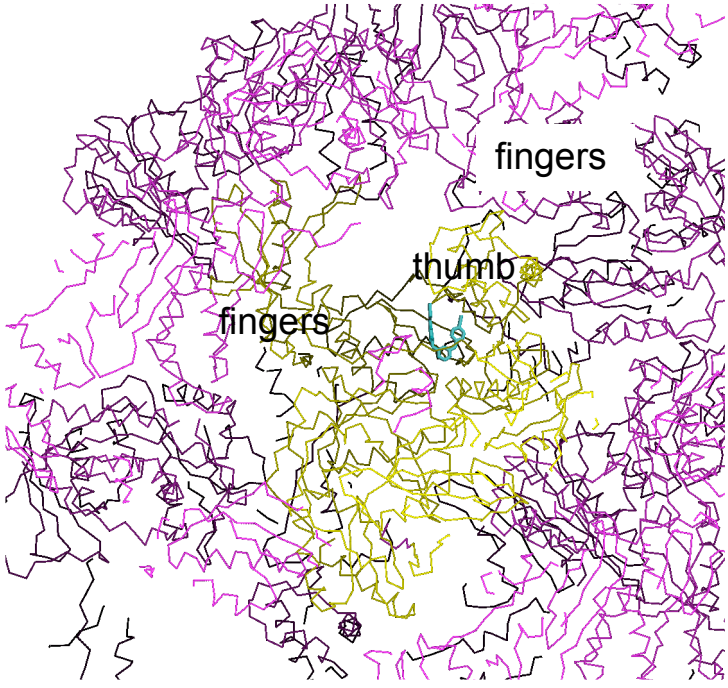

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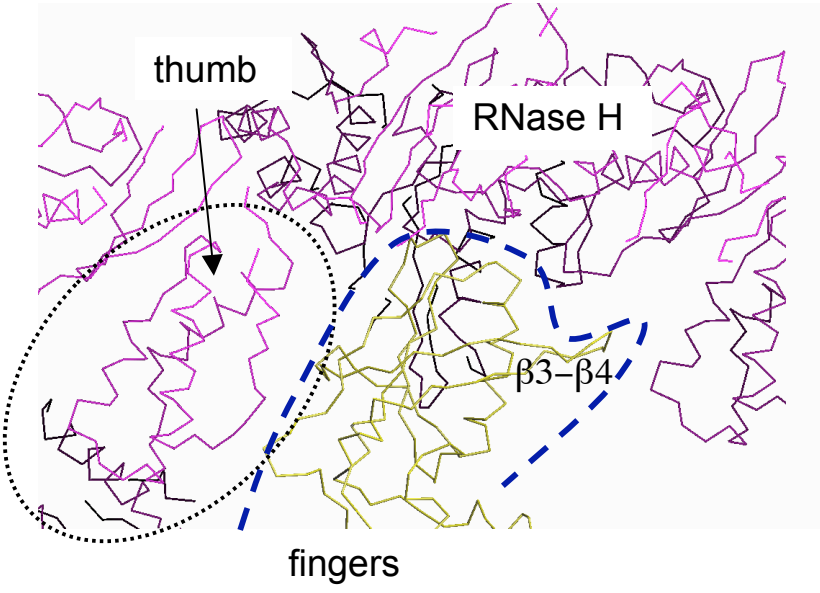

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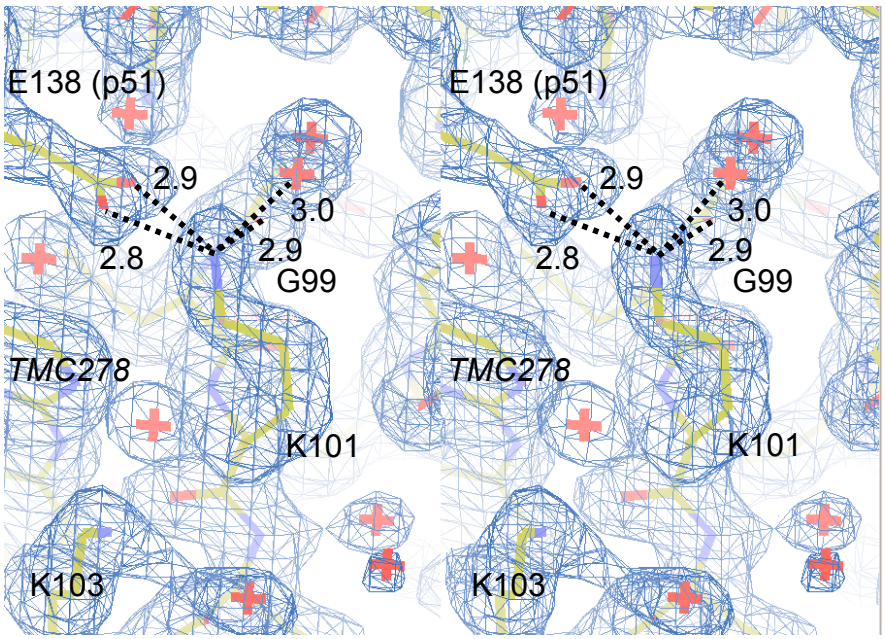

