Supplementary information

Figure S1. RMSD profiles for simulations Apo1, Apo2, Complex1 and Complex2.

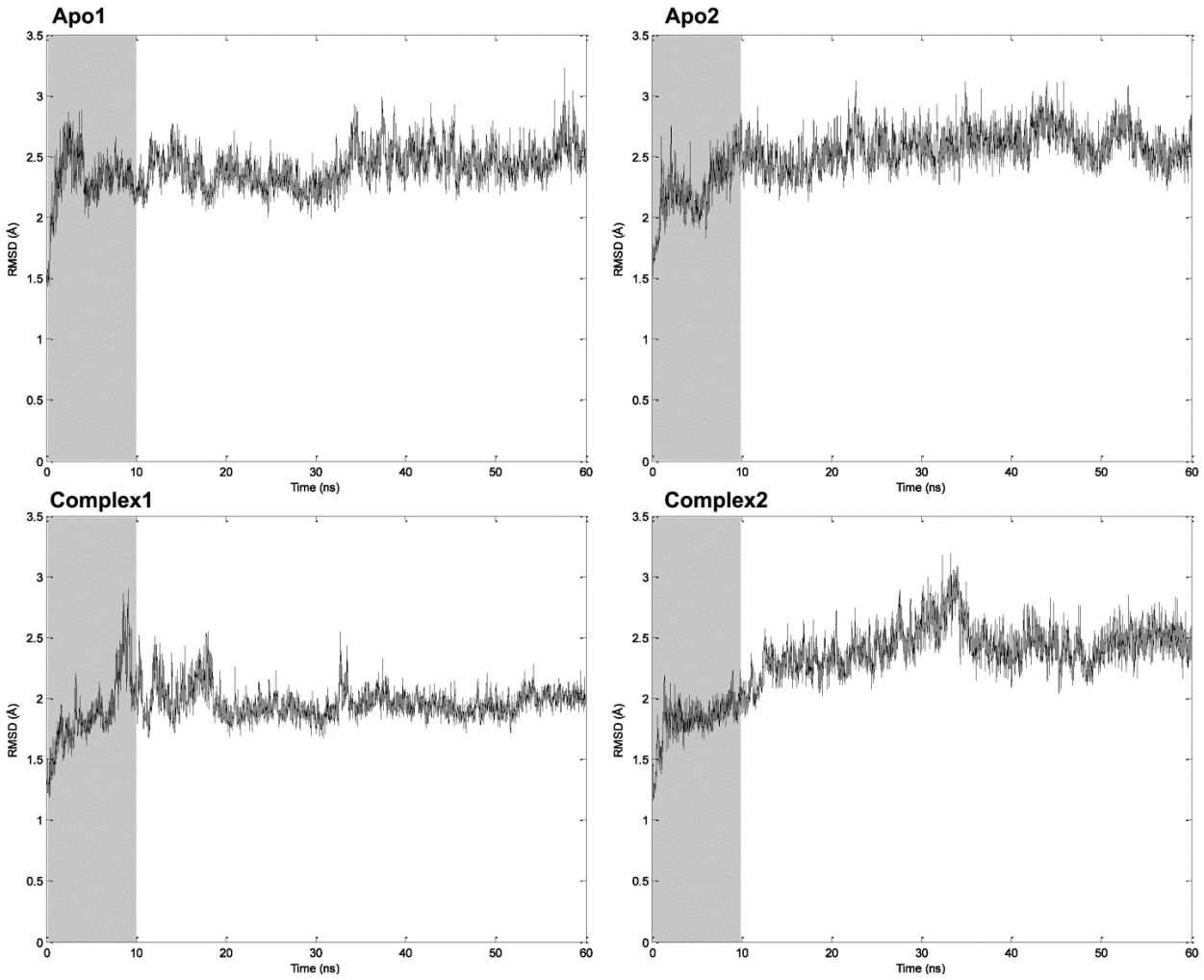

Figure S2. Residues making H-bonding with DHAP throughout the complex simulations: (**a**) Complex1, (**b**) Complex2 for subunit A and B. In (**a**) and (**b**), number of H-bonds between the residue and DHAP is represented with following color scheme: blue (no H-bond), green (1 H-bond), red (2 H-bonds). In (**b**), 9-13 ns, H-bonds between DHAP and key residues are sequentially broken and resulting in the detachment of DHAP from the catalytic site of subunit A. In (**c**), total number of H-bonds between TIM residues and DHAP in Complex1 A and B subunits and in Complex2 B subunit is given.

