The Redox Players I: Fe-S clusters

Rising reduction potentials = oxidation power

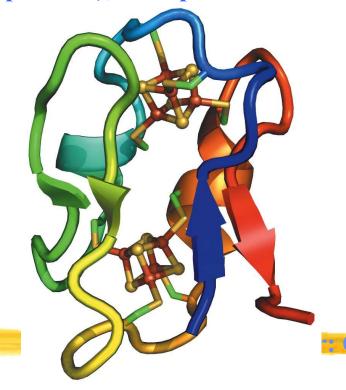
Table 22-1 Reduction Potentials of Electron-Transport Chain Components in Resting Mitochondria

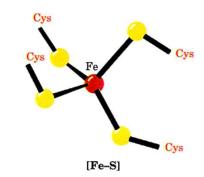
Component	$\mathscr{E}^{\circ\prime}(V)$
NADH	-0.315
Complex I (NADH:CoQ oxidoreductase; ~900 kD, 45 subunits):	
FMN	-0.380
[2Fe-2S]N1a	-0.370
[2Fe-2S]N1b	-0.250
[4Fe-4S]N3, 4, 5, 6a, 6b, 7	-0.250
[4Fe-4S]N2	-0.150
Succinate	0.031
Complex II (succinate-CoQ oxidoreductase; ~420 kl 4 subunits):	D,
FAD	-0.040
[2Fe-2S]	-0.030
[4Fe-4S]	-0.245
[3Fe-4S]	-0.060
Heme b_{560}	-0.080
Coenzyme Q	0.045
Complex III (CoQ-cytochrome c oxidoreductase; ~450 kD, 9-11 subunits):	
	0.020
Heme $b_{\rm H} (b_{562})$	0.030
Heme b_L (b_{566}) [2Fe–2S]	-0.030
	0.280
Heme c_1	0.215
Cytochrome c	0.235
Complex IV (cytochrome c oxidase; ~410 kD, 8–13 st	,
Heme a	0.210
Cu _A	0.245
Cu _B	0.340
Heme a_3	0.385
O ₂	0.815

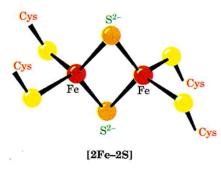
Source: Mainly Wilson, D.F., Erecinska, M., and Dutton, P.L., Annu. Rev. Biophys. Bioeng. 3, 205 and 208 (1974); and Wilson, D.F., In Bittar, E.E. (Ed.), Membrane Structure and Function, Vol. 1, p. 160, Wiley (1980).

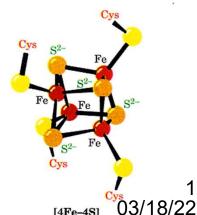
The oxidized and reduced forms of iron-sulfur clusters differ by 1 formal charge in the conjugated system (e.g., $Fe(II)/Fe(III)_3 \rightarrow Fe(II)_2/Fe(III)_2$):

- ➤ All irons are tetrahedrally coordinated to Cys or S²-
- > Contained in iron-sulfur proteins (= non-heme iron proteins), example ferredoxin:









The Redox Players II: Quinones

The coenzymes of Complex I (NADH-Q reductase)

➤ FMN and CoQ are both quinones that are stable as one-electron reduced semiquinones (radicals!) and two-electron reduced hydroquinones

⇒ mediate between 2 e

donor NADH and the 1 e⁻

complexes III and IV

acceptors (cytochromes) of

 $ightharpoonup 10 C_5$ isoprenoid unit of mammals' CoQ leads to nomenclature "coenzyme Q_{10} " (other organisms Q_6 or Q_8) ⇒ hydrophobic tail that mediates membrane solubility!

