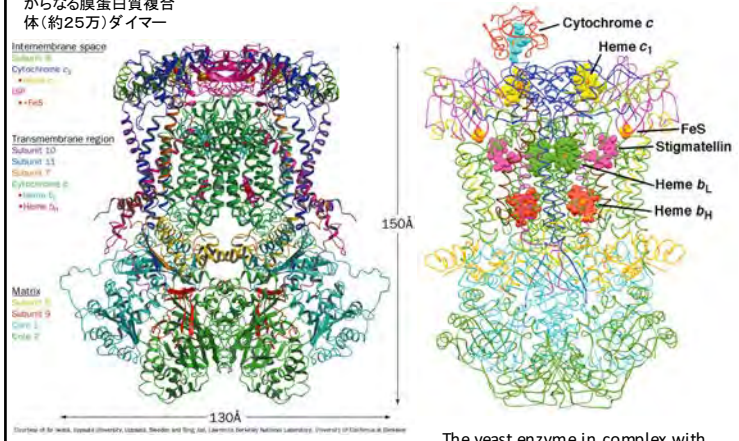
11サブユニット蛋白質からなる膜蛋白質複合体（約25万）ダイマー

X-ray structures of cytochrome bc_1.

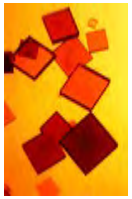


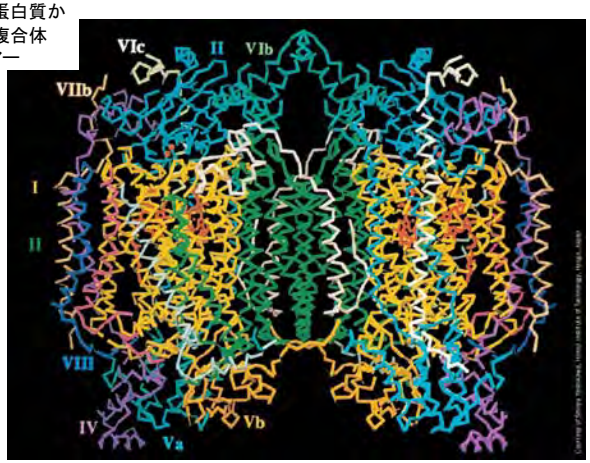
The dimeric bovine complex is viewed perpendicular to its 2-fold axis and parallel to the membrane with the matrix below.

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

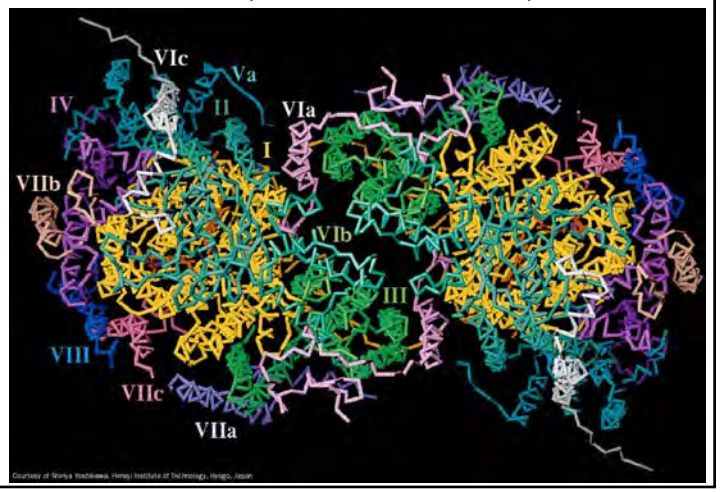
X-ray structure of fully oxidized bovine heart cytochrome *c* oxidase.

