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Structure at 2.8 Å resolution of F1-ATPase from bovine heart mitochondria

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In the crystal structure of bovine mitochondrial F-1-ATPase determined at 2.8 Angstrom resolution, the three catalytic beta-subunits differ in conformation and in the bound nucleotide. The structure supports a catalytic mechanism in intact ATP synthase in which the three catalytic subunits are in different states of the catalytic cycle at any instant. Interconversion of the states may be achieved by rotation of the alpha(3) beta(3) subassembly relative to an alpha-helical domain of the gamma-subunit.

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