Analysis of binding properties of influenza hemagglutinins and human receptor analog

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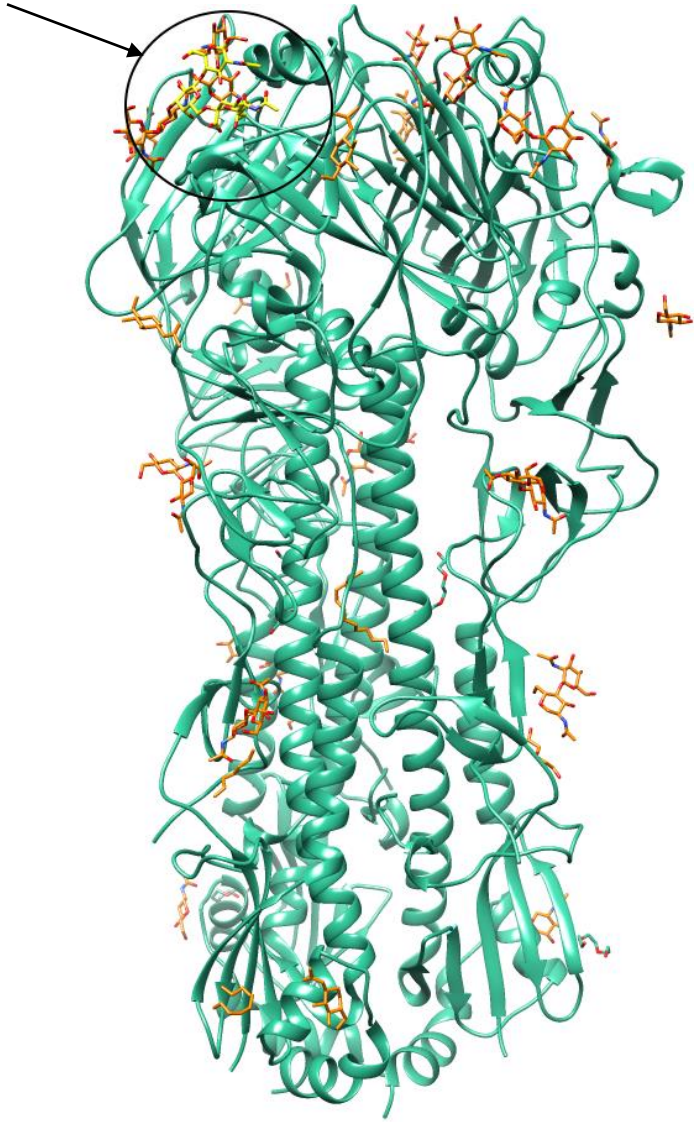
Influenza virus hemagglutinin

- The virus binds to the receptor via the protein hemagglutinin
- The new group of the Influenza virus – Bangladesh, spread and practically displaced other viruses of its A(H3N2) subtype

The aim: To assess the free binding energy difference between Bangladesh representative and the international vaccine strain A(H3N2) with AutoDock Vina program



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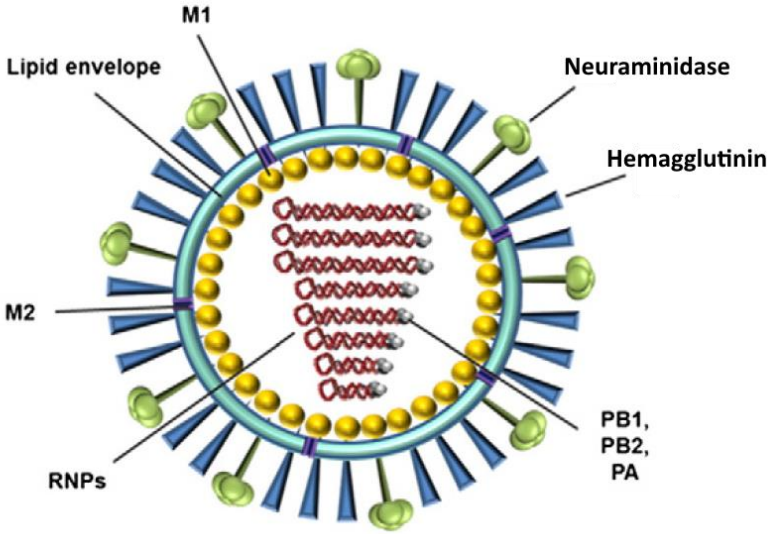
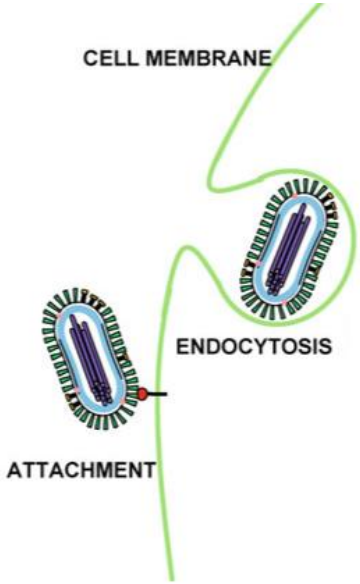


