# August 24, 2012

Used the scripts in "automate cluster download" to download all the HHOMP clusters. Put them in the folder "automated sequence alignment/clusters".

Copied the folder "aligned structures" from the folder "june 2012 lab meeting"

Copied the fodler "TMout" from the folder "bbtm derivation".

Wrote code that does not use ClustalW's "reset all gaps before alignment option". I am not sure if this is necessary but eventually I should ue this option to be safe.