Effective modelling of Resonance Raman spectra of doxorubicin in aqueous solution

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The system investigated in the present work is doxorubicin (DOX), an anti-cancer drug amply studied experimentally using the RR spectroscopy [1,2]. The structure of the drug consists of a planar part (chromophore) of three condensed aromatic rings, an aliphatic ring and an aminosugar moiety situated out of plane of the chromophore (Figure 1). The tumor-inhibiting behavior of doxorubicin may be explained by the process of intercalation of the drug molecule into DNA helix.

A theoretical investigation of the Resonance Raman (RR) effect has been performed within the time-independent formalism. Our approach includes the vibronic effects at the Franck-Condon and Herzberg-Teller level [3,4]. We also account for possible differences between ground and excited states' potential energy surfaces. For this reason it is extremely important to describe in an accurate manner the geometries and normal modes of both states involved in the process.

As a biologically active system, DOX occurs mainly in aqueous solutions. This fact needs to be accounted for while calculating its properties. The most popular approach to modeling environmental effects is the Polarizable Continuum Model (PCM) [5]. Here we will present both advantages and limitations of this model applied to calculate the IR, UV-Vis and Resonance Raman spectra of DOX in a strongly interacting environment. An attempt to explain the nature of these limitations is provided based on Molecular Dynamics simulations and a possible way of overcoming them is proposed.

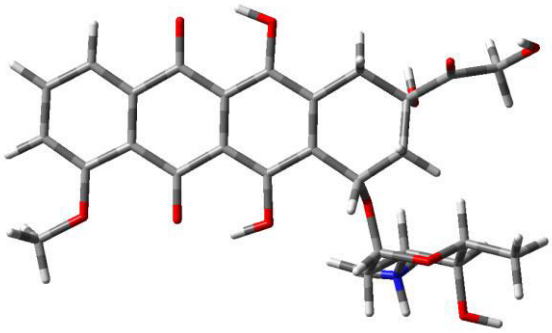

Figure 1. Structure of the doxorubicin molecule

References

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