When the online visualization web page is first launched, the default display for the protein will be a backbone format shown to the right. In backbone, only the alpha carbon of each amino acid is shown with these alpha carbons connected by a thin line. Backbone format is able to be turned on and off using the **backbone on** and **backbone off** commands. When these commands are entered, the text box below the input line says that the jmol display has received the command, calling it a script, and completed it.

There are two other main formats that can be used when modeling a protein. These are the spacefill format and the wireframe format. To display a protein in spacefill format, enter the command **spacefill on**. Spacefill displays all the atoms in a file - each represented by a single sphere. Spacefill can be turned back off using the **spacefill off** command.

The third format, wireframe, can be turned on by using the **wireframe on** command. In wireframe format, each atom is included and the bonds between the atoms are represented by connected lines. Again, wireframe can be turned off using the **wireframe off** command.

The thickness of each of these three displays can be changed simply by adding a number after the command. For example, instead of entering wireframe on, use the command **wireframe 200**. This will allow the wireframe format to remain but it is displayed with much more thickness. The same is true for both backbone format and spacefill format.

More than one of the three display formats can be seen at the same time. For example, if a backbone of 300 is turned on using the **backbone 300** command and then the **wireframe on** command is used, the standard wireframe format will be displayed along with the backbone of 300 - both being shown at the same time.