Electronic Supplementary Material (ESI) for RSC Advances.

Fig. s1 (a) the 3D structure of Ac-Leu-*p*NA; (b) The 3D structure *p*NPC8.

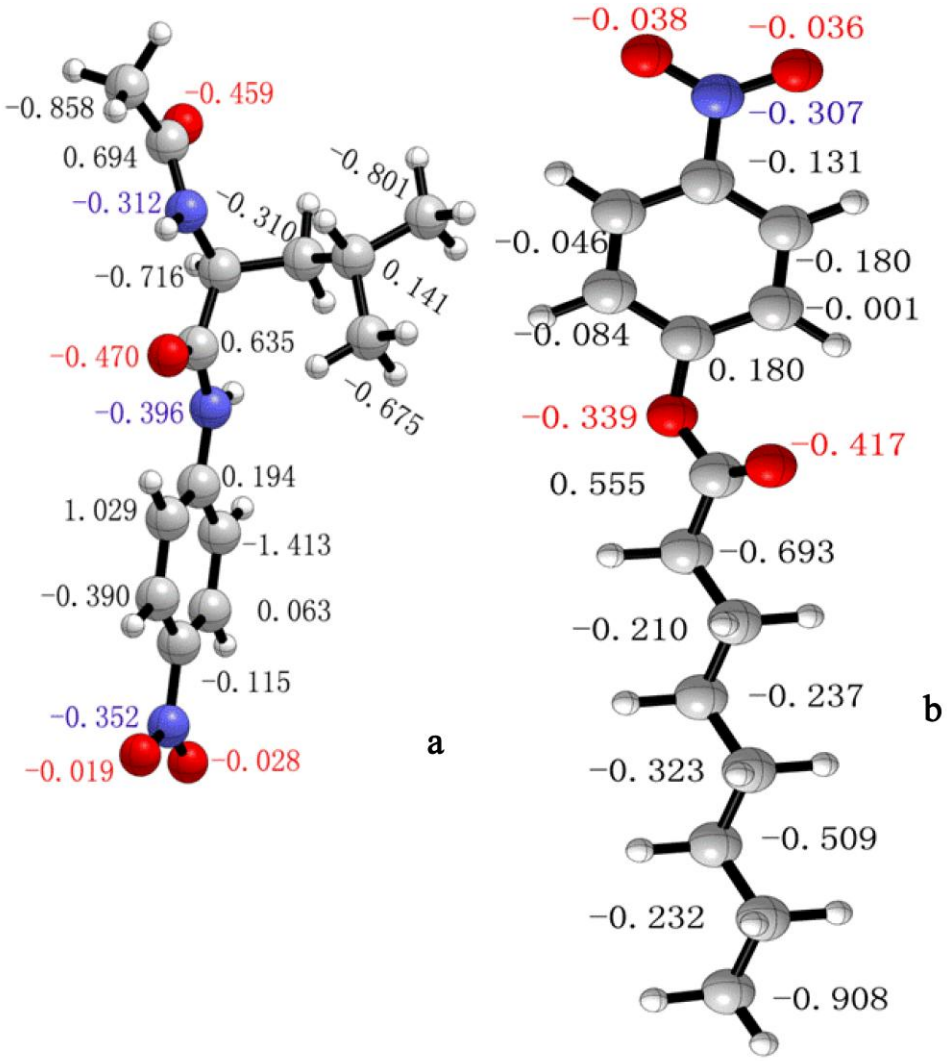

Fig. s2 (a) Three similar docked poses with different scores for Ac-Leu-*p*NA (blue (-7.8 kcal/mol), magenta (-7.2 kcal/mol), cyan (-6.8 kcal/mol)). Snapshots of Ac-Leu-*p*NA/APH at (b) 0.6, (c) 1.2 and (d) 2ns.

