SUPPLEMENTARY TEXT

ATP OPLS-AA/L Validation

As discussed in the main paper, simulations were performed using both the OPLS-AA/L and AMBER-03 force fields. However, one initial problem was that (as far as we are aware) there are no published polyphosphate parameters for use with the OPLS-AA/L force field, meaning this it is was not possible to simulate ATP. However, there are published parameters for use with the AMBER force fields[1] and so a series of simulations were performed to test if these parameters would be suitable for use in the OPLS-AA/L force field to simulate ATP. In the original paper where these AMBER parameters were published, minimisations were performed of four different protein structures (PDB codes: 1F2U, 1F9A, 1GOL and 1NSF) containing one or more ATP molecules. The RMSD with respect to the crystal structure was used to determine if these parameters performed more accurately than the existing AMBER parameters. Whilst also repeating the minimisations of these four structures for both AMBER-03 and OPLS-AA/L force fields within GROMACS, we also performed 10 ns of molecular dynamics simulations after minimisation for each system. The dynamics of the ATP molecules during these simulations were also compared to the same simulations performed using the united-atom GROMOS 43A1 force field[2] and the standard GROMOS ATP parameters. The only difference in the setup of the simulations compared to the normal GroEL simulations was in the minimisation procedure. The protein backbone was restrained in position using a harmonic restraint of 1000 kJ mol^{-1} nm^{-2} during the minimisation, the minimisations used the l-BFGS algorithm and were performed for 50,000 steps or until the maximum force on any atom was less than 1 kJ mol^{-1} nm^{-1}. Supporting figures S1 and S2 show the structure of the ATP molecules from the end of the 10 ns simulations and the RMSF of the

ATP atoms during the simulations respectively. These results show that the ATP parameters used in combination with the OPLS-AA/L force field perform with an adequate accuracy when compared to the AMBER-03 force field simulations. Both sets of AMBER-03 and OPLS-AA/L simulations also compare favourably to the GROMOS 43A1 simulations and ATP parameters under these simulation conditions.

SUPPLEMENTARY REFERENCES

1. Meagher, K. L., Redman, L. T., and Carlson, H. A. (2003) Development of polyphosphate parameters for use with the AMBER force field. *J Comp Chem 24*, 1016-1025.

2. van Gunsteren, W. F., Billeter, S. R., Eising, A. A., Hünenberger, P. H., Krüger, P., Mark, A. E., Scott, W. R. P., and Toroni, I. G. (1996) Biomolecular simulation: The GROMOS96 manual and user guide.

SUPPLEMENTARY FIGURES

FIGURE S1

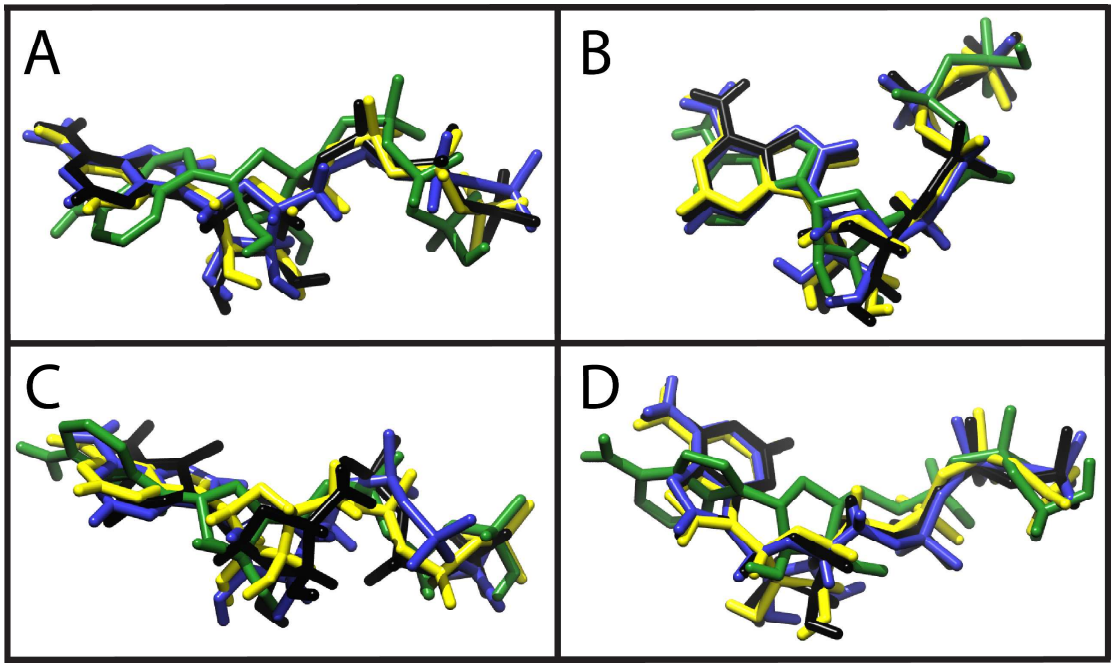


Figure S1: ATP conformations after 10 ns simulations of structures A) 1F2U, B) 1F9A, C) 1GOL and D) 1NSF using the AMBER-03 (yellow), OPLS-AA/L (blue) and GROMOS 43A1 (green) force fields. The structures were superimposed using a least squares fit to the crystal structures (black).

