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Supporting information for article:

Molecular architecture of the nucleoprotein C-terminal domain from the Ebola and Marburg viruses

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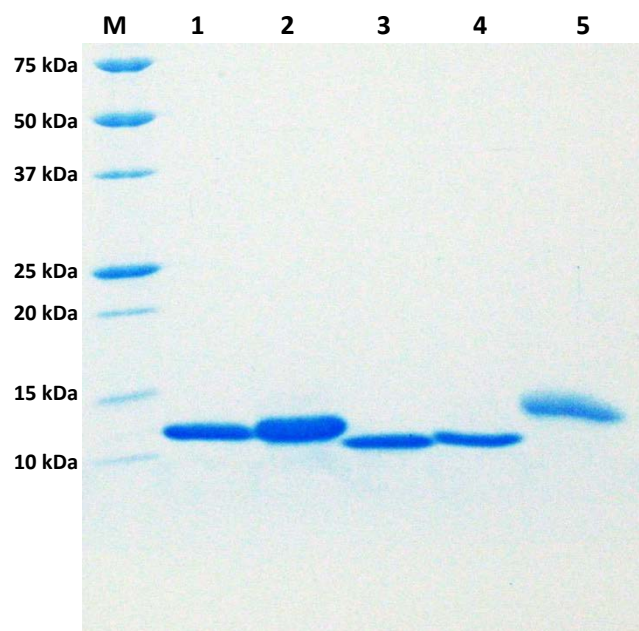


Figure S1. A Coomassie-stained 15% SDS-PAGE gel showing the final NP^{Ct} samples used for crystallization. The lanes are as follows: M) molecular-weight markers, 1) RESTV NP^{Ct}, 2) BDBV NP^{Ct}, 3) SUDV NP^{Ct}, 4) TAFV NP^{Ct}, and 5) MARV NP^{Ct}.

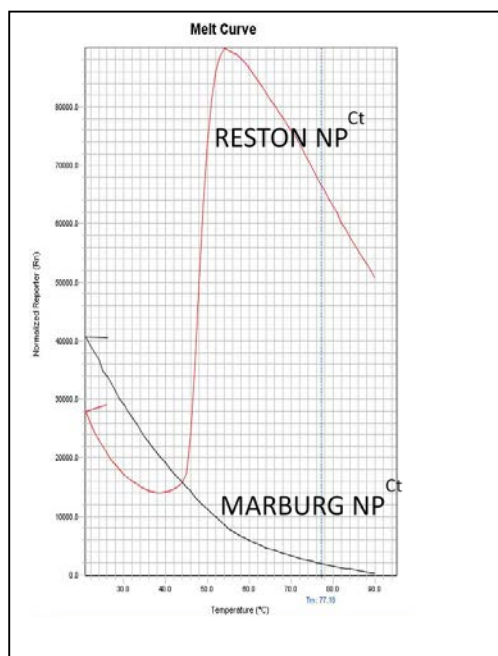
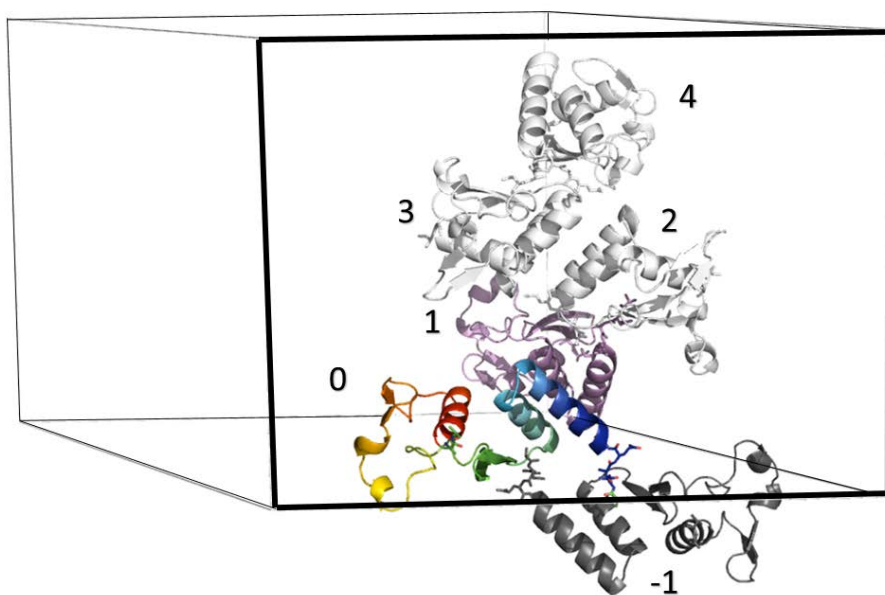


Figure S2. Raw data for scanning fluorescence (Thermal stability assay) for the Reston and Marburg NP^{Ct} proteins. Details in the text.