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

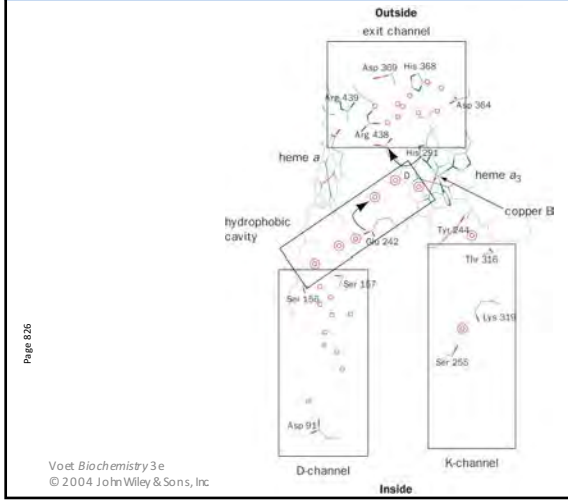




X-Ray structure of fully oxidized bovine heart cytochrome *c* oxidase.
The complex as viewed from the top



The proton-translocating channels in bovine complex IV



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Voet *Biochemistry* 3e
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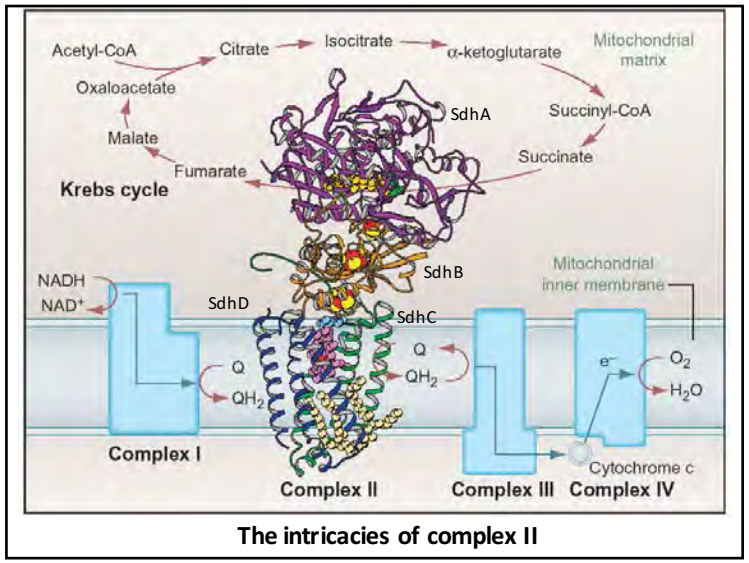
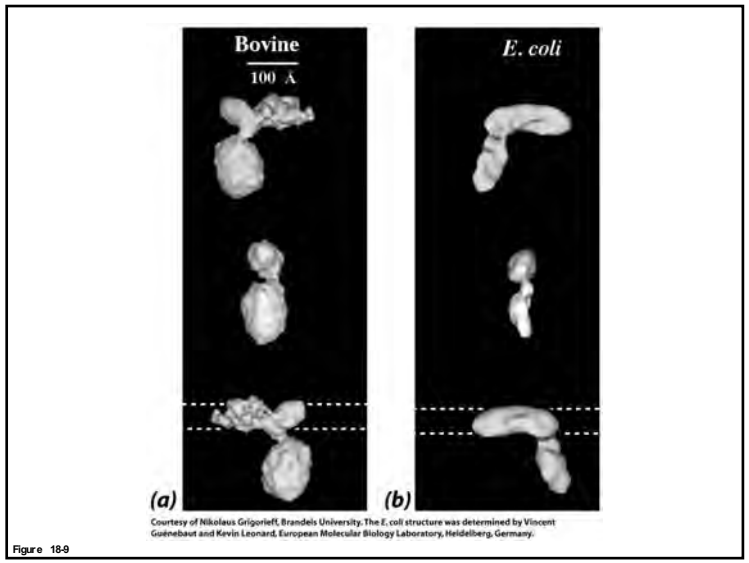
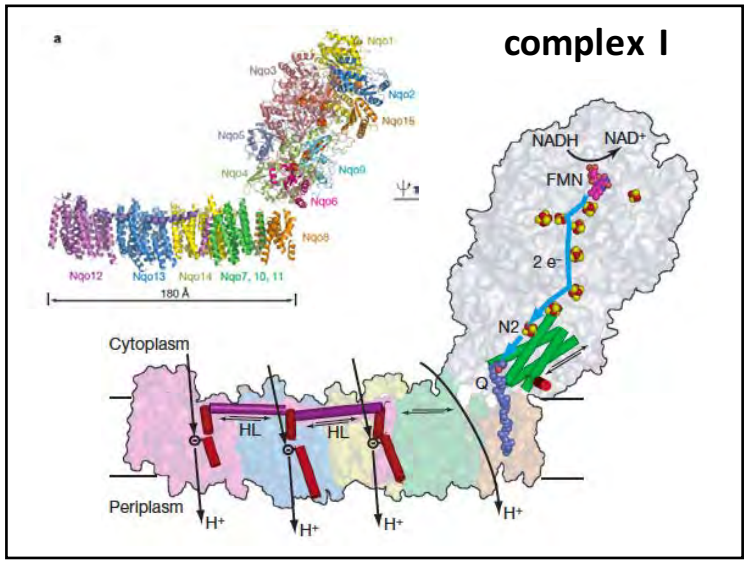
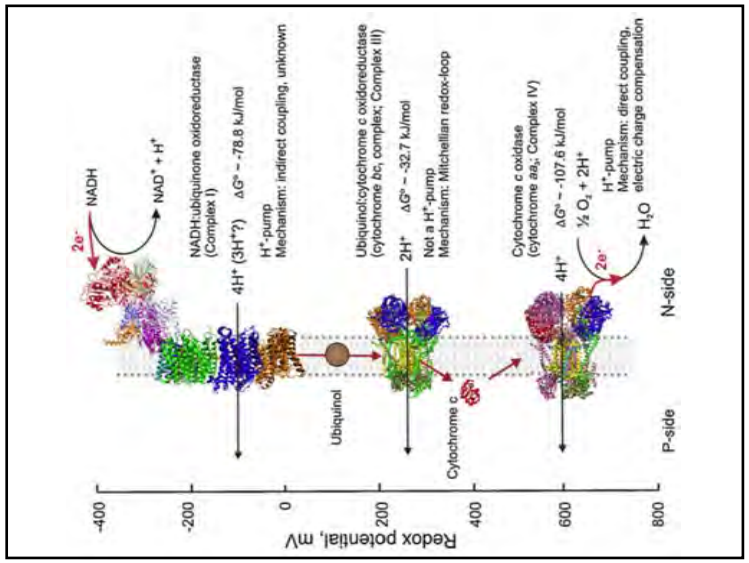


