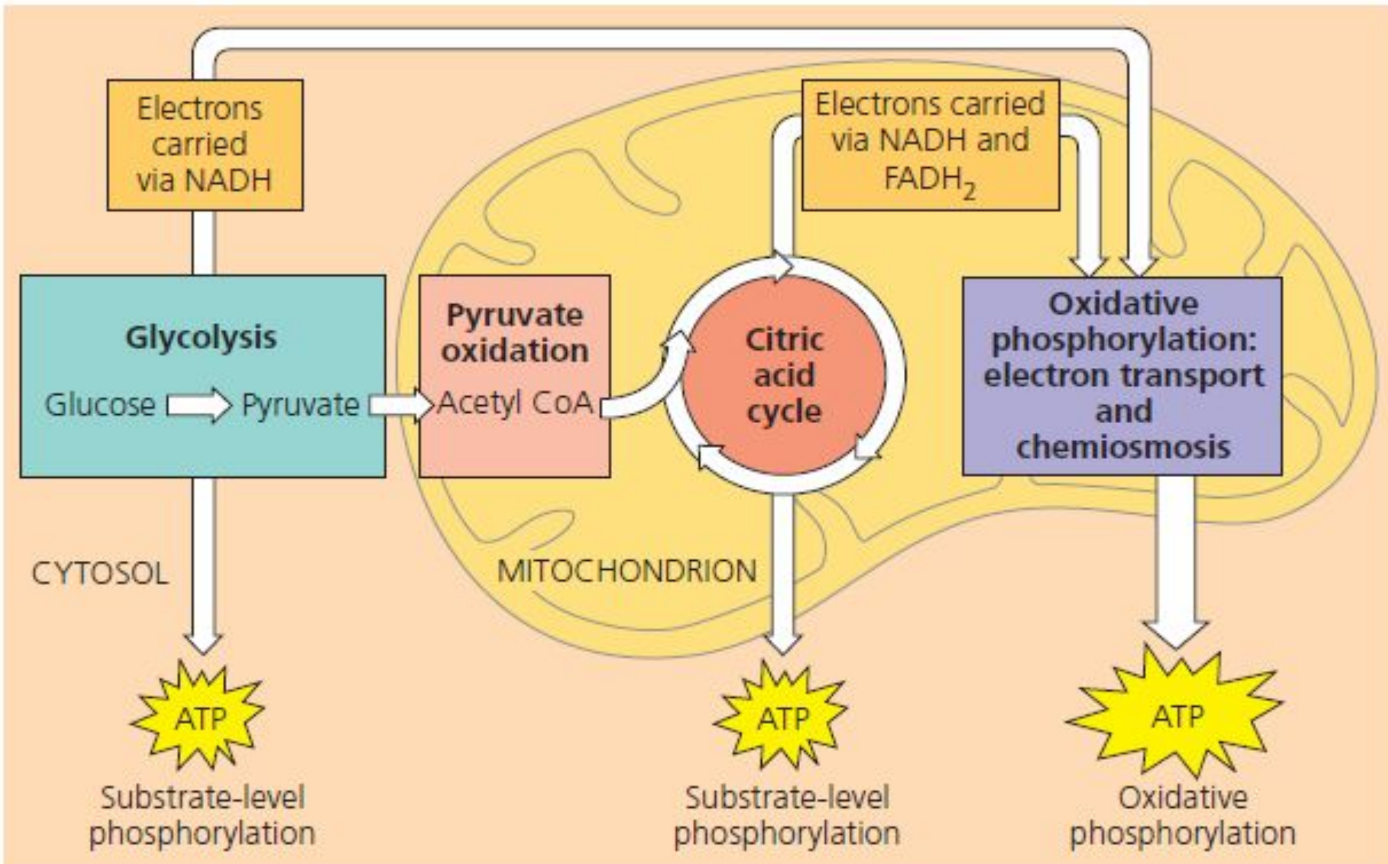
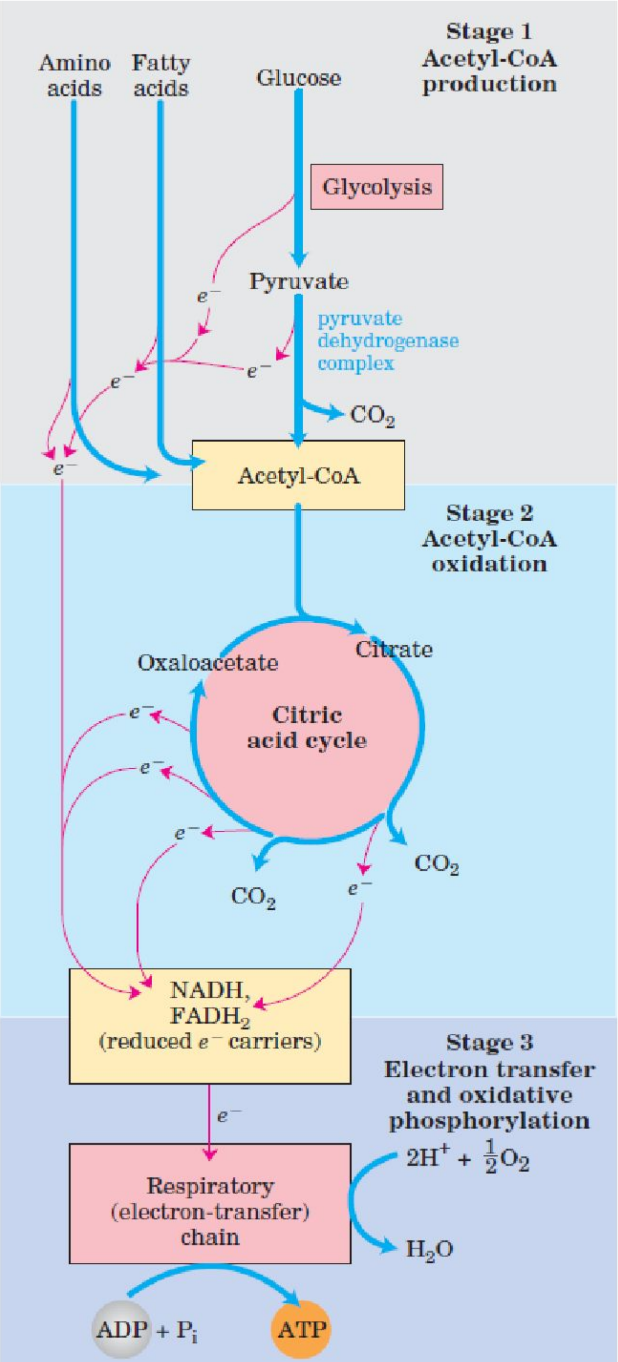
Цикл Кребса.

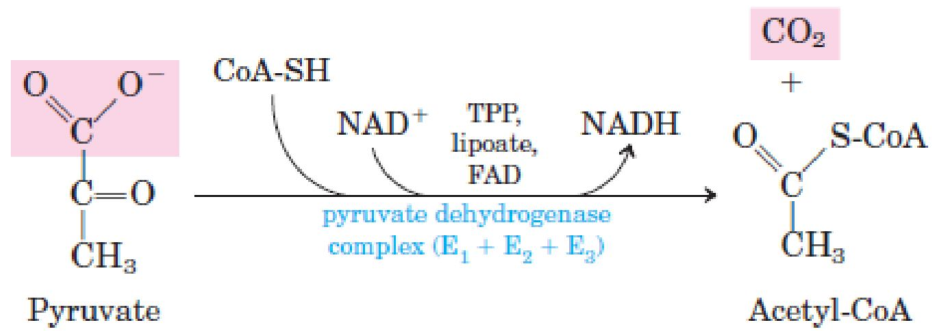
Дыхательная цепь.


Electrons carried via NADH
Electrons carried via NADH and $FADH_2$
Glycolysis
Glucose
Pyruvate
Pyruvate oxidation
Acetyl CoA
Citric acid cycle
Oxidative phosphorylation: electron transport and chemiosmosis
CYTOSOL
MITOCHONDRION
ATP
ATP
ATP
Substrate-level phosphorylation
Substrate-level phosphorylation
Oxidative phosphorylation

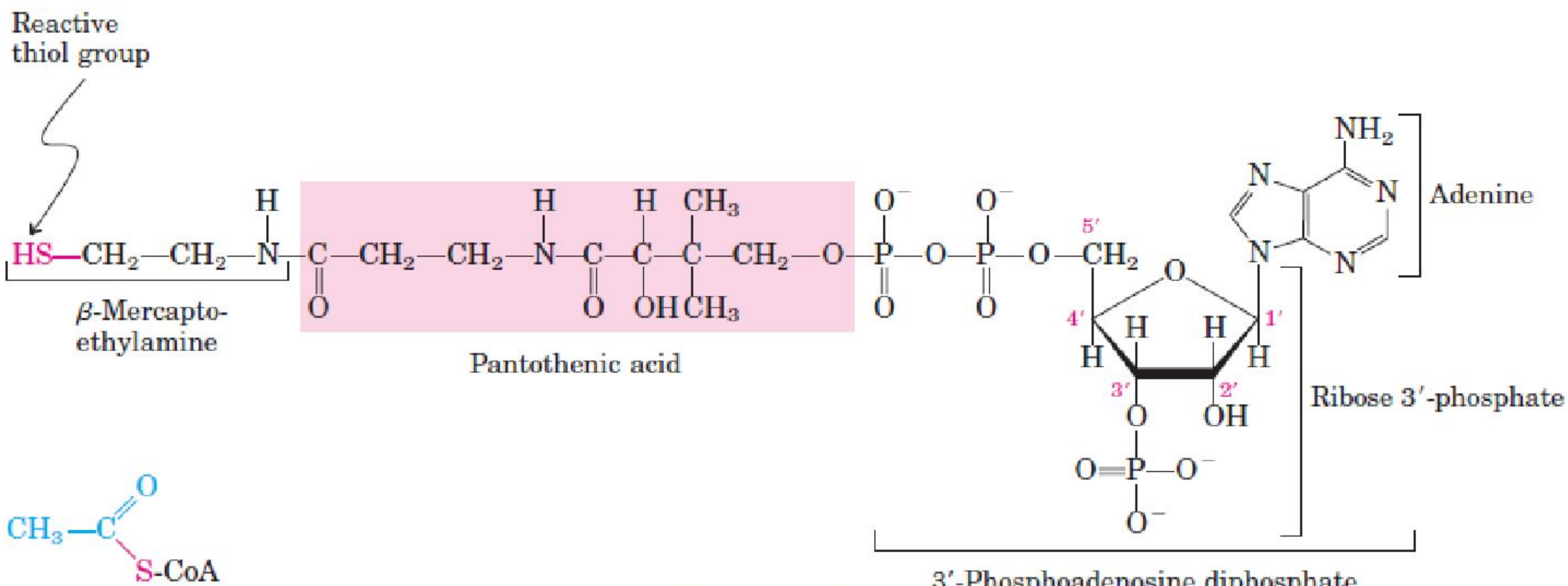


Stage 1
Acetyl-CoA
production
Amino acids
Fatty acids
Glucose
Glycolysis
Pyruvate
pyruvate dehydrogenase complex
e^-
CO_2
Acetyl-CoA
Stage 2
Acetyl-CoA
oxidation
Oxaloacetate
Citrate
Citric acid cycle
CO_2
CO_2
NADH,
$FADH_2$
(reduced e^- carriers)
Stage 3
Electron transfer
and oxidative
phosphorylation
$2H^+ + \frac{1}{2}O_2$
H_2O
Respiratory
(electron-transfer)
chain
ADP + P_i
ATP

Окислительное декарбоксилирование Pyr (PDH)



$\Delta G'° = -33.4$ kJ/mol



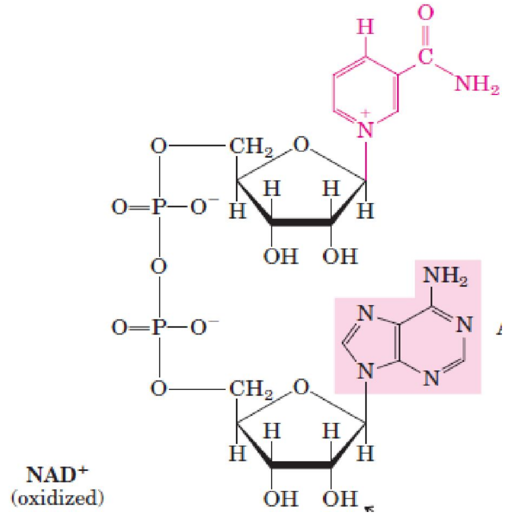
Acetyl-CoA

Coenzyme A

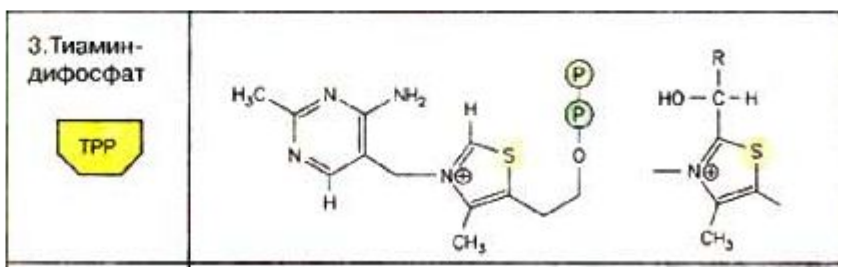
Коферменты PDH

1) CoA

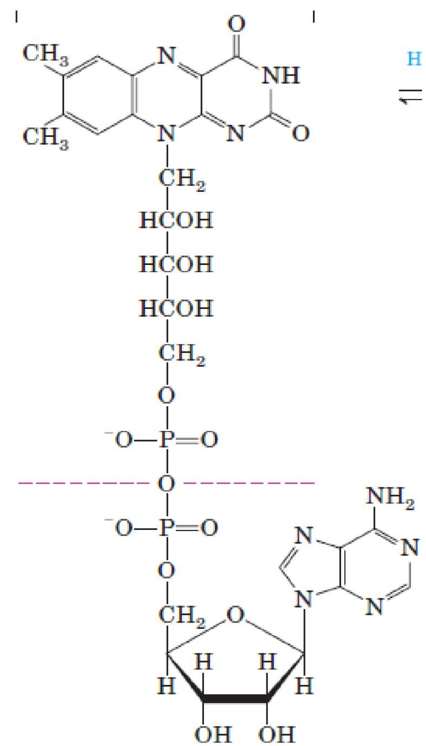
2) NAD



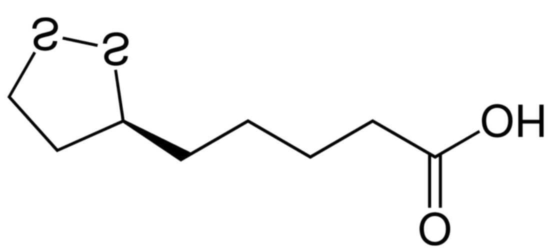
3) TPP

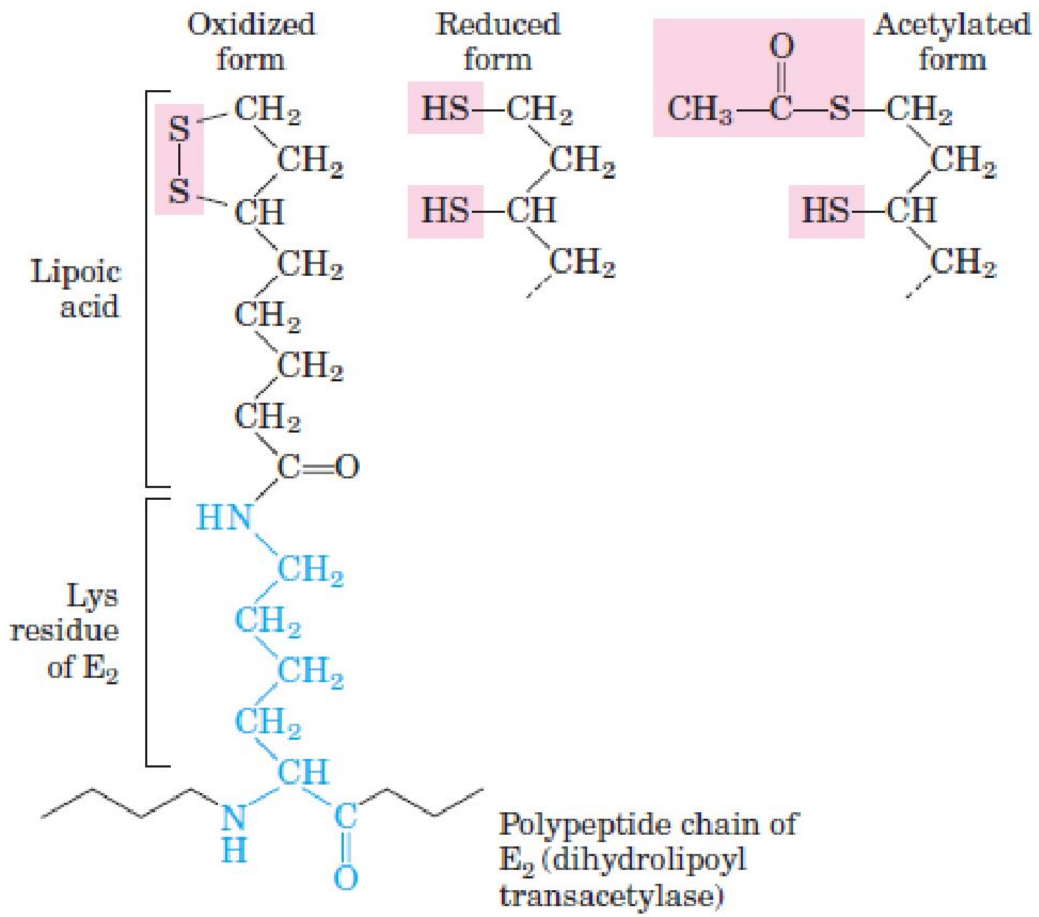


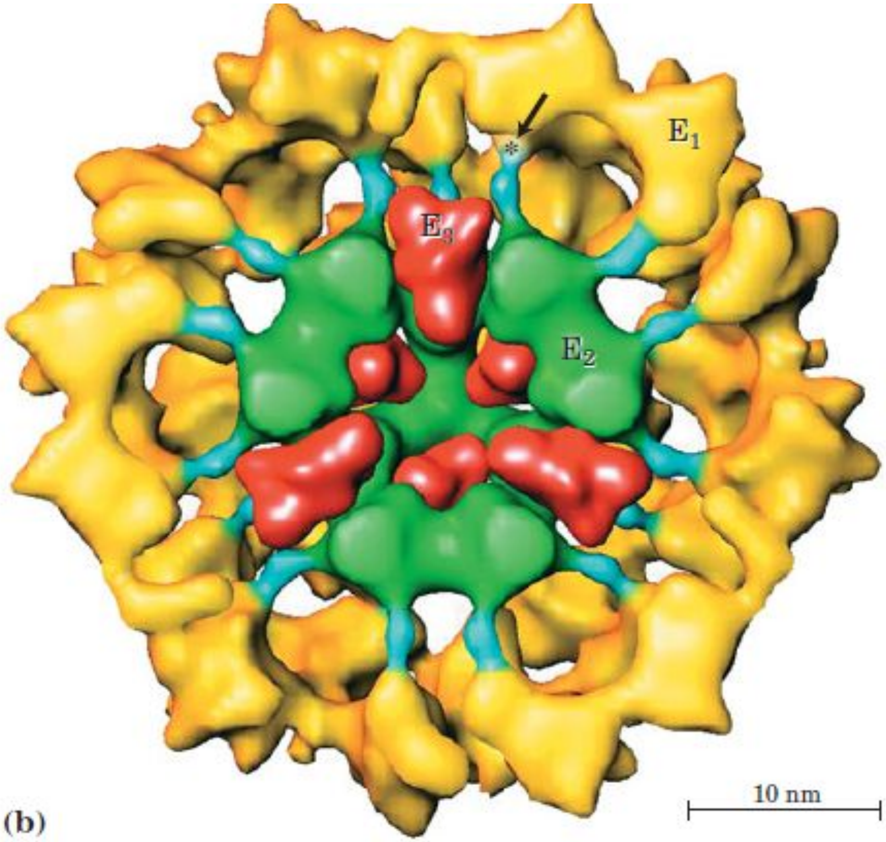
4) FAD



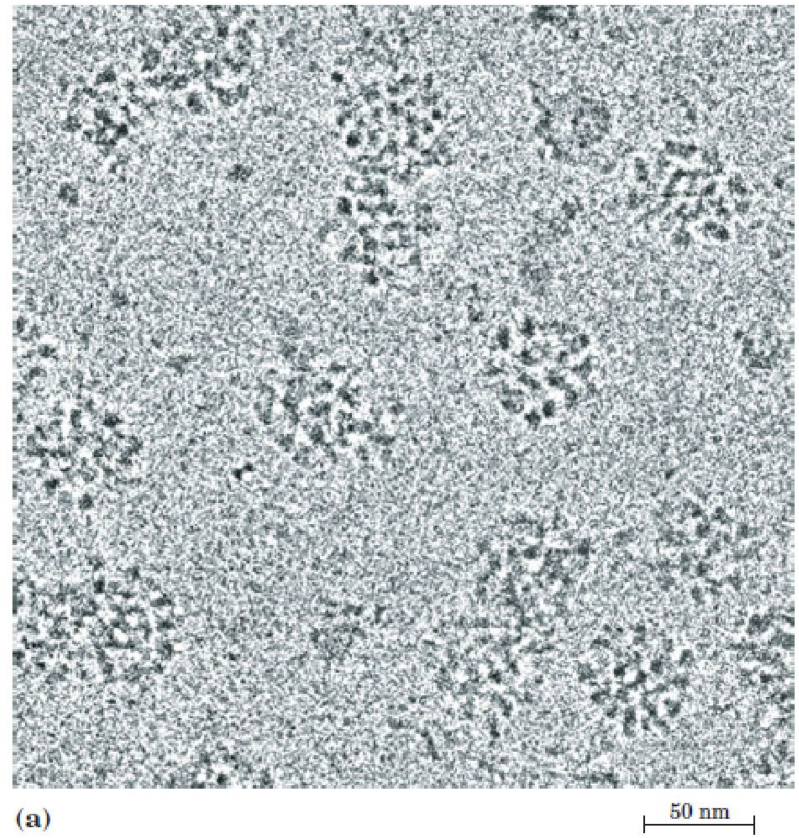
5) липоат




Oxidized form
Reduced form
Acetylated form
Lipoic acid
Lys residue of E_2
Polypeptide chain of E_2 (dihydrolipoyl transacetylase)



