CHemical Energy Wise Decomposition (CHEWD)

CHEWD plugin can be downloaded from

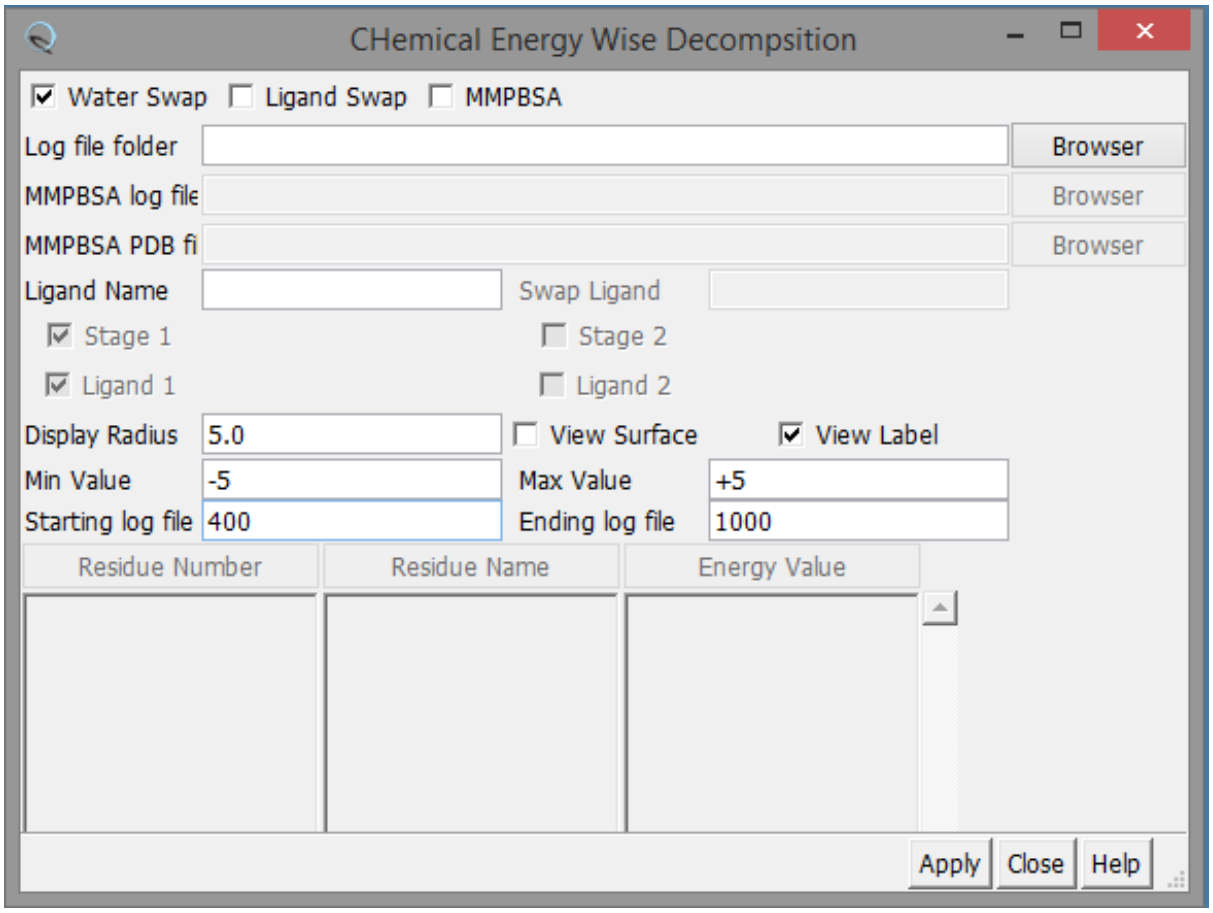
https://github.com/saadraza128/CHEWD

For installation in Chimera:

Download the folder Chimera-CHEWD .

Open Chimera, go to favorites tab > Preferences. Change category to Tools. Click Add, then browse and select Chimera-CHEWD. Click save.

The plugin will be located in the menu Tools | Utilities CHEWD. Clicking on this option will open the below GUI dialog:

