When $\Phi = 180°$ and $\Psi = 0°$, there is a large steric interaction between adjacent peptide H atoms as shown in the figure.

Ramachandran has calculated the distances between atoms in a tripeptide of L-ala for all sets of $\Phi$ and $\Psi$ angles to determine which are sterically forbidden based on distances less than the sum of the van der Waals radii of the atoms.

The handout table gives the minimum contact distances between atoms using both the normally accepted radii and the minimum radii of atoms.

The Ramachandran plot shown in Fig 6-9 indicates regions of $\Phi$ and $\Psi$ angles that are normally allowed, minimally allowed and forbidden.

White areas correspond to $\Phi$ and $\Psi$ angles for which there is no steric interaction using normally accepted van der Waals radii of atoms.

The darkest areas correspond to $\Phi$ and $\Psi$ angles for which there is no steric interaction using minimum radii of atoms.

All other areas are forbidden because of large steric interactions.

Note that the plot is not symmetric; left-handed helical regions have different areas of stability than right-handed helical regions.

The lack of symmetry is due to the fact that the plot is for an L-amino acid since steric interactions of the side chains also occur for particular angles of $\Phi$ and $\Psi$.

For bulkier a.a., the allowed areas may be considerably reduced.

Among allowed regions of the plot are particular angles of $\Phi$ and $\Psi$ which yield helical structures found in proteins.

These structures are referred to as $\beta_A$, $\beta_P$, C, and $\alpha_R$.

The $\Phi$ and $\Psi$ angles corresponding to these structures are shown in the handout table.

For example, the right-handed $\alpha$ helix results when $\Phi$ = -57° and $\Psi$ = –47°.

The formation of these structures among other possible structures is due to the stabilizing effect of H-bonding between peptide N-H and C=O groups.

Helical structures stabilized by H-bonds between these peptide groups are referred to as the secondary structure of proteins.

Consider the structures of these helices and some proteins in which they are found.

The $3_{10}$ helix is described in the handout figure.

The $3_{10}$ helix is right-handed and results from $\Phi$ and $\Psi$ angles of -49° and -26° respectively that corresponds to a minimally allowed region of the Ramachandran plot.

In the $3_{10}$ helix, n = 3 and the carbonyl O of the 1st a.a. is H-bonded to the N-H group of the 4th a.a. along the chain to form a 10-membered ring.

Note that the intrapeptide H-bond is approximately parallel to the axis of the helix.

The $3_{10}$ helix is often found within $\alpha$-helical segments of proteins including myoglobin that participates in $O_2$ storage in muscle.