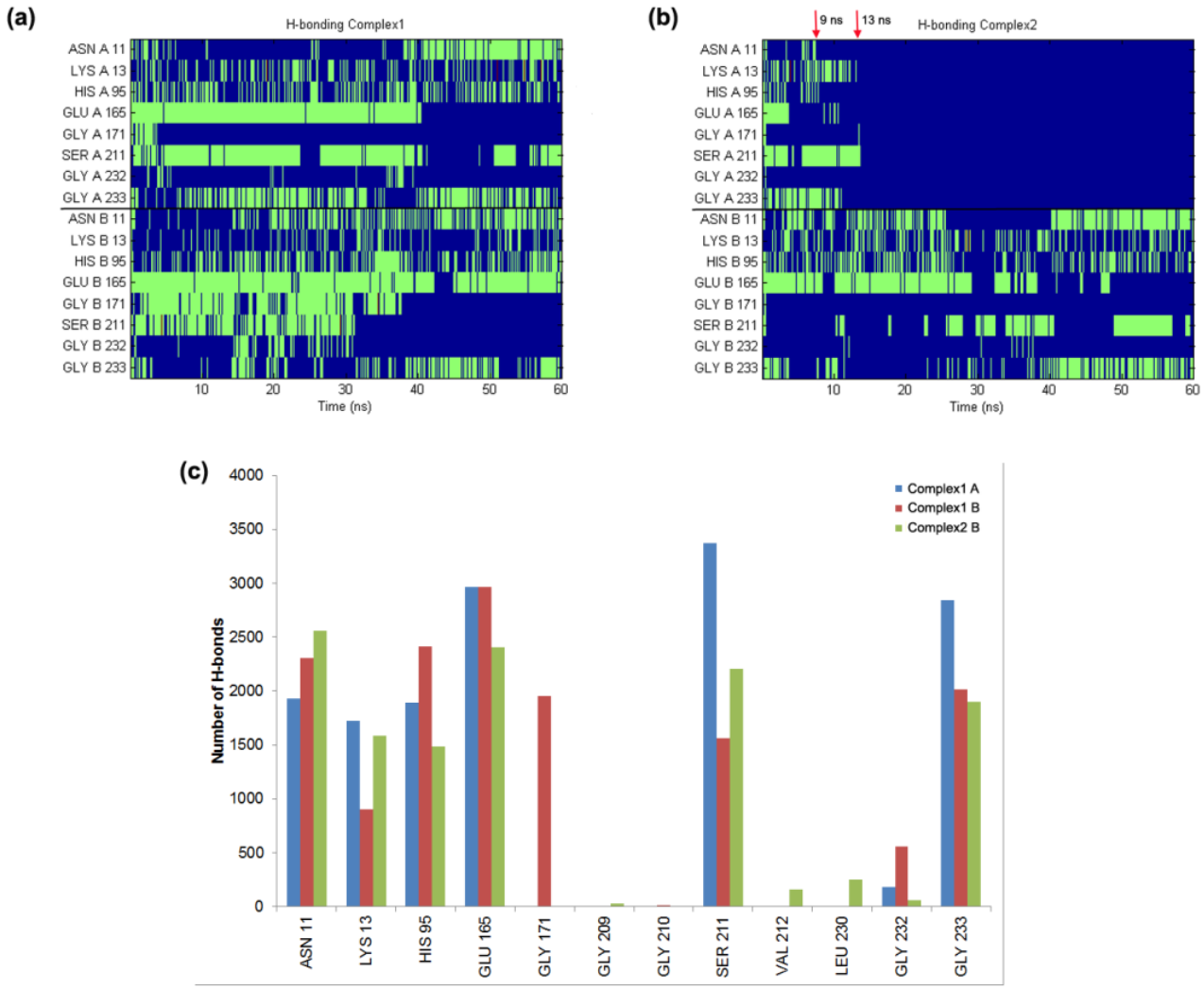

Figure S3. The distance between C^{α} atoms of loop 6 tip residue (G171) and a reference residue (Y208) as a function of time. Solid and dashed lines indicate the respective closed and open states of the loop based on crystal structures.

