viewMOL-by Nitesh Turaga

Readme:

Please go to www.vpython.org and install the file based on your computers specifications. There is a clear instruction on the opening page on which version to choose and install. It will guide you smoothly. You would have to install python 2.7.1 and/or a newer version. The program mainly works on vPython and python’s inbuilt Tkinter.

NOTE: The amino acids in view are implicitly indicated. The atoms in yellow are “always” meant to be CARBON atoms and the cyan and the green cylinders are meant to be the NH2 and COOH bonds.

The program is meant to be educational and also meant for research purposes. The protein files need to be downloaded from [www.pdb.org](http://www.pdb.org), in which you can type in the name of the protein and download a PDB text file on to the DESKTOP. The program will not function on wrong/ improperly placed PDB files.

NOTE: The PDB text files need to be on the desktop.