**Answer : 01**

The structures of the dipeptides glutamine-aspartic acid and isoleucine-threonine with NH2 and COOH at the amine and carboxylic acid ends, as well as their three-letter and one-letter abbreviations for the amino acid residues, are as follows:

1. **Glutamine-aspartic acid:**
   * Structure: Glutamine (Gln)-Aspartic acid (Asp)  
     Glutamine-aspartic acid
   * Three-letter abbreviations: NH₂-Gln-Asp-COOH
   * One-letter abbreviations: NH₂-Q-D-COOH
2. **Isoleucine-threonine:**
   * Structure: Isoleucine (Ile)-Threonine (Thr)  
     Isoleucine-threonine
   * Three-letter abbreviations: NH₂-Ile-Thr-COOH
   * One-letter abbreviations: NH₂-I-T-COOH

In both structures, NH2 represents the amino group (N-terminus), COOH represents the carboxylic acid group (C-terminus), and the amino acid residues are connected through a peptide bond.

**Answer : 02**

**Part (A): The chemical structure of the short peptide CYS-ALA-LYS-SER at pH 9.0 is as follows:**

**Part (B): Full Names of Amino Acids:**

* CYS: Cysteine
* ALA: Alanine
* LYS: Lysine
* SER: Serine

**Part (C): Moles of Water Liberated:**

* For each peptide bond formed, one mole of water is liberated. Since there are three peptide bonds formed in the tetrapeptide (CYS-ALA-LYS-SER), three moles of water would be liberated when 1 mole of each amino acid reacts to form the peptide.

**Part (D): Net Charge at pH 9.0:**

At pH 9.0, the NH3+ groups on lysine (LYS) and the N-terminus are protonated, and the COO- groups on cysteine (CYS) and serine (SER) are deprotonated. The net charge is calculated as the sum of the charges on individual amino acids.

Charge of CYS: 0 (S-) - 0 (NH3+) = -1

Charge of ALA: 0

Charge of LYS: +1 (NH3+) - 0 = +1

Charge of SER: 0 (COO-) - 0 = 0

Net charge = (-1) + 0 + 1 + 0 = 0

Therefore, the net charge on the peptide at pH 9.0 is 0.

**Part (E): pH for -2 Charge (Isoelectric Point):**

The isoelectric point (pI) is the pH where the peptide has a net charge of 0. Using the provided pKa table and calculating the net charge at different pH values, we can estimate the pH to be around 10.2.

* Cysteine's thiol group contributes a negative charge only for pH values above its pKa (8.3).
* Lysine's side chain ammonium group contributes a positive charge only for pH values below its pKa (8.95).
* Serine's hydroxyl group has a negligible effect on the charge within the relevant pH range.

By balancing the +1 charge from lysine with two -1 charges from cysteine's thiol groups, we reach around pH 10.2.

**Answer : 03**

**Part (A): Net Charge at Different pH Values:**

* pH 2:
  + At pH 2, all amino acids are likely to be in their protonated forms.
  + Net charge: (+1) + 0 (+1) + 0 = +2
* pH 3:
  + CYS (Cysteine) and LYS (Lysine) side chains may be partially deprotonated at pH 3.
  + Net charge: (-1) + 0 (+1) + 0 = 0
* pH 7:
  + At physiological pH, the carboxyl groups are deprotonated, and the amino groups are protonated.
  + Net charge: (-1) + 0 (+1) + 0 = 0
* pH 10:
  + At pH 10, CYS and SER (Serine) side chains are likely to be deprotonated.
  + Net charge: (-1) + 0 0 (-1) = -2
* pH 11:
  + At pH 11, most amino acids are likely to be deprotonated.
  + Net charge: 0 + 0 0 (-1) = -1

**Part (B): Estimate Isoelectric Point (pI):**

* The isoelectric point (pI) is the pH at which a molecule carries no net electrical charge.
* The pI can be estimated as the average of the two pKa values surrounding the pH at which the net charge is closest to zero.

**From the analysis:**

* pH 7 has a net charge of 0.
* The nearest pKa values are for CYS (pKa ~ 2) and SER (pKa ~ 9).

An estimate for the pI would be the average of these pKa values:

pI ≈ (2 + 9) / 2 = 5.5

**So, the estimated pI for the peptide is around 5.5.**

**Top of Form**

**Answer : 04**

**Part (A): Four Levels of Protein Structure:**

**1. Primary Structure:** This is the linear sequence of amino acids in a protein chain. Changing the order of amino acids, even just one, can significantly alter the folding and therefore the function of the protein. Imagine building a puzzle; swapping tiles will likely change the resulting picture.

**2. Secondary Structure:** This refers to the local spatial arrangements of the polypeptide chain, mainly held by hydrogen bonds. These arrangements, like alpha helices and beta sheets, contribute to overall protein shape. Modifications in secondary structure can impact folding and potentially function, depending on the location and extent of the change.

**3. Tertiary Structure:** This is the overall 3D conformation of the protein, arising from interactions between side chains of amino acids. It's crucial for function, as specific shapes create pockets, grooves, and binding sites for other molecules. Minor changes in tertiary structure could disrupt these interactions and alter function, while major changes may completely abolish it.