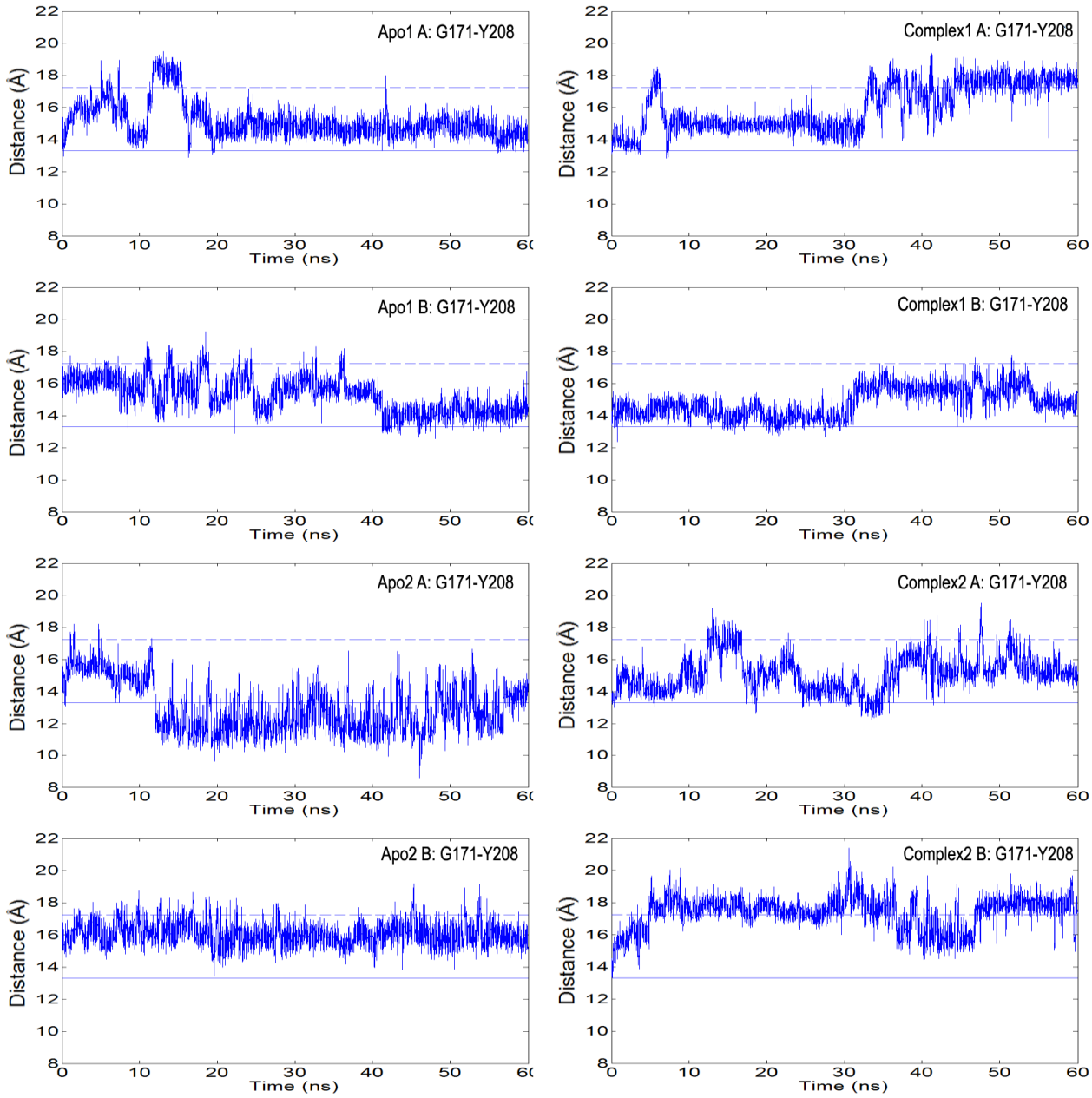

Figure S4. The distance between C^{α} atoms of loop 6 tip residue (T172) and a reference residue (Y208) as a function of time. Solid and dashed lines indicate the respective closed and open states of the loop based on crystal structures.