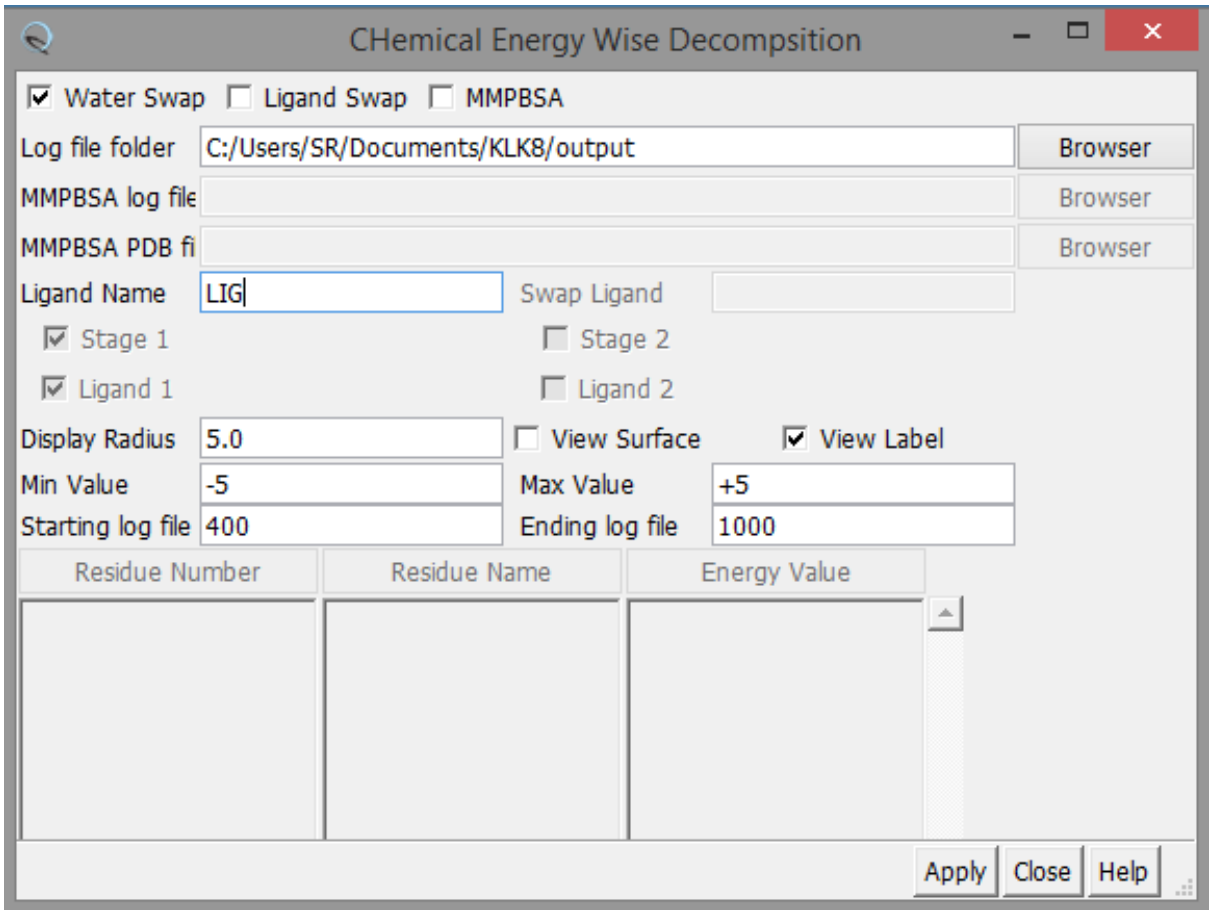


For Waterswap unzip the output folder in the example directory.

Click Browser to open a file browser. Navigate to and select the example output directory containing all of the example results.

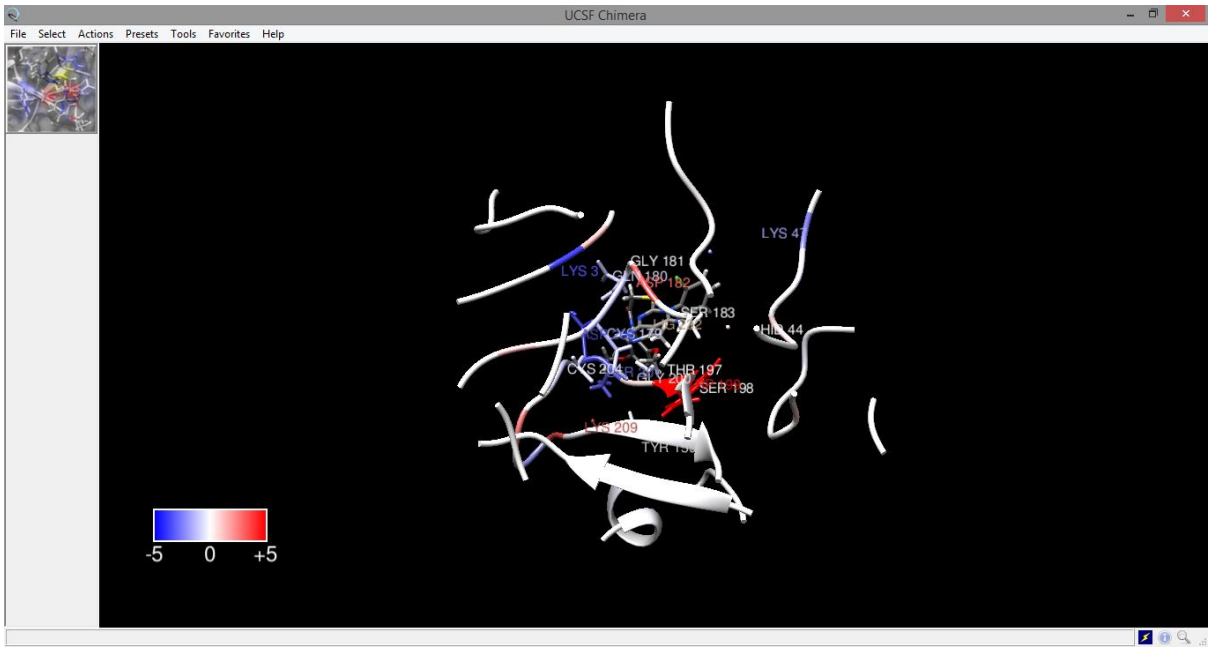
Next, make sure that the Water Swap box is checked at the top of the dialog. This puts the plugin into Waterswap mode. Next, set the Ligand Name according to your topology file (In this example we set it to LIG).

