Electronic Supplementary Material (ESI) for Molecular BioSystems.

SUPPLEMENTARY INFORMATION

The *Henipavirus* V protein is a prevalently unfolded protein with a zinc-finger domain involved in binding to DDB1

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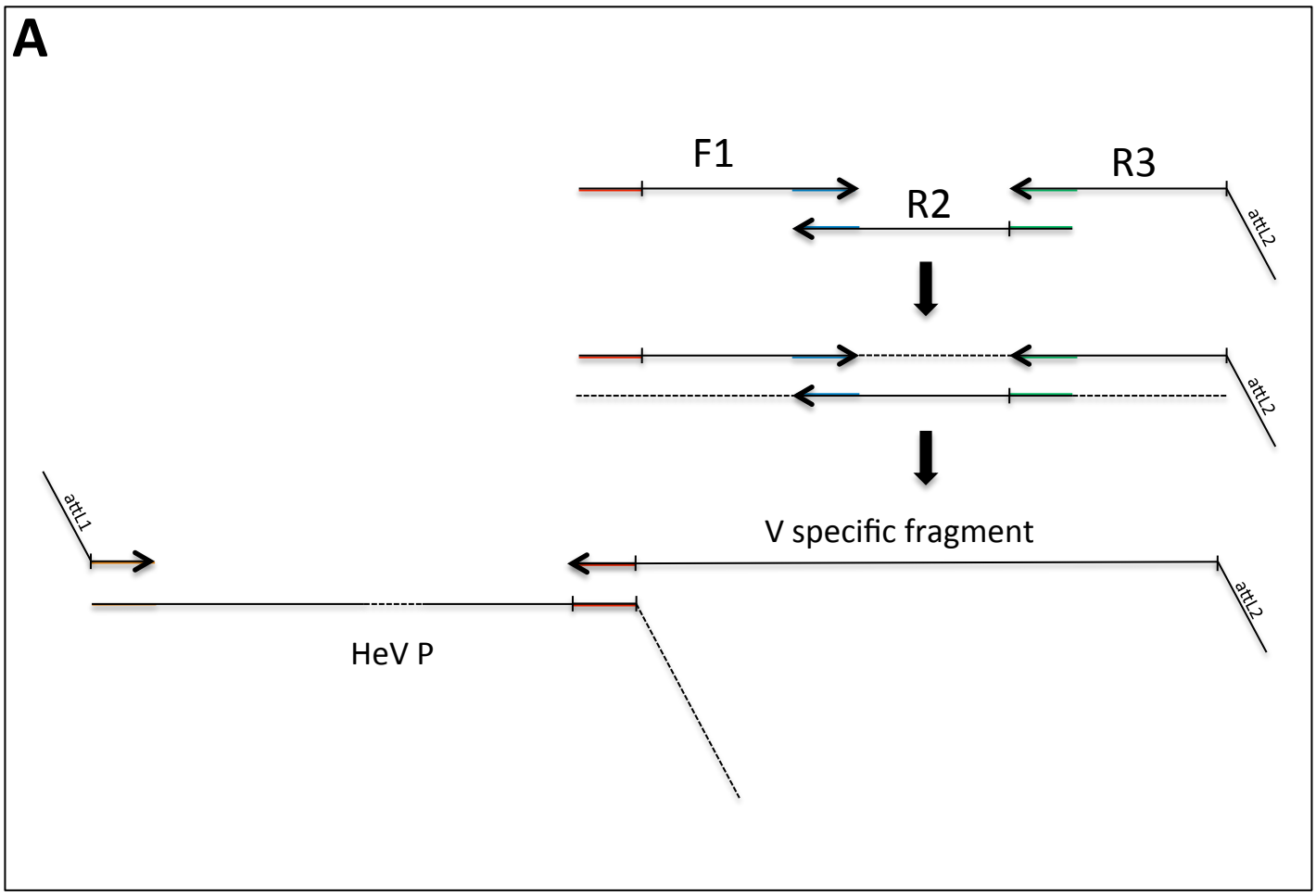
Legends of supplementary figures

