```
PyMOL>super 6JFK, fold_mfn2_model_0
 MatchAlign: aligning residues (439 vs 758)...
 MatchAlign: score 2138.739
 ExecutiveAlign: 3218 atoms aligned.
 ExecutiveRMS: 182 atoms rejected during cycle 1 (RMSD=24.75).
 ExecutiveRMS: 94 atoms rejected during cycle 2 (RMSD=6.79).
 ExecutiveRMS: 186 atoms rejected during cycle 3 (RMSD=2.14).
 ExecutiveRMS: 219 atoms rejected during cycle 4 (RMSD=1.32).
 ExecutiveRMS: 204 atoms rejected during cycle 5 (RMSD=0.92).
 Executive: RMSD =    0.677 (2333 to 2333 atoms)

PyMOL>super 6jfl, fold_mfn2_model_0
 MatchAlign: aligning residues (438 vs 758)...
 MatchAlign: score 1785.651
 ExecutiveAlign: 3092 atoms aligned.
 ExecutiveRMS: 179 atoms rejected during cycle 1 (RMSD=24.04).
 ExecutiveRMS: 87 atoms rejected during cycle 2 (RMSD=6.52).
 ExecutiveRMS: 124 atoms rejected during cycle 3 (RMSD=2.04).
 ExecutiveRMS: 168 atoms rejected during cycle 4 (RMSD=1.33).
 ExecutiveRMS: 131 atoms rejected during cycle 5 (RMSD=1.10).
 Executive: RMSD =    0.974 (2403 to 2403 atoms)
```