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Supporting information for article:

Structure of LCMV Nucleoprotein Provides a Template for Understanding Arenavirus Replication and Immunosuppression

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Table S1 Structural Alignments

Molecule 1	Molecule 2	r.m.s.d. (Å)
LCMV NPΔ340 $P6_5$ chain A	Lassa NP CTD (PDB 3Q7C)	0.479
LCMV NPΔ340 $P6_5$ chain A	Tacaribe NP CTD (PDB 4GVE)	0.787
LCMV NPΔ340 $P6_5$ chain A	Junin NP CTD (PDB 4K7E)	1.491
LCMV NPΔ340 Monomers		r.m.s.d. (Å)
$P6_5$ chain A aligned to $P6_5$ chain B		0.133
Average for all $P2_1$ Chains aligned to each other		0.345
Average for all $P6_5$ chains aligned to all $P2_1$ chains		0.385
LCMV NPΔ340 Dimers		r.m.s.d. (Å)
Average for all $P2_1$ dimers aligned to each other		0.377
Average for the $P6_5$ dimer aligned to each $P2_1$ dimer		1.880

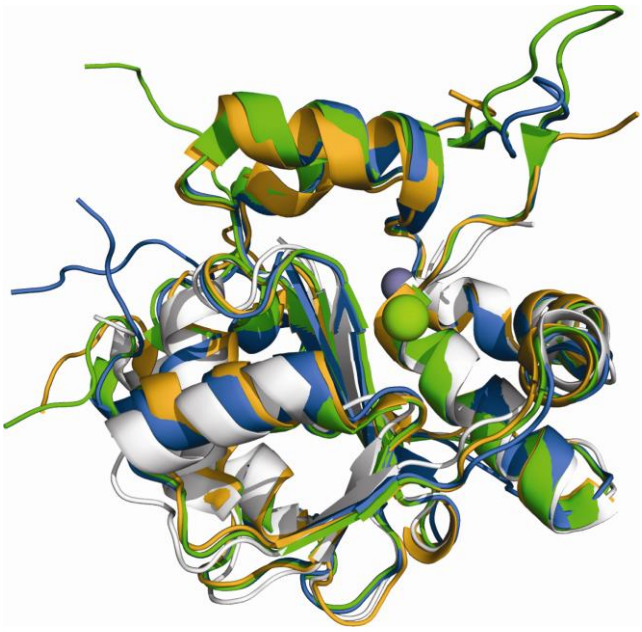

Figure S1 LCMV NPΔ340 structural Alignments. The LCMV C-terminal domain structure (blue) is aligned to previously characterized C-terminal NP structures from Lassa (green), Tacaribe (orange) and Junin virus (white).