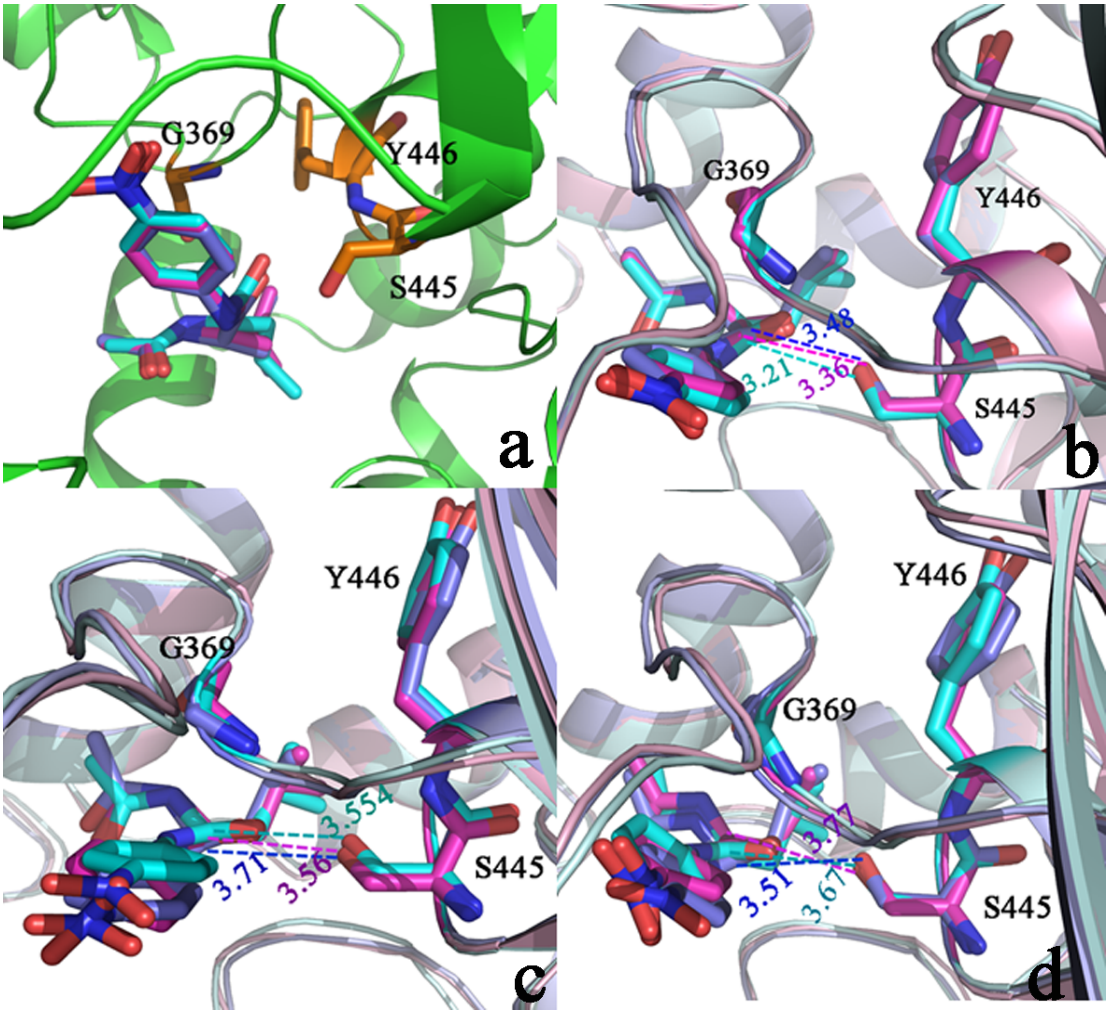

Fig. s3 (a) Three similar docked poses with different scores for *p*NPC8 (blue (-7.9 kcal/mol), magenta (-7.4 kcal/mol), cyan (-7.0 kcal/mol)). Snapshots of *p*NPC8/APH at (b) 0.6, (c) 1.2 and (d) 2ns.

