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Structure-dynamics-function relationships of inward rectifier K⁺ channels probed by *in silico* methods

Inwardly rectifying potassium channels play a critical role in stabilizing membrane potentials and control numerous physiological processes in excitable and inexcitable cells. Their activity is controlled by dynamical conformational changes that regulate ion flow through a central pore. Understanding the dynamical rearrangements of these channels during gating requires high-resolution structure information from channels crystallized in different conformations and insights into the gating transition steps, which are difficult to access experimentally. My group is using computational methods to gain in depth structural insights into gating perturbations of these channels, including gating changes resulting from disease causing mutations. In particular we focus on Cantú syndrome, a rare genetic disorder causing hypertrichosis and cardiac abnormalities. The genetic cause of this disease, are gain-of-function mutations in the ATP-sensitive potassium channel KATP consisting of pore forming Kir6.1 subunits and ancillary SUR2 subunits. The availability of cryo-EM structures of the KATP channel enables us to investigate the binding sites of channel modulators and to develop dynamic pharmacophore models, which should facilitate the development of novel inhibitors, needed for the treatment of Cantú disease.

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