Fig. S2. Stereoview of the region surrounding amino acid residues K101 and K103 of the wild-type HIV-1 RT/TMC278 complex. The electron density map calculated at 1.8 Å resolution demonstrates accurate positioning of the side chains and solvent molecules. A striking feature is that the K101 Nζ atom makes close contacts with four oxygen atoms (represented by dotted lines), including a bifurcated hydrogen bond with the carboxylate oxygens of p51 residue E138.

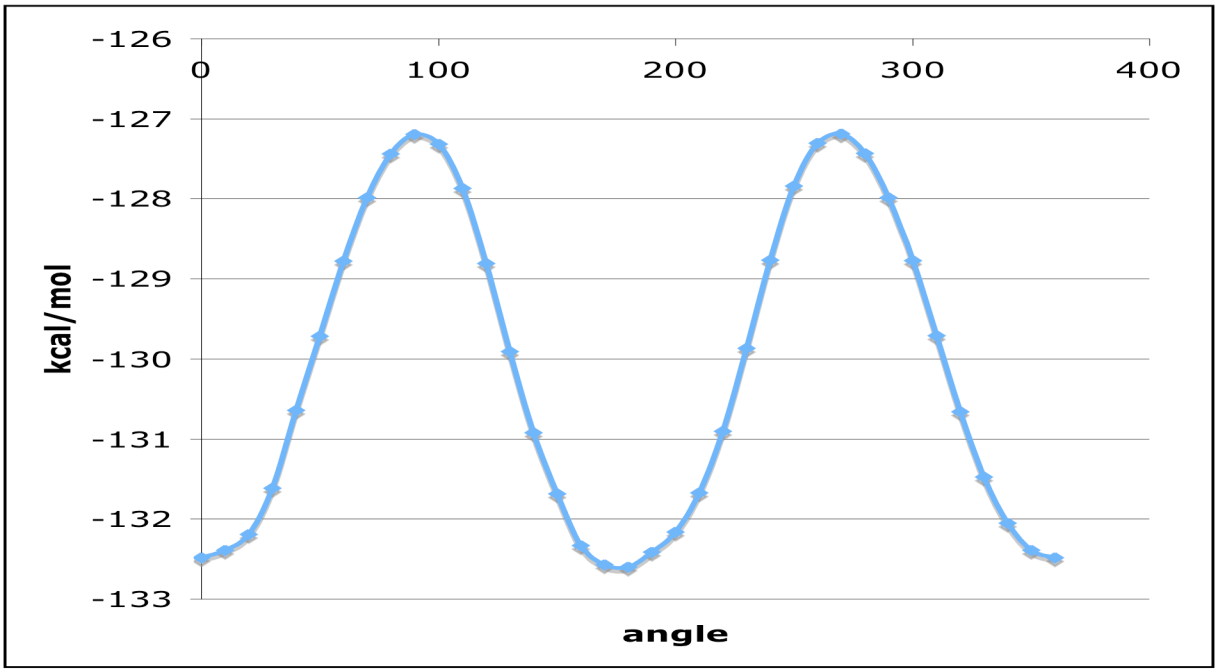

Fig. S3: Plot of total energy calculated for a free TMC278 molecule while varying the torsion angle τ5. The conformation of TMC278 molecule from the wild-type RT/TMC278 structure was used as starting model. In the energy minimization, the torsion angle τ5 was rotated from 0 to 360º in steps of 10º and each conformation was energy minimized keeping other four rotatable torsion angles (τ1–τ4) fixed; the energy minimization was carried out using program MACROMODEL in the software package Schrödinger V8.0 (http://www.schrodinger.com/).