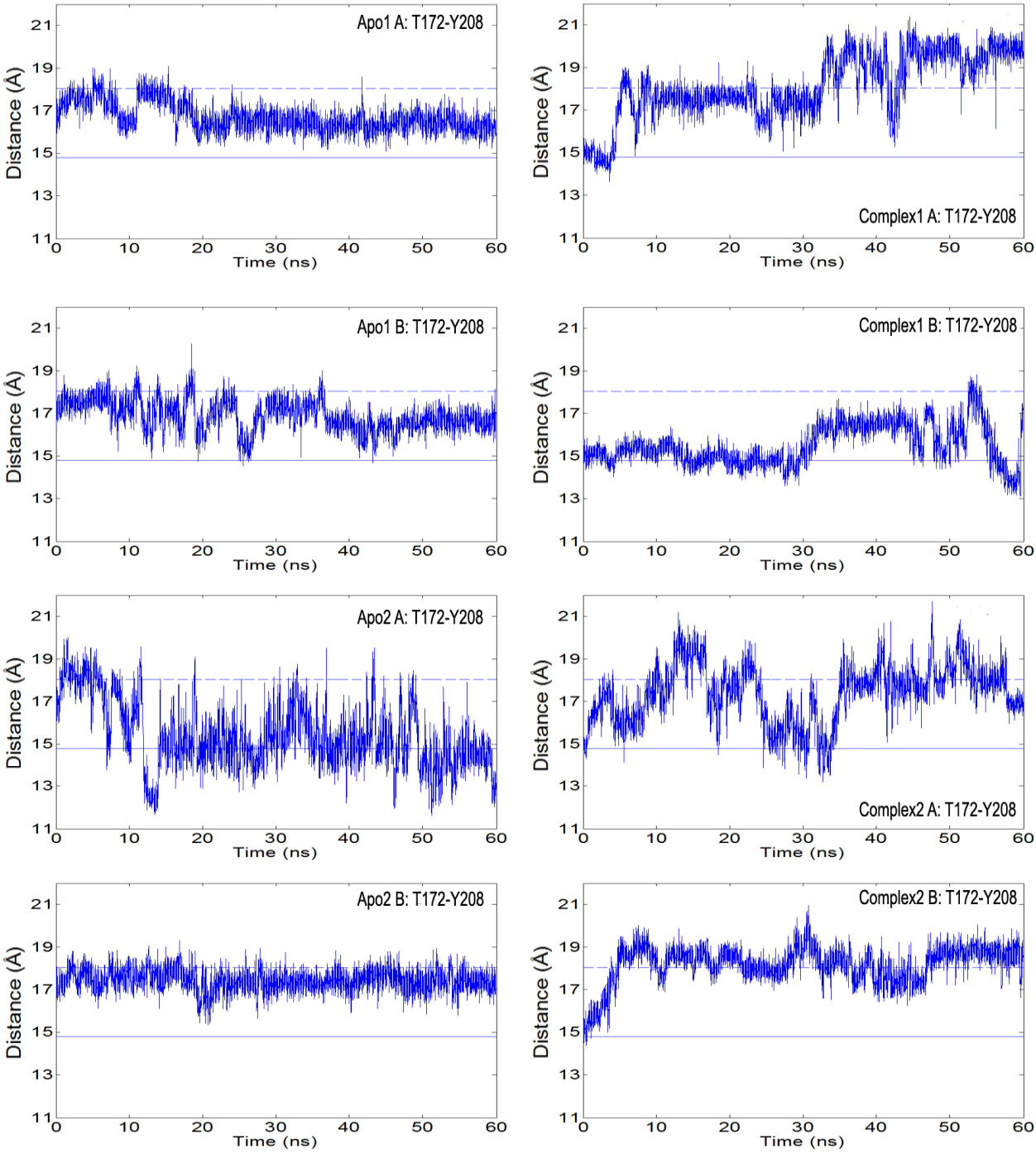

Figure S5. Overlap of first 10 PCs of the simulations.

