

# On the Association of the Base Pairs on the Silica Surface based on Free Energy Biased Molecular Dynamics Simulation and Quantum Mechanical Calculations

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The adsorption of the DNA bases and base pairs on the hydrophobic silica surface has been investigated by ab initio quantum mechanical (QM) methods (DFT-D) and molecular mechanics (MM) and also by biased molecular dynamics (MD) simulations (metadynamics). The structures of all the clusters (surface with single-bases and base pairs) predicted by means of the force field are compared with the results of direct QM calculations. The MM interaction energies for all clusters agreed well with the QM ones, which justifies the use of MM methods in the evaluation of accurate adsorption free energies. Rigid rotor-harmonic oscillator-ideal gas (RR-HO-IG) calculations based on QM and MM entropies as well as biased metadynamics (MTD) simulations based on MM demonstrated that mA-mT (Adenine-Thymine) and mG-mC (Guanine-Cytosine) base pairs are adsorbed on a fully solvated silica surface in different H-bonded forms. Both QM and MM techniques convincingly demonstrated that adsorptions of any H-bonded (Watson-Crick (WC), non-WC and Hoogsteen) structures on the surface are stronger than that of any  $\pi$ - $\pi$  stacked structures.