LSM2241 Lecture 7 supplement and exercises: β turns

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Contents

1 Introduction

This supplement discusses a few concepts from the structural biology material we cover in the structure lecture, and in the associated practical. I've included a few exercises for you to work through. I will provide solutions to the exercises after I receive the first five (5) attempted solutions from students, sent to me via email.

Exercise on canonical secondary structures

The diagram of **??** is called a Newman projection. The ϕ angle for a typical anti-parallel beta sheet is shown, as it is in the lecture. Draw the Newman projection for the typical ϕ and ψ angles of a *parallel* beta sheet, and the typical ϕ and ψ angles of an alpha helix. Given the handedness of amino acids in proteins, we know that the alpha carbon C_α is asymmetric for all amino acids except glycine. As a consequence, where will the H_α and R groups appear on the projections?

Consider the angles you just drew for the α helix. Which direction does it appear to turn? Is an α helix left handed or right handed? Does this make sense? What if anything is missing for it to make sense?

Note on the answers provided

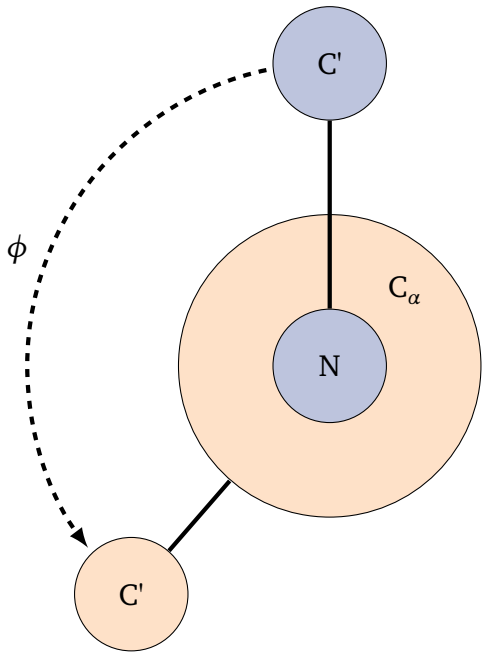


Figure 1. Diagram for a ϕ angle calculation. Note that the angle is measured from the atom in the front to the atom in the back. This diagram shows a ϕ angle of -139°, corresponding to a canonical antiparallel β sheet

The text for answers provided will be in shaded boxes like this. They are accompanied by diagrams, which use standard chemical shading for atomic elements: green for carbon, blue for nitrogen, and red for oxygen. The coloring is to make it easier to understand the diagrams.

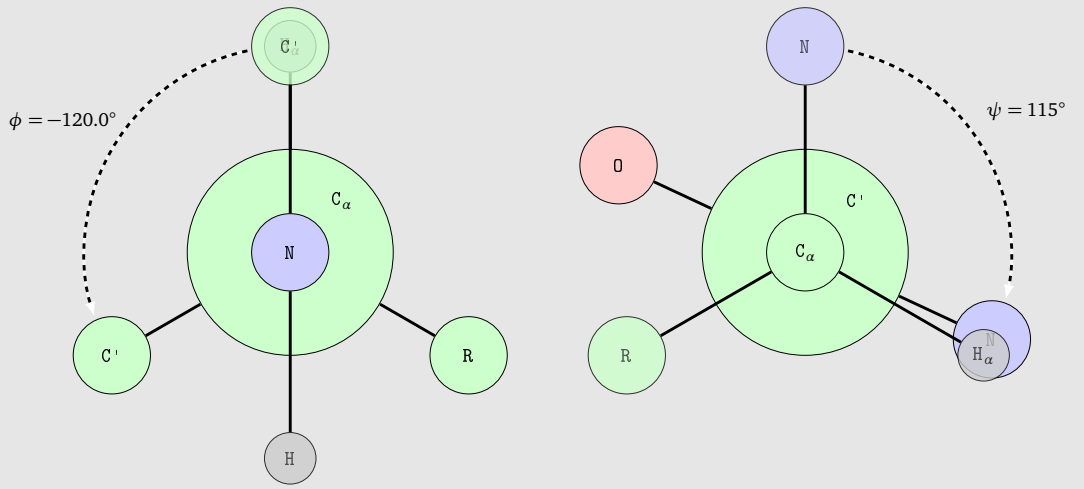
I did not provide the exact angles for canonical sheets, helices, and turns, because these are trivial to look up on the internet.