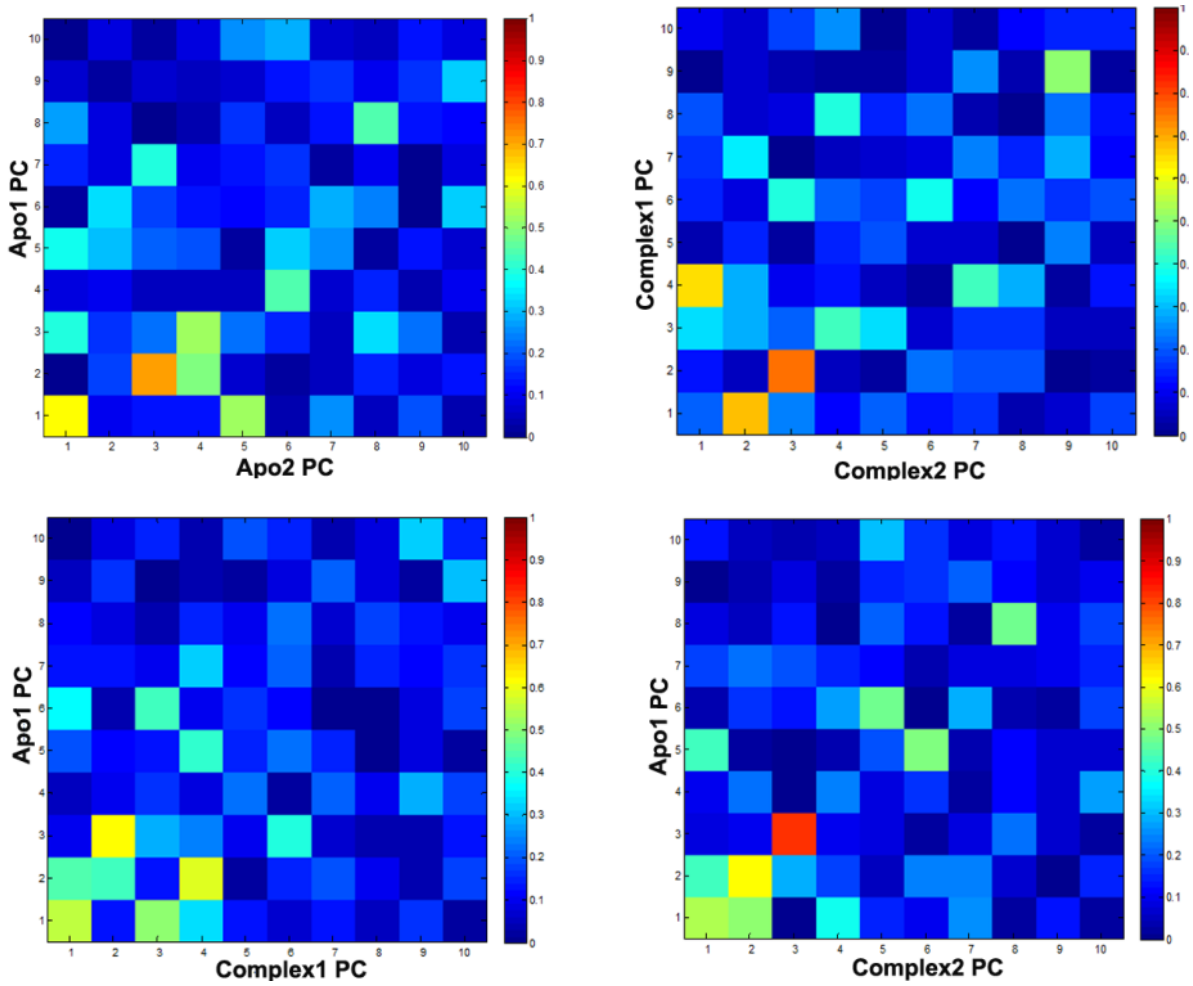

Figure S6. Normalized orientational cross-correlation map for all runs.

