May 1

Saved “cluster73.clu” from HHOMP database to “spring 2012 final paper/typical seq id/cluster73.clu”.

Saved “spring 2012 final paper/typical seq id/1A0S.fasta” from the PDB page for 1A0S. In previous work (“structure comparisons” folder I think?) I found that the sequence labeled chain P in this file is the same as the sequence of chain P from the PDB file.

Saved “DJ-M\_BBTMALL.txt”, Jie Liang's BBTMALL matrix, from an email Daniel sent me on March 7.

Using ClustalX with the following settings (default unless indicated):  
Alignment->Alignment Parameters->Multiple Alignment parameters, User Defined Matrix: BBTMALL

Alignment->Alignment Parameters->Reset All Gaps Before Alignment: checked

I aligned the protein sequences from cluster73.clu (removed consensus sequences, and stuff like bb\_pred that isn't really proteins equences) with the chain P sequence from 1A0S.fasta

Saved result as “cluster 73 1a0s.aln”

Ran script “compare\_id.py” with input “cluster73 1a0s.aln” and “1A0S”, saved output as “identities.txt”

May 2

Renamed "cluster73 1a0s.aln" to "cluster73 1a0s bbtmall.aln"

Re-aligned with the gonnet series matrices and saved as "cluster73 1a0s gonnet.aln"

Renamed "identities.txt" to "bbtmall identities.txt"

Made this histogram of the resulting sequence identities