

Figure 22-1 The sites of electron transfer that form NADH and FAD₂ in glycolysis and the citric acid cycle.

NAD⁺ as an electron shuttle

C1=NC(=O)NC(=O)N1
 Oxidized form of NICOTINAMIDE

$\xrightleftharpoons[\text{Oxidation}]{\text{Reduction}}$

C1=NC(=O)N[C@@H](C1)O
 Reduced form of NICOTINAMIDE

$+ H^+$

$+ 2[H]$
 (from food)

\rightarrow

C1=NC(=O)N[C@@H](C1)O
 NADH

$\Delta E_0 = -0.320 \text{ V}$

C1=NC(=O)N[C@@H](C1)O
 NAD⁺
 (nicotinamide adenine dinucleotide)

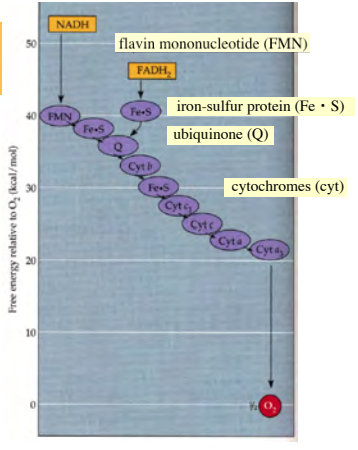
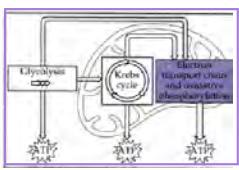
\rightarrow

coenzyme

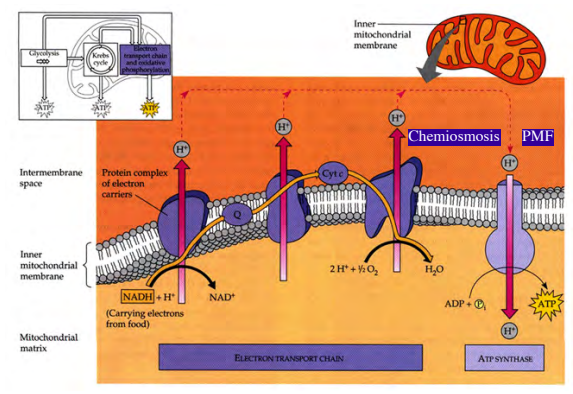
$\Delta G^0 = -nF\Delta E_0^0$
 $= -(2 \text{ mol}) (23.06 \text{ kcal/mol V}) (-0.320 \text{ V})$
 $= 14.8 \text{ kcal/mol}$

F: Faraday constant
 n: number of electrons

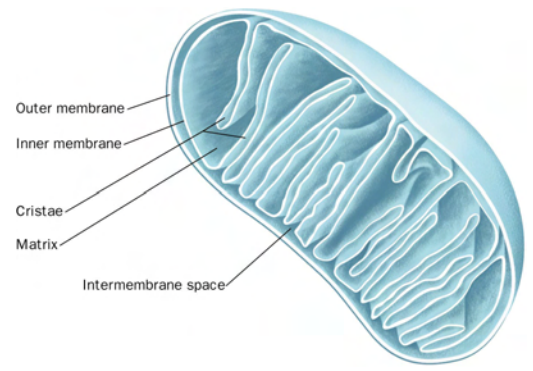
electron transport chain



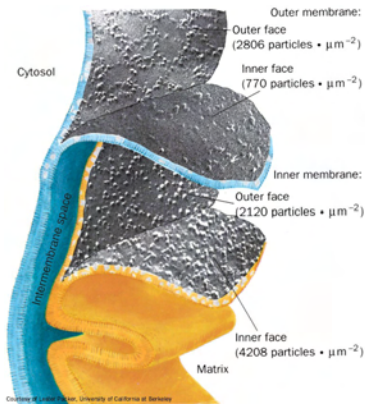
Chemiosmosis: How the mitochondrial membrane couples electron transport to oxidative phosphorylation



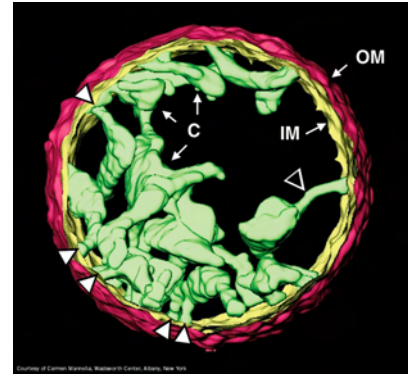
Mitochondria. (a) An electron micrograph of an animal mitochondrion.