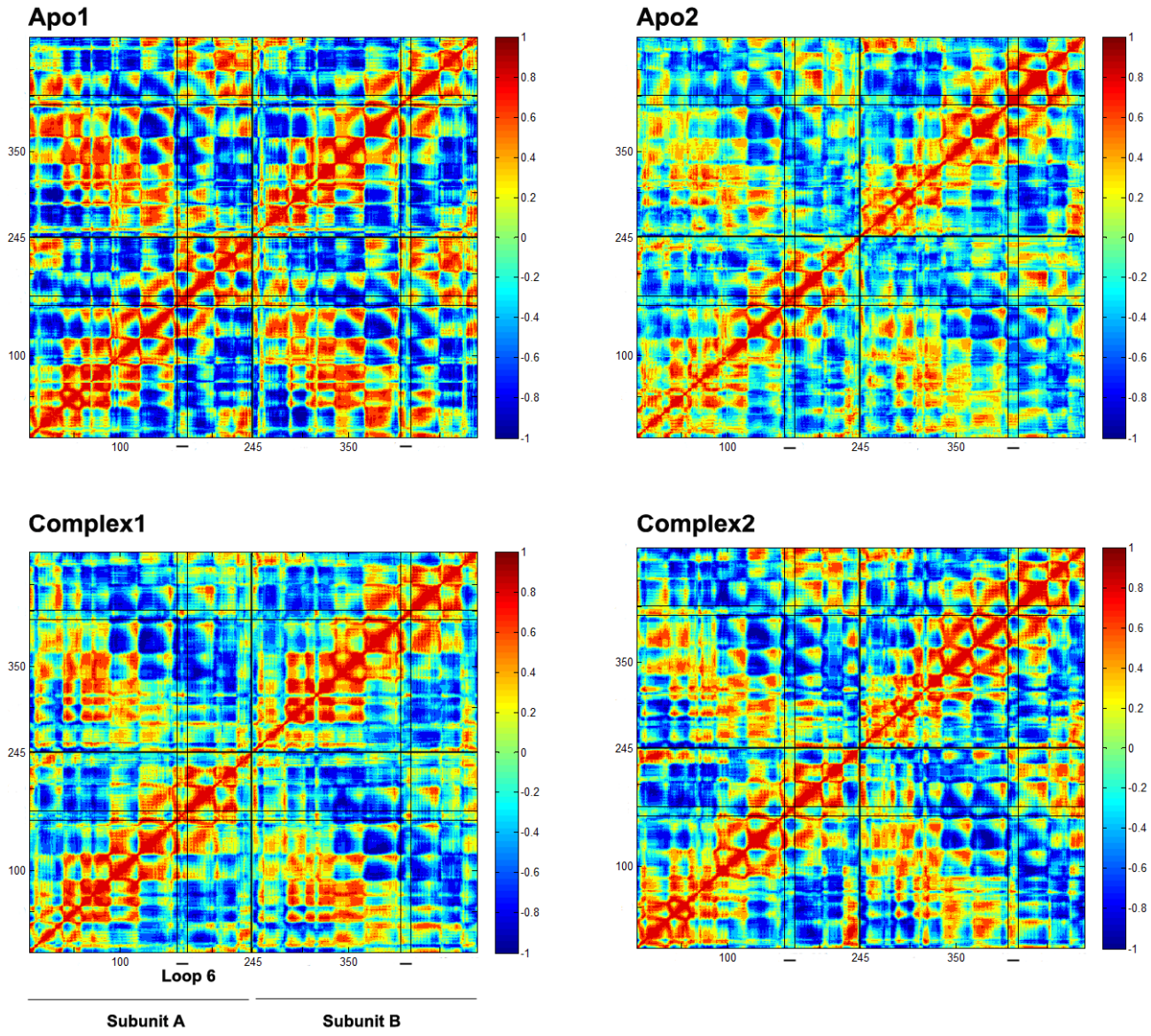

Figure S7. Normalized orientational cross correlations averaged for three N-terminus residues of the loop 6 (P166-W168) with respect to residue index in apo and complex.