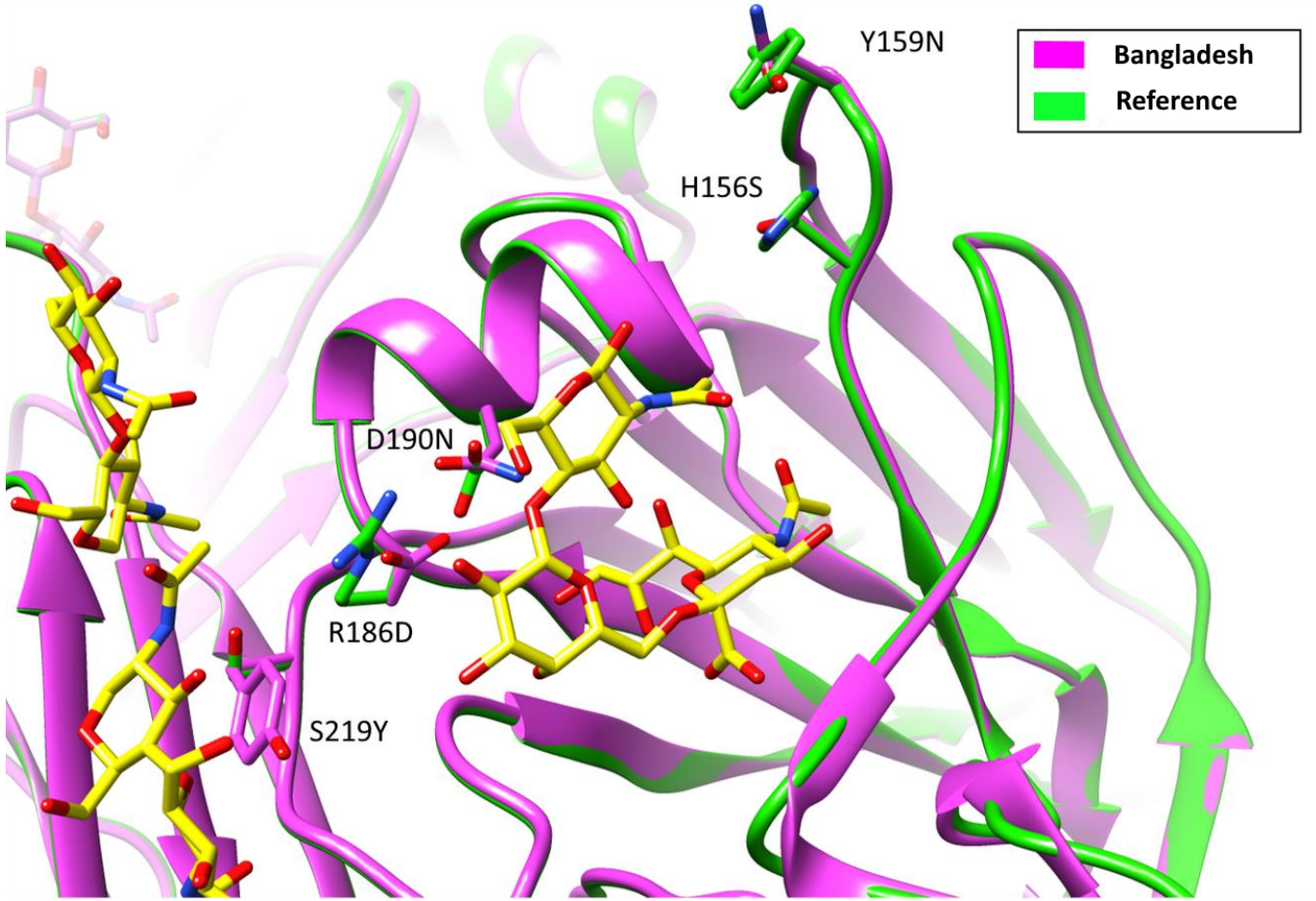


Michael G. Rossmann, Venigalla B. Rao, viral molecular machines (2012), 210

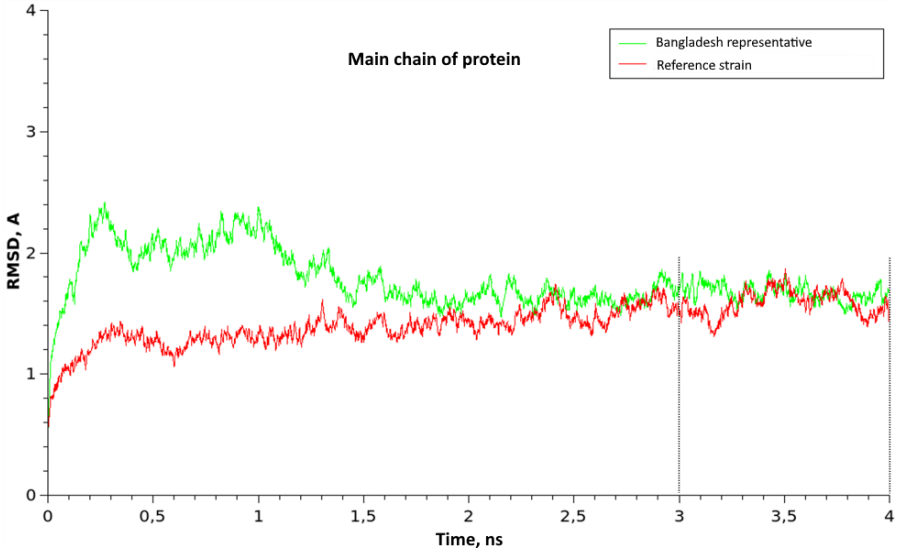