Mitochondria. (b) Cutaway diagram of a mitochondrion.

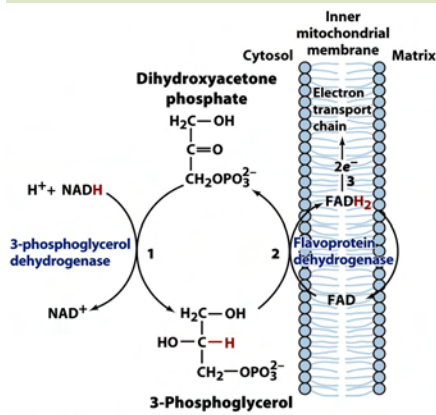


Freeze-fracture and freeze-etch electron micrographs of the inner and outer mitochondrial membranes.

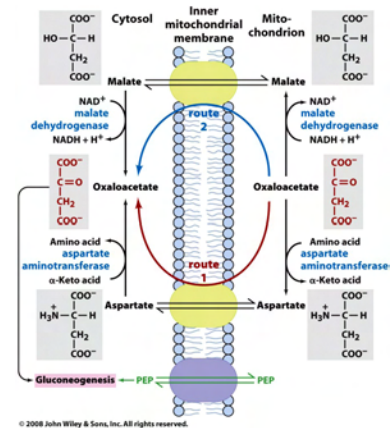


Electron microscopy-based three-dimensional image reconstruction of a rat liver mitochondrion.

The glycerophosphate shuttle.



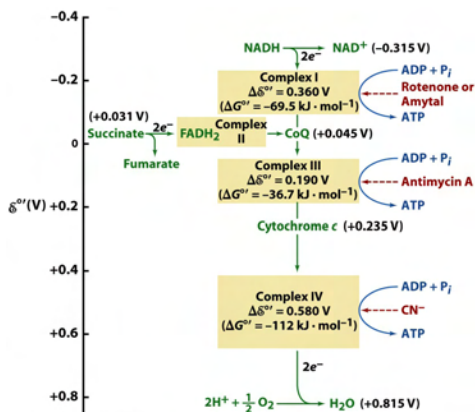
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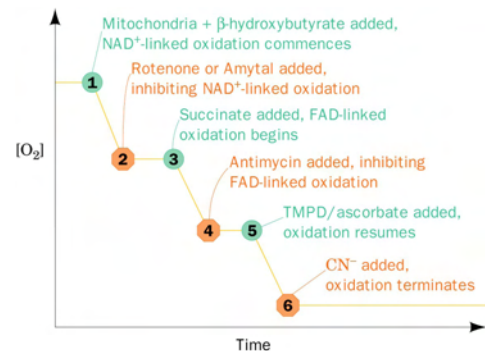
Figure 16-20

The mitochondrial electron-transport chain.

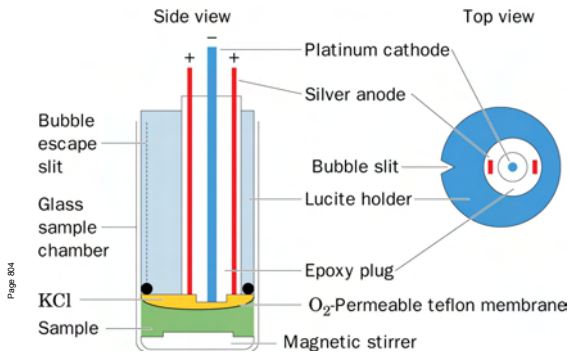


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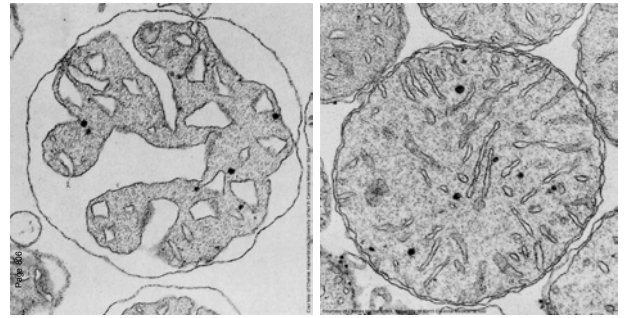
Effect of inhibitors on electron transport.



