

Crystal structure of the tetramerization domain of the *Shaker* potassium channel

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Voltage-dependent, ion-selective channels such as Na⁺, Ca²⁺ and K⁺ channel proteins function as tetrameric assemblies of identical or similar subunits¹⁻⁴. The clustering of four subunits is thought to create an aqueous pore^{5,6} centred at the four-fold symmetry axis. The highly conserved, amino-terminal cytoplasmic domain (~130 amino acids) immediately preceding the first putative transmembrane helix S1 is designated T1. It is known to confer specificity for tetramer formation^{7,8}, so the heteromeric assembly of K⁺-channel subunits is an important mechanism for the observed channel diversity⁹⁻¹¹. We have determined the crystal structure of the T1 domain of a *Shaker* potassium channel at 1.55 Å resolution. The structure reveals that four identical subunits are arranged in a four-fold symmetry surrounding a centrally located pore about 20 Å in length. Subfamily-specific