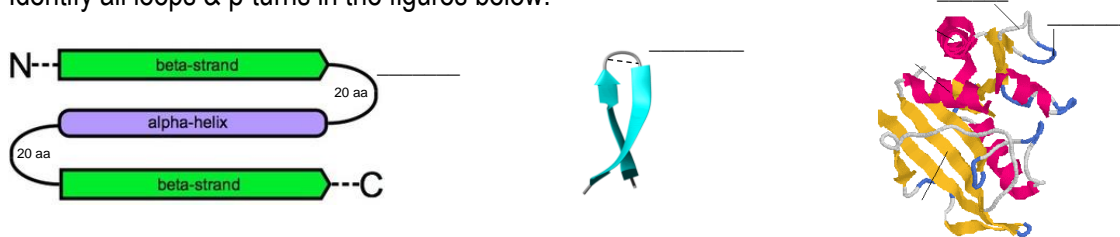


## CONCEPT: BETA TURNS

- \_\_\_\_\_ & loops: non-repetitive secondary structures causing the peptide backbone to \_\_\_\_\_ directions.
  - Usually found on the *surface* of proteins with \_\_\_\_\_ residues & allow for a folded, compact shape.
- Loop: \_\_\_\_\_ links of amino acids causing changes in backbone direction \_\_\_\_\_ fixed, internal hydrogen bonds.
- $\beta$ -Turns (or *Reverse turns*): \_\_\_\_\_ loops ( $\leq 4$  amino acid residues) causing \_\_\_\_\_ changes in backbone direction.
  - Stabilized by fixed, internal hydrogen bonds.

**EXAMPLE:** Identify all loops &  $\beta$ -turns in the figures below.



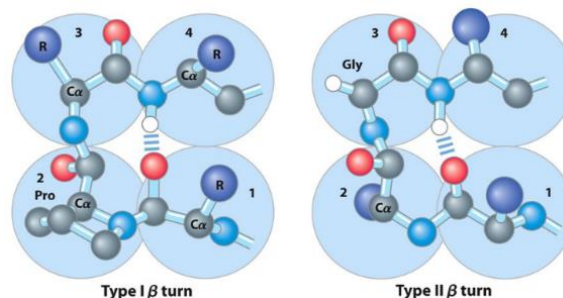
**PRACTICE:** Which of the following options contains a true statement about protein turns & loops?

- Loops & turns can interact with other proteins & the environment.
- Loops are short links causing abrupt changes in direction & extend only from  $\beta$  strands.
- Loops and turns usually contain hydrophilic residues located on the interior of proteins.
- Loops exposed to an aqueous environment are usually composed of hydrophobic amino acids.

## Type I & II $\beta$ -Turns

- Two common types of  $\beta$ -turns: 1) *Type I  $\beta$ -turn* & 2) *Type II  $\beta$ -turn*.
- Both types produce abrupt \_\_\_\_\_ in direction, contain \_\_\_\_\_ amino acid residues, & are stabilized by \_\_\_\_\_ bonding.
  - Type I  $\beta$ -turns: *more* common & usually contain a \_\_\_\_\_ amino acid residue at position #2 of the turn.
  - Type II  $\beta$ -turns: contain a \_\_\_\_\_ amino acid residue at position #3 of the turn.

**EXAMPLE:**



**PRACTICE:** In the peptide below, circle the *individual* amino acid residues indicating the most likely positions for  $\beta$ -turns:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28  
Ile-Ala-His-Thr-Tyr-Gly-Pro-Phe-Glu-Ala-Ala-Met-Cys-Lys-Trp-Glu-Ala-Gln-Pro-Asp-Gly-Met-Glu-Cys-Ala-Phe-His-Arg

## CONCEPT: BETA TURNS

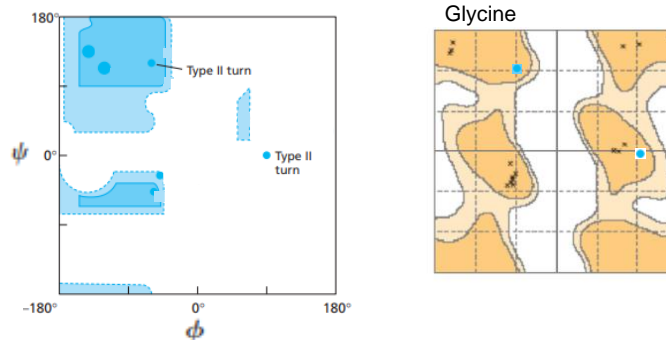
**PRACTICE:** Which of the following statements is true regarding  $\beta$ -turns?

- a) Only Type I  $\beta$ -turns are stabilized by hydrogen bonds, not Type II  $\beta$ -turns.
- b) Type II  $\beta$ -turns have a Pro residue at position #2 of the turn.
- c) Type I  $\beta$ -turns have a Gly residue at position #4 of the turn.
- d) Type II  $\beta$ -turns have a Gly residue at position #3 of the turn.

## Beta Turn Bond Angles

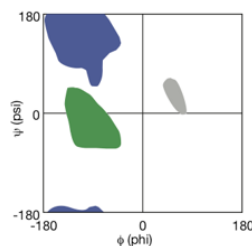
- Bond angles for loops & turns are found in \_\_\_\_\_ regions of a Ramachandran plot.
  - Type II  $\beta$ -turns: some  $\phi$  and  $\psi$  angles lie \_\_\_\_\_ expected permissible angles.
- \_\_\_\_\_ can adopt a wide range of  $\phi$  and  $\psi$  angles because of its small R-group that avoids steric hindrance.
  - Glycine is often a residue found in type \_\_\_\_  $\beta$ -turns.

**EXAMPLE:**



**PRACTICE:** If the phi & psi angles of loop regions are plotted, where do they tend to fall on the Ramachandran plot below?

- a) The area labeled in green.
- b) The area labeled in blue.
- c) The area labeled in grey.
- d) All the above.



**PRACTICE:** Which of the following statements is correct?

- a) Loops and turns are usually found tucked away on the interior of folded proteins.
- b) An  $\alpha$ -helix peptide backbone located in the interior of a protein will H-bond to R-groups of other residues.
- c) In extended fibrous proteins that are elongated, we would expect to find numerous  $\beta$ -turns & loops.
- d) Tightly compact spherical/globular proteins tend to have more  $\beta$ -turns than elongated fibrous proteins.
- e) A membrane-embedded  $\alpha$ -helix is likely rich in Asp residues.