Supplementary information

Structural Insights into HIV-1 Protease Flap Opening Process and Key Intermediates

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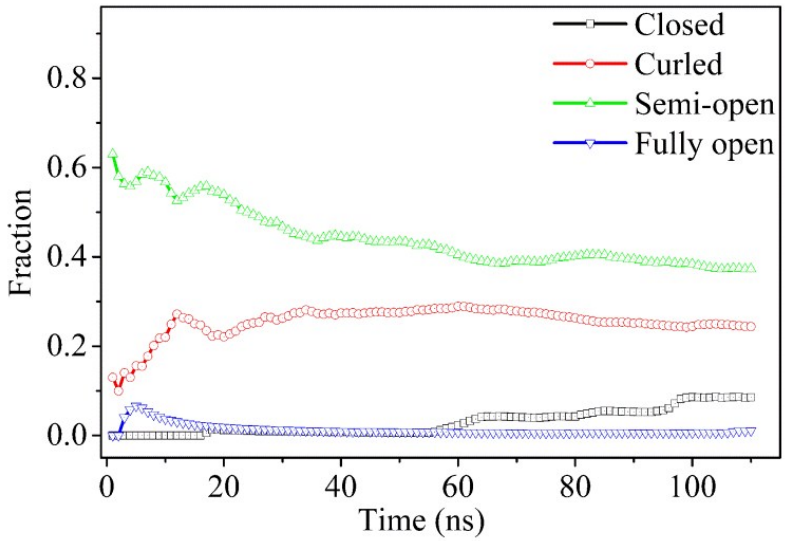

Figure S1. Time series of the fraction of all distinct states in the conformational transition pathway of HIV-1 PR at 300 K measured by hREMD simulation.

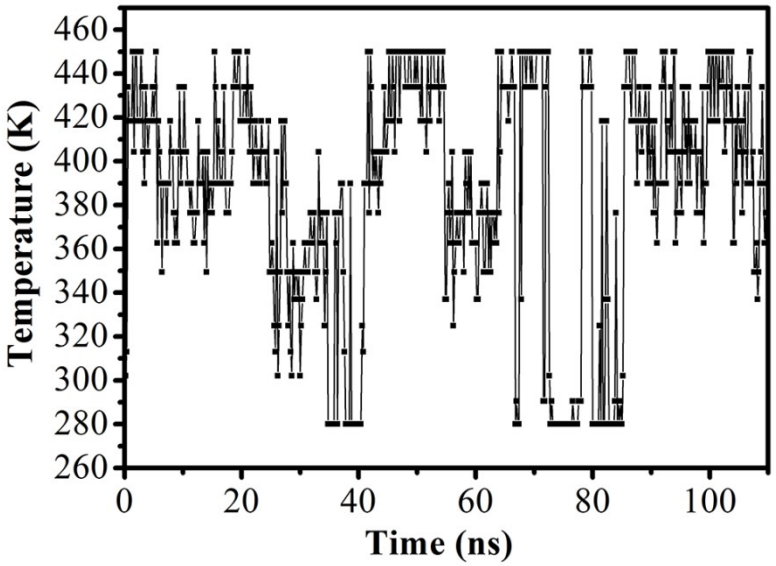

Figure S2. Temperature history of a representative replica in the hREMD simulation of HIV-1 PR in water. For clarity, we sampled the data every 100 exchanges.