A



B

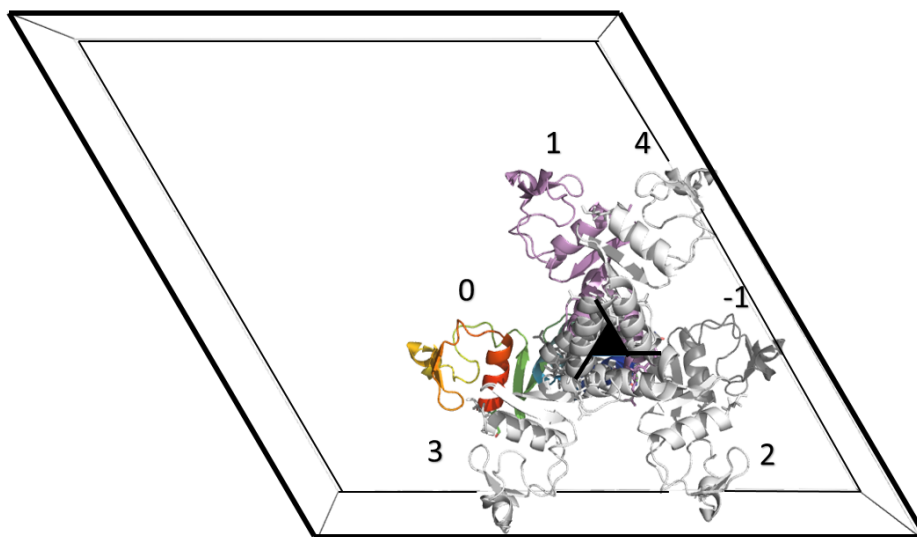


Figure S3: Two perpendicular views of the packing of molecules of Bundibugyo NP^{Ct} around the three-fold screw axis. (A) View perpendicular to the symmetry axis; the contact between molecules 0 (rainbow) and -1 (grey) involves the N-termini (shown as sticks); the contact between molecules 0 and 1 (magenta) involves the interaction of the α -helical hairpins. The 0/-1 dimer is then rotated 120° and translates 1/3 along the crystallographic three-fold screw axis. Molecules 2-4 are shown in white. (B) View down the crystallographic three-fold screw axis.

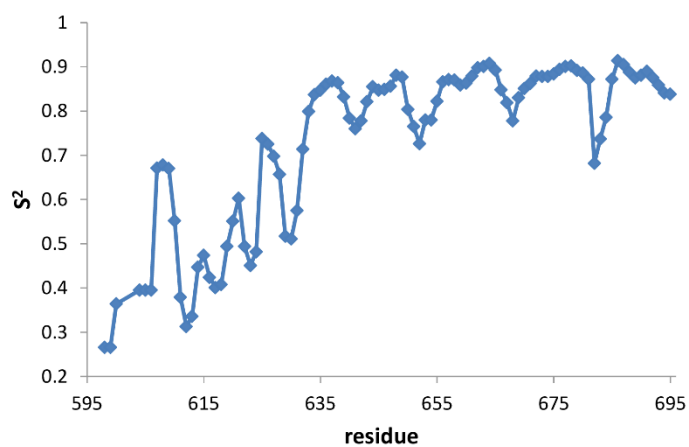


Figure S4. Backbone segmental order parameter versus residue number. Order parameters were obtained from backbone ^1H (except $\text{H}\alpha$), ^{13}C , and ^{15}N chemical shifts by the method of (Berjanskii & Wishart, 2005).

Berjanskii, M. V. & Wishart, D. S. (2005). *J Am Chem Soc* **127**, 14970-14971.