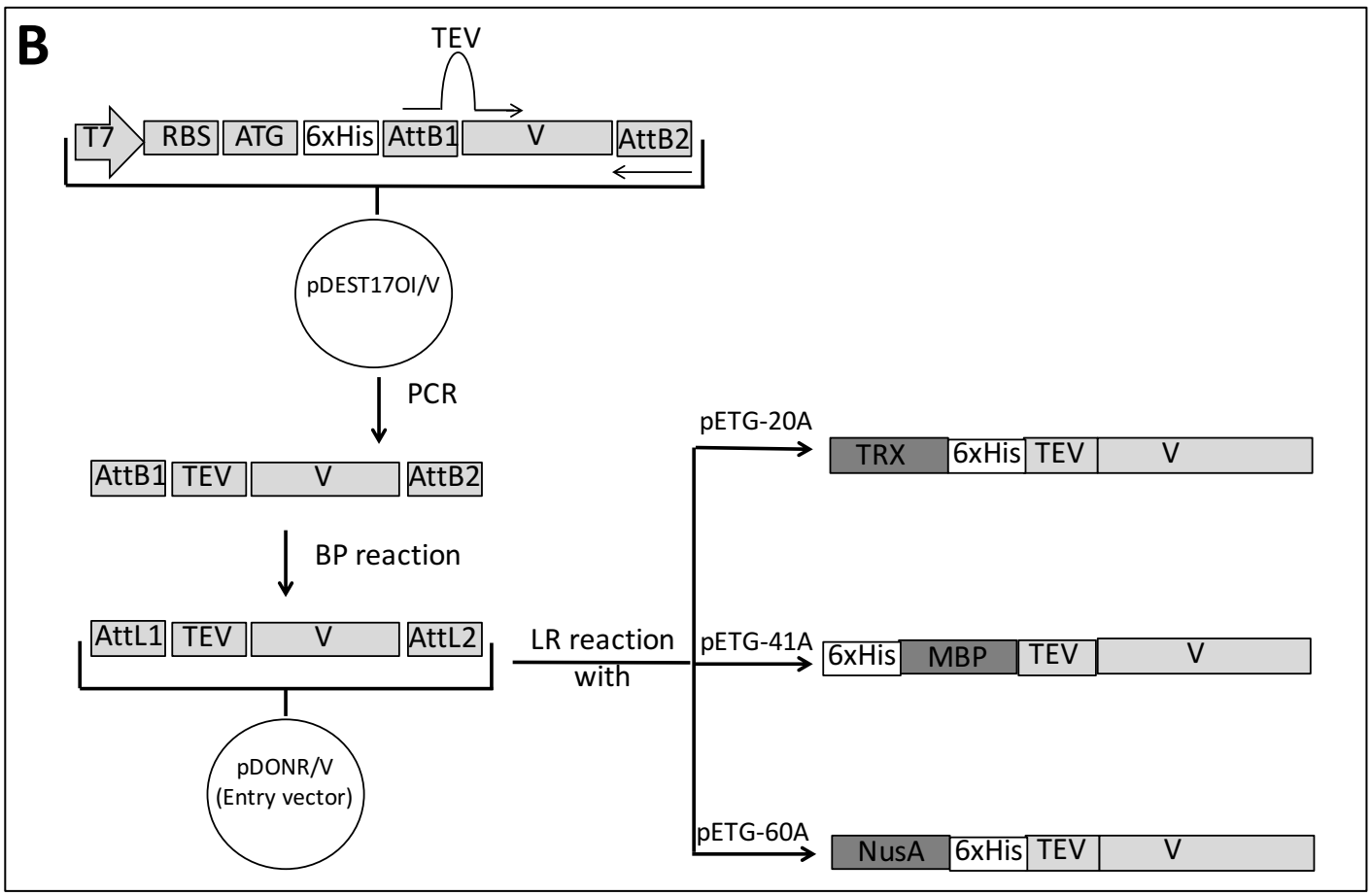
Supplementary Figure S1. (A) Scheme of the strategy used to build the V gene. Forward primer 1 (F1) was 56 nucleotides in length and was designed to bear a fragment of 18 nucleotides at its 5' end (see portion in red) annealing on the 3' end of the PNT-encoding fragment. Reverse primer 3 (R3) was designed to introduce an AttL2 site at the 3' end of the amplicon. The resulting amplicon was used as reverse megaprimer in a final PCR step that used a PNT-specific forward primer bearing an AttL1 site at its 5' end. (**B**) Schematic description of the ensuing cloning steps.