(b)

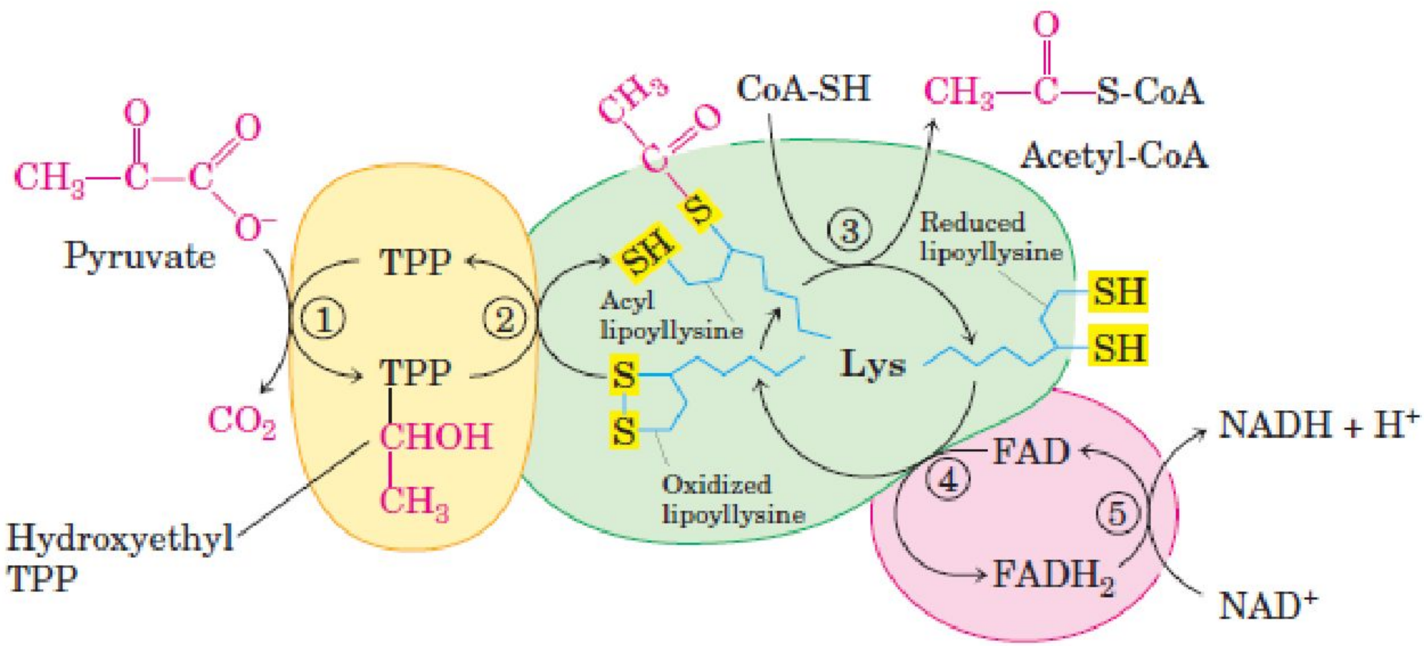


(a)

E1 – пируват дегидрогеназа

E2 – дигидролипоил трансацетилаза

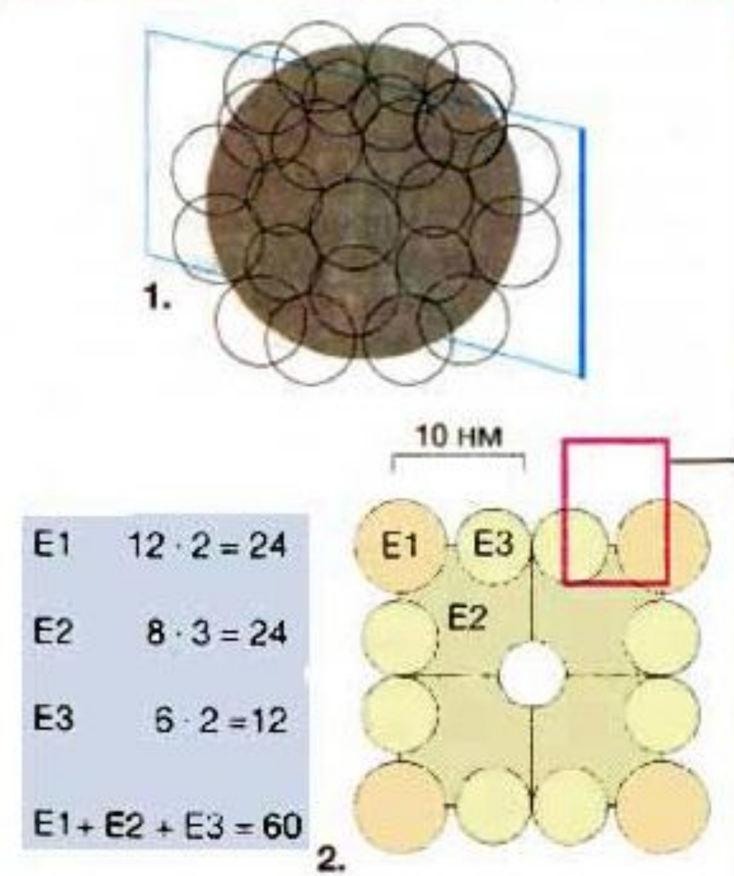
E3 – дигидролипоил дегидрогеназа

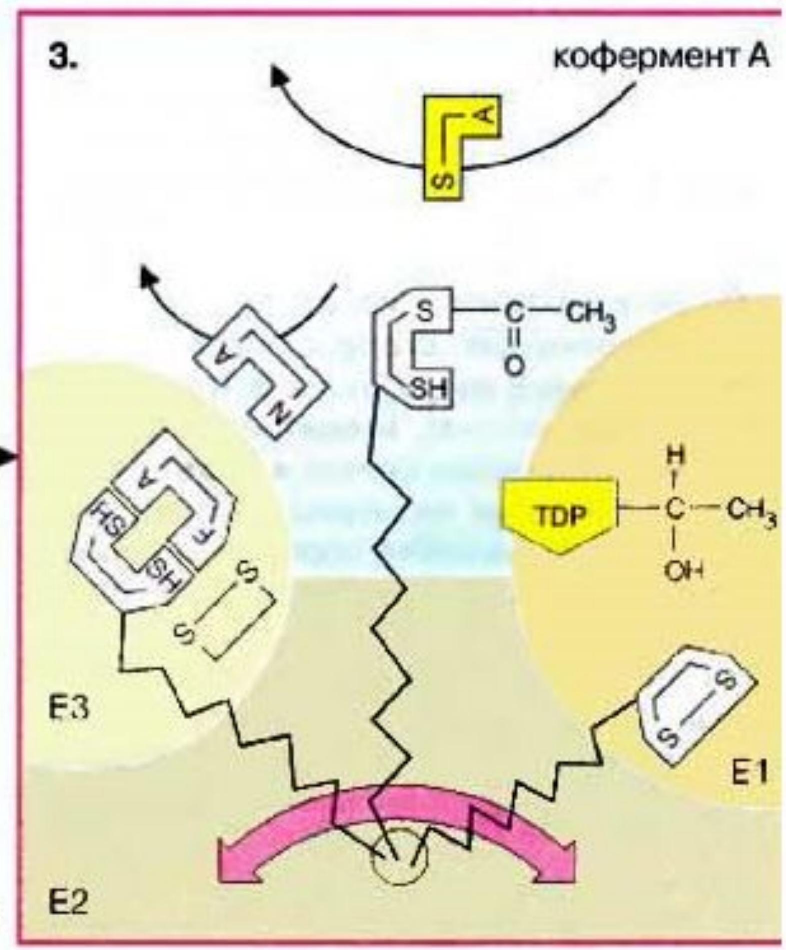


Pyruvate dehydrogenase, E_1

Dihydrolipoyl transacetylase, E_2

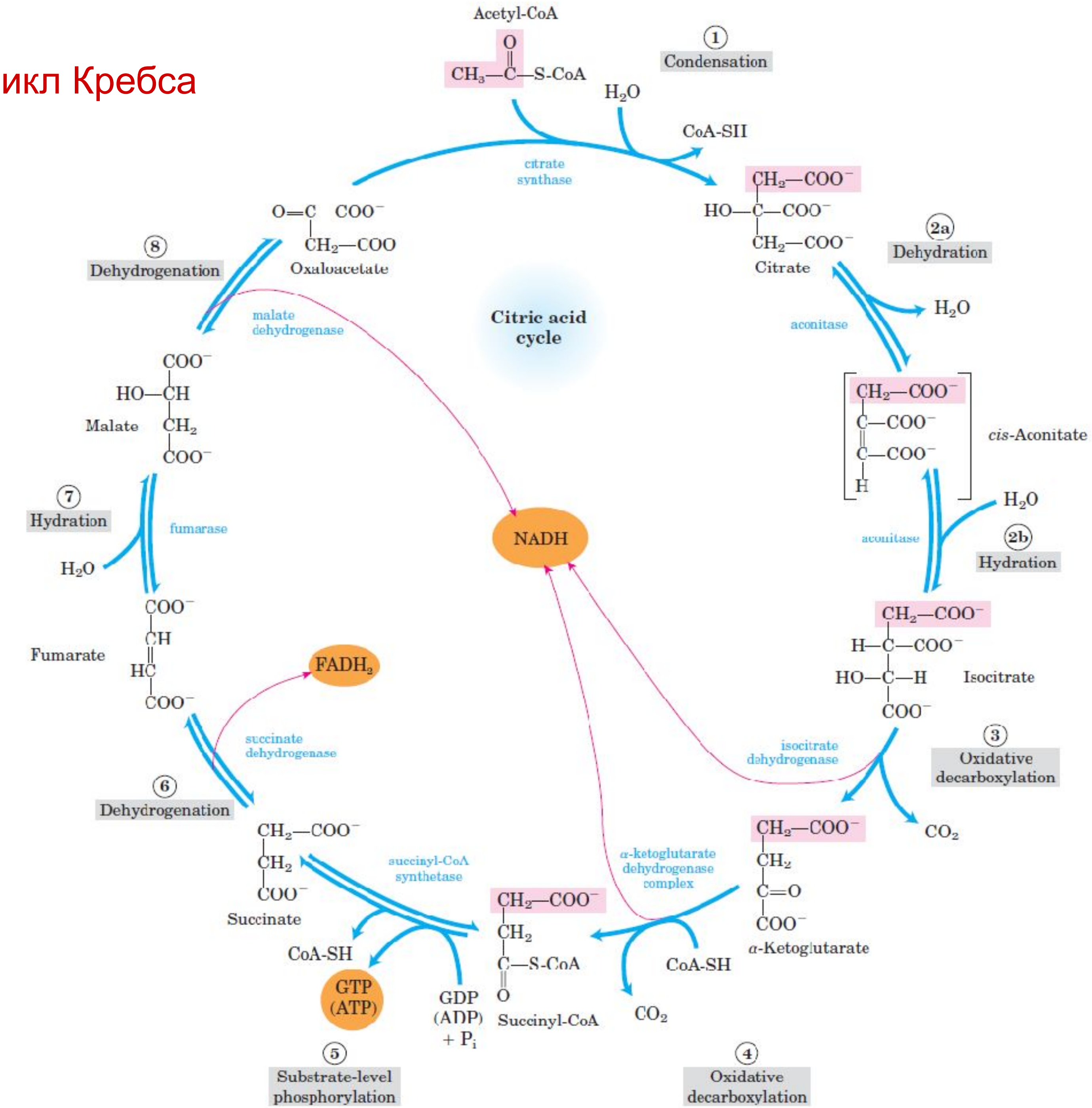
Dihydrolipoyl dehydrogenase, E_3



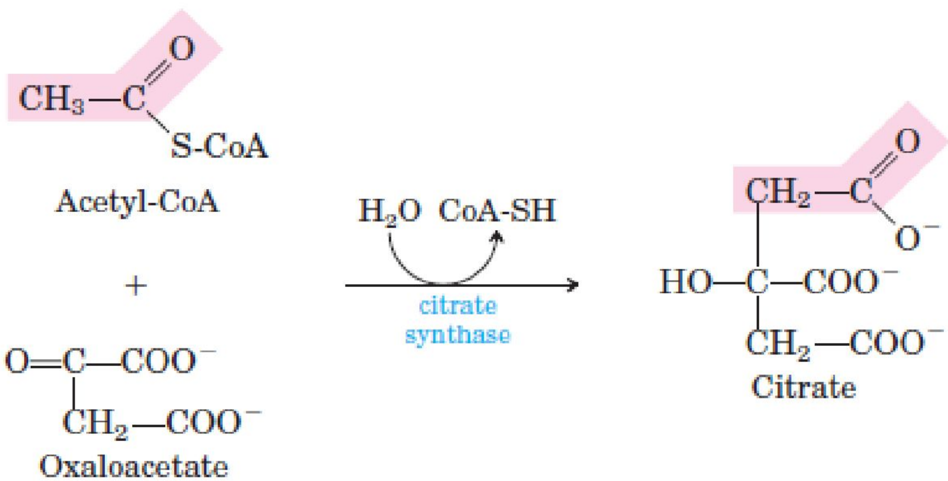


Б. Пируватдегидрогеназный комплекс
Escherichia coli

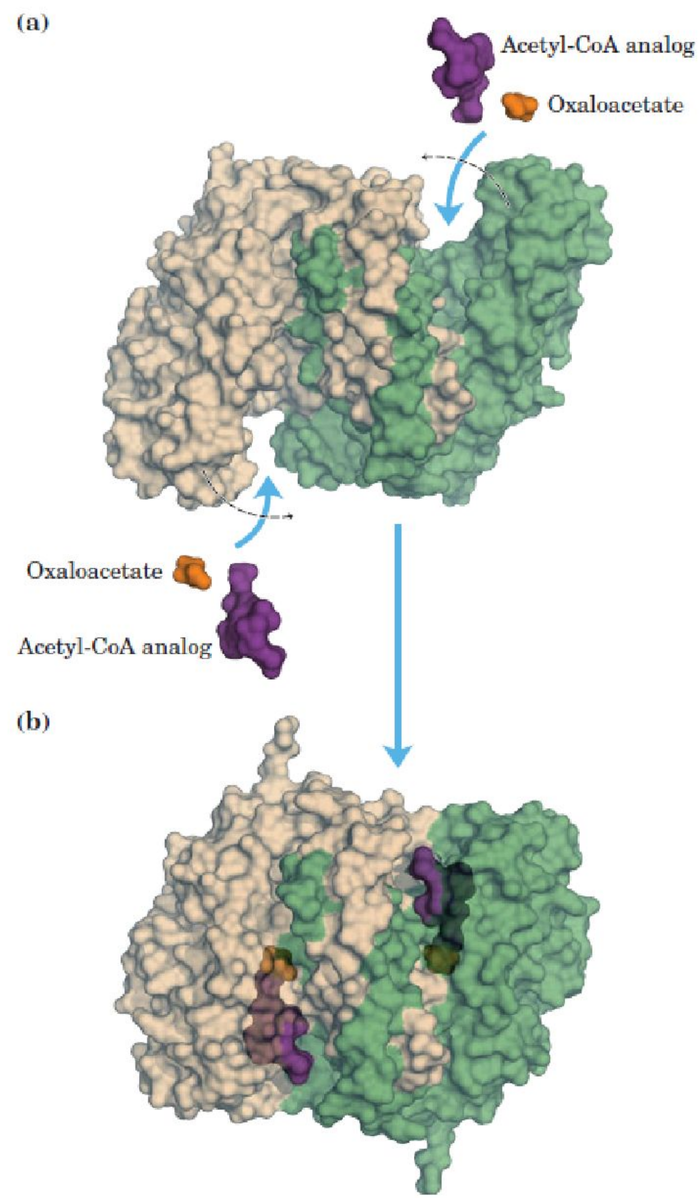
Цикл Кребса

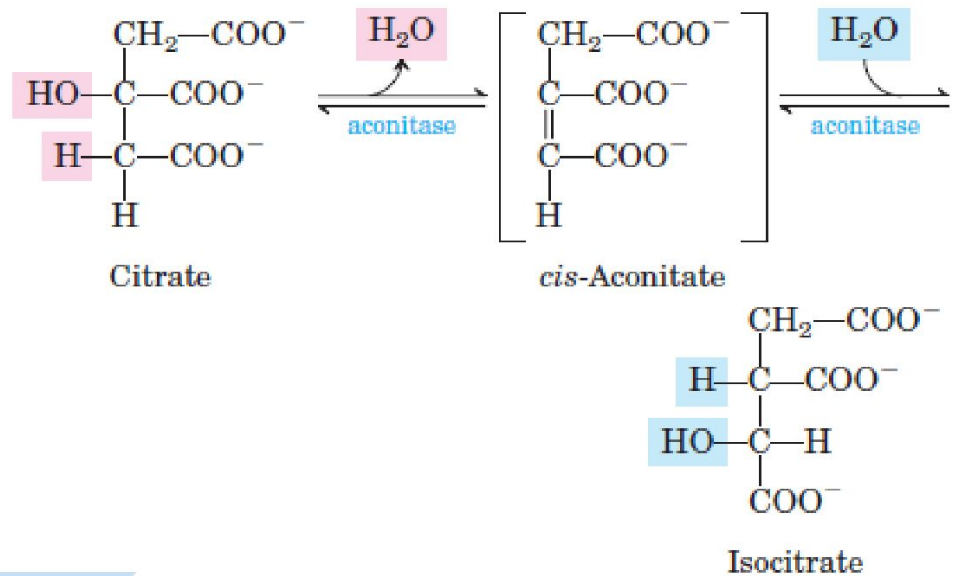


Acetyl-CoA
Condensation
H_2O
CoA-SH
citrate synthase
Citrate
Dehydration
aconitase
cis-Aconitate
Hydration
Isocitrate
Oxidative decarboxylation
isocitrate dehydrogenase
CO_2
α-Ketoglutarate
α-ketoglutarate dehydrogenase complex
Succinyl-CoA
Oxidative decarboxylation
succinyl-CoA synthetase
GTP (ATP)
GDP (ADP) + P_i
Substrate-level phosphorylation
Succinate
succinate dehydrogenase
Dehydrogenation
$FADH_2$
Fumarate
fumarase
Hydration
Malate
malate dehydrogenase
Dehydrogenation
Oxaloacetate
Citric acid cycle
NADH

