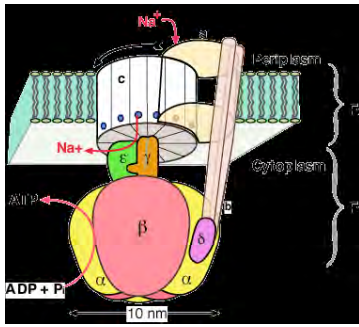
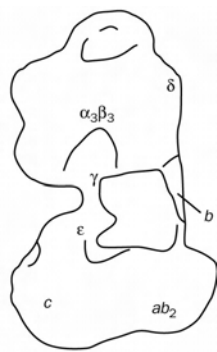
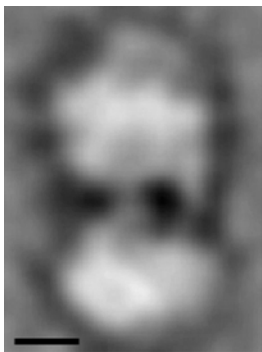
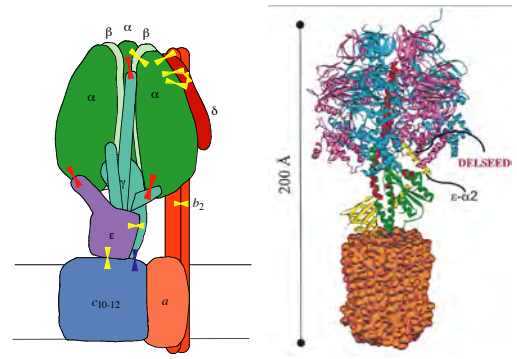


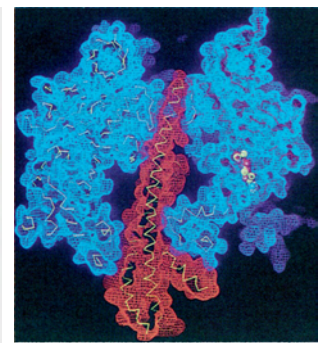
F型ATPaseモーターの構造



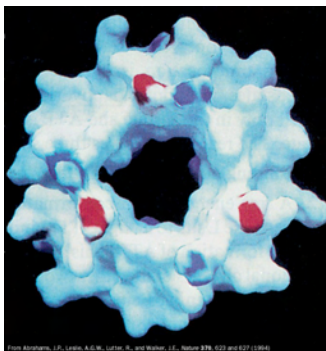
F型ATPase



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

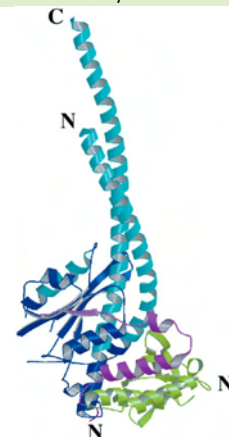


X-Ray structure of F₁-ATPase from bovine heart mitochondria.



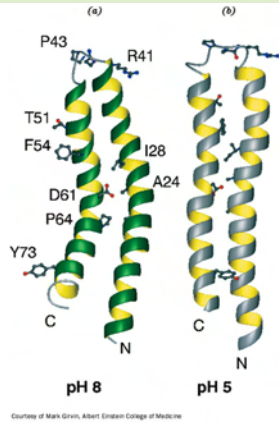
X-Ray structure of F₁-ATPase from bovine heart mitochondria. The surface of the inner portion of the $\alpha_3\beta_3$ assembly.

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

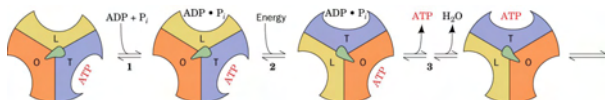
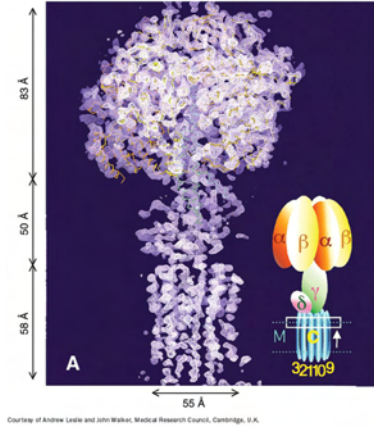


Courtesy of Andrew Leslie and John Walker, Medical Research Council, Cambridge, UK.