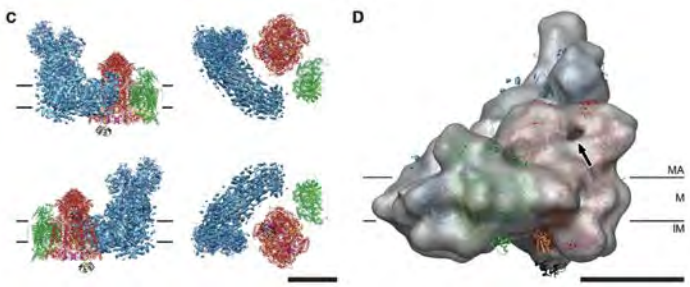
The intricacies of complex II





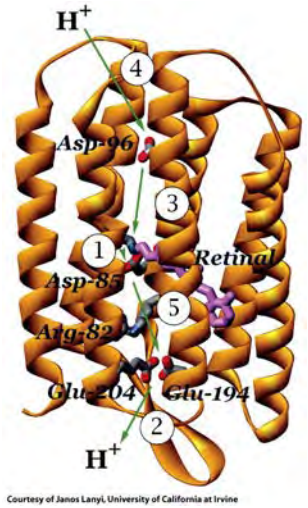


Complexes I, III, IV from bovine heart



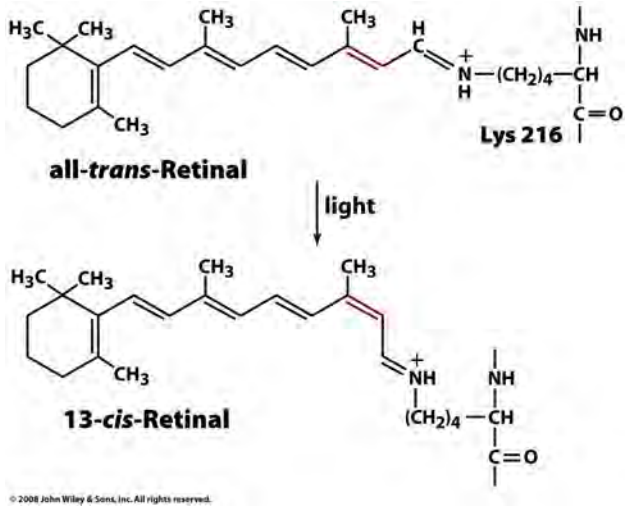
(blue, complex I; red, complex III; green, complex IV) and cytochrome c (black)

