BCH222 :: Structure of Biological Macromolecules
Helix Worksheet

Since hydrogen bonds are crucial to understanding helices, and important to much of the later work in this course, 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. Refer also to the page of IUPAC-IUB definitions handed out in class.

1. A classic alpha-helix
Open file 2hmqHlx.kin (24KB) (helix B from a hemerythrin subunit) in KiNG.

Confirm for yourself that this helix is righthanded. 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 n to n+ _____).
List the other 11 backbone atoms that complete its H-bonded loop:
O_n _____ _____ _____ _____ _____ _____ _____ _____ _____ _____ _____ H_{n+4}.
How many n to n+4 H-bonds are shown for this helix? _____

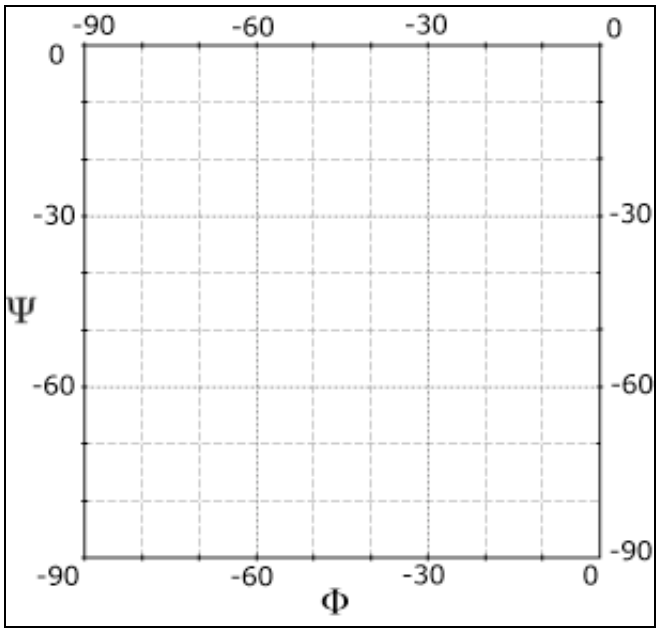
Choose View3, which looks at one turn of helix end-on from the N-terminus, and turn off labels, H-bonds, and N and O atoms. In the box at right, sketch the pattern formed by the backbone in this view:

Turn on the side chains. Show on your sketch some of the Cα-Cβ bonds.
Do they extend out radially, spiral clockwise, or spiral counterclockwise? _____
How do they look viewed from the other end of the helix?
_____

Turn off side chains and on labels again. In the end view, decide which Cα of the top turn is most exactly in line with 55 Cα. _____
Count between the two: there is an interval of _____ residues in _____ turns, so the pitch is _____ residues per turn.

Is the H-bonding regular in the first turn of the helix? _____ (use View5)
Find the first residue that makes a helical H-bond: _____ _____ . It is half-in and half-out of the helix, and is called the helix N-cap residue.
Find the three NH groups in the first turn that cannot make helical H-bonds. Turn on side chains. What atom of what residue satisfies one of those bonds? _____ of _____ _____

Turn on "Measure angle & dihedral" under the Tools menu. Practice measuring dihedral angles along the backbone, checking agreement with the ϕ,ψ data table. [Remember that the dihedral value shown on screen is the rotation around the bond joining the two central atoms of the 4 last picked and highlighted.]
Plot the phi, psi values for residues 41-65 (use the ϕ,ψ data table).).



Do they cluster around the helical value of -57, -47 given in the IUPAC-IUB definition? _____
By IUPAC rule 6.2, what would be the first and last residues of helix B? _____ _____
By their rule 6.3, what would be the first and last residue?
_____ _____

The header for the PDB file lists 41-64; a generous definition based on Cα positions would give 40-66. Each of these definitions suits different purposes; we have found the Cα definition correlates best with amino-acid preferences (such as for N-cap or C-cap positions.)

2. Helix caps
Study kinemage II.A_hlxCaps.kin from Anatax II.A to recognize the N and C-cap residues, the characteristic N-cap and cap-box sidechain-backbone H-bonds, the backbone H-bonds of an Lα Gly C-cap, and the "hydrophobic staple" pairs when present.