Atoms are all the drawn the same size, except for the centre rear atom in the projections, which is larger so you can see it, and the hydrogen atom, which are smaller by convention. The term C' refers to the carbonyl carbon of an amino acid backbone.

I strongly encourage you to review the Ramachandran plots in studying these scenarios.

Answers to exercise

parallel sheet



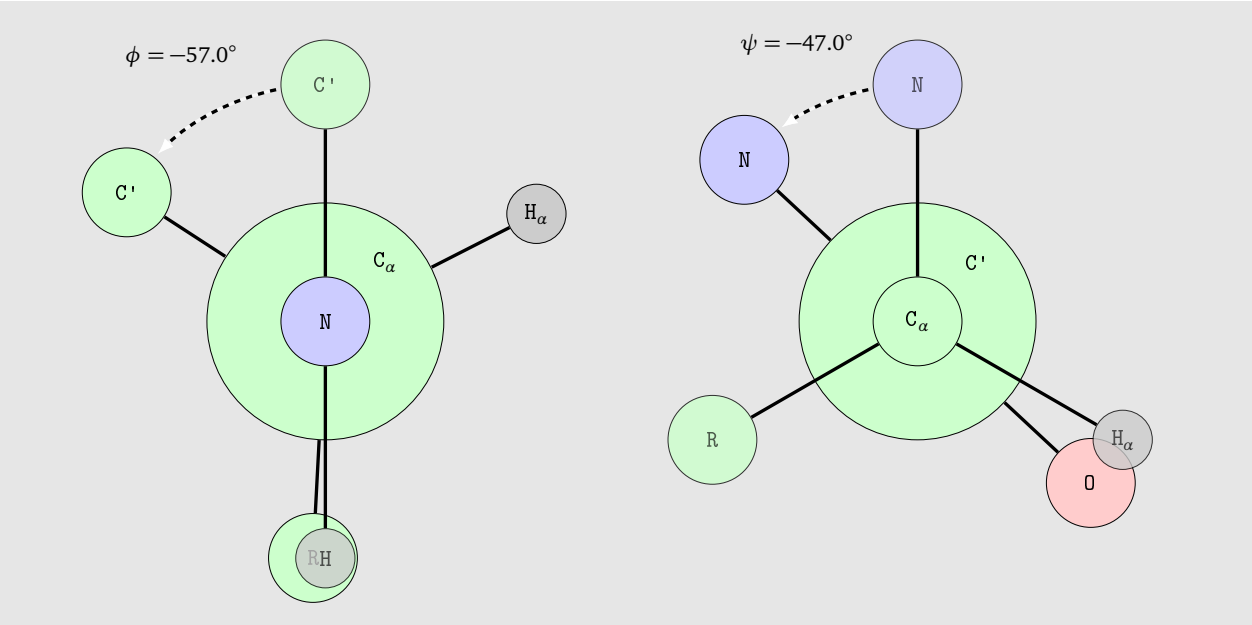
On the left above is a Newman projection for a canonical parallel β sheet ϕ angle of -120°, with R groups and H_α positions show. The planar peptide bond is also shown by illustration of the amide hydrogen atom.

On the right is shown the canonical ψ angle of 115° for a parallel beta sheet.

Note how the carbonyl carbon and the H_α are nearly overlapping in the ϕ angle projection, while the H_α and amide nitrogen are nearly overlapping in the ψ angle projection. This should be familiar to you, as these are the atoms that stick out of the thin sides of the cartoon representation of the beta strands.

Alpha helix

The idealized α helix ϕ and ψ projections are shown below. Note the near overlap of the R group and the amide hydrogen. A proline would replace the amide hydrogen with a carbon as part of the five atom ring side chain, which must be nearly planar.



2 What defines a β turn?

A β turn is a tight turn that involves four residues (*three* peptide bonds) between two close amino acids in adjacent elements of secondary structure. (A β turn is unrelated to β sheets; β turns can occur between sheets or helices.) We usually refer to the amino acids in the turn by number: n, $n+1$, $n+2$, and $n+3$. The n and $n+3$ residues must have C_α atoms within 7Å of each other to be considered a beta turn. The different types of β turns are characterized by different backbone angles and propensities of different amino acids.

