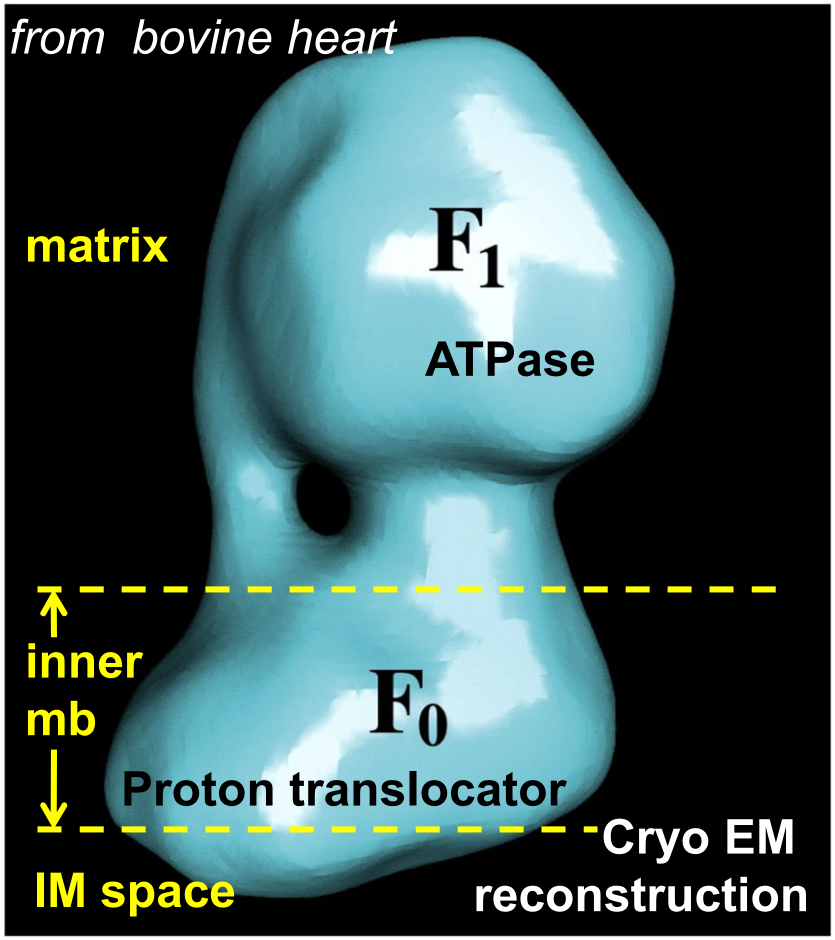
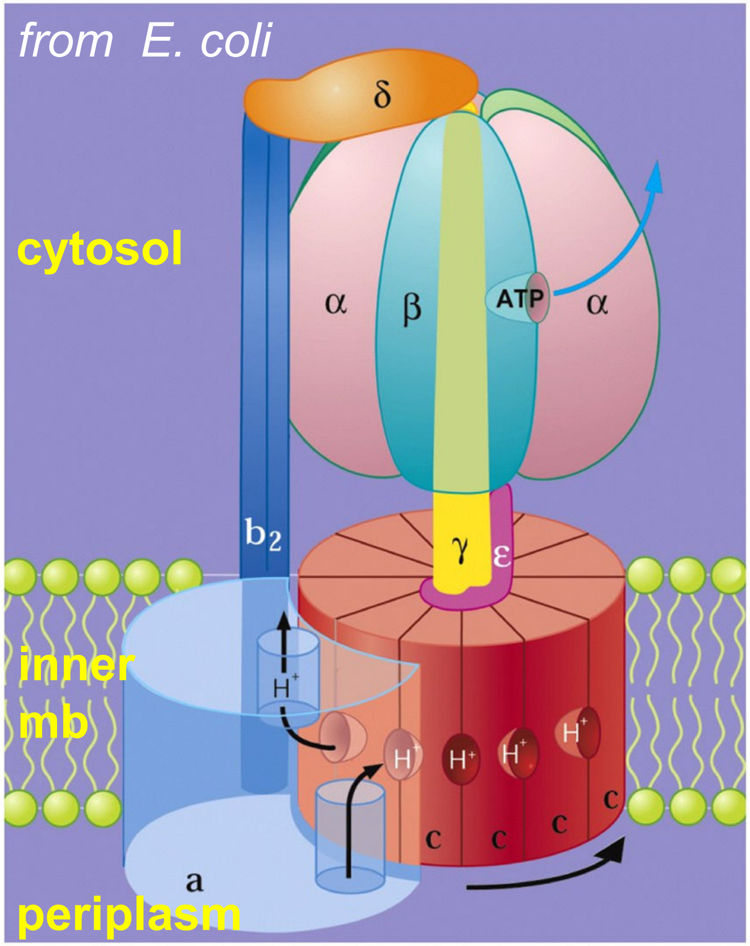
ATP synthase is a multi-subunit complex with membrane and matrix components



