Conformational motions of HIV-1 Protease identified using Reversible Digitally Filtered Molecular Dynamics

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Supporting Information

It is worth explaining the sudden changes in graphs of RDFMD trajectories, such as those seen in the second flap when moving between closed and curled conformations, and in the increasing flap separation. The apparent discontinuities indicate that the conformational change is induced entirely during one set of digital filter applications. As previously stated, the trajectories shown are pieced together from the 4 ps simulations between each of the 100 filter sequences, and do not include information from the filter sequences themselves. Such information can be constructed from the forward portions of NVE simulation. However, the timescale of these forward portions is not sufficiently significant for inclusion on plots of the 400 ps simulation.

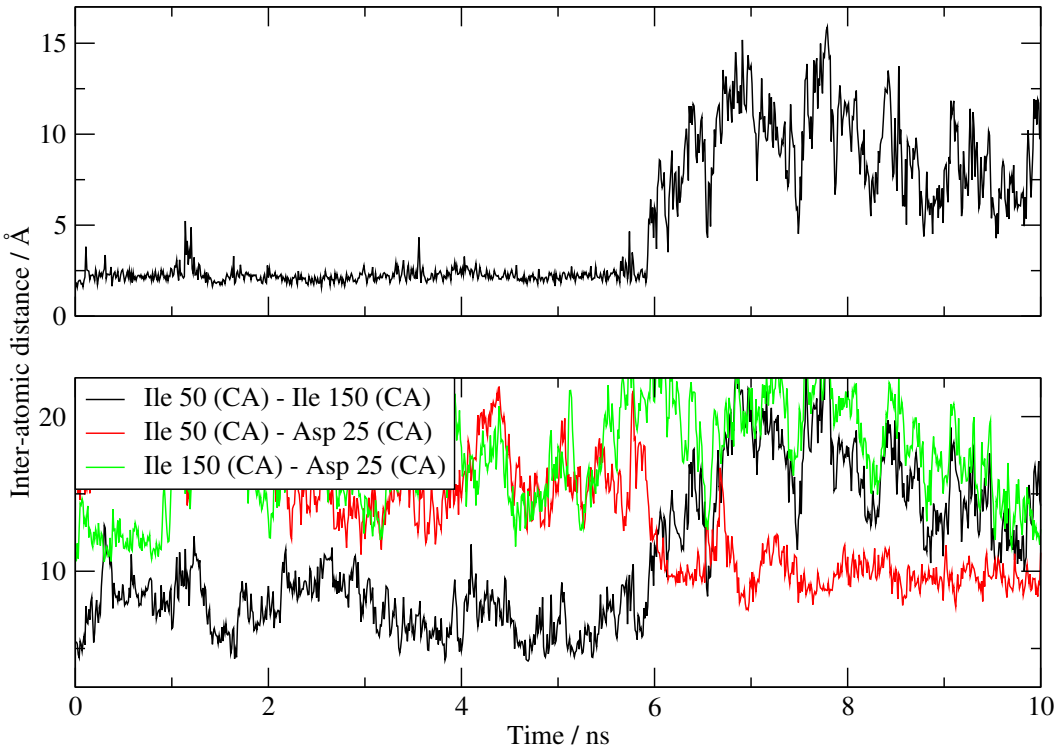

Figure 1: Analysis of the 10 ns 450 K NVT MD simulation of HIV-1 PR with a monoprotonated aspartic acid dyad. Top: flap separation shown by the shortest distance between all atoms of residues 45 to 55 and 145 to 155. Bottom: α-carbon distances.