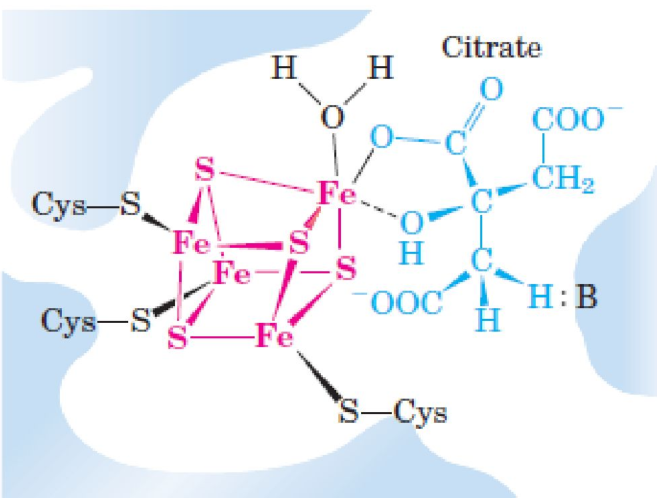


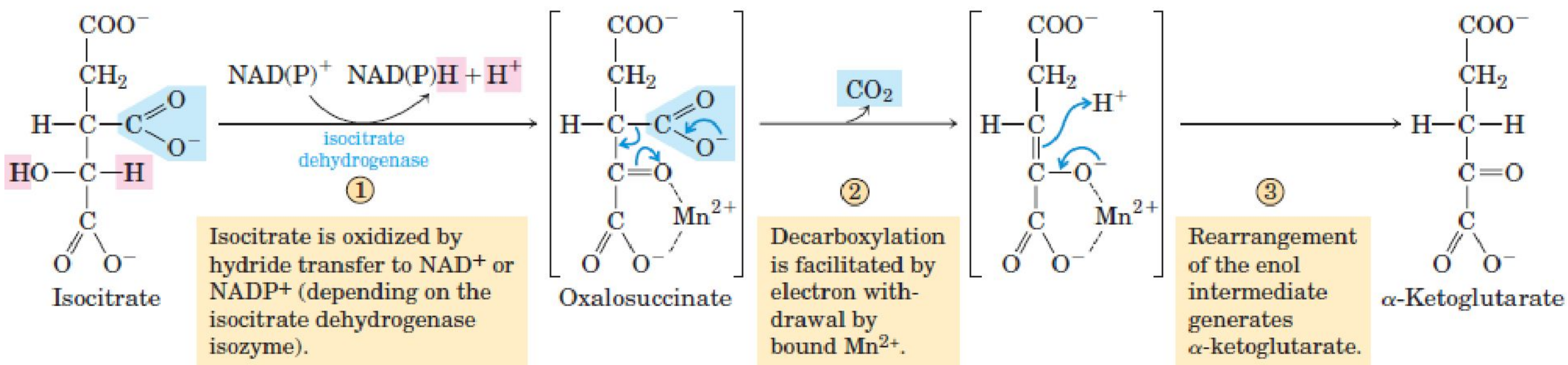
$$\Delta G'^{\circ} = -32.2\ \text{kJ/mol}$$



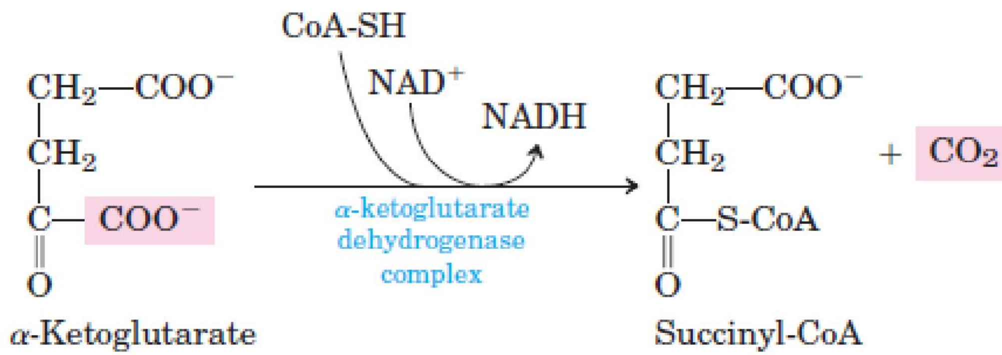


$\Delta G'^{\circ} = 13.3\ \mathrm{kJ/mol}$

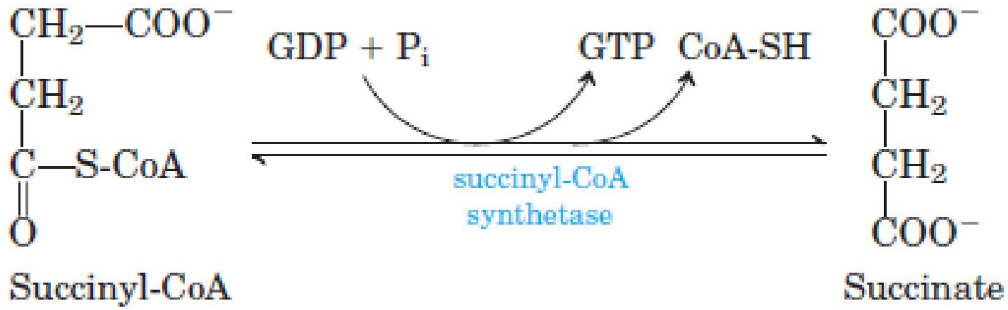




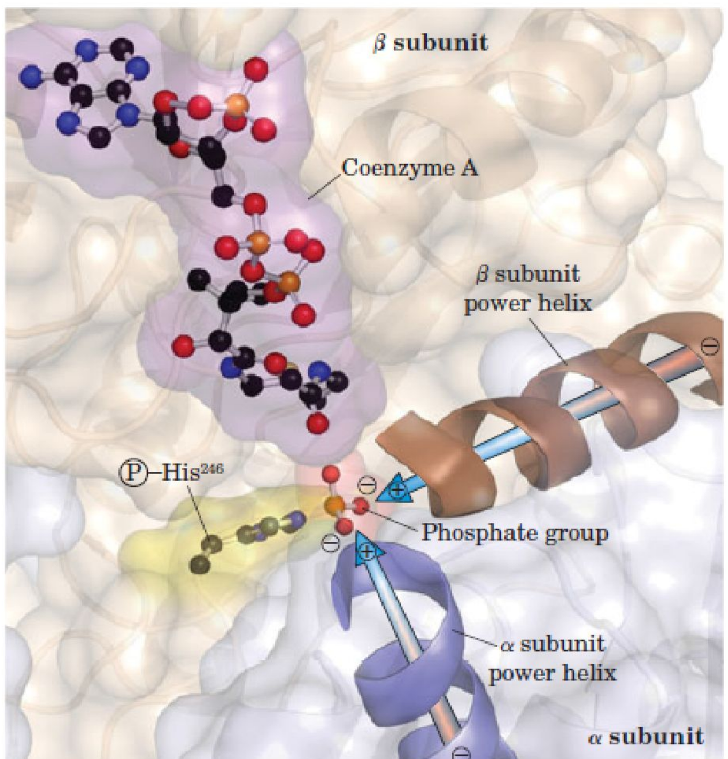
COO⁻
CH₂
H—C—C
O
O⁻
HO—C—H
C
O
O⁻
Isocitrate
NAD(P)⁺
NAD(P)H + H⁺
isocitrate
dehydrogenase
1
Isocitrate is oxidized by hydride transfer to NAD⁺ or NADP⁺ (depending on the isocitrate dehydrogenase isozyme).
Oxalosuccinate
Mn²⁺
CO₂
2
Decarboxylation is facilitated by electron withdrawal by bound Mn²⁺.
H⁺
3
Rearrangement of the enol intermediate generates α-ketoglutarate.
α-Ketoglutarate

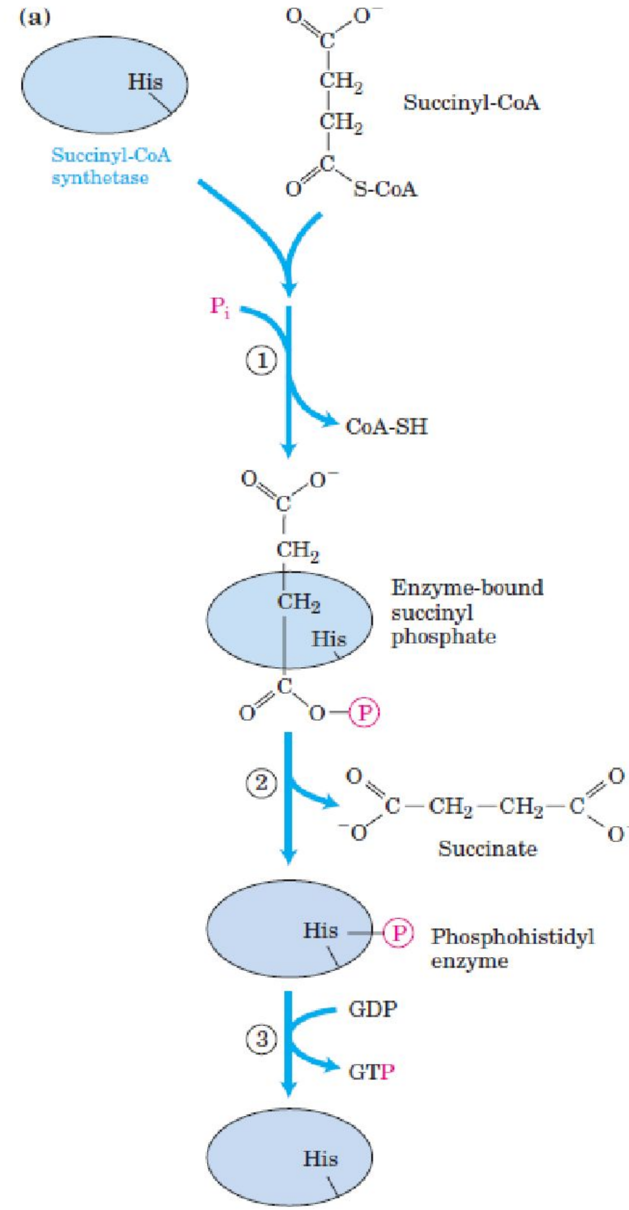


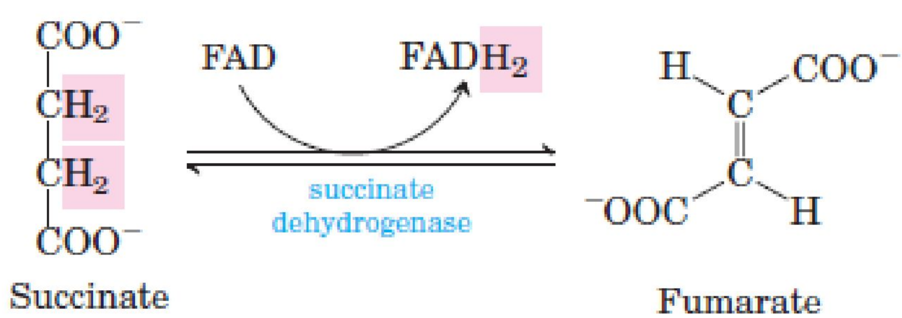
$$\Delta G'^{\circ} = -33.5 \text{ kJ/mol}$$



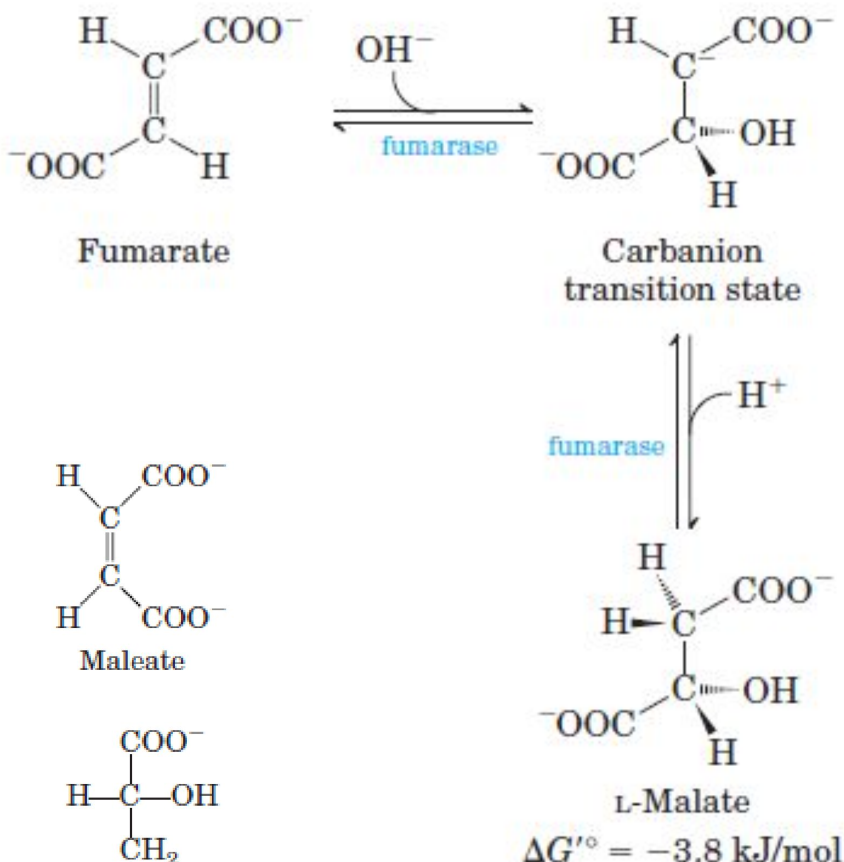
$$\Delta G'^{\circ} = -2.9\ \text{kJ/mol}$$



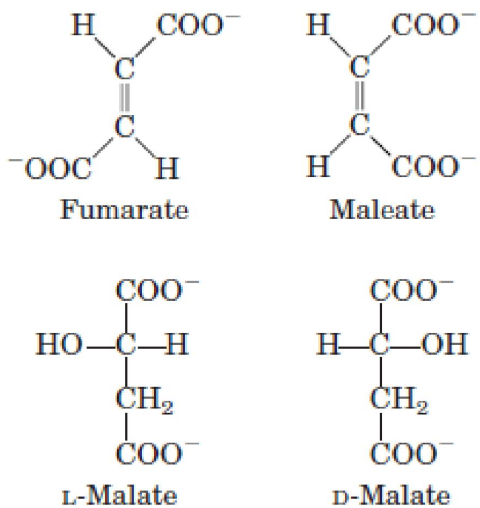




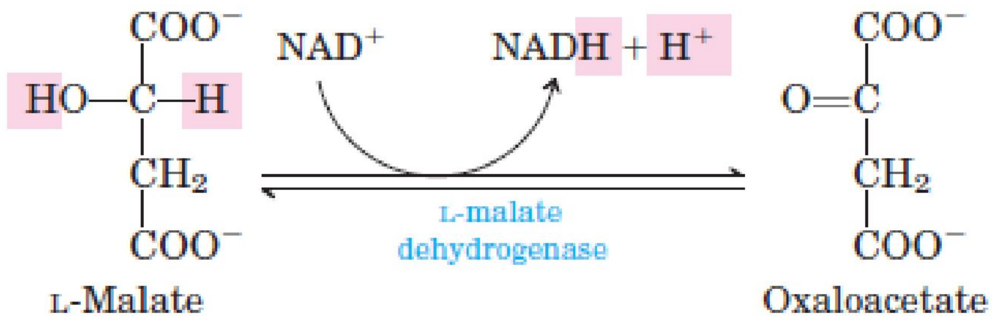
$$\Delta G'^{\circ} = 0 \text{ kJ/mol}$$



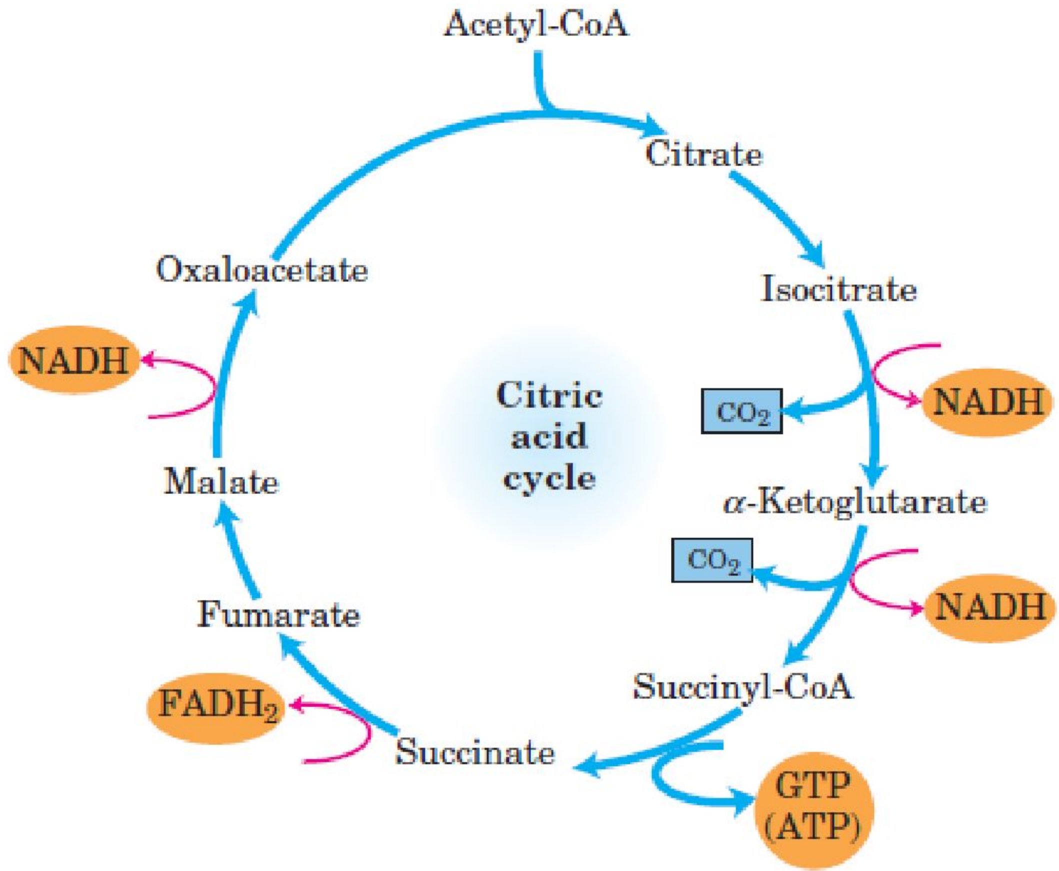
fumarase
fumarase
Fumarate
Carbanion transition state
L-Malate
$\Delta G'^{\circ} = -3.8$ kJ/mol

