

## **Supporting information**

### **Secondary structure of influenza A virus genomic segment 8 RNA folded in a cellular environment**

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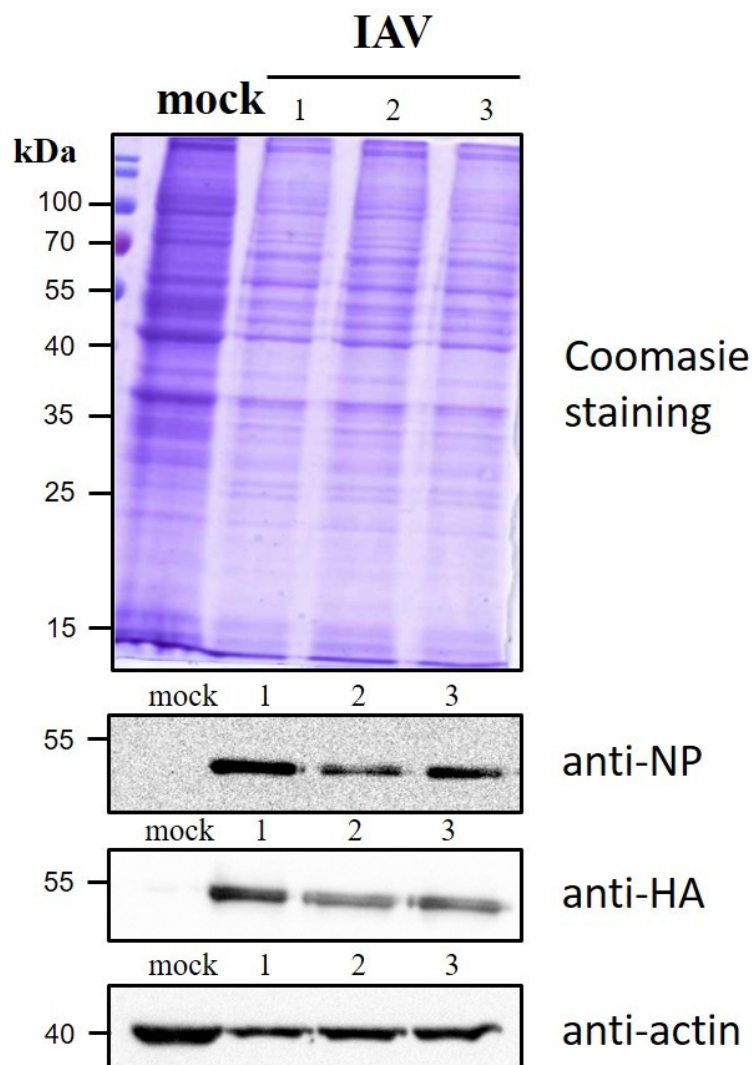