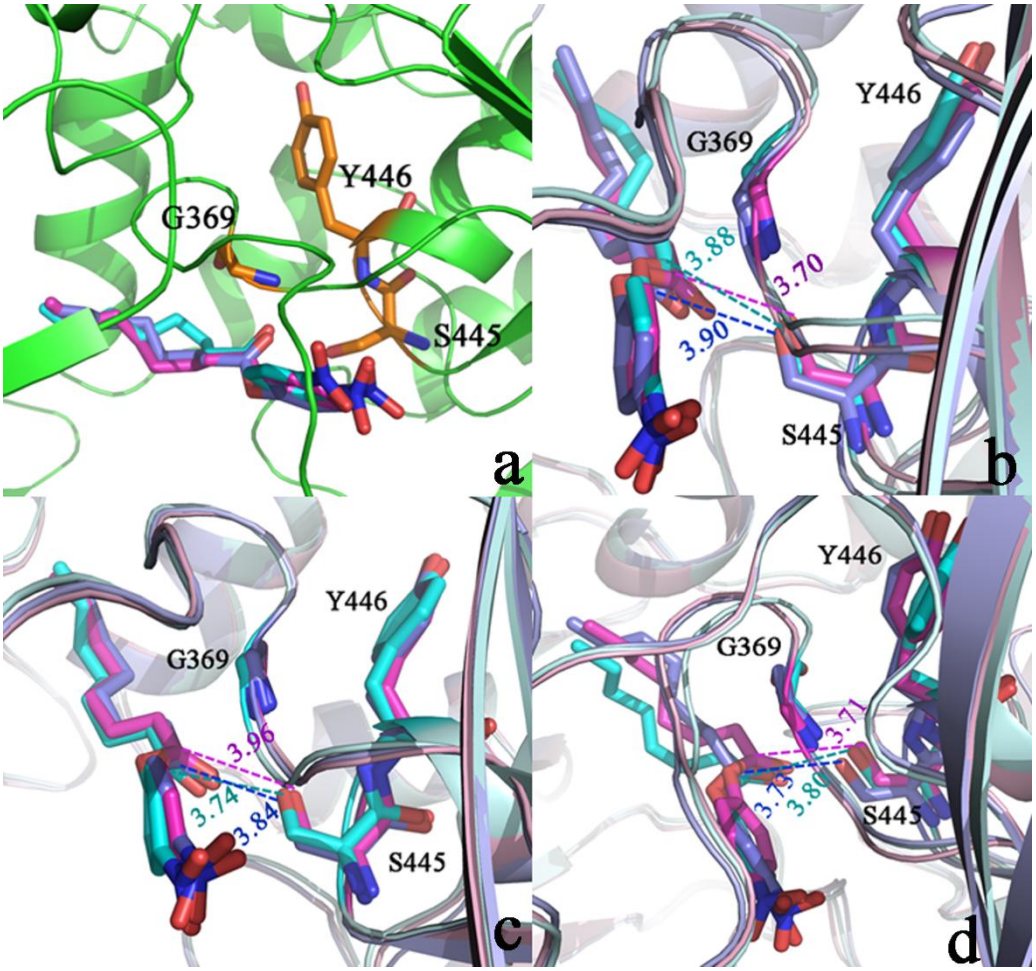

Fig. s4 The binding mode of *p*NPC8 at force peak via P2A.