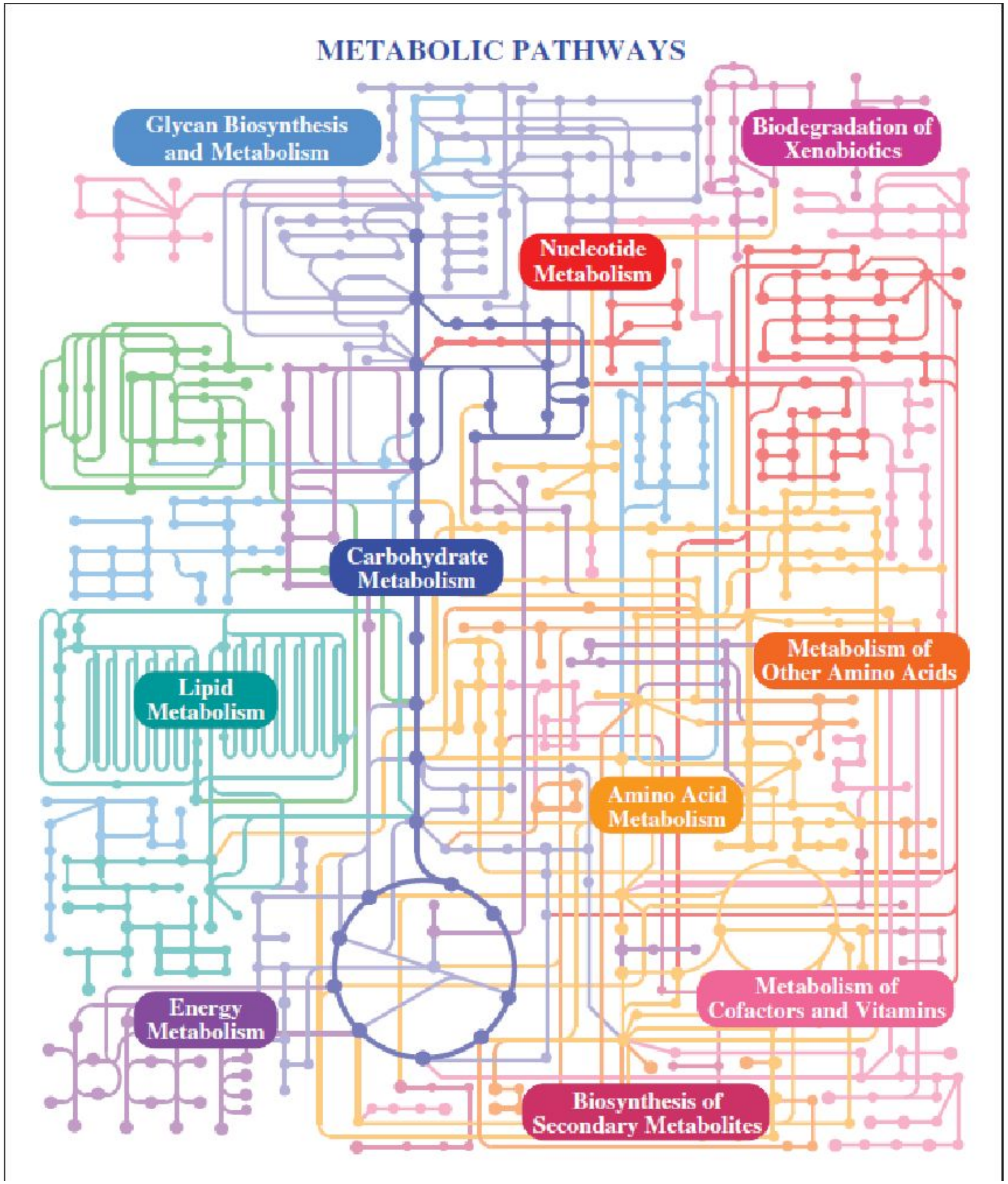


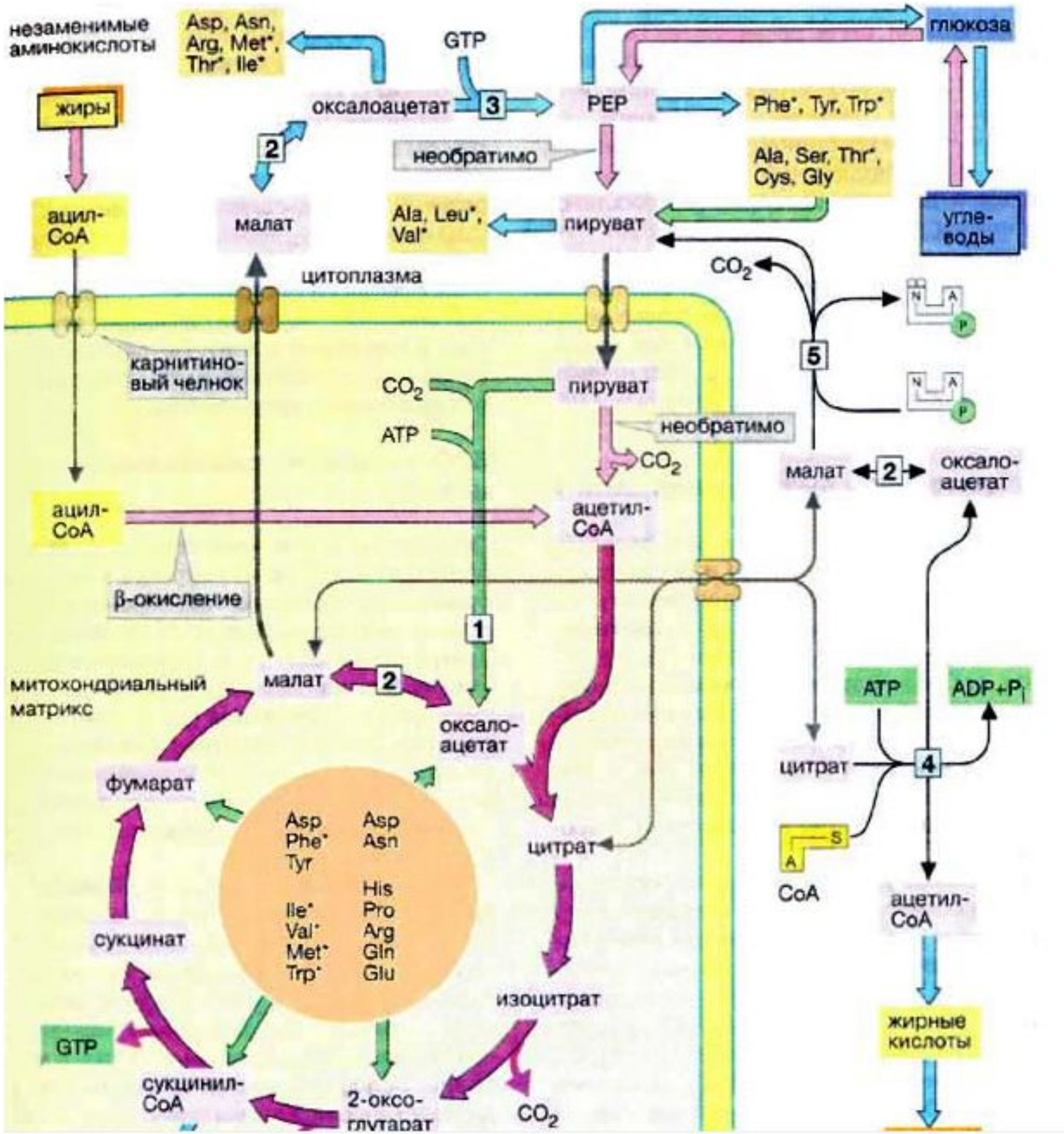
Fumarate
Maleate
L-Malate
D-Malate

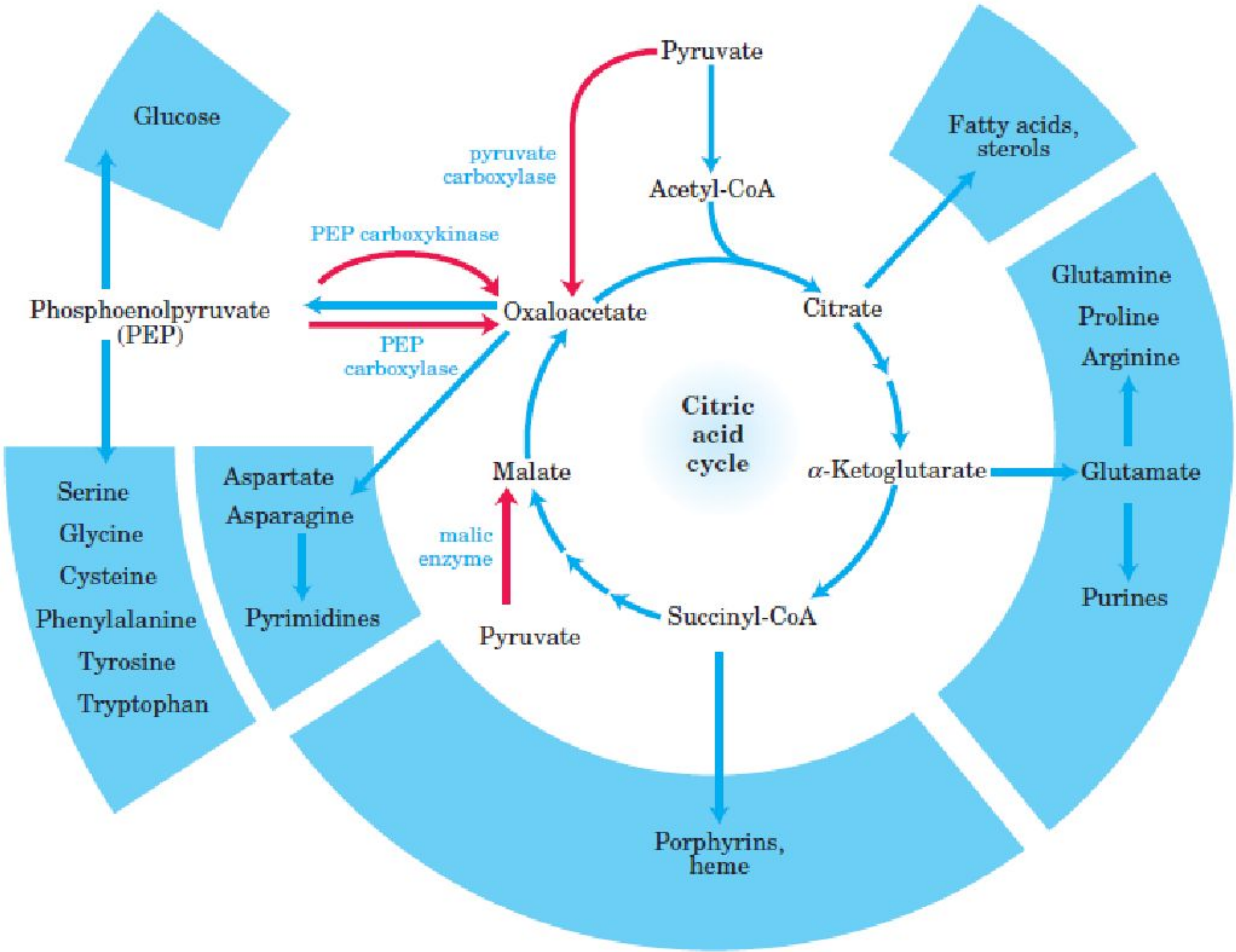


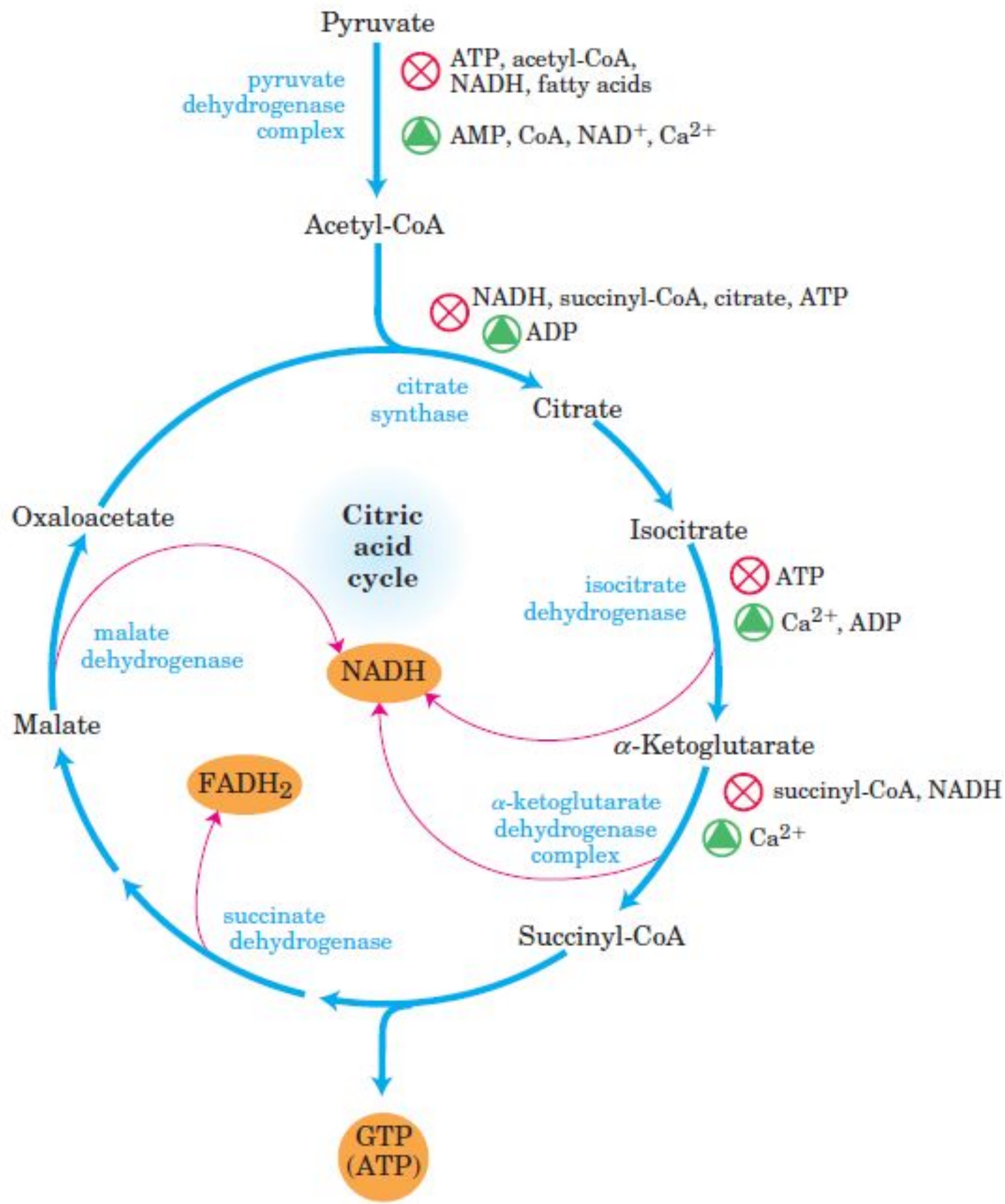
$$\Delta G'^{\circ} = 29.7 \text{ kJ/mol}$$


Acetyl-CoA
Citrate
Isocitrate
CO_2
NADH
α-Ketoglutarate
CO_2
NADH
Succinyl-CoA
GTP
(ATP)
Succinate
$FADH_2$
Fumarate
Malate
NADH
Oxaloacetate
Citric
acid
cycle


METABOLIC PATHWAYS
Glycan Biosynthesis and Metabolism
Biodegradation of Xenobiotics
Nucleotide Metabolism
Carbohydrate Metabolism
Lipid Metabolism
Metabolism of Other Amino Acids
Amino Acid Metabolism
Energy Metabolism
Metabolism of Cofactors and Vitamins
Biosynthesis of Secondary Metabolites

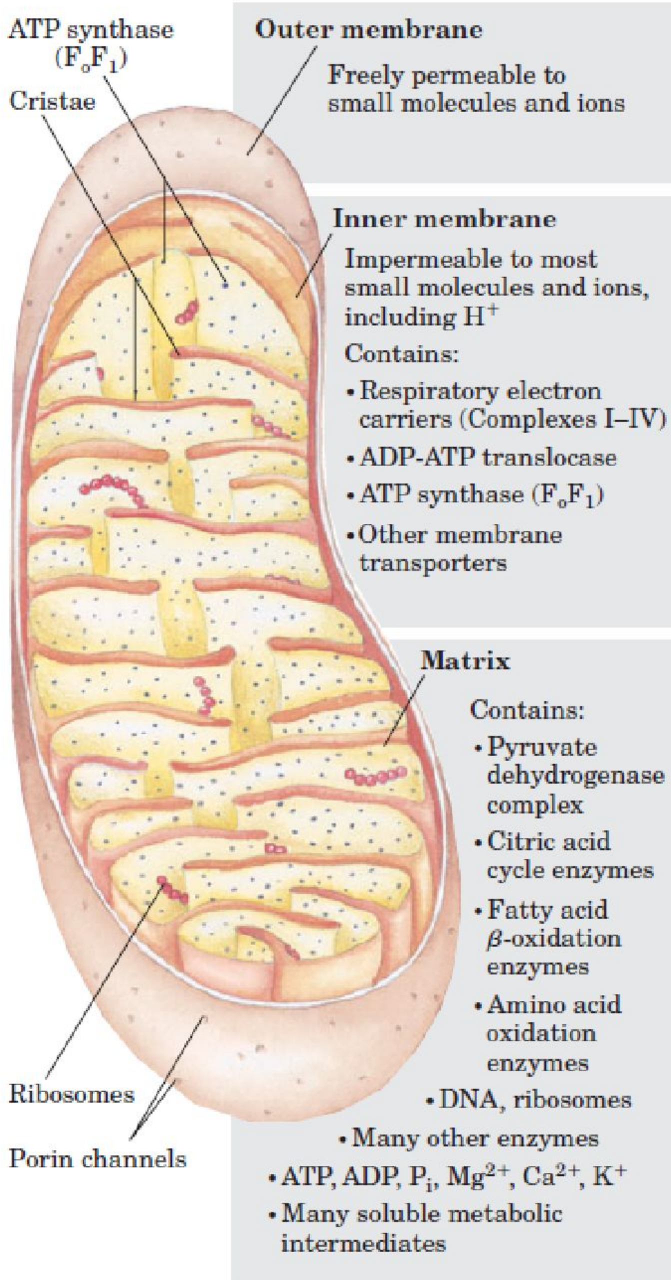

незаменимые аминокислоты
Asp, Asn, Arg, Met*, Thr*, Ile*
GTP
оксалоацетат
3
PEP
глюкоза
Phe*, Tyr, Trp*
жиры
2
необратимо
Ala, Ser, Thr*, Cys, Gly
ацил-CoA
малат
Ala, Leu*, Val*
пируват
угле-воды
цитоплазма
CO_2
карнитино-вый челнок
5
CO_2
пируват
ATP
необратимо
CO_2
малат
2
оксало-ацетат
ацил-CoA
ацетил-CoA
β-окисление
1
митохондриальный матрикс
малат
2
оксало-ацетат
ATP
ADP+P_i
фумарат
цитрат
4
Asp Phe* Tyr
Asp Asn
Ile* Val* Met* Trp*
His Pro Arg Gln Glu
цитрат
CoA
сукцинат
ацетил-CoA
изоцитрат
жирные кислоты
GTP
сукцинил-CoA
2-оксо-глутарат
CO_2