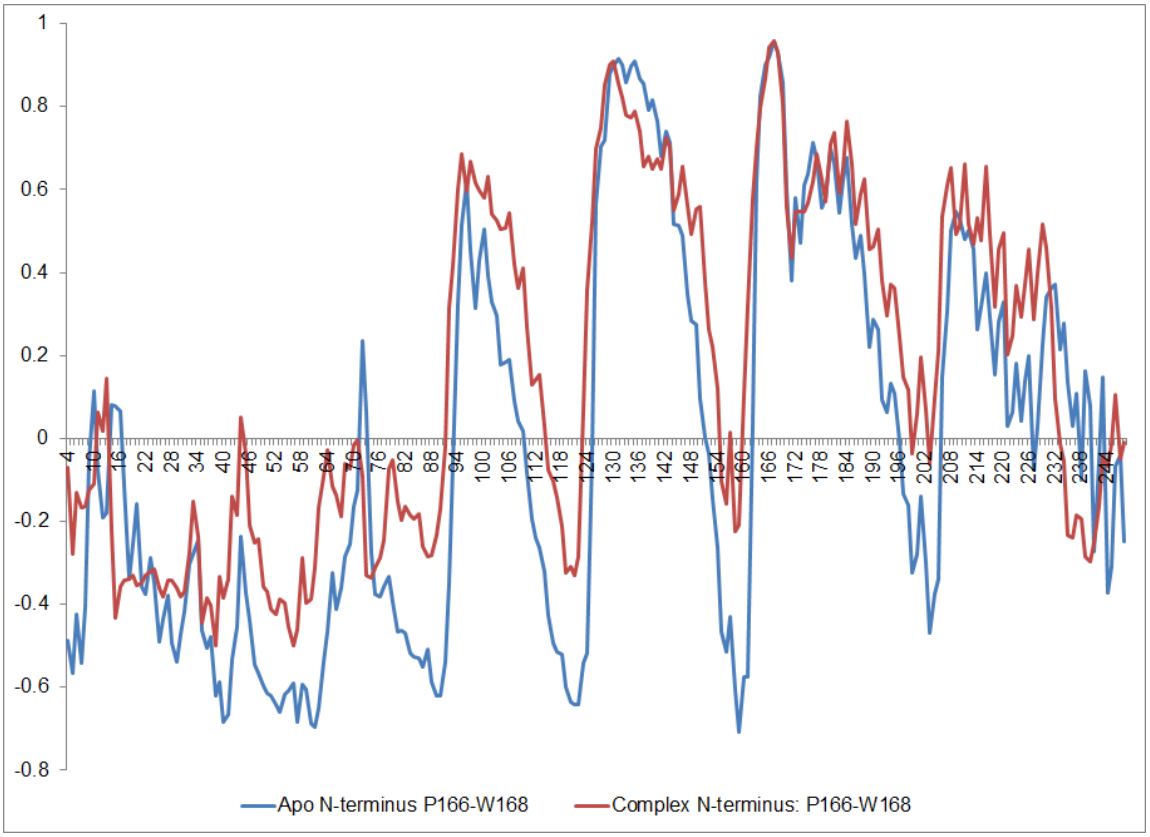

Figure S8. Normalized orientational cross correlations averaged for three tip residues of the loop 6 (I170-T172) with respect to residue index in apo and complex.