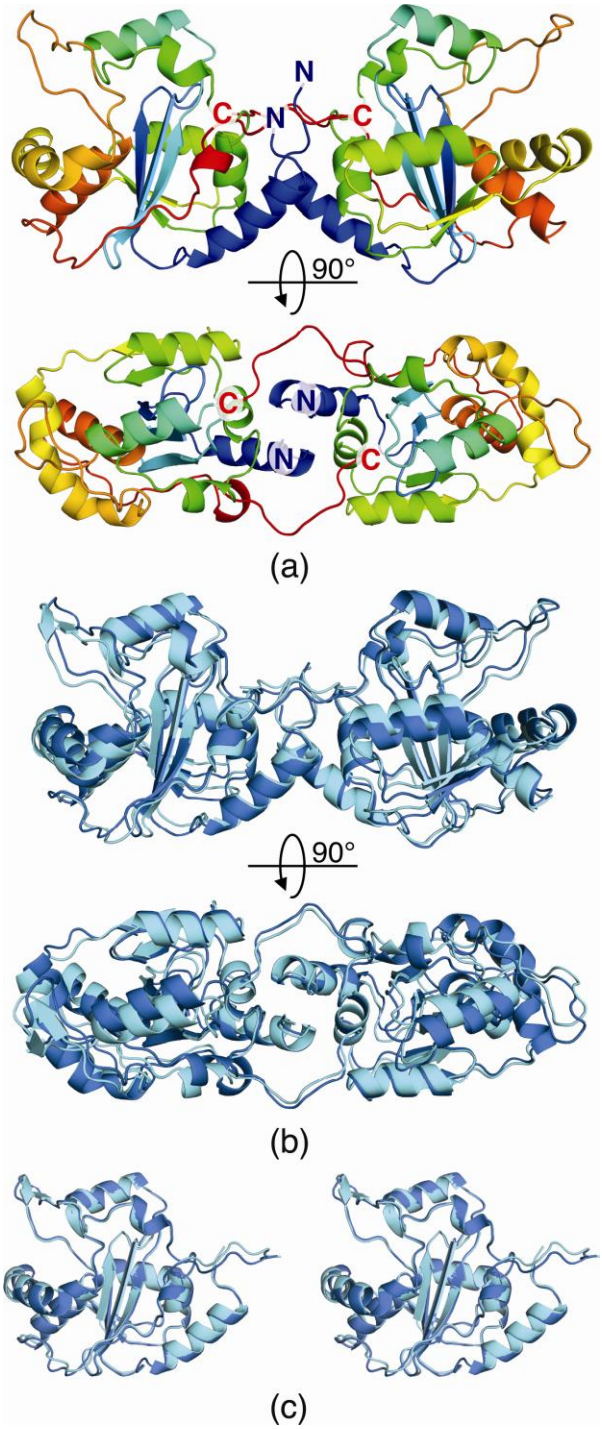

Figure S2 Alignment of LCMV NPΔ340 from the $P2_1$ and $P6_5$ crystals. (a) Side view and 90° rotated top-down view of the A/B chain dimer of LCMV NPΔ340 from the $P6_5$ crystal. Each monomer is displayed as a cartoon colored as a rainbow from the N- (blue) to C-terminus (red). The N- and C-termini are labeled with an N and C respectively. (b) Alignment of the A/B chain dimer from the $P6_5$ crystal (dark blue) to the A/D chain dimer from the $P2_1$ crystal (light blue). The structures align best in the dimeric interface region while showing the greatest deviation in the helices and loops distal to the dimeric interface. (c) Stereo view of the structural alignment between the two A chains from the P65 (dark blue) and P21 (light blue) crystals.

