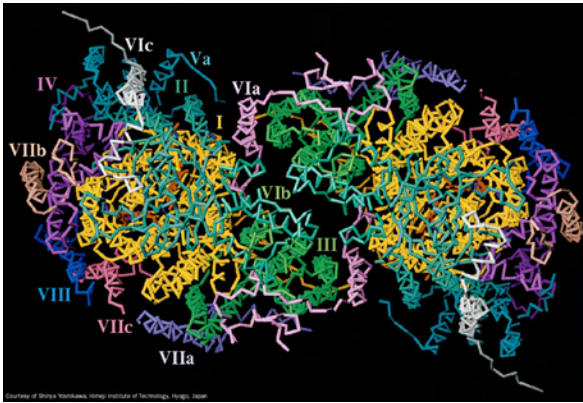
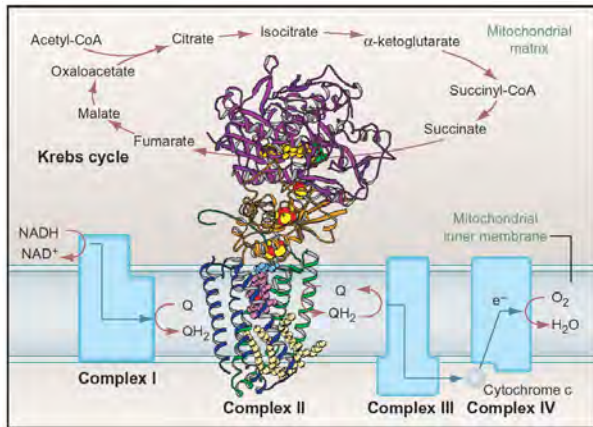
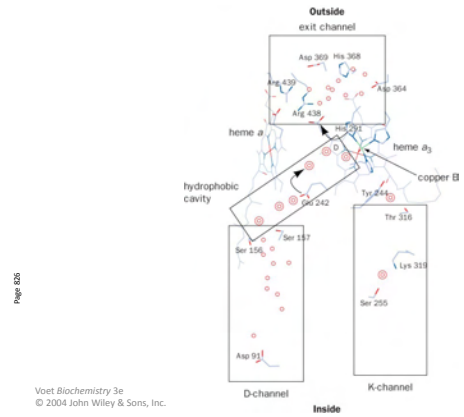


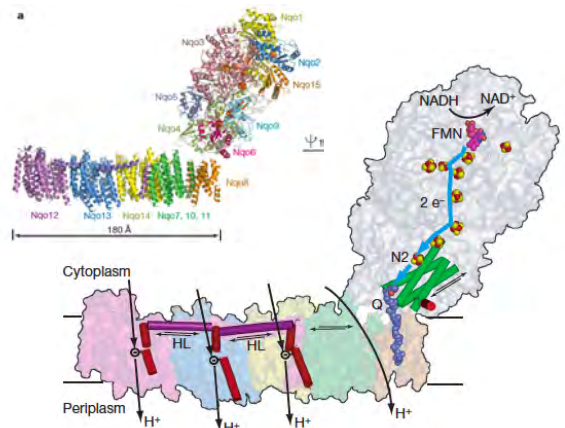
X-Ray structure of fully oxidized bovine heart cytochrome c oxidase.
The complex as viewed from the top



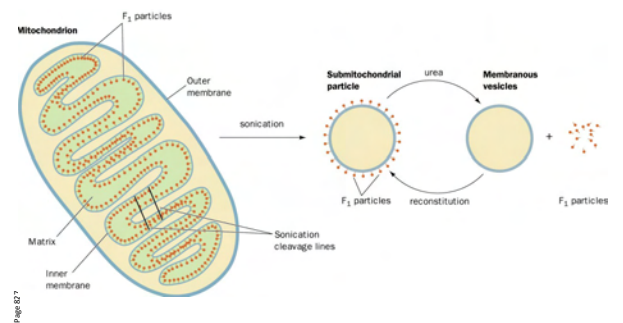
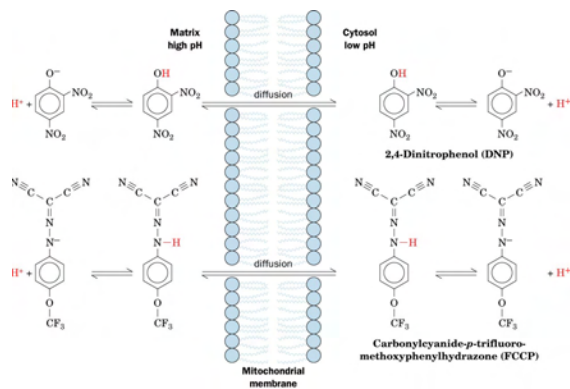
The proton-translocating channels in bovine COX.



