問題

1）呼吸酵素では様々なクロームが反応に関与している。NADHからクロームへの電子の流れの順序を決める方法を経てせよ。

2）ミトコンドリアを調整し、NADHをいったって酸素消費を調べた。これに、ロテノンという薬剤をいれ、そこにトピド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を明かし、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。

答え用紙に名前を書くのを忘れないこと。

Figure 22-21a Visible absorption spectra of cytochromes.
(a) Absorption spectrum of reduced cytochrome c showing its characteristic α, β, and γ (Soret) absorption bands.

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.

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 bc₁. (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 22-26 The redox centers in the X-Ray structure of bovine heart cytochrome c oxidase.

Figure 22-27 Synthetic model of the cytochrome α₃–CuB binuclear complex.
Figure 22-28  Proposed reaction sequence for the reduction of O₂ by the cytochrome a₃–CuB 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 Qₒ binding site of the chicken cytochrome bc₁ complex occupied by inhibitors. (a) This structure shows its complex with stigmatellin.

Figure 22-32b X-Ray structures of the Qₒ binding site of the chicken cytochrome bc₁ 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 22-35 The proton-translocating channels in bovine COX.

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.

ATP synthase, a molecular machine (fig9-14)
Figure 22-37 Electron microscopy–based image of *E. coli* $F_1F_0$–ATPase.

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 $\alpha_5\beta_2$ assembly.
**Figure 22-39** The γ, δ, and ε subunits in the X-ray structure of bovine F$_1$–ATPase.

**Figure 22-40** NMR structures of the c subunit of *E. coli* F$_1$F$_0$–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.

**Figure 22-42** Energy-dependent binding change mechanism for ATP synthesis by proton-translocating ATP synthase.
Figure 22-44b  Rotation of the c-ring in *E. coli*.

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*F*$_{1}$*F*$_{0}$–ATPase. (b) The rotation of a 3.6-µm-long actin filament in the presence of 5 mM MgATP.