
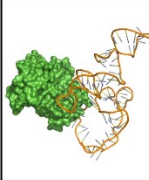
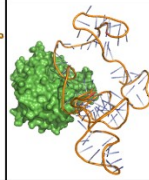
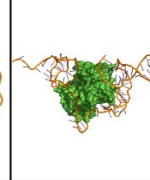
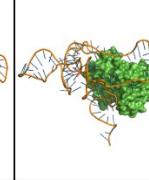
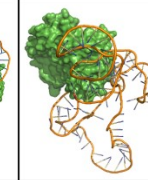
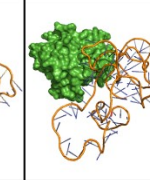
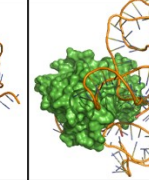
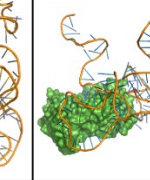
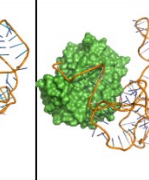
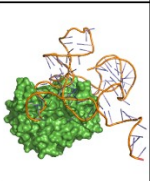
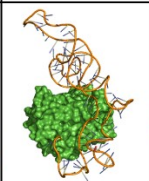
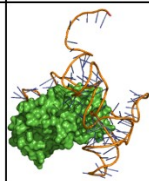
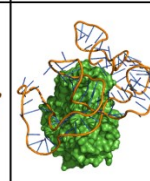
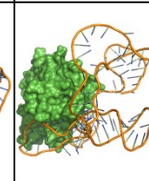
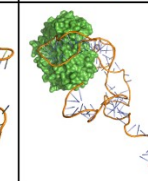
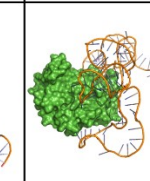
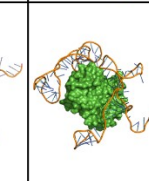
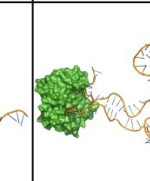
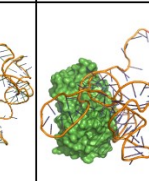
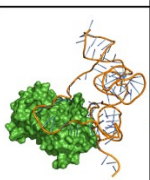

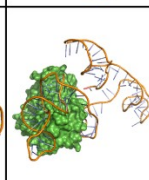
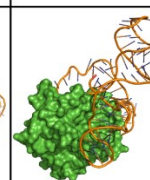
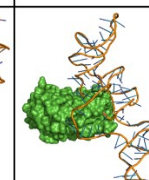
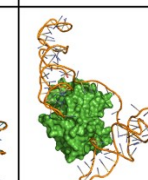
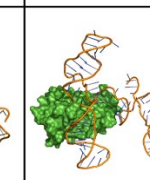
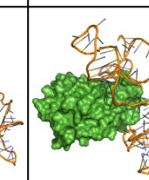
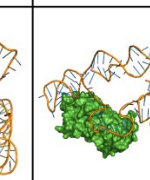
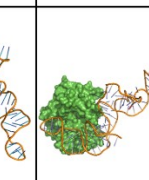


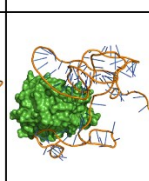
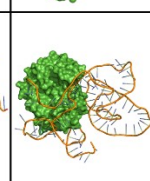
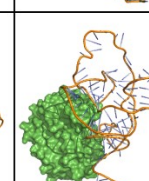
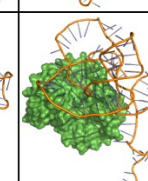
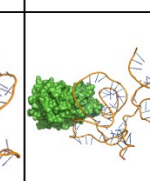
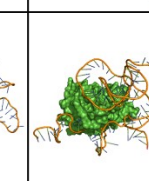
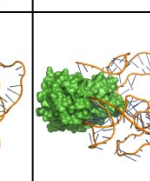





Secondary/ tertiary structure	1	2	3	4	5	6	7	8	9	10
<b>A</b>										
<b>B</b>										
<b>C</b>										
<b>D</b>										

**Figure S2.** Predictions of the three-dimensional structures of all Apt5 secondary structures as well as their docking with the target molecule, SEA. The tertiary structures of the aptamer were predicted by the 3dRNA webserver and docking by the HDock webserver.