(a) CH₂OPO₃²⁻
HO-C-H
HO-C-H
HO-C-H
CH₂

H₃C
N
N
N
O
H
H₃C
N
H

Flavin mononucleotide (FMN) (oxidized or quinone form)

FMNH• (radical or semiquinone form)

$$\begin{array}{c|c} & & & \\ & & &$$

FMNH₂ (reduced or hydroquinone form)

$$\begin{array}{c} \text{CH}_3\text{CO} \\ \text{H}_3\text{CO} \\ \text{H}_3\text{CO} \\ \text{O} \end{array} \begin{array}{c} \text{CH}_3 \\ \text{(CH}_2\text{-CH} = \text{C} - \text{CH}_2)_n \text{ H} \\ \text{Isoprenoid units} \end{array}$$

Coenzyme Q (CoQ) or obiquinone (oxidized or quinone form)

$$H_3CO$$
 CH_3
 H_3CO
 R

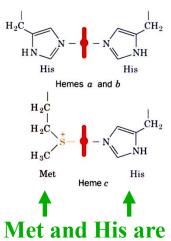
Coenzyme QH• or Ubisemiquinone (radical or semiquinone form)

$$\begin{array}{c} & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ &$$

Coenzyme QH₂ or Ubiquinol (reduced or hydroquinone form)

03/18/22

CH_3 (a) $CH_2+CH_2-CH=\dot{C}-CH_2+\frac{\dot{C}}{2}H$ но-сн CH₃ $CH = CH_{2}$ porphyrin rings are the HCequatorial ligands to iron CH₂ CH₂ coo COO Heme a Similar to hemoglobin $CH_2 = CH$ CH_3 $CH = CH_2$ CHo CH₂ COO coo Heme b (iron-protoporphyrin IX) Protein CH-CH₃ CH_3 CHo CH2 COO Heme c



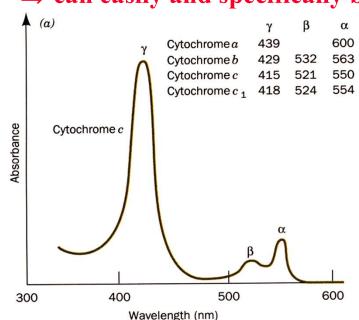
Met and His are the axial ligands to iron (and shield it from O₂!)

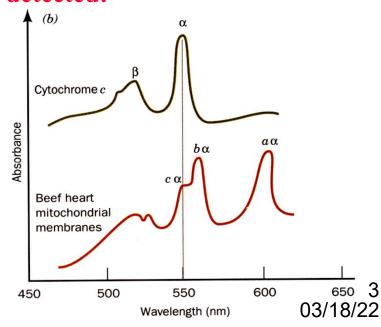
The Redox Players III: Cytochromes

Cytochromes = Redox-active proteins with heme groups:
Fe(II) Fe(III)

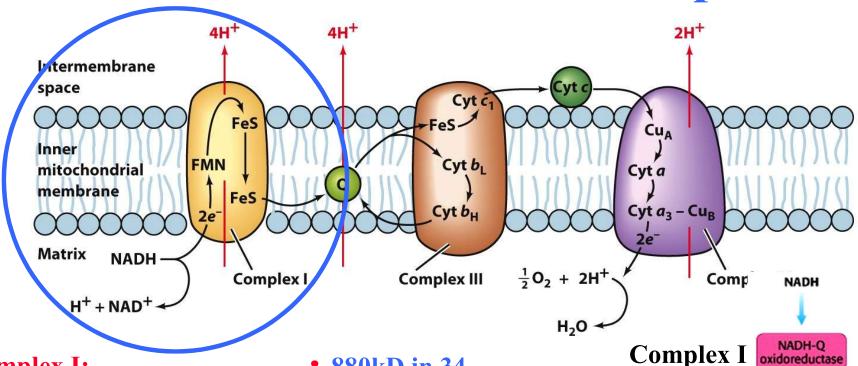
Cytochromes transfer electrons through sigma bonds over distances of 10-20 Å at physiologically significant rates!

