

Enzyme-bound ATP is released

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24/04/2024

Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

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Reactome database release: 88

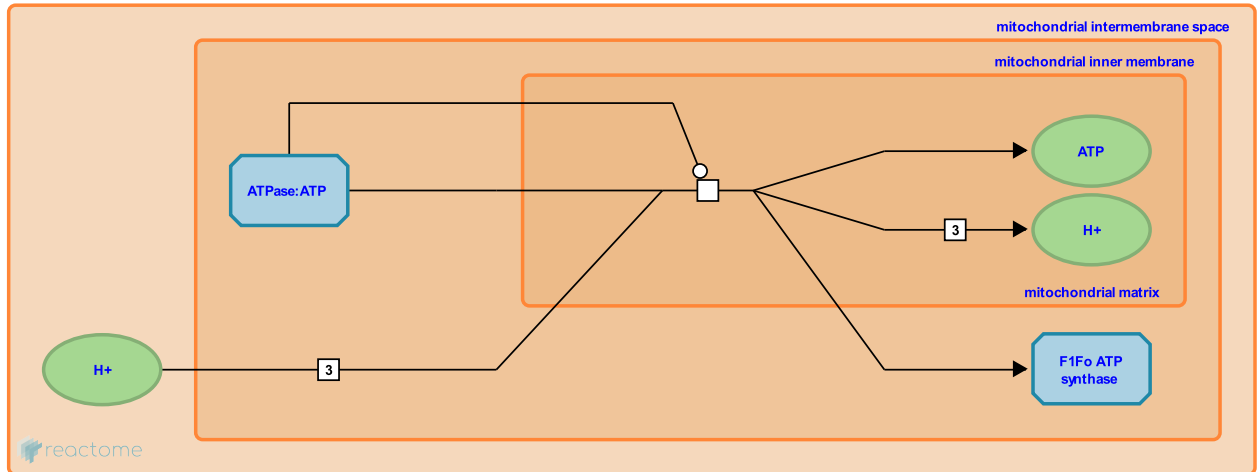
This document contains 1 reaction ([see Table of Contents](#))

Enzyme-bound ATP is released [↗](#)

Stable identifier: R-HSA-164834

Type: transition

Compartments: mitochondrial matrix



In the last step, the beta subunit is converted to the open form and ATP is released. Passage of protons through the Fo part causes a ring of approximately 10 subunits to rotate. This rotation in turn drives the rotation of the gamma subunits, which forms part of one of the stalks. The gamma subunit moves between the three beta subunits which are held in place by the second stalk which can be regarded as a stator. The polypeptide called OSCP connects the stator stalk to the assembly of alpha and beta subunits. It is this step that is coupled to proton translocation as energy is required to break the strong bond between ATP and the protein.

Literature references

Boyer, PD., Momsen, W., Cross, RL. (1973). A new concept for energy coupling in oxidative phosphorylation based on a. *Proc Natl Acad Sci U S A*, 70, 2837-9. [↗](#)

Editions

2005-06-30

Authored

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