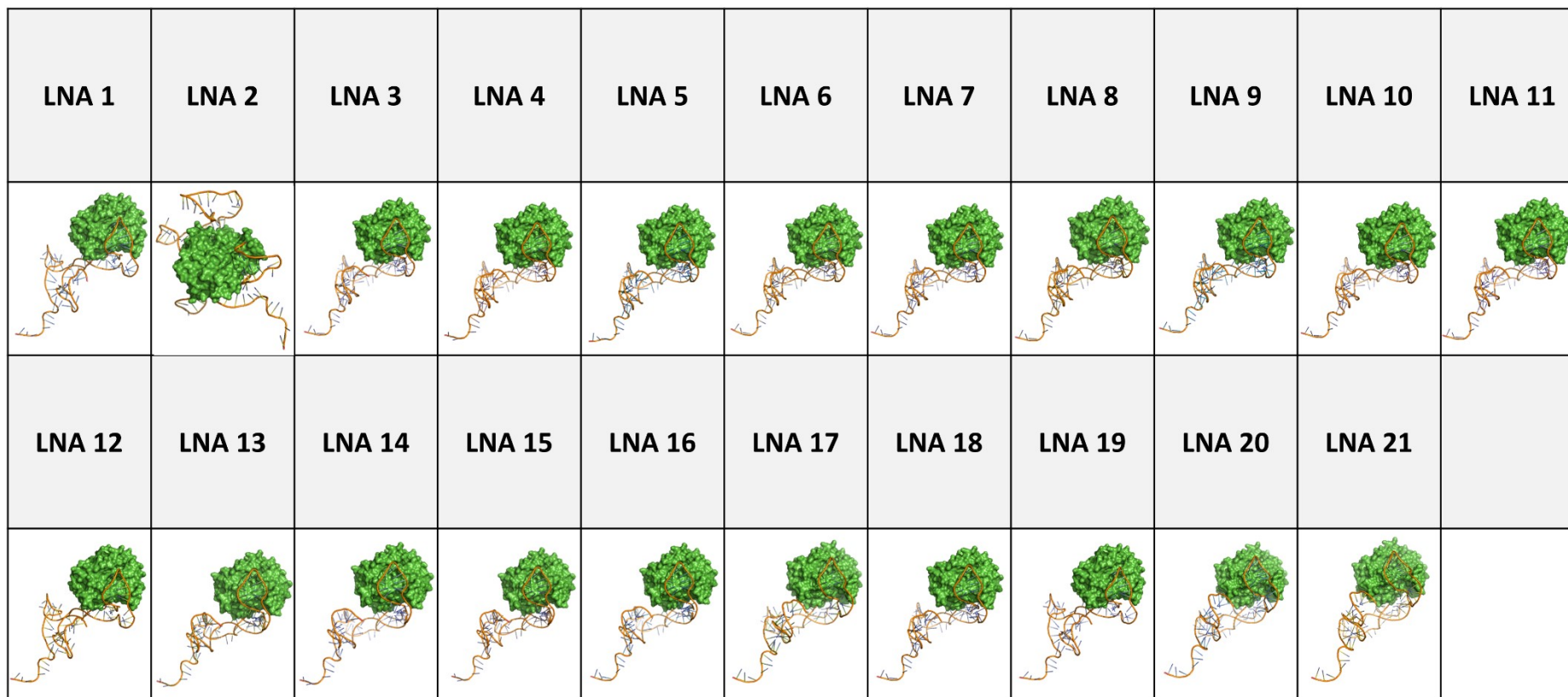


Figure S4. Predictions of the three-dimensional structures of LNA versions as well as their docking with the target molecule, SEA. The tertiary structures correspond to the most likely structure of the original Apt5 modified with LNA using BIOVIA software and docking by HDock webserver.

