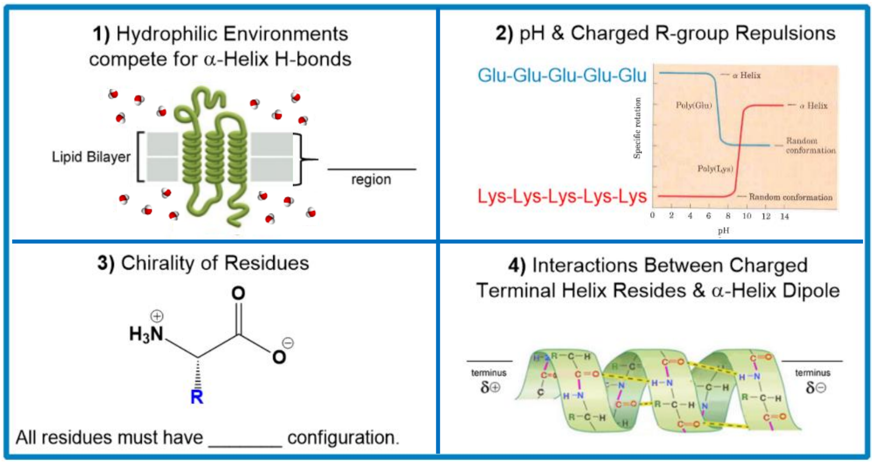
CONCEPT: ALPHA HELIX DISRUPTION

●Several factors can ________ or prevent formation of the α-helix structure.

1. α-helices typically found ____________ the *hydrophobic* area within a membrane.
2. α-helices are __________ to destabilizing interactions between neighboring residues (ex. bulky/charged groups).
3. All α-helix residues must have the same ________________.

EXAMPLE: Disrupting α-helix structure.



PRACTICE: Why does poly-L-Glutamate adopt an α-helical structure at low pH but a random conformation above pH 5?

a) Positively charged residues destabilize α-helices.

b) At high pH, the (-) Glu repulsion destabilizes α-helices.

c) Negatively charged residues destabilize α-helices.

d) < pH 5, the (+) Glu repulsion destabilizes α-helices.

5) <u>Gly & Pro Disrupt α-Helices</u>

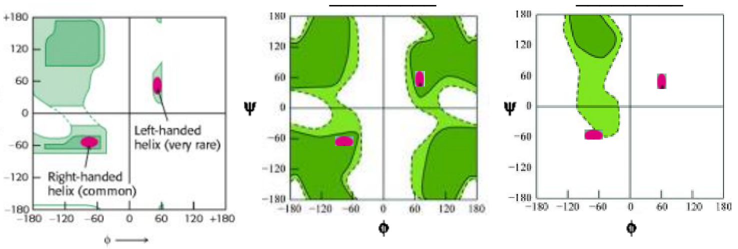
●α-helix formation requires specific φ and ψ bond ________ to stabilize the required hydrogen bonds.

- □ Recall: α-helix bond angles appear in the __________ left quadrant of a Ramachandran plot.

●Both ________ & _________ amino acids *destabilize* α-helices.

- □ Glycine's R-group (H) is too ______ and steric hindrance cannot limit its bond angles enough to conform.
- □ Pro residues lack a ___-atom for hydrogen bonding & create a ______ in the α-helix.

EXAMPLE: Gly & Pro disrupt α-helices.



PRACTICE: Which of the following peptides is more likely to take up an α-helical structure and why?

a) LKAENDEAARAMSEA.

b) CRAGGFPWDQPGTSN.

CONCEPT: ALPHA HELIX DISRUPTION

PRACTICE: An α-helix would be destabilized most by:

a) DNA missense mutation leading to a Gly residue placed in the α-helix sequence.
b) Interactions between neighboring Asp & Arg residues.
c) A hydrophobic environment competing for hydrogen bonds.
d) DNA missense mutation leading to a Pro residue placed in the α-helix sequence.
e) A net electric dipole spanning several peptide bonds throughout the α-helix.

PRACTICE: At pH 6.8, which of the following peptides is least likely to form an α-helix?

Peptide # 1: RSEDNFGAPKSILWE

Peptide # 2: DQKASVEMAVRNSGK

a) Peptide # 1.
b) Peptide # 2.
c) Both peptides are equally likely to form an α-helix.
d) Neither peptide is likely to form an α-helix.

PRACTICE: Why does proline often “break” an alpha helix?

a) Its amino group has no free hydrogen to bond with a carbonyl because of the imino ring.
b) It is impossible for it to adopt the psi and phi angles required to form an alpha helix.
c) Its peptide bond often adopts the trans conformation, unlike other amino acids.
d) Its peptide bond flips frequently between the cis and trans conformations.