Electron diffraction of a bacterial ClC-type chloride channel

Abstract
CIC-type Cl- channels, as two-pore homodimers, display an architecture unprecedented in selective ion channels, yet little is known regarding their mechanisms of selectivity and gating. In contrast to the great successes with K+ channels, a decade of mutagenic analysis has revealed little about the structure and function of the ClCs: even the number of ion-conducting pores per complex is controversial. Thus, for these proteins direct structural information is particularly important. We have formed two-dimensional crystals of a bacterial CIC homologue, and are analysing their structure using cryo-electron microscopy of glucose-embedded specimens. Here we report the measurement of electron diffraction patterns from these crystals. Unfettered by the imaging limitations of the electron microscope, the diffraction patterns reveal ordering of the crystals to at least 3.8 Å resolution, suggesting that they can be used to generate an atomic model of the protein. We present an improved projection structure of the channel at 6.5 Å using amplitude data derived from four electron diffraction patterns, with crystallographic statistics comparable to those reported for other high-quality two-dimensional crystals.

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