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Investigating Molecular Power Converters

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Rotary ATPases are ubiquitous protein complexes that couple the translocation of protons through membranes to the synthesis or hydrolysis of ATP and are thus central to biological energy conversion. Eukaryotic F-type ATP synthases use energy stored in transmembrane proton gradients to synthesise the biological energy carrier ATP from ADP and inorganic phosphate. The evolutionary related V-type ATPases operate in reverse by utilising energy derived from ATP hydrolysis to build up transmembrane ion gradients thereby enabling transport processes across membranes. Most eubacteria have F-type ATPases, but some eubacteria and all known archaea have ATPases of the A-type, which are close homologues of V-ATPases. A-ATPases are simpler in design than their eukaryotic counterparts, but are bifunctional and can operate in either direction in dependence of their cellular environment (1).
We are using a combination of X-ray structure analysis, electron microscopy and other biochemical and biophysical techniques to obtain a pseudo-atomic model of an A-ATPase (2, 3). In addition, X-ray structures in different conformations along with normal mode analysis suggest a greater dynamics of the intact complex than previously envisioned. This might be important for cooperativity and regulation of intact rotary ATPases (4, 5).
1. Stewart et al. BioArchitecture 3 (2013)
2. Zhou, et al. Science 334, 380-385 (2011)
3. Lee, et al. Nat. Struct. Mol. Biol. 17, 373-378 (2010)
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Summary

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