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CONFORMATIONAL STUDY OF VANCOMYCIN ANALOGS

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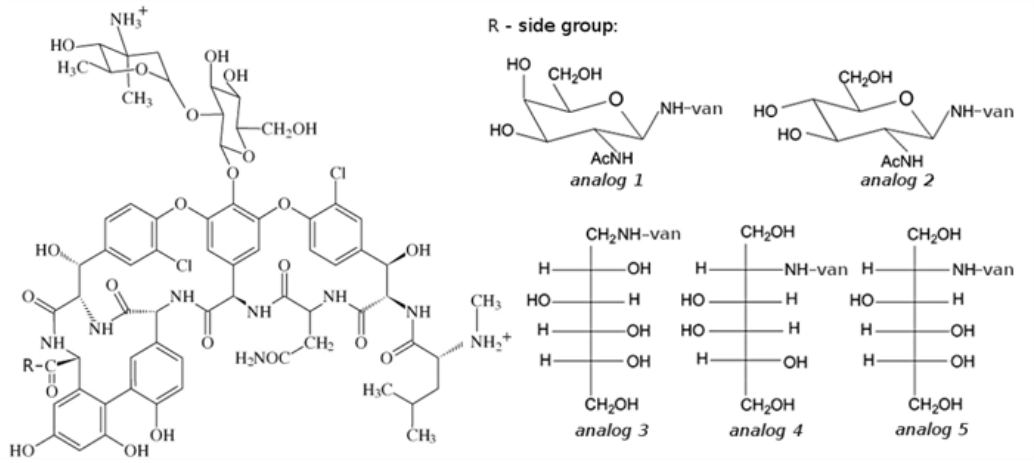
An extensive computational investigations have been performed to examine the effects of the addition of 2-acetamido-2-deoxy-b-D-galactopyranosylamine (*analog 1*), 2-acetamido-2-deoxy-b-D-glucopyranosylamine (*analog 2*), 1-amino-1-deoxy-D-glucitol (*analog 3*), 2-amino-2-deoxy-D-galactitol (*analog 4*) and 2-amino-2-deoxy-D-glucitol (*analog 5*) to the C-terminal amino acid group in the vancomycin. All non standard groups have been parametrized for the *gaff* and *glycam06* force fields, and connected to the heptapeptide macrocyclic vancomycin ring C-termini by a peptide bond. A pentapeptide cell wall precursor mimic AcAla-D-iGlu-Lys-D-Ala-D-Ala has been added in the position known to form active complex with vancomycin. To the computational system there has been also added a periodical, pre-equilibrated water box, TIP3P model.
Every vancomycin analog-peptidoglycan precursor complex has been optimized, submitted to the isothermal-isobaric molecular dynamics in the AMBER package and then analyzed. The analysis of overall RMSd changes, changes in position and interactions involving modified part of vancomycin as well as comparative study of possible interactions with cyclic and chain forms of modified groups are discussed.



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