Supplementary information for

Recognition of the HIV capsid by the TRIM5a restriction factor is mediated by a subset of pre-existing conformations of the TRIM5a SPRY domain.

Dmytro B. Kovalskyy, Dmitri N. Ivanov*.

Department of Biochemistry and Cancer Therapy and Research Center, University of Texas Health Science Center at San Antonio, 7703 Floyd Curl Drive, San Antonio, TX 78229, USA.

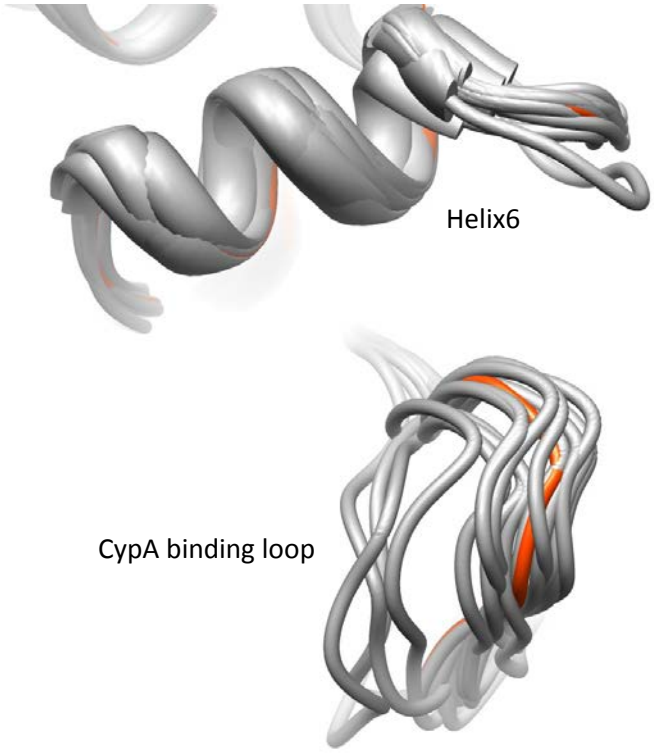

Figure S1. Superposition of the HIV-1 CA NTDs from X-Ray structures found in PDB with CypA binding loops resolved. Structures were overlaid using Cα atoms of the α-helixes from NTD domain. A consistently stable shape of the backbone suggests a preferred conformation of the CypA binding loop.

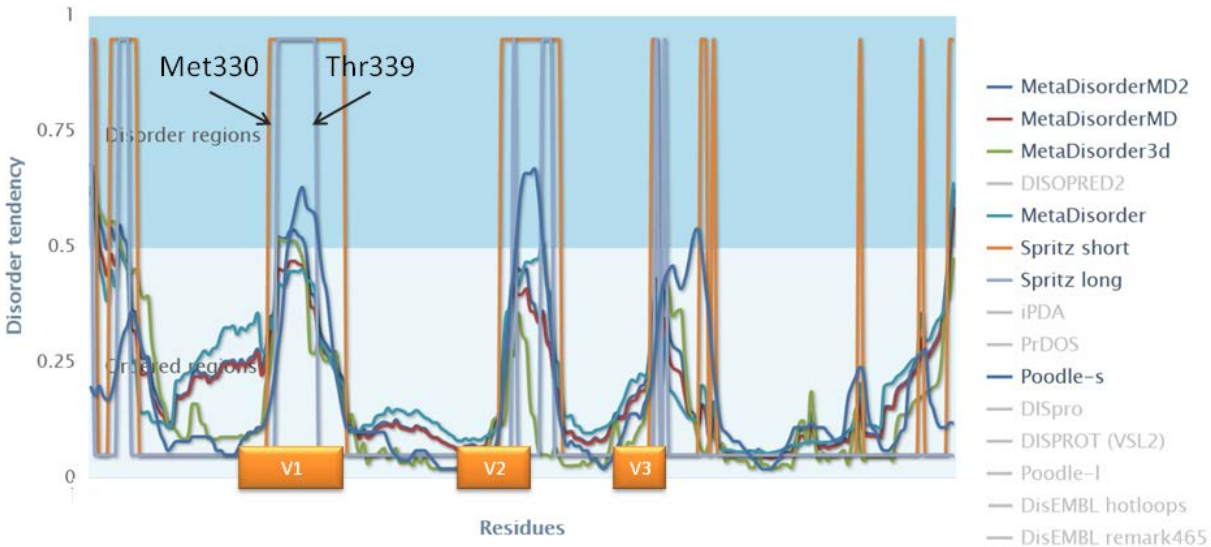

Figure S2. Prediction of IDP propensity for SPRY domain of rhesus.[(1)] **A**lgorithms that returned acceptable predictions are shown.

