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Supporting information for article:

Structure and oligomerization state of the C-terminal region of the *Middle East respiratory syndrome coronavirus* nucleoprotein

Thi Hong Van Nguyen, Julie Lichière, Bruno Canard, Nicolas Papageorgiou, Sarah Attoumani, François Ferron and Bruno Coutard

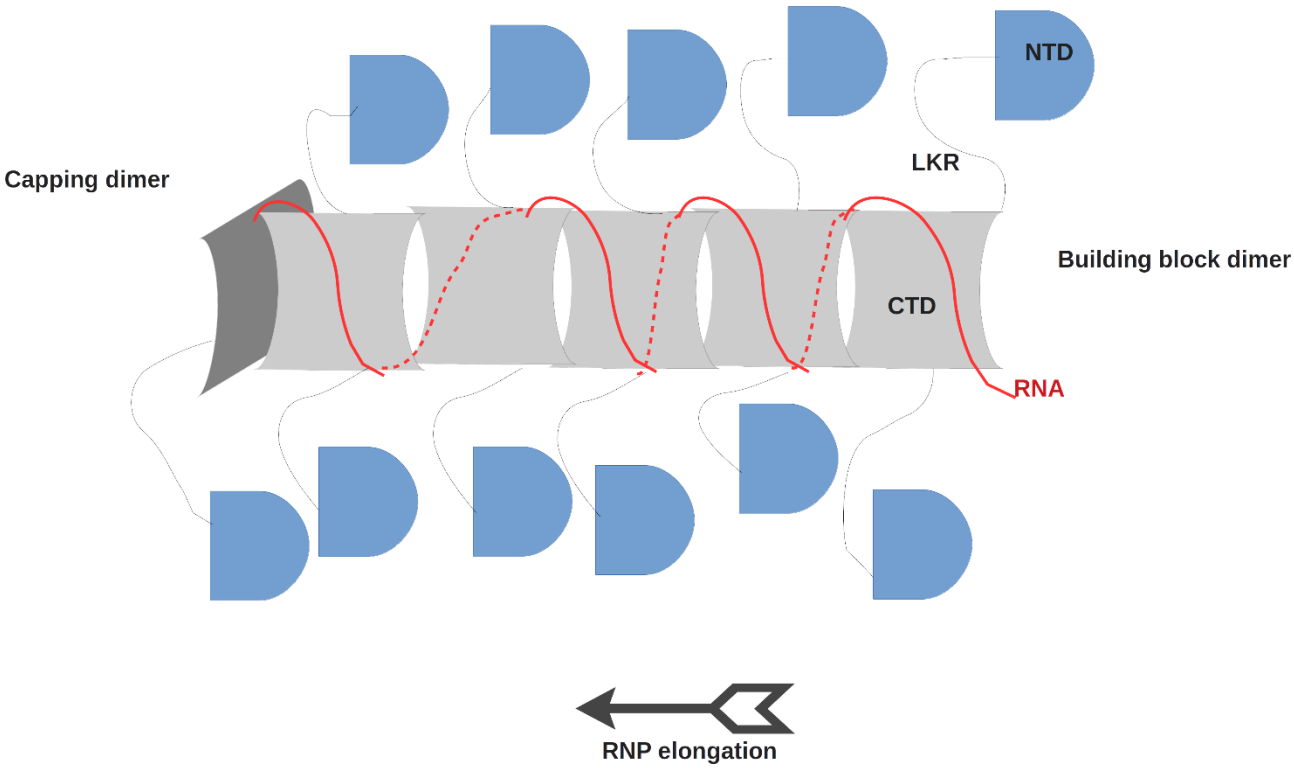

Figure S1 The N assembly mechanism in coronavirus. The CTDs dimerize to providing a platform to recruit viral RNA. The prominent NTD is also responsible for recruiting RNA. The LKR domains between NTD and CTD may act as a flexible arm to change the relative position of the two domains. Growth of the filament is sideway and and control of growth is achieved by a dimer capping the growing extremity.