FIGURE S2

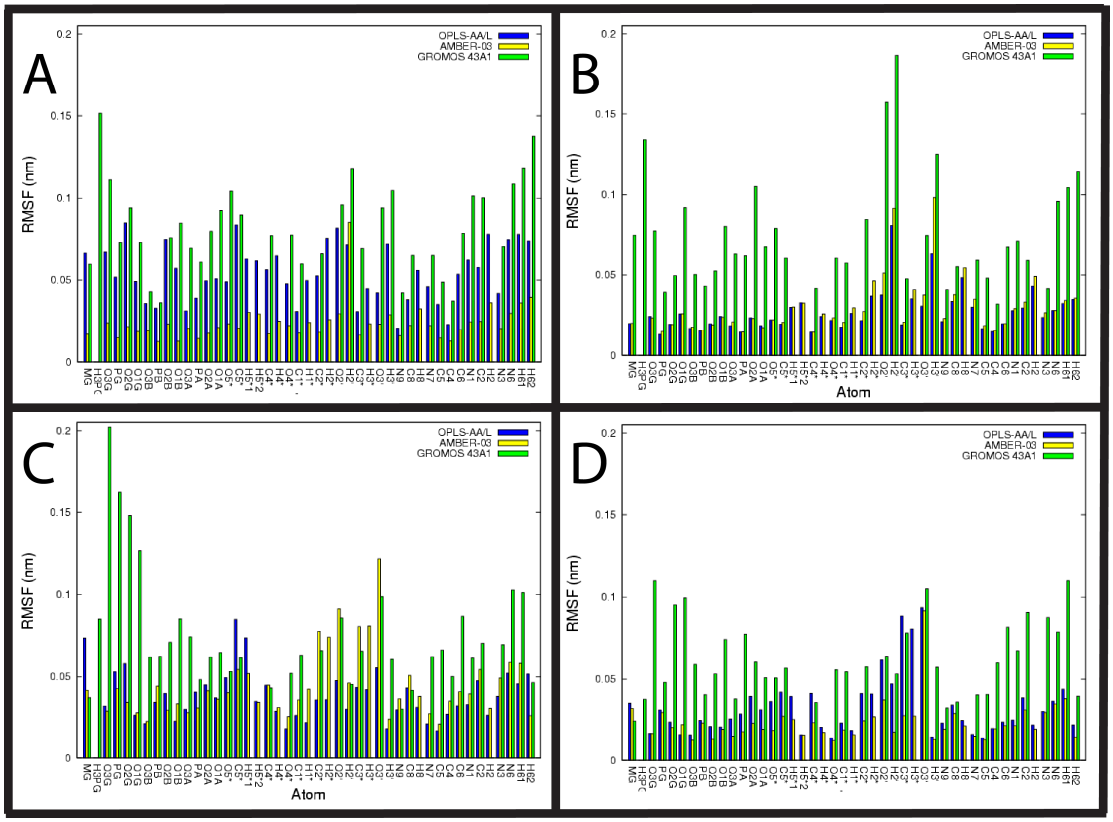


Figure S2: RMSF's of the ATP atoms during the 10 ns simulations of structures A) 1F2U, B) 1F9A, C) 1GOL and D) 1NSF. The AMBER-03 simulations are shown in yellow, the OPLS-AA/L simulations in blue and the GROMOS 43A1 simulations in green.

