How do antimicrobial peptides disrupt membranes?

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Abstract

Recent molecular dynamics (MD) simulations indicate that membrane pores made by two different peptides have remarkably different stabilities. Six alamethicin remained in a barrel stave arrangement for the duration of the 14 μs trajectory. In contrast, all six peptides in a similar barrel stave pore formed by piscidin 1 diffused to the membrane surface by 15 μs. This result has important implications for the understanding and design of antimicrobial peptides. It also directly follows from the simulations of simple liquids run on the Los Alamos computers shortly after the end of World War II. Following a brief review the history of the field, the talk will focus on the essential steps needed to get from simple liquids to complex membranes, and some problems that must be solved to proceed further. The talk will conclude with a grid of human behavior that I find useful but some others hate.

Some references (should you wish to include them):

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