The oxygen electrode.



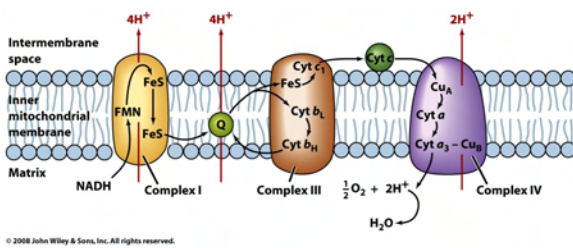
Electron micrographs of mouse liver mitochondria.



(a) In the actively respiring state.

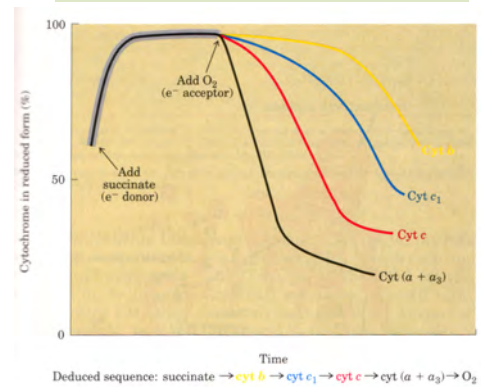
(b) In the resting state.

The mitochondrial electron-transport chain.

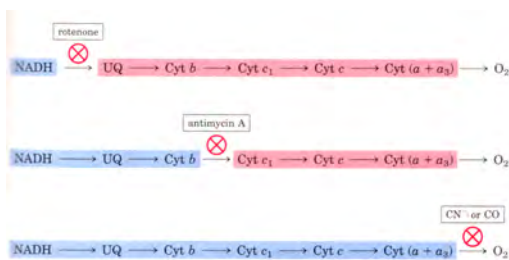


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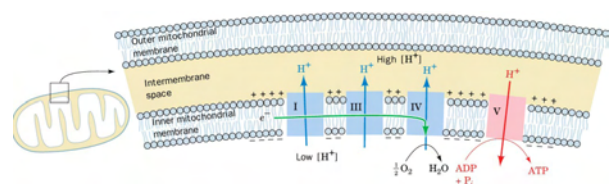
Cytochromeの電子の流れの順序



阻害剤と電子の流れ



Coupling of electron transport (green arrow) and ATP synthesis.



Uncoupling of oxidative phosphorylation.

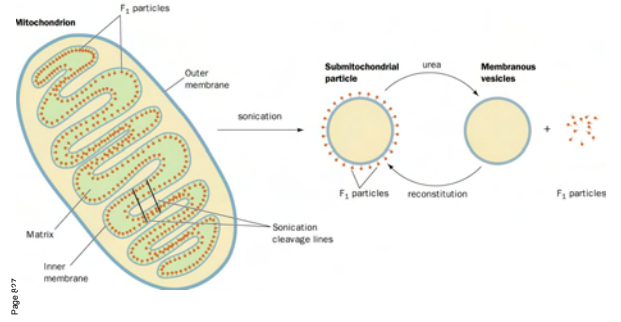
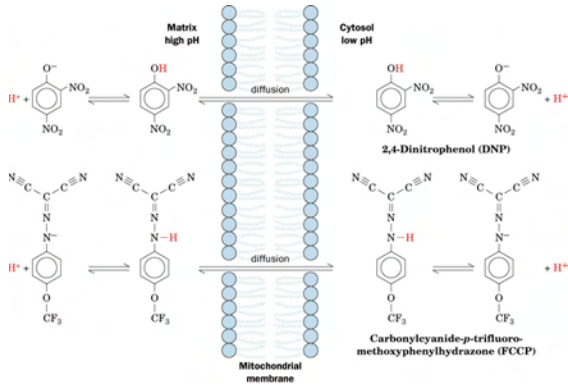
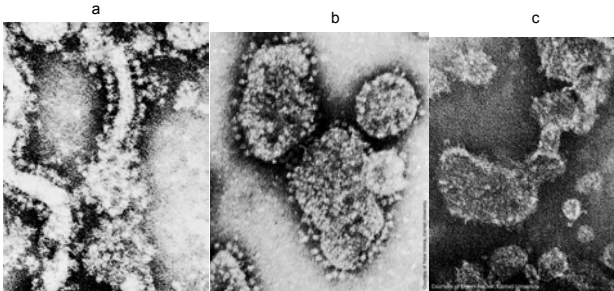
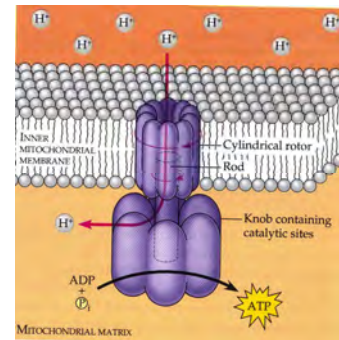


