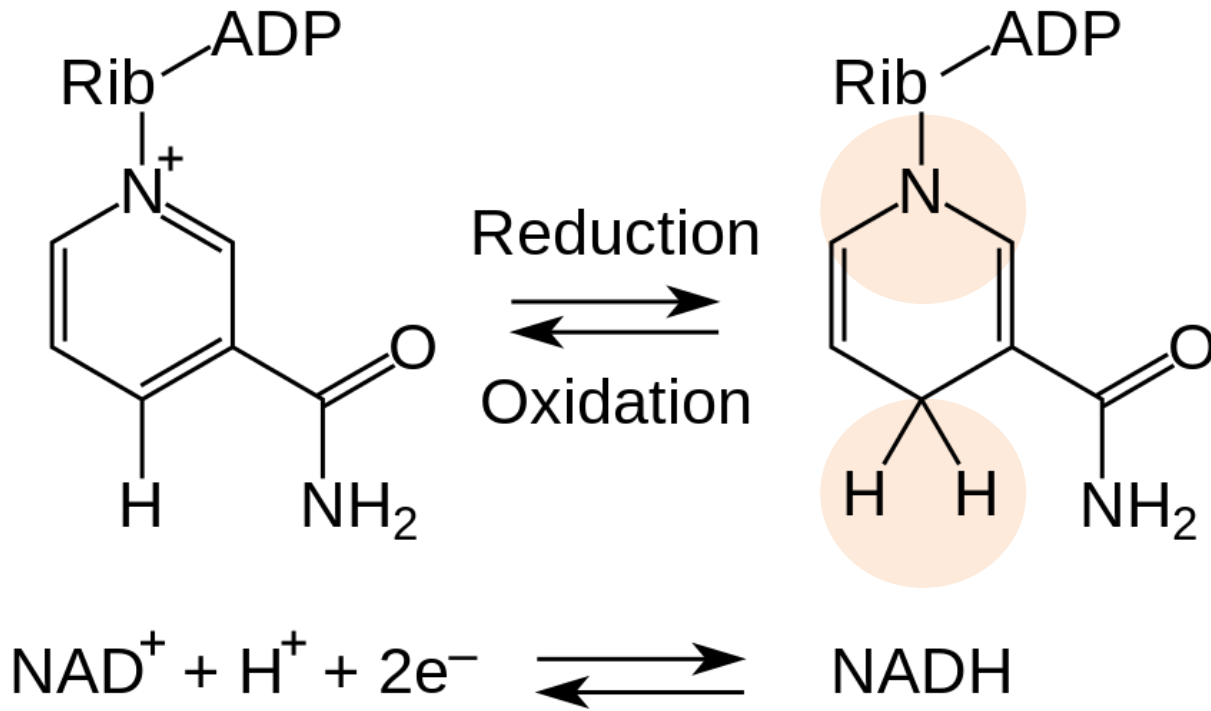
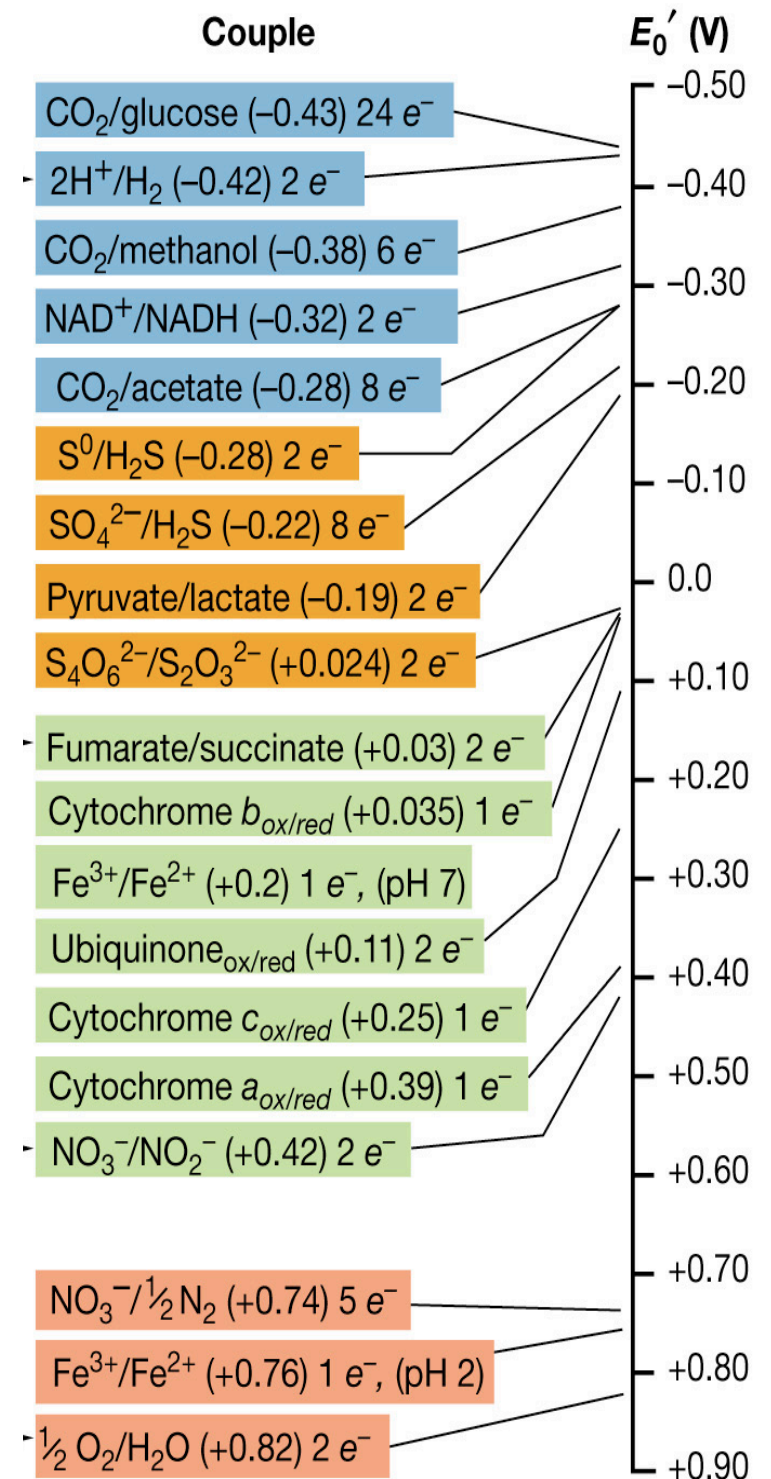