Since the amino acids n and $n+3$ are within 7Å, the major distinctions between types of β turns are in the backbone ϕ and ψ angles for the amino acids $n+1$ and $n+2$. However, analysis of turns in the PDB shows that some amino acids are more likely to occur than others at particular types of turns. This propensity can be used to predict the occurrence of a turn.

3 Type I β turn

The most common β turn is a type I turn. It is defined by idealized ϕ and ψ angles at $n+1$ and $n+2$ positions, but of course the real angles may deviate from the ideal. Hutchinson and Thornton looked at a large number of turns in the PDB, and found average backbone dihedral angles for Type I turns corresponding to the values in **??** (Hutchinson and Thornton 1994).

Type I turns very often have a proline at either position n or $n+1$, and very *rarely* have a proline at position $n+2$. Hydrogen bond acceptors (histidine, apsaragine, aspartate, serine, and cystine) are common at position n, so they can accept a hydrogen bond from the backbone nitrogen of position $n+3$. The propensities for different amino acids at different turn types can be found at this page.

An example type I turn can be seen in residues 39-42 of the structure of subtilisin Carlsberg (PDB entry 1CSE) which has the sequence `HPDL`. A close up stereo diagram is show in **??**. In the practical you may give yourself a headache trying to see three dimensional figures from stereo diagrams on the screen, but you can do the same on the printed page without the headache. Try it!

position	ϕ	ψ
$n+1$	-64(-60)	-27(-30)
$n+2$	-90(-90)	-7(0)

Table 1. Average ϕ and ψ angles at the key positions in Type I β turns in the PDB, from Hutchinson and Thornton 1994. Values in parentheses correspond to idealized turns, rather than actual turns.

Type I β turns commonly show hydrogen bonding between the carbonyl carbon of position n and the amino group of position $n+3$. This is highlighted as a dashed line in the figure. There is an additional hydrogen bond, also shown, in this structure from the backbone amino nitrogen of position $n+2$ to the histidine ring nitrogen at position n.

The actual dihedral angles for this structure are show in Table~**??**.

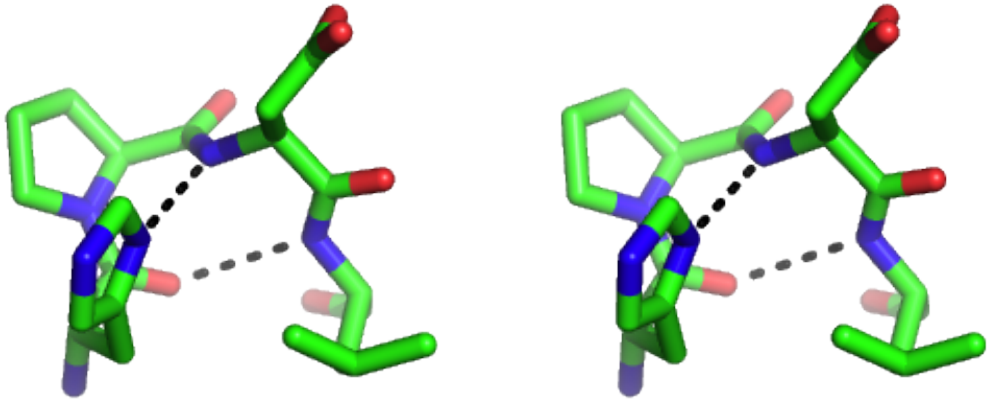


Figure 2. Stereo diagram of type I β turn of residues 39-42 of subtilisin from PDB entry 1CSE. Hydrogen bonding within the turn is shown as dashed lines. If you have learned how to see stereo diagrams in the practical, you should be able to see this turn in three dimensions.

position	ϕ	ψ
40	-62	-22
41	-90	13.8

Table 2. Actual dihedral angles for the key positions of the turn shown in **??**. These angles were measured in PyMol.