Initial structures

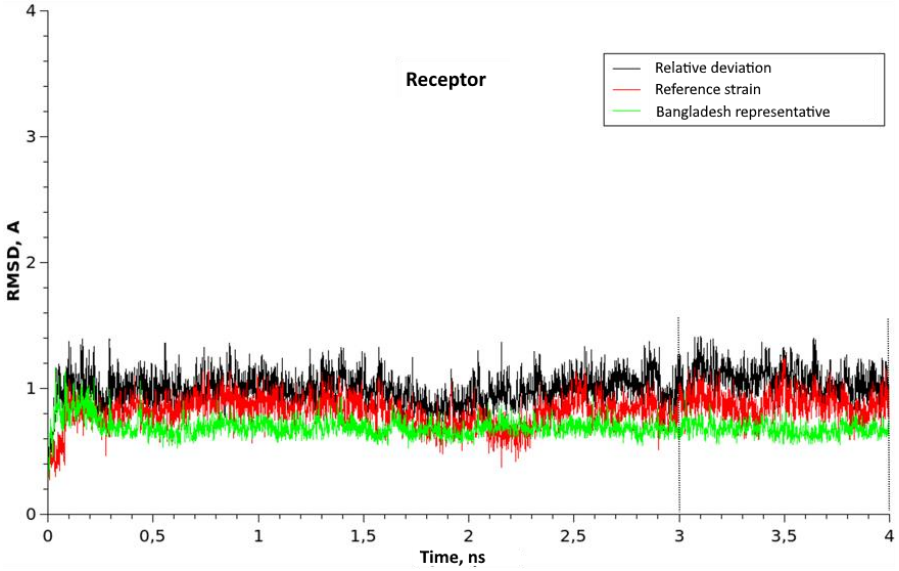
- Initial structures were modelled by comparative modelling method with MODELLER