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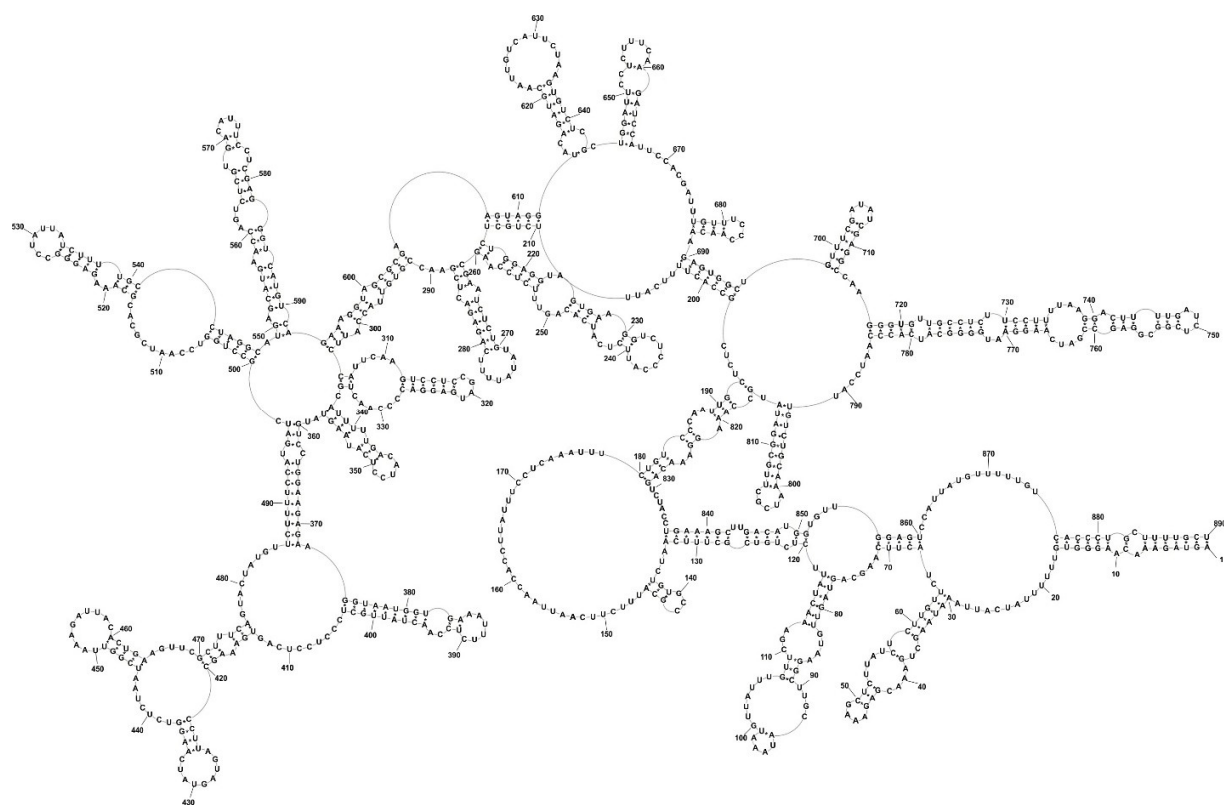
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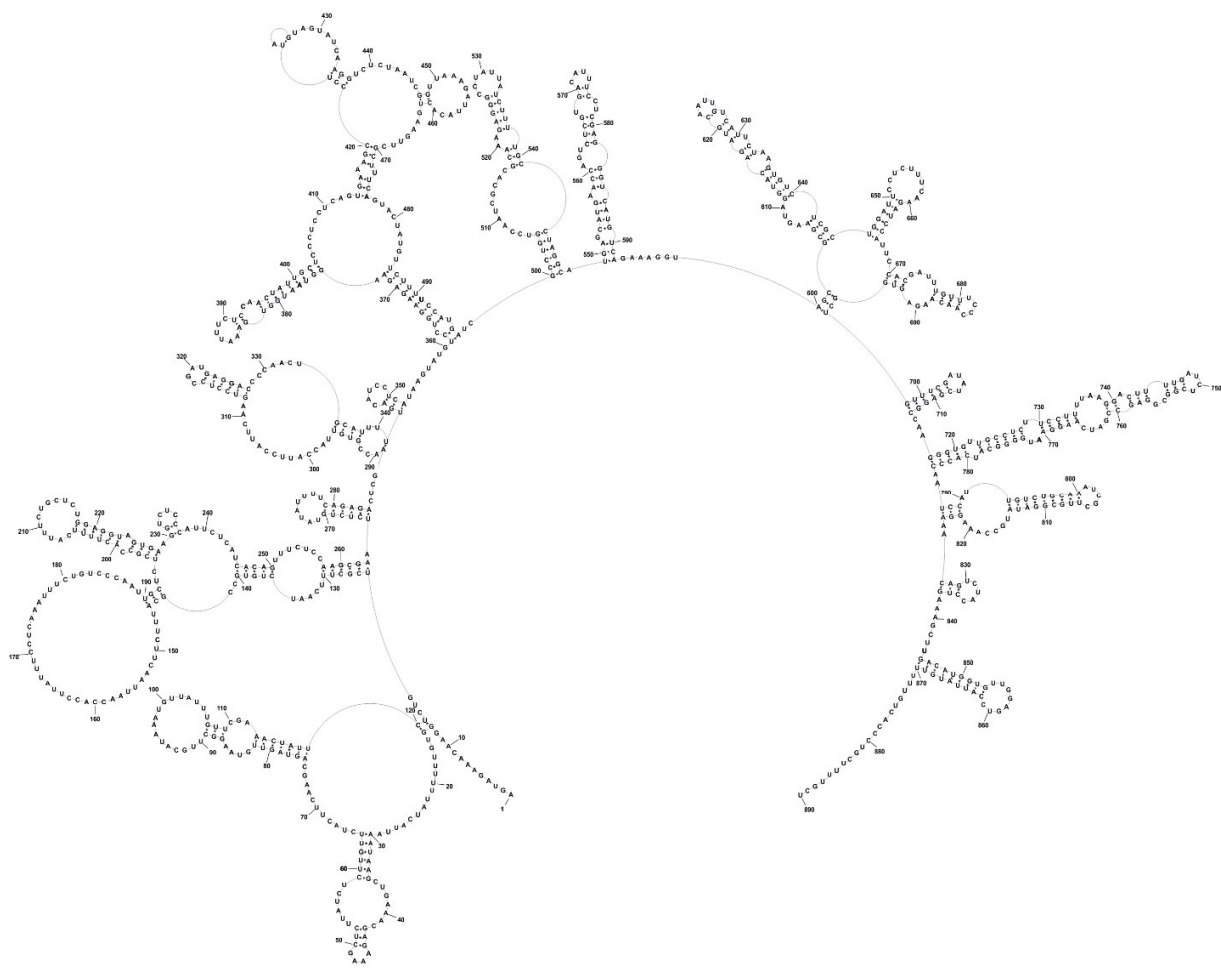
E-mail: elzbieta.kierzek@ibch.poznan.pl (EK)



