Early Pauling and Corey devised a novel for the combination of phrases known as beta-turns. In this configuration, the polypeptide backbone winds around itself. In other words, it loops back on itself to reform the helix.

### Beta-turns

- **Beta-turns** are short segments of the polypeptide chain that are stabilized by hydrogen bonds between the backbone atoms. These hydrogen bonds form a turn, or a bend, in the chain.
- **4-helix bundle** is a type of protein structure composed of four alpha helices that are packed together.
- **Alpha-helices** are a common type of protein structure characterized by a hydrogen-bonded turns between every third residue. These turns are stabilized by hydrogen bonds between the backbone atoms.
- **β-strands** are segments of the polypeptide chain that are stabilized by hydrogen bonds between the backbone atoms.

### Alpha-helices

- **Alpha-helices** are common in globular proteins.
- **Beta-sheets** are also common in globular proteins.
- **Three of the greatest structural scientists of the 20th century** were Pauling, Corey, and Kendrew.

### Beta-sheets

- **Beta-sheets** are common in globular proteins.
- **Parallel sheets** are observed, but **antiparallel sheets** with less than four strands are rare.

### Comparison of alpha helix and beta pleated sheet

- **Axial distance between adjacent residues** is 3.5 Angstroms.
- There are two residues per repeat unit, which gives the beta-strand a 7 Angstrom pitch.
- This compares with the alpha-helix where the axial distance is 3.5 Angstroms.

### Imagining two strands parallel to this, one above the plane of the screen and one behind, it is possible to grasp how the pleated appearance of the beta-sheet arises. Note that in the classical Pauling-Corey models the parallel beta-sheet has somewhat more distorted and bent strands than the antiparallel beta-sheet with its flat, folded appearance and no bending.