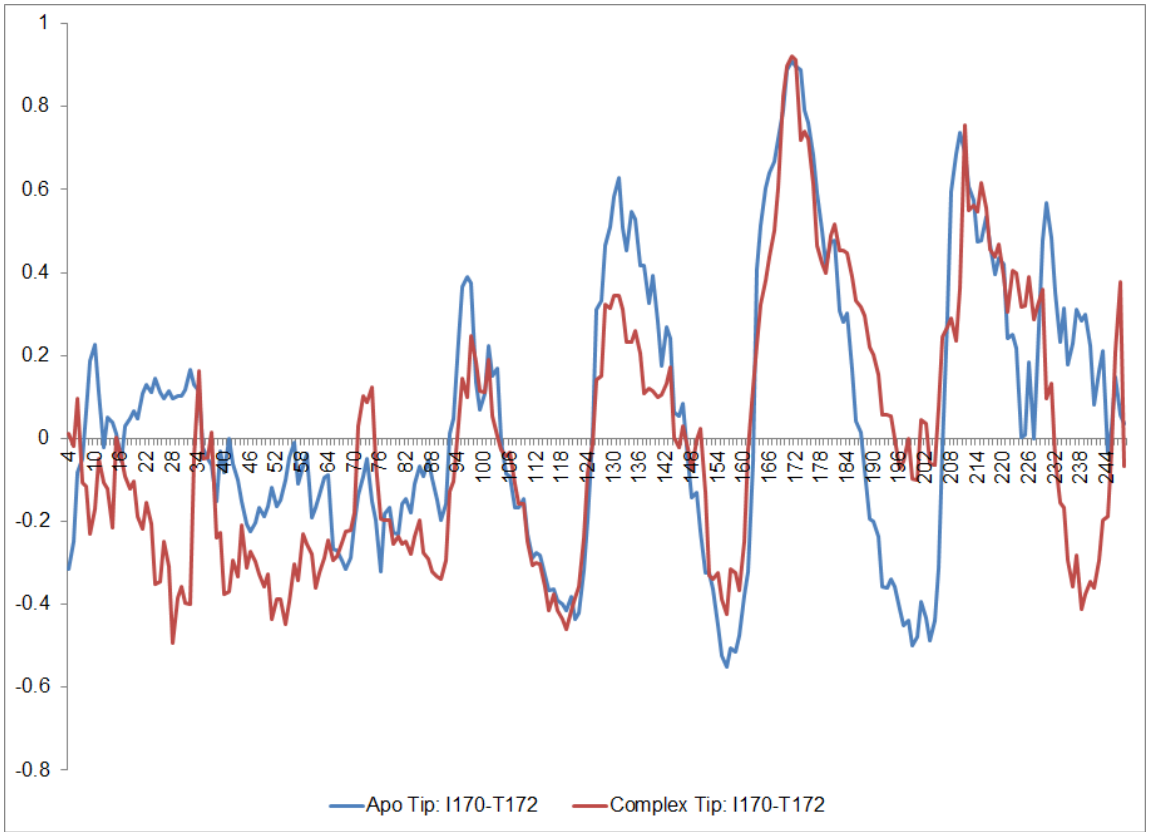

Figure S9. Normalized orientational cross correlations averaged for three C-terminus residues of the loop 6 (K174-A176) with respect to residue index in apo and complex

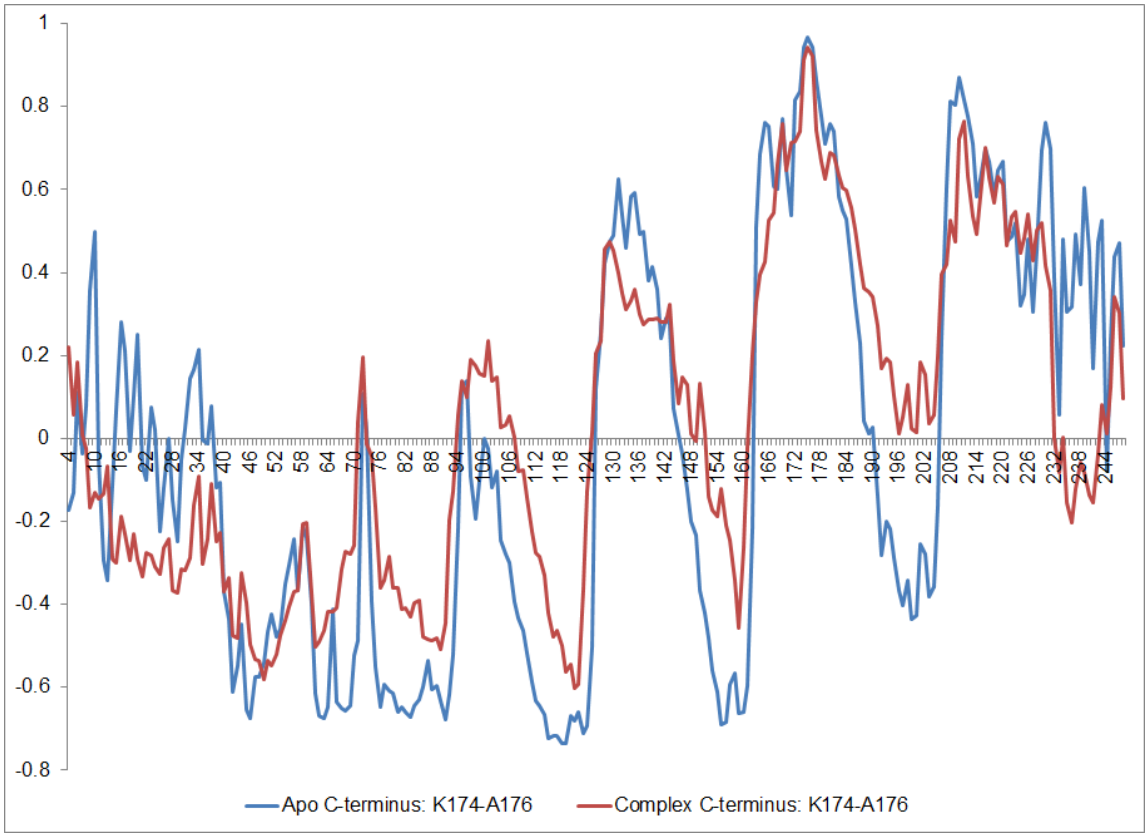

Table S1. Percentage Variance Captured by PC modes (overall PCA).

PC	Apo1	Apo2	Complex1	Complex2
1	34	19	24	23
2	8.0	11	8.9	19
3	7.3	7.3	7.5	8.0
4	4.7	5.2	4.9	5.1
5	3.2	4.5	4.0	2.9