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Peptide Bonds & Levels of Protein Structure

Exam — 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 — Printable Exam

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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

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

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

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

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

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

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

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

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

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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

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

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

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

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

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

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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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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)

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

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

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

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

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

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

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

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

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

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D Only peptide bond rearrangement creating a new sequence

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

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

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

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

A -helix

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- B -sheet
- C DNA double helix
- D Coiled-coil always more extended than -sheet
- E There is no difference; both are equally extended

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

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

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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

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

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

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

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

Answer Key

#	Ans	Answer Text
1	B	Condensation (dehydration) reaction that releases water
2	D	The carboxyl group of one amino acid and the amino group of another amin…
3	C	The peptide bond has partial double-bond character, restricting rotation…
4	A	N-terminus to C-terminus
5	B	C-terminus (carboxyl end)
6	C	Peptide bond hydrolysis is favored by proteases in cells because it is s…
7	B	8
8	C	The linear amino acid sequence (order of residues) in the polypeptide
9	D	Hydrogen bonds between backbone C=O and N–H groups
10	B	-helices are stabilized by H-bonds within one segment of a chain; -she…
11	A	Has a rigid ring that disrupts helix geometry and lacks a backbone N–H f…
12	C	It has a very small side chain (H), allowing unusual backbone angles and…
13	D	A covalent bond between the sulfur atoms of two cysteine side chains
14	A	Denaturation usually disrupts secondary/tertiary/quaternary structure bu…
15	E	It breaks disulfide bonds, separating chains or domains linked by S–S bo…
16	B	Hydrophobic effect (burying nonpolar side chains away from water)
17	C	The complete 3D shape of a single polypeptide chain, including side-chai…
18	C	A protein consists of two or more polypeptide chains (subunits) that ass…
19	C	Quaternary structure (multiple subunits)
20	D	Quaternary structure
21	B	Ionic (salt-bridge) interactions between charged side chains
22	D	Help other proteins fold correctly and prevent aggregation without perma…
23	B	A protein's amino acid sequence contains the information needed for its …
24	C	Rotation is restricted around the C–N peptide bond due to partial double…
25	A	It minimizes steric clashes between side chains across the peptide bond
26	B	Their hydrogen bonds can be more linear and optimal
27	B	Point outward from the helix backbone
28	C	Primary structure
29	C	They can have different primary structures and potentially different fol…
30	B	The high-energy bond linking an amino acid to its tRNA (aminoacyl-tRNA)
31	E	rRNA in the large ribosomal subunit (a ribozyme)
32	A	A region of a polypeptide that can fold independently and often has a sp…
33	D	The amino acid sequence (primary structure in the sequence sense) is unc…
34	C	Peptide bond
35	C	Hydrophobic residues mostly buried in the interior, hydrophilic residues…
36	B	The lumen of the endoplasmic reticulum or extracellular environment (mor…
37	A	Denaturation usually disrupts folding without breaking most peptide bond…
38		Heating caused denaturation and misfolding/aggregation, preventing corre…

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