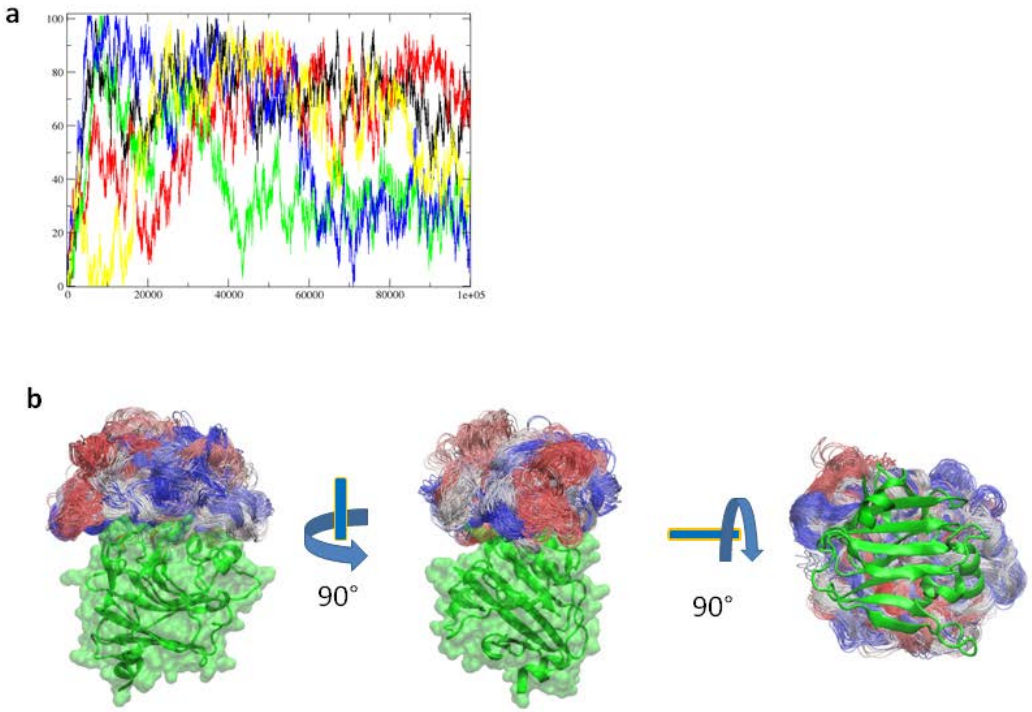

Figure S3. ***a***. Replica walk in the temperature corridor during 100 ns of REMD. First 5 replicas are shown. Random behavior and wide motions suggest sufficient amount of successful exchanges between replicas along simulated time. ***b***. Distribution of the v1 loop conformations along REMD trajectory. The core is colored in green. v1 loop is represented as wires and colored after time step in the trajectory. The extensive coverage of conformational space is evident.

