

Publication

1MO7: ATPase

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The Na,K-ATPase hydrolyzes ATP to drive the coupled extrusion and uptake of Na⁺ and K⁺ ions across the plasma membrane. Here, we report two high-resolution NMR structures of the 213-residue nucleotide-binding domain of rat alpha1 Na,K-ATPase, determined in the absence and the presence of ATP. The nucleotide binds in the anti conformation and shows a relative paucity of interactions with the protein, reflecting the low-affinity ATP-binding state. Binding of ATP induces substantial conformational changes in the binding pocket and in residues located in the hinge region connecting the N- and P-domains. Structural comparison with the Ca-ATPase stabilized by the inhibitor thapsigargin, E2(TG), and the model of the H-ATPase in the E1 form suggests that the observed changes may trigger the series of events necessary for the release of the K⁺ ions and/or disengagement of the A-domain, leading to the eventual transfer of the gamma-phosphate group to the invariant Asp369.

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