1. Go to the Protein Data Bank (google it)
2. Search on the site for PDB ID “1SNC”, this should bring up a protein structure with a short strand of DNA.
   1. What is the name of the protein?

Staphylococcal nuclease

* 1. When was the structure deposited into the PDB?

1989-07-21

* 1. What method was used to obtain the structure?

X-RAY DIFFRACTION

* 1. What resolution is the structure? What does resolution mean?

1.65 Å

Resolution means the ability to separate a chemical compound or mixture into its constituents rather a single fuzzy dot.

* 1. What is the title of the paper from which the structure is detailed?

The crystal structure of the ternary complex of staphylococcal nuclease, Ca2+, and the inhibitor pdTp, refined at 1.65 A.

1. Make a PNG of the protein shown with “sticks”
2. You can select parts of the protein via their secondary structure assignment. In the command window type “select ss s” to select the beta sheet residues. Rename the selection to beta and color it to a blue. Show as a cartoon.
3. Select the alpha helix residues “select ss h”. Rename the selection alpha and color red. Show as a cartoon.
4. Select all the other residues (loops and unassigned) with: select ss l+””. Rename the selection to other and color it magenta. Show as a ribbon.
5. Displace the sequence and find the Calcium atom. Select it and color it yellow. Show as a sphere.
6. Create a PNG with each secondary structure colored as described above.
7. Display only the beta sheet residues.
   1. Which element is the donor for the hydrogen bonding that stabilizes the beta sheet structure and which element is the acceptor?

Oxygen is the hydrogen acceptor and nitrogen is the hydrogen donor.

* 1. I18/T22 and Y91/E75 are donor acceptor pairs in the backbone. What is the distance between the atoms forming the hydrogen bond for these two pairs?

I18/T22: 3.0Å (1 hydrogen bond).

Y91/E75: 2.75Å (on average; 2 hydrogen bonds, 2.7Å and 2.8Å each)