FIGURE S3

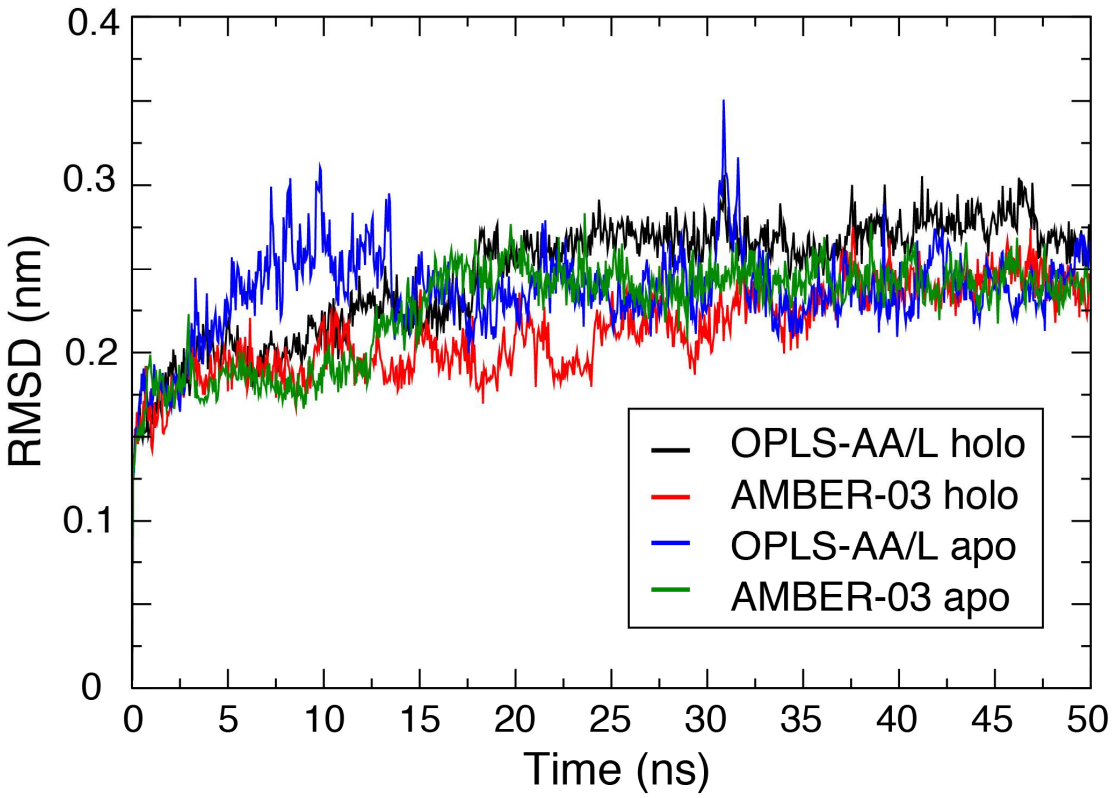


Figure S3: RMSD's of the apical domain during the single subunit simulations.

