The stabilization is only possible if the planes defined by the $\mathrm{sp}^{2}$ bonding units of the carbonyl C and N atoms are coplanar as shown.

If the two bonding units are not coplanar, the $2 p_{z}$ orbitals of the $O, C$ and $N$ atoms would not all overlap as shown for the hybrid.

This means that rotation about the peptide bond is restricted.

As a result of the lack of free rotation, cis and trans peptide bonds are possible as follows:

The peptide bond in proteins is in the trans form. This form is more stable because there is less steric interaction between R groups of adjacent a.a..

Fig 6-4 shows a representation of a polypeptide chain with planar peptide groups.

Fig 6-4 also indicates that only the single bonds to the $\alpha$-carbon atoms in the polypeptide backbone are free to rotate.

Thus it is rotation about these bonds which gives rise to the conformations of proteins.

Angles of rotation about the $\mathrm{C}_{\alpha}-\mathrm{C}$ and $\mathrm{C}_{\alpha}-\mathrm{N}$ bonds are referred to by the letters $\Psi$ (psi) and $\Phi$ (phi) respectively as shown in the handout figure.
$\Psi=180^{\circ}$ when adjacent peptide planes are coplanar with $\mathrm{N}_{1}$ and $\mathrm{N}_{2}$ trans to the $\mathrm{C}_{\alpha}-\mathrm{C}$ bond.
$\Phi=180^{\circ}$ when adjacent peptide planes are coplanar with carbonyl $\mathrm{C}_{1}$ and $\mathrm{C}_{2}$ trans to the N $C_{\alpha}$ bond.

The handout figure shows an amino acid with $\Psi$ and $\Phi$ angles of $180^{\circ}$.

Let's also define positive and negative angles of rotation.

While looking along a bond from one atom to another, a clockwise rotation of the farthest atom corresponds to a positive rotation.

Rotation of carbonyl $\mathrm{C}_{2}$ (farthest atom) about the $\mathrm{C}_{\alpha}$ in the direction shown in the figure corresponds to a positive rotation.

Rotation of $\mathrm{N}_{1}$ (farthest atom) about the $\mathrm{C}_{\alpha}$ in the direction shown in the figure corresponds to a positive rotation.

If the $\Phi$ and $\Psi$ angles are constant throughout a polypeptide chain, the polypeptide will have the shape of a helix.

A given set of $\Phi$ and $\Psi$ angles will determine the type of helix, i.e., $n$, the number a.a. per turn, p , the pitch, and d, the distance traversed by one a.a. along the helix axis.

The handout figure defines $\mathrm{n}, \mathrm{p}$ and d .

The same n can result from other angles of $\Phi$ and $\Psi$ as shown below

For a given value of $\Phi$ and different values of $\Psi$, helices of different n will result as represented below

Not all values of $\Phi$ and $\Psi$ are equally favorable because of steric interactions within the polypeptide chain.

When $\Phi=0^{\circ}$ and $\Psi=180^{\circ}$, there is a large steric interaction between adjacent carbonyl 0 atoms as shown in the handout figure.