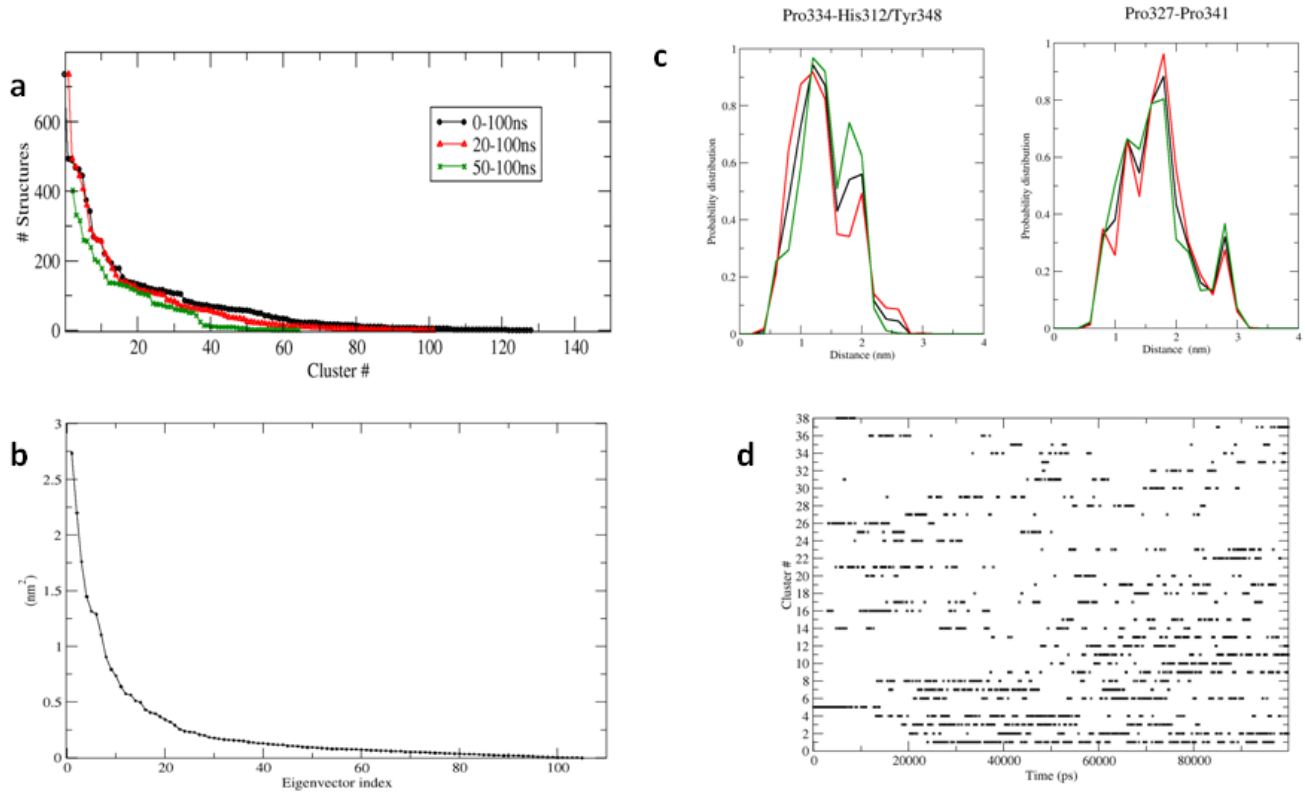

Figure S4. ***a***. Size of clusters derived from clusterization of REMD trajectory at 300K (10000 snapshots). To compare cluster sizes distribution across trajectory three versions of the trajectory where clustered. ***b***. Eigenvalues of corresponding eigenvectors for the REMD trajectory at 300K. ***c***. Distance probability distribution between v1 loop basement (H312/Y349) and loop tip (P334) . Black whole 100ns trajectory at 300K; green 0-49ns; red – 50-100ns. ***d***. distribution of cluster members across timeline.