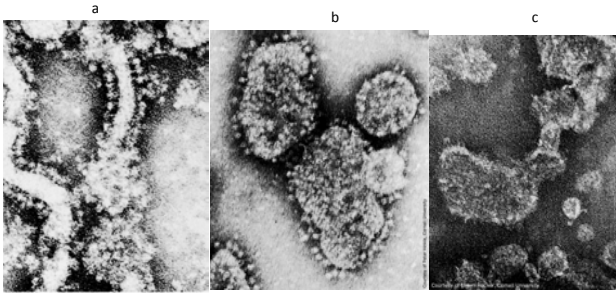
The intricacies of complex II



Uncoupling of oxidative phosphorylation.



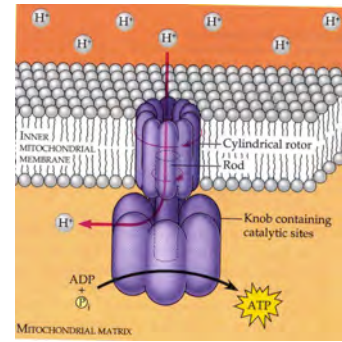
Interpretive drawings of the mitochondrial membrane at various stages of dissection.



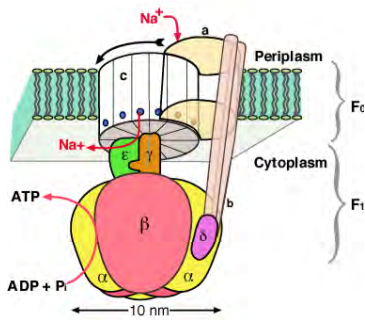
From Peterson, D.J., *Science* 246: 989 (1991).
Copyright © 1991 American Association for the Advancement of Science.
Used by permission.

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.

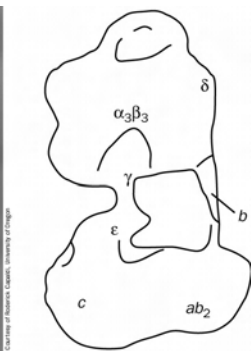
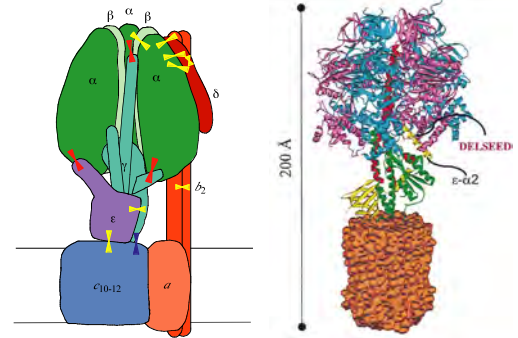
ATP synthase, a molecular machine



F型ATPaseモーターの構造



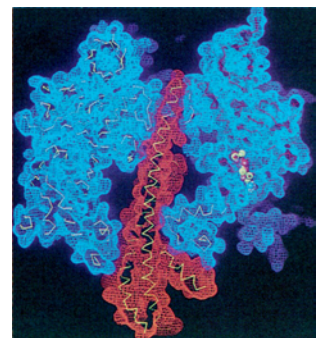
F型ATPase



Electron microscopy-based image of *E. coli* F₁F₀-ATPase.



From Kohnhans, J.F., Leslie, A.G.W., Leslie, A., and Walker, J.E., *Nature* 370: 622 and 627 (1994).

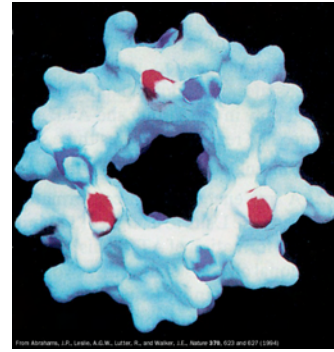


From Kohnhans, J.F., Leslie, A.G.W., Leslie, A., and Walker, J.E., *Nature* 370: 622 and 627 (1994).

X-Ray structure of F₁-ATPase from bovine heart mitochondria.



X-Ray structure of F₁-ATPase from bovine heart mitochondria.



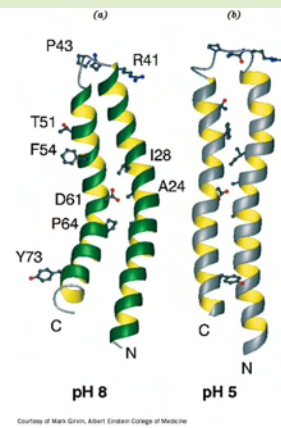
X-Ray structure of F₁-ATPase from bovine heart mitochondria. The surface of the inner portion of the $\alpha_3\beta_3$ assembly.

The γ , δ , and ϵ subunits in the X-ray structure of bovine F₁-ATPase.