Figure 22-36 Interpretive drawings of the mitochondrial membrane at various stages of dissection.

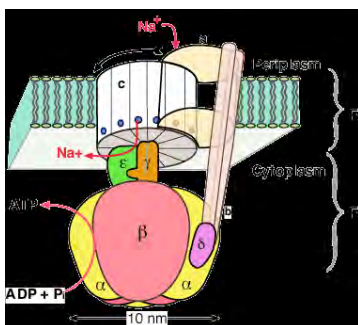


Electron micrographs of cristae from (a) intact mitochondria showing their F₁ "lollipops" projecting into the matrix, (b) submitochondrial particles, showing their outwardly projecting F₁ lollipops, and (c) submitochondrial particles after treatment with urea.

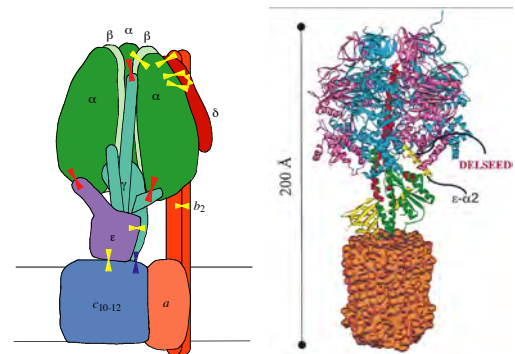
ATP synthase, a molecular machine (fig9-14)

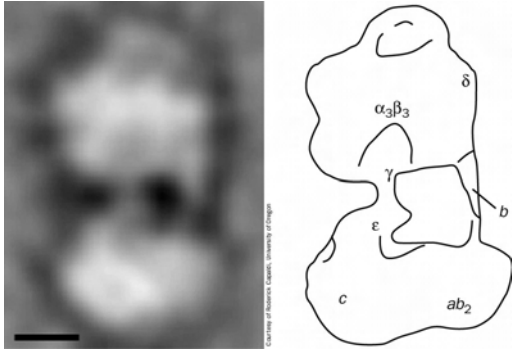


F型ATPaseモーターの構造



F₁F₀ATPase

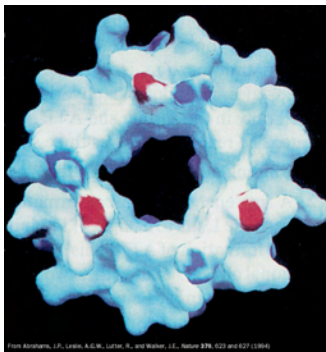




Electron microscopy-based image of *E. coli* F₁F₀-ATPase.



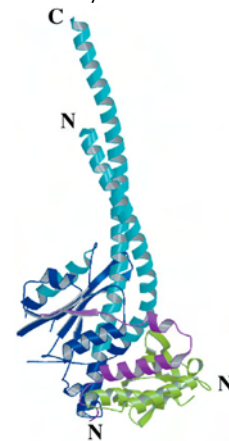
X-Ray structure of F₁-ATPase from bovine heart mitochondria.



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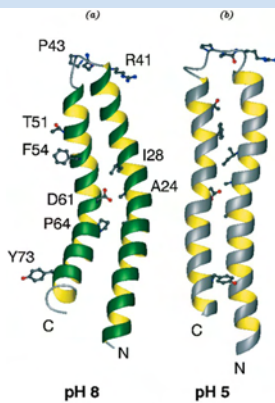
X-Ray structure of F₁-ATPase from bovine heart mitochondria. The surface of the inner portion of the $\alpha_3\beta_3$ assembly.