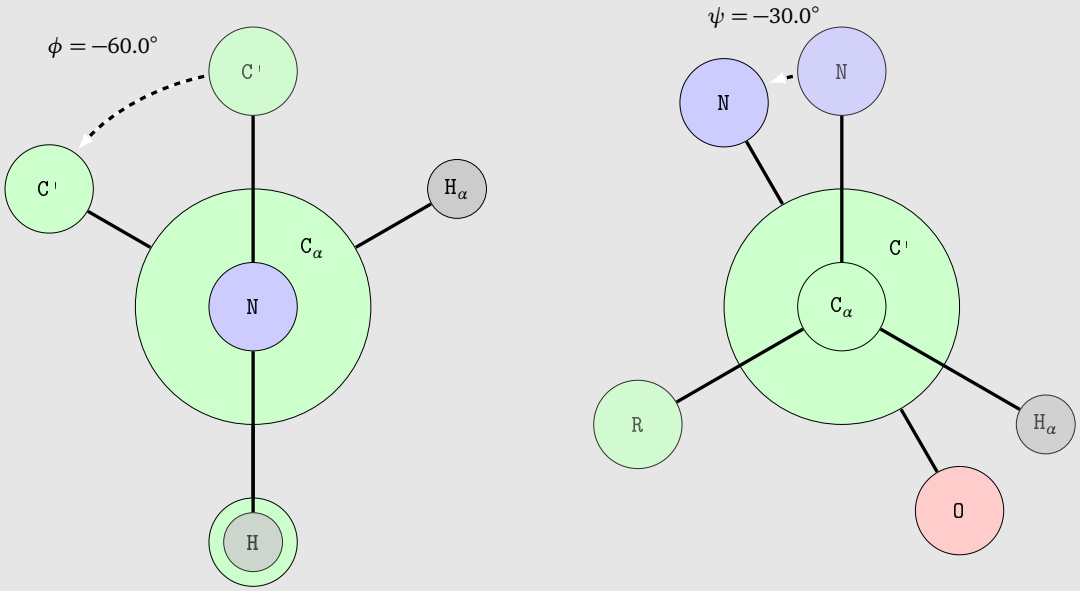
Exercise

Draw the ϕ and ψ angles in a Newman projection for the $n+1$ and $n+2$ residues of a type I β turn. Given the L handedness of amino acids, where on the projection would the H_α and the side chain (the R group) appear?

Imagine a proline at position $n+1$, and draw the side chain connected to the backbone of the protein. Can you see why proline is preferred at this position?

