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Title: Sequence Diversity in the Pore-Forming Motifs of the Membrane-Damaging Protein Toxins

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Abstract:

Abstract: Pore-forming proteins/toxins (PFPs/PFTs) are the distinct class of membrane-damaging proteins. They act by forming oligomeric pores in the plasma membranes. PFTs and PFPs from diverse organisms share a common mechanism of action, in which the designated pore-forming motifs of the membrane-bound protein molecules insert into the membrane lipid bilayer to create the water-filled pores. One common characteristic of these pore-forming motifs is that they are amphipathic in nature. In general, the hydrophobic sidechains of the pore-forming motifs face toward the hydrophobic core of the membranes, while the hydrophilic residues create the lining of the water-filled pore lumen. Interestingly, pore-forming motifs of the distinct subclass of PFPs/PFTs share very little sequence similarity with each other. Therefore, the common guiding principle that governs the sequence-to-structure paradigm in the mechanism of action of these PFPs/PFTs still remains an enigma. In this article, we discuss this notion using the examples of diverse groups of membrane-damaging PFPs/PFTs.

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