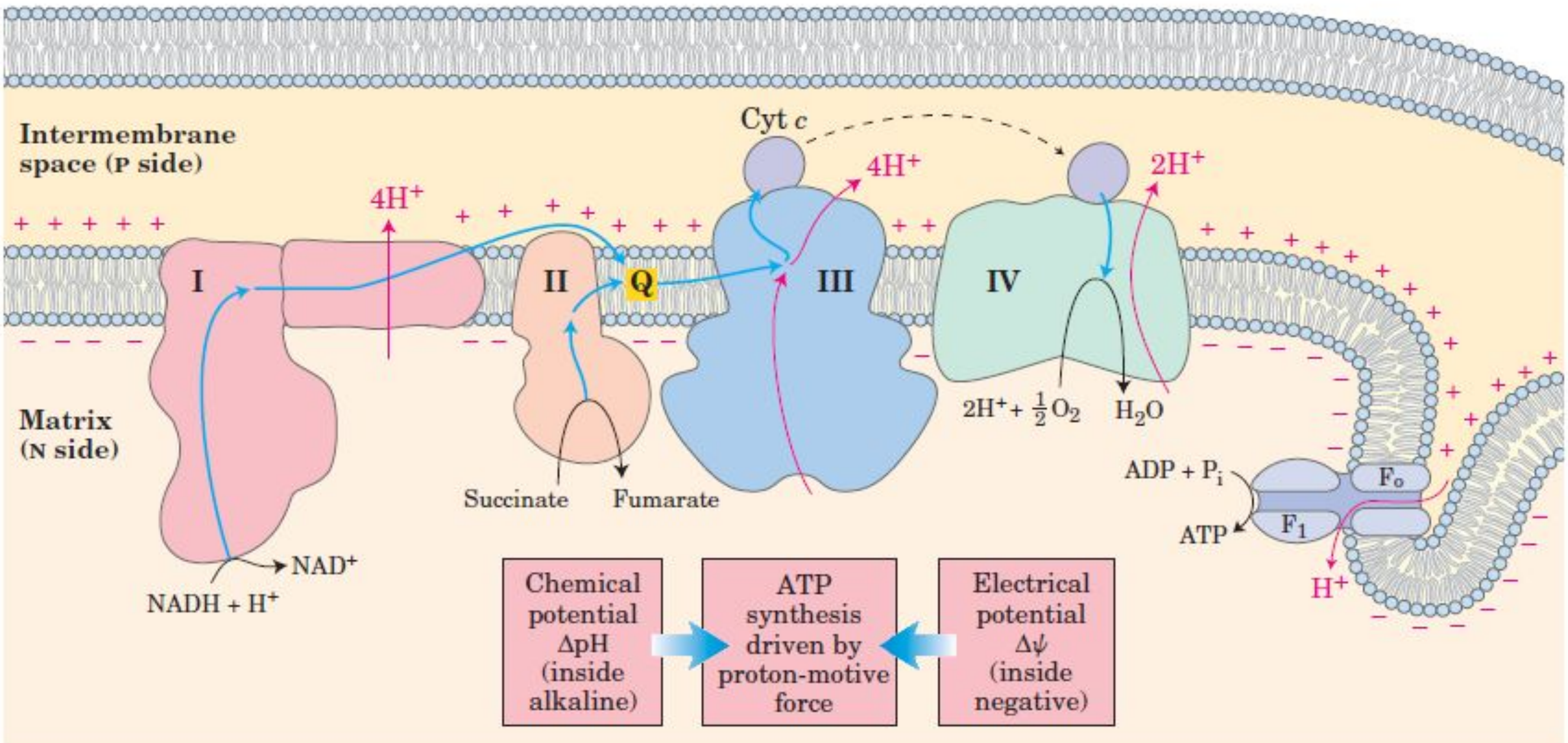

Pyruvate
Glucose
pyruvate carboxylase
Acetyl-CoA
Fatty acids, sterols
PEP carboxykinase
Phosphoenolpyruvate (PEP)
Oxaloacetate
Citrate
PEP carboxylase
Glutamine
Proline
Arginine
Citric acid cycle
Malate
α-Ketoglutarate
Glutamate
Serine
Glycine
Cysteine
Phenylalanine
Tyrosine
Tryptophan
Aspartate
Asparagine
Pyrimidines
malic enzyme
Pyruvate
Succinyl-CoA
Purines
Porphyrins, heme



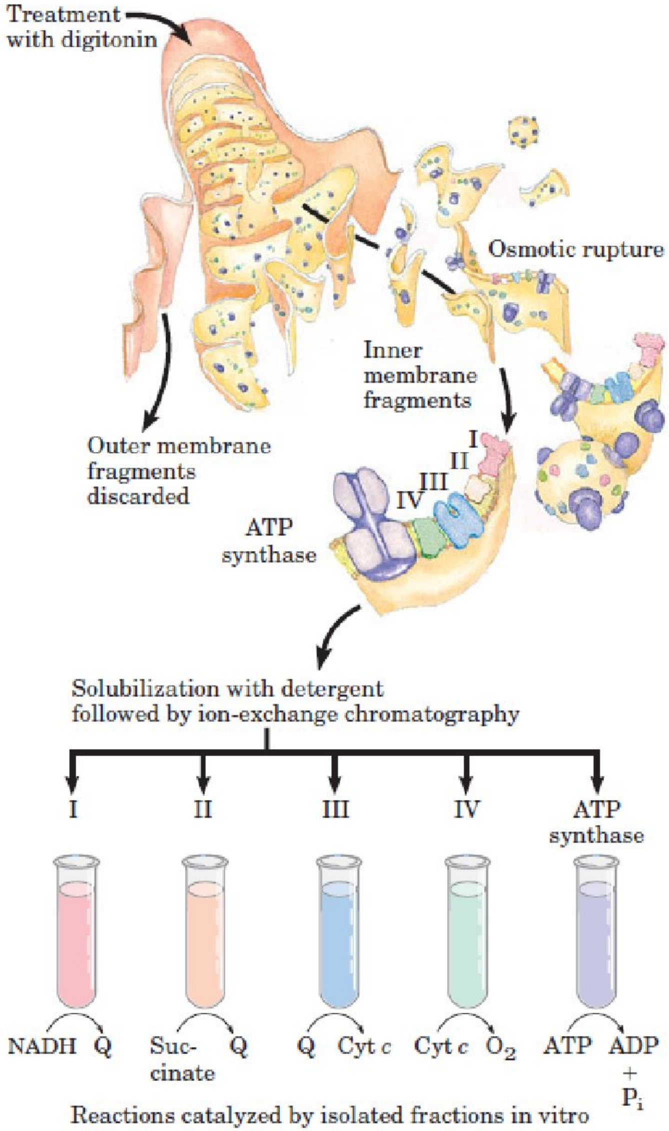
Pyruvate
pyruvate dehydrogenase complex
ATP, acetyl-CoA, NADH, fatty acids
AMP, CoA, NAD+, Ca2+
Acetyl-CoA
NADH, succinyl-CoA, citrate, ATP
ADP
citrate synthase
Citrate
Isocitrate
ATP
Ca2+, ADP
isocitrate dehydrogenase
Citric acid cycle
Oxaloacetate
malate dehydrogenase
NADH
Malate
α-Ketoglutarate
succinyl-CoA, NADH
Ca2+
α-ketoglutarate dehydrogenase complex
FADH2
succinate dehydrogenase
Succinyl-CoA
GTP (ATP)

Дыхательная цепь

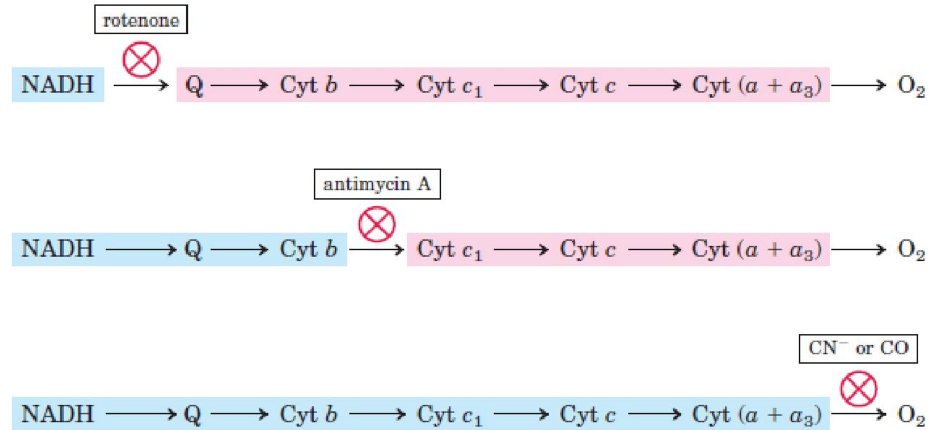




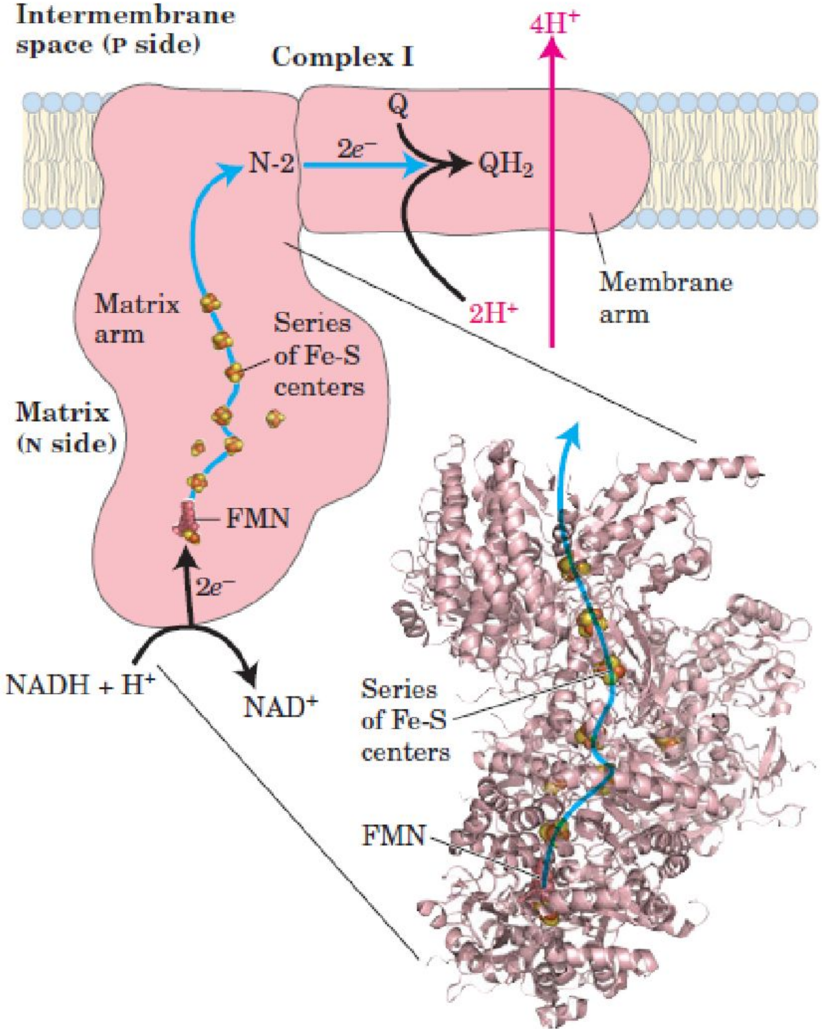
Intermembrane space (P side)
Cyt c
4H+
4H+
2H+
I
II
Q
III
IV
Matrix (N side)
NADH + H+
NAD+
Succinate
Fumarate
2H+ + ½ O2
H2O
ADP + Pi
ATP
Fo
F1
H+
Chemical potential ΔpH (inside alkaline)
ATP synthesis driven by proton-motive force
Electrical potential Δψ (inside negative)



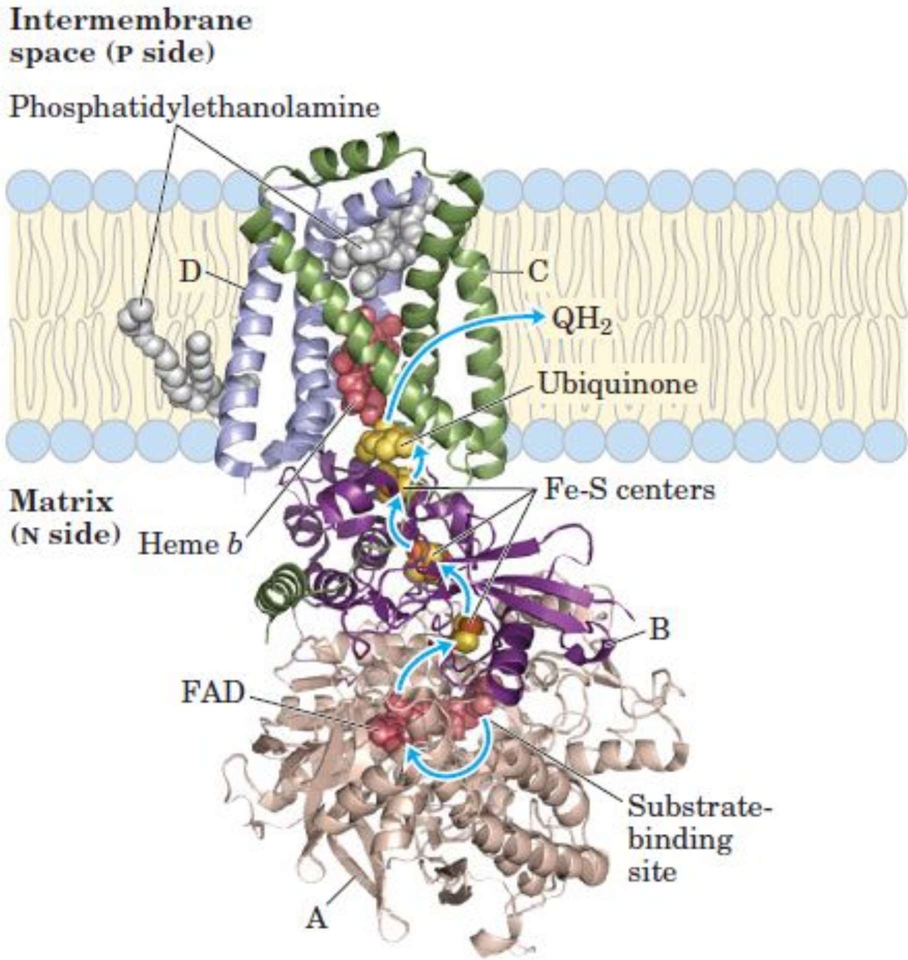
Treatment with digitonin
Osmotic rupture
Outer membrane fragments discarded
Inner membrane fragments
I
II
III
IV
ATP synthase
Solubilization with detergent followed by ion-exchange chromatography
I
II
III
IV
ATP synthase
NADH Q
Suc-cinate Q
Q Cyt c
Cyt c O2
ATP ADP + Pi
Reactions catalyzed by isolated fractions in vitro



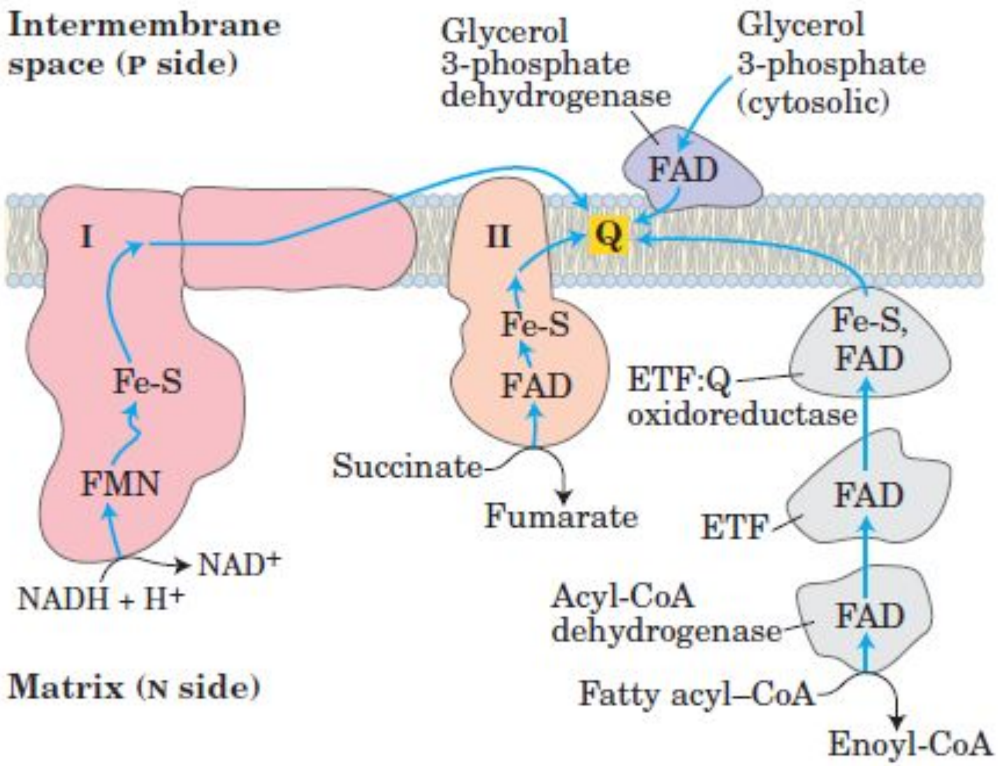
rotenone
NADH → Q → Cyt b → Cyt c1 → Cyt c → Cyt (a + a3) → O2
antimycin A
NADH → Q → Cyt b → Cyt c1 → Cyt c → Cyt (a + a3) → O2
CN⁻ or CO
NADH → Q → Cyt b → Cyt c1 → Cyt c → Cyt (a + a3) → O2



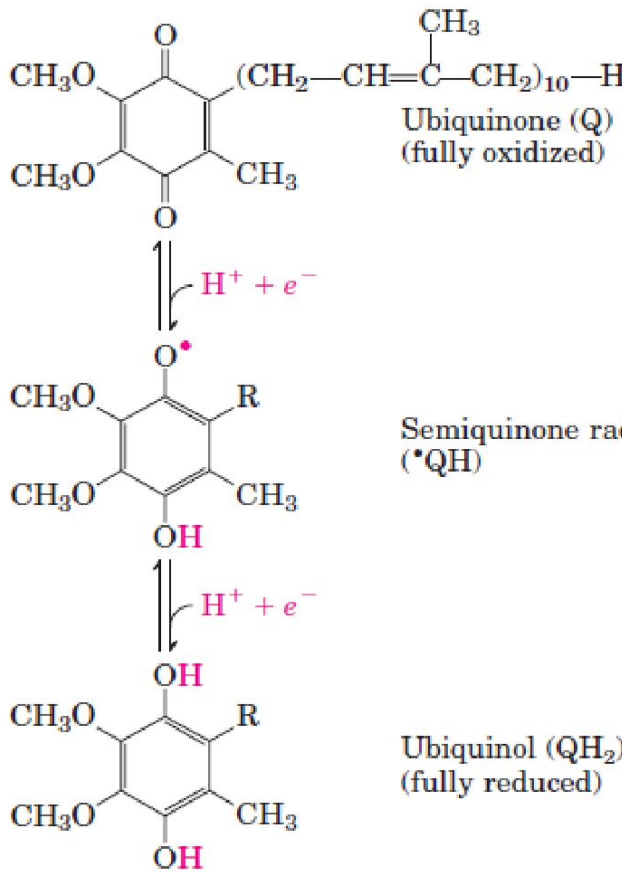
$$NADH + 5H_N^+ + Q \longrightarrow NAD^+ + QH_2 + 4H_P^+$$



Intermembrane space (P side)
Phosphatidylethanolamine
D
C
QH_2
Ubiquinone
Fe-S centers
Matrix (N side)
Heme b
B
FAD
Substrate-binding site
A



