STRUCTURE OF CRIMEAN-CONGO HAEMORRAGHIC FEVER VIRUS NUCLEOPROTEIN: SUPERHELICAL HOMO-OLIGOMERS AND THE ROLE OF CASPASE-3 CLEAVAGE

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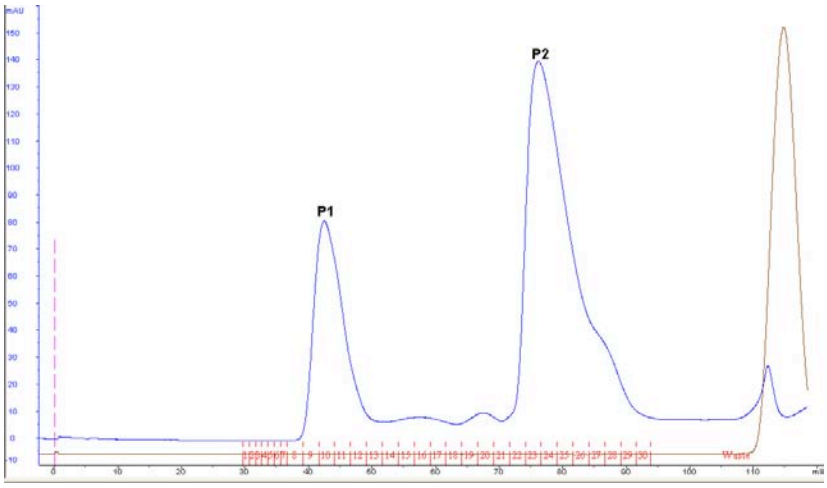
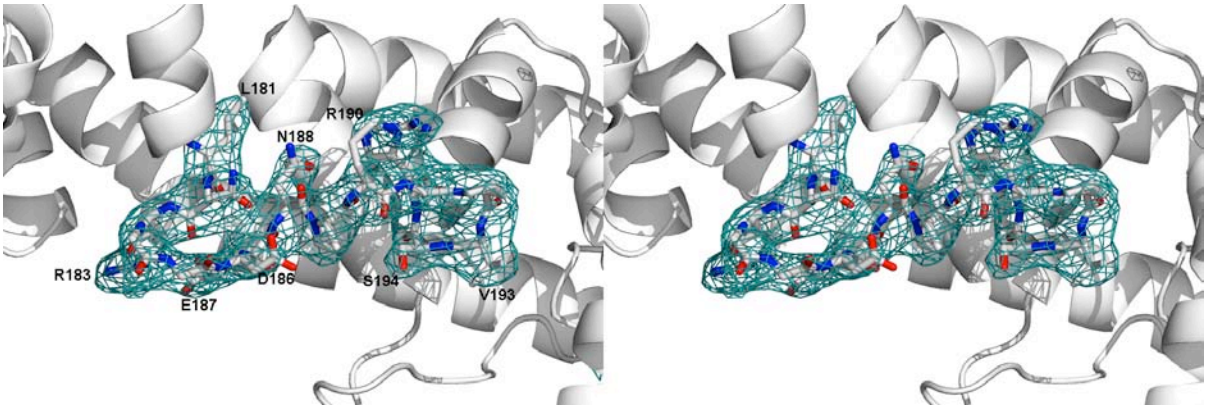
SUPPLEMENTAL INFORMATION

