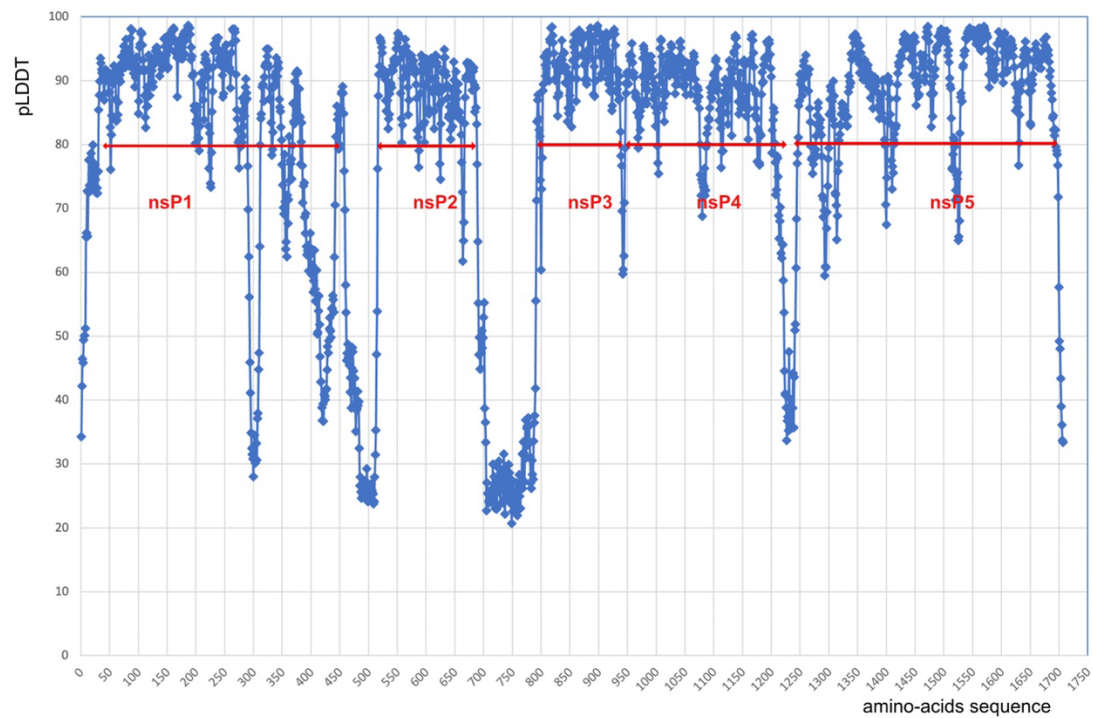


**Supplementary Figure S1.** pLDDT values of the HEV3 polyprotein predicted structure . pLDDT values for each residue along protein sequences are plotted. The five domains are identified in the sequence by red double arrows.



**Supplementary Figure S2.** Comparison of predicted and experimentally determined SARS machinery structure. A/ complex of nsP7(yellow), nsP8 (green) and nsP12 (salmon) predicted by AF2. B/ Experimental structure of nsP7(green), 2xnsP8 (salmon and yellow) and nsP12 (violet) in complex with dsRNA (green and yellow).C/ pLDDT of the predicted nsP7, nsP8 and nsP12 proteins. D/ Predicted aligned errors of the nsP7/nsP8/nsP12 predicted complex.