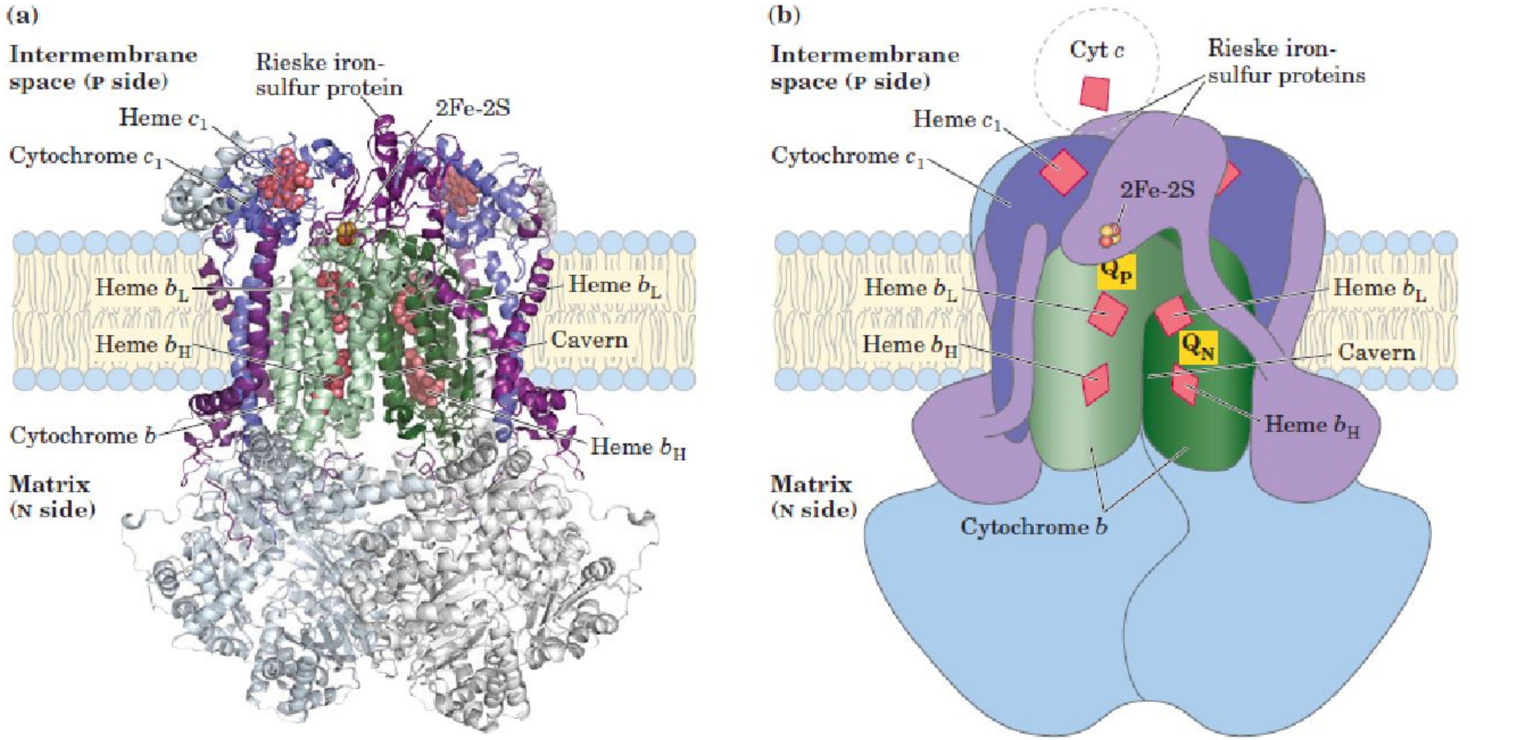
Intermembrane space (P side)
Glycerol 3-phosphate dehydrogenase
Glycerol 3-phosphate (cytosolic)
FAD
I
II
Q
Fe-S
FMN
NADH + H+
NAD+
Fe-S
FAD
Succinate
Fumarate
Fe-S, FAD
ETF:Q oxidoreductase
FAD
ETF
Acyl-CoA dehydrogenase
FAD
Fatty acyl–CoA
Enoyl-CoA
Matrix (N side)



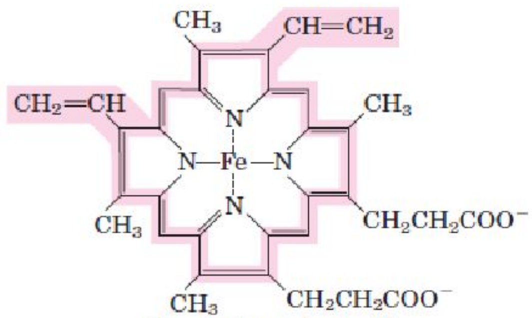
Ubiquinone (Q)
(fully oxidized)

Semiquinone radical
($^{\bullet}QH$)

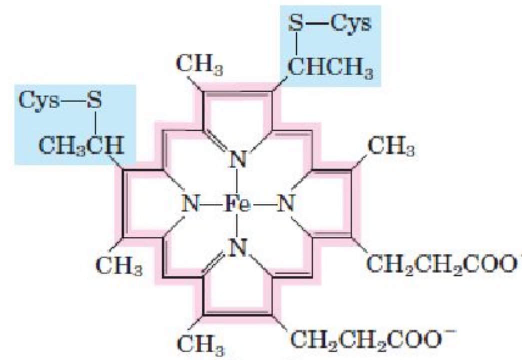
Ubiquinol (QH_2)
(fully reduced)



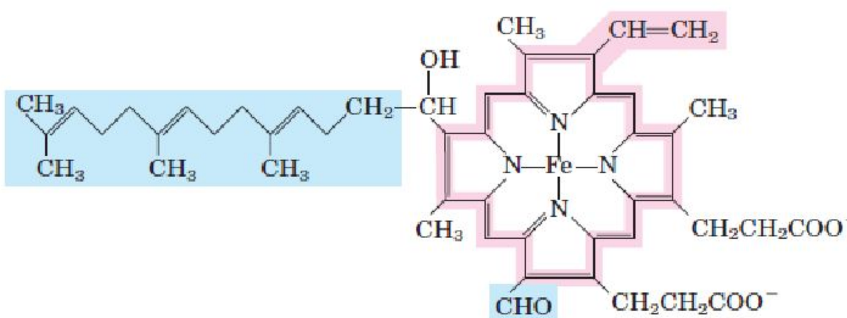
$$
\begin{aligned}
QH_2 + 2\ \text{cyt}\ c_1\ (\text{oxidized}) + 2H_N^+ \longrightarrow \\
Q + 2\ \text{cyt}\ c_1\ (\text{reduced}) + 4H_P^+
\end{aligned}
$$



Iron protoporphyrin IX
(in *b*-type cytochromes)

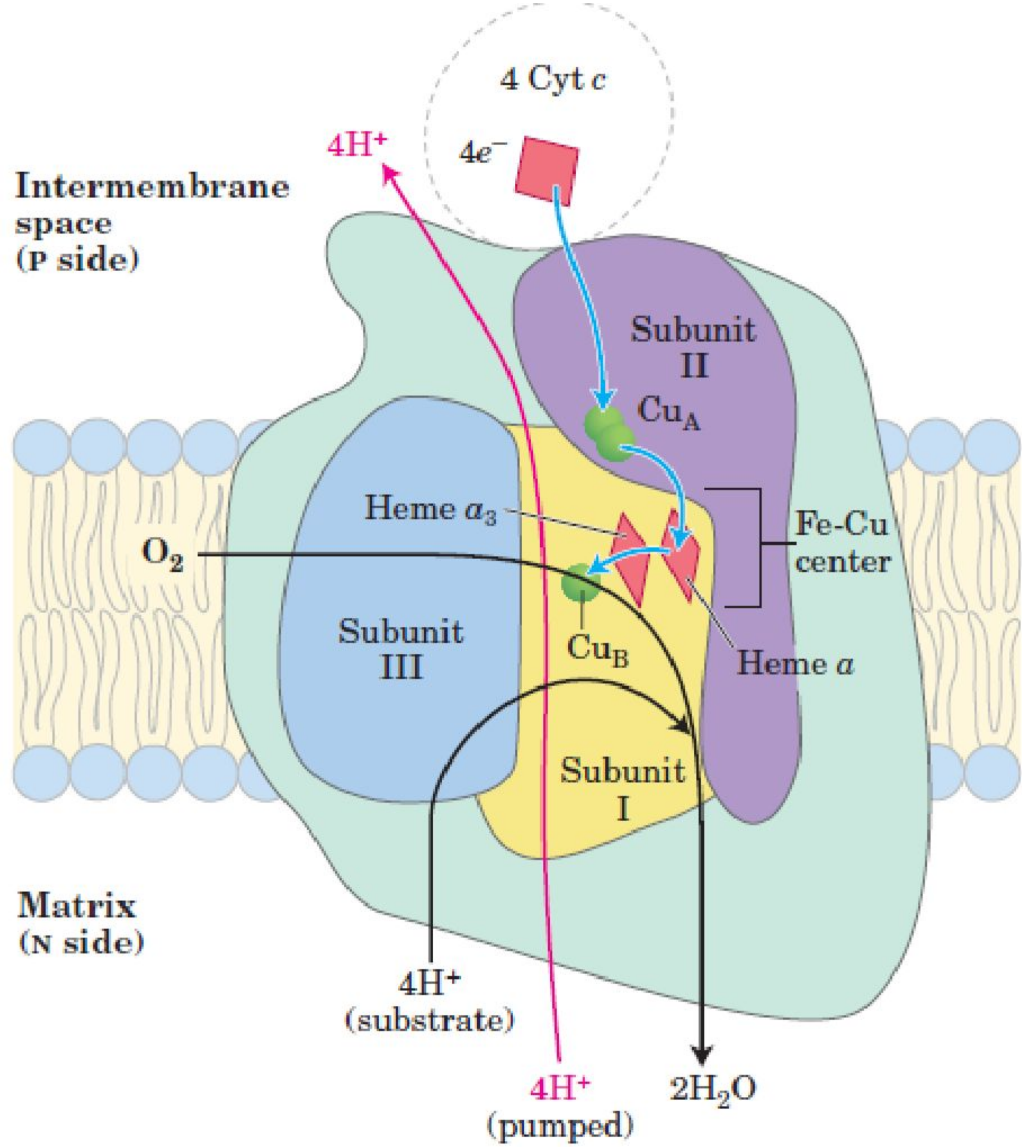


Heme C
(in *c*-type cytochromes)

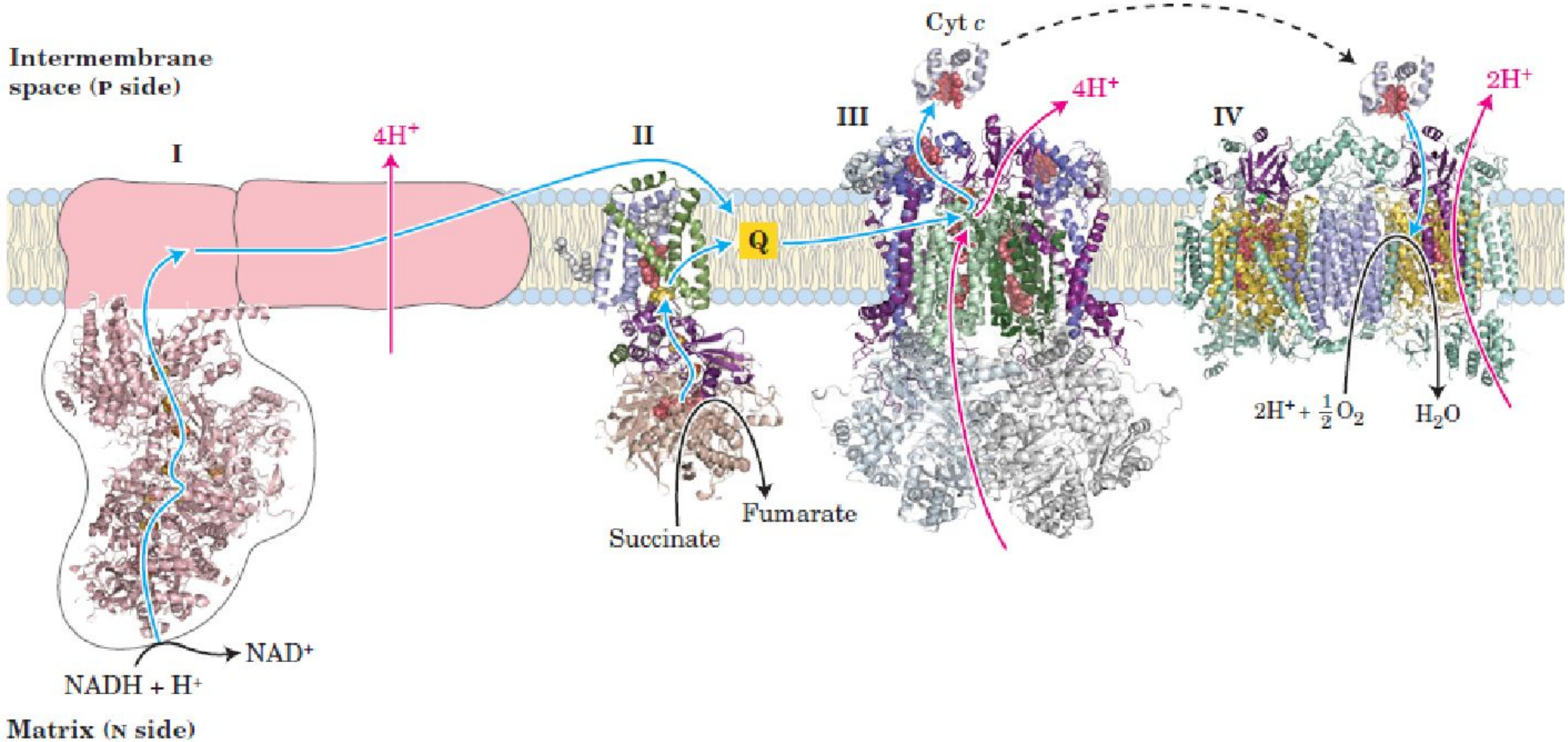


Heme A
(in *a*-type cytochromes)

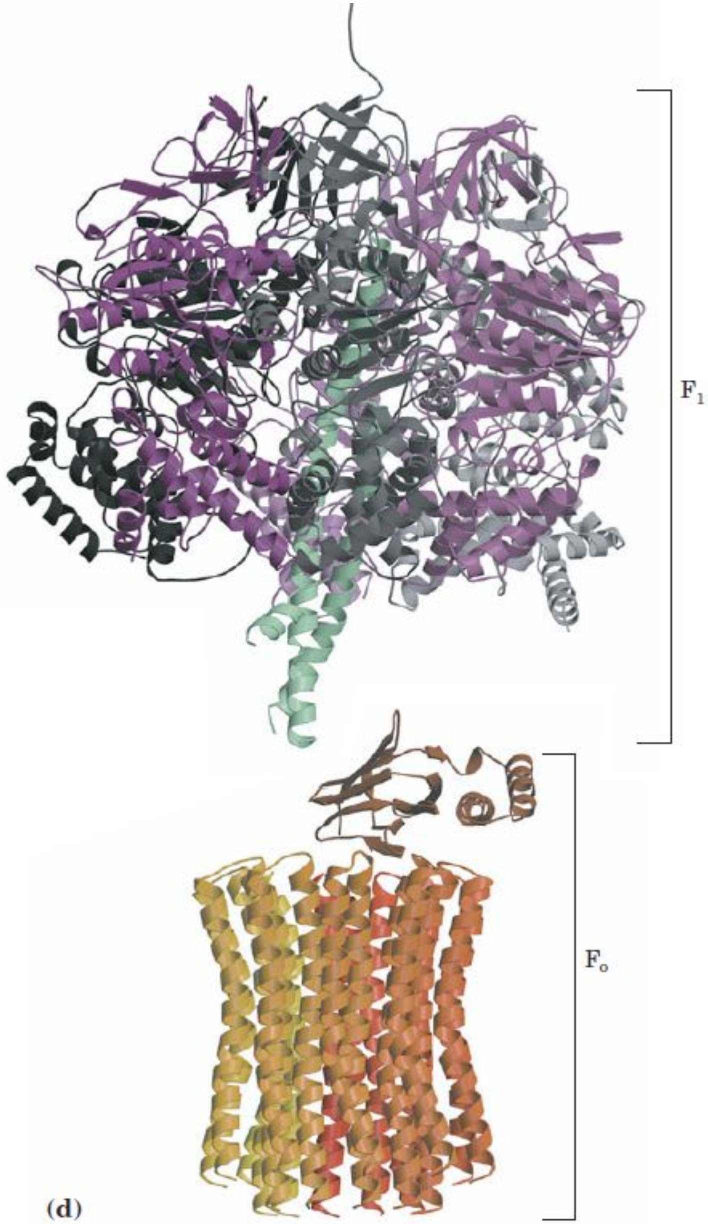
FIGURE 19–3 Prosthetic groups of cytochromes. Each group consists of four five-membered, nitrogen-containing rings in a cyclic structure called a porphyrin. The four nitrogen atoms are coordinated with a central Fe ion, either Fe^{2+} or Fe^{3+}. Iron protoporphyrin IX is found in *b*-type cytochromes and in hemoglobin and myoglobin (see Fig. 4–16). Heme *c* is covalently bound to the protein of cytochrome *c* through thioether bonds to two Cys residues. Heme *a*, found in *a*-type cytochromes, has a long isoprenoid tail attached to one of the five-membered rings. The conjugated double-bond system (shaded pink) of the porphyrin ring accounts for the absorption of visible light by these hemes.



$$4 \text{ Cyt } c \text{ (reduced)} + 8H^+_N + O_2 \longrightarrow$$
$$4 \text{ cyt } c \text{ (oxidized)} + 4H^+_P + 2H_2O$$

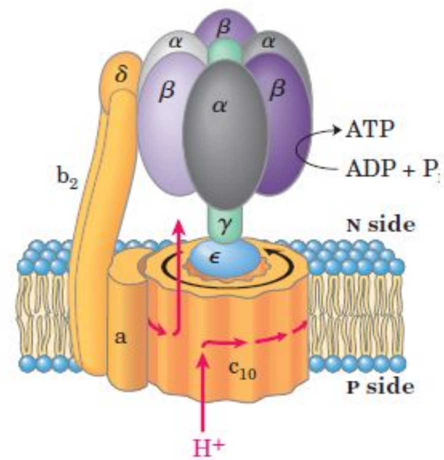


Intermembrane space (P side)
Cyt c
4H+
2H+
I
II
III
IV
Q
Succinate
Fumarate
2H+ + ½ O2
H2O
NADH + H+
NAD+
Matrix (N side)

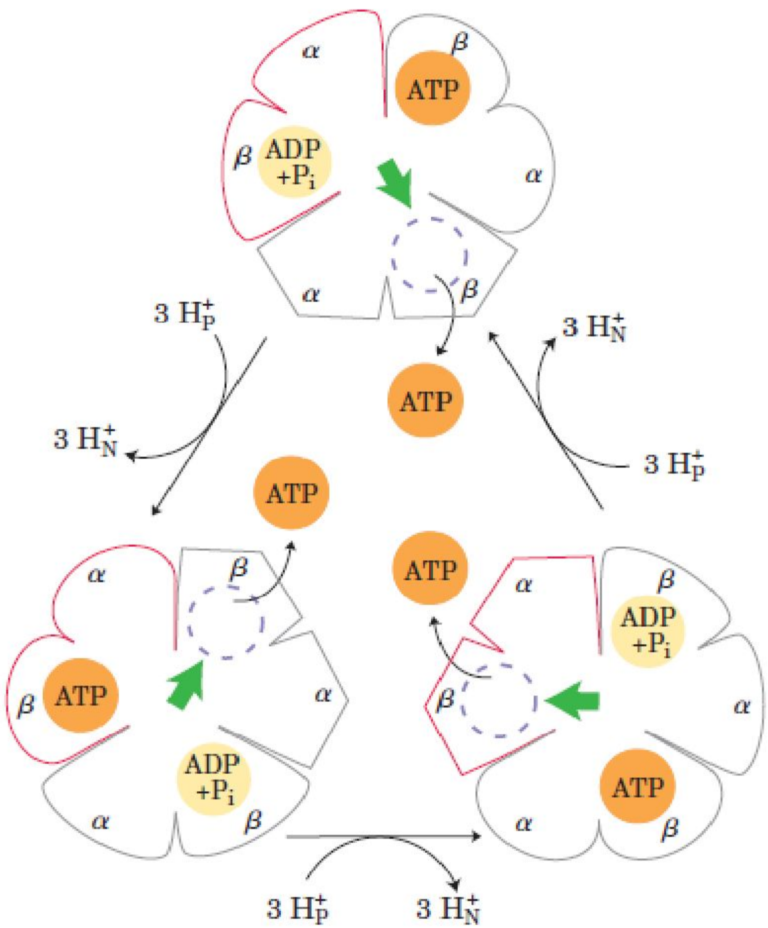


(d)