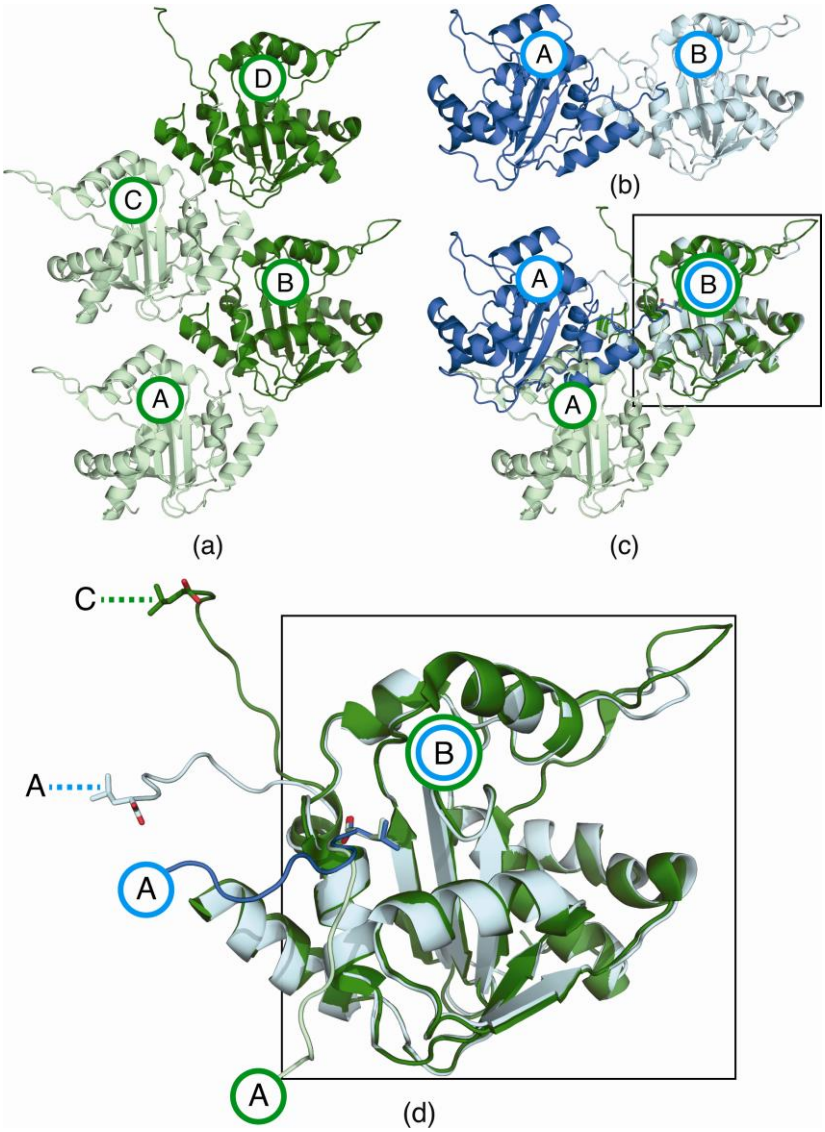

Figure S3 LCMV NPΔ340 versus LASV NP C-terminal domain crystal packing. (a) LASV C-terminal domain (PDB 3Q7C) crystal packing polymer. Each monomer is shown as a cartoon in an alternating green and light green color scheme. The C-terminal residue from each monomer extends up and attaches to a neighboring monomer (A-B, B-C, C-D, etc…). (b) LCMV NPΔ340 crystal packing dimer. The A chain monomer is shown in dark blue, and the B chain monomer is shown in light blue. The C-terminal residue from each monomer connects reciprocally between two monomers (A-B, and B-A). (c) The A-B subunit from the LASV and LCMV NP C-terminal domain crystal packing are shown aligned via the B chains. The LASV dimer is in green and the LCMV dimer is in blue. Note that the position of the A monomers differs relative to the B monomer. (d) Zoomed in view of the region boxed in (c). Here we can clearly see that despite the large shift in the location of the two A monomers relative to the B monomer, the ultimate C-terminal Leu residue (shown as sticks connected to the two circled A chains) inserts into the same pocket on a neighboring monomer. Also evident is the flexibility shown by the C-terminal tail to accommodate a dimeric versus a polymeric interaction (A-B/B-A versus A-B/B-C).

