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Structure of complete ATP synthase and its role as a new drug target against tuberculosis

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 \mathbf{F}_{o} -ATP synthases are paradigmatic molecular machines, which use the transmembrane electrochemical ion gradient to power ATP synthesis. The enzymes belong to the class of rotary ATPases, which all share a common architecture, consisting of a rotor and stator entity. While ions are shuttled through the \mathbf{F}_{o} complex of the enzyme, torque is generated at the rotor/stator and transferred to the F1-catalytic subunits for ATP synthesis. In the opposite direction, ATP hydrolysis can be used to drive ion pumping. In this present research the structure of the complete ATP synthase analysed by electron cryo-microscopy and X-ray crystallography shall be discussed. Also focus on biochemical and structural investigations of the ATP synthase with respect to the development of new antibiotics in the fight against infectious diseases such as tuberculosis.

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