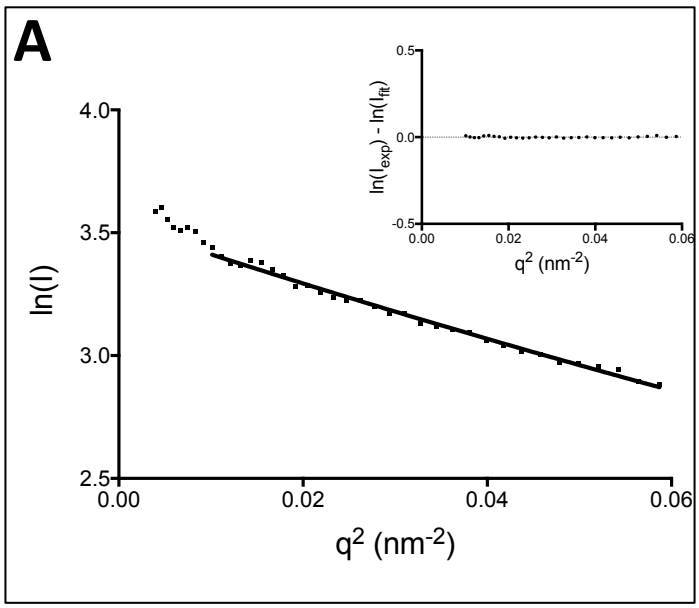
Supplementary Figure S2. SAXS studies of NiV V. (**A**) Representation of the Guinier plot for the protein at 4.0 g/L. Inset: residuals. (**B**) Pair distance distribution, P(r), function of the data for the 4.0 g/L concentration. (**C**) Dimensionless Kratky plot of the SAXS data obtained at 4.0 g/L. The inset shows the Kratky plots of a disordered, folded and partially folded protein. Data were taken from. [1] (**D**) Experimental scattering curve of the protein at 4.0 g/L (red) and GAJOE fit (black). (**E**) Distribution of Rg of the ensemble of randomly generated conformers by Flexible-Meccano without constraints (red) and of the sub-ensemble of selected conformers using GAJOE (black). (**F**) Final conformational sub-ensemble. All the conformers are superimposed on their ZnFD. Structures were drawn using Chimera [2].

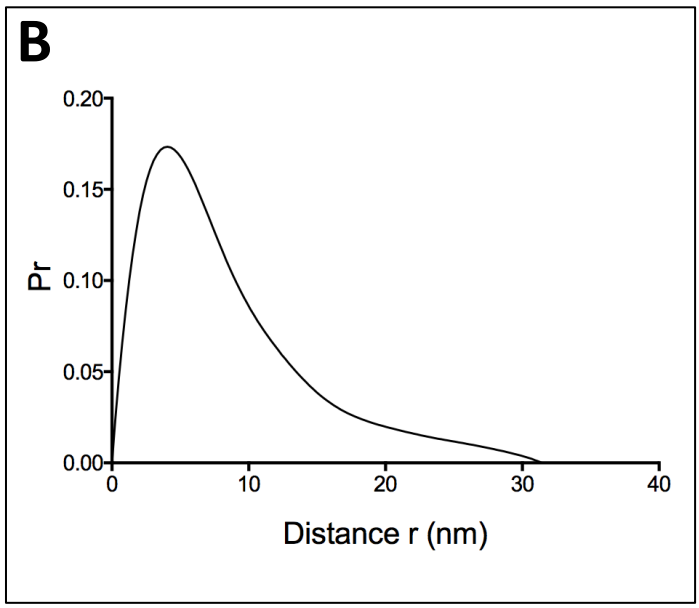
References

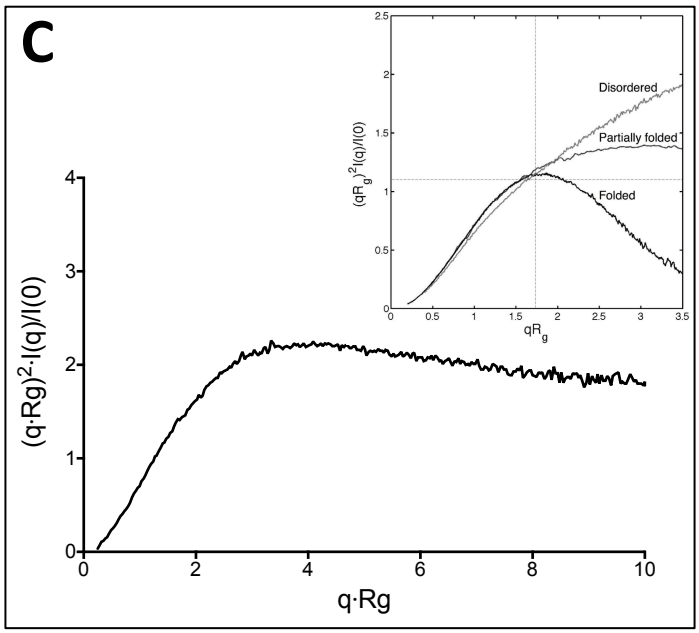
1. V. M. Burger, D. J. Arenas and C. M. Stultz, *Sci Rep*, 2016, **6**, 29040.
2. E. F. Pettersen, T. D. Goddard, C. C. Huang, G. S. Couch, D. M. Greenblatt, E. C. Meng and T. E. Ferrin, *J Comput Chem*, 2004, **25**, 1605-1612.