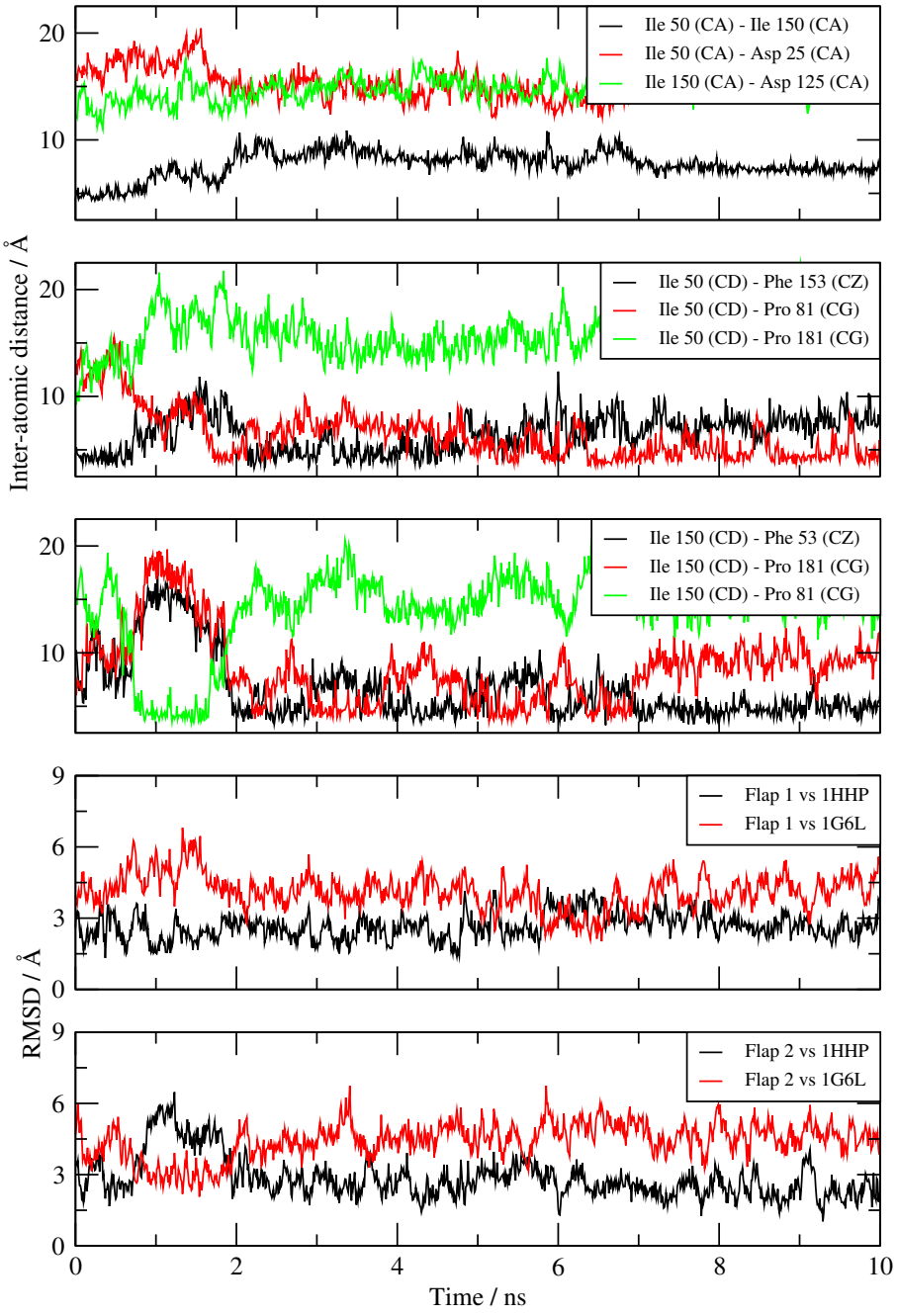

Figure 2: Analysis of the 10 ns NVT MD simulation of HIV-1 PR with a monoprotonated aspartic acid dyad. Top: α-carbon distance between flap tips. Upper middle: location of flap 1 tip with respect to nearby hydrophobic residues (semi-open, curled and closed conformations are indicated by black, red and green respectively). Middle: location of flap 2 tip with respect to nearby hydrophobic residues. Lower middle: RMSD of flap 1 (residues 46 to 54) against semi-open (1HHP) and closed (1G6L) structures. Bottom: RMSD of flap 2 (residues 146 to 154) against semi-open (1HHP) and closed (1G6L) structures.

