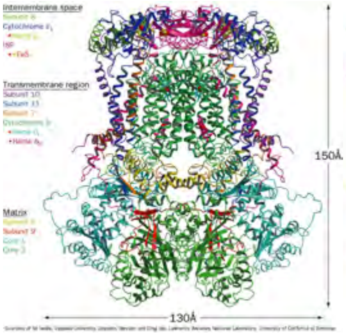
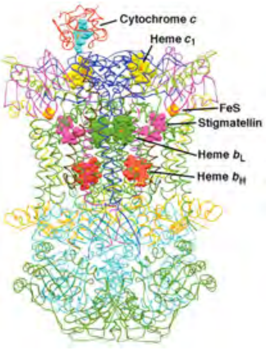
１１サブユニット蛋白質からなる膜蛋白質複合体（約２５万）ダイマー

X-ray structures of cytochrome bc_1.



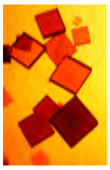
The dimeric bovine complex is viewed perpendicular to its 2-fold axis and parallel to the membrane with the matrix below.

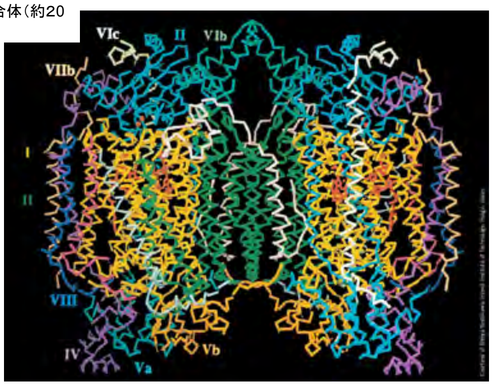


The yeast enzyme in complex with cytochrome *c* and the inhibitor stigmatellin viewed with a ~90° rotation about its 2-fold axis.

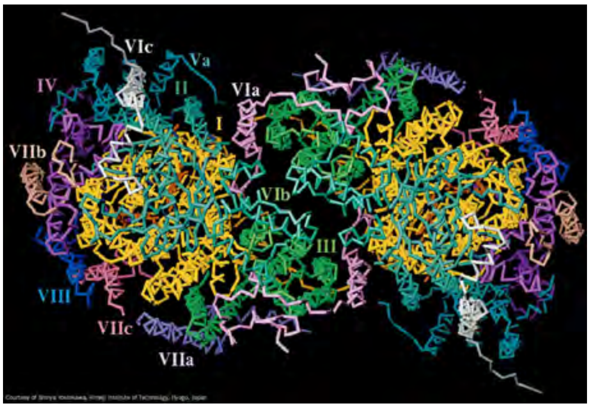
X-Ray structure of fully oxidized bovine heart cytochrome *c* oxidase.

１３サブユニット蛋白質からなる膜蛋白質複合体（約２０万）ダイマー





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



Courtesy of Shinya Yoshikawa, Himeji Institute of Technology, Hyogo, Japan

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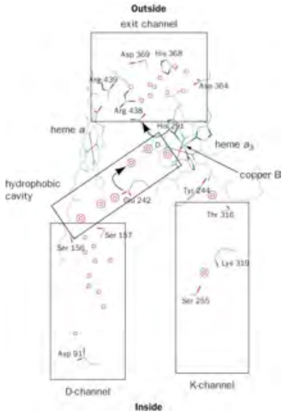
The proton-translocating channels in bovine complex IV



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Voet *Biochemistry* 3e
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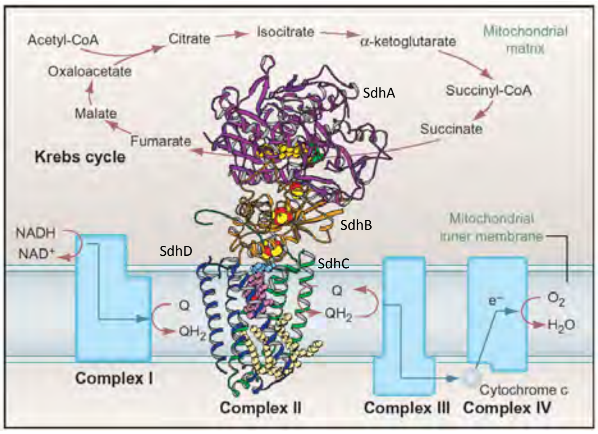

