To do this homework assignment I used Chimera to model proteins. Initially I felt that Chimera had a pretty steep learning curve, but in hindsight I realize that the curve is nowhere as steep as learning to use pymol, comparing both to the ease of use of rasmol. The program’s stability is questionable I installed both the Linux and windows version. I noticed the Linux version had a lower frame rate, but there was also a disclaimer on the website about video driver with the Linux version. Most importantly, under Linux I was able to make the program crash (segmentation fault), while trying to do surface rendering. I tried to repeat my steps as best as I could recall, but was unable to make it seg fault again. This led me to try the windows version which has a considerably higher frame rate, and I was unable to make it crash.

The biggest issue I noticed is that there is no obvious way to select a residue with the mouse. After searching the manual I discovered that you must control click to select a residue, and this solved the problem but it was still rather counter-intuitive. The command line was also very little help. Pymol, while complicated, has a console help menu and information about commands, Chimera pointed all help issues to the internet, which was not only annoying, but also could make it difficult to work offline. Was not very forgiving as it was either menu clicking or command line both of which lack a lot of polish that would come with commercial software, it was very apparent that the GUI was put in as minimally as possible and that appropriate way to use the program was through the command line. Another problem is that the frame rate would sometimes drop significantly while rending surfaces or very high quality model pictures (specifically using the publishing presets). I have experienced bother very slow and unchanged frame rates from the normal ribbon modeling.

One of the things that was most appealing was the image quality. The surfaces were rendered very well, and looked very nice compare to other programs. One of the large pluses I encountered was the powerful selection abilities. While this interface was rather clunky, it allowed for set selection operations as well as selecting base don classifications like polar, negative charge, backbone, functional groups and many other options. This made it very easy to take a pdb file and select certain properties and isolate them and look at them very quickly.

Overall, I think this program is not bad, but I am not sure it is a strong candidate to replace rasmol and/or pymol. It does have some powerful capabilities, but I doubt that the interface is ready to hook into something like a wiimote. Once you get used to the program, though, the interface becomes less awkward (though still not very intuitive) and the some the power of the program shines. I personally would consider it as a replacement to pymol/rasmol, for personal use, especially as the program improves.