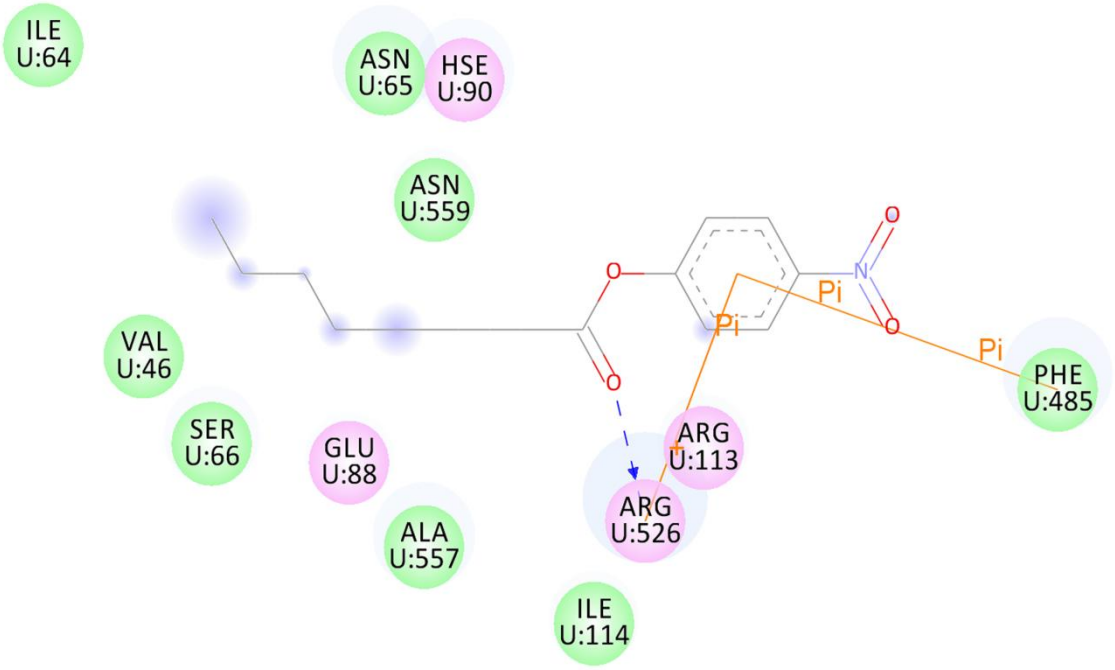

Fig. s5 The binding mode of Ac-Leu-*p*NA at force peak via P1.