 \triangleright have visible absorption spectra with α, β, and γ (Soret) bands \Rightarrow can easily and specifically be detected:



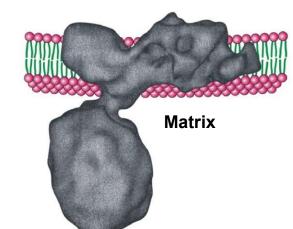


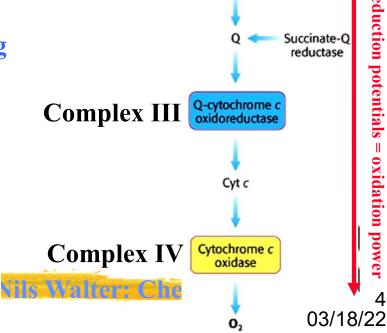
How It All Works: Electron Transport Chain



- **Complex I:**
- electrons are transferred from the 2 e⁻ carrier NADH to the 1 or 2 e carrier FMN and the Fe-S clusters:
- they are then passed on to Coenzyme Q that is lipid soluble and takes them to **Complex III;**
- ♣ 4 H⁺ are concomitantly pumped out of the matrix

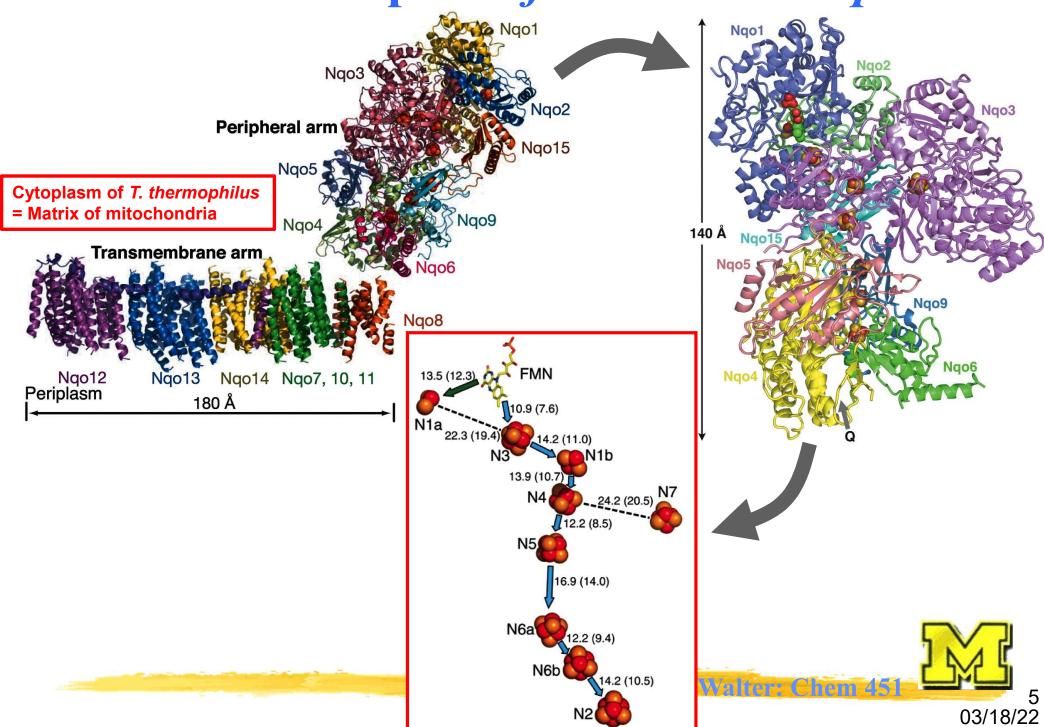
- 880kD in 34 polypeptide chains;
- **♣** large, NADH binding matrix arm:



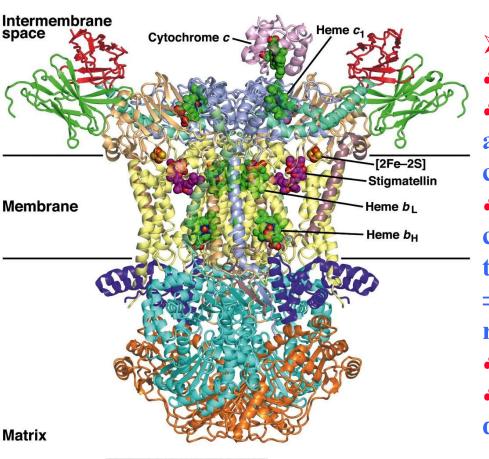


Rising reduction potentials = oxidation power

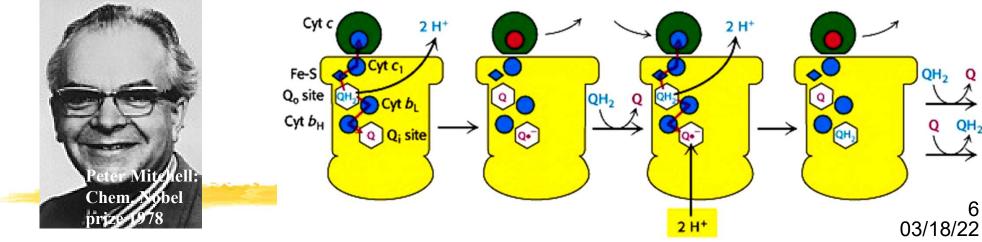
Details of Complex I from T. thermophilus



Complex III: Q-Cytochrome c Reductase



- **Complex III:**
- **4** dimer with 11 polypeptide chains/monomer;
- \clubsuit hemes b_L (for <u>Low</u> affinity) and b_H (for <u>High</u> affinity) within cytochrome b, one c-type heme in cytochrome c_1 ;
- * contains one 2Fe-2S cluster (Rieske center) with one Fe coordinated by two His (instead of Cys)
- ⇒ stabilizes reduced form = raises reduction potential!
- * oxidizes CoQ, reduces cytochrome c
- ♣ 4 H⁺ are pumped out of the matrix during the "Q cycle":



Complex IV: Cytochrome c Oxidase

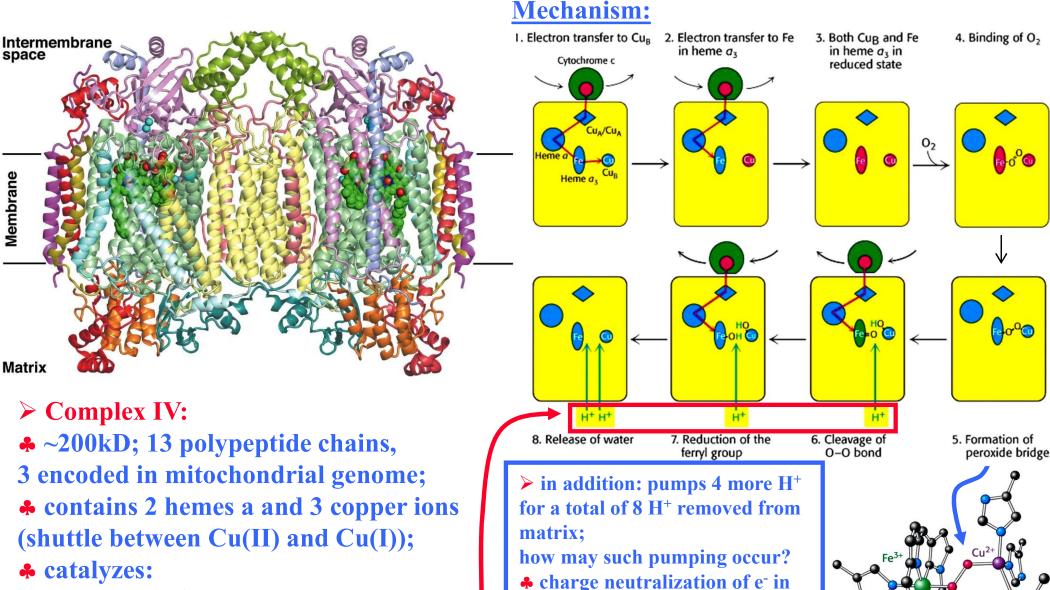


protein core by H⁺

conformational changes that guide H⁺ from matrix to cytosolic

side (as in bacteriorhodopsin!)

Peroxide



4cytochrome $c^{2+} + 4H^+ + O_2 \rightarrow$ 4cytochrome $c^{3+} + 2H_2O$

 \Rightarrow removes 4 H⁺ from matrix!