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

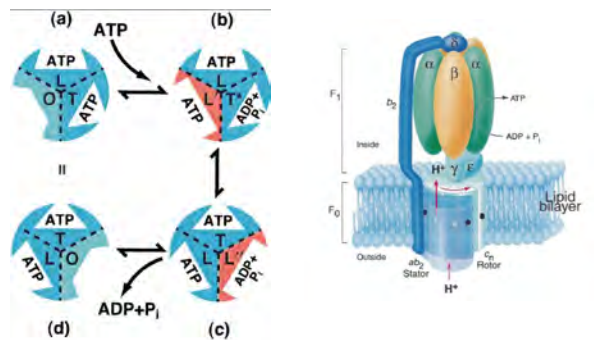


Electron density map of the yeast mitochondrial F₁-c₁₀ complex.



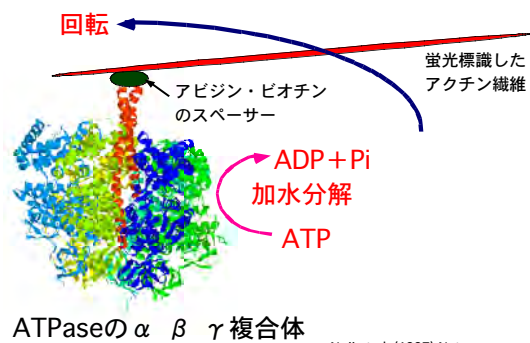
Energy-dependent binding change mechanism for ATP synthesis by proton-translocating ATP synthase.

ATPaseの構造変化と触媒活性モデル

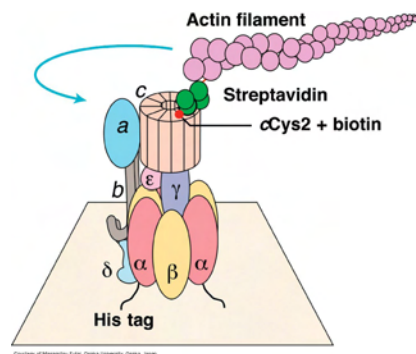


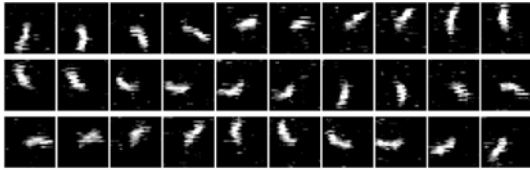
O(オープン)型: 触媒不活性で基質・生成物に親和性なし
 L(ルーズ)型: 弱い親和性をもつが、触媒活性なし
 T(タイト)型: 強い親和性をもち、触媒活性をもつ

F型ATPase回転実証の実験系



Rotation of the c-ring in *E. coli* F₁F₀-ATPase

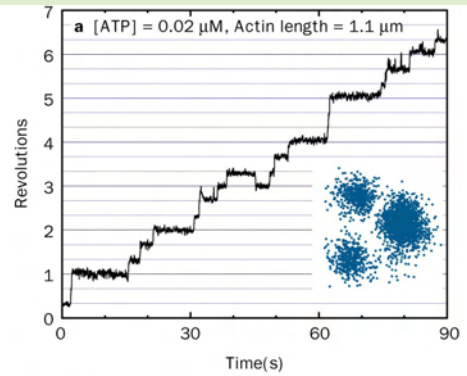




Courtesy of Masamitsu Futai, Osaka University, Osaka, Japan

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

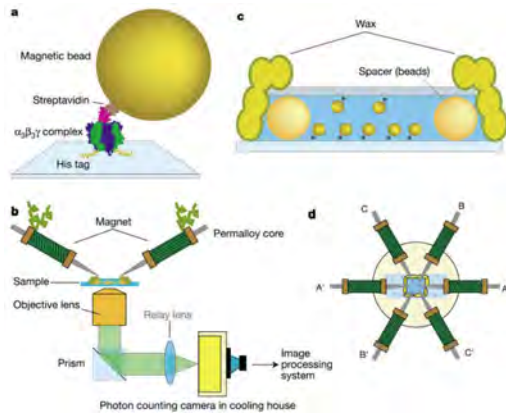
Stepwise rotation of the γ subunit of F_1 relative to an immobilized $\alpha_3\beta_3$ unit at low ATP concentration.