Answers to exercise

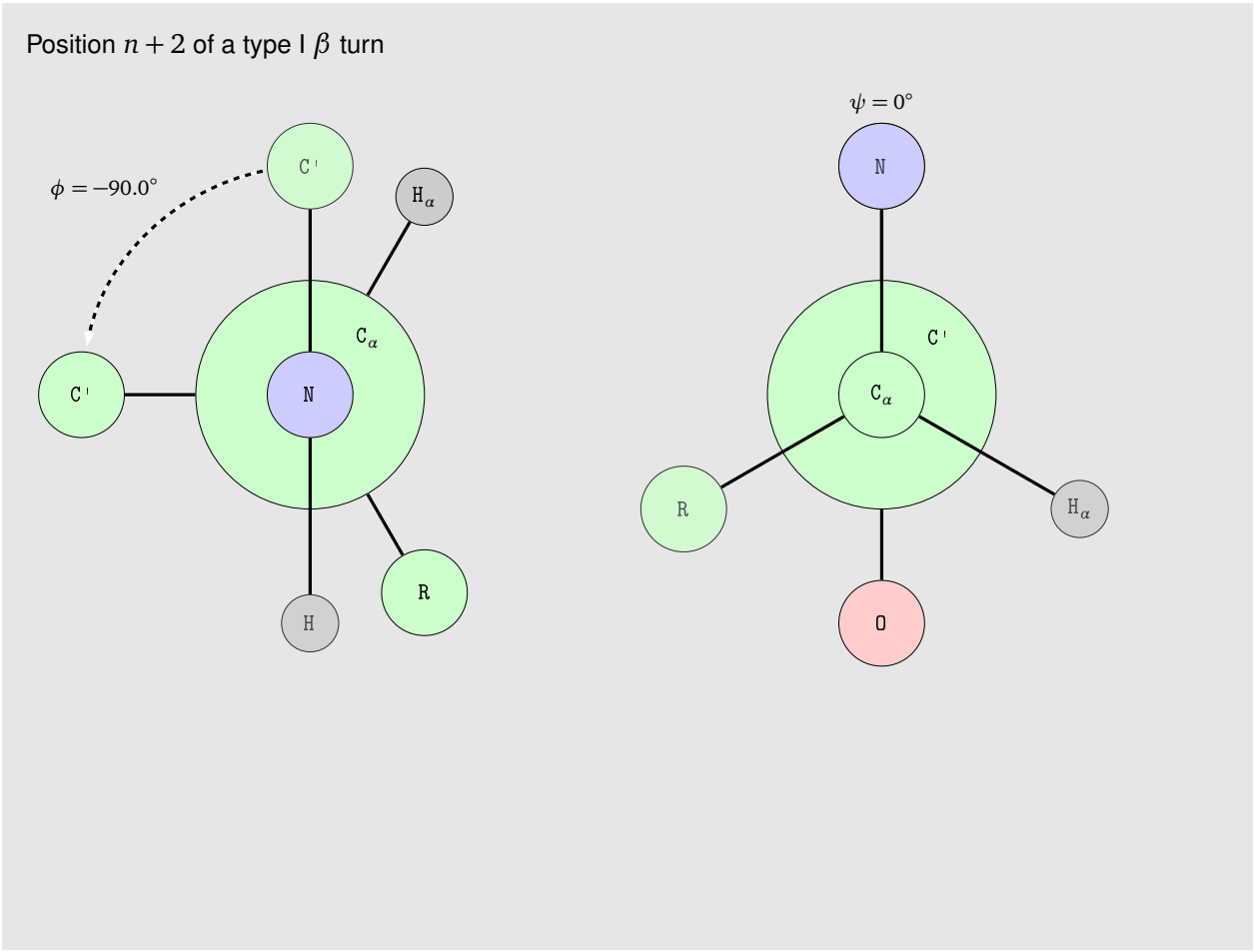
Position $n+1$ of a type I β turn



The $n + 1$ position is shown above. Note how the R group position is eclipsed by the amide hydrogen. In a proline, the amide hydrogen doesn't exist, but is replaced by a carbon that is part of the proline ring. This ϕ angle is not only compatible with the proline ring, but the proline ring must have a ϕ angle very close to this value.

An idealized α helix angle of -57° is not very different than this, so why do people often say prolines are not compatible with α helices? One reason is that the loss of the amide hydrogen bond destabilizes the helix. A second reason is that the carbon of a proline replaces a hydrogen of other amino acids, and occupies more space by itself and within the ring. Finally, the restrictions imposed by a proline prevent the amino acid that precedes it from forming an alpha helix. See the Ramachandran plot (the "pre-pro" panel) in the lecture notes.

While proline is the most common amino acid at position $n+1$, serine and glutamate may also occur here. What about their side chains might favour the $\phi = -60°$ torsion? A serine is easiest to visualise; the hydroxyl oxygen can form a hydrogen bonded five atom ring with the amide nitrogen which mimics the structure of the proline ring.



4 Type II β turns

Type II β turns are distinguished from type I by the ϕ and ψ angles at positions $n+1$ and $n+2$. Type II turns also characteristically have a hydrogen bond from the carbonyl carbon of position n to the amino nitrogen of position $n+3$, but the ψ angle at position $n+1$ and the ϕ angle at position $n+2$ are almost completely opposite the type I turn case. The average and ideal values for a large number of Type II β turns in the PDB, identified by Hutchinson and Thornton 1994, are shown in **??**.

Like type I turns, proline is favored at position $n+1$. Note the similarity of the ϕ angle for this position in both types of turns.

Because of the angular requirements at position $n+2$ of a type II turn, this amino acid is a glycine in about 90% of cases, but may also be an asparagine or aspartate.

position	ϕ	ψ
$n+1$	-60(-60)	131(120)
$n+2$	84(80)	1(0)

Table 3. Average ϕ and ψ angles at the key positions in Type II β turns in the PDB, from Hutchinson and Thornton 1994. Values in parentheses correspond to idealized turns, rather than actual turns.

An example of a type II β turn is residues 75-78 of yeast iso-1-cytochrome c (PDB entry 1YCC), which has the sequence `IPGT` and is illustrated in **??**. This shows the characteristic type II turn propensity for a glycine at position $n+2$.