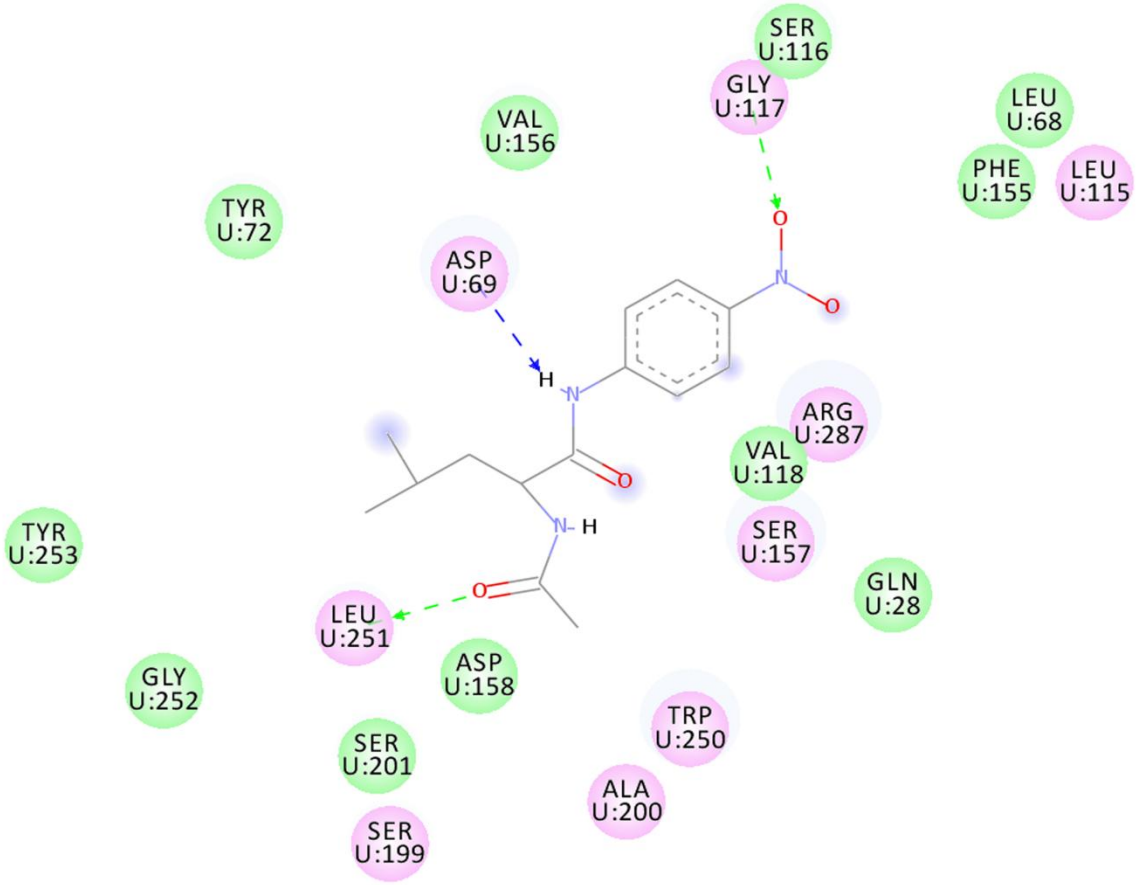

Fig. s6 Snapshots of *p*NPC8 unbinding from APH along P3 at (a) 1.5, (b) 2.2, (c) 4.5, and (d) 6.6 ns.