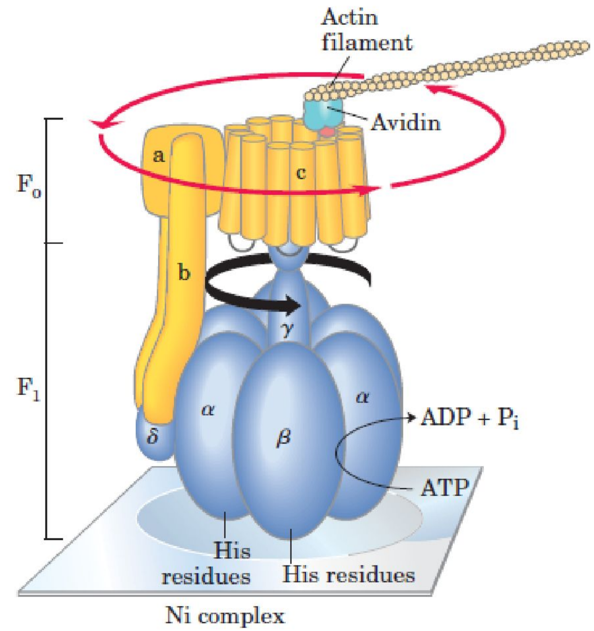
(e)



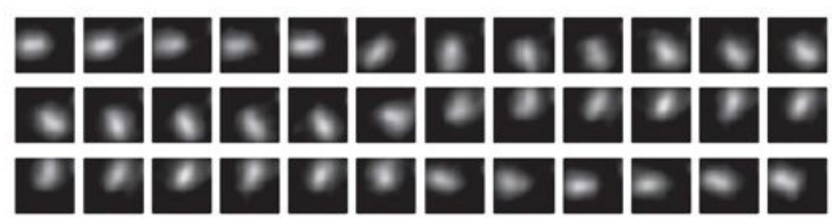
(f)



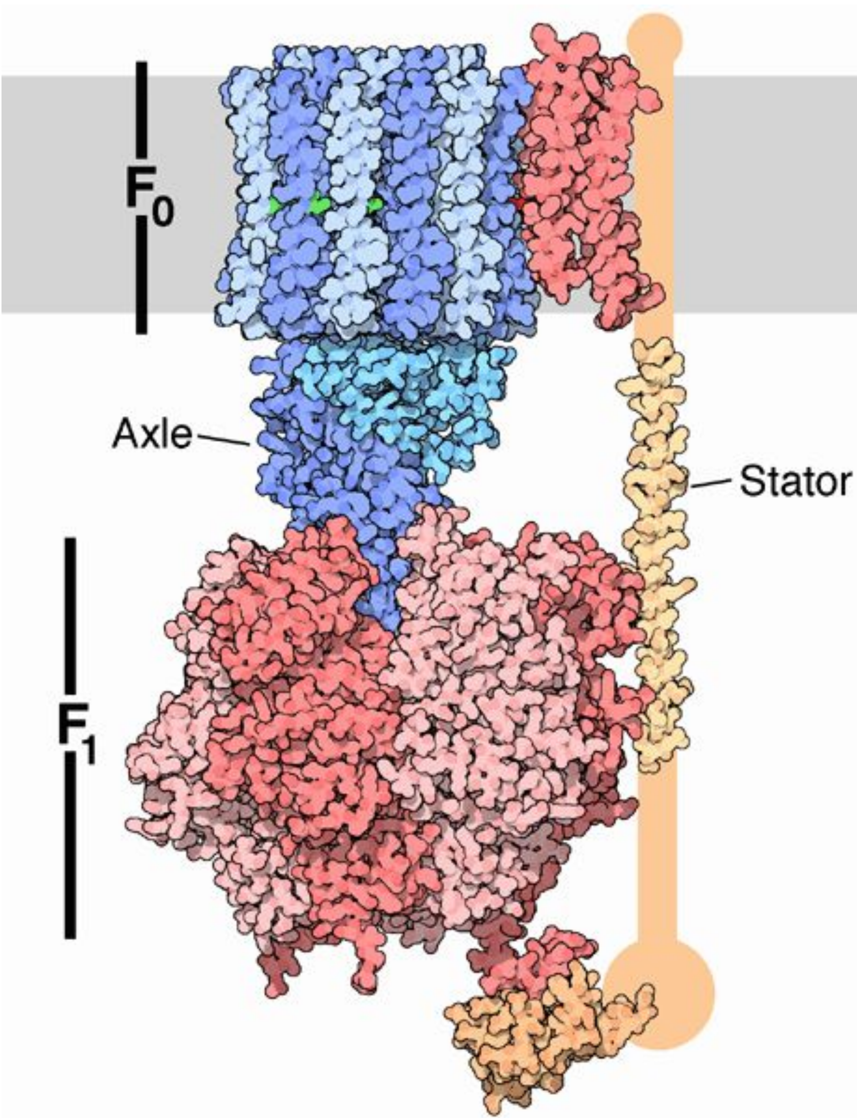
α
β
ATP
ADP +Pi
3 H+P
3 H+N



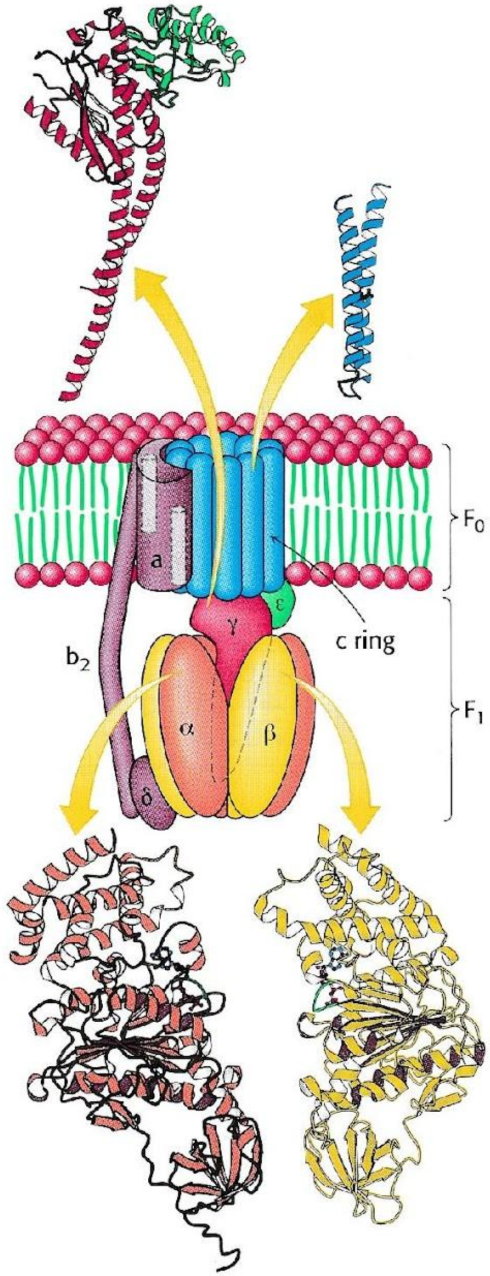
Actin filament
Avidin
Fo
F1
a
b
c
δ
γ
α
β
ADP + Pi
ATP
His residues
His residues
Ni complex

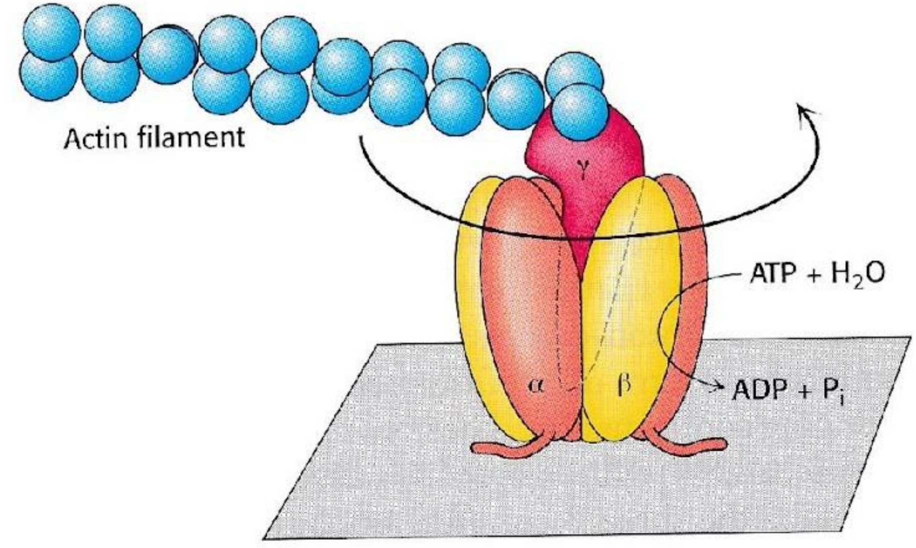


АТФ-синтаза

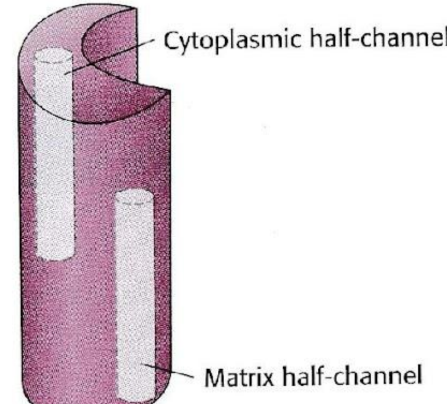


Electron density map of the F_1-ATPase associated with a ring of 10 c-subunits from the F_0 domain of ATP synthase, a molecular machine that carries out the synthesis of ATP in eubacteria, chloroplasts, and mitochondria. [Courtesy of Andrew Leslie, MRC Laboratory of Molecular Biology, Cambridge, UK.]

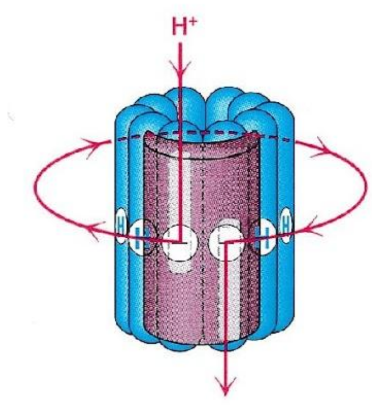


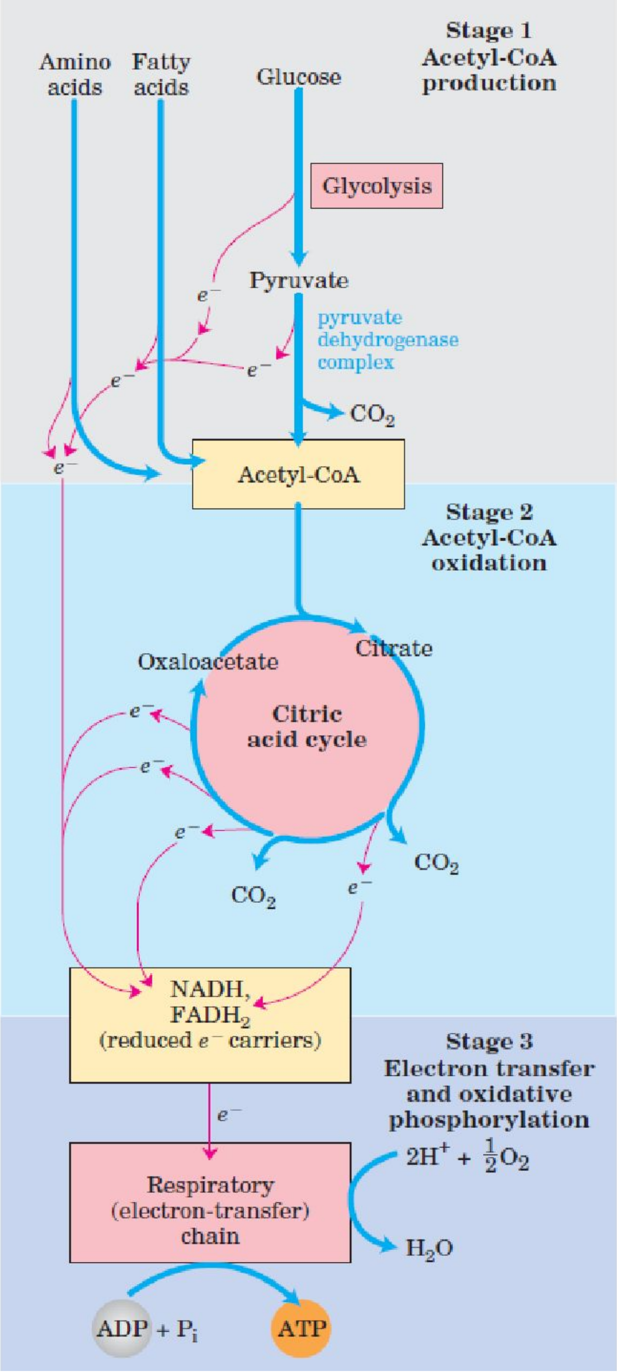


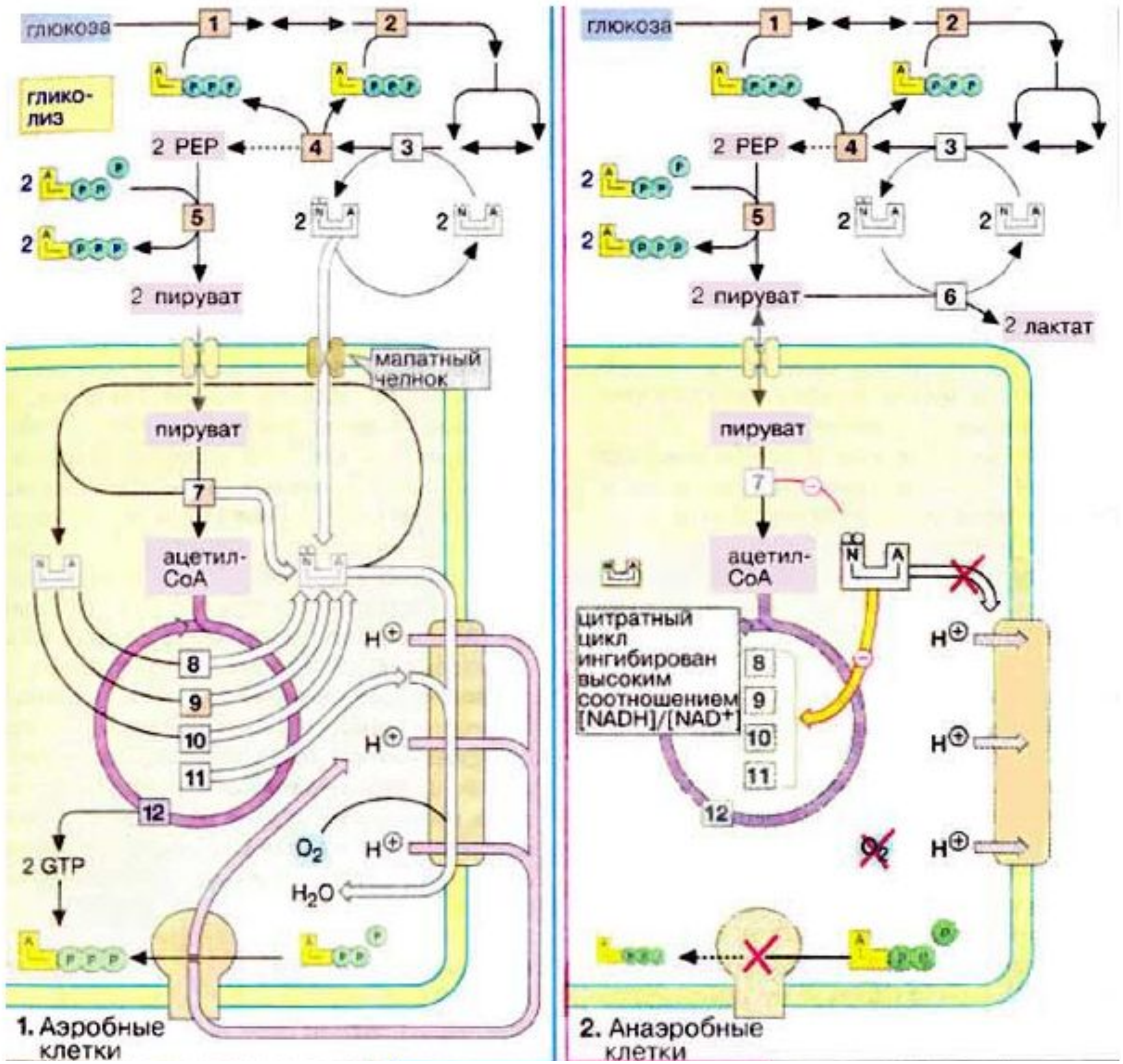
Subunit **c**



Subunit **a**

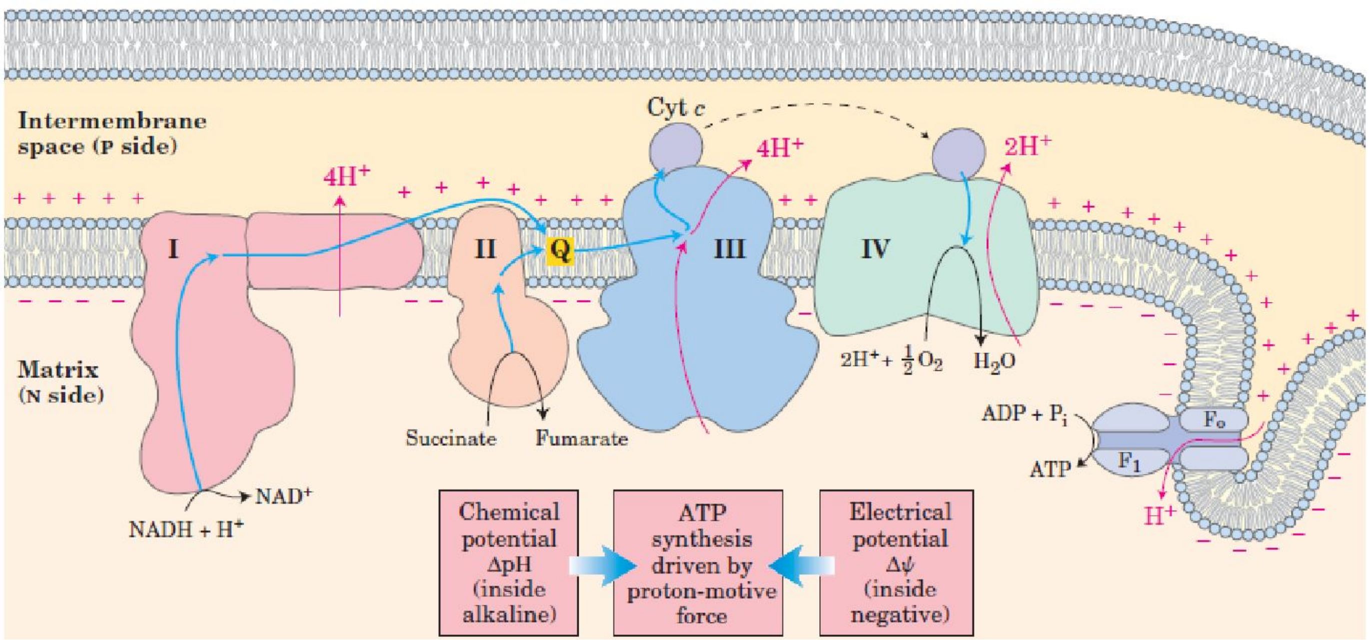


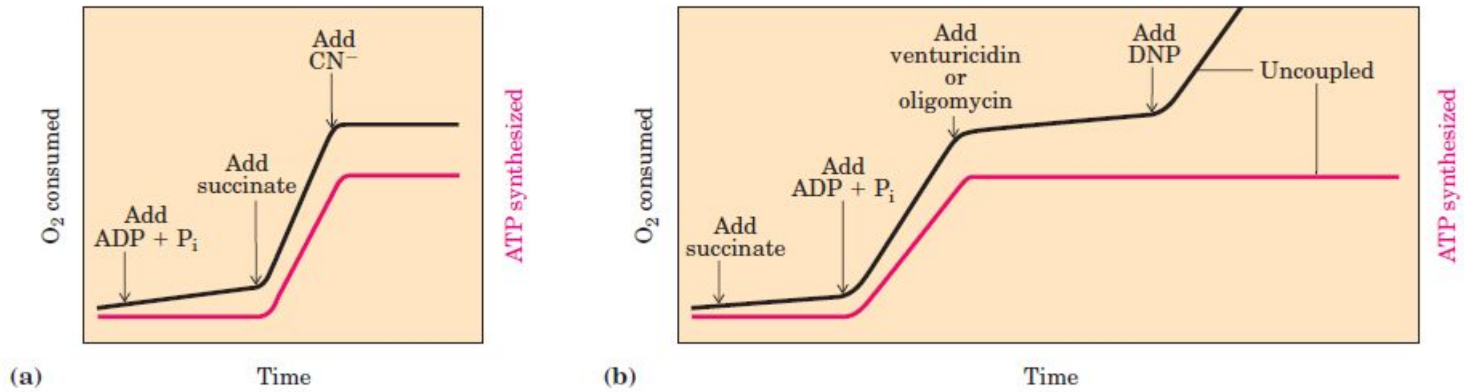

Stage 1
Acetyl-CoA
production
Amino acids
Fatty acids
Glucose
Glycolysis
Pyruvate
pyruvate dehydrogenase complex
e^-
CO_2
Acetyl-CoA
Stage 2
Acetyl-CoA
oxidation
Oxaloacetate
Citrate
Citric acid cycle
CO_2
CO_2
NADH,
$FADH_2$
(reduced e^- carriers)
Stage 3
Electron transfer
and oxidative
phosphorylation
$2H^+ + \frac{1}{2}O_2$
Respiratory
(electron-transfer)
chain
H_2O
ADP + P_i
ATP

