



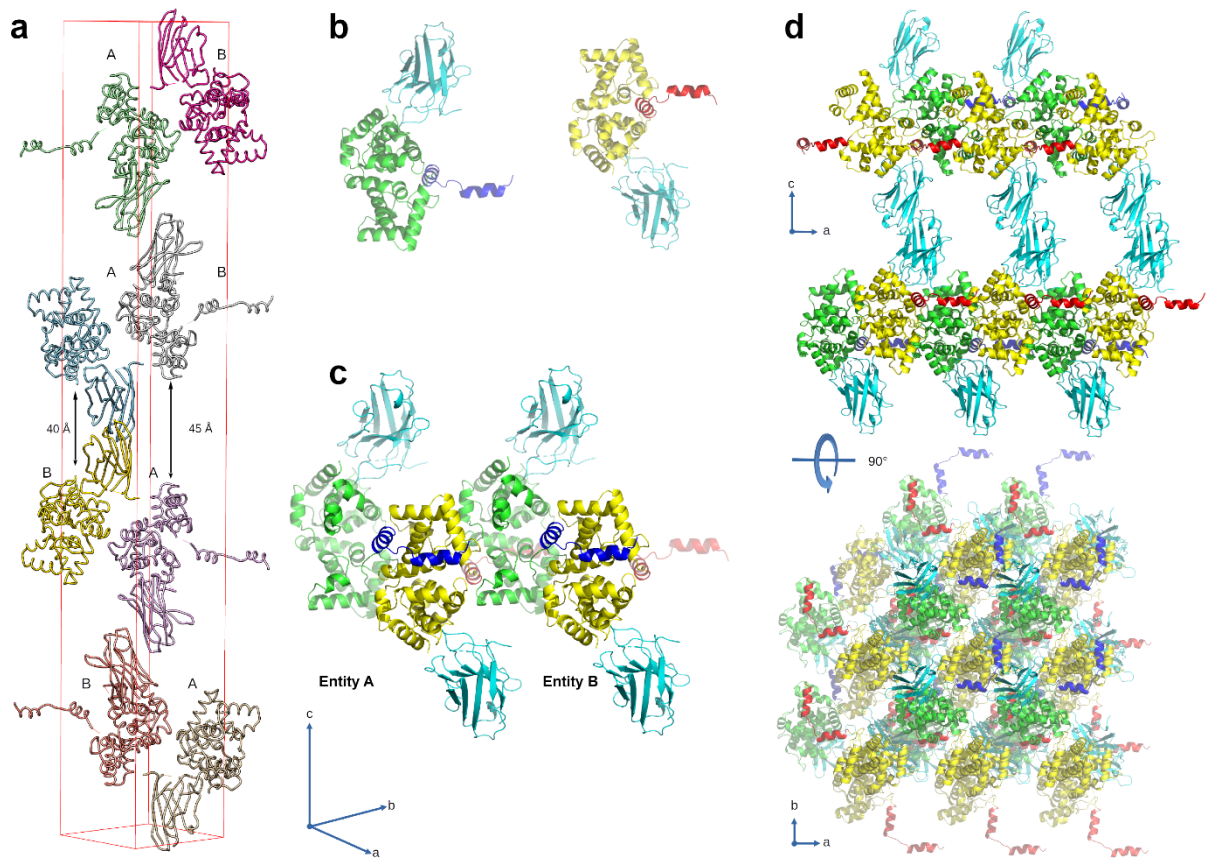
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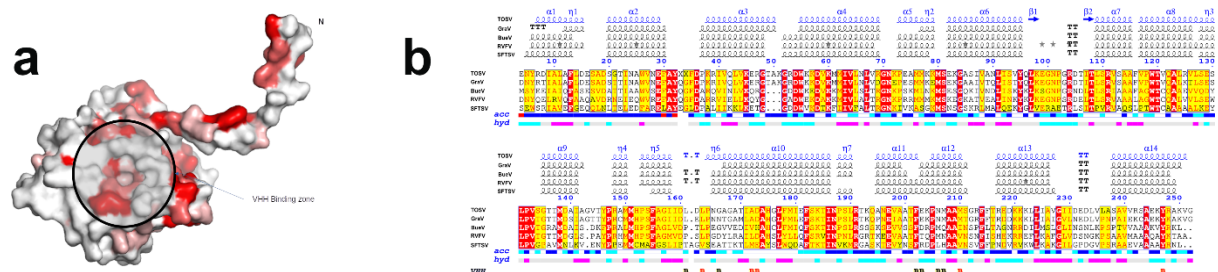
**Supporting information for article:**

**Structural flexibility of Toscana virus nucleoprotein in the presence of a single-chain camelid antibody**

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**Figure S1** The unit cell of the Toscana virus N-VHH heterodimer and its different orientation within the unit cell. (a) One heterodimer is labelled A and the other B. (b) Dissociation of each heterodimer is shown in ribbon. N core of A is coloured in yellow and its N-terminal is in red, while N core of B is coloured in green and its N-terminal is in blue. The bound VHH on A and B is coloured in cyan. (c) Detail of 4 heterodimers named Entity A interacting with the neighbouring 4 heterodimers named Entity B. This assembly Entity A & B is the basic structural motif repeated along the a axis forming a fiber. (d) *Top* Representation of the crystal packing along a axis forming the fibers separated by two interacting VHH. *Bottom* Representation of the crystal packing at 90° showing a tight compact crystal.



**Figure S2** (a) Sequence conservation of N-TOSV of the VHH binding site plotted on the surface. Conservation is plotted according to ENDSCRIPT parameter (White color no conservation Red Identical). (b) Sequence alignment of Phleboviruses N sequences retrieved by ENDSCRIPT (Robert 2014)(default search parameter) using TOSV N-VHH structure as input search. Residues involved in binding are marked with B in red if the distance is less than 3.2 Å and in black if it is in the range 3.2-4.0 Å.