Figure 9-22



Courtesy of Janos Lanyi, University of California at Irvine

Figure 18-12



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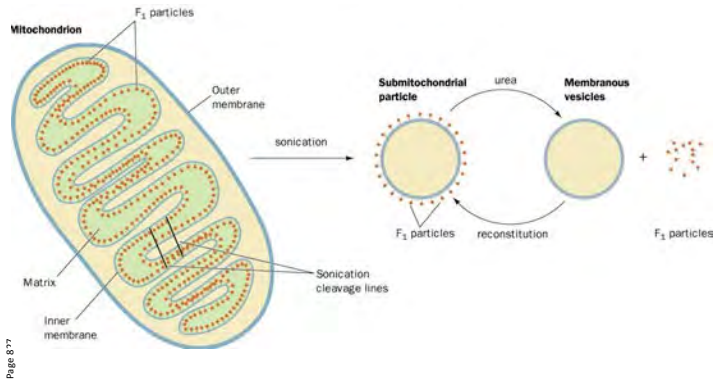
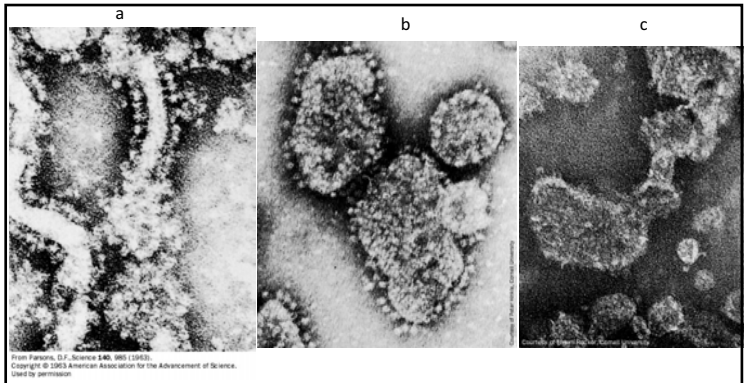
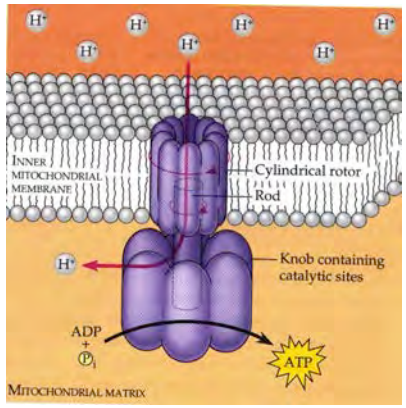


Interpretive drawings of the mitochondrial membrane at various stages of dissection.

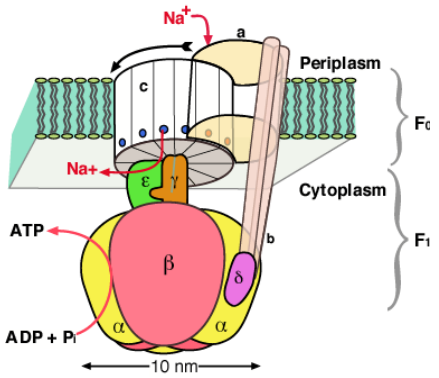


Electron micrographs of cristae from (a) intact mitochondria showing their F1 "lollipops" projecting into the matrix, (b) submitochondrial particles, showing their outwardly projecting F1 lollipops, and (c) submitochondrial particles after treatment with urea.