3. 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.

4. 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 residues 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? _____

5. 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?

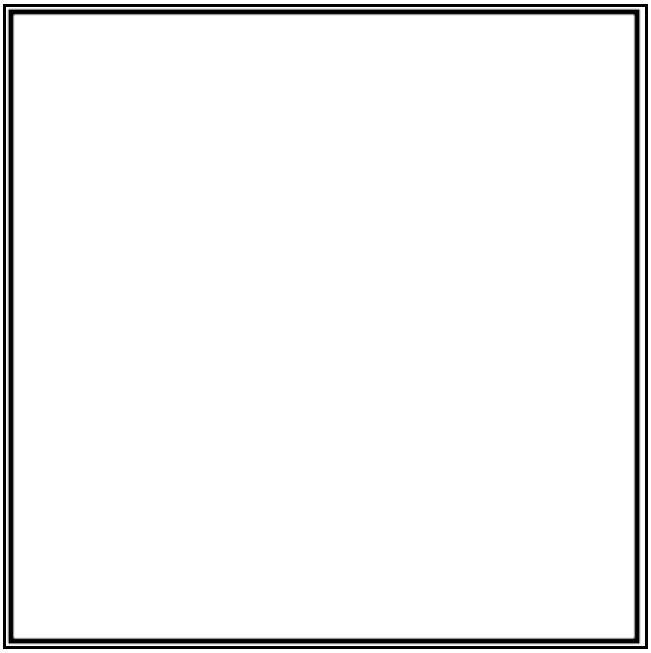
_____

What is the typical H-bond pattern for the first half of the helix (res. 164-170)? n to n+ _____

Now turn to look end-on from the C-terminal; sketch the pattern of the backbone:
What is the typical H-bond pattern for residues 171-177?

_____

Turn on side chains and add Cα-Cβ 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 longest 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 Cα's in successive turns lined up parallel to the helix axis? _____
For which one are the H-bonds approximately parallel to the helix axis? _____
Relate that to the 3 versus 3.6 pitch.

6. All-atom contacts for an alpha-helix

2erl.hlxContacts.kin (76KB)

This kinemage shows all-atom contact dots for a classic piece of alpha-helix in a very accurate structure (at 1.0 Å resolution, with all H atoms refined) for the insect pheromone ER-1, a small ss-rich helix bundle. Turn off the buttons marked "vdw contact" and "small overlap", to see dots only for the H-bonds (in pale green); they form intersecting lens shapes, because the favorable H-bond interaction pulls them closer than van der Waals distance. Choose View2 to look at the helix N-cap; that first H-bond mimics a helical one, but is actually made by the sidechain _____ atom of _____ _____ .

Choose View3 to look end-on at the helix C-cap, where the main chain makes an abrupt turn at _____ _____ .
If the helix continued, the NH of residue 10 would bond back to the CO of 6 and the NH of 11 to the CO of 7 (normal n to n+4 pattern), but here NH 10 bonds to CO _____ and NH 11 to CO _____ .
This is a very common way to end a helix, but which amino-acid would normally be used? _____
Measure the phi _____ and psi _____ of Cys 10 to see why. (Remember that "measures" is on the Tools pulldown menu, and you click on 4 successive atoms to get a dihedral angle.)

Choose View4 and turn "vdw contacts and "small overlap", and "H's" on, to see the set of interactions surrounding a peptide in the middle of the helix. What atom _____ of this peptide makes a good van der Waals contact with what atom _____ of the side chain on the turn above it?
Measure the chi1 angle of that side chain (defined by the N, Calpha, Cbeta, Cgamma atoms): _____ ; not surprisingly, that is very close to the commonest chi1 angle on helices.

Notice that all the backbone CO bonds splay outward a bit from lying parallel to the helix axis. To see what pushes them out, turn off vdw and H-bonds to see only bumps (there are not many, since this is a very good structure). At each residue thru the helix middle there is a yellow patch of small overlap between which atom types? _____ and _____