

Name: _____



Worksheet 2: Handedness & Amino Acid Roles

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Kinemage file -- [c1Basics-A-KiNG.kin](#)

Study the kinemages in this file, following along on this worksheet and answering its questions. Use chapter 1 of the Branden & Tooze textbook for background. Practice dragging back & forth slowly with the mouse to rotate the molecule and see it as 3-dimensional, and clicking on an atom to identify it. Turn things on & off with the button boxes. To animate, either click the “Animate” button or press “a” on the keyboard. For a closer view, turn on “Pickcenter”, click an atom, and zoom in on the scale scrollbar (alternatively, center with a right-click). In kinemages 1 and 6, move the rotatable bonds with the horizontal sliders provided. (If you need additional help in using the KiNG program, review the tutorial file [Demo5_4a-KiNG.kin](#).)

Kinemage 1

Kinemage 1 illustrates a 5-residue fragment of polypeptide chain, to show its geometry and atom names and to allow rotation of one residue’s worth of the variable dihedral angles Phi, Psi, and Chi. Hydrogen atoms (in brown) are included, so this illustrates the full chemical geometry of a protein. Turn them off (with the “H” button box) to see the heavy atoms alone, more typical of what is directly known for most crystal structures since hydrogen atoms diffract x-rays very weakly. Atoms are depicted in this type of “skeletal” or “stick” representation as the intersections or ends of lines which show the chemical connectivity of the molecule. In this case, non-carbon atoms are shown as colored balls (red for O and blue for N), giving a partial “ball&stick” representation. For a skeletal model, one aspect of the basic physical nature of the molecule - namely the chemical bonding arrangement - is explicitly clear, and the model does not hide parts of itself; on the other hand, another important physical aspect - the bulk and the steric constraints - can only be inferred by the relative position of the atoms. Choose View3 (on the VIEWS pulldown menu) and turn on the “spheres” button temporarily to see a rough space-filling representation, which has the opposite properties of showing how big the atoms are but of hiding things that are inside. Note that in Mage and KiNG you can click on a sphere and identify it.

Can you turn the H atoms on & off in this representation? _____

Now turn off the spheres and go back to View1. Selected atom labels can be turned on, or the angle labels turned off, with the button box controls on the right side of the screen. They identify the atom names along the backbone, or they label the variable dihedral angles that determine conformation. (Of course, an atom can also be identified just by clicking on it, but then the residues will have specific numbers, such as 45 for the Phe, rather than being called n, n+1, etc.) The dihedral angles Phi (around the N-Calpha bond) and Psi (around the Calpha-C bond) of the central Phe residue can be

changed using the Tools: Specialty: Suite Rotation. The Suite Rotation box has one dial and a set of axis choices. Dragging the dial “hand” changes the angle freely, clicking in the + - boxes to right or left of the dial will change the angle by 0.1° degrees at a time for fine control. A double-click on the dial resets it to its original angle. One angle value below the middle changes as you change the angle, while the other stays at the original value. As you change one of the angles, look for positions at which atoms on either side are too close together (that is what determines the allowed conformations). For instance, try setting phi to about 0 and psi to about 180. Does that look possible? _____
What bumps? _____

The central Phe (residue n) is shown in cyan with a full side chain and a green ball at its C α . The C α -C β bonds are colored seagreen, both to better illustrate the tetrahedral geometry of the C α atom and also to point out that the C β position is fixed with respect to the polypeptide backbone. Were it not for the unique amino acid glycine which lacks a C β , one would probably consider the C β as part of the main chain rather than the side chain. View2 looks down the C β -C α bond, showing that the starting conformation is close to one of the three staggered positions of Chi1 (the first side-chain dihedral angle) expected from simple steric considerations around a carbon-carbon single bond: $+60^\circ$, -60° , or 180° . What is the actual Chi1 value? _____
(One can return to the startup view by choosing View1.) Try rotating Chi1 and Chi2.

Choose “Kinemage #2” in the upper-right panel (which scrolls if there are more than 3 or 4 kinemages in the file).

