

5 Conclusions

Present work was aimed to explore equilibrium properties of tautomeric forms of nucleic acid bases in the gas-phase, in a microhydrated environment and in aqueous solution. The study also presents thorough comparison of different methods used for calculations in water environment. Such calculations were supposed to reveal the accuracy of these methods and the possibility of their usage for more biologically relevant calculations. This was true for the last presented paper where the knowledge of equilibrium properties together with geometry properties of different tautomers was used for base pairs calculations.

We explored the tautomeric equilibrium properties of adenine, uracil and thymine. Adenine case ended in the theoretical prediction of coexistence of several tautomers in water phase. Uracil/thymine case confirmed that population of rare *enol* forms in bulk water is very low in this case and canonical structure is also clearly dominant in this phase.

The hydration free energies of nucleic acid bases tautomers were calculated using two different methods bare COSMO and MD-TI. Although results are in a good agreement in our calculations, some minor differences still remain. This difference becomes smaller when optimization of the geometry in the water phase was performed.

We believe that correctly described specific hydration can also minimize this difference. This belief lead us to introduce the hybrid model which should more or less cover the specific hydration. In the most cases the inclusion of explicit water molecules neither improved nor deteriorated results obtained for rare tautomers. It can thus be concluded that introduction of specific hydration, which is physically fully adequate, does not bring any improvement over bare COSMO. The use of our hybrid model is thus recommended only if the solute dipole moment becomes very large (approximately $>10D$).

The consequential part of this work was focused on broadening our knowledge about nucleic acid base pairs constructed from unusual nucleic acid base tautomers. Their common presence in the native DNA was not discovered yet although some structures containing a single nucleic acid base tautomer are known. This was the first thorough study of these tautomeric base pairs which ment to be a solid background for forthcoming studies (e.g. hydration, nucleotide studies). It was mainly concerned about geometries and accurate interaction energies.

We optimized all sterically possible tautomeric base pairs which according to their spatial properties could be incorporated into DNA molecule. For all structures we calculated

total interaction energies including complete basis set extrapolation and including the higher-order correlation effects energy contributions.

Some optimized structures of studied base pairs possess interesting motifs which we believe become more important after inclusion of a water molecule. Stabilization energies of some tautomeric base pairs were very high (even higher than in the case of Watson-Crick base pair) and those structures deserve further investigation. Even for optimized H-bonded tautomeric base pairs it is evident that the CCSD(T) correction term is negligible.