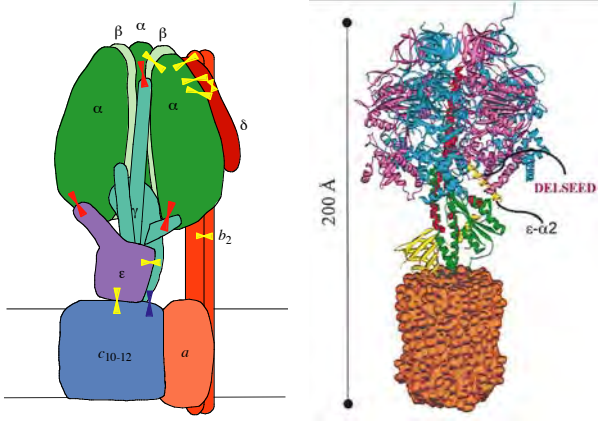
ATP synthase, a molecular machine

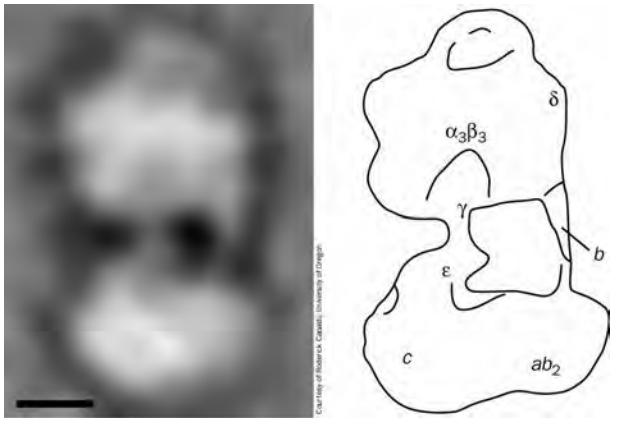


F型ATPaseモーターの構造



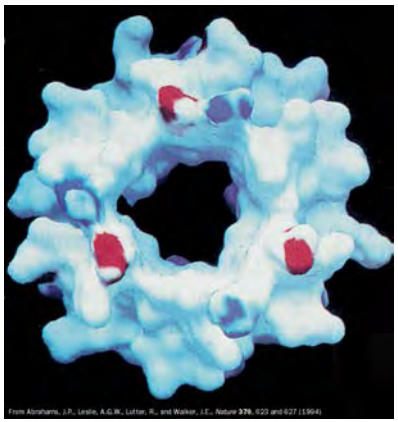
F型ATPase





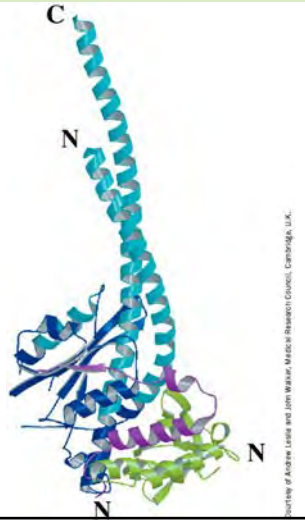
Electron microscopy–based image of *E. coli* F_1F_0–ATPase.

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

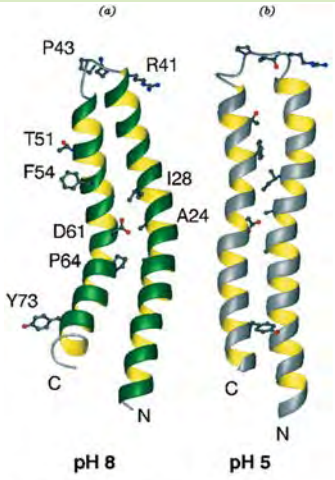


X-Ray structure of F_1–ATPase from bovine heart mitochondria.
The surface of the inner portion of the $\alpha_3\beta_3$ assembly.

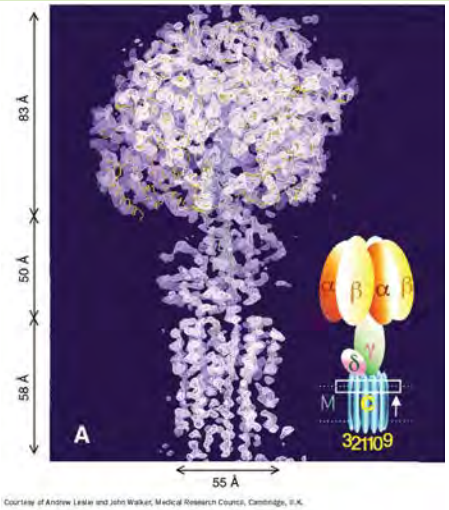
The ■ ♥ and ■ subunits in the X-ray structure of bovine F_1–ATPase.