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



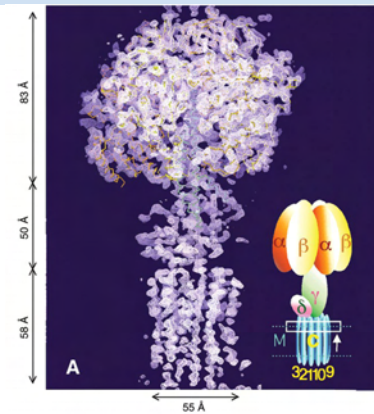
Courtesy of Andrew Leslie and John Walker, Medical Research Council, Cambridge, U.K.

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

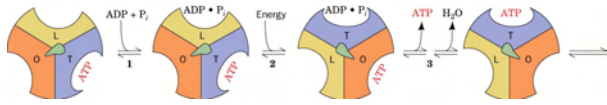


Courtesy of Mark Girvin, Albert Einstein College of Medicine

Electron density map of the yeast mitochondrial F₁- complex.

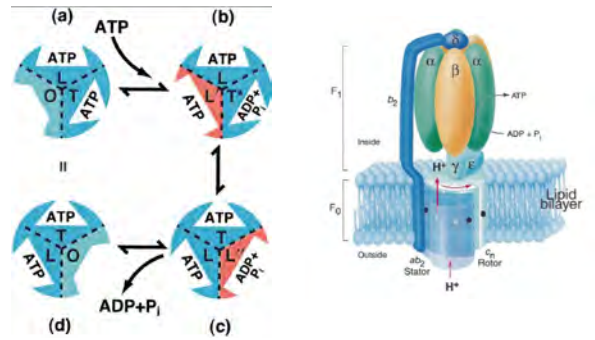


Courtesy of Andrew Leslie and John Walker, Medical Research Council, Cambridge, U.K.



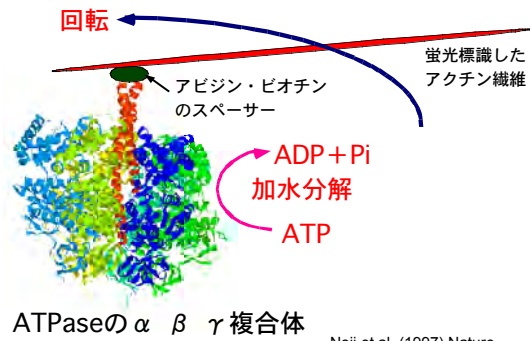
Energy-dependent binding change mechanism for ATP synthesis by proton-translocating ATP synthase.

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

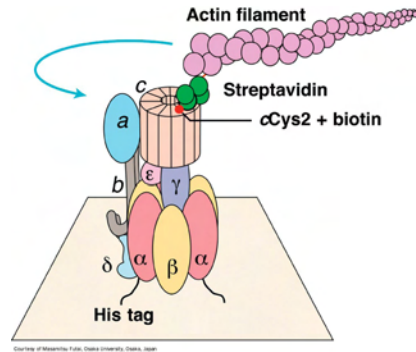
F型ATPase回転実証の実験系



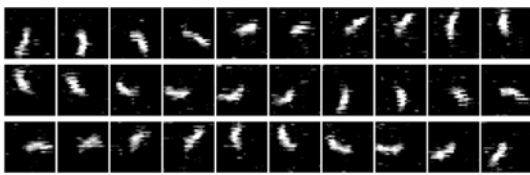
ATPaseの α β γ 複合体

Noji et al. (1997) Nature

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

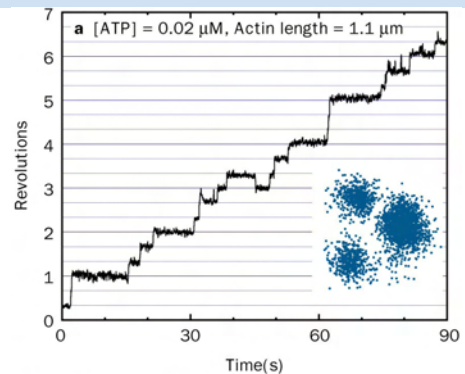


Stepwise rotation of the γ subunit of F₁ relative to an immobilized $\alpha_3\beta_3$ unit at low ATP concentration.



Courtesy of Masahito Futai, Osaka University, Osaka, Japan

Rotation of the c-ring in *E. coli* F₁F₀-ATPase. (b) The rotation of a 3.6- μ m-long actin filament in the presence of 5 mM MgATP.



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Courtesy of Kazuhiko Aizawa et al., Keio University, Yokohama, Japan