Full-length protein

Match: read scoring matrix.
Match: assigning 531 x 531 pairwise scores.
MatchAlign: aligning residues (531 vs 531)...
MatchAlign: score 2596.000
ExecutiveAlign: 531 atoms aligned.
ExecutiveRMS: 16 atoms rejected during cycle 1 (RMSD=3.25).
ExecutiveRMS: 18 atoms rejected during cycle 2 (RMSD=0.95).
ExecutiveRMS: 35 atoms rejected during cycle 3 (RMSD=0.70).
ExecutiveRMS: 27 atoms rejected during cycle 4 (RMSD=0.56).
ExecutiveRMS: 25 atoms rejected during cycle 5 (RMSD=0.46).
Executive: RMSD = 0.383 (410 to 410 atoms)
Executive: object "aln_533698_to_533699" created.

Divergent region (2 a-helices)

Match: read scoring matrix.
Match: assigning 40 x 40 pairwise scores.
MatchAlign: aligning residues (40 vs 40)...
MatchAlign: score 94.000
ExecutiveAlign: 40 atoms aligned.
ExecutiveRMS: 3 atoms rejected during cycle 1 (RMSD=1.22).
ExecutiveRMS: 2 atoms rejected during cycle 2 (RMSD=0.95).
ExecutiveRMS: 2 atoms rejected during cycle 3 (RMSD=0.77).
ExecutiveRMS: 2 atoms rejected during cycle 4 (RMSD=0.67).
ExecutiveRMS: 1 atoms rejected during cycle 5 (RMSD=0.57).
Executive: RMSD = 0.536 (30 to 30 atoms)

Full-length protein excluding the divergent region

Match: read scoring matrix.
Match: assigning 477 x 477 pairwise scores.
MatchAlign: aligning residues (477 vs 477)...
MatchAlign: score 2427.000
ExecutiveAlign: 477 atoms aligned.
ExecutiveRMS: 8 atoms rejected during cycle 1 (RMSD=1.15).
ExecutiveRMS: 30 atoms rejected during cycle 2 (RMSD=0.72).
ExecutiveRMS: 28 atoms rejected during cycle 3 (RMSD=0.58).
ExecutiveRMS: 23 atoms rejected during cycle 4 (RMSD=0.46).
ExecutiveRMS: 15 atoms rejected during cycle 5 (RMSD=0.38).
Executive: RMSD = 0.333 (373 to 373 atoms)
Executive: object "aln_R1_to_R2" created.