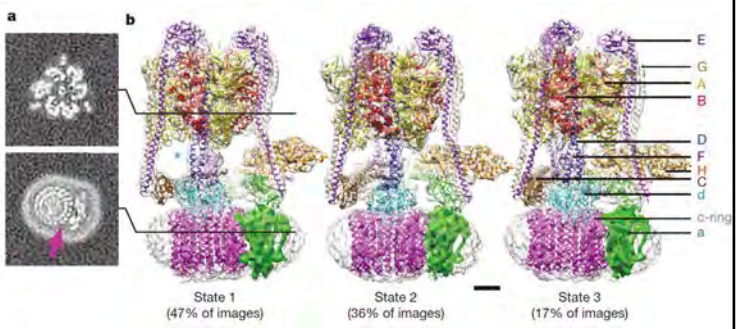
NMR structures of the *c* subunit of *E. coli* F_1F_0–ATPase.



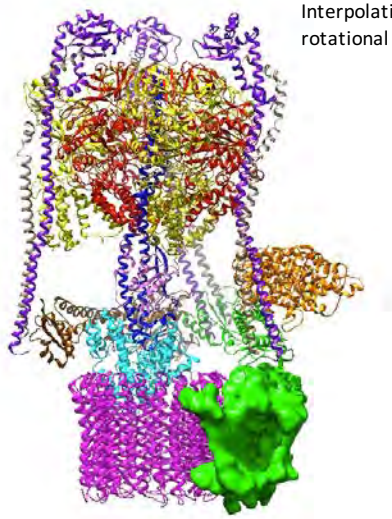
Electron density map of the yeast mitochondrial F_1–c_{10} complex.



Electron cryomicroscopy to obtain structures for rotational states of the V-ATPase from the yeast *S. cerevisiae.*

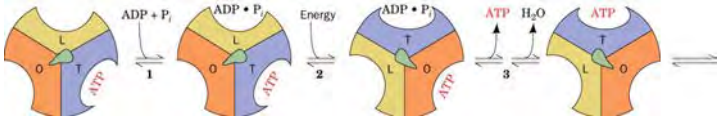


Nature **521**, 241–245 (14 May 2015)



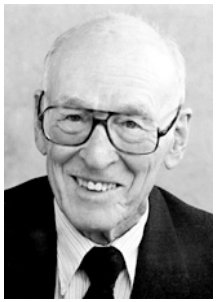
Interpolation between the three observed rotational states of the V-ATPase.

The resulting series of structures shows ten proteolipid subunits in the c-ring, setting the ATP:H^+ ratio for proton pumping by the V-ATPase at 3:10, and reveals long and highly tilted transmembrane α-helices in the a-subunit that interact with the c-ring. The three different maps reveal the conformational changes that occur to couple rotation in the symmetry-mismatched soluble catalytic region to the membrane-bound proton-translocating region. Almost all of the subunits of the enzyme undergo conformational changes during the transitions between these three rotational states. The structures of these states provide direct evidence that deformation during rotation enables the smooth transmission of power through rotary ATPases.

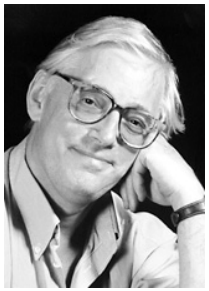


Energy-dependent binding change mechanism for ATP synthesis by proton-translocating ATP synthase.