FIGURE S4

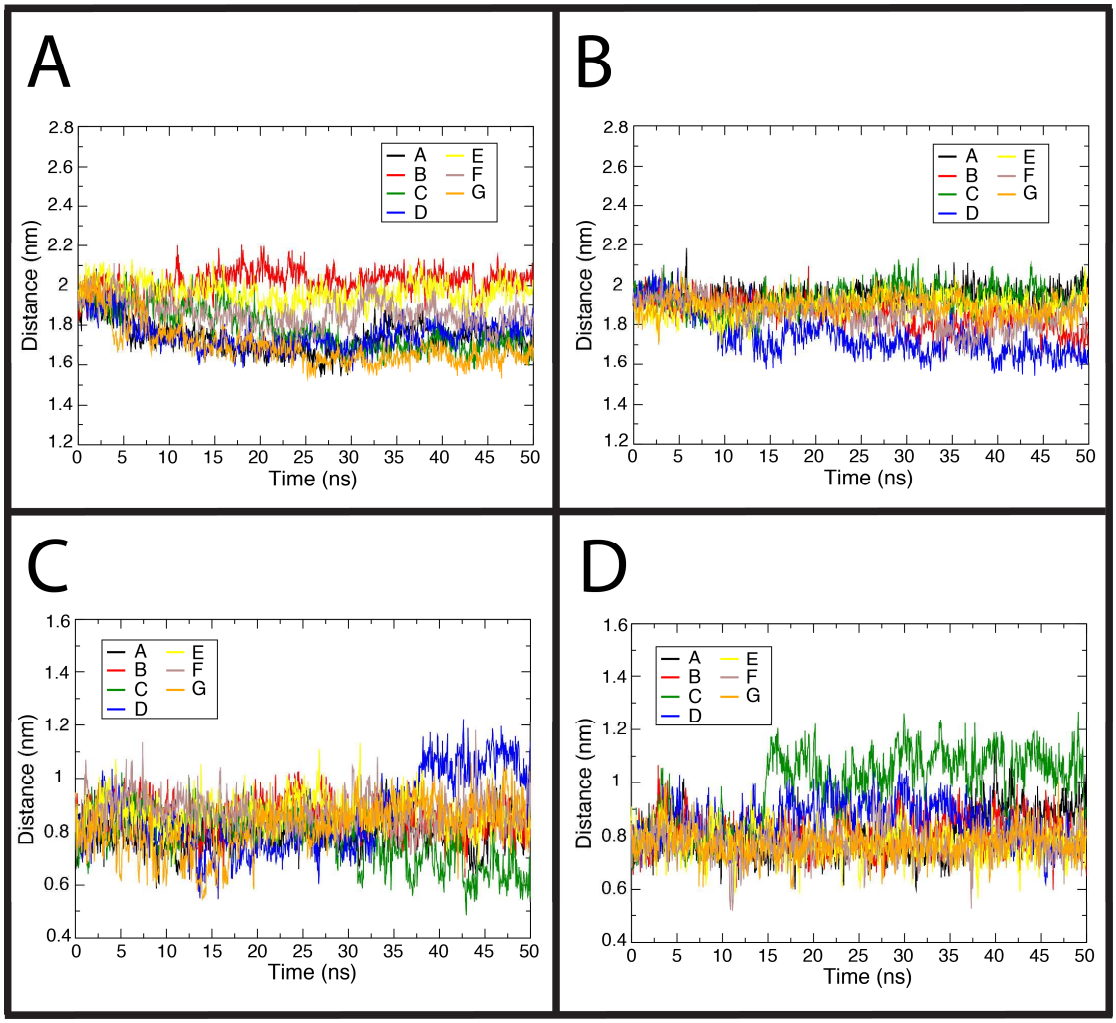


Figure S4**:** The distance between the COM of Thr-91 and the COM of the final turn of helix F at the end located closest to Thr-91 as it varies for each subunit during the (A) *holo* and (B) *apo* GroEL AMBER-03 single-ring simulations. The distance between the Cγ carbon of the catalytic residue Asp-398 and the Cγ carbon of Asp-87, the active site residue coordinated to the Mg^{2+} ion, during the (C) *holo* and (D) apo AMBER-03 single-ring simulations.