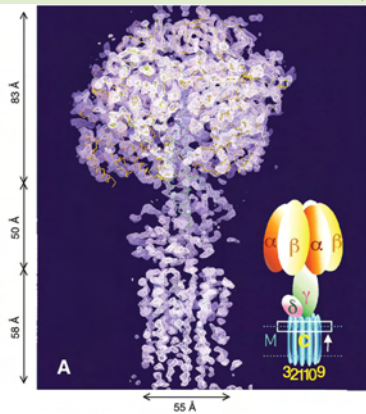
Courtesy of Andrew Leslie and John Walker, Medical Research Council, Cambridge, U.K.

NMR structures of the c subunit of *E. coli* F₁F₀-ATPase.

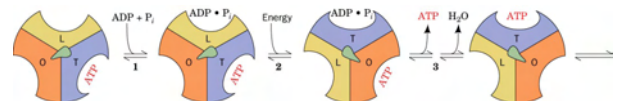


Courtesy of Mark Grinn, Albert Einstein College of Medicine

Electron density map of the yeast mitochondrial F₁-C₁₀ complex.

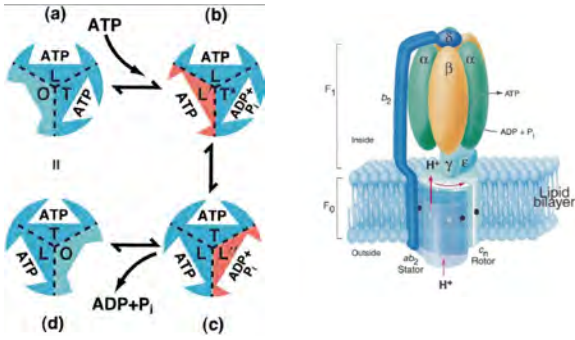


Courtesy of Andrew Leslie and John Walker, Medical Research Council, Cambridge, U.K.



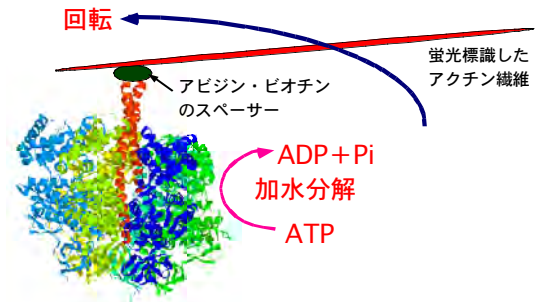
Energy-dependent binding change mechanism for ATP synthesis by proton-translocating ATP synthase.

ATPaseの構造変化と触媒活性モデル



O(オープン)型: 触媒不活性で基質・生成物に親和性なし
 L(ルーズ)型: 弱い親和性をもつが、触媒活性なし
 T(タイト)型: 強い親和性をもち、触媒活性をもつ

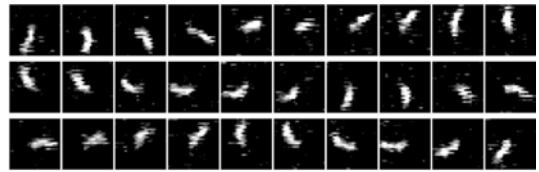
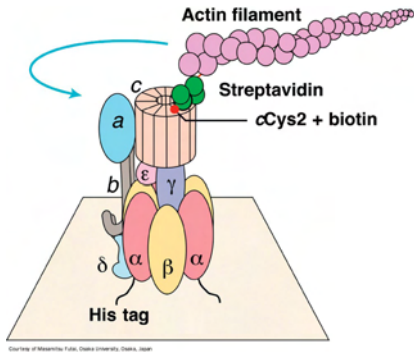
F型ATPase回転実証の実験系



ATPaseの α β γ 複合体

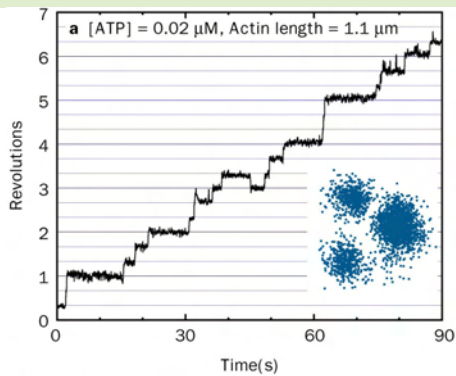
Noji et al. (1997) Nature

Rotation of the c -ring in *E. coli* F_1F_0 -ATPase



Rotation of the c -ring in *E. coli* F_1F_0 -ATPase. (b) The rotation of a 3.6- μm -long actin filament in the presence of 5 mM MgATP.

Stepwise rotation of the γ subunit of F_1 relative to an immobilized $\alpha_3\beta_3$ unit at low ATP concentration.



Courtesy of Kazuhiko Aoyama, Keio University, Yokohama, Japan