# 电子载体的化学性质和运载电子的方式各不相同

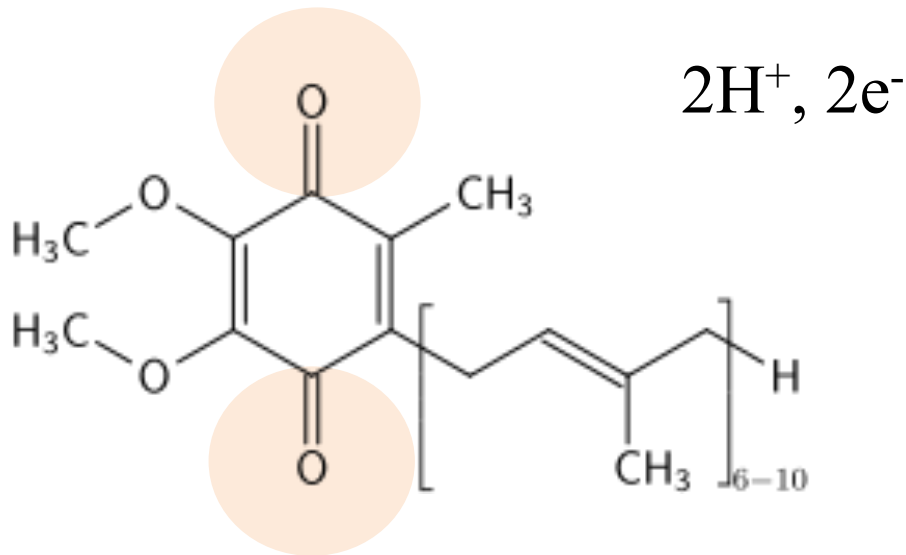


NAD<sup>+</sup>  
(Nicotinamide adenine dinucleotide)(细胞质)\*

- 烟酰胺腺嘌呤二核苷酸的烟酰胺环从供体获得两个电子和一个质子
- 烟酰胺腺嘌呤二核苷酸磷酸(NADP<sup>+</sup>)类似



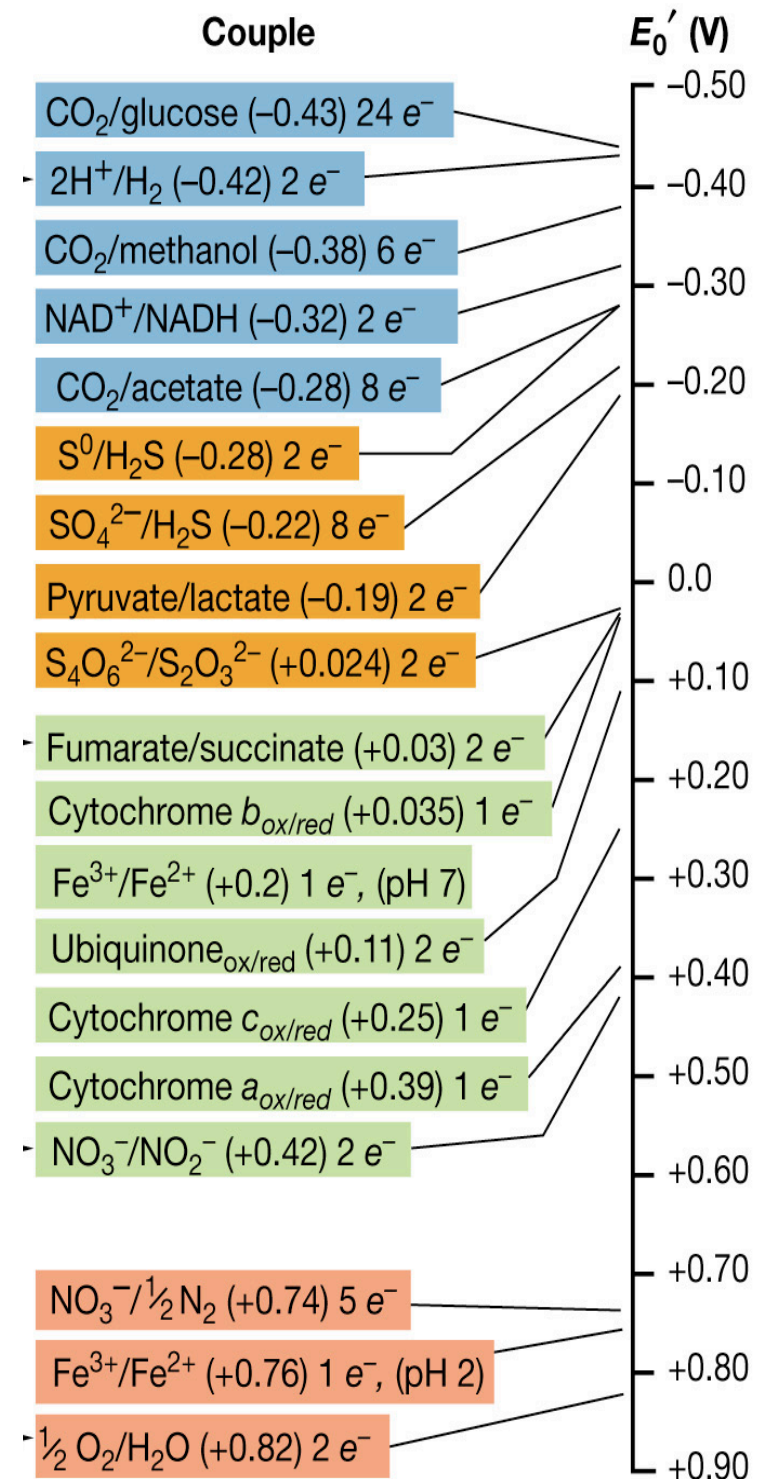
# 电子载体的化学性质和运载电子的方式各不相同



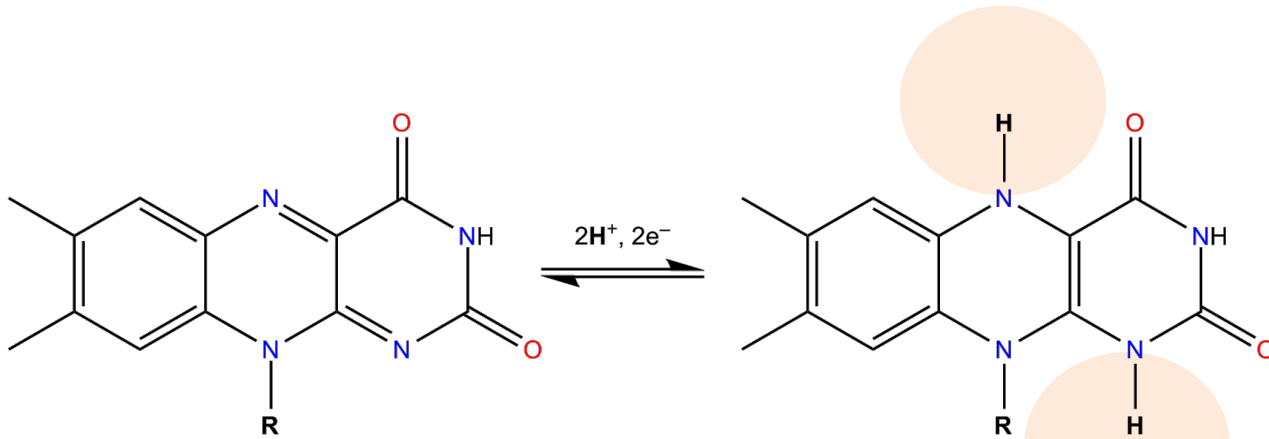
CoQ

(Coenzyme Q; ubiquinone) (脂溶性)\*

泛醌可从供体获得两个电子和两个质子

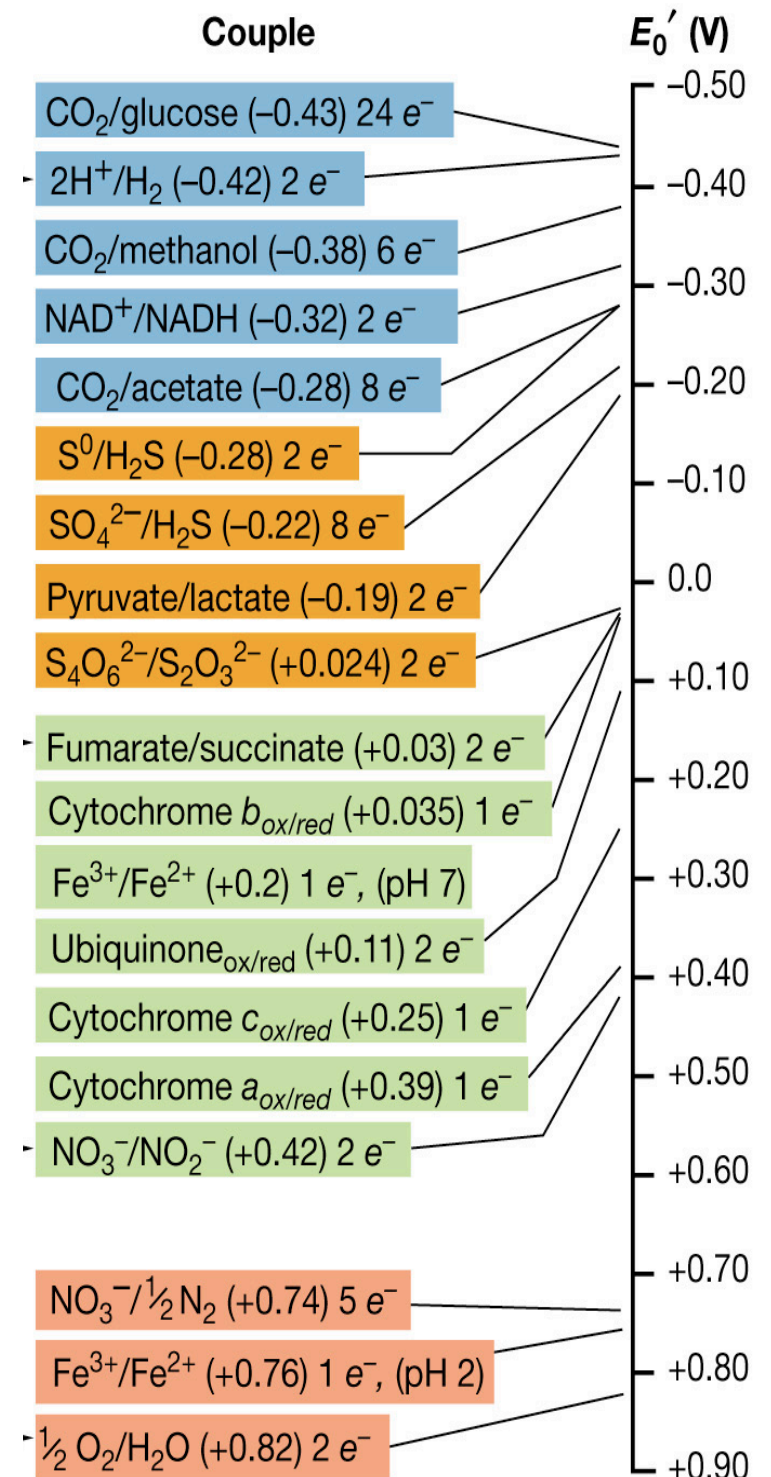


# 电子载体的化学性质和运载电子的方式各不相同

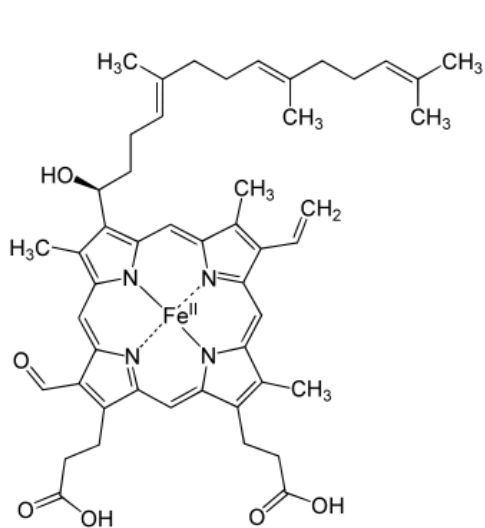


FAD  
(Flavin adenine dinucleotide)

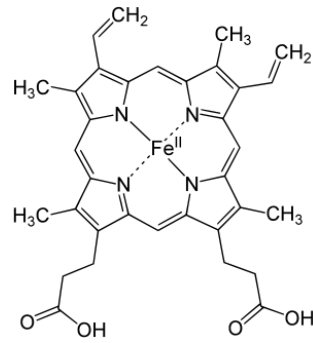
- 黄素腺嘌呤二核苷酸(FAD)的异咯嗪环从供体获得两个电子和两个质子；
- 黄素单核苷酸(FMN)类似；
- 含有FAD和FMN的蛋白质叫黄素蛋白\*