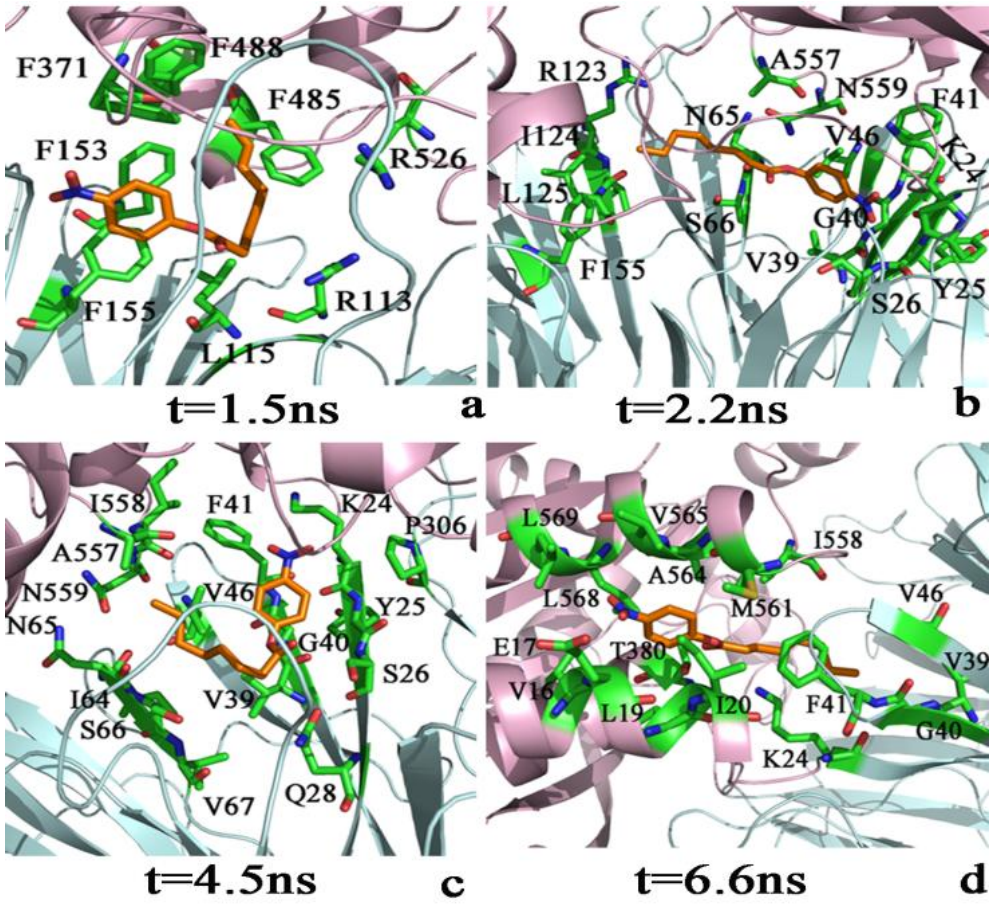

Fig. s7 The binding mode of *p*NPC8 at force peak via P3.

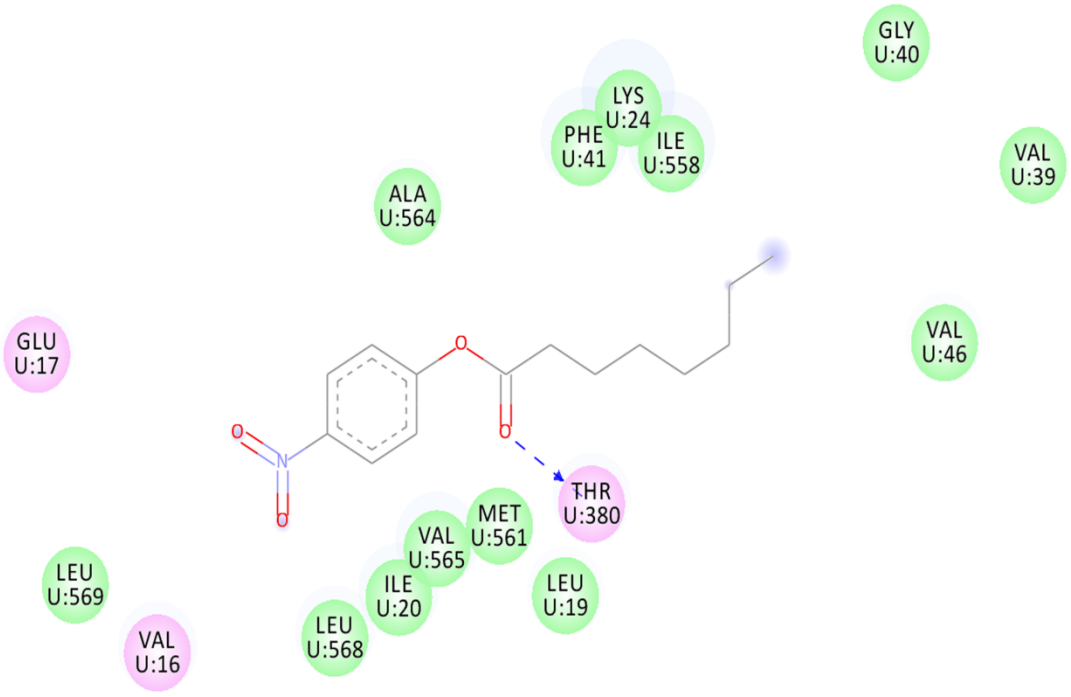

Fig. s8 Snapshots of Ac-Leu-*p*NA unbinding from APH along P3 at (a) 1.9, (b) 2.6, (c) 2.7, and (d) 7.1 ns.