FIGURE

S5

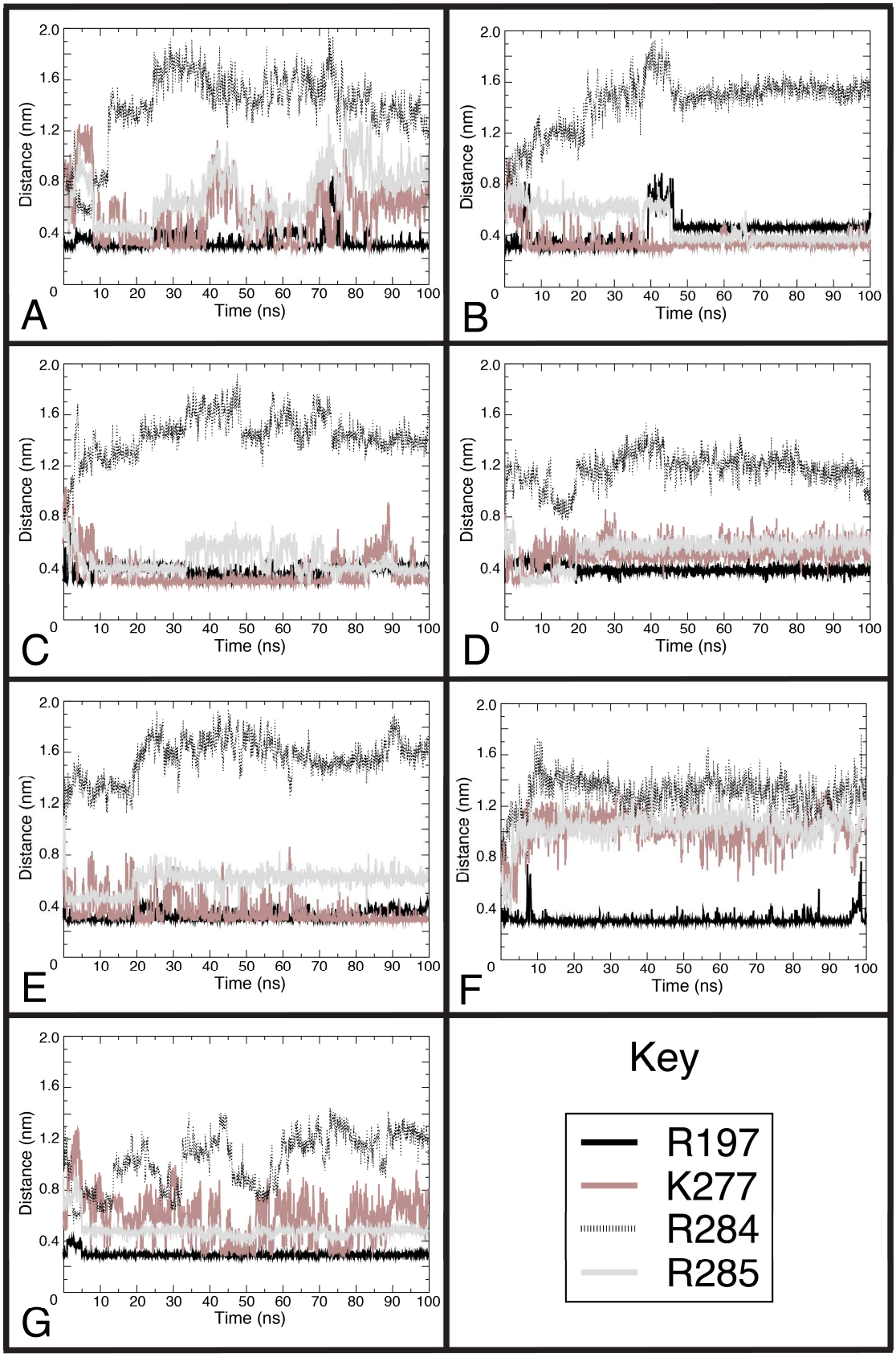
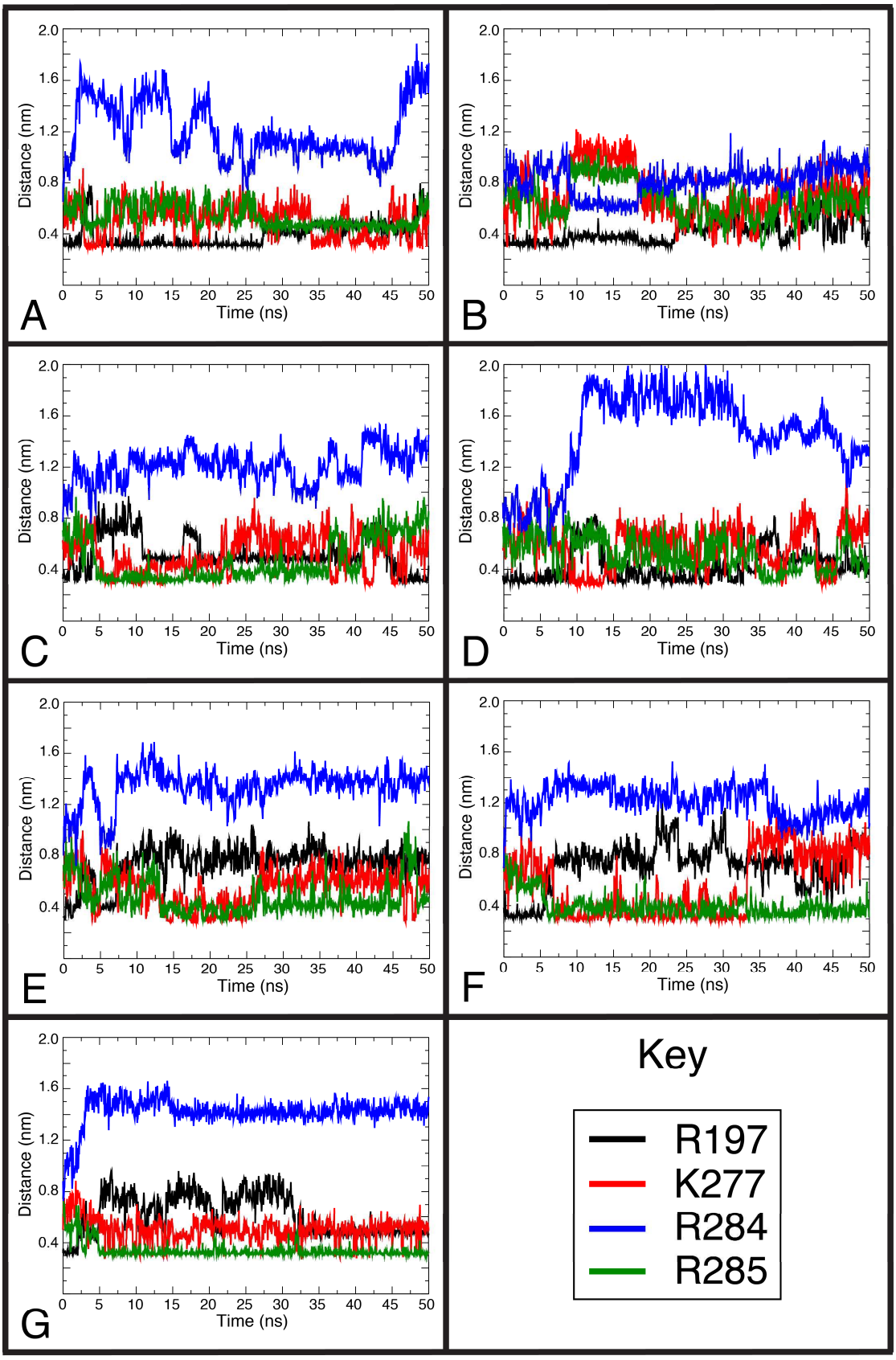