The intricacies of complex II

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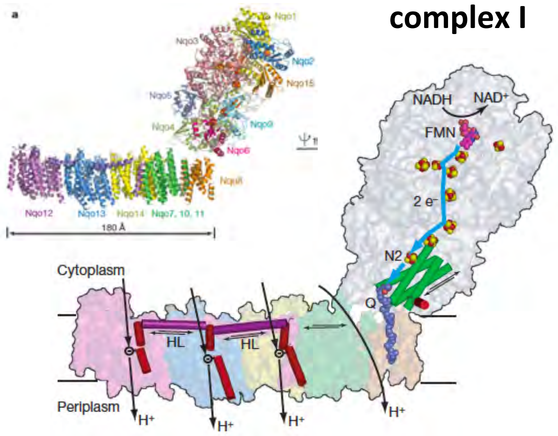
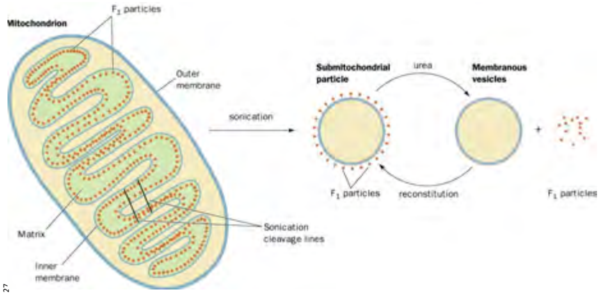
complex I





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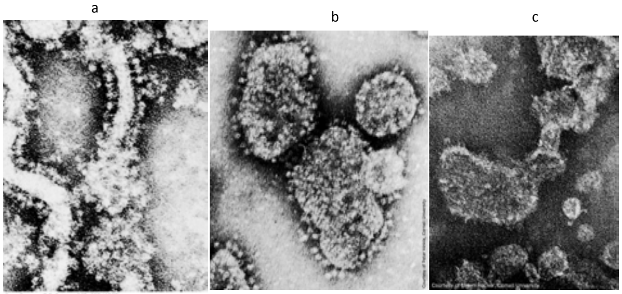
Interpretive drawings of the mitochondrial membrane at various stages of dissection.



From Parsons, D.F., Science 140, 985 (1963).
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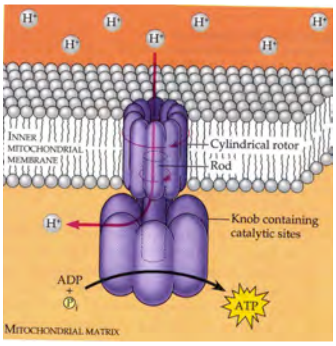
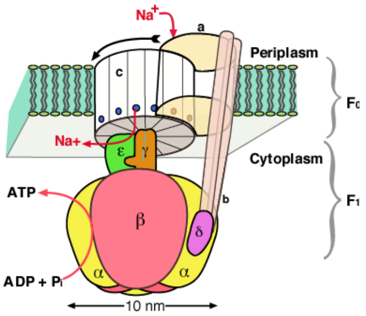
Electron micrographs of cristae from (a) intact mitochondria showing their F1 “lollipops” projecting into the matrix, (b) submitochondrial particles, showing their outwardly projecting F1 lollipops, and (c) submitochondrial particles after treatment with urea.

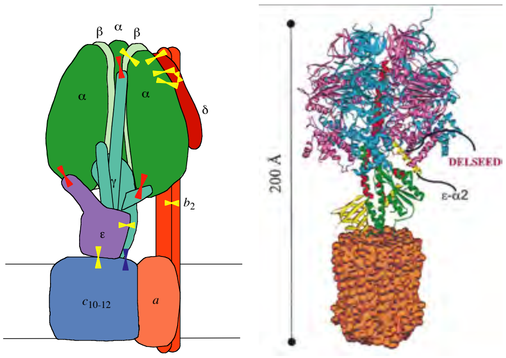
ATP synthase, a molecular machine

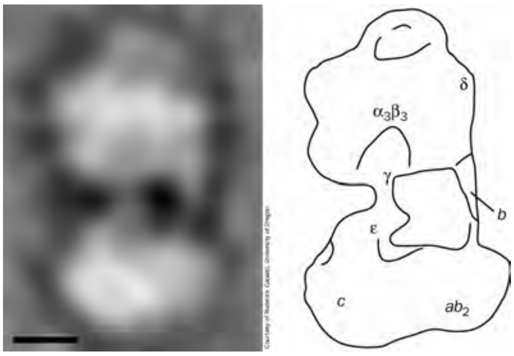


F型ATPaseモーターの構造



F型ATPase



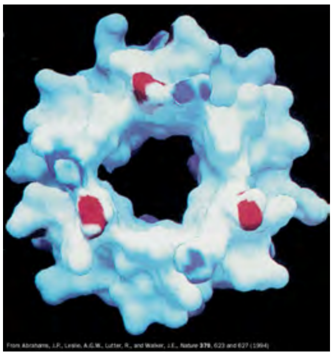


Courtesy of Roderick Capaldi, University of Oregon

Electron microscopy–based image of *E. coli* F_1F_0–ATPase.


From Abrahams, J.P., Leslie, A.G.W., Lutter, R., and Walker, J.E., Nature 370, 622 and 627 (1994)

X-Ray structure of F_1–ATPase from bovine heart mitochondria.