(the template is the structure received by X-ray diffraction analysis from the Protein Data Bank in complex with the receptor analog **6'-sialyl-N-acetyllactosamine**, similarity of sequences **95%**)



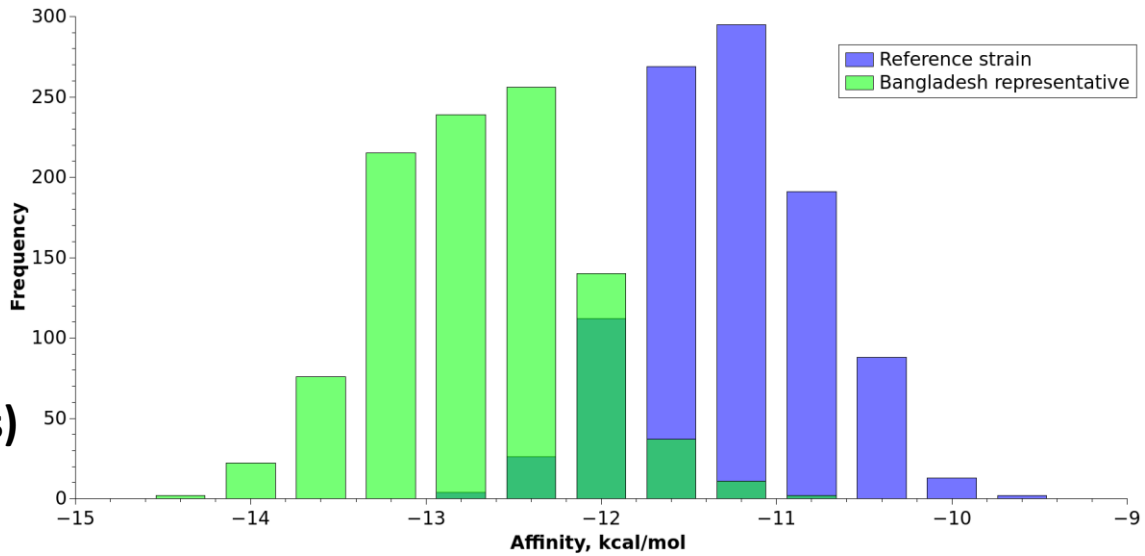
Molecular dynamics simulations and Autodock Vina analysis





AutoDock Vina (1000 configurations)

(the range is from 3 to 4 ns, the step is 1 ps)

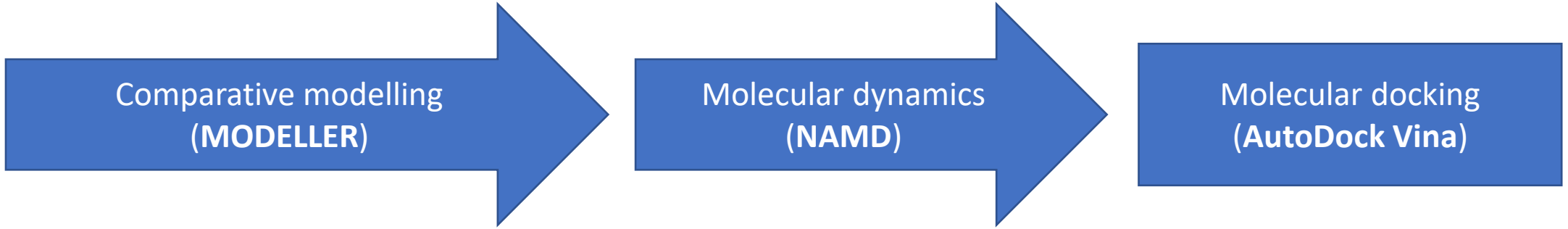


Average values: -12.7 and -11.27 kcal/mol
Standard deviations: 0.58 and 0.5 kcal/mol

for Bangladesh and reference strains correspondingly.

Average difference - 1.43 kcal/mol.

Conclusion



- Three amino acid replacements detected in the receptor binding site which contact with the receptor and can affect on the binding affinity
- Higher affinity was demonstrated for Bangladesh representative by molecular docking analysis
- The analysis of the separate replacement influences on the results can give the information about the role of every replacement in the change of the binding affinity