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THE ORIGINS OF TRANSMEMBRANE ION CHANNELS

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Even though membrane proteins that mediate transport of ions and small molecules across cell walls are among the largest and least understood biopolymers in contemporary cells, it is still possible to shed light on their origins and early evolution. The central observation is that transmembrane portions of most ion channels are simply bundles of α -helices. By combining results of experimental and computer simulation studies on synthetic models and natural channels, mostly of non-genomic origin, we show that the emergence of α -helical channels was protobiologically plausible, and did not require highly specific amino acid sequences. Despite their simple structure, such channels could possess properties that, at the first sight, appear to require markedly larger complexity. Specifically, we explain how the antiamoebin channels, which are made of identical helices, 16 amino acids in length, achieve efficiency comparable to that of highly evolved channels. We further show that antiamoebin channels are extremely flexible, compared to modern, genetically coded channels. On the basis of our results, we propose that channels evolved further towards high structural complexity because they needed to acquire stable rigid structures and mechanisms for precise regulation rather than improve efficiency. In general, even though architectures of membrane proteins are not nearly as diverse as those of water-soluble proteins, they are sufficiently flexible to adapt readily to the functional demands arising during evolution.