Courtesy of John Rubinstein, University of Toronto, Canada, and John Walker and Richard Henderson, MRC Laboratory of Molecular Biology, Cambridge, U.K.



Courtesy of Richard Cross, State University of New York, Syracuse, New York

ATP synthesis happens in the F1 complex

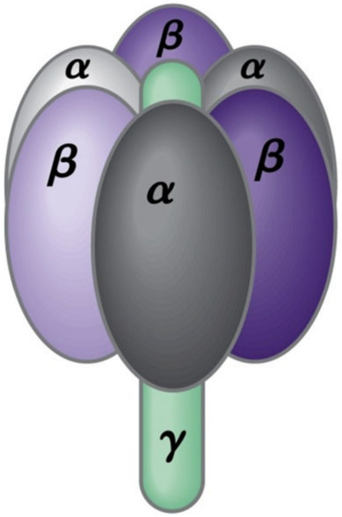


Figure 19-25a
Lehninger Principles of Biochemistry, Fifth Edition

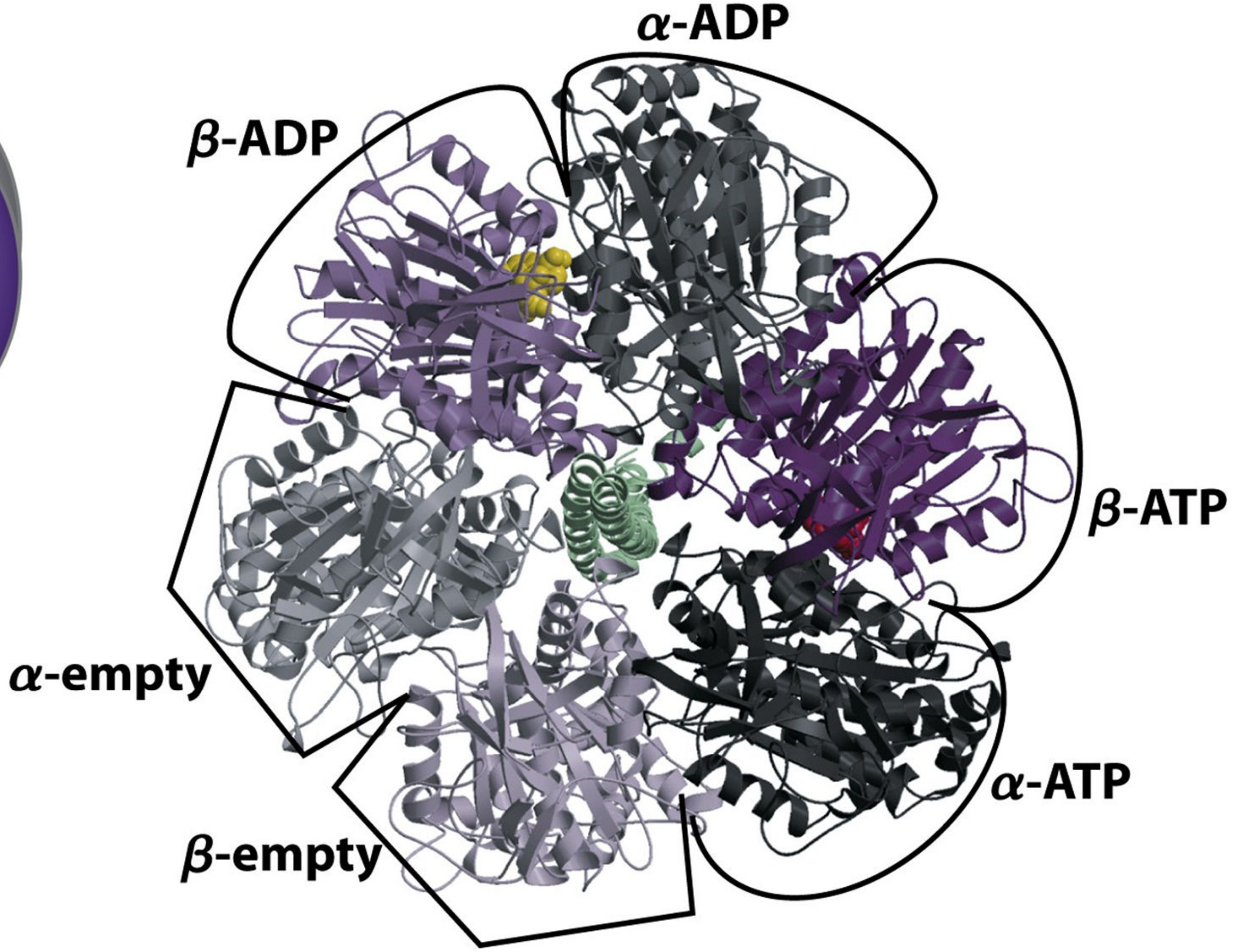


Figure 19-25c
Lehninger Principles of Biochemistry, Fifth Edition

Unlike most enzymes, product release is the rate-determining step for ATP synthase

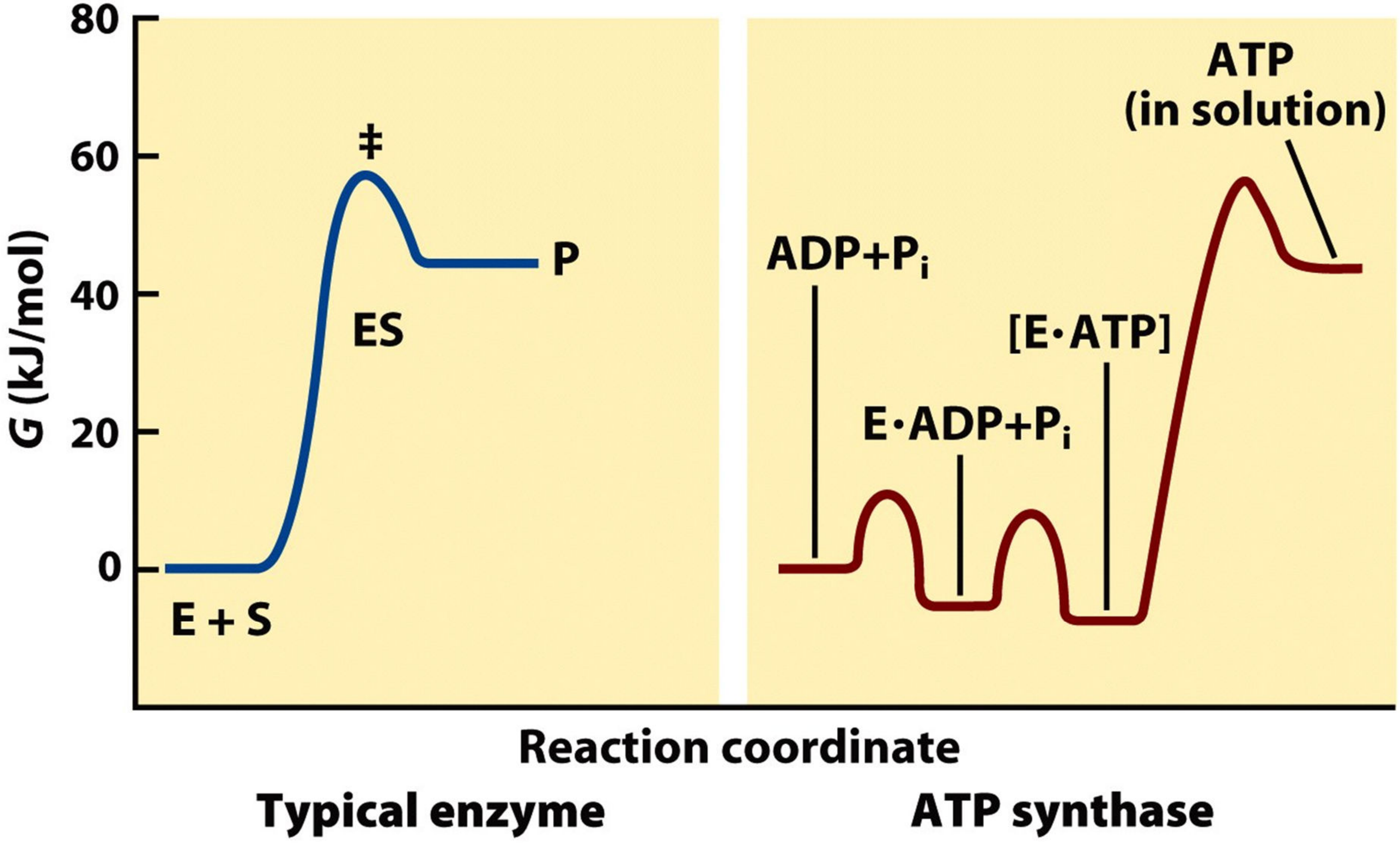
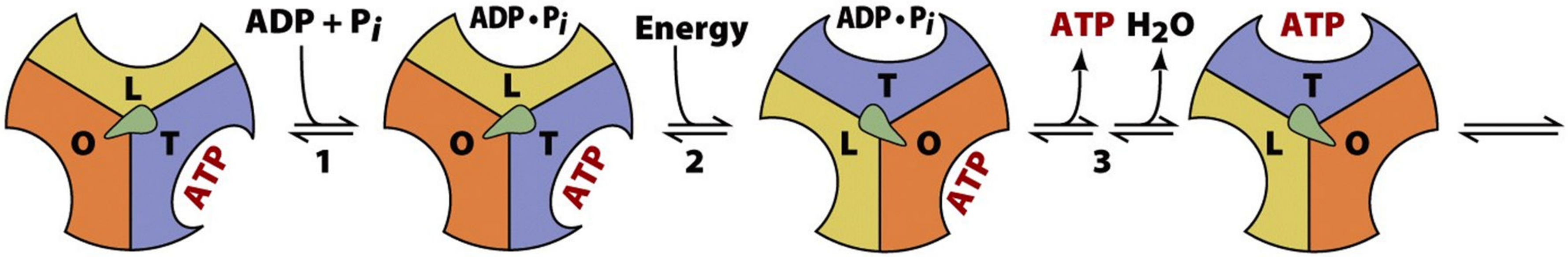