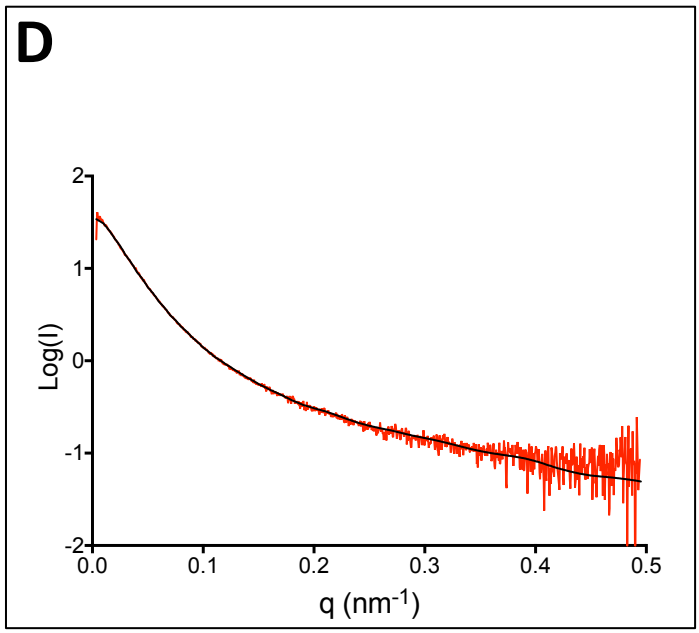

A
F1
R2
R3
attL2
attL2
attL1
V specific fragment
attL2
HeV P

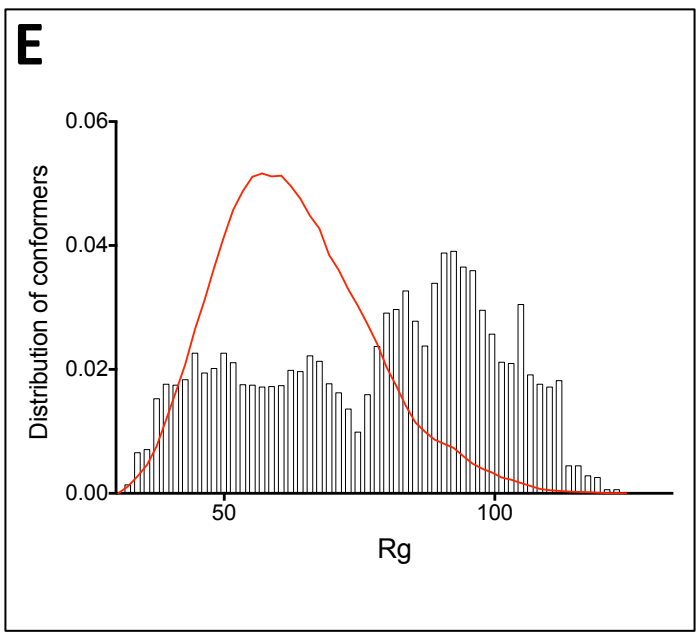

B
TEV
T7
RBS
ATG
6xHis
AttB1
V
AttB2
pDEST17OI/V
PCR
AttB1
TEV
V
AttB2
BP reaction
AttL1
TEV
V
AttL2
pDONR/V
(Entry vector)
LR reaction
with
pETG-20A
TRX
6xHis
TEV
V
pETG-41A
6xHis
MBP
TEV
V
pETG-60A
NusA
6xHis
TEV
V

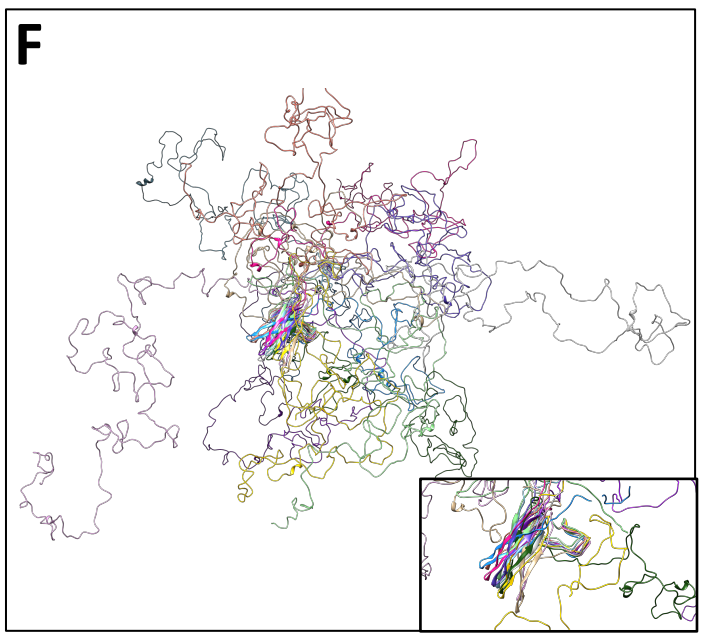

A
ln(I)
q² (nm⁻²)
ln(I_exp) - ln(I_fit)


B
Pr
Distance r (nm)


C
(q·Rg)²·I(q)/I(0)
q·Rg
Disordered
Partially folded
Folded


D
Log(I)
q (nm⁻¹)


E
Distribution of conformers
Rg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