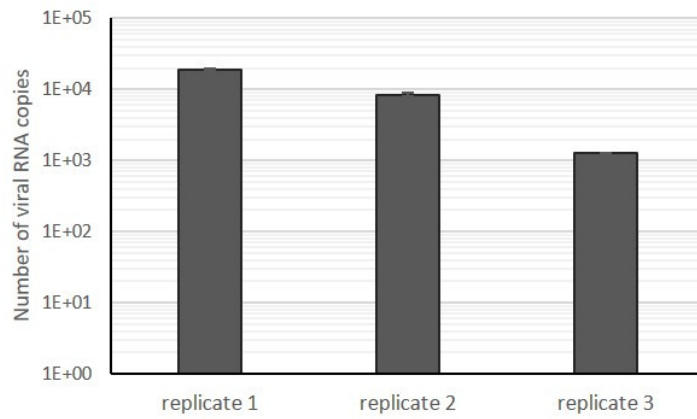
**Figure S1. The IAV proteins expression in the infected cell lysates.** The MDCK cells were infected with influenza virus A/California/04/2009 at MOI 0.01 and incubated for 24 hours. Next, the cells were treated with lysis buffer, and the total protein was stained with Coomassie blue (Bio-Rad). Additionally, the IAV proteins expression was detected by Western blot analysis using anti-NP (Thermo Scientific) and anti-HA (Merck) antibodies. Expression of actin, detected with anti-actin antibody (Thermo Scientific), served as a loading control.



**Figure S2.** MEA global structure of vRNA8 A/California/04/2009 folded according to the experimental data. For the probability file calculation partition function in RNAStructure (6.2) experimental data (SHAPE and DMS), as well as panhandle base-pairing, were used. Visualization via PseudoViewer.



**Figure S3. MEA local structure of vRNA8 A/California/04/2009 folded according to the experimental data.** For the probability file calculation partition function in RNAstructure (6.2) experimental data (SHAPE and DMS) with maximum pairing distance set to 150 nt. The panhandle region was excluded from the calculation. Visualization via PseudoViewer.



**Figure S4. Amount of viral RNA8 copies in the independent replicates.** The copies of vRNA8 were analyzed by RT-qPCR. The mean was calculated from three technical repeats by independent RT-qPCR reactions and the standard deviation is shown.