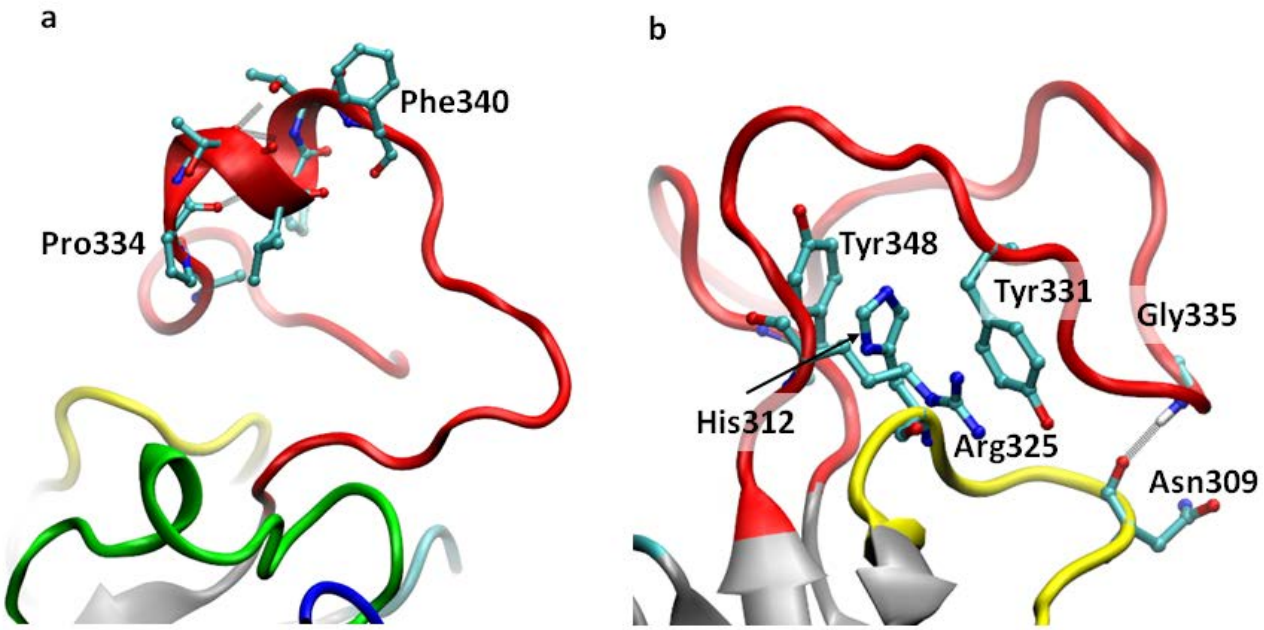

Figure S5. Two types of the v1 loop stabilization. Loop colors same as on Figure 1 of the main text. ***a***. Stabilization through helices formation. Centroid #6 with a-helix in the P334-F340 region is shown. ***b***. Hydrophobic collapse is stabilized through pi-pi and cation-pi interactions. Residues contributing to the hydrophobic core of the centroid #1 are shown.

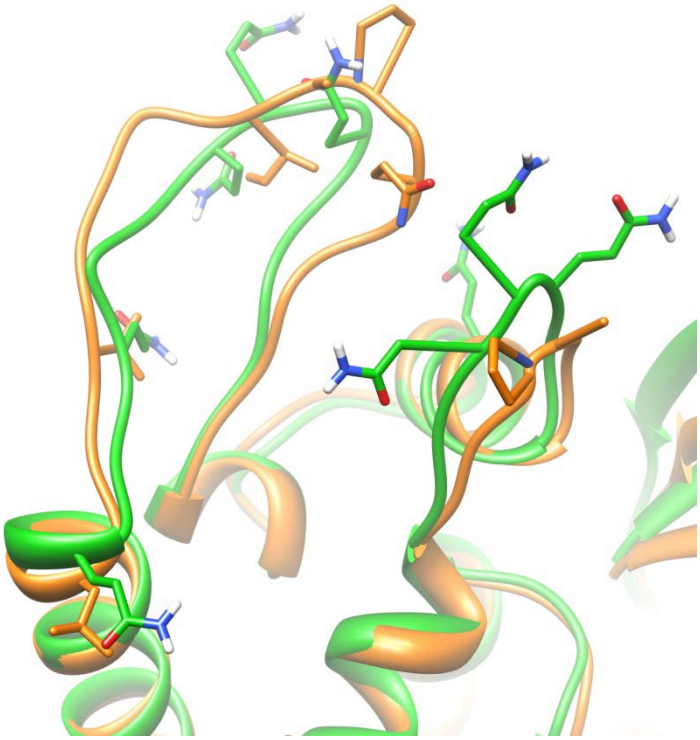

Figure S6. Solvent exposed segments of the HIV-1 (*gold*) and SIVmac239 (*green*) capsids differ not only in conformation of the CypA binding loop but also in amino acid composition. SIVmac239 in enriched with polar not charged residues glutamines and asparagines. Amino acids in corresponding HIV-1 CA positions are hydrophobic with only one glutamine residue Q95.

REFERENCES:

1. Kozlowski, L. P., and Bujnicki, J. M. (2012) MetaDisorder: a meta-server for the prediction of intrinsic disorder in proteins, *BMC bioinformatics 13*, 111.