Figure S5: Distances between the COM of the side chain carboxylate group of Glu-386 and either the COM of the Cζ and both side chain NH_2 groups of Arg-197, Arg-284 and Arg-285, or the COM of the side chain amine group of Lys-277. The distance shown is between each pair of adjacent subunits in the *holo* GroEL single-ring OPLS-AA/L simulation. Panel A shows the interaction of Glu-386 in subunit A and Arg-197, Arg-284, Arg-285 and Lys-277 in subunit B. Panel B shows the interactions of subunits B and C and so forth.

FIGURE S6


A
B
C
D
E
F
G
Distance (nm)
Time (ns)
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1.6
1.2
0.8
0.4
0
5
10
15
20
25
30
35
40
45
50
Key
R197
K277
R284
R285

Figure S6: Distances between the COM of the side chain carboxylate group of Glu-386 and either the COM of the Cζ and both side chain NH_2 groups of Arg-197, Arg-284 and Arg-285, or the COM of the side chain amine group of Lys-277. The distance shown is between each pair of adjacent subunits in the *holo* GroEL single-ring AMBER-03 simulation. Panel A shows the interaction of Glu-386 in subunit A and Arg-197, Arg-284, Arg-285 and Lys-277 in subunit B. Panel B shows the interactions of subunits B and C and so forth.