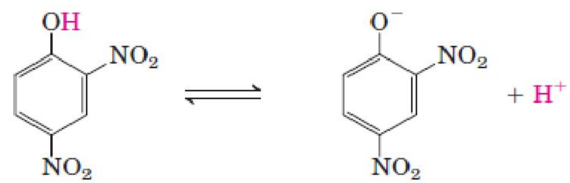


глюкоза
1
2
глико-
лиз
2 PEP
4
3
5
2 пируват
малатный
челнок
пируват
7
ацетил-
CoA
8
9
10
11
12
2 GTP
H^+
O_2
H_2O
1. Аэробные
клетки
глюкоза
1
2
2 PEP
4
3
5
2 пируват
6
2 лактат
пируват
7
ацетил-
CoA
цитратный
цикл
ингибирован
высоким
соотношением
[NADH]/[NAD+]
8
9
10
11
12
H^+
O_2
2. Анаэробные
клетки

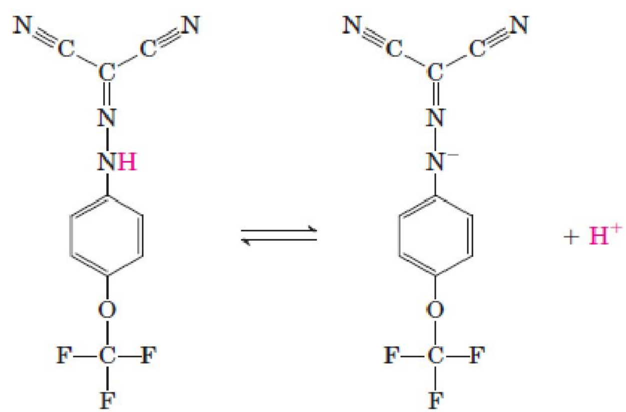
$$\mathrm{ADP} + \mathrm{P_i} + n\mathrm{H_P^+} \longrightarrow \mathrm{ATP} + \mathrm{H_2O} + n\mathrm{H_N^+}$$



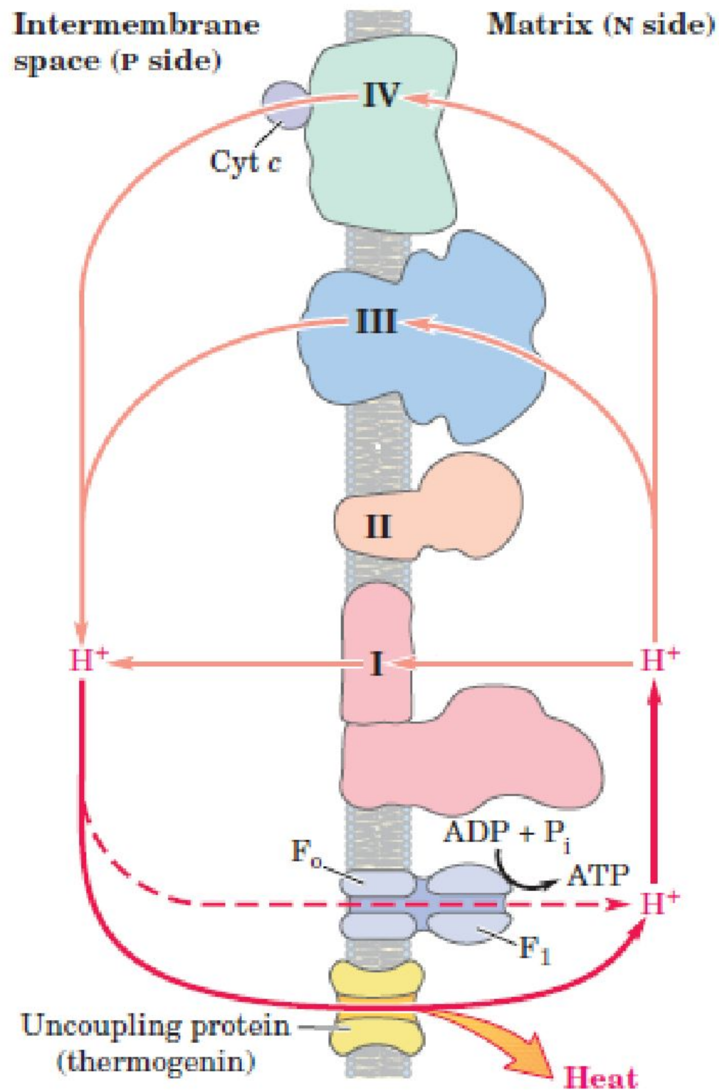




2,4-Dinitrophenol
(DNP)



Carbonylcyanide-*p*-
trifluoromethoxyphenylhydrazone
(FCCP)



Intermembrane space (P side)
Matrix (N side)
IV
Cyt c
III
II
I
H+
H+
ADP + Pi
ATP
Fo
H+
F1
Uncoupling protein (thermogenin)
Heat

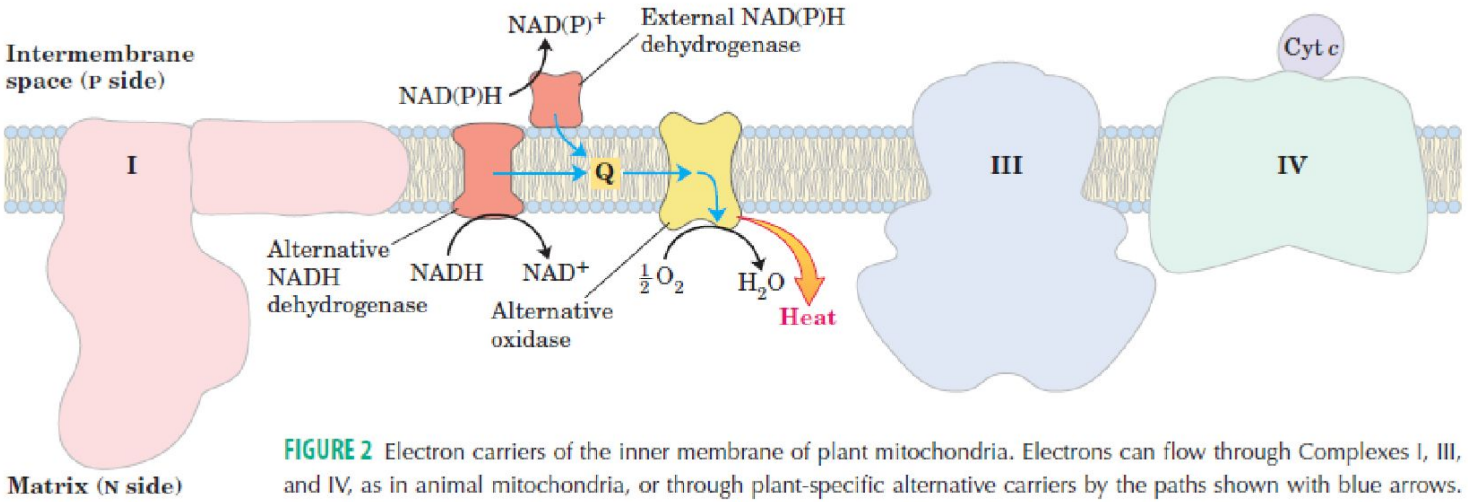
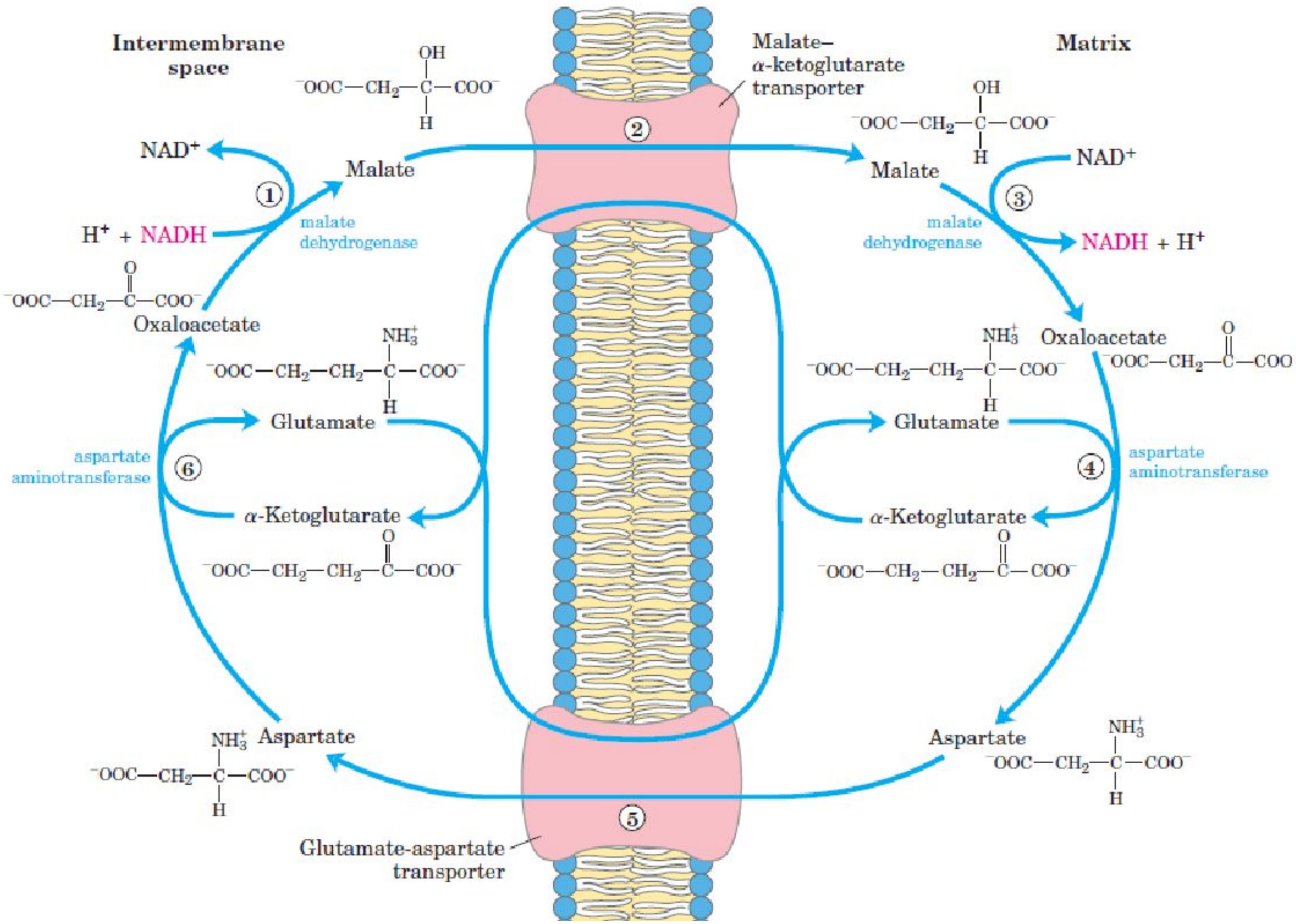
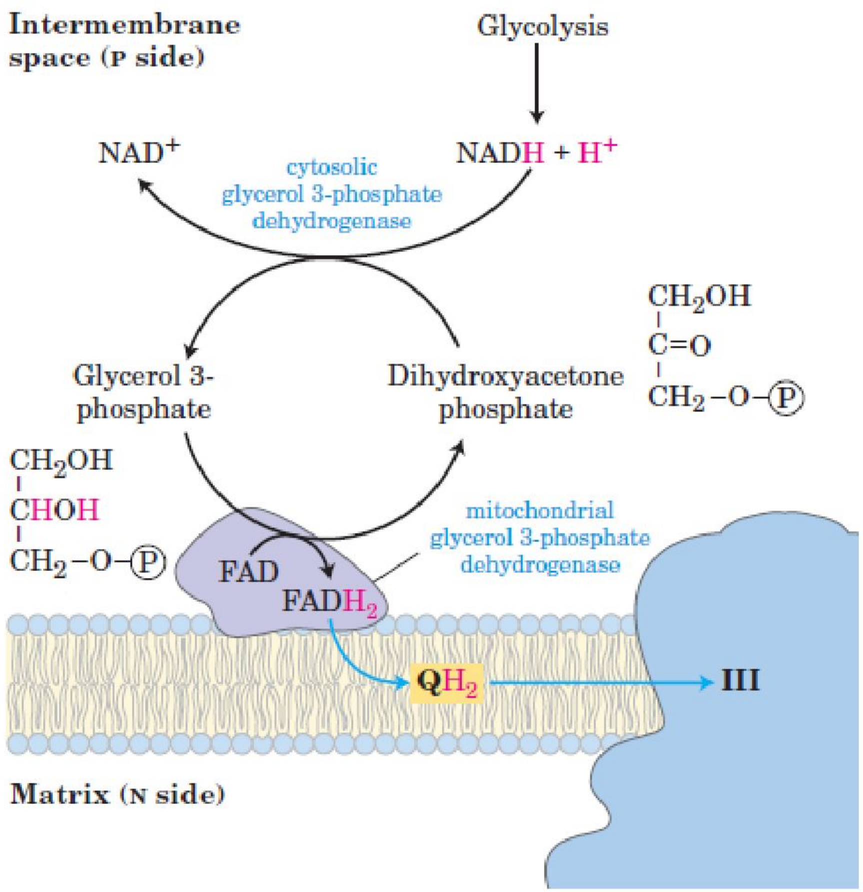


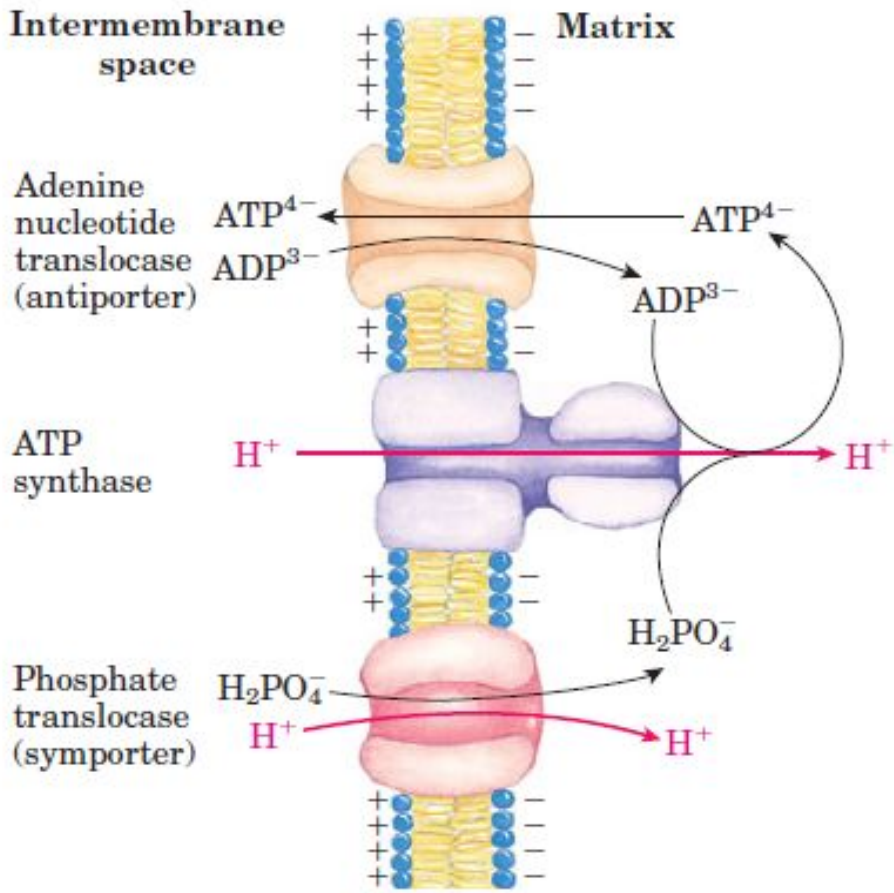
FIGURE 2 Electron carriers of the inner membrane of plant mitochondria. Electrons can flow through Complexes I, III, and IV, as in animal mitochondria, or through plant-specific alternative carriers by the paths shown with blue arrows.



Intermembrane space
Matrix
Malate–
α-ketoglutarate transporter
NAD⁺
H⁺ + NADH
Malate
malate dehydrogenase
Oxaloacetate
Glutamate
aspartate aminotransferase
α-Ketoglutarate
Aspartate
Glutamate-aspartate transporter



Intermembrane space (P side)
Glycolysis
NAD$^+$
NADH + H$^+$
cytosolic glycerol 3-phosphate dehydrogenase
CH_2OH
$C=O$
CH_2-O-P
Glycerol 3-phosphate
Dihydroxyacetone phosphate
CH_2OH
$CHOH$
CH_2-O-P
mitochondrial glycerol 3-phosphate dehydrogenase
FAD
$FADH_2$
QH_2
III
Matrix (N side)



Intermembrane space
Matrix
Adenine nucleotide translocase (antiporter)
ATP^{4-}
ADP^{3-}
ATP^{4-}
ADP^{3-}
ATP synthase
H^+
H^+
$H_2PO_4^-$
Phosphate translocase (symporter)
$H_2PO_4^-$
H^+
H^+

TABLE 19–5 ATP Yield from Complete Oxidation of Glucose

Process	Direct product	Final ATP
Glycolysis	2 NADH (cytosolic)	3 or 5*
	2 ATP	2
Pyruvate oxidation (two per glucose)	2 NADH (mitochondrial matrix)	5
Acetyl-CoA oxidation in citric acid cycle (two per glucose)	6 NADH (mitochondrial matrix)	15
	2 $FADH_2$	3
	2 ATP or 2 GTP	2
Total yield per glucose		30 or 32