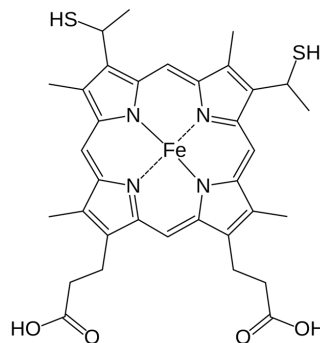
# 电子载体的化学性质和运载电子的方式各不相同



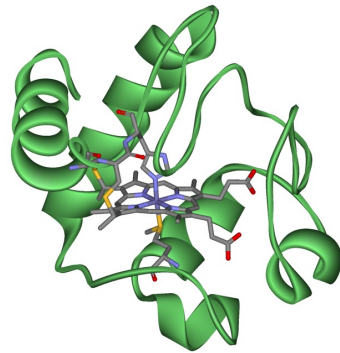
血红素a



血红素b



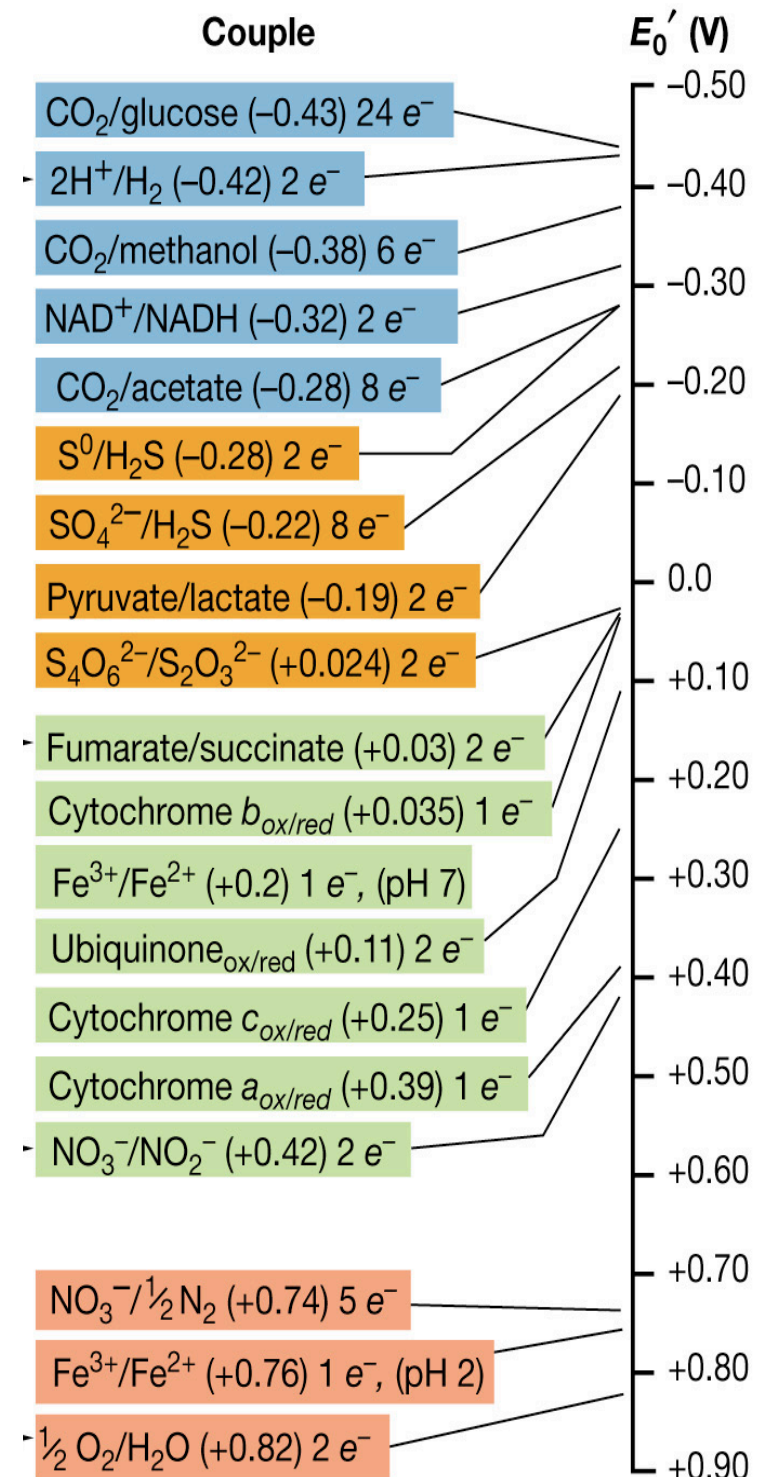
血红素c



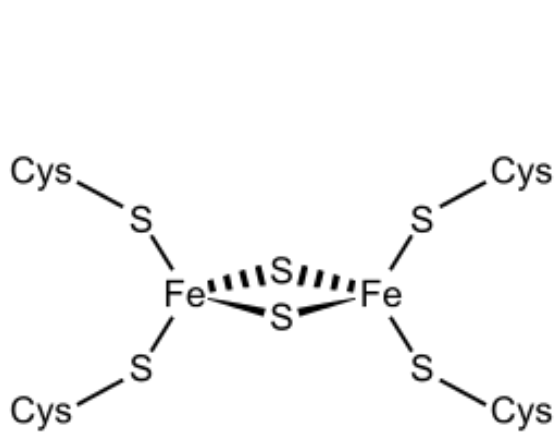
细胞色素c  
(含有血红素c)



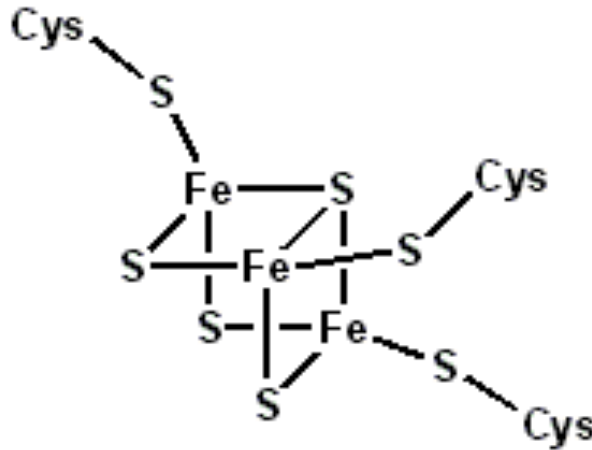
细胞色素(cytochrome)中，铁原子参与血红素或其他类似卟啉环的组成，由蛋白质和铁卟啉环组成。通过Fe原子的可逆的氧化还原反应，每次传递一个电子。



# 电子载体的化学性质和运载电子的方式各不相同



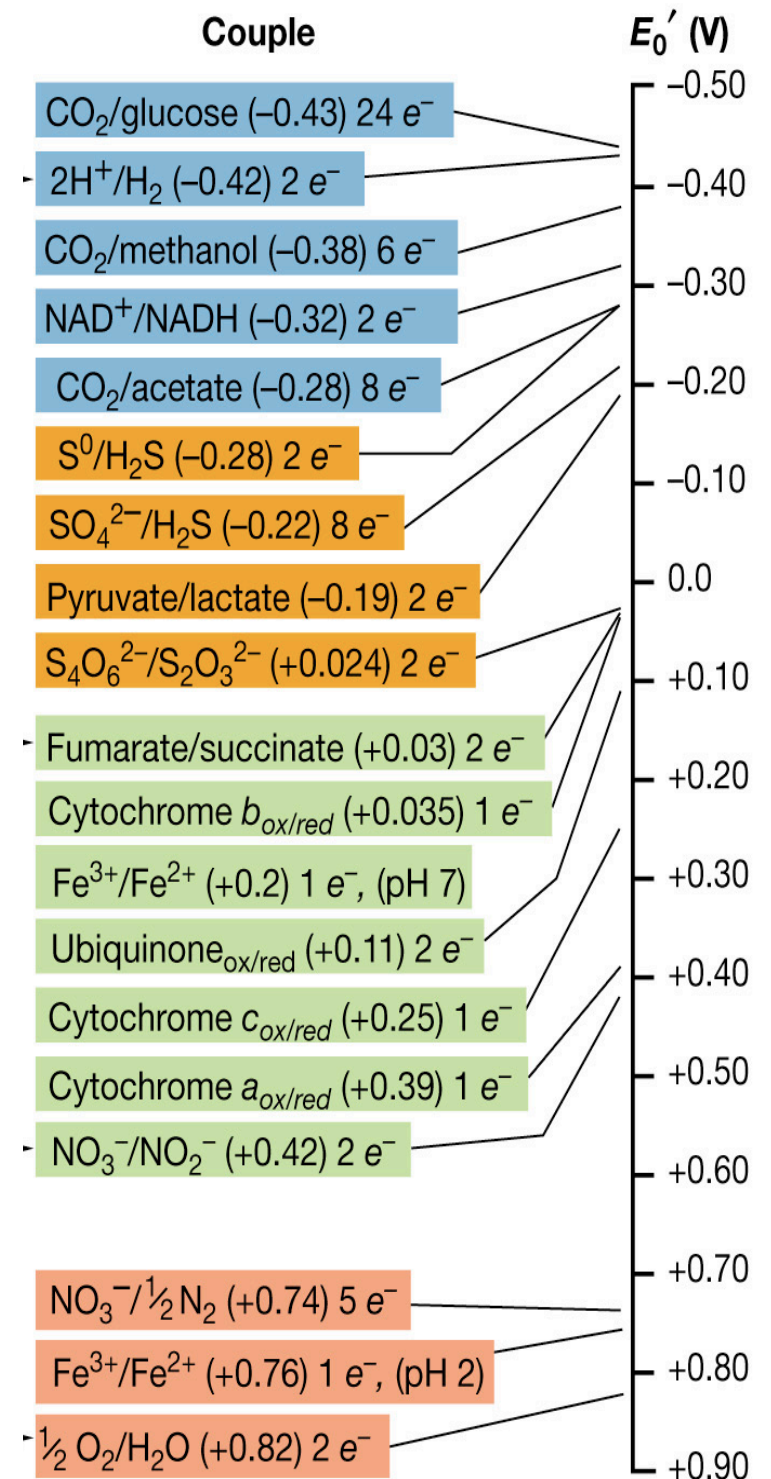
Fe<sub>2</sub>S<sub>2</sub> 铁氧还蛋白  
保守区域



Fe<sub>3</sub>S<sub>4</sub> 铁氧还蛋白  
保守区域



非血红素铁蛋白：含铁原子但无血红素的电子传递蛋白。例如：铁氧还蛋白(ferredoxin)，虽然不含血红素，但仍有可逆的氧化还原反应。Fd可分为Fe<sub>2</sub>S<sub>2</sub>、Fe<sub>4</sub>S<sub>4</sub>、Fe<sub>3</sub>S<sub>4</sub>等类型。



# *E. coli* 如何选择电子受体？\*

$O_2 > NO_3^- > DMSO$  (二甲基亚砷)  $> TMAO$  (三甲胺氮氧化物)  $>$  延胡索酸

TABLE 18-1. Characteristics of Electron Transport Systems in *E. coli*

Electron Acceptor	$\delta G^{0a}$ (kJ/mol)	Terminal Respiratory Enzyme	Operon	Chromosomal Location (min)
$O_2$	-233	Cytochrome <i>o</i> oxidase	<i>cyoABCDE</i>	10
$O_2$	-233	Cytochrome <i>d</i> oxidase	<i>cydAB</i>	17
$NO_3^-$	-144	Nitrate reductase	<i>narGHJI</i>	27
$NO_3^-$	-144	Nitrate reductase	<i>narZYWV</i>	33
DMSO	-92	DMSO/TMAO reductase	<i>dmsABC</i>	20
TMAO	-87	TMAO reductase	<i>torA</i>	28
Fumarate	-67	Fumarate reductase	<i>frdABCD</i>	94

<sup>a</sup>Free energy calculated by using NADH as an electron donor to the indicated electron acceptor.

