The p66 Immature Precursor of HIV-1 Reverse Transcriptase.

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List of the Supplementary data.

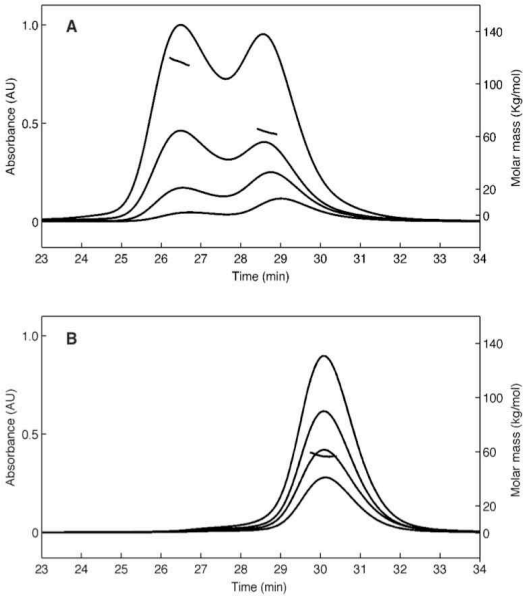

Figure S1. Multi-angle light scattering (MALS) elution profiles of (A) the p66 and (B) the p51 protein samples. Experiments were repeated at different protein concentrations from 10.9 μM to 59.9 μM and 19.3 μM to 58.6 μM, for p66 and p51 samples, respectively. Assuming that the samples are diluted approximately 10-fold on the gel-filtration column, homodimer dissociation constants for p66 and p51, calculated from the observed MALS results, are 4.3 ± 0.7 μM and 318 ± 116 μM, respectively, which are in excellent agreement with the published homodimer dissociation constants of ~4 μM and ~230 μM for p66 and p51, respectively, as descried in the main text.

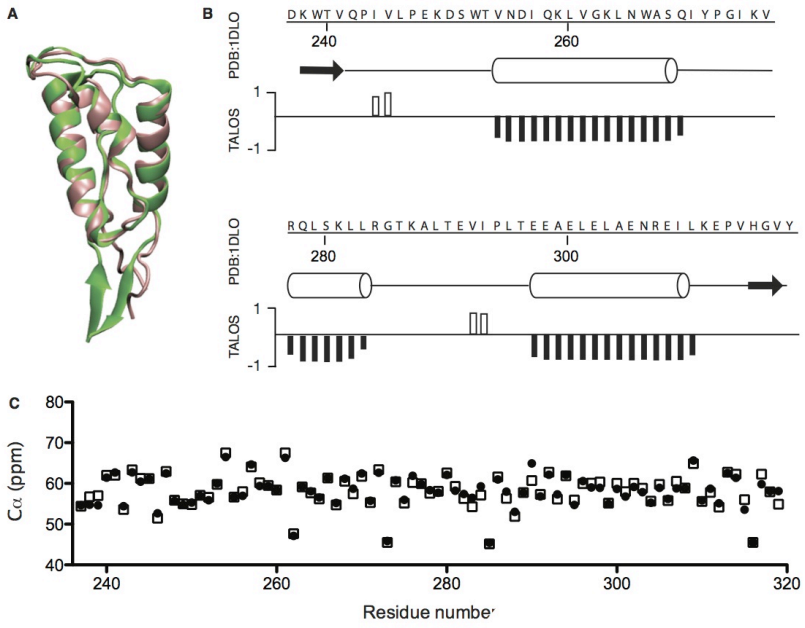

Figure S2. Thumb domain structure comparison: (A) Thumb domain structure in the p66 (green) and p51 (pink) subunits in the RT crystal structure (PDB: 1DLO), (B) TALOS+ derived secondary structure of the isolated Thumb domain, based on C_α, C_β, C', N, and H_N chemical shifts. The amino acid sequence and secondary structure elements in the RT crystal structure are depicted on top. (The N-terminal methionine and the C-terminal 6 histidines are omitted), (C) Experimentally determined C_α chemical shifts for the isolated Thumb domain (black circles) compared with those back-calculated from the coordinates of the Thumb domain in 1DLO, using Sparta (open square).

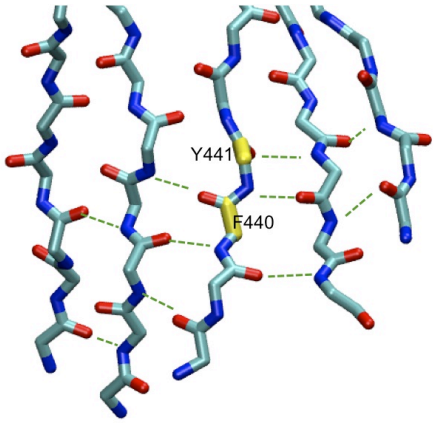

Figure S3. Region of the RNH backbone structure with a subset of hydrogen bonds highlighted (dashed lines). In the ^{1}H-^{15}N HSQC TROSY spectrum of the p66 homodimer, cross-peaks reside at similar positions, in frequencies, to these highlighted amide ones of the isolated RNH fragment (±27 Hz). NMR structure of the isolated RNH domain (PDB = 1O1W) was used to generate the graphics.