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Supporting information for article:

Crystallographic analysis of the N-terminal domain of *Middle East respiratory syndrome coronavirus* nucleocapsid protein

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Figure S1 Sequences of CoV NP-NTDs were aligned using ClustalW. Visualization of the multiple sequence alignment was performed with BioEdit. The consensus region is colored according to sequence conservation: orange, highly conserved (more than 80% sequence identity); yellow, moderately conserved (more than 80% sequence similarity); and white, not conserved. Amino acid sequences of MERS (MERS-CoV; AFY13314), OC43 (HCoV-OC43; AAT84366), SARS (SARS-CoV; ABI96968), 229E (HCoV-229E; AAG48597) and IBV (Infectious Bronchitis virus; AAB24054) NP-NTD were obtained from GenBank.