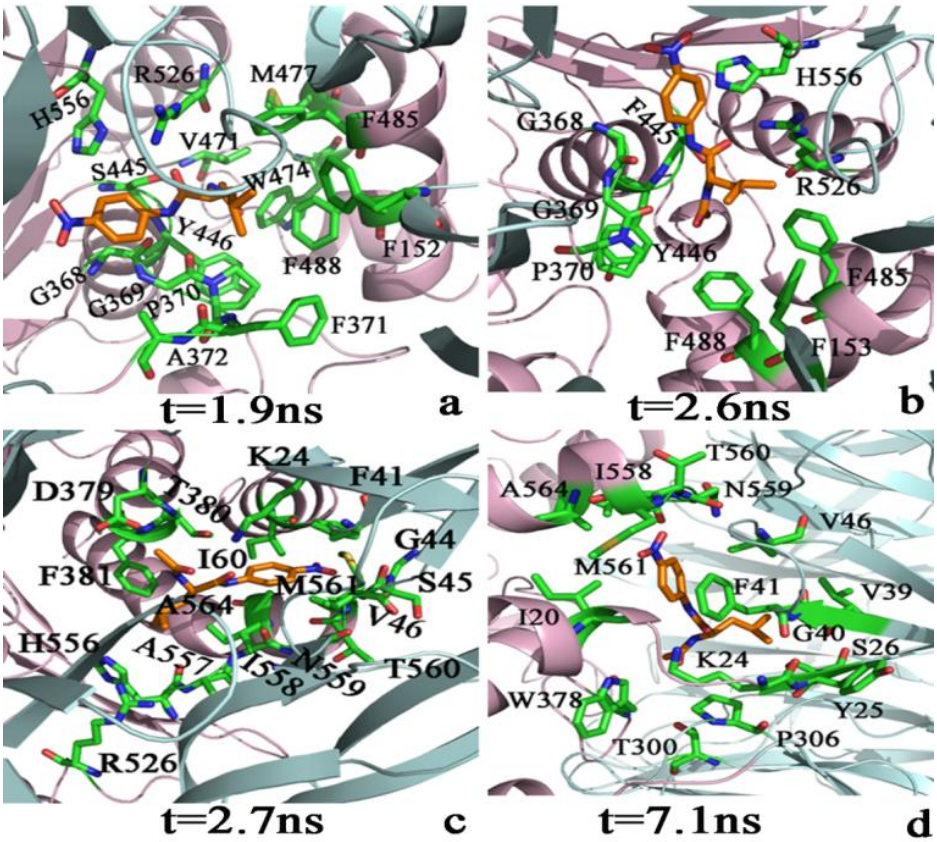

Fig. s9 The binding mode of Ac-Leu-*p*NA at force peak via P3.