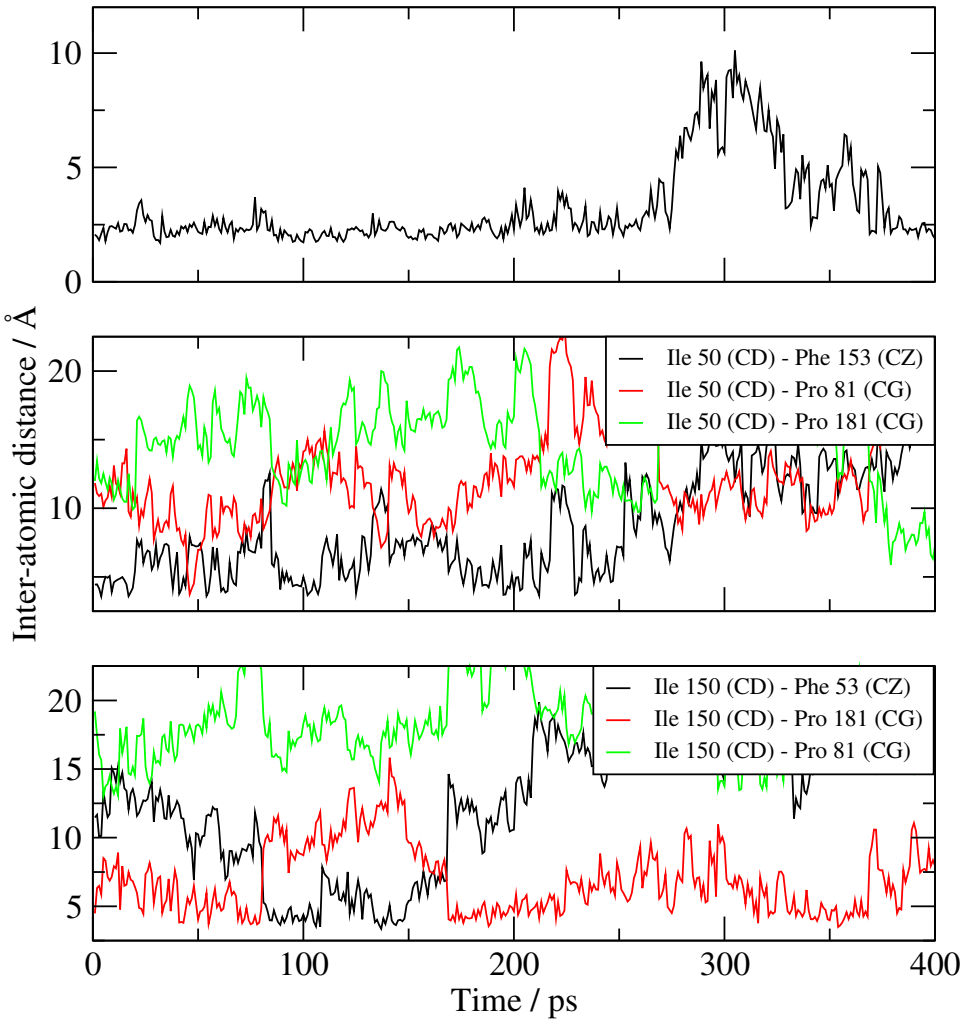

Figure 3: Analysis of the 400 ps RDFMD simulation using a filter delay of 100 steps and an internal temperature cap of 1100 K with NPT MD between filter sequences. Top: flap separation shown by the shortest distance between all atoms of residues 45 to 55 and 145 to 155. Middle: location of flap 1 tip with respect to nearby hydrophobic residues (semi-open, curled and closed conformations are indicated by black, red and green respectively). Bottom: location of flap 2 tip with respect to nearby hydrophobic residues.