能产生更多能量的电子受体被优先利用！

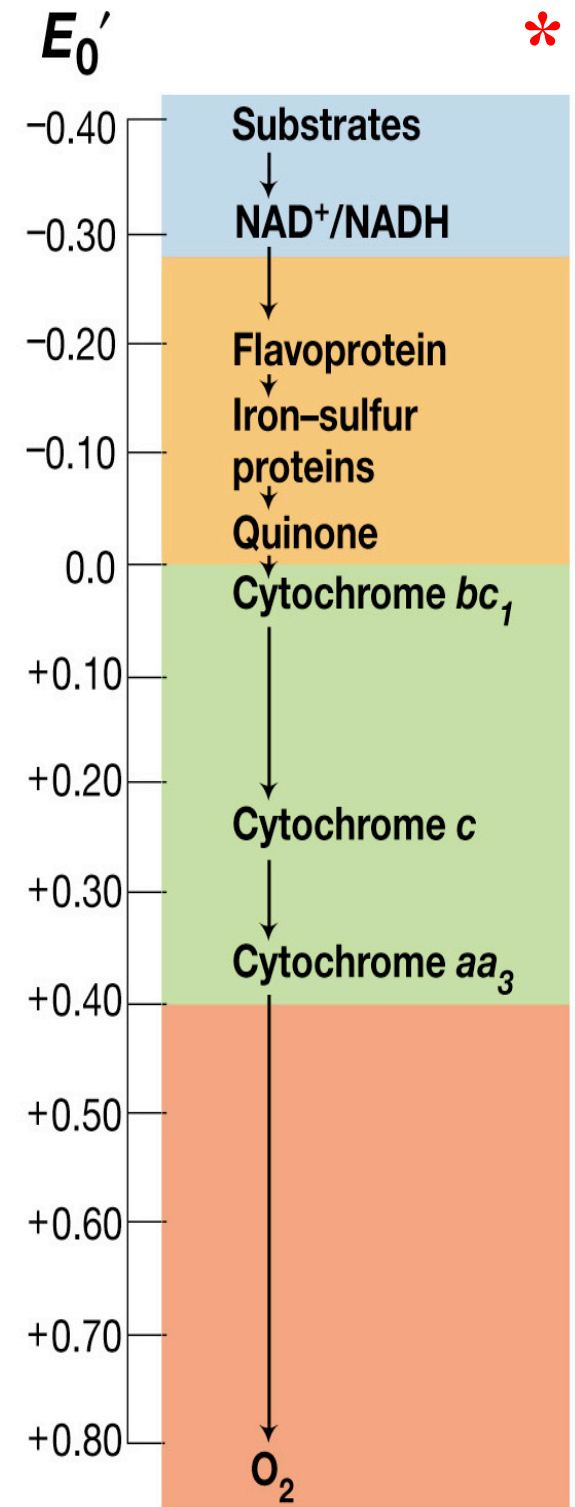
# 电子传递链/系统 (electron transport chain/system)

电子传递链/系统：电子从电子供体向最终电子受体的传递，要通过一系列的载体，这些电子载体组成的系统。

- 第一个载体有最负的 $E_0'$ ，每一个接下来的载体的 $E_0'$ 都依次升高（如右图）。
- 存储在发动电子流的氧化还原电对里的势能释放，用来形成ATP。



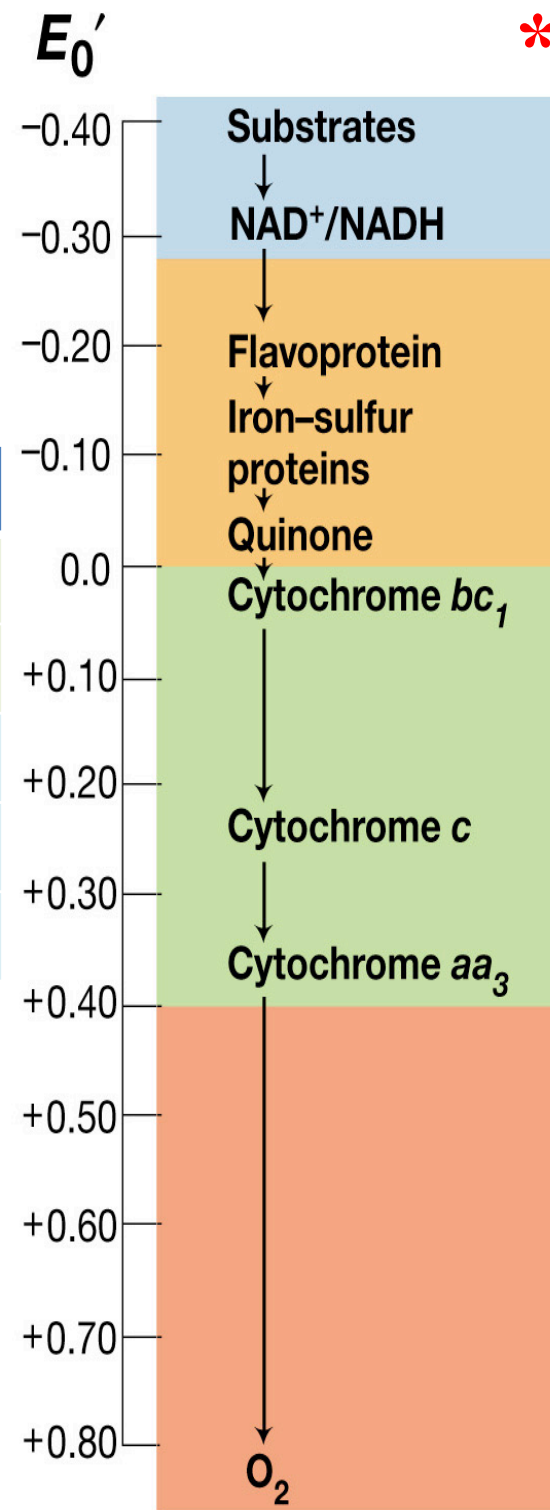
<https://www.bilibili.com/video/av926235438>



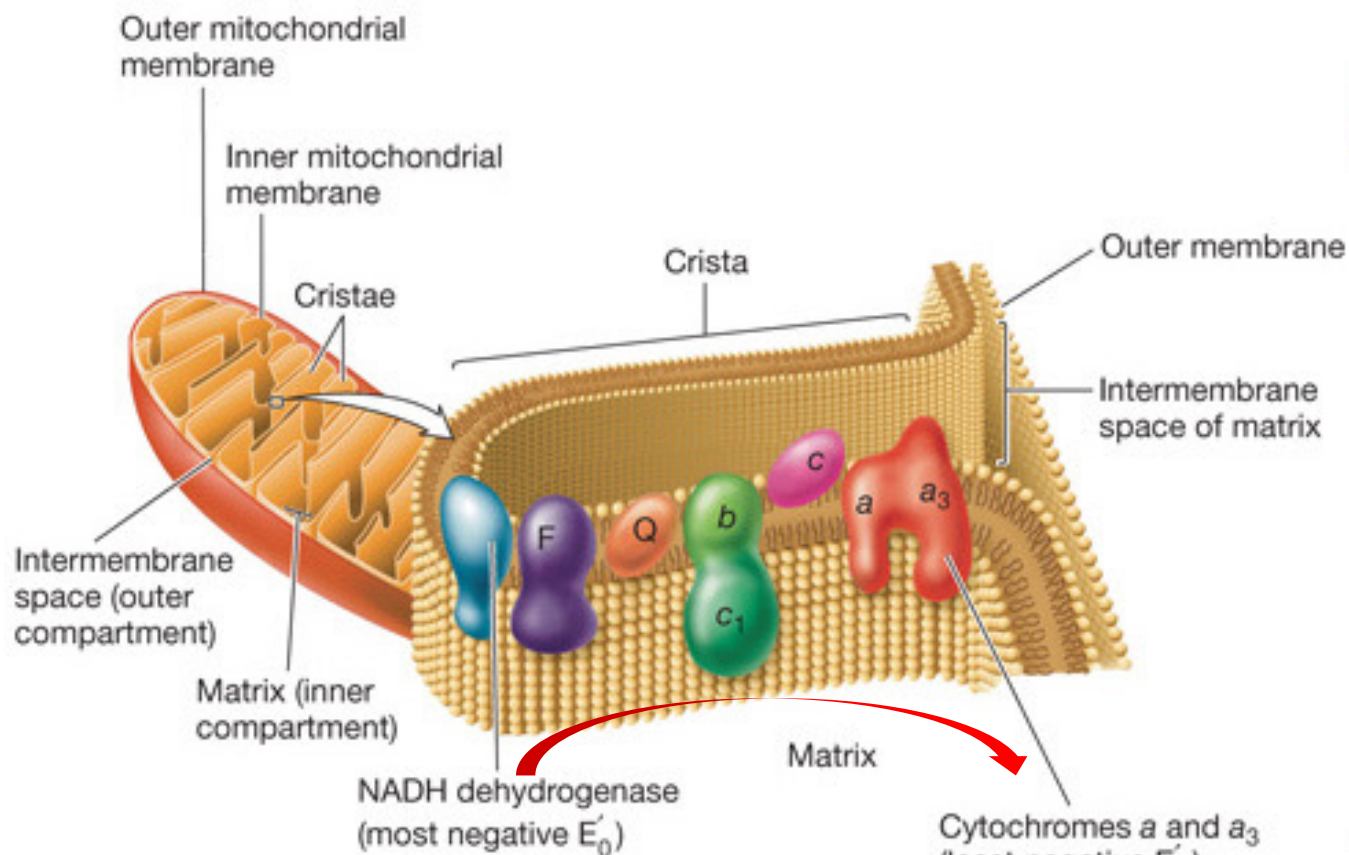
# 电子传递链/系统的亚细胞定位 (electron transport chain/system)

	营养类型	电子传递链位置
真核微生物	化能有机营养型	线粒体内膜
	光能营养型	叶绿体类囊体膜
原核微生物	有机营养型	质膜
	化能无机营养	质膜或内膜系统
	光能营养	质膜或内膜系统