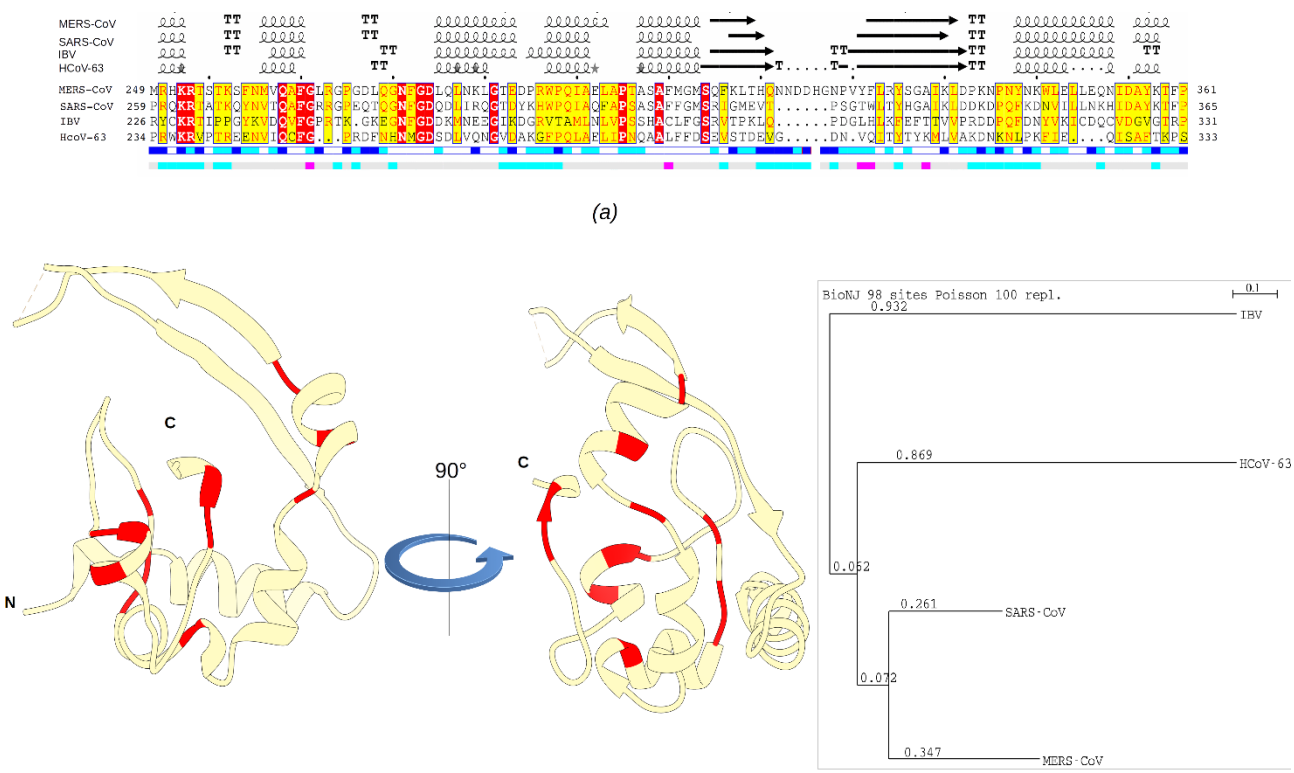

Figure S2 Sequence to structure analysis of the MERS-CoV CTD with homologous domains. (a) Sequence alignment featuring homologous viral domains including the ones of : IBV (PDB : 2CA1 / 2GE7), HCoV-NL63 (PDB : 5EPW), SARS-CoV (PDB : 2CJR) and MERS-CoV (PDB : 6G13). Conserved residues are shaded in red. Secondary-structure elements corresponding to each crystal structure are displayed above the sequence alignment. (b) Conserved residues are highlighted in red on the structure MERS-CoV CTD. Conserved residues are facing the core of the structure. (c) Phylogenic distribution presented a BioNJ tree bootstrapped of the different structures.

