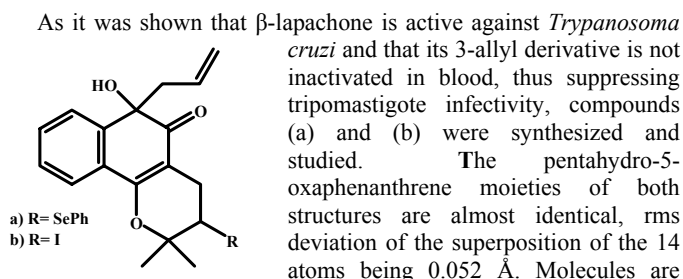


Structural and Docking Studies of β -lapachone Derivatives

Ignéz Caracelli^a, Julio Zukerman-Schpector^b, Carlos Alberto Brandt^c,
^aDepartment of Physics, UNESP-Bauru, Brazil. ^bDQ-UFSCar, São Carlos, Brazil. ^cI. Butantan, São Paulo, Brazil. E-mail: ignez@fc.unesp.br



packed in a same ladder fashion through OH...O, CH...O and CH... π (in (a)) interactions.

Docking studies were carried out with DOCK3.5 [1,2], for (a) and (b) and their dione analogs modelled based on the crystal structures, in the active site (AS) and the interface site (IS) of human glutathione and *T. cruzi* trypanothione reductases (GR and TR). For the modelled dione ligands, it was possible to choose a preferred orientation in each site with total energies of *ca* -20 kcal/mol in TR-AS, -28 kcal/mol in TR-IS and GR-AS and -30 kcal/mol in GR-IS. On the other hand, docking studies with (a) and (b) did not show any preferred orientation. These results are in agreement with the showed trypanocidal activity, *in vitro*, of the dione derivatives and the inactivity of (a) and (b).

FUNDUNESP, FAPESP, CAPES, CNPq

[1] Shoichet B.K., Kuntz I.D., *J. Mol. Biol.*, 1991, **221**, 327. [2] Shoichet B.K., Bodian D.L., Kuntz I.D., *J. Comp. Chem.*, 1992, **13**, 380.

Keywords: docking, drug-receptor modelling, stereochemistry