

## BCH222 :: Helix Worksheet

Hydrogen bonds are crucial to understanding helices, and H-bonds and helices are important to understanding and analyzing both individual structures and data compilations such as Ramachandran plots. Therefore, your first step should be to go through the H-bond Worksheet and HbondPractice.kin at whatever level of detail you need in order to feel comfortable with the definitions and with the practical skill of recognizing the geometry of H-bonds in graphics (or figures) - good or bad or marginal.

Then read the helix section in Anatomy and Taxonomy (IIA), including the green update comments, and use it as background for this worksheet.

### 1. Classic alpha-helices and helix caps

Open file [2hmqHlx.kin](#) (24KB) (helix B from a hemerythrin subunit) in KiNG.

Confirm for yourself that this helix is righthanded (point & move your right thumb in the direction the COs point, and check that your right-hand fingers can follow the backbone direction around the helical spiral). Is it approximately straight? \_\_\_\_\_

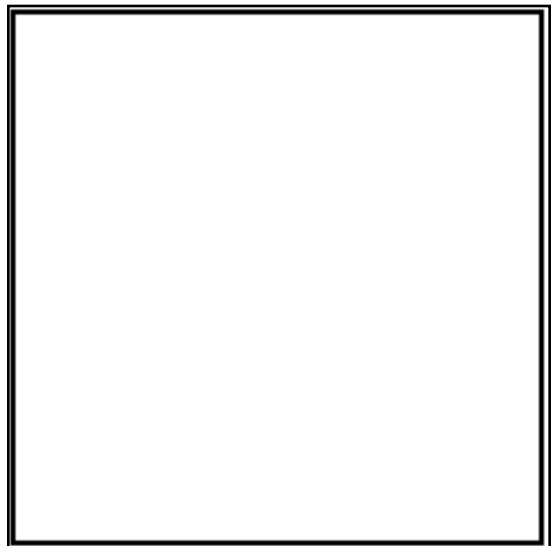
In the central section (View2) where the H-bonding is regular, choose one helical H-bond: it is from the carbonyl O of residue \_\_\_\_\_ to the amide H of residue \_\_\_\_\_ (that is, residues  $i$  to  $i +$  \_\_\_\_\_). What is the distance between O and N atoms? \_\_\_\_\_ Å (H atoms are not shown in this kin.) On the Tools menu, turn on Measures, and measure the phi angle value (click C, N, C $\alpha$ , C atoms) of a good  $\alpha$ -helical residue: \_\_\_\_\_°, then its psi angle (click on one more atom, the next N): \_\_\_\_\_°. Turn off Measures. List the other 10 backbone atoms (besides the O...H-N) that complete its H-bonded loop, for a total of 13:

O <sub>$i$</sub>  \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ \_\_\_\_\_ N <sub>$i+4$</sub> .

How many total  $i$  to  $i+4$  H-bonds are shown for this helix? \_\_\_\_\_ How many that are NOT  $i$  to  $i+4$ ? \_\_\_\_\_ To check yourself, turn "Extras" on, then off again.

Choose View3 (ca 55, N close), which looks at two turns of helix end-on from the N-terminus, and turn off all list buttons except "mainchain". In the box at right, sketch the pattern formed by the backbone in this view. Turn on the side chains. Show on your sketch some of the C $\alpha$ -C $\beta$  bonds.

Do they extend out radially, spiral clockwise, or spiral counterclockwise? \_\_\_\_\_



Answer the same question, as viewed from the other end of the helix (View4)

Turn on labels again, and choose View5 (N end to 55). Locate the C $\alpha$  of Phe 55; which C $\alpha$  of the top turn is most exactly in line with 55 C $\alpha$ ? \_\_\_\_\_

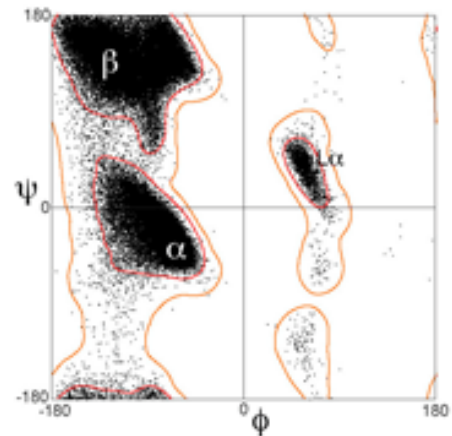
Subtract those residue numbers: there is an interval of \_\_\_\_\_ residues in 3 turns, so the helical pitch is \_\_\_\_\_ residues per turn.