FIGURE S7

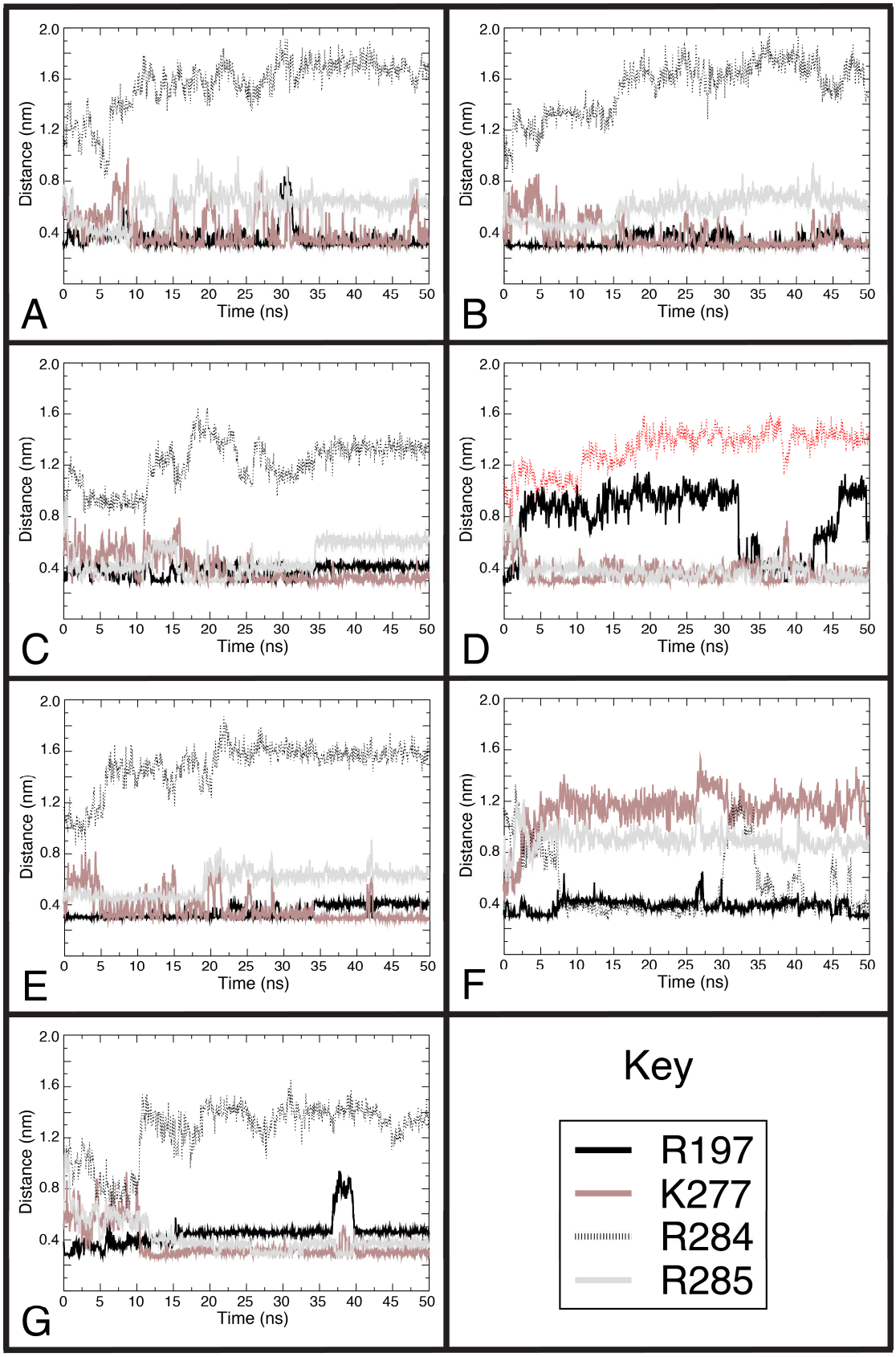

Figure S7: Distances between the COM of the side chain carboxylate group of Glu-386 and either the COM of the Cζ and both side chain NH_2 groups of Arg-197, Arg-284 and Arg-285, or the COM of the side chain amine group of Lys-277. The distance shown is between each pair of adjacent subunits in the *apo* GroEL single-ring OPLS-AA/L simulation. Panel A shows the interaction of Glu-386 in subunit A with Arg-197, Arg-284, Arg-285 and Lys-277 in subunit B. Panel B shows the interactions of subunits B and C and so forth.

FIGURE S8

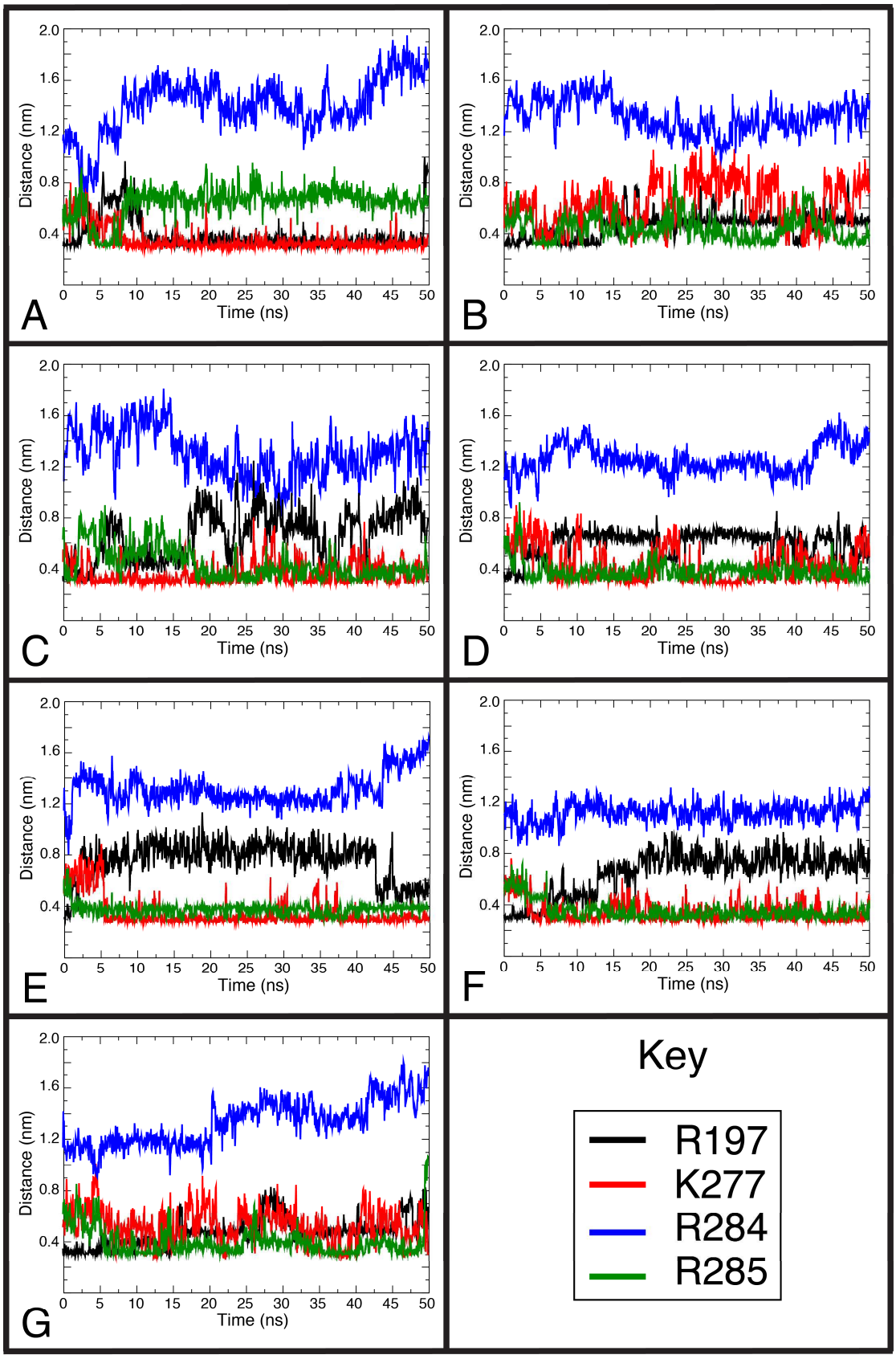
A
B
C
D
E
F
G
Distance (nm)
Time (ns)
0.4
0.8
1.2
1.6
2.0
0 5 10 15 20 25 30 35 40 45 50
Key
R197
K277
R284
R285