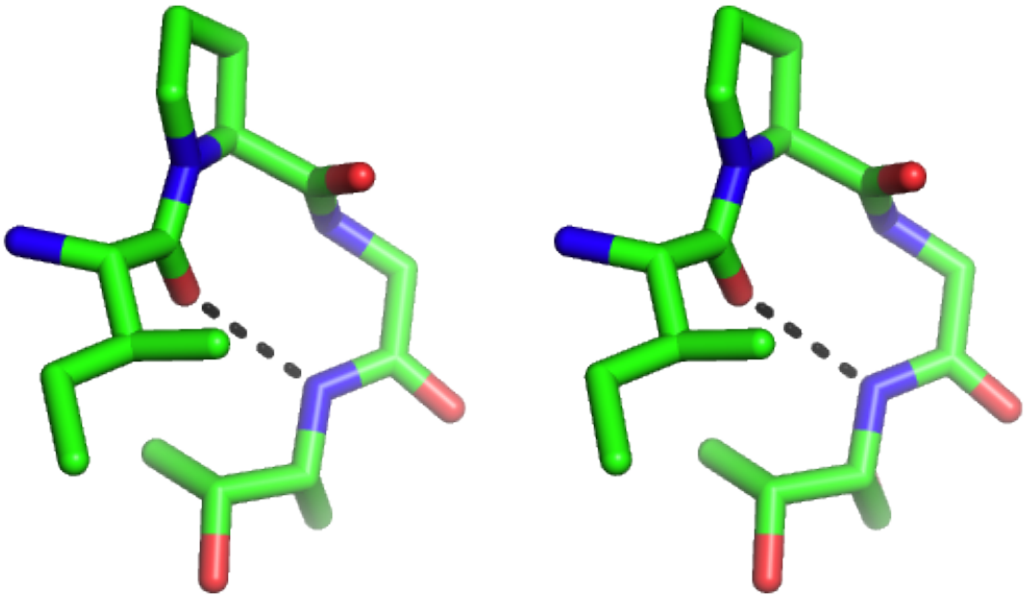


Figure 3. Type II β turn of residues 75-78 of yeast yeast iso-1-cytochrome c (PDB entry 1YCC). The hydrogen bond along the backbone between residues n and $n+3$ is shown with a dashed line. If you can see this in stereo, the difference from a Type I turn will be clear.

Again, the stereo diagram should give you a sense of how these torsion are different from those of type I turns, but to be specific, in this case the actual torsion angles are in **??**.

position	ϕ	ψ
76	-66.3	128.8
77	99.7	-1.5

Table 4. Actual dihedral angles for the key positions of the turn shown in **??**

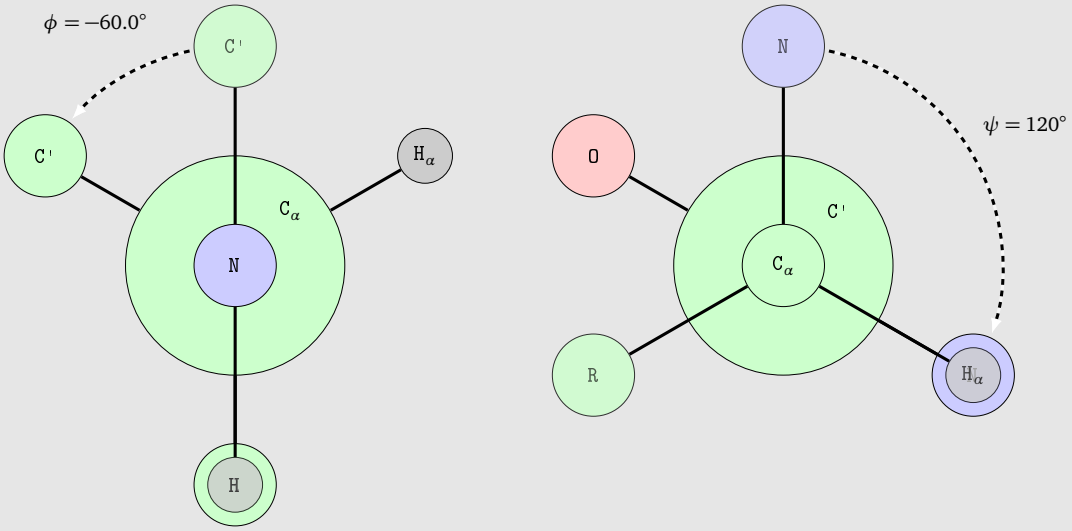
Exercise

Draw the ϕ and ψ angles in a Newman projection for the $n+1$ and $n+2$ residues of a type II β turn. Given the L handedness of amino acids, where on the projection would the H_α and the side chain (the R group) appear?