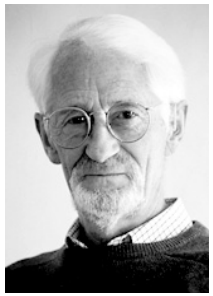
The Nobel Prize in Chemistry 1997



Paul D. Boyer



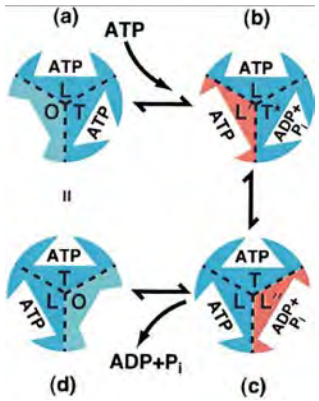
John E. Walker

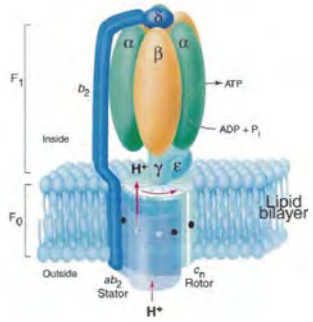


Jens C. Skou

The Nobel Prize in Chemistry 1997 was divided, one half jointly to Paul D. Boyer and John E. Walker *"for their elucidation of the enzymatic mechanism underlying the synthesis of adenosine triphosphate (ATP)"* and the other half to Jens C. Skou *"for the first discovery of an ion-transporting enzyme, Na^+, K^+ -ATPase"*.

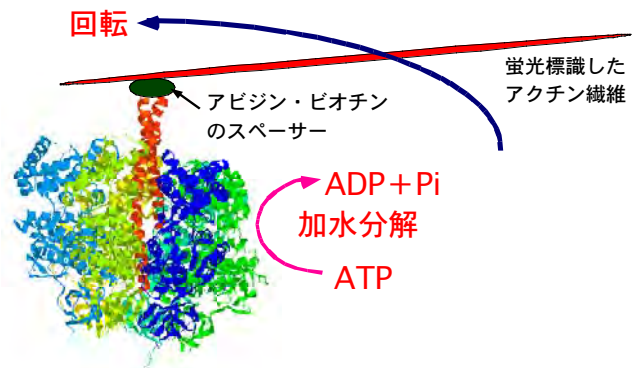
ATPaseの構造変化と触媒活性モデル





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

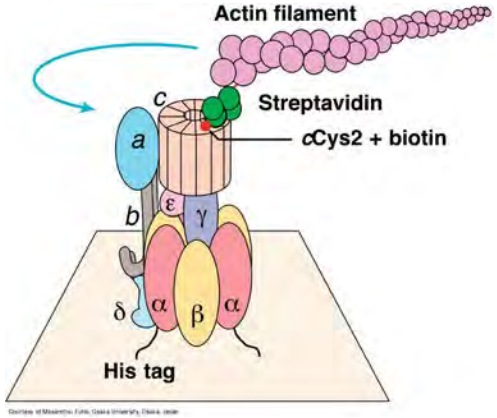
F型ATPase回転実証の実験系

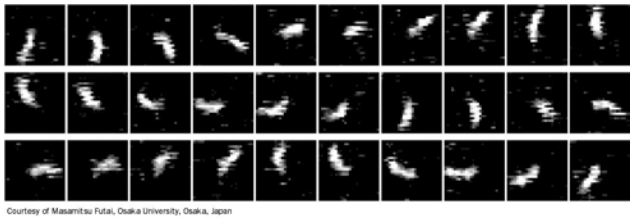


ATPaseのα　β　γ複合体

Noji et al. (1997) Nature

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

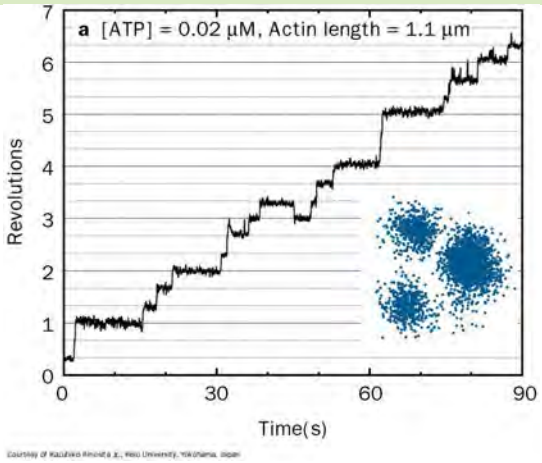




Courtesy of Masamitsu Futai, Osaka University, Osaka, Japan

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.



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