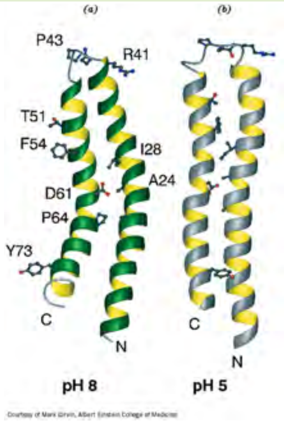

From Abrahams, J.P., Leslie, A.G.W., Lutter, R., and Walker, J.E., Nature 370, 622 and 627 (1994)

X-Ray structure of F_1–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 F_1–ATPase.

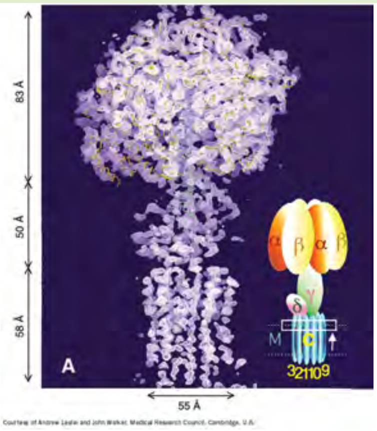
Courtesy of Andrew Leslie and John Walker, Medical Research Council, Cambridge, U.K.

NMR structures of the *c* subunit of *E. coli* F_1F_0–ATPase.

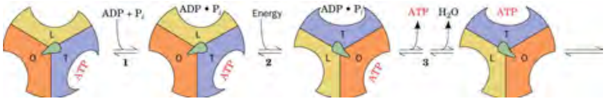


Courtesy of Mark Girvin, Albert Einstein College of Medicine

Electron density map of the yeast mitochondrial F_1–c_{10} complex.

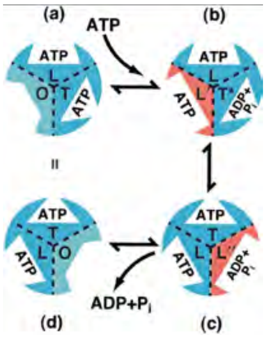


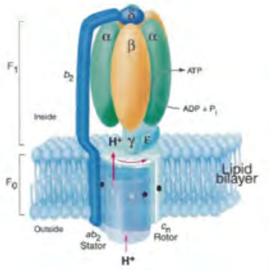
Courtesy of Andrew Leslie and John Walker, Medical Research Council, Cambridge, U.K.



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

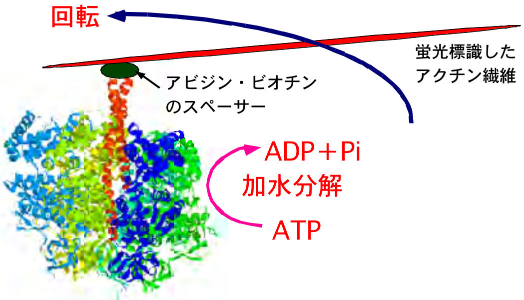
ATPaseの構造変化と触媒活性モデル





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

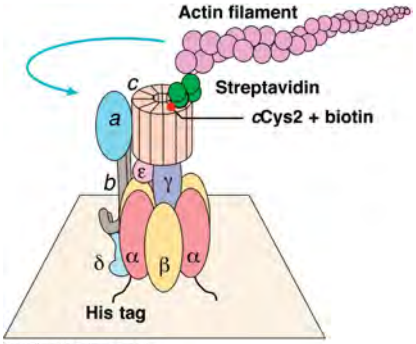
F型ATPase回転実証の実験系

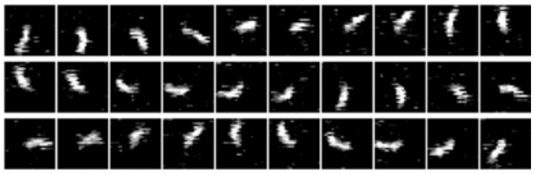


ATPaseのα　β　γ複合体

Noji et al. (1997) Nature

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

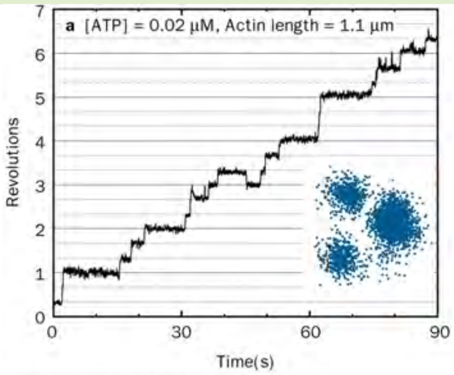




Courtesy of Masamitsu Futai, Osaka University, Osaka, Japan

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 m*M* 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 Kinosita Jr., Keio University, Yokohama, Japan

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