线粒体和叶绿体都起源于革兰氏阴性菌



# 真核生物中化能有机营养型微生物的电子传递链在线粒体内膜

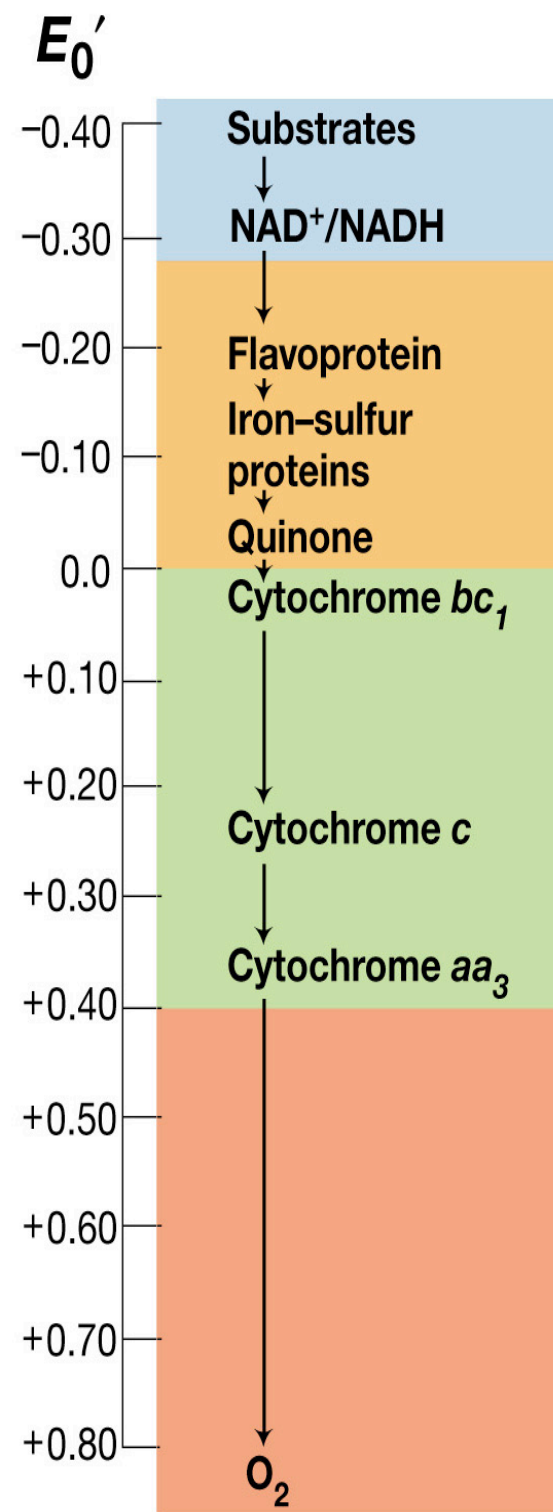


还原电势最负

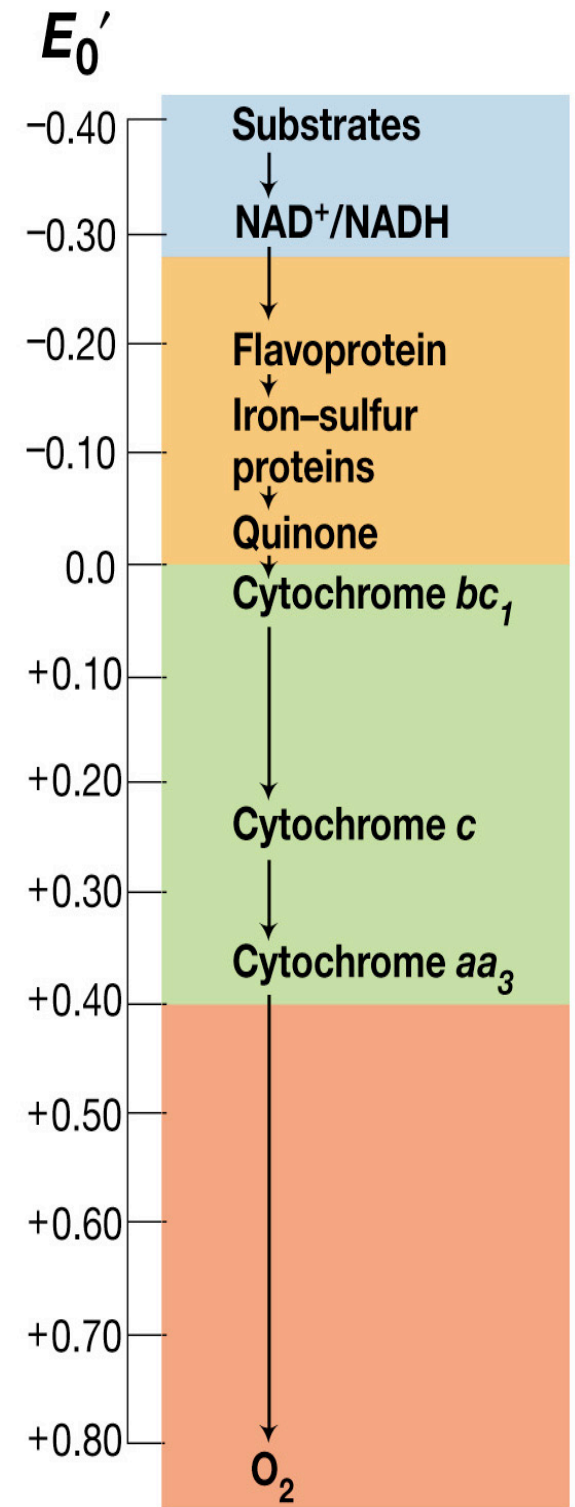
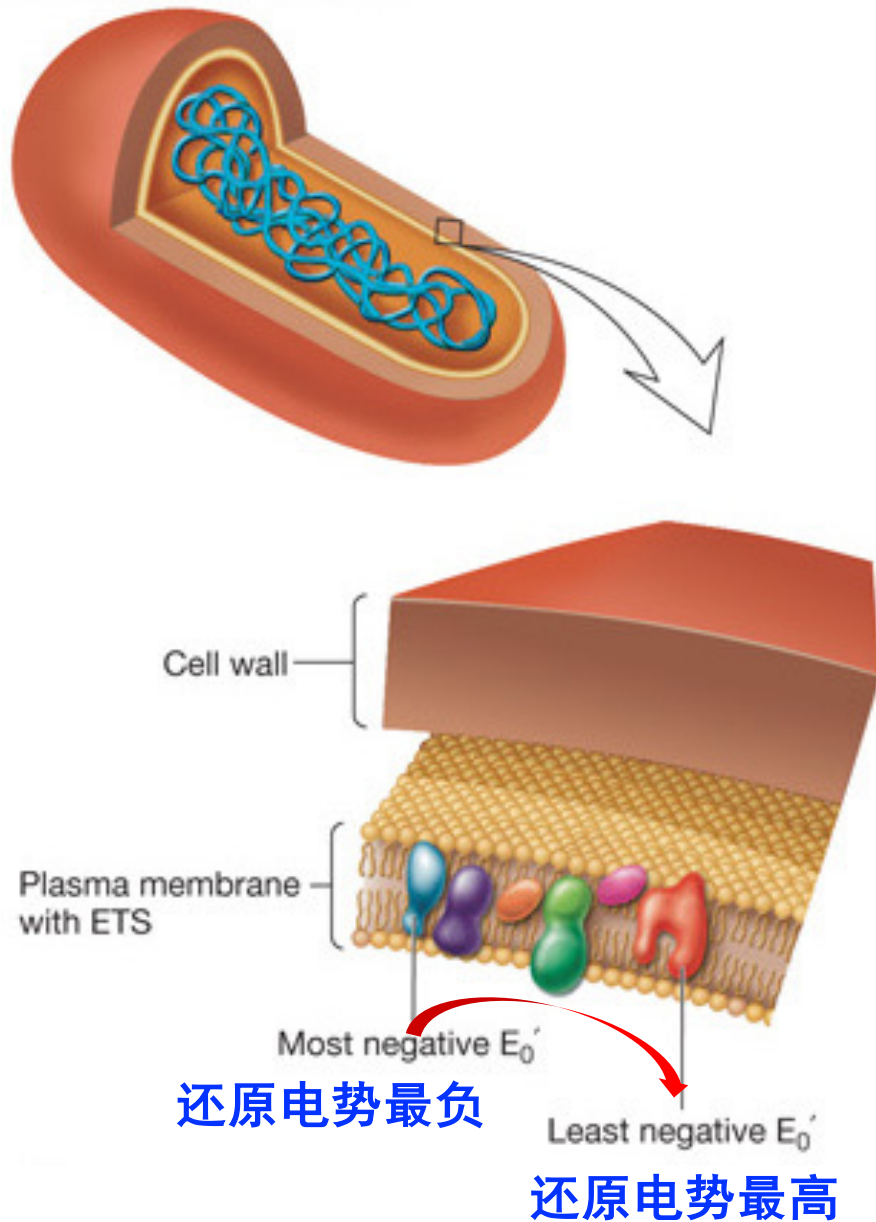
还原电势依次升高

- FMN
- Coenzyme Q
- Cytochrome  $c_1$
- Cytochrome c
- Cytochrome b

(a)



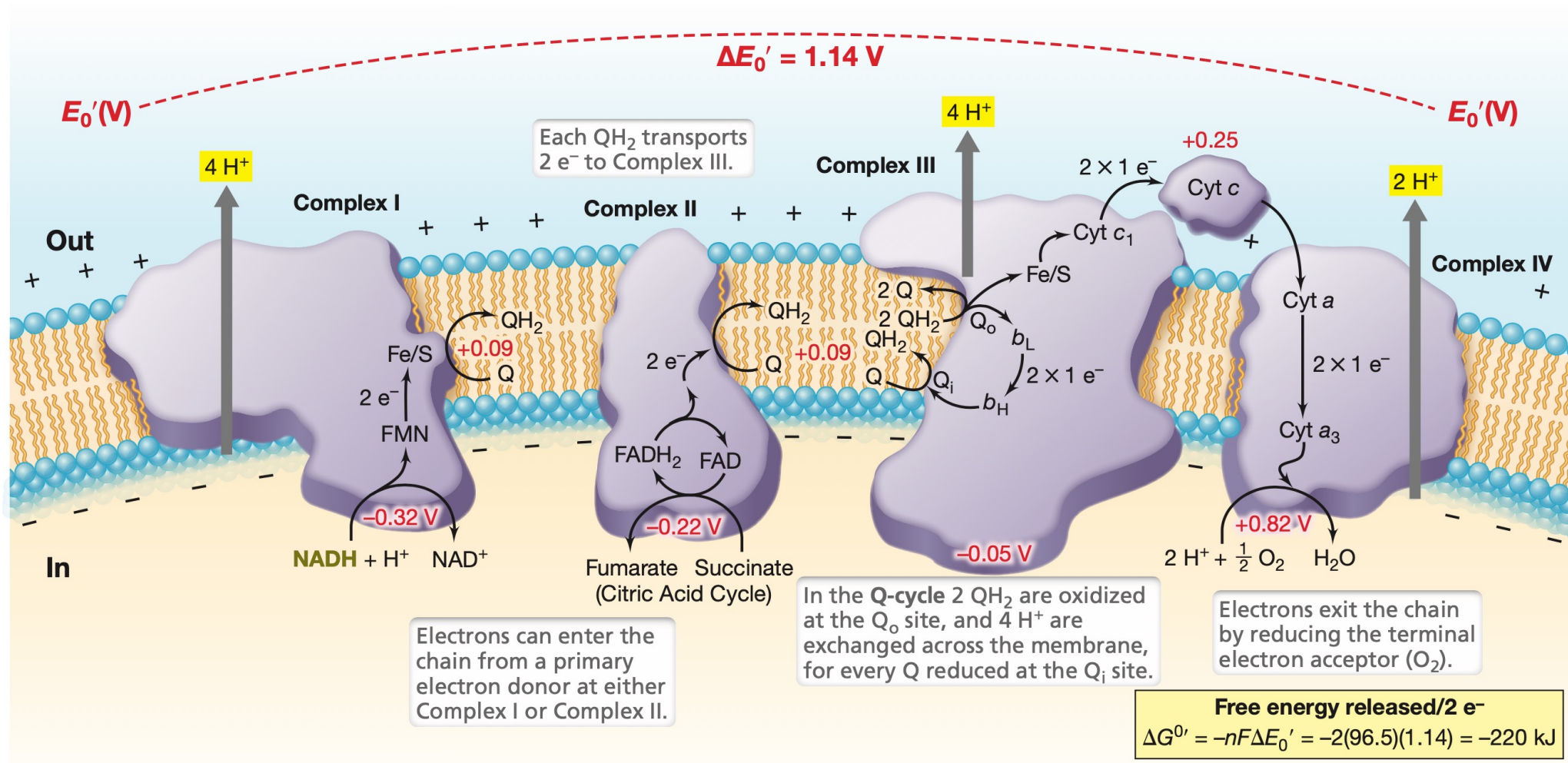
# 原核生物的电子传递链(质膜)





