Molecular gating characteristics in variants of the potassium ion channel Kcv_{ATCV}

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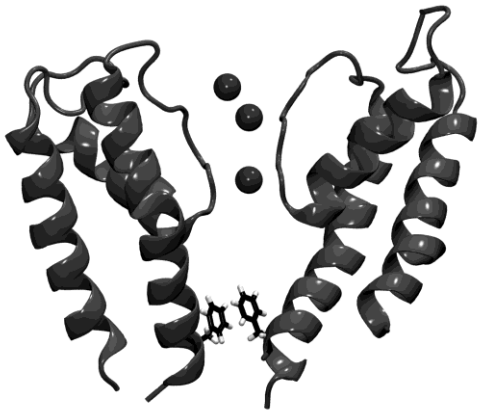
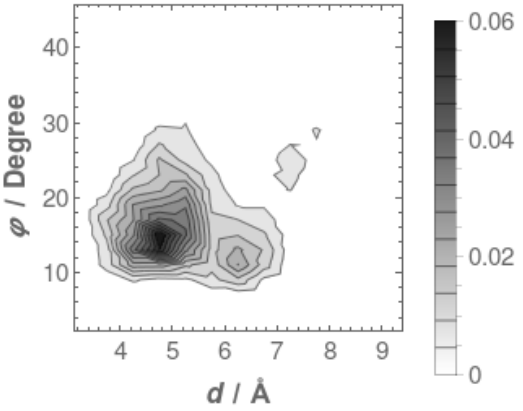
Ion channels fluctuate stochastically between "open" and "closed" states, which determine the ion flux through biological membranes, also known as "gating". This crucial feature of ion channels is necessary in cellular, biological systems to regulate the ion concentration level, which is essential for the processes of homeostasis or second messaging. Yet the origin of gating is not fully understood. A suitable ion channel model for investigations of gating is the tetrameric potassium-selective ion channel Kcv_{ATCV-1}. This minimalistic channel is found in chlorella viruses, and comprised of only 82 amino acids per monomer [1-3]. While electrophysiological experiments have already identified two gates in the wild-type channel, an additional 3rd gating state is found in the related channel Kcv_{ATCV}-"Smith" (Kcv_{ATCV-S}). This 3rd gate leads to a predominantly closed channel (over 70%) in comparison with the wild-type Kcv_{ATCV} and the related Kcv_{ATCV}-"next to Smith" ($Kcv_{ATCV-NTS}$) channel, which both lack this additional gate. Site directed mutagenesis experiments revealed a significant dependency of this gate on the presence of phenylalanine at position 78.

To investigate the characteristics of this 3rd gate with molecular dynamic (MD) simulations, initial homology models were created for the three related channels Kcv_{ATCV-1}, Kcv_{ATCV-S} and $Kcv_{ATCV-NTS}$. For the description of the different behavior in gating, potential π-π-interactions of the Phe78 residues were analyzed in terms of angle/distance probabilities, considering also interactions between different monomers. The results allow for a microscopic interpretation of the gating states in Kcv_{ATCV} variants.





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