1. Write the primary structure of the peptide RDHQWMI, indicating the predominant ionization forms that would be found for the sidechains at pH 5.

2. For the peptide GKDLG, what will its approximate NET charge (rounded off to the nearest whole integer) be at:
   (a) pH 7 0
   (b) pH 1 +2
   (c) pH 13 -3

3. Draw the maximally hydrogen-bonded interactions between the SIDE CHAINS of the following pairs of amino acids:

   (a) Gln and Asn

   (b) Arg and Asp
4. Shown below are ribbon diagrams of different protein structures. For each of them, find one end of the polypeptide chain, and trace it through to the other end. Then:

(a) Classify the type of domain structure of each domain. (β-barrel, helical bundle, α-β, etc.)

(b) For proteins containing β structure, indicate whether the β-strands are parallel or antiparallel.

(c) For the parallel β-strands, identify the crossovers, and indicate the types of crossovers (α-helices or loops).

(d) Identify the proteins that contain packed α-helices. Which Chothia angles are made between the different pairs of adjacent α-helices?

(e) Which proteins have multiple domains, and how many domains do you find?
parallel β-barrel
α-helical crossovers

α-helical bundle
+19°

anti-parallel β-barrel/sheet
multiple domains

5 domains:
1. anti-parallel β-barrel
2. 3α/β open-face
   (anti-parallel sheet)
3. parallel β-sheet
4. α-β-α sandwich
6. Propose a specific mechanism for recognition of an A-T base pair in the major groove of DNA by H-bonding with the side chain of Asn in a regulatory protein, with a structural drawing.

![Structural drawing](image)

7. Compare the geometry of A-form RNA, B-form DNA helices and protein α-helices and β-sheets, with respect to the following parameters:

<table>
<thead>
<tr>
<th>Parameter</th>
<th>A-form RNA</th>
<th>B-form DNA</th>
<th>α-helices</th>
<th>β-sheets</th>
</tr>
</thead>
<tbody>
<tr>
<td>(a) spacing of monomers along the helical axis</td>
<td>~2.4 Å</td>
<td>~3.4 Å</td>
<td>1.5 Å</td>
<td>3-3.5 Å</td>
</tr>
<tr>
<td>(b) pitch (helical repeat)</td>
<td>~2.8 Å</td>
<td>~3.4 Å</td>
<td>5.4 Å</td>
<td>6-7 Å</td>
</tr>
<tr>
<td>(c) diameter</td>
<td>~2.2 Å</td>
<td>~2.0 Å</td>
<td>5 Å</td>
<td>4.7 Å</td>
</tr>
<tr>
<td>(d) monomers per helical repeat</td>
<td>~12 x 2</td>
<td>10 x 2</td>
<td>3.6</td>
<td>2</td>
</tr>
<tr>
<td>(e) twist angle per monomeric repeat</td>
<td>~30°</td>
<td>~36°</td>
<td>100°</td>
<td>180°</td>
</tr>
</tbody>
</table>