# 还原电势越来越高

NADH --- 黄素单核苷酸FMN --- 辅酶Q --- 细胞色素 $bc_1$  --- 细胞色素 $c$  --- 细胞色素 $aa_3$



(脱氮副球菌 *Paracoccus denitrificans*)

# *E. coli* 等有两种类型的末端氧化酶



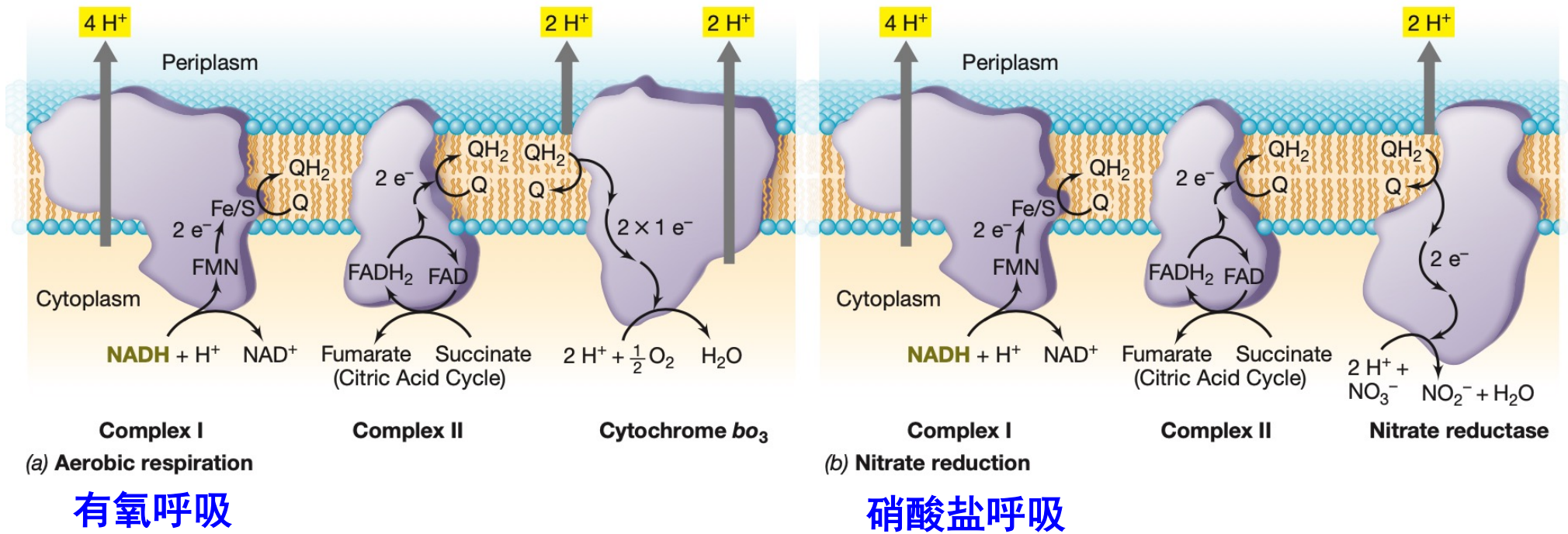
## (1) *bo-type* (对数期、高氧)

- a heme copper protein
- an integral membrane protein
- subunit that contains oxygen binding site has twelve membrane spanning domains
- a redox driven proton pump.

## (2) *bd-type* (稳定期、低氧)

- Not structurally related to the *bo-type* or *mitochondrial type* oxidases
- **unique to bacteria**
- **a very high affinity for O<sub>2</sub>**

# *E. coli* 的有氧呼吸和硝酸盐呼吸



## 真核生物呼吸链的蛋白质组成 (组分I-IV)

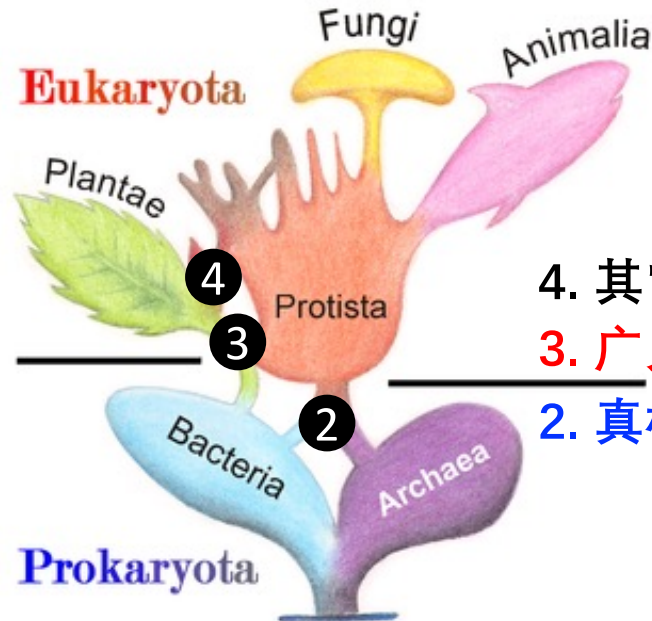
**Protein Components of the Mitochondrial Electron-Transfer Chain**

Enzyme complex	Mass (kDa)	Number of subunits*	Prosthetic group(s)
I NADH dehydrogenase	850	42 (14)	FMN, Fe-S
II Succinate dehydrogenase	140	5	FAD, Fe-S
III Ubiquinone: cytochrome <i>c</i> oxidoreductase	250	11	Hemes, Fe-S
Cytochrome <i>c</i> <sup>†</sup>	13	1	Heme
IV Cytochrome oxidase	160	13 (3–4)	Hemes; Cu <sub>A</sub> , Cu <sub>B</sub>

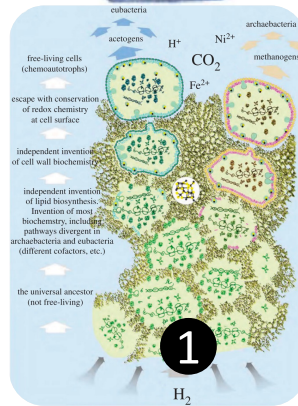
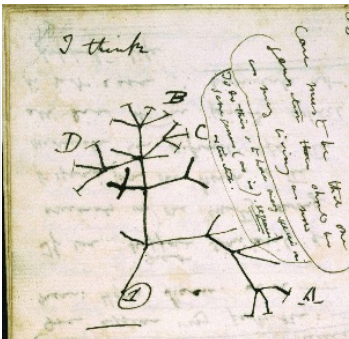
\*Numbers of subunits in the bacterial equivalents in parentheses.

<sup>†</sup>Cytochrome *c* is not part of an enzyme complex; it moves between Complexes III and IV as a freely soluble protein.

# 原核生物与生命树的发生和发展



- 4. 其它光合藻类 (第二次内共生)
- 3. 广义植物起源 (蓝细菌的内共生)
- 2. 真核生物起源 (古菌内吞alpha变形菌)



## 1.2 细菌和古菌的独立进化

## 1.1 祖先细胞的起源 (非自生细胞)

# Engineering yeast endosymbionts as a step toward the evolution of mitochondria

Angad P. Mehta<sup>a,1</sup>, Lubica Supekova<sup>a,1</sup>, Jian-Hua Chen<sup>b</sup>, Kersi Pestonjamas<sup>c</sup>, Paul Webster<sup>d</sup>, Yeonjin Ko<sup>a</sup>, Scott C. Henderson<sup>c</sup>, Gerry McDermott<sup>b</sup>, Frantisek Supek<sup>e,2</sup>, and Peter G. Schultz<sup>a,2</sup>

<sup>a</sup>Department of Chemistry, The Scripps Research Institute, La Jolla, CA 92037; <sup>b</sup>Department of Anatomy, School of Medicine, University of California, San Francisco, CA 94158; <sup>c</sup>Core Microscopy Facility, The Scripps Research Institute, La Jolla, CA 92037; <sup>d</sup>Department of Advanced Imaging and Microscopy, Oak Crest Institute of Science, Monrovia, CA 91016; and <sup>e</sup>Department of General Medical Biology, Genomics Institute of the Novartis Research Foundation, La Jolla, CA 92121

Contributed by Peter G. Schultz, September 14, 2018 (sent for review July 31, 2018; reviewed by Jay D. Keasling and David R. Liu)

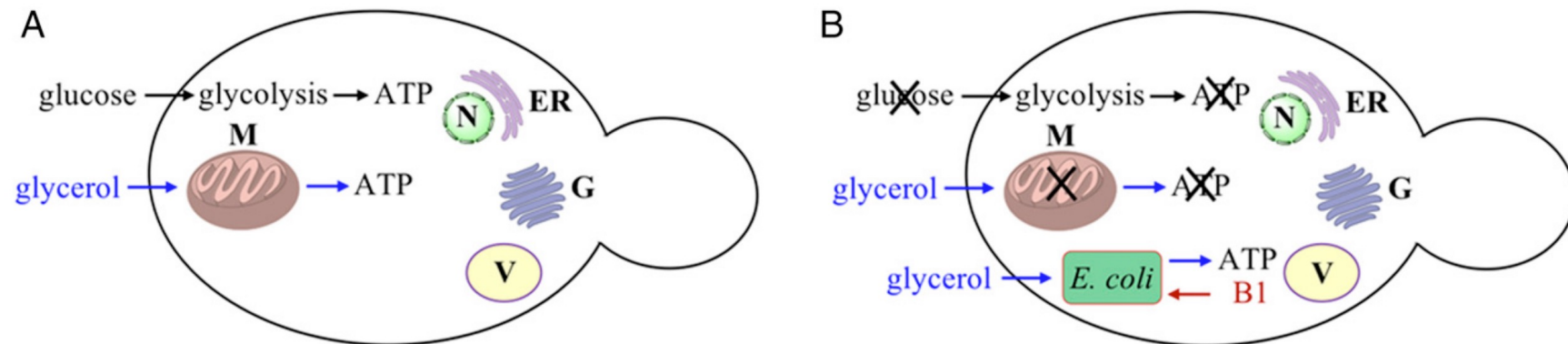


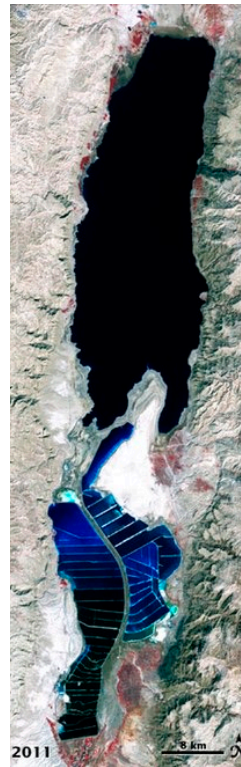
Fig. 1. Strategy to engineer *S. cerevisiae*–*E. coli* endosymbiont chimera. (A) Wild-type *S. cerevisiae* can grow on medium with glucose or glycerol due to ATP production by **glycolysis in the cytoplasm** and **oxidative phosphorylation in mitochondria**. (B) Yeast cells with a **defect in oxidative phosphorylation cannot utilize glycerol for ATP synthesis and cannot grow in the absence of glucose**. Introduction of *E. coli*-expressing ADP/ATP translocase and SNARE proteins into such mutant yeast can restore yeast growth with glycerol as the sole carbon source. Growth of intracellular *E. coli* is dependent on thiamin diphosphate (vitamin B1) provided by yeast. ER, endoplasmic reticulum; G, Golgi apparatus; M, mitochondria; N, nucleus; V, vacuole.