**4. Quaternary Structure:** This involves the arrangement of multiple polypeptide chains in a multi-subunit protein. Changes in how these subunits interact can affect both structure and function. For example, dissociation of subunits might deactivate the protein.

**Part (B): Serine to Threonine Replacement:**

* Both serine (Ser) and threonine (Thr) are polar, uncharged amino acids. They have similar structures, with threonine having an additional methyl group. The replacement is a conservative substitution.
* The change is not likely to significantly alter the protein's function because both amino acids have similar chemical properties. It might affect local interactions, but overall, the protein's structure and function may remain relatively unchanged.

**Part (C): Serine to Leucine Replacement:**

* Leucine is a nonpolar, hydrophobic amino acid, while serine is polar and hydrophilic. This substitution is non-conservative.
* The change could disrupt hydrogen bonding or other interactions, potentially affecting the protein's structure and function. It might lead to misfolding or altered binding properties.

**Part (D): Serine to Cysteine Replacement:**

* Both serine and cysteine are polar amino acids, but cysteine has a thiol group (SH) that can form disulfide bonds. This substitution introduces a thiol group.
* The change could lead to the formation of disulfide bonds, affecting the protein's tertiary and quaternary structures. This modification might impact stability, interactions, or the protein's redox properties.

**Part (E): Aspartic Acid to Tryptophan in the Active Site:**

* Aspartic acid (Asp) is acidic and polar, while tryptophan (Trp) is neutral, aromatic, and hydrophobic. This substitution is non-conservative.
* The replacement in the active site may disrupt the local environment necessary for catalysis. It could affect substrate binding, the orientation of residues, or the charge distribution, likely altering enzymatic activity.

**Part (F): Aspartic Acid to Tryptophan in a Non-Active Site:**

* In a non-active site, the impact is likely less severe because the local environment and interactions might not be critical for catalysis.
* The substitution might still cause changes in the local structure, but since it's not in the active site, the overall protein function may be less affected.

In summary, the qualitative assessment depends on the specific amino acids involved, their chemical properties, and the context of their location in the protein (active site or non-active site). Conservative substitutions are less likely to significantly alter protein function compared to non-conservative substitutions.

**Answer : 05**

**Part (A):** The sequence of both polypeptide chains in insulin as the one-letter abbreviations for each amino acid are as follows:

* Chain A: GIVEQCCTSICSLYQLENYCN
* Chain B: FVNQHLCGSHLVEALYLVCGERGFFYTPKT

**Part (B):** Insulin has several ionizable functional groups in aqueous solution. The amino acid residues that have these ionizable groups are as follows:

* Aspartic acid (Asp, D): carboxyl group (-COOH)
* Glutamic acid (Glu, E): carboxyl group (-COOH)
* Histidine (His, H): imidazole group (-C3H3N2)
* Lysine (Lys, K): amino group (-NH3+)
* Tyrosine (Tyr, Y): phenol group (-C6H4OH)
* Cysteine (Cys, C): thiol group (-SH)

The pKa and pKb values (including the R groups) that are on both polypeptide chains that make up insulin are as follows:

* Aspartic acid (Asp, D): pKa = 3.9
* Glutamic acid (Glu, E): pKa = 4.3
* Histidine (His, H): pKa = 6.0 (imidazole ring), pKa = 7.6 (amino group)
* Lysine (Lys, K): pKa = 10.8
* Tyrosine (Tyr, Y): pKa = 10.1
* Cysteine (Cys, C): pKa = 8.3 (thiol group), pKR = 10.8 (ionization of thiol group)

**Part (C):** The isoelectric point (pI) of insulin is reported to be around 5.3-5.35. Using the method covered in class, we can estimate the pI of insulin by averaging the pKa values of the ionizable groups. The pI of insulin can be calculated as follows:  
pI = (pKa1 + pKa2) / 2  
where pKa1 and pKa2 are the pKa values of the ionizable groups that are closest in pH to the measured pI. For insulin, the closest pKa values are those of the carboxyl group of aspartic acid (pKa = 3.9) and the amino group of lysine (pKa = 10.8). Therefore, the estimated pI of insulin is:  
pI = (3.9 + 10.8) / 2 = 7.35

The estimated pI of insulin is higher than the reported range of 5.3-5.35. This could be due to differences in the method used to measure the pI or the specific insulin analog being studied.

**Part (D):** For a polypeptide to be soluble in an aqueous solution, it is generally not good to be near the isoelectric point. This is because at the isoelectric point, the net charge of the polypeptide is zero, and the polypeptide tends to aggregate and precipitate out of solution. Therefore, it is generally better for a polypeptide to be either positively or negatively charged in an aqueous solution, rather than having no net charge.

**Answer : 06**

**Major Differences between Nuclear and Plasmid DNA:**

**Organism:**

* Nuclear DNA: Present in all organisms, from bacteria to plants and animals.
* Plasmid DNA: Primarily found in bacteria and archaea, although some eukaryotes also harbor them.

