Name:

1. Download PyMol to your computer from the OIT downloads page

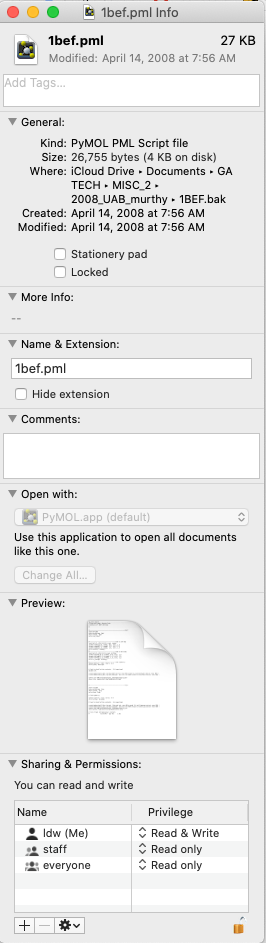
For this class we will be extensively using a program called [PyMol](https://www.compchems.com/an-introduction-to-pymol/#what-is-pymol). You will need this program for many of the problem sets.

Before you start the PyMol install, save the license to a known directory on your computer. Get the license [here](https://williams.chemistry.gatech.edu/course_Information/biochemistry/misc/pymol_license_2024.lic).

Download PyMol from [this site](https://www.pymol.org/#download). You will need the license to complete the installation.

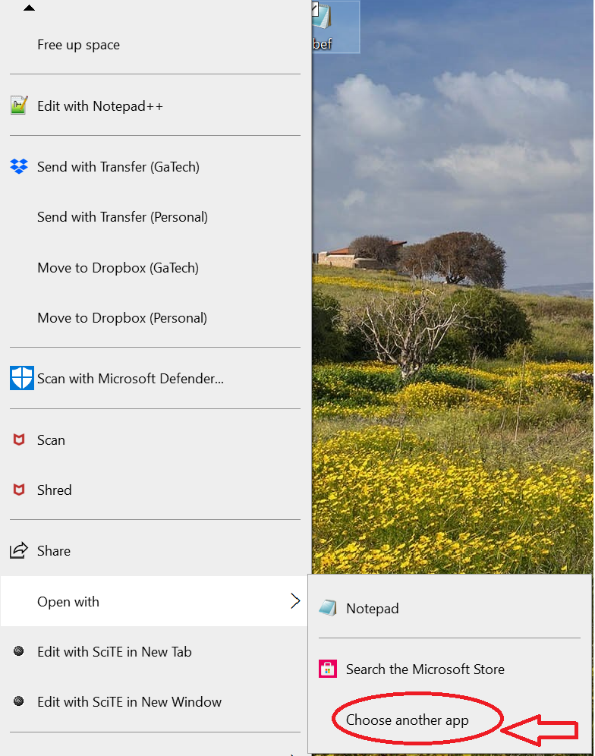
1. Launch Pymol.
2. Set your computer so that when it sees file.pdb or file.pml, it runs Pymol.

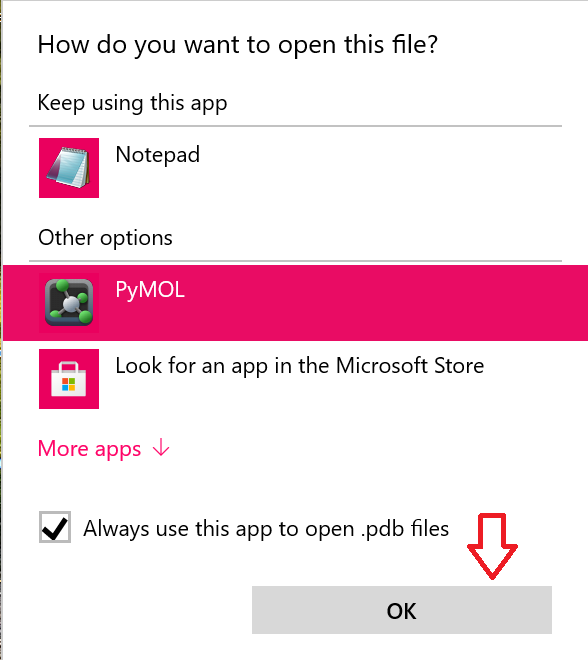
(i) For a Mac, click on the pml file in this directory (atp\_mg.pml), then Finder -> File -> Get Info and set “Open with” to PyMol (use this application to open all documents like this one). Do the same for atp\_mg.pdb.