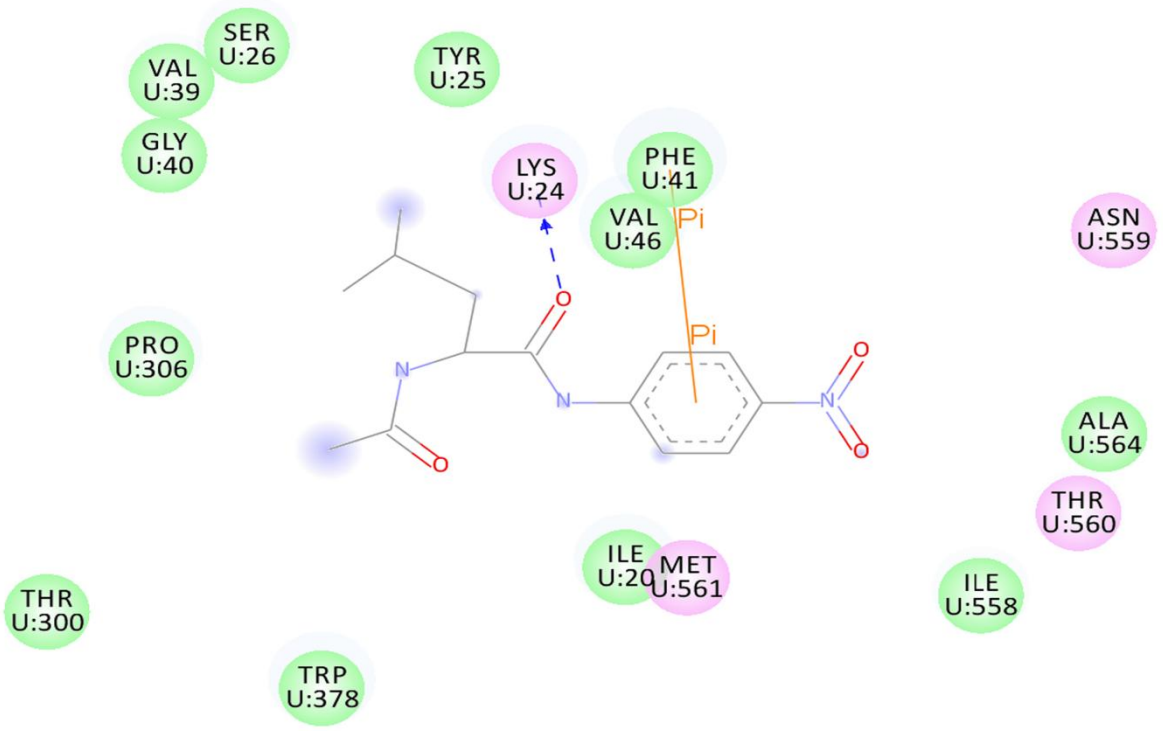

Fig. s10 The distance between aromatic ring of Phe485 and guanidine group of Arg526 (P2A).

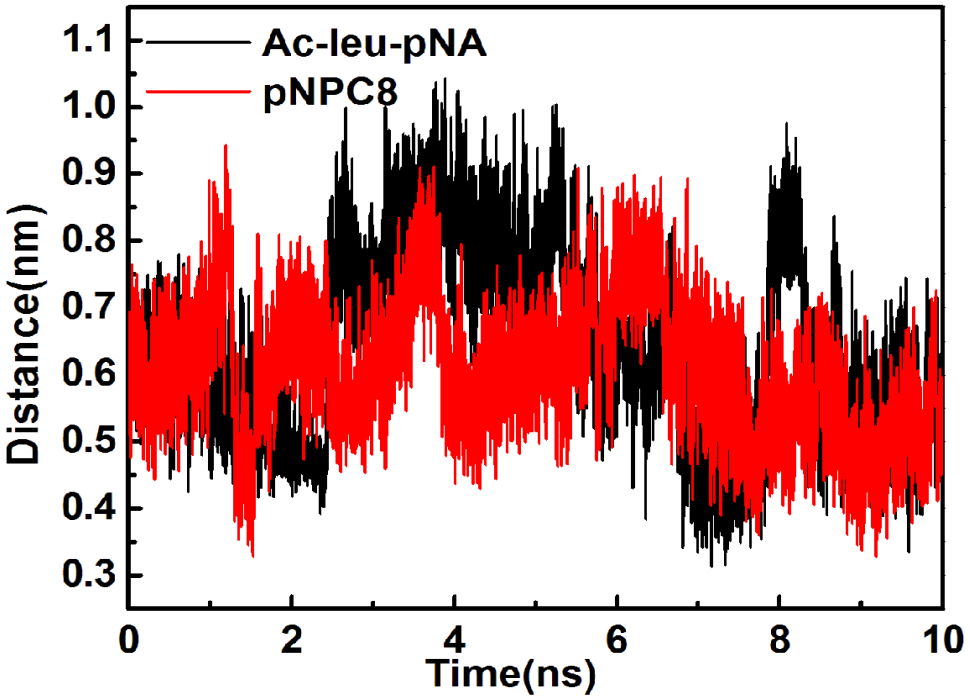

Fig. s11 PMF profile along the unbinding pathway of *p*NPC8 via (a) P2A, (b) P1, and (c) P3; and of Ac-Leu-*p*NA via (d) P1, (e) P2A, and (f) P3. Given that the process is reversible, the free energy profile also applies to the binding process.