Structure prediction of antimicrobial peptide Melectin in membrane mimicking environment

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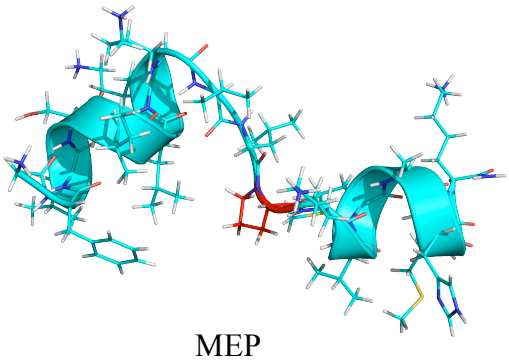
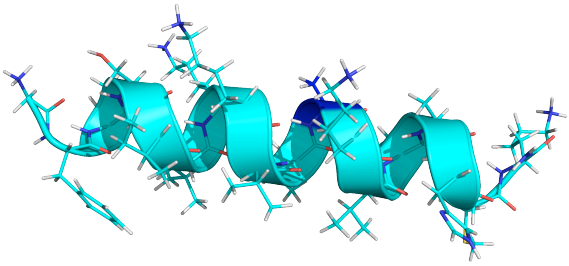
Melectin (MEP) is an antimicrobial peptide (AMP) recently isolated from the venom of cleptoparasitic bee Melecta alfibrons exhibiting both antimicrobial (against both gram-positive and -negative bacteria) and mast cell degranulating activity but low hemolytic activity. [1] This unique combination of properties owes to the proline residue in position 11. Mutation of this residue causes a dramatic increase in hemolytic activity and thus in toxicity for eukaryotic cells.
Secondary structures of the short (19AAs) antimicrobial peptide MEP and the mutant MEP3(P11A) in 40% trifluorethanol(TFE)/water solution were modeled and studied in molecular dynamics simulations. Such TFE/water mixtures have been used for more than three decades in experimental studies (mainly NMR and CD) of secondary-structure-forming peptides in solution as a membrane mimicking environment. Recently also a few theoretical studies using different force fields were published[2,3]. Here, in order to afford for consistent peptide-TFE-water simulation studies, we have parametrized TFE within the AMBER framework[4] and studied the effect of TFE on the peptide structure.



MEP



MEP3

[1] V.Cerovsky et al*, Chem. Bio. Chem*, **2008**, *9*, 2815-2821.
[2] D. Roccatano et al, *PNAS*, **2002**, *99*, 12179-12184.
[3] A. R. van Buuren and H. J. C. Berendsen*, Biopolymers*, **1993**, *33*, 1159-1166.
[4] Y. Duan et al, *J. Comp. Chem.*, **2003**, *24*, 1999-2012.