# 生境多样性

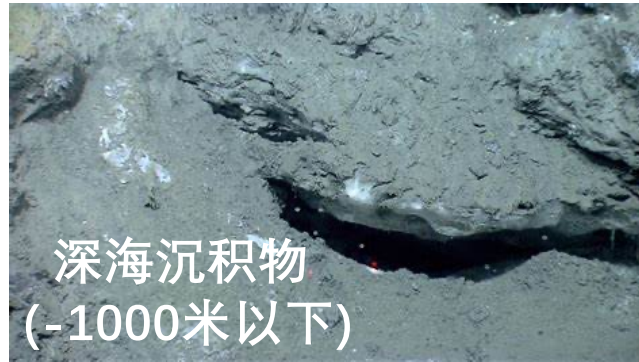
## 微生物多样性



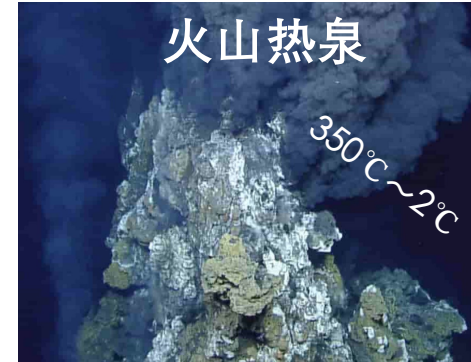
平流层  
(41千米)



死海  
(-304米)(年均降水量低于0.1毫米)



深海沉积物  
(-1000米以下)



火山热泉

350°C~2°C



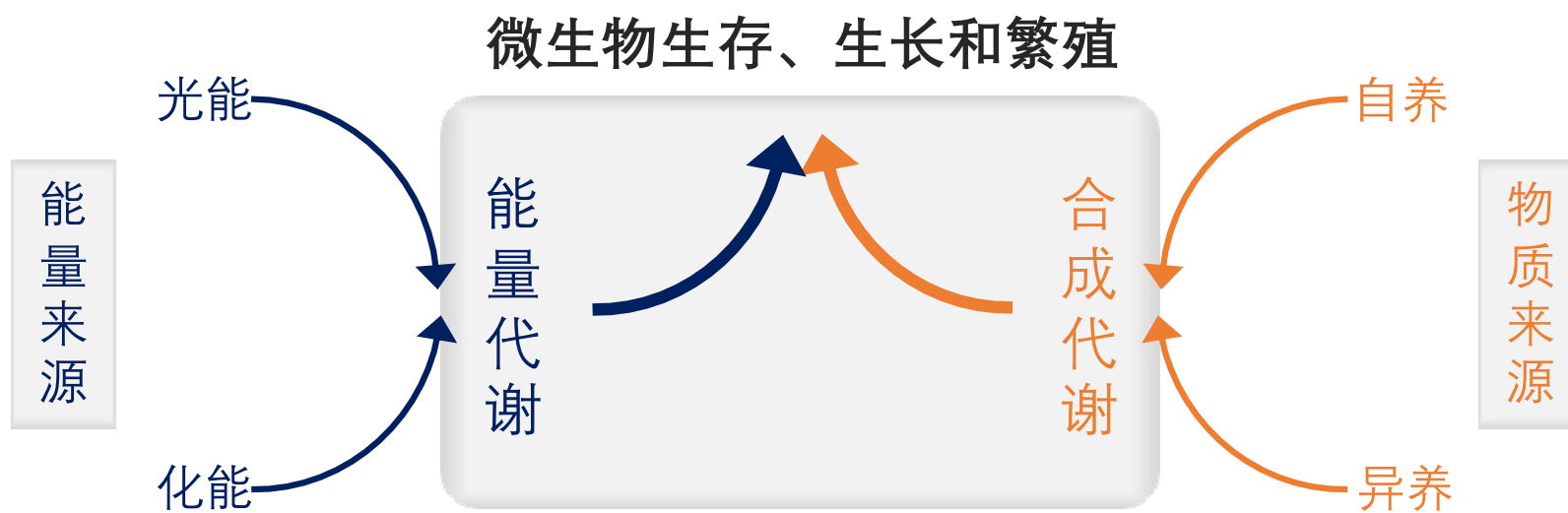
阿塔卡马沙漠

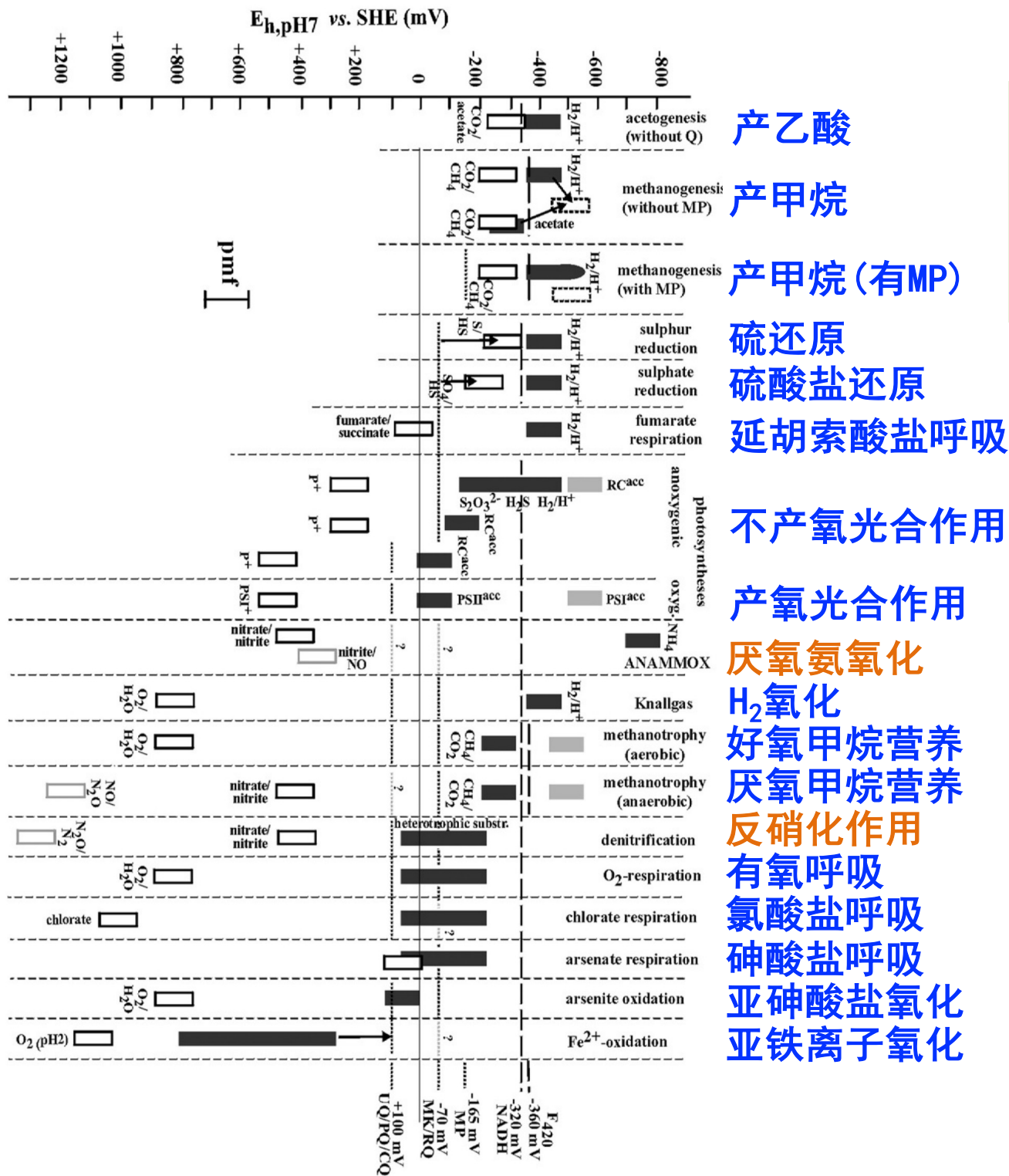
(年均降水量低于0.1毫米)



喜马拉雅山无植被土壤  
(海拔5100米以上)