Can you see from your Newman projections why a glycine is so strongly favored at position $n+2$?

Answers to exercise

Position $n+1$ of a type II β turn

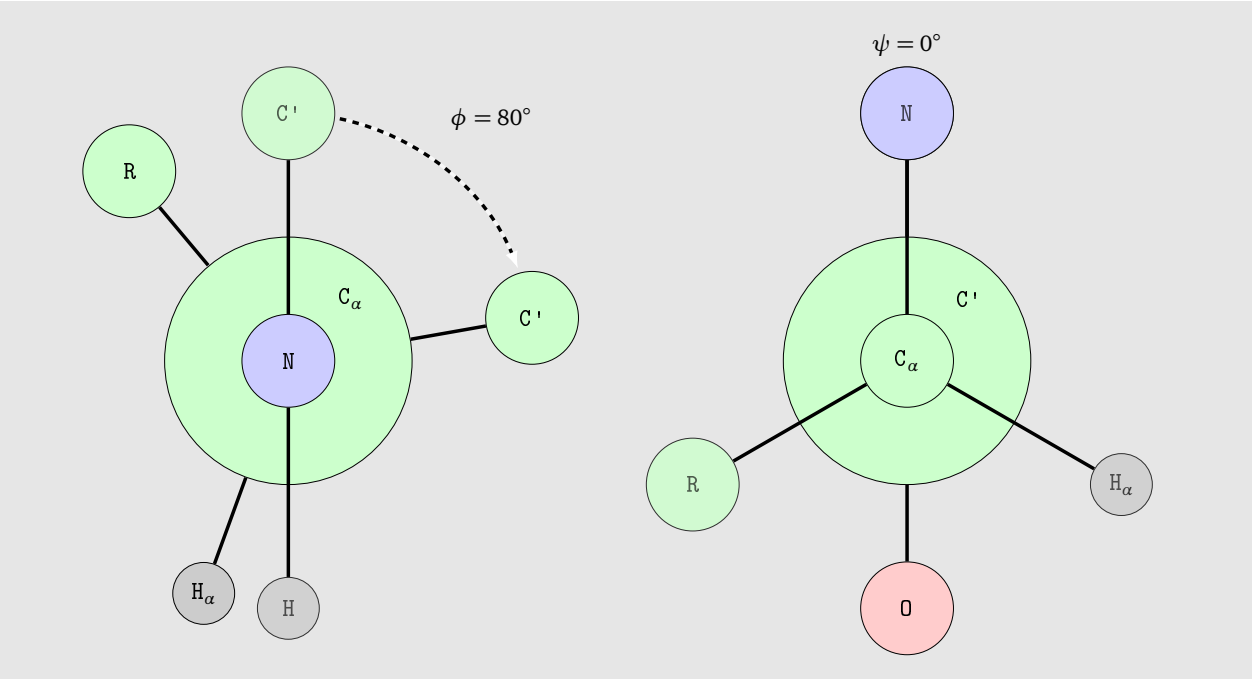


This ϕ angle at this position looks similar to the $n + 1$ position of a Type I β turn. Like a Type I turn, proline is favoured, being ideal for this ϕ angle. The ψ angle is quite different, however, as you can see from both the Newman projection and the stereo diagram of **??**. Note how the H_α in the projection eclipses the following amino nitrogen.

Position $n+2$ of a type II β turn

The (ϕ,ψ) combination at position $n + 2$ position of a type II β turn is called an α_L configuration. One thing that is striking is that the ϕ angle of 80° puts the R group of the side chain very close to the carbonyl carbon and its associated oxygen (which would be pointed upwards in this representation). The lack of a side chain in glycine allows it to assume this confirmation, which most other amino acids could not.

Asparagine is an exception, and sometimes appears at this position. Why do you think asparagine could form an α_L configuation?



5 Other turn types

The other β turn types are also defined by characteristic torsion angles, and empirical amino acid propensities that make sense from structural considerations. The Type I' and Type II' turns are roughly the mirror images of the Type I and Type II turns, respectively, with the signs of all dihedral angles reversed.

References

Hutchinson, E G and J M Thornton (1994). "A revised set of potentials for beta-turn formation in proteins." In: *Protein science : a publication of the Protein Society* 3.12, pp. 2207–16. DOI: 10.1002/pro.5560031206 (cit. on pp. 4, 5, 7).

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