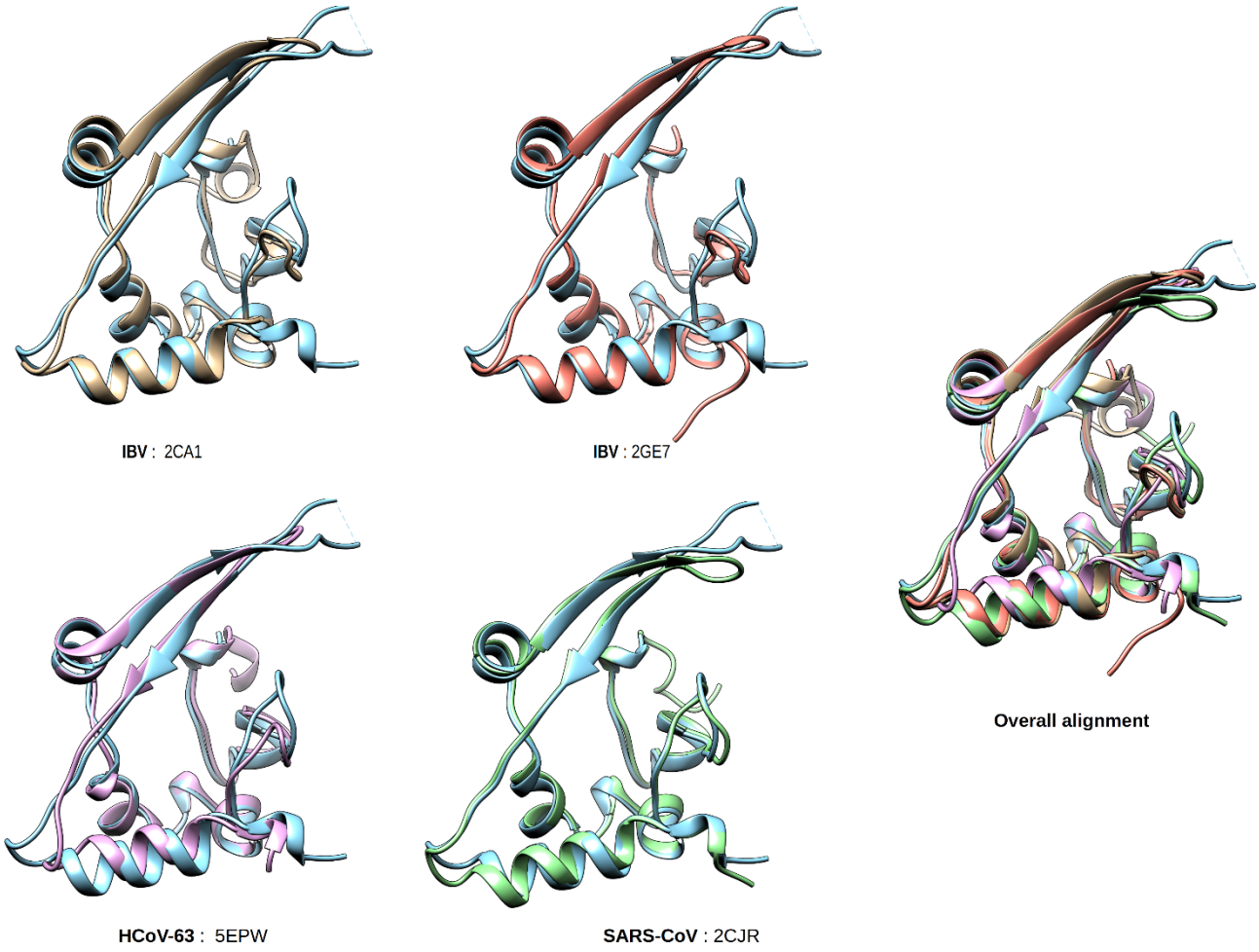

Figure S3 Structural superimposition of MERS-CoV CTD (blue) with homologous viral domains including : IBV (PDB : 2CA1 / 2GE7), HCoV-NL63 (PDB : 5EPW), SARS-CoV (PDB : 2CJR).