Turn on H-bonds and N & O atoms again. Is the H-bonding regular in the first turn of the helix? \_\_\_\_\_ (use View6)

Find the first residue that makes one helical H-bond: \_\_\_\_\_ . It is half-in and half-out of the helix, with the peptide after its C $\alpha$  in good helix geometry and the peptide before it going off in a completely different direction. It is called the helix N-cap residue. Turn and look at it from all directions, to learn to recognize this important N-cap relationship. Three backbone N atoms in the first turn cannot make helical H-bonds. What atom of what residue is theoretically in position to H-bond with the N of residue 43? \_\_\_\_\_ of \_\_\_\_\_ . At what distance? \_\_\_\_\_ To check yourself, turn "Extras" on, then off again. As you know, it should really be the sidechain O atom making that H-bond. In this structure, the N-cap Asn has been incorrectly fit flipped over by 180°; such sidechain amide flips are not uncommon because the electron density looks nearly identical for an N and an O.

In View8, study the more complex (but classic) relationships at the helix C-cap. Near the helix end, the H-bonds shift to the *i* to *i*+3 pattern of 3-10 helix, starting with a bifurcated H-bond shared at the NH of \_\_\_\_\_ . How many 3-10 H-bonds are there? \_\_\_\_\_ (To check yourself, turn on Extras, where the 3-10 bonds are colored yellow or orange.)

The final flinging-outward of the backbone at this C-cap happens at residue Gln 66, surrounded by two H-bonds which join the expected two pairs of atoms but in reverse order, so they are an *i*+3 and an *i*+5 rather than two *i*+4s. (Turn on Extras to see them in orange and red.) Measure the phi angle of Gln 66: \_\_\_\_\_°, and the psi angle: \_\_\_\_\_°; those values put it in the \_\_\_\_\_ region of the Ramachandran plot ( $\alpha$ ,  $\beta$ , or  $L\alpha$ ).



Now study kinemage II.A\_hlxCaps.kin from Anatax II.A (on-line, click on the KiNG icon to open the kinemage). Practice recognizing the N and C-cap residues, the characteristic N-cap and cap-box sidechain-backbone H-bonds, the backbone H-bonds of an L $\alpha$  Gly C-cap, and

the "hydrophobic staple" pairs when present. [Refer to the Fasman chapter if you need further background describing helix caps.] The N-cap residue of helix 1 is \_\_\_\_\_, and the N-cap of helix 2 is \_\_\_\_\_. [Note that the chainID is "4".]  
 The hydrophobic staple of helix 1 is between residues \_\_\_\_\_ and \_\_\_\_\_.  
 \_\_\_\_\_.  
 The C-cap residue of helix 4 is \_\_\_\_\_.

## 2. Helix variants

### A. Coiled-coil (supercoiled) helices

🔗 [2tma.kin](#) (52KB) (tropomyosin)

The two chains are related by an exact twofold parallel to their length. Instead of being fairly short and straight, like typical globular-protein helices, these helices are about \_\_\_\_\_ turns long and coil around one another. Neighboring pairs stay the same distance apart all along, and the internal packing of hydrophobic side chains repeats approximately in multiples of seven residues.

### B. A bent helix

🔗 [2mlt.a.kin](#) (20KB) (one melittin chain)

This helix has an unusually sharp bend in the middle, of around \_\_\_\_\_ degrees.

Center on Pro 14, and turn on the side chains. How many helical H-bonds are missing at the bend? \_\_\_\_\_

Which peptide has the most distorted configuration? \_\_\_\_\_

Which CO would have been the H-bond partner of a residue 14 NH? \_\_\_\_\_

What is the effect of the Pro ring on the above residue and its backbone? \_\_\_\_\_

This helix is membrane-active, and has a rather extreme segregation of charges and hydrophobics. With side chains off but labels on, look down each half of it end-on, and locate the charged side and the hydrophobic side. Which is toward the inside (concave side) of the bend? \_\_\_\_\_

### C. A 3-10 helix

🔗 [2cyp.kin](#) (164KB) (cytochrome C peroxidase)

Look at the main chain and the heme and Fe (and H-bonds if you want them), just to get some feeling for the overall molecule.