# 能量代谢 (多样性与规律)





自然界存在多种多样的基于电子传递链的化学渗透系统

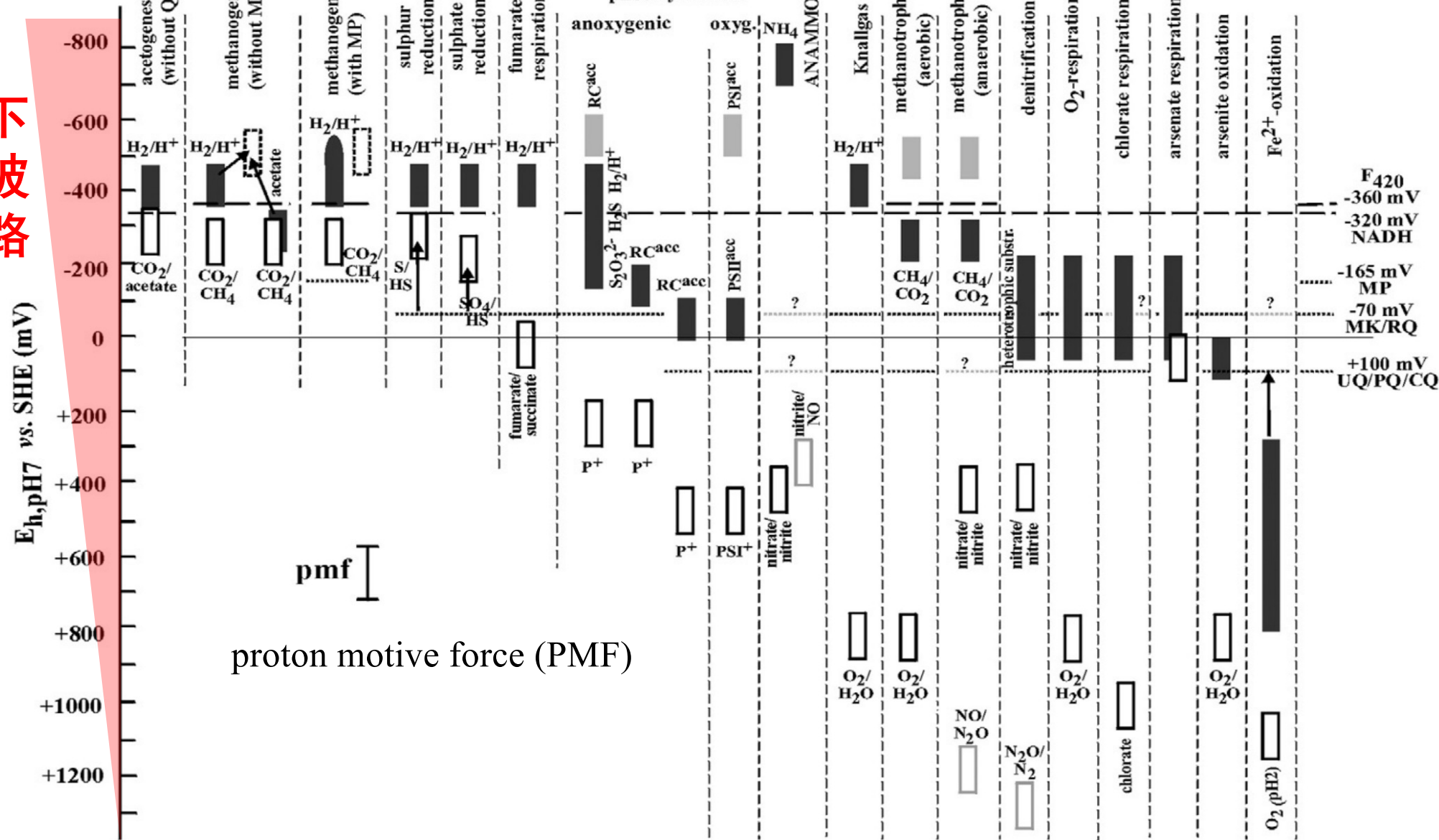
与生物的生存环境和适应机制紧密相关

还原底物

氧化底物

下坡路

$E_{h,pH7}$  vs. SHE (mV)



还原底物

氧化底物

Useful conversions between electrochemical parameters and Gibbs free energy.

---

Effective electrochemical potential  $E_h$  at pH 7 of a redox compound:

$$(1) E_{h,7} = E_{m,7} + 59 \text{ mV}/n * \log ([\text{ox}]/[\text{red}])$$

with  $E_{m,7}$  denoting the redox midpoint potential at pH 7

and  $n$ , number of transferred electrons

Electrochemical driving force for redox equilibrations

between a donor (D) and an acceptor (A) molecule:

$$(2) \Delta E_h = E_h (A) - E_h (D)$$

Gibbs free energy of redox reaction:

$$(3) \Delta G = -nF\Delta E_h$$

with  $n$ , number of transferred electrons and  $F$ , Faraday constant

---

## 氧化还原底物的多样性对产生能量多少的影响

在给定的环境条件下， $\Delta G$  受以下因素影响：



1. 电子供体与电子受体之间的标准还原电势差 ( $\Delta E_{m,7}$ )
2. 电子供体与电子受体的绝对浓度
3. 电子供体与电子受体的氧化/还原水平

下坡路

$E_{h,pH7}$  vs. SHE (mV)

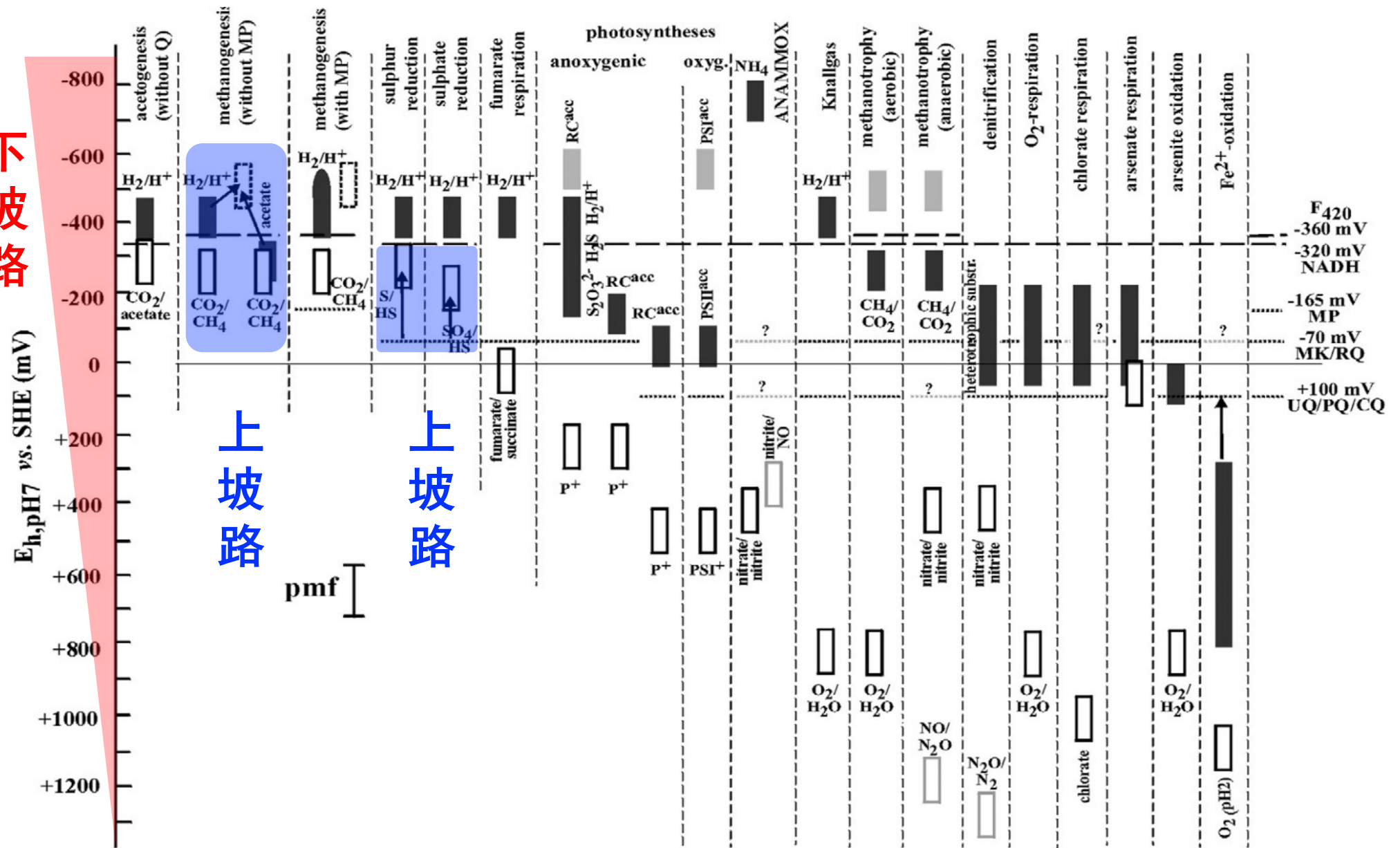
上坡路

上坡路

pmf

还原底物

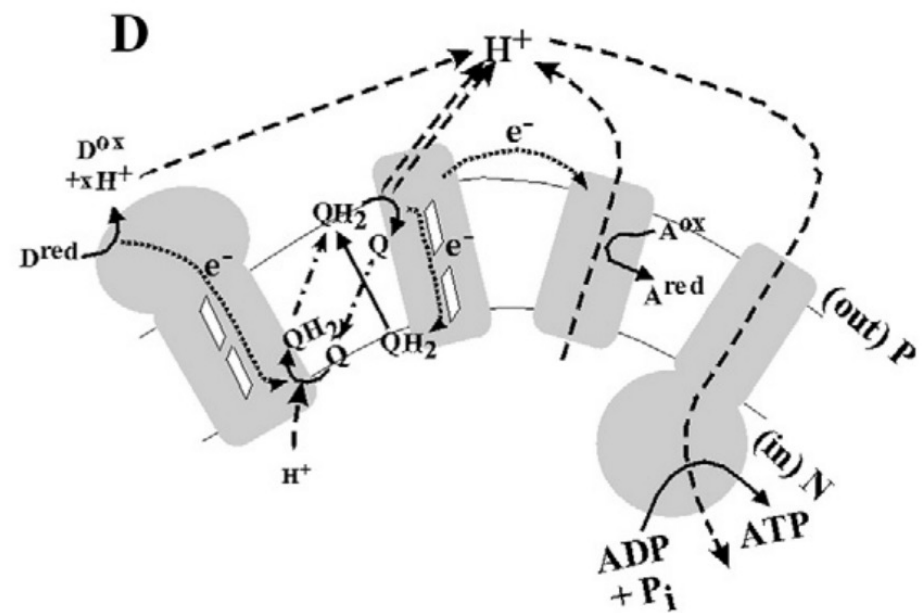
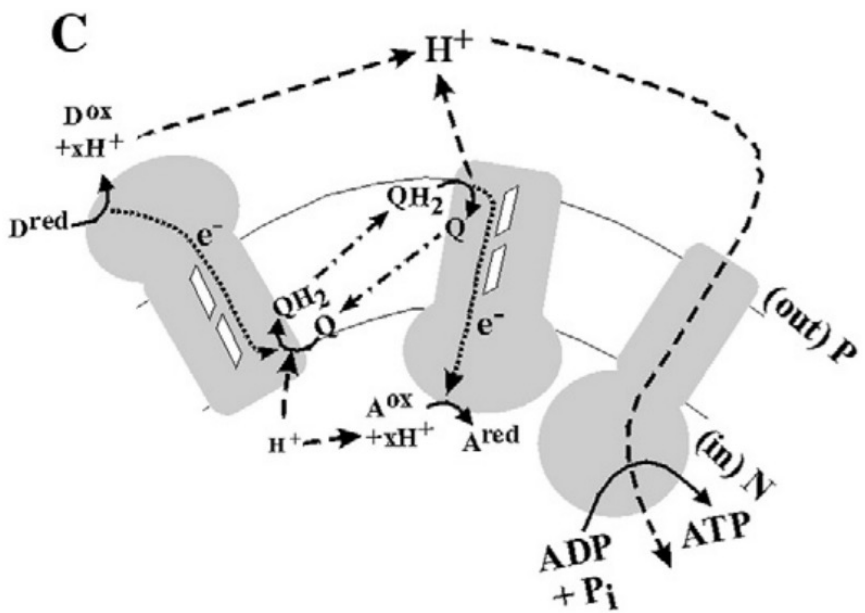