Doing this, you should see that the dialog looks something like this;



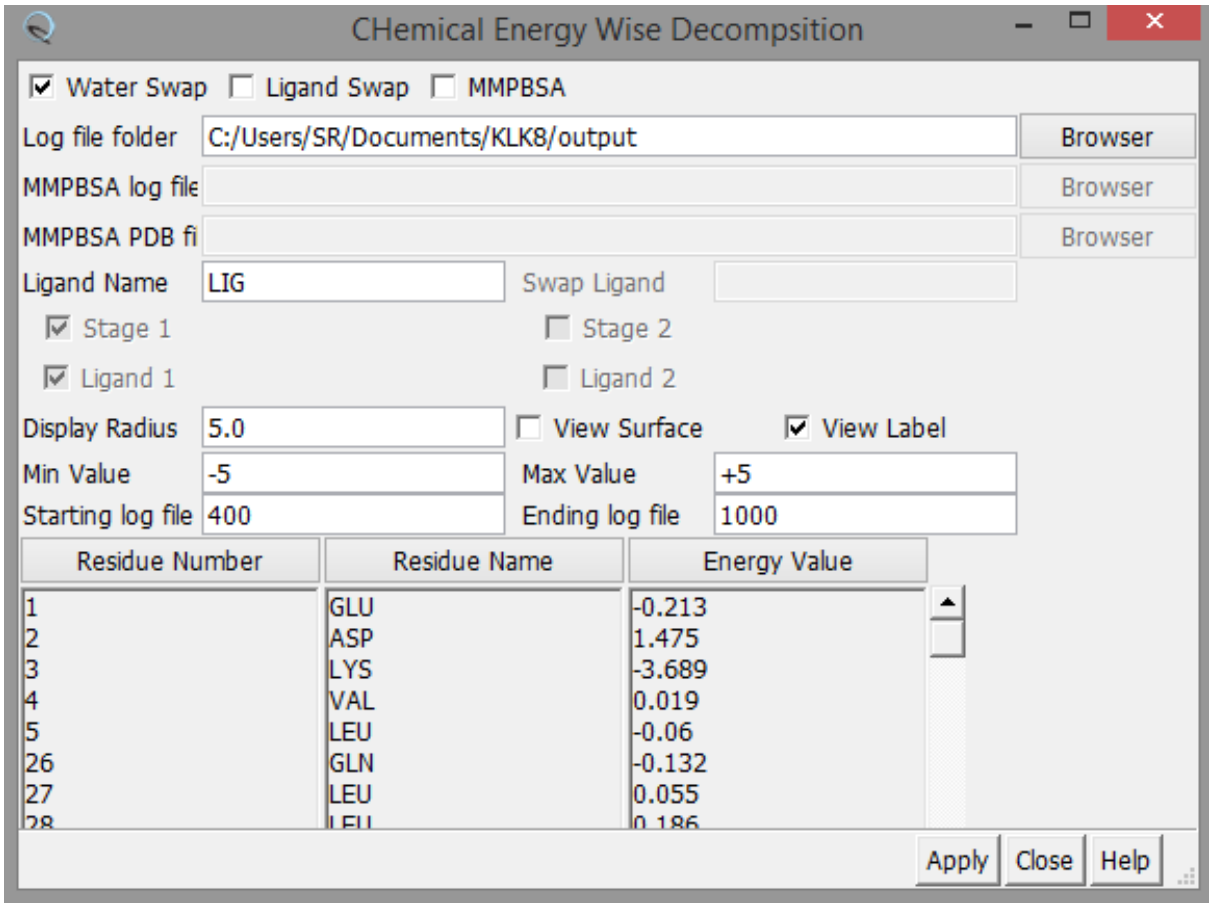
Now click Apply. This will take a while to load up all of the output.

Once loaded, you should see that the main chimera window looks something like this;



This shows a cutout of the full protein-ligand-water system, showing only the protein and ligand atoms that were mobile during the waterswap calculation (everything within 15 angstroms of the swapped ligand). The residues are colour-coded according to their preference for either ligand or water. Red shows a preference for water, with stronger colours indicating a stronger preference. Blue shows a preference for ligand, again with a stronger colour implying a stronger preference.

The exact values of these free energy component preferences are shown in the CHEWD dialog, which looks something like this;



For MMPBSA the load the “FINAL_DECOMP_MMPBSA.dat” in log file tab and “KLK8-complex.pdb” in the pdb file tab. The decomposition file has been written using MMPBSA.py of amber simulation package. This log output was done by setting the verbosity to 1 in the input file for MMPBSA.py.