Now turn on just the fragment in order to examine residues 164-177, which form a rather unusual helix buried in the middle of CYP, on one side of the heme. Look end-on from the N-term; does the shape look familiar? \_\_\_\_\_

What is the typical H-bond pattern for the first half of the helix (res. 164-170)?  $i$  to  $i+$  \_\_\_\_\_

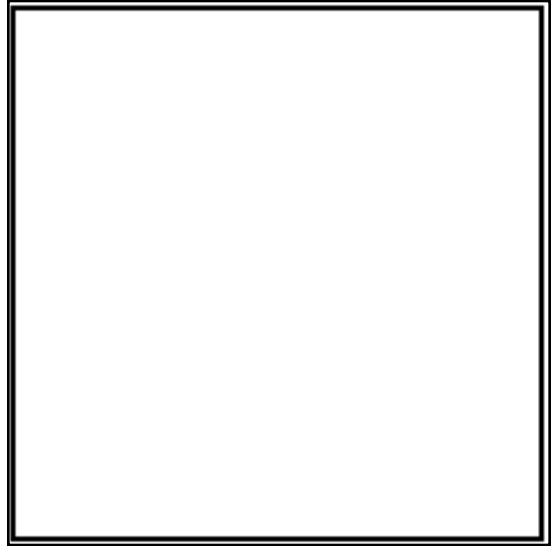
Now turn to look end-on from the C-terminal.  
Sketch the pattern of backbone in box at right.

What is the typical H-bond pattern for residues 171-177? \_\_\_\_\_

Turn on side chains and add  $C\alpha$ - $C\beta$  vectors to your sketch. What is different about 3-10- versus alpha helix that might be of use here in this protein?

The N term part is quite classic alpha-helix; it even starts with an Asn, again, which is the commonest side chain in that position, and has 2 negative charges in the first turn (also typical). This is one of the longer pieces of 3-10 helix in the data bank, but it does hold to the usual feature of short 3-10 in occurring at the C-term end of an alpha-helix. Comparing the alpha half with the 3-10 half, for which one are  $C\alpha$ 's in successive turns lined up parallel to the helix axis? \_\_\_\_\_

For which one are the H-bonds approximately parallel to the helix axis? \_\_\_\_\_



### 3. Helices on the Ramachandran plot

Go to the MolProbity site (<http://molprobity.biochem.duke.edu>) and fetch the 2MLT structure from the PDB. On the main page, choose "Analyze geometry without all-atom contacts" and run with the defaults.

Click to view the Ramachandran-plot kinemage. Animate three steps, to the Pro data, where the only points are in the \_\_\_\_\_ region of the plot; then one more step to the pre-Pro, with points in the \_\_\_\_\_ region. Animate back to "All data", and click to identify the data point that lies farthest from the main cluster: \_\_\_\_\_. It is one of the chain termini, so less constrained. The other, to the left of alpha, is \_\_\_\_\_ A 11, on one side of the helix bend. Use "Edit/Find point" with markers turned on to locate residue B 11. Is its conformation more helix-like? \_\_\_\_\_ A conclusion, then, is that even as a dramatic bend as this one can be formed with only rather subtle local changes in phi,psi values. Close the Rama window, continue to the main page, and log out of MolProbity.

Open file [general-noGPIVpreP\\_whbkg.kin.gz](#) (9MB) in KiNG. It is a general-case Ramachandran plot from 4400 high-resolution files, yielding over half a million residues with backbone B-factors < 30. View2 zooms in on the "comet" shape in the alpha region. The 3-10 helix in 2CYP has phi,psi values of about -68,-12. Turn on Tools/Show xyz coordinates, and click on datapoints to locate ones near those values. Where do they lie relative to the main alpha cluster? \_\_\_\_\_ relative to the "comet" tail? \_\_\_\_\_ There is a lot

of local detail in such a plot that no one yet fully understands.

In the view3 closeup, pick a datapoint at the center of the most highly populated cluster; its phi,psi values are \_\_\_\_\_,\_\_\_\_\_. Ideal alpha-helix is often cited as -60,-40, which is not too far away. The official IUPAC-IUB value (from 1970) is -57,-47; find where that lies relative to the cluster: \_\_\_\_\_.

Only one point in 2000 is outside the outer contour, and most of those are close to the allowed regions. Click to identify one of the 3 data points near the middle of an ellipse that outlines a drastically disallowed steric clash: \_\_\_\_\_ in file \_\_\_\_\_. One of those cases is a clearly misfit peptide out of density, while the other two are basically a nomenclature problem: an autocatalytic active site modification in related ammonia lyase enzymes that puts a covalent bond between adjacent peptides - these should have been flagged as "het" groups in the PDB file but were not.

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This page last updated 20 January 2011.