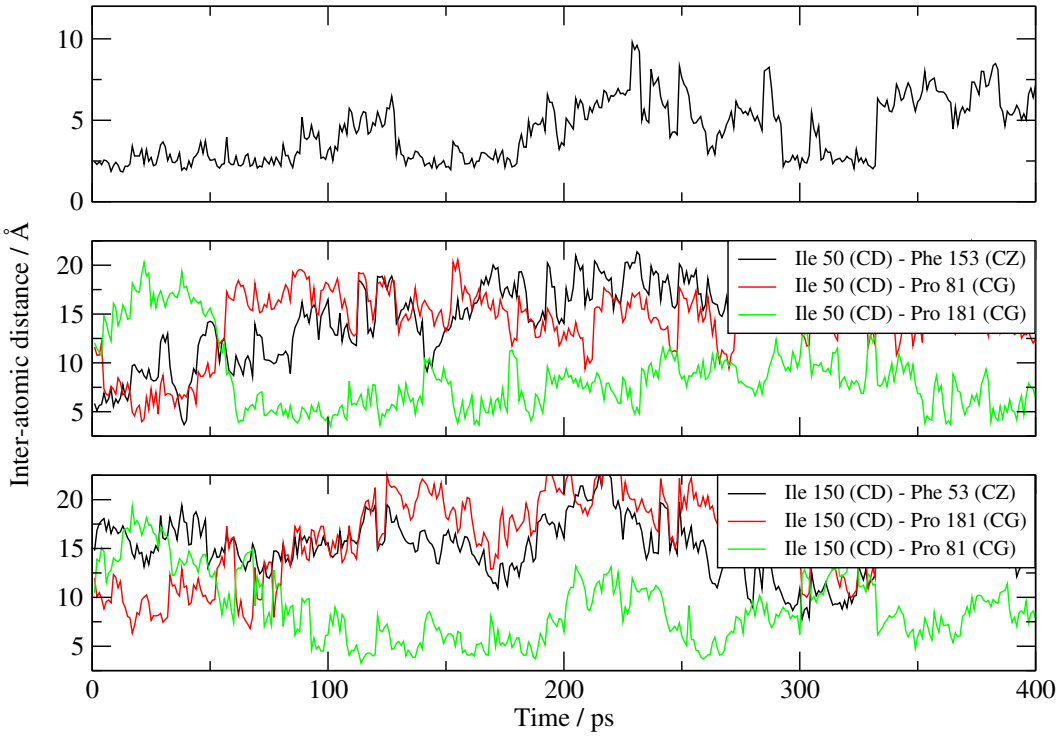

Figure 4: Analysis of the 400 ps RDFMD simulation using a filter delay of 100 steps and an internal temperature cap of 1300 K with NPT MD between filter sequences. Top: flap separation shown by the shortest distance between all atoms of residues 45 to 55 and 145 to 155. Middle: location of flap 1 tip with respect to nearby hydrophobic residues (semi-open, curled and closed conformations are indicated by black, red and green respectively). Bottom: location of flap 2 tip with respect to nearby hydrophobic residues.

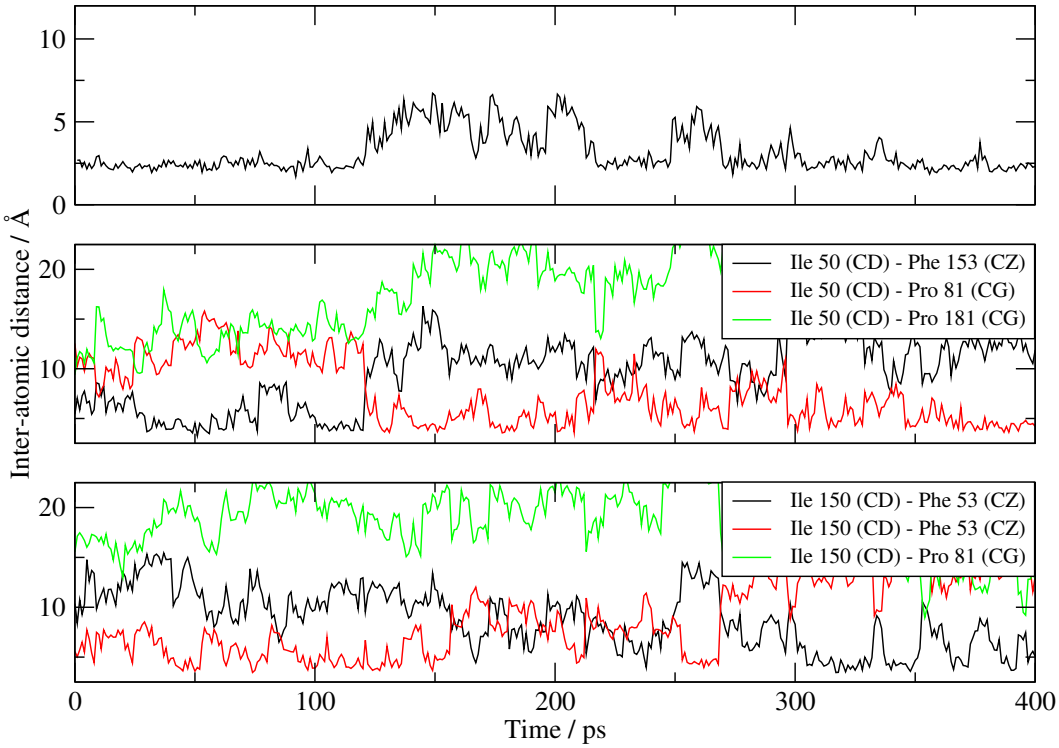

Figure 5: Analysis of the 400 ps RDFMD simulation using a filter delay of 100 steps and an internal temperature cap of 1100 K with NVT MD between filter sequences. Top: flap separation shown by the shortest distance between all atoms of residues 45 to 55 and 145 to 155. Middle: location of flap 1 tip with respect to nearby hydrophobic residues (semi-open, curled and closed conformations are indicated by black, red and green respectively). Bottom: location of flap 2 tip with respect to nearby hydrophobic residues.