**Location:**

* Nuclear DNA: Contained within the nucleus of eukaryotic cells and the single circular chromosome of prokaryotes.
* Plasmid DNA: Independent, extrachromosomal elements existing free in the cytoplasm.

**Function:**

* Nuclear DNA: Encodes essential genes for the organism's structure, growth, development, and reproduction. Crucial for cell survival and organismic function.
* Plasmid DNA: Often carries non-essential genes that provide auxiliary functions like antibiotic resistance, toxin production, or metabolic pathways. Some plasmids are conjugative, enabling transfer between cells.

**Transcription and Translation:**

**1. Transcription:**

* **Process:** Transcription is the synthesis of RNA from a DNA template. It takes place in the nucleus for eukaryotes and in the cytoplasm for prokaryotes.
* **Initiation:** RNA polymerase binds to the promoter region of the DNA, initiating the process.
* **Elongation:** RNA polymerase synthesizes a complementary RNA strand by adding nucleotides based on the DNA template.
* **Termination:** Transcription concludes when RNA polymerase reaches a terminator sequence, and the newly formed RNA molecule is released.

**2. Translation:**

* **Process:** Translation is the synthesis of a protein using the information encoded in mRNA. It occurs in the cytoplasm for both prokaryotes and eukaryotes.
* **Initiation:** The small ribosomal subunit binds to the mRNA, and the initiator tRNA binds to the start codon.
* **Elongation:** The ribosome moves along the mRNA, and tRNA molecules bring amino acids to the ribosome, forming a polypeptide chain.
* **Termination:** Translation stops when a stop codon is reached. The ribosome releases the completed polypeptide, and the components dissociate.

In summary, nuclear DNA is essential genetic material found in the nucleus of eukaryotic cells, while plasmid DNA is typically non-essential and found in the cytoplasm of prokaryotic cells. Transcription involves the synthesis of RNA from DNA, and translation is the process of protein synthesis using the information encoded in mRNA.

**Answer : 07**

**Part (A):** The three-letter abbreviations for the first five amino acids in the globular protein myoglobin are:

* V: Valine
* N: Asparagine
* F: Phenylalanine
* K: Lysine
* L: Leucine

**Part (B):** One possible corresponding RNA sequence that would code for synthesizing the first five amino acids in the ribosomes is:

* AUG (initiation codon for methionine, which is usually removed before the polypeptide chain is completed)
* GUG (valine)
* GAU (asparagine)
* UUG (phenylalanine)
* AUG (lysine)
* UUG (leucine)

Note that the actual RNA sequence would depend on the specific genetic code used by the organism synthesizing the myoglobin protein.

**Answer : 08**  
**Part (A): Polypeptide Chemical Structure at pH 10:**

Here's the chemical structure of the new polypeptide, MAGVRSPIDFWK, in aqueous solution at pH 10:

H₃N⁺-CH₂-C=O-Gly-A-Gly-Val-Arg-Ser-Pro-Ile-Asp-Phe-Trp-Lys-COOH

| | | | | | | | | | | |

OH OH OH OH NH₂⁺ OH OH OH OH OH OH OH NH₂⁺

* Aminoacids: M=Methionine, A=Alanine, G=Glycine, V=Valine, R=Arginine, S=Serine, P=Proline, I=Isoleucine, D=Aspartic acid, F=Phenylalanine, W=Tryptophan, K=Lysine.
* Protonation states at pH 10:
  + N-terminal group: positively charged (NH₃⁺) due to pKa values of most N-terminal groups being around 8-9.
  + Arginine (R): side chain guanidinium group is positively charged (NH₂⁺) due to its high pKa (12.5).
  + Aspartic acid (D): side chain carboxyl group is deprotonated (COO⁻) due to its low pKa (3.86).
  + Other amino acids: all other side chains are neutral at pH 10, as their pKa values lie between 4 and 10.

**Part (B): Microcapsule Formation Procedure:**

1. **Preparation of Polypeptide Solution:** Dissolve the polypeptide in an aqueous solution at a specific pH, considering the pI of the polypeptide. The pH should be chosen such that the polypeptide has a net charge, which can interact with the alginate.
2. **Preparation of Alginate Solution:** Prepare an alginate solution in water at a pH above 3.2 to ensure that alginate has a net negative charge due to the ionization of its carboxylic groups.
3. **Mixing of Solutions:** Slowly add the polypeptide solution to the alginate solution while stirring gently. The oppositely charged polypeptide and alginate molecules will interact through electrostatic forces, leading to the formation of coacervates (microcapsules) entrapping the essential oil.
4. **Collection of Microcapsules:** Once the coacervation is complete, the microcapsules can be collected by centrifugation or filtration.
5. **Crosslinking (Optional):** If needed, the microcapsules can be further stabilized by crosslinking the coacervate droplets using divalent cations such as calcium ions.

The pH of the solutions is crucial as it affects the net charge of the polypeptide and alginate, influencing their interaction during coacervation. The pI of the polypeptide should be considered to ensure that it has a net charge opposite to that of alginate, promoting coacervate formation. Additionally, the pH of the system can influence the stability and properties of the microcapsules.

**END**