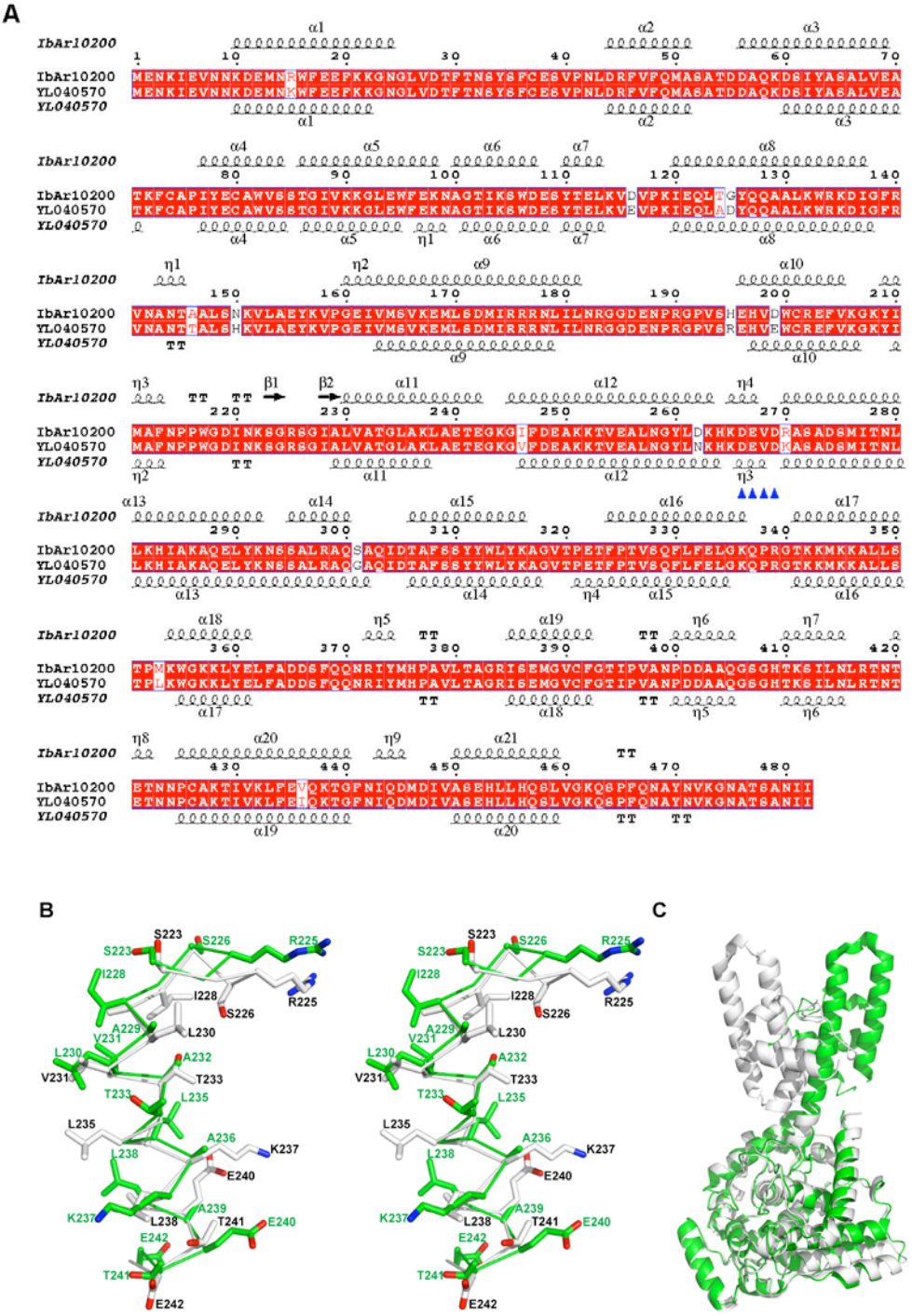
Supplemental figure 1. Gel filtration profile of CCHFV N on superdex200 16/60 column (GE Healthcare). Peak 1 (P1) is eluted at a position which corresponds to an apparent molecular weight of > 300 kDa. Peak 2 (P2) is eluted at a position corresponding to an apparent molecular weight of ~60 kDa.



