## <u>Calculation of Q-scores from Command Line – NEW (Simpler method)</u>

First, download and install UCSF Chimera and the MapQ plugin: <a href="https://github.com/gregdp/mapq">https://github.com/gregdp/mapq</a>

Then, Q-scores can be calculated from the command line using a python script that is in the zip file downloaded when installing the MapQ plugin. The command has the following format:

```
python mapq_cmd.py [path to Chimera] [path to map] [path to model 1] [path to model 2]
[path to model ...] np=N
```

## Example:

```
python mapq_cmd.py ~/_mol/Chimera/bin/chimera ~/Dropbox/_data/Ferritin/k175/k175_fi.mrc
~/Dropbox/_data/Ferritin/k175/3ajo_f.pdb np=4
```

## Notes:

- the np=4 argument is optional; if left out, a single process will be used.
- [map to Chimera] is just the path where Chimera is installed, not the actual binary itself

The output should be something like this (will vary slightly depending on whether multiprocessing was used or not, and whether more than one model was specified):

```
O Scores:
 - map: emd_20026.map
 - mol: 3ajo.pdb, chain: _all_
 - sigma: 0.50
- mind: -0.061, maxd: 0.109
- atoms to do: 1714
- path: /Users/greg/Desktop/Chimera.app/Contents/Resources/share/mapqp.py
- on mac
[...]
- done, time: 70.172916
 - done, time: 1 min, 10.2 sec
Saving pdb with Q-scores: /Users/greg/_data/mmetrics/emd_20026/3ajo__Q__emd_20026.pdb
Q for 413 res...
Model Q-score: 0.776
Chain Avg.Q-score
                     Est.Res.(A)
chain A (hoh) 0.506
                     3.45
chain A (mg) 0.510 3.42
chain A (protein)
                     0.820 1.69
Type
      Avg.Q-score
                     Est.Res.(A)
Protein 0.820
                     1.69
      0.510
              3.42
     0.506 3.45
Map: emd_20026.map, Model: 3ajo.pdb
--> avg. Q score: 0.776
```

- The score for the entire model is on the last line (0.776).
- The other few last lines summarize the scores by atom type: protein, nucleic acids, and other, e.g. Mg, Hoh (water atoms).

•	Per-atom Q-scores are stored in the pdb file [model name]Q[map name] in the <b>Occupancy</b> column. Note that the full path to the model must be given in the command for this file to be put in the same folder as this model.