**Results from Pymol and UCSF Chimera.**

Proteins used for Project:

Accession number1: Q3B890

Accession number2: Q3B891

PYMOL

Match: read scoring matrix.  
Match: assigning 259 x 480 pairwise scores.  
MatchAlign: aligning residues (259 vs 480)...  
MatchAlign: score 29.000  
ExecutiveAlign: 26 atoms aligned.  
ExecutiveRMS: 1 atoms rejected during cycle 1 (RMSD=11.37).  
Executive: RMSD =    6.093 (25 to 25 atoms)  
Executive: object "aln\_AF-Q3B890-F1-model\_v3\_to\_4ole" created.

UCSF CHIMERA

Computing secondary structure assignments for model(s) #1, #0

using ksdssp (Kabsch and Sander Define Secondary Structure

of Proteins) with the parameters:

energy cutoff -0.5

minimum helix length 3

minimum strand length 3

Matchmaker 4ole.pdb, chain A (#1) with AF-Q3B890-F1-model\_v3.pdb, chain A (#0), sequence alignment score = 15.4

with these parameters:

chain pairing: bb

Needleman-Wunsch using BLOSUM-62

ss fraction: 0.3

gap open (HH/SS/other) 18/18/6, extend 1

ss matrix: (O, S): -6 (H, O): -6 (H, H): 6 (S, S): 6 (H, S): -9 (O, O): 4

iteration cutoff: 2

RMSD between 6 pruned atom pairs is 1.285 angstroms; (across all 7 pairs: 1.957)