問題

- 呼吸鎖では種々のチトクロームが反応に関与している。NADHからチトクロームへの電子の流れの順序を 決める方法を概説せよ。
- 2) ミトコンドリアを調整し、NADHをいれて酸素消費 を調べた。また、ここに、ロテノンという薬剤をい れ、そこにTMPDとアスコルビン酸を入れた。このと きの、アスコルビン酸の役割説明し、ロテノンを入れ た場合と入れない場合のATP産生の量比を答えよ。ま た、酸素消費の量比も答えよ。

答案用紙に名前を書くのを忘れないこと。







Figure 22-21b The three separate α bands in the spectrum of beef heart mitochondrial membranes indicate the presence of cytochromes *a*, *b*, and *c*.

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Figure 22-22a Porphyrin rings in cytochromes. *(a)* Chemical structures.



Figure 22-22b Porphyrin rings in cytochromes. (*b*) Axial liganding of the heme groups contained in cytochromes *a*, *b*, and *c* are shown.



Cytochrome Cの構造



Figure 22-23 X-ray structures of cytochrome bc_1 . (*a*) The dimeric bovine complex. (*b*) The yeast enzyme in complex with cytochrome *c*



Figure 22-24 Ribbon diagram of cytochrome *c* showing the Lys residues involved in intermolecular complex formation.





Figure 22-25c X-Ray structure of fully oxidized bovine heart cytochrome c oxidase. (c) A protomer viewed similarly to Part a showing the positions of the complex's redox centers.





Figure 22-27 Synthetic model of the cytochrome a_3 -Cu_B binuclear complex.



Figure 22-28 Proposed reaction sequence for the reduction of O_2 by the cytochrome a_3 -Cu_B binuclear complex of cytochrome *c* oxidase.



Figure 22-30 The redox loop mechanism for electron transport–linked H⁺ translocation.



Figure 22-31 The Q cycle.





Figure 22-32a X-Ray structures of the Q_o binding site of the chicken cytochrome bc_1 complex occupied by inhibitors. (*a*) This structure shows its complex with stigmatellin.



Figure 22-32b X-Ray structures of the Q_o binding site of the chicken cytochrome bc_1 complex occupied by inhibitors. (*b*) This structure shows its complex with myxothiazol.



Figure 22-33 Proton pump mechanism of electron transport–linked proton translocation.



Figure 22-34 Proton pump of bacteriorhodopsin.





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



Figure 22-36 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.









Figure 22-37 Electron microscopy–based image of *E. coli* F_1F_0 –ATPase.



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Figure 22-38a X-Ray structure of F_1 -ATPase from bovine heart mitochondria. (*a*) A ribbon diagram.



Figure 22-38b X-Ray structure of F_1 -ATPase from bovine heart mitochondria. (*b*) Cross section through the electron density map of the protein.



Figure 22-38c X-Ray structure of F_1 -ATPase from bovine heart mitochondria. (c) The surface of the inner portion of the $\alpha_3\beta_3$ assembly.



Figure 22-39 The $\gamma, \delta,$ and ϵ subunits in the X-ray structure of bovine $F_1\text{-}ATPase.$



Figure 22-40 NMR structures of the *c* subunit of *E. coli* F_1F_0 -ATPase.



Figure 22-41a Low (3.9 Å) resolution electron density map of the yeast mitochondrial F_1-c_{10} complex. (*a*) A view from within the inner mitochondrial membrane with the matrix above.



Figure 22-41b The electron density map of the yeast mitochondrial F_1-c_{10} complex. View of the boxed section in Part *a* from the intermembrane space.



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Figure 22-42 Energy-dependent binding change mechanism for ATP synthesis by proton-translocating ATP synthase.



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



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Figure 22-44b 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.

ATPaseの α β γ 複合体 Noji et al. (1997) Nature