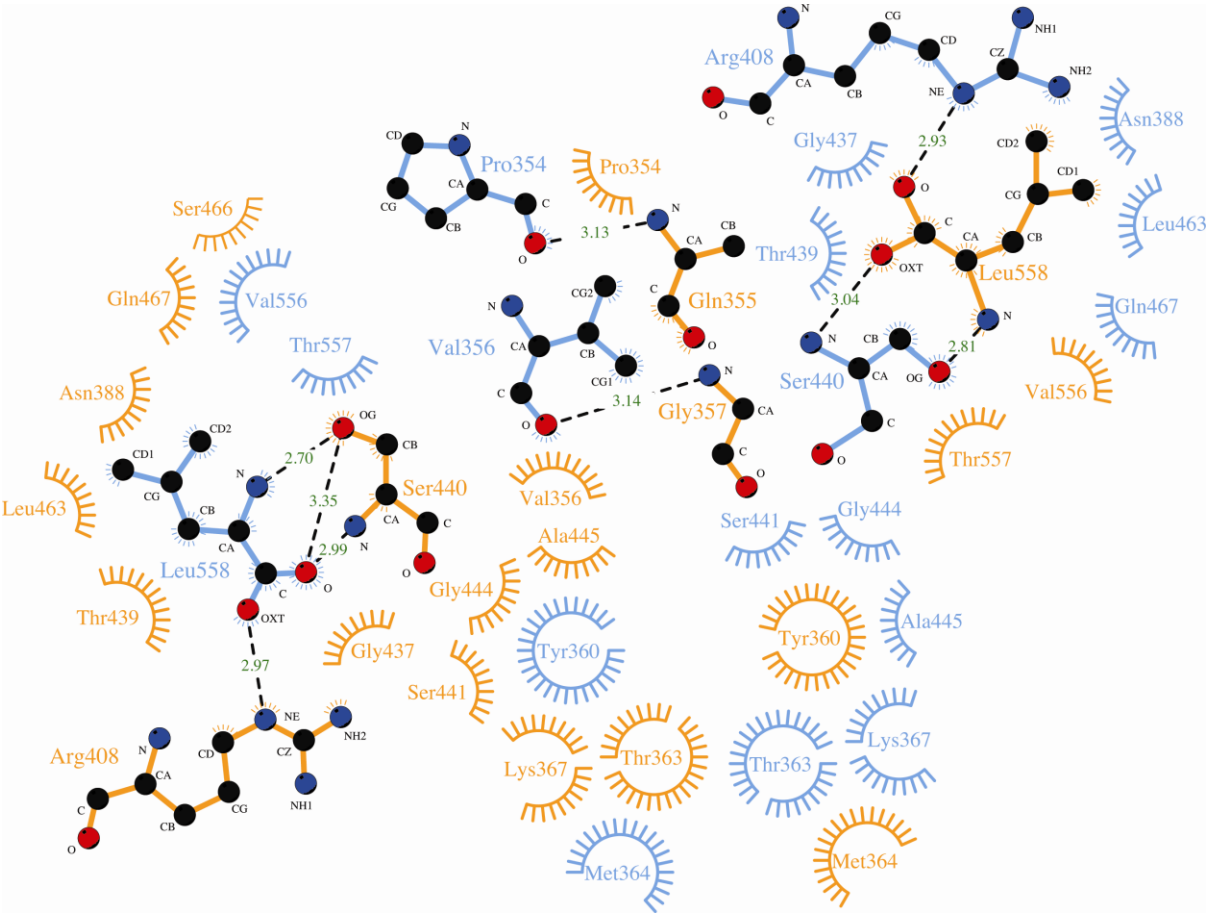

Figure S4 Interactions across the dimeric interface of the LCMV NPΔ340 asymmetric unit. (a) Interactions between monomers of the asymmetric unit are displayed using LigPlot^{+} (Laskowski & Swindells, 2011), with the two monomers in orange and blue, respectively (consistent with the coloring of Figure 3). Hydrogen bonds are displayed as dashed lines with their distances indicated. Hydrophobic interactions are shown as radial lines directed towards the interaction partner.

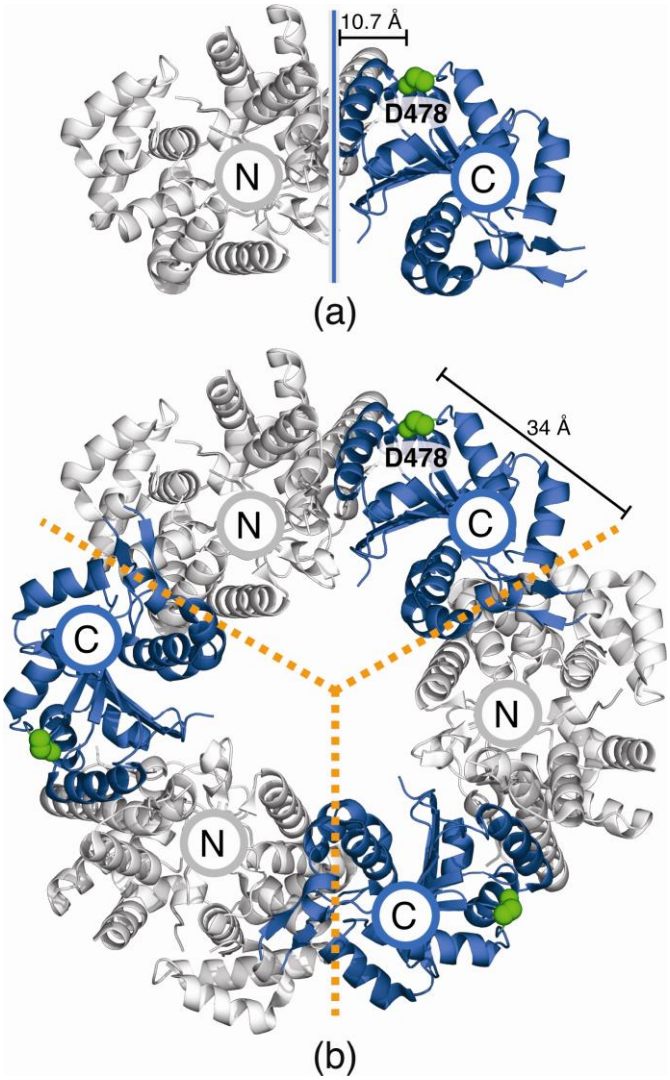

Figure S5 Location of D478 in LASV NP structure. (a) A monomer of LASV NP (PDB 3MWP) with the N-terminal domain shown in grey, and the C-terminal domain shown in blue. A grey line is shown between the two domains. The minimum distance from the N-terminal domain to residue D478 (depicted as green spheres and equivalent to LCMV D471) is indicated as 10.7 Å. (b) The trimeric form of LASV NP observed in the 3MWP crystal packing with the interfaces between monomers indicated with dashed orange lines. The minimum distance from D478 to this interface is indicated as 34 Å.