Comparison of two AMBER force fields for investigating the ligand binding properties of maltose-binding protein

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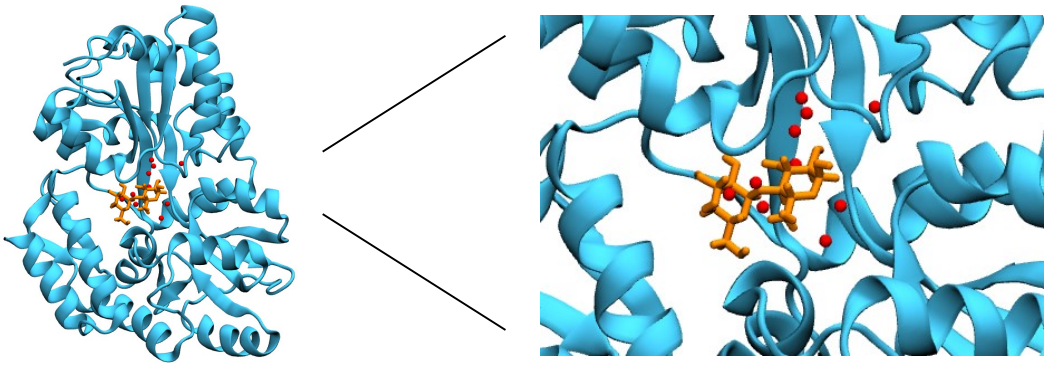
Maltose-binding protein (MBP) belongs to a superfamily of bacterial receptor proteins. It consists of two domains exhibiting a large conformational change upon ligand binding, which can be utilized to engineer biosensors that report ligand concentration. [1]



To set the necessary groundwork for designing an MBP-based biosensor, here we performed molecular dynamics (MD) simulations of MBP with maltose as its ligand starting from the known complex crystal structure [2]. This allows the analysis of MPB conformational stability and ligand binding properties within a dynamic state. A comparison of the two AMBER force fields *ff14SB* (with TIP3P water model) and *ff19SB* (with OPC water model) was done to assess whether they produce similar results.

We could show that both force fields produce highly similar protein dynamics and ligand binding properties. Large fluctuations of the water molecules in the ligand binding pocket were observed regardless of the force field and water model used, indicating that these water molecules are much more dynamic than previously expected from the static crystal structures. This finding is relevant for the future design of altered ligand binding specificity and further demonstrates the need to investigate the ligand binding properties of MBP in a dynamic setting.

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[2] F. A. Quiocho, J. C. Spurlino, L. E. Rodseth, *Structure*, **1997**, *5* (8), 997–1015.