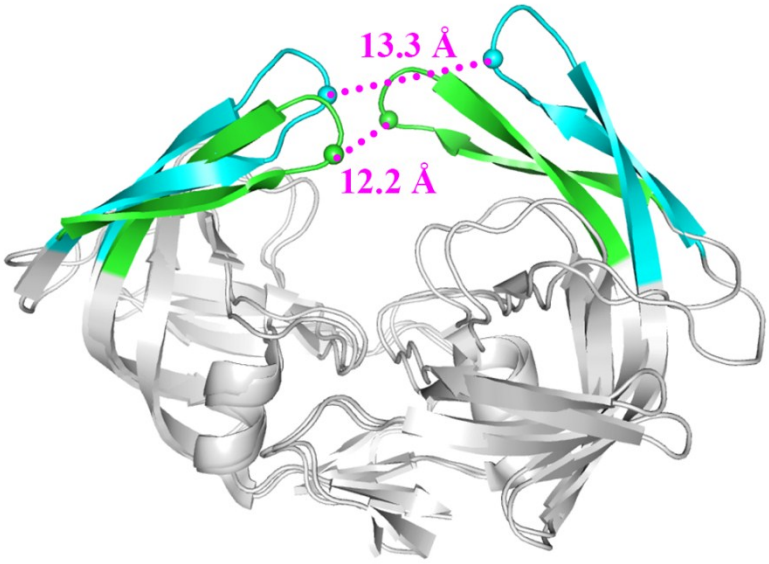

Figure S3. The fully open structure from hREMD simulation (cyan flap) superimposed onto crystal wide-open structure 1TW7 (green flap). Ile50 and Ile50' are shown as balls and their distance is shown by dash line.

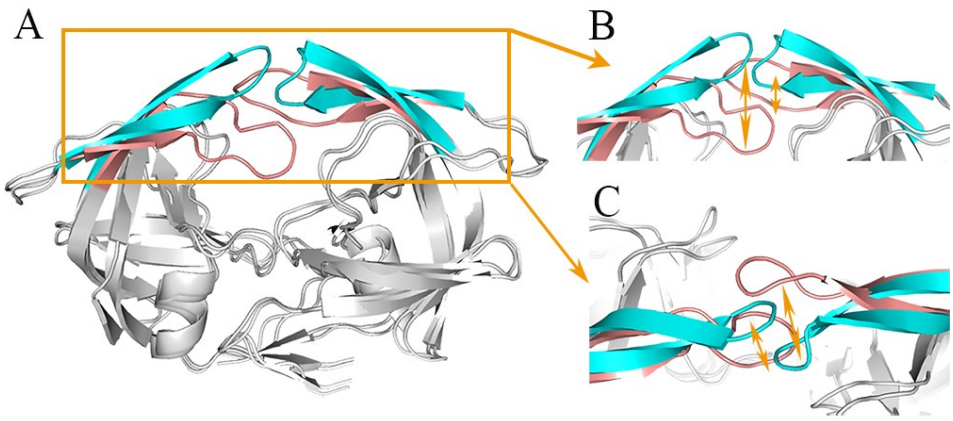

Figure S4. (A) The semi-open structure from hREMD simulation of wild-type HIV-1 PR (cyan flap) superimposed onto the “semi-open” structure from conventional MD simulation of Act variant (wine flap). (B, C) The side view and top view indicating the structure difference in flaps.

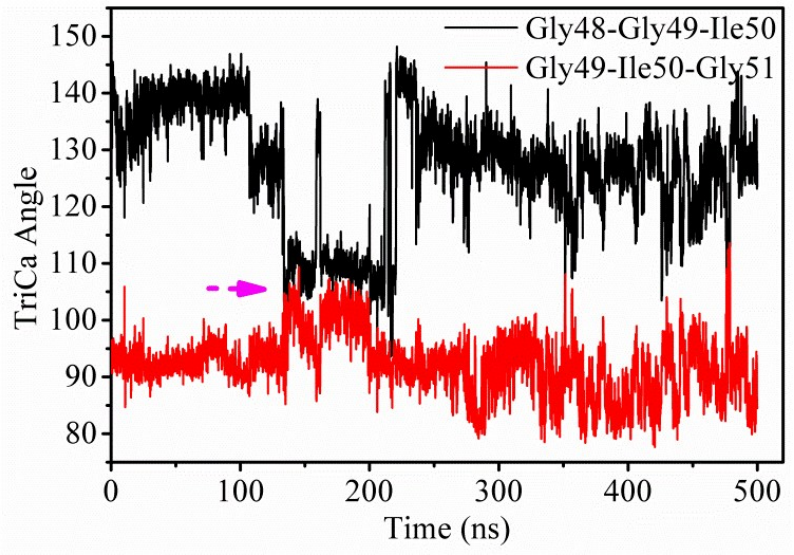

Figure S5. Time series of TriCa angles of Gly48-Gly49-Ile50 and Gly49-Ile50-Gly51 in the conventional MD simulation of Act variant (arrow indicates the time for the occurrence of flap curling).