X-Ray structure of fully oxidized bovine heart cytochrome c oxidase. The complex as viewed from the top.

The intricacies of complex II.

Uncoupling of oxidative phosphorylation.

The proton-translocating channels in bovine COX.

Interpretive drawings of the mitochondrial membrane at various stages of dissection.
Electron micrographs of cristae from (a) intact mitochondria showing their F1 “lollipops” projecting into the matrix, (b) submitochondrial particles, showing their outwardly projecting F1 lollipops, and (c) submitochondrial particles after treatment with urea.

F型ATPaseモーターの構造

Electron microscopy–based image of E. coli F$_{1}$F$_{0}$-ATPase.

X-Ray structure of F$_{1}$-ATPase from bovine heart mitochondria.

ATP synthase, a molecular machine

F型ATPase
X-Ray structure of F$_{1}$–ATPase from bovine heart mitochondria.

The γ, δ, and ε subunits in the X-ray structure of bovine F$_{1}$–ATPase.

Electron density map of the yeast mitochondrial F$_{1}$–c$_{10}$ complex.

X-Ray structure of F$_{1}$–ATPase from bovine heart mitochondria. The surface of the inner portion of the α$_{3}$β$_{3}$ assembly.

NMR structures of the c subunit of E. coli F$_{1}$F$_{0}$–ATPase.

Energy-dependent binding change mechanism for ATP synthesis by proton-translocating ATP synthase.
Rotation of the c-ring in *E. coli* F\(_{1}\)F\(_{0}\)-ATPase.

(a) The rotation of a 3.8-μm-long actin filament in the presence of 5 mM MgATP.