Figure 19-24

Lehninger Principles of Biochemistry, Fifth Edition

The “binding change” mechanism explains how rotational motion drives ATP synthesis



Rotation of the γ subunit induces sequential conformational changes in the α and β subunits. The conformations promote:

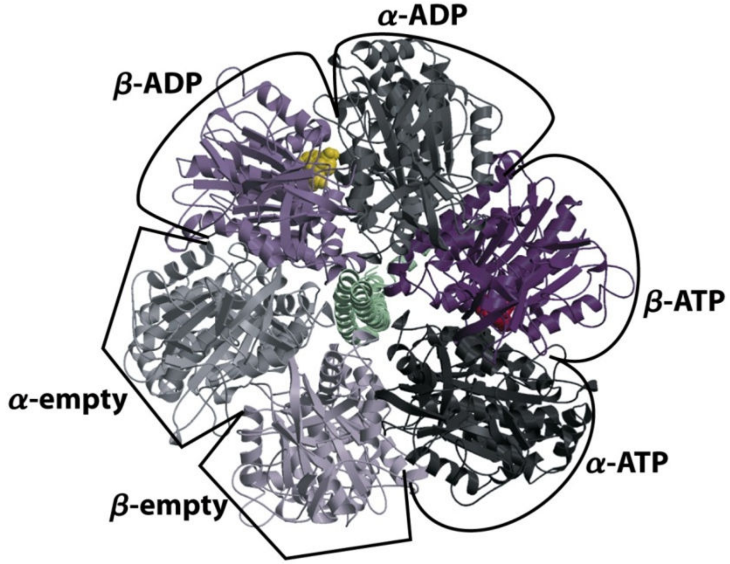


Figure 19-25c
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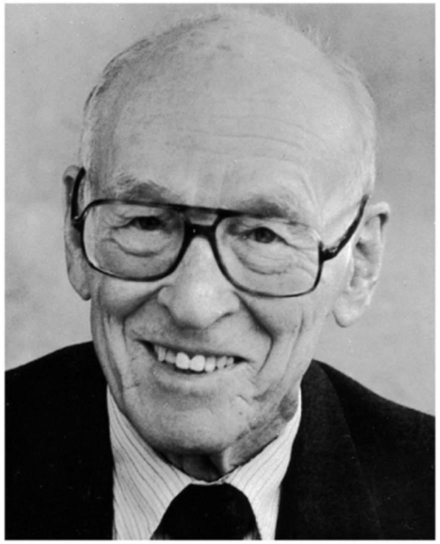
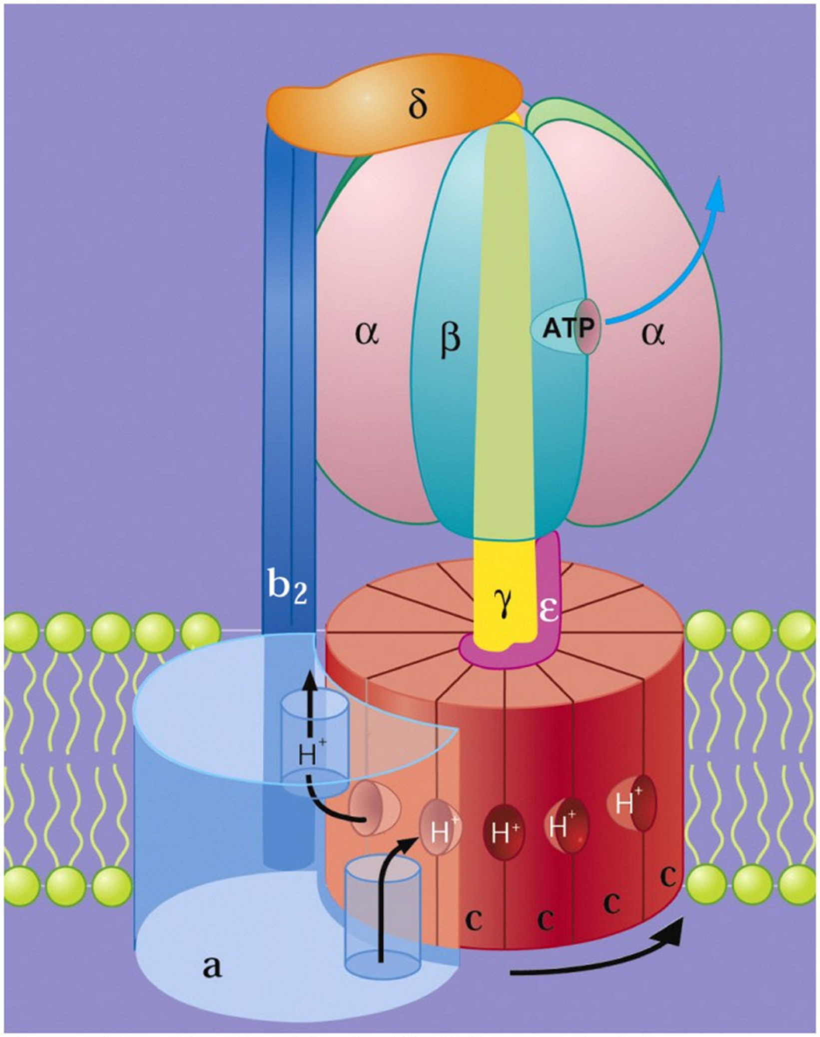
1. ADP and P_i binding
   (<u>L</u>oose or ADP conformation)
2. ATP formation
   (<u>T</u>ight or ATP conformation)
3. ATP release
   (<u>O</u>pen or empty conformation)



Paul Boyer

Proton movement across the membrane spins the rotor and drives ATP synthesis



Courtesy of Richard Cross, State University of New York, Syracuse, New York

Binding and release of 3 protons turns the rotor 120°, resulting in the synthesis of one ATP

Rotor: Ring of *c* subunits plus γ and ε
(The rotor rotates.)

Stator: α/β ring plus *a*, b_2 and δ
(The stator is stationary.)

Transporters allow substrates and products of ATP synthesis to cross the inner mitochondrial membrane

The electrochemical gradient provides the driving force for this transmembrane movement