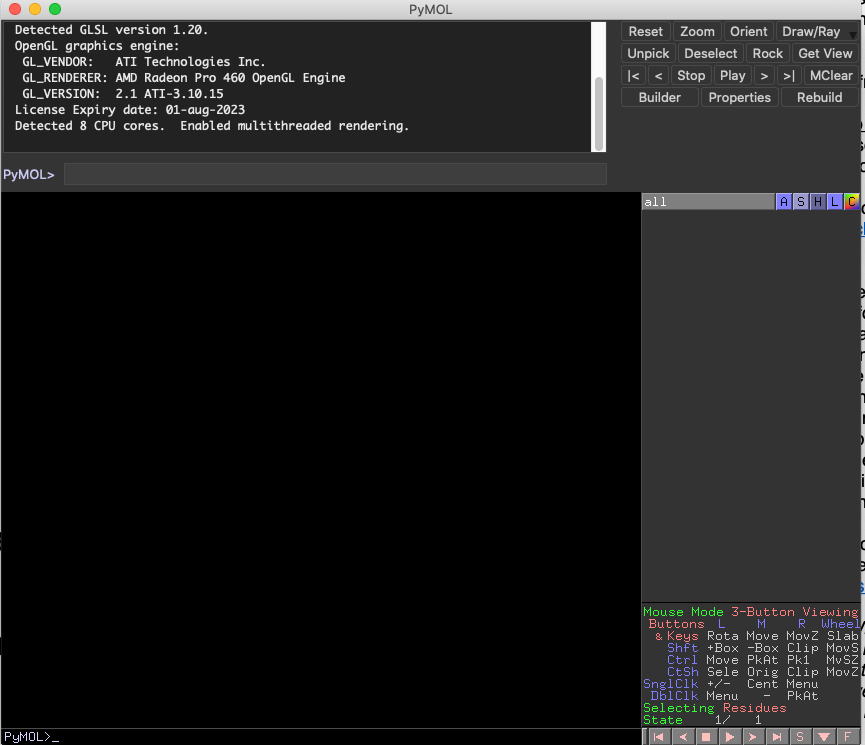


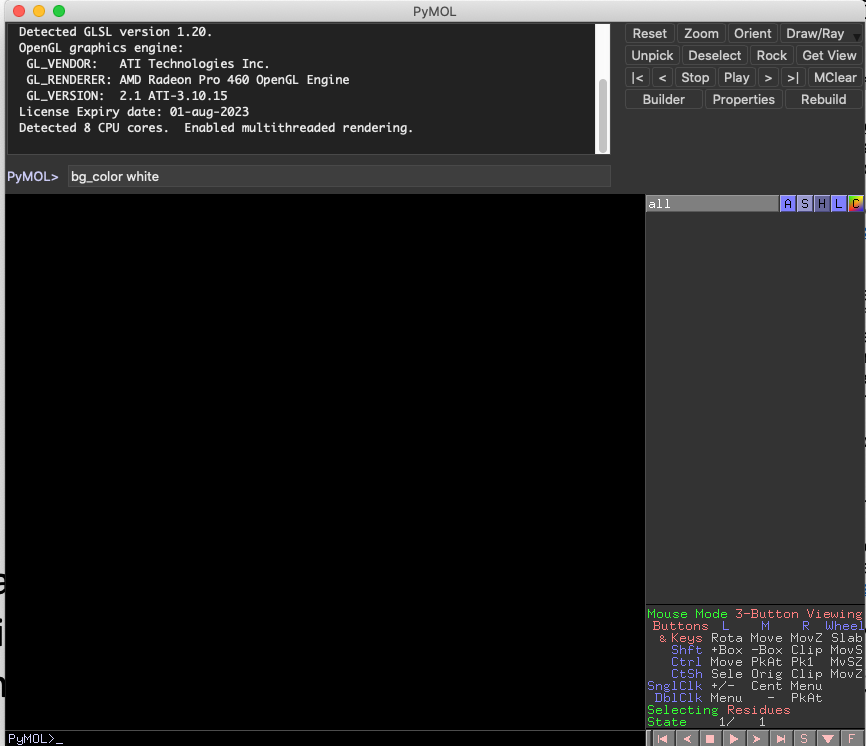
(ii) For a PC



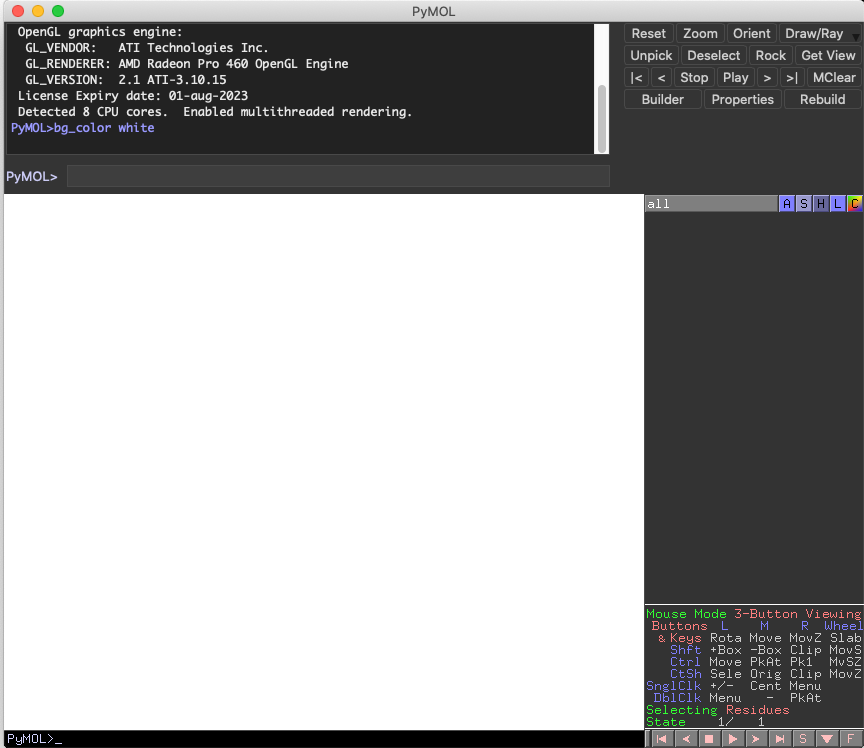




1. Launch PyMol by double-clicking on application icon. Pymol should look like this.
2. Set the background color to white.  
   In the command line type

 “bg\_color white”



1. PyMol should look like this.

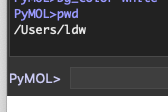
Set the background to your favorite color  
 bg\_color cyan

bg\_color pink

or whatever you like

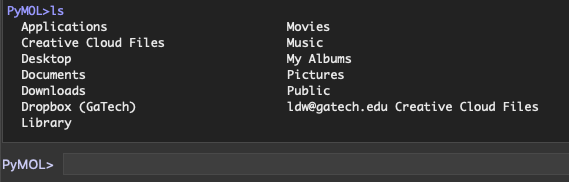
1. Type

“pwd”

(this command shows your present working directory and can be very useful when looking for PyMol output files).

1. Type

“ls”

(This commands lists the contents of the directory and can also be use when looking for lost files.)

1. type

“cd *some directory*”

(This is the command you can use to change the directory. You might not need this command much.)

For more on cd look here: https://www.rapidtables.com/code/linux/cd.html

1. Set the mouse, to whatever kind of mouse you are using.  
     
     
     
   For a trackpad, use “one button mouse”.



1. Use PyMol to visualize a protein from the PDB (Protein Databank).

Type “fetch 6M1D” in the command line.

This command downloads Angiotnesion Converting Enzyme 2 (ACE2) from the PDB. This enzyme is part of the **Renin-Angiotensin System (RAS)**, which controls blood pressure and fluid balance. ACE2 converts **angiotensin II** (a potent vasoconstrictor that increases blood pressure) into **angiotensin-(1-7)**, which has the opposite effect.

1. Rotate the ACE2 around, zoom in, etc.  
   Take two screen shots and paste them below.
2. Type “reinitialize” in the command line. This command deletes everything and brings PyMol back to initial conditions.
3. Drag and drop atp\_mg.pml (not atp\_mg.pdb) onto the main PyMol window. This script will set the background white and load the coordinates of ATP. [**Important** **Note for PC users**. You must first extract the zip file, before you load it into PyMol. Please check on the top of the course homepage for instructions on how to extract zip files.]
4. rotate the structure around, zoom in, etc,   
   take two screen shots and paste them below,