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### **How antimicrobial peptides disrupt lipid bilayers?**

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The molecular basis for the activity of cyclic and linear antimicrobial peptides is analysed. We performed multi-scale molecular dynamics simulations and biophysical measurements to probe the interaction of antimicrobial peptides with model membranes. Two linear antimicrobial peptides, magainin and melittin and a cyclic one, BPC194 have been studied. We test different models to determine the generic and specific forces that lead to bilayer disruption. We probe whether interfacial stress or local membrane perturbation is more likely to lead to the porated state. We further analyse the reasons that determine specificity and increase of activity in antimicrobial peptides. The results provide detailed insight in the mode of action of antimicrobial peptides.