Structure and conformation
(Three dimensional shape)
Two principle secondary structural elements in protein structures:

**Alpha helix**

**Beta strand**

(a) Carboxyl terminus  (b)

3.5 Å  5.7 Å

Ala side chain  Gly side chain
Polypeptide chain folds up into a self stabilizing secondary structural element
**Beta strand**

Polypeptide chain folds up into beta strand secondary structural element and interacts with other beta strands to form a beta sheet.
Secondary structural elements depend on the peptide torsion angles

\[
\begin{align*}
\text{phi (}\varphi\text{)} & \quad \text{N - C}_{\alpha} \\
\text{psi (}\psi\text{)} & \quad \text{C}_{\alpha} - \text{C} \\
\text{omega (}\omega\text{)} & \quad \text{C} - \text{N (peptide bond)}
\end{align*}
\]
The planarity of the peptide bond restricts omega to 180 degrees (in very nearly all of the main chain peptide bonds – other than proline) leaving rotation in the phi and psi bonds.
Alpha-Helix Structure

Pauling and Corey (alpha-keratin)
The most simple and elegant arrangement is a right-handed spiral conformation known as the 'alpha-helix'
The helix is stabilized by hydrogen bonds between main chain atoms

-N-H.............O-C
Right-handed alpha-helix.

White dots show the hydrogen bonds.
Right/Left handed Helices

A right-handed helix differs from a left-handed one. An easy way to remember this is to hold both your hands in front of you with your thumbs pointing up and your fingers curled towards you. For each hand the thumbs indicate the direction of translation and the fingers indicate the direction of rotation.
Characteristics of Helix:

Hand

Number of amino acids per turn

Rise per residue

Radius of helix

H-bonding
### Parameters of helical structures

<table>
<thead>
<tr>
<th>Helix</th>
<th>Residues/Turn</th>
<th>Rise (nm) H-bonding</th>
<th>#atoms</th>
<th>phi (°)</th>
<th>Psi (°)</th>
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</thead>
<tbody>
<tr>
<td>$3_{10}$</td>
<td>3.0</td>
<td>.2</td>
<td>10</td>
<td>-49</td>
<td>-26</td>
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<tr>
<td>$\alpha$</td>
<td>3.6</td>
<td>.15</td>
<td>13</td>
<td>-57</td>
<td>-47</td>
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<tr>
<td>$\pi$</td>
<td>4.4</td>
<td>.12</td>
<td>16</td>
<td>-57</td>
<td>-70</td>
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</tbody>
</table>
Helical Wheels
Helical Wheels

- Hydrophobic
- Polar
- Charged
4-helix bundle

- Green: Hydrophobic surface
- Red: Hydrophilic surface
Topology of ferritin four-helix bundle

Topology of myohemerythrin four-helix bundle
Pauling and Corey (beta-keratins)

In this conformation the polypeptide does not form a coil
Instead, it zig-zags in a more extended conformation
A diagram of a polypeptide in the beta conformation.

The peptide bonds of adjacent residues point in opposite directions towards and away from the plane of the screen.

Note the pronounced zig-zag appearance.

Can you recognise the amino acids in this beta strand?

Alternate side chains also point in opposite directions approximately in the plane of the screen.
Amino acid residues in the beta-conformation have typical phi, psi values

\[ \text{phi} = -140 \text{ degrees} \]
\[ \text{psi} = 130 \text{ degrees} \]

A section of polypeptide with residues in the beta-conformation is referred to as a beta-strand and these strands can associate by main chain hydrogen bonding interactions to form a beta sheet

In a beta-sheet two or more polypeptide chains run alongside each other and are linked in a regular manner by hydrogen bonds between the main chain C=O and N-H groups. Therefore all hydrogen bonds in a beta-sheet are between different segments of polypeptide. This contrasts with the alpha-helix where all hydrogen bonds involve the same element of secondary structure. The R-groups (side chains) of neighboring residues in a beta-strand point in opposite directions
Note that peptide groups of adjacent residues point in opposite directions whereas with alpha-helices the peptide bonds all point one way.

The axial distance between adjacent residues is 3.5 Angstroms (.35nm). 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 between adjacent residues is only 1.5 Angstroms.

Clearly, polypeptides in the beta-conformation are far more extended than those in the alpha-helical conformation.
Parallel, antiparallel and mixed beta-sheets

In parallel beta-sheets the strands all run in the same direction.
In antiparallel sheets they all run in opposite directions.
In mixed sheets some strands are parallel and others are antiparallel.
Diagram of a three-stranded antiparallel beta-sheet

Emphasizes the highly regular pattern of hydrogen bonds between the main chain NH and CO groups of the constituent strands

Can you identify the amino- and carboxy- termini of the strands?
In the classical Pauling-Corey models the parallel beta-sheet has somewhat more distorted and consequently weaker hydrogen bonds between the strands.

Beta-sheets are very common in globular proteins and most contain less than six strands. The width of a six-stranded beta-sheet is approximately 25 Angstroms.

No preference for parallel or antiparallel beta-sheets is observed, but parallel sheets with less than four strands are rare, perhaps reflecting their lower stability.

Sheets tend to be either all parallel or all antiparallel, but mixed sheets do occur.
The Pauling-Corey model of the beta-sheet is planar.

However, most beta-sheets found in globular proteins are twisted. This twist is left-handed.

The overall twisting of the sheet results from a relative rotation of each residue in the strands by 30 degrees per amino acid in a right-handed sense.
The right-handed beta-alpha-beta unit. The helix lies above the plane of the strands.

The Rossman fold
The Ramachandran Plot

In a polypeptide the main chain \([\phi (\varphi) \text{N-C}_{\text{alpha}}]\) and \([\psi (\psi) \text{C}_{\text{alpha}}-\text{C}]\) bonds are relatively free to rotate

These rotations are represented by the torsion angles \(\phi\) and \(\psi\), respectively

Ramachandran used computer models of small polypeptides to systematically vary \(\phi\) and \(\psi\) with the objective of finding stable conformations
-胎-sheet.

Left handed alpha-helix.

Right handed alpha-helix.
In the previous figure the white areas correspond to conformations where atoms in the polypeptide come closer than the sum of their van der Waals radii. These regions are sterically disallowed for all amino acids except glycine which is unique in that it lacks a side chain.

The red regions correspond to conformations where there are no steric clashes, i.e. these are the allowed regions namely the alpha-helical and beta-sheet conformations. The yellow areas show the allowed regions if slightly shorter van der Waals radii are used in the calculation, i.e. the atoms are allowed to come a little closer together. This brings out an additional region which corresponds to the left-handed alpha-helix.