

Common Mechanism of Pore Opening Shared by Five Potassium Channels Elucidated by Gaussian Network Model.

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One of the fundamental questions associated with the function of ion channels is their gating mechanism. The recently elucidated crystal structures of five potassium (K⁺) channels reveal similar structural motifs at their pore-forming region despite their different 3-d structures, suggesting that they could share a common gating mechanism. The validity of this hypothesis is explored by analyzing their collective dynamics using the Gaussian Network Model (GNM). A common gating mechanism is clearly demonstrated by the close superposition of the most cooperative mode profiles of the five proteins, after optimal alignment of their sequences. The identified common mechanism is a global counter-rotation of the extracellular and cytoplasmic (CP) halves of the proteins, leading to the opening of the CP end of the pore. A second cooperative mechanism of motion shared by all five K⁺ channels is the alternating opening and closing of the EC ends (turret region) of the diagonally opposite pairs of monomers.