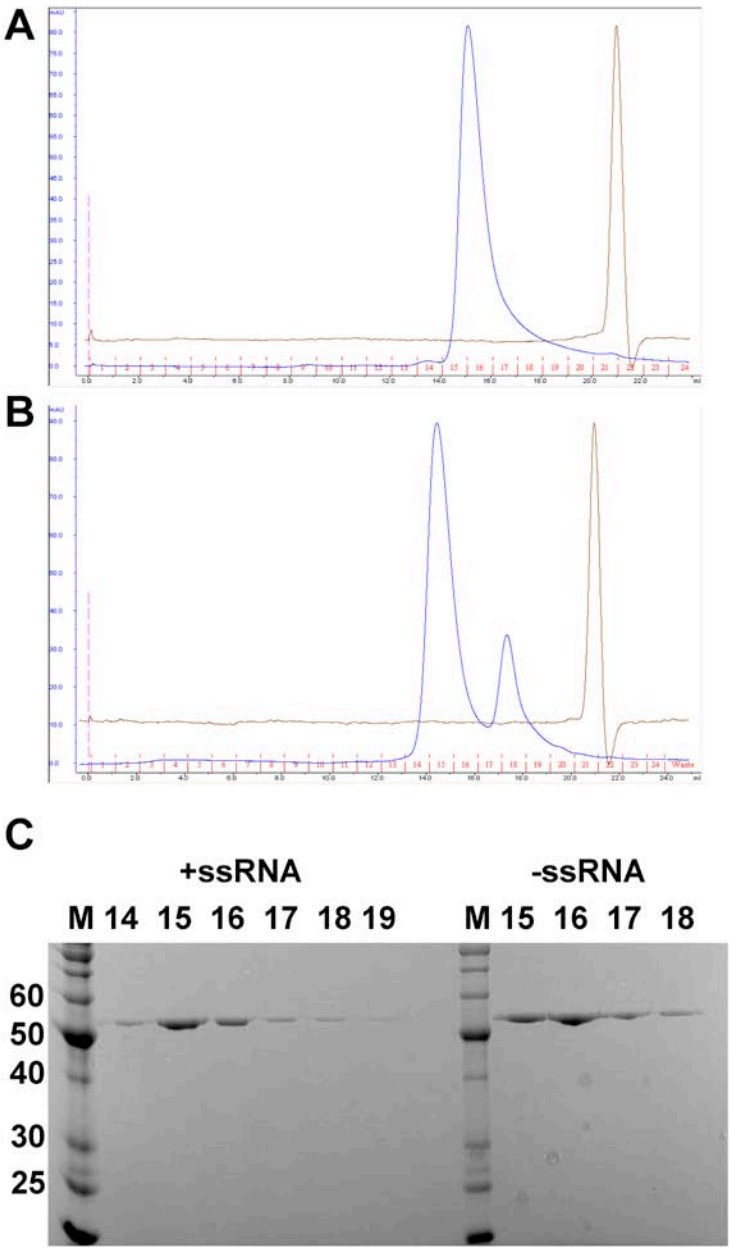
Supplemental figure 2. Stereoview of interdomain linker observed in molecule B of CCHFV N crystallised in oligomerised form. Simulated annealing omit map is contoured at 4σ.



Supplemental figure 3. Comparison of crystal structures of CCHFV N strain IbAr10200 against strain YL040570. A. Sequence alignment of CCHFV N of the two strains. The conserved caspase-3 cleavage sequence is highlighted by blue triangles. B. Stereoview depicting the one amino acid shift difference observed between in α11of CCHFV N strain IbAr10200 and strain YL040570. CCHFV N of strain IbAr10200 is coloured in white while strain YL040570 is shown in green. C. The difference in the position of the stalk of CCHFV N of the two strains. The structures are coloured in accordance to Figure B.



Supplemental figure 4. Gel filtration profile of CCHFV N on superdex200 10/300 analytical column (GE Healthcare). A. Profile of purified recombinant CCHFV N without RNA eluted at a position which corresponds to an apparent molecular weight of > 60 kDa. B. Profile of purified recombinant CCHFV N incubated with 100 μM 12U ssRNA. CCHFV N is eluted at two positions. One corresponds to an apparent molecular weight of > 60 kDa and latter peak corresponds to an apparent molecular weight of ~40 kDa. C. SDS-PAGE analysis of CCHFV N eluted from superdex 200 10/300 analytical column. Lanes corresponds to the fraction number collected for the peaks seen in Figures A and B.



Supplemental figure 5. Sequence alignment of CCHFV N against Ns of other Nairoviruses including Dugbe virus, Hazara virus, Kupe virus and Nairobi sheep disease virus (NSDV). Magenta stars depict conserved positively charged residues and the conserved caspase-3 cleavage sequence is highlighted by blue triangles.