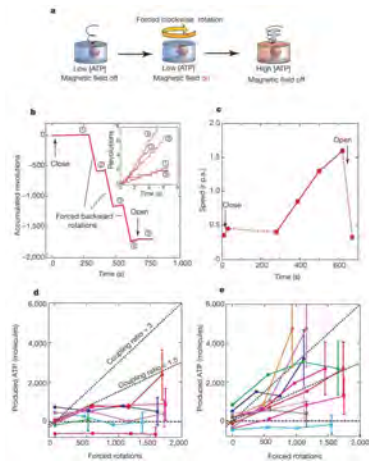
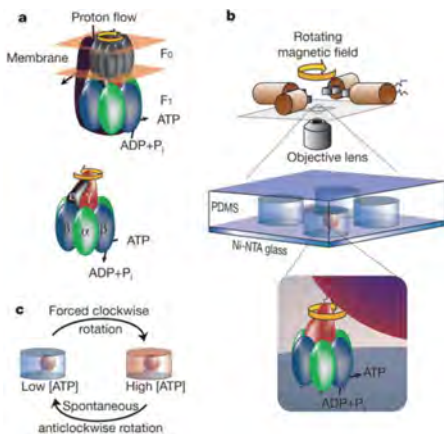
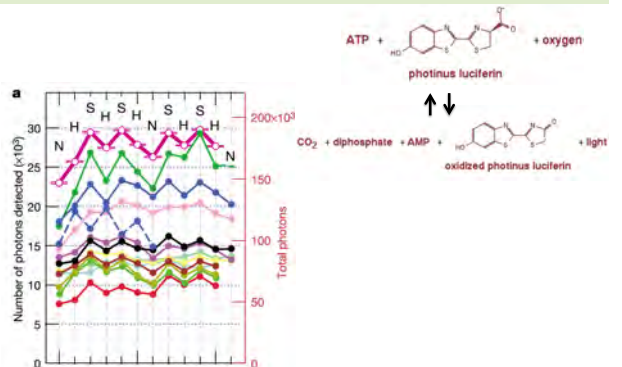
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Courtesy of Naohiko Kinoshita J., Keio University, Yokohama, Japan

ATPaseを強制的に回転することでATP合成を行う

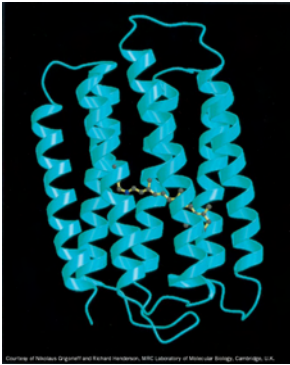


ルシフェラーゼによるATPの検出

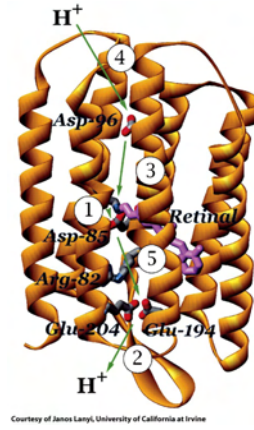
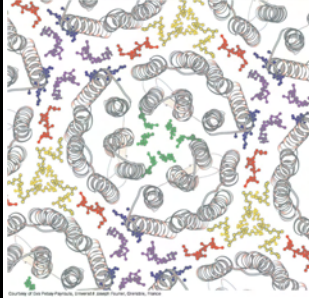


Structure of bacteriorhodopsin.

(a) The electron crystallography-based structure.

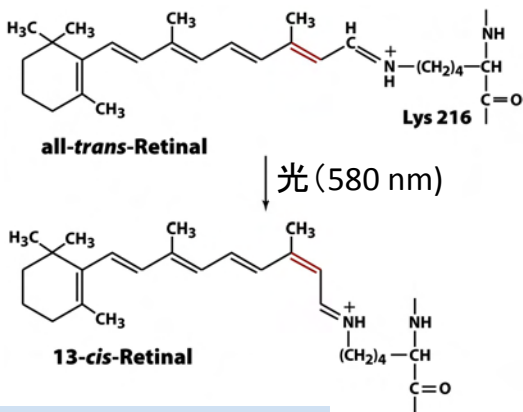


(b) The X-ray structure of a trimer.



Courtesy of James Lanyi, University of California at Irvine

Figure 18-12



レチナールの構造

Proton pump of bacteriorhodopsin.