Figure S8: Distances between the COM of the side chain carboxylate group of Glu-386 and either the COM of the Cζ and both side chain NH_2 groups of Arg-197, Arg-284 and Arg-285, or the COM of the side chain amine group of Lys-277. The distance shown is between each pair of adjacent subunits in the *apo* GroEL single-ring AMBER-03 simulation. Panel A shows the interaction of Glu-386 in subunit A with Arg-197, Arg-284, Arg-285 and Lys-277 in subunit B. Panel B shows the interactions of subunits B and C and so forth.

FIGURE S9

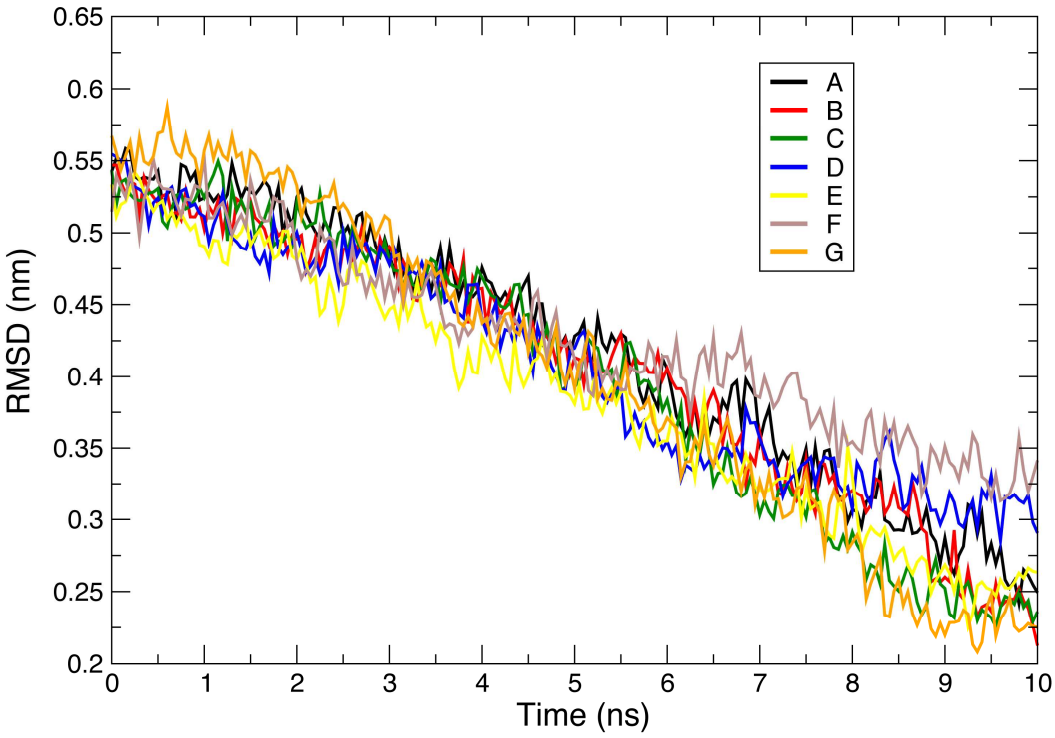

Figure S9: RMSD of the subunits in the single ring to the cryoEM target structure (all protein atoms) during the DRB simulation.