Kinemage 2

Kinemage 2 animates disulfide formation in an engineered mutant of T4 phage lysozyme. Click repeatedly on the onscreen button labeled “ANIMATE” (or press the ‘a’ keyboard key) to change between the reduced form, with SH Cys, and the oxidized form, in which the Cys sulfurs are covalently bonded into a disulfide. Sulfur atoms are shown as gold balls, and H atoms (only present in the reduced SH form) in brown. Often there is essentially no backbone movement when a disulfide forms, but in this case two separate domains of the T4 lysozyme structure hinge to come somewhat closer together when the SS bond forms; choose View2 to see this motion. View3 is a closeup of the SS bridge, which is in the righthand hook conformation, one of the two commonest conformations for disulfides; the other common one is the lefthand spiral. For the LH spiral the 3 dihedral angles across the SS are -, -, - while for the RH hook they are +, +, - (the handedness is named after the central dihedral around the S to S bond). We’ll practice measuring dihedrals in kinemage 6, but to try this one choose “Measure angle & dihedral” on the TOOLS menu and click successively on the C β , S γ , S γ' , and C β' of the SS; the dihedral angle is the last number shown: _____.
Try it in the opposite order, which should give the same number.

Kinemage 3

Kinemage 3 shows the Calpha backbone of dihydrofolate reductase (DHFR), with each type of side chain on a separate button. View1 shows the central beta sheet from the side. View2 is an edge view, showing the twist of the beta sheet. Click “Animate” to switch among the four groupings of side chains (use View2) and see how they differ in overall location. The strongly hydrophobic residues Cys, Phe, Ile, Leu, Met, Val, Trp (in gold) predominantly pack against each other to form the inside core of the protein, while the permanent charges Asp, Glu, Lys, Arg (+ in skyblue and - in pink) are nearly always on the outside. The neutral and polar groups (in cyan) are more evenly distributed, with a more modest preference for the outside. Pro (green) is also usually outside, even though its side chain has no polar atoms, since it is so good at ending helices and turning corners. Gly (labeled with a “G” at the Calpha) has 3 different sorts of roles: it occurs a) at corners or at ends of pieces of secondary structure (often with otherwise disallowed conformational angles), b) at especially tight contacts inside a protein, and c) where flexibility of motion is needed. Many amino acids have roles at particular positions in specific secondary structures. Gly is by far the commonest amino acid at helix C-termini; to see Gly 86 (green G label) ending an alpha helix, click in the hypertext jump command in the text window; it looks like `*{Kin3, view3 ... }*`. Turn to view from the helix end, to see that at this typical Gly “C-cap” the backbone turns insideout relative to the normal pattern in helix; the peptides on either side of the Gly both make H-bonds to the previous helical turn, but in the wrong order. The N atom of Gly 86 is too far (3.62 Å) to H-bond with the usual n-4 CO; how far is it from the n-3 CO?

_____ Å

Ser 77 is the “N-cap” residue at the start of this same alpha helix. The N-cap residue is defined as the one whose preceding peptide is out of the helix but whose following peptide is in the helix. Turn the image around, and perhaps zoom it smaller, to see that the backbone past the Ser N-cap follows the helical spiral, while the backbone before it goes in a completely different direction; the Calpha of the N-cap residue is where that abrupt change takes place. Ser, Thr, Asn, and Asp are all very common in N-cap positions, usually making an H-bond from the side-chain oxygen to a free backbone NH group in the first turn of the helix, as in this case (H-bond shown in purple). Interestingly, Gln is the least preferred residue in the N-cap position (the extra methylene group in its side chain, vs. Asn, does not allow the side-chain oxygen to get into the correct geometry for the H-bond), which emphasizes that residues whose properties look superficially similar do not always play equivalent roles in protein structure. Gln, on the other hand, is especially common in exposed positions in the middle of helices; to see one in such a place, choose “Find” on the “Edit” pulldown menu, enter “gln 102”, and accept. Zoom smaller and rotate the image, to see that the Gln is indeed exposed. Pro prefers corners in the backbone, many of which are at one end of a piece of secondary structure. To see Pro 25 at the beginning of a helix (at top) and 3 other Pro (bottom) at the ends of beta strands, click at the

hypertext jump which begins: `*{Kin 3 v=4 ...}`?. Which position is Pro 25 (Ncap, Ncap+1, etc.)?

Arg and Lys are another pair of similar residues with often-divergent roles. Click on the hypertext in the text window which looks like: `*{Kin 3 v=5, alloff ...}` for a close-up of Arg 158: the aliphatic part of its side chain makes hydrophobic contacts to the Trp 133 ring, while the positively charged guanidinium group at its end reaches over to interact electrostatically with the negative helix dipole at the C-terminus of a helix and also H-bonds to one of the free backbone CO groups. Zoom out to see that helix; its Ncap is residue _____ (for a double blank, please give the residue name and number). [Remember that the cap residue C α is the dividing point between peptides clearly in the helix and peptides clearly not in the helix.] An Arg guanidinium can make as many as 5 planar H-bonds to oxygens and often does so, therefore tending to have a well-defined, tied-down position. Lys, in contrast, makes H-bonds with its very freely rotatable NH₃ group, which is often quite mobile in proteins and interacts well with bulk solvent. Of the 7 Lys in DHFR, 2 of them were so mobile that only a few side-chain atoms could be located in the crystallographic structure: use “Find point” on the edit menu to center on Lys 76, which is only shown out to its C β since the rest was mobile and invisible.

The main function of the large hydrophobic residues is to form hydrophobic cores; the different types pack together in distinctive geometries and have different preferences for backbone conformation. Click on the hypertext jump: `*{Kin 3 v=6, ...}` to see 4 aromatic side chains in a row (Y151, F153, & Y111 on the beta sheet and W30 from a helix), some interacting with their rings perpendicular (the more common arrangement) and one pair with stacked rings: _____ and _____. Click in the hypertext jump, `*{Kin 3 v=7, ...}` to see a set of 8 Ile and Val on both sides of the beta sheet. Of the aliphatic side chains, the ones with branched C β s (Ile, Val) prefer beta sheet, while Leu and Met prefer alpha helices. Individual residue types can be toggled on one at a time in this kinemage - try that, back in View1 (note that buttons are labeled with both one-letter and 3-letter amino acid codes). If all amino acids were equally represented in DHFR, there would be approximately 159 residues/20 = 8 of each. Amino acids that occur much more often than that in DHFR include Asp (14), Ala (13), and Ile (12). What is the least common hydrophobic amino acid in DHFR? _____ with _____ examples

Kinemage 4

Kinemage 4 has backbone in white, and shows 27 superimposed examples of leucine side chains from 11 protein structures at 0.9 to 1.2 Å resolution (the button for each example gives its 4-character PDB code and residue number). Only a few combinations of side-chain “Chi” dihedral angles occur in these very accurate structures; such clusters of preferred conformations are known as “rotamers”. All of them have one of the three possible staggered values for both Chi1 and Chi2 (near -60°, near 180° or trans, or near +60° degrees). Leu is surprisingly strongly constrained, with over 90% in one of just

two rotamers: either Chi1=-60,Chi2=trans (examples shown in gold) or Chi1=trans,Chi2=+60 (in cyan). To understand better where the constraints might come from, turn off the minor rotamers (in pink), turn on “H”, and move around.

Kinemage 5

Kinemage 5 shows in 3-D the di-iron center in ribonucleotide reductase, which produces a catalytically important free radical on the neighboring tyrosine (upper left). Each Fe has 6 ligands arranged octahedrally, including the bridging oxygen ion, a bridging Glu, waters, and other carboxyl O's and histidine N's (marked with color-coded balls). What is the shortest distance for one of the O-Fe bonds? _____ Å To see the local environment of these side chains within the mostly-helical protein subunit, choose View2 and turn on “Calphas”.