 **Tertiary structure refers to:**

A The linear amino acid sequence

B The local folding into -helices and -sheets only

C The complete 3D shape of a single polypeptide chain, including side-chain interactions ✓

D The assembly of multiple different proteins into one complex always

E The shape of DNA wrapped around histones

▶ **Explanation:** Tertiary structure is the overall 3D fold of one polypeptide, stabilized by interactions among side chains (hydrophobic, ionic, H-bonds, disulfides). Quaternary structure involves multiple polypeptide subunits.

18 **Quaternary structure is present only when:**

A A protein contains -helices

B A protein contains -sheets

C A protein consists of two or more polypeptide chains (subunits) that assemble into one functional complex ✓

D A protein contains disulfide bonds

E A protein is an enzyme

▶ **Explanation:** Quaternary structure refers specifically to the arrangement of multiple polypeptide subunits. A single-chain protein can have secondary and tertiary structure without quaternary structure.

19 **Hemoglobin is a classic example of a protein with:**

A Only primary structure

B Only secondary structure

C **Quaternary structure (multiple subunits)** ✓

D No tertiary structure

E No peptide bonds

▶ **Explanation:** Hemoglobin is made of multiple polypeptide subunits assembled together, which is quaternary structure. Like most proteins, each subunit also has primary, secondary, and tertiary structure.

20 **Three separate polypeptide chains wrap together to form a single stable triple-helix protein complex. The interaction between these chains is best classified as:**

A Primary structure

B Secondary structure

C Tertiary structure only

D **Quaternary structure** ✓

E A peptide bond network

▶ **Explanation:** When multiple polypeptide chains (subunits) associate to form a functional complex, that is quaternary structure. Primary and secondary structure describe features within a single chain; tertiary describes the full fold of one chain.

21 **A drop in pH (more acidic) is most likely to disrupt which stabilizing interaction in a folded protein?**

A Peptide bonds in the backbone immediately

B Ionic (salt-bridge) interactions between charged side chains ✓

C The order of amino acids in the sequence

D Covalent bond lengths within amino acids

E The existence of the N-terminus

▶ **Explanation:** Changing pH changes protonation states of side chains (e.g., Asp/Glu, Lys/Arg/His), weakening ionic interactions and often H-bond patterns. It typically does not instantly hydrolyze peptide bonds or change the amino acid sequence.

22 Molecular chaperones are best described as proteins that:

A Rewrite the amino acid sequence to ensure proper folding

B Catalyze peptide bond formation in the nucleus

C Are part of the DNA replication machinery

D Help other proteins fold correctly and prevent aggregation without permanently becoming part of the final structure ✓

E Break peptide bonds to activate enzymes

▶ **Explanation:** Chaperones assist folding by preventing misfolding/aggregation (often using ATP), but the final folded structure is mainly determined by the protein's primary sequence. They do not change the sequence or act as proteases by default.

23 Anfinsen's classic experiment (refolding of ribonuclease) is most commonly used to support which conclusion?

A Quaternary structure determines primary structure

B A protein's amino acid sequence contains the information needed for its native 3D structure ✓

C Chaperones always determine a protein's final fold

D Denaturation breaks peptide bonds irreversibly

E Secondary structure is independent of primary structure

▶ **Explanation:** Anfinsen showed that under the right conditions some proteins can refold to a functional native state after denaturation, supporting the idea that primary structure largely determines higher-level structure.

24 **Which statement about rotation in the protein backbone is most accurate?**

A The C–N peptide bond rotates freely like a single bond

B Rotation is mainly restricted around the N–C and C –C bonds, while C–N rotates freely

C **Rotation is restricted around the C–N peptide bond due to partial double-bond character** ✓

D No rotation is possible anywhere in the backbone

E Rotation occurs only in proteins with quaternary structure

▶ **Explanation:** The peptide bond C–N is planar and restricted by resonance. The N–C and C –C bonds have more rotational freedom and largely determine backbone conformation (though still limited by steric effects).

25 **Most peptide bonds in proteins adopt the trans configuration because:**

A **It minimizes steric clashes between side chains across the peptide bond** ✓

B Trans peptide bonds are always covalent and cis are not

C Trans peptide bonds allow free rotation of the C–N bond

D Cis peptide bonds cannot exist in biology

E Trans peptide bonds require ATP and cis do not

▶ **Explanation:** Trans is energetically favored because it reduces steric hindrance between adjacent side chains. Cis peptide bonds can occur (especially with proline) but are less common overall.

26 **Compared with parallel -sheets, antiparallel -sheets are often considered more stable because:**

A They contain disulfide bonds between all strands

B **Their hydrogen bonds can be more linear and optimal** ✓

C They do not require any hydrogen bonds

D They can exist only in fibrous proteins

E They are held together mainly by peptide bonds between strands

▶ **Explanation:** Antiparallel -sheets often form more linear (stronger) backbone hydrogen bonds than parallel sheets. Strands are not covalently linked by peptide bonds between them; peptide bonds form within each chain.

27 **In an -helix, the side chains (R groups) typically:**

A Point inward toward the helix axis and hydrogen bond with each other

B **Point outward from the helix backbone** ✓

C Are always charged

D Form peptide bonds with each other

E Are removed during protein folding

▶ **Explanation:** In -helices, side chains project outward from the backbone. The helix is stabilized mainly by backbone hydrogen bonds, not by peptide bonds between side chains.

28 **A single amino acid substitution (missense mutation) directly changes which level of protein structure first?**

A Quaternary structure

B Tertiary structure

C **Primary structure** ✓

D Secondary structure only

E It cannot change any level of structure

▶ **Explanation:** A missense mutation changes the amino acid sequence (primary structure). This may or may not alter secondary/tertiary/quaternary structure depending on the location and chemical properties of the substituted residue.

29 **Two proteins have exactly the same amino acid composition (same counts of each amino acid) but in a different order. Which statement is correct?**

A They must have identical primary structure

B They must have identical tertiary structure

C **They can have different primary structures and potentially different folding and function** ✓

D They cannot form peptide bonds

E They must have the same quaternary structure

▶ **Explanation:** Primary structure depends on sequence order, not just composition. Different sequences can fold differently and perform different functions even if they contain the same numbers of each amino acid.

30 **What provides the immediate energy that drives formation of each peptide bond during translation elongation at the ribosome?**

A Direct ATP hydrolysis at the peptide bond site

B **The high-energy bond linking an amino acid to its tRNA (aminoacyl-tRNA)** ✓

C The hydrogen bonds between mRNA codons and tRNA anticodons

D Breaking disulfide bonds in the growing peptide

E Oxidation of NADH in the cytosol

▶ **Explanation:** Peptide bond formation is powered by the energy stored in the aminoacyl-tRNA ester bond (created earlier using ATP during tRNA charging). ATP is used before elongation to activate amino acids, not directly at the peptide bond step.

31 **The ribosome's peptidyl transferase activity is mainly carried out by:**

A A DNA enzyme in the nucleus

B A membrane-bound ATPase

C A cytosolic protease

D A protein enzyme in the ribosome's large subunit

E **rRNA in the large ribosomal subunit (a ribozyme)** ✓

▶ **Explanation:** Peptide bond formation is catalyzed mainly by rRNA (not a ribosomal protein), making the ribosome a ribozyme. DNA enzymes and proteases do not catalyze peptide bond formation.

32 **A "protein domain" is best described as:**

A **A region of a polypeptide that can fold independently and often has a specific function** ✓

B A single peptide bond between two amino acids

C Only the quaternary structure of a multi-subunit protein

D A short DNA sequence coding for one amino acid

E A carbohydrate chain attached to a protein

▶ **Explanation:** Domains are independently folding parts of a protein that often correspond to functional modules. They are not single bonds, DNA sequences, or carbohydrate chains.

33 A serine residue in a protein becomes phosphorylated, but the amino acid sequence itself is unchanged. Which statement is MOST accurate?

A Primary structure must change because any covalent change counts as a new sequence

B Secondary structure must change in every case

C Tertiary structure cannot change because only the sequence matters

D The amino acid sequence (primary structure in the sequence sense) is unchanged, but charge/interaction patterns can change, altering folding or interactions ✓

E Phosphorylation breaks peptide bonds

▶ **Explanation:** Phosphorylation does not change the order of amino acids, but it adds a negatively charged group that can change ionic interactions, binding, and sometimes conformation. It does not necessarily force secondary structure changes in every case.

34 Which type of bond links amino acids together in a polypeptide chain?

A Phosphodiester bond

B Glycosidic bond

C Peptide bond ✓

D Hydrogen bond

E Ionic bond

▶ **Explanation:** A polypeptide is formed by covalent peptide bonds. Phosphodiester bonds are for nucleic acids, and glycosidic bonds are for carbohydrates. Hydrogen/ionic bonds may stabilize folding but do not link residues into a chain.

35 **In a typical soluble globular protein, which distribution of amino acids is most expected?**

A Hydrophobic residues mostly on the surface, hydrophilic residues mostly buried

B Only charged residues are found in the protein core

C **Hydrophobic residues mostly buried in the interior, hydrophilic residues more exposed to water** ✓

D All residues are equally likely to be on the surface

E Only glycine can be buried inside proteins

▶ **Explanation:** Water disfavors exposure of nonpolar side chains, so hydrophobic residues tend to be buried, while polar/charged residues are more often exposed. This pattern is a major consequence of the hydrophobic effect.

36 **Disulfide bonds are most likely to form and persist in which cellular environment?**

A The cytosol (highly reducing)

B **The lumen of the endoplasmic reticulum or extracellular environment (more oxidizing)** ✓

C The mitochondrial matrix only

D Inside ribosomes during peptide bond formation only

E Only in bacterial cytosol because bacteria lack membranes

▶ **Explanation:** Disulfide bonds require an oxidizing environment. In eukaryotes, this is typical of the ER lumen and extracellular space, while the cytosol is generally reducing and disfavors disulfide formation.

37 **Which statement best distinguishes denaturation from digestion of a protein?**

A **Denaturation usually disrupts folding without breaking most peptide bonds; digestion breaks peptide bonds into smaller peptides/amino acids** ✓

B Denaturation breaks peptide bonds; digestion changes only tertiary structure

C Both processes leave the protein's 3D shape unchanged

D Denaturation occurs only in the stomach; digestion occurs only in the cytosol

E Digestion forms new peptide bonds to stabilize proteins

▶ **Explanation:** Denaturation disrupts noncovalent interactions and often function, while peptide bonds remain mostly intact. Digestion (proteolysis) hydrolyzes peptide bonds, changing primary structure and producing smaller fragments.

38 **An enzyme loses activity after heating, and activity does NOT return after cooling. Which explanation is most likely?**

A Heating changed the amino acid sequence irreversibly in every case

B Heating increased peptide bond formation, locking the active site open

C Cooling cannot restore activity because proteins never refold

D **Heating caused denaturation and misfolding/aggregation, preventing correct refolding** ✓

E Heating only breaks disulfide bonds, which are impossible to reform

▶ **Explanation:** Heat can unfold proteins and expose hydrophobic regions that stick together, causing aggregation. Aggregated proteins often cannot refold properly on cooling. Primary structure is not necessarily changed by moderate heating.

39 **Which statement about quaternary structure is correct?**

A All proteins must have quaternary structure

B Quaternary structure refers to -helices only

C Many proteins have no quaternary structure because they are single polypeptide chains ✓

D Quaternary structure is the same thing as primary structure

E Quaternary structure is created by peptide bonds between different polypeptides

▶ **Explanation:** Only proteins composed of multiple polypeptide subunits have quaternary structure. Subunits usually associate via noncovalent interactions (and sometimes disulfides), not peptide bonds between chains.

40 **A single amino acid change in hemoglobin leads to abnormal clumping of hemoglobin molecules under low oxygen conditions. Which level(s) of structure are directly involved in this change?**

A Only secondary structure

B Primary structure change that alters interactions between subunits (affecting quaternary associations) ✓

C Only quaternary structure with no primary change

D Only peptide bond rearrangement creating a new sequence

E It must be caused by changes in DNA base pairing, not proteins

▶ **Explanation:** A substitution changes primary structure. In hemoglobin, such a change can create new surface properties that promote abnormal interactions between hemoglobin molecules/subunits, affecting quaternary-level behavior (aggregation/polymerization).

41 **Which interaction is LEAST likely to be a major stabilizer of tertiary structure in a typical protein?**

A Hydrophobic packing of nonpolar side chains

B Hydrogen bonds between side chains and/or backbone

C Ionic interactions (salt bridges) between charged side chains

D Disulfide bonds (in some proteins)

E **Phosphodiester bonds linking amino acids** ✓

▶ **Explanation:** Tertiary structure is stabilized by hydrophobic interactions, H-bonds, ionic interactions, and sometimes disulfide bonds. Phosphodiester bonds are characteristic of nucleic acids, not proteins.

42 **Which statement about secondary structure is MOST accurate?**

A Secondary structure depends only on disulfide bonds between cysteines

B Secondary structure is primarily determined by interactions between side chains only

C **Secondary structure refers to local folding patterns like -helices and -sheets** ✓

D Secondary structure requires multiple polypeptide chains

E Secondary structure is the same as the amino acid sequence

▶ **Explanation:** Secondary structure describes local backbone folding patterns such as -helices and -sheets, mainly stabilized by backbone hydrogen bonds. It can occur within a single polypeptide chain.

43 **Which secondary structure generally produces a more extended (stretched) backbone conformation?**

A -helix

B **-sheet** ✓

C DNA double helix

D Coiled-coil always more extended than -sheet

E There is no difference; both are equally extended

▶ **Explanation:** -strands in -sheets are relatively extended compared with -helices, which are compact coils. DNA helix is not a protein secondary structure.

44 **Urea is a classic protein denaturant. Its main effect is to:**

A Create new peptide bonds between proteins

B **Disrupt noncovalent interactions, including hydrogen bonding and hydrophobic interactions, favoring unfolding** ✓

C Specifically cut peptide bonds after lysine residues

D Force all proteins to form disulfide bonds

E Convert amino acids into nucleotides

▶ **Explanation:** Urea disrupts the stabilizing noncovalent interactions that maintain protein folding, promoting denaturation. It does not enzymatically cut peptide bonds or create disulfides.

45 **At a protein's isoelectric point (pI), the protein typically has:**

A A net positive charge

B A net negative charge

C **A net charge of approximately zero** ✓

D No amino acids with charged side chains

E No peptide bonds

▶ **Explanation:** The isoelectric point is the pH at which the protein's positive and negative charges balance (net ~0). Charged residues can still be present; they just balance overall.

46 **Which statement about the peptide bond is correct?**

A It is nonpolar and cannot participate in hydrogen bonding

B **It is polar and can participate in hydrogen bonding, helping form secondary structure** ✓

C It is an ionizable bond that becomes positive or negative depending on pH

D It is a disulfide bond between cysteines

E It links side chains together, not the backbone

▶ **Explanation:** The peptide bond is polar (C=O and N–H) and participates in hydrogen bonding that stabilizes -helices and -sheets. It is not typically ionizable like side-chain groups, and it is not a disulfide bond.

47 **At physiological pH, which description best matches the typical charges at the ends of a polypeptide?**

A Both N-terminus and C-terminus are neutral

B **N-terminus is usually positively charged ($NH3^+$), and C-terminus is usually negatively charged ($COO-$)** ✓

C N-terminus is negative and C-terminus is positive

D Both ends are always positively charged

E Both ends are always negatively charged

▶ **Explanation:** The N-terminus commonly carries a protonated amino group ($NH3^+$) and the C-terminus commonly carries a deprotonated carboxyl group ($COO-$) near physiological pH. Exact charge can vary with pH and modifications.

48 **A protease cuts a protein into smaller fragments by cleaving peptide bonds. Which level of structure is definitively altered by this action?**

A Only secondary structure

B Only tertiary structure

C Only quaternary structure

D Only the isoelectric point

E **Primary structure** ✓

▶ **Explanation:** Cleaving peptide bonds changes the covalent backbone and therefore the primary structure. Secondary/tertiary/quaternary structure may also change, but primary structure is guaranteed to be altered when peptide bonds are cut.

49 **Which statement is MOST accurate about "secondary structure" versus "tertiary structure"?**

A Secondary structure is the overall 3D shape of a protein; tertiary structure is the amino acid sequence

B **Secondary structure is local backbone folding (/); tertiary structure is the overall 3D fold of one chain including side-chain packing** ✓

C Secondary structure requires multiple subunits; tertiary structure does not

D Tertiary structure is stabilized only by peptide bonds

E Secondary structure is stabilized only by disulfide bonds

▶ **Explanation:** Secondary structure is local backbone folding stabilized mainly by backbone H-bonds. Tertiary structure is the full 3D fold of a single polypeptide, stabilized by many side-chain interactions and sometimes disulfides.

50 **A protein forms a -barrel made from antiparallel -sheets that fold into a closed cylinder within a single polypeptide chain. This -barrel is best classified as part of the protein's:**

A Primary structure

B Secondary structure only

C Quaternary structure

D **Tertiary structure** ✓

E Genetic code

▶ **Explanation:** While -strands are secondary structure elements, a -barrel describes a larger 3D arrangement of these elements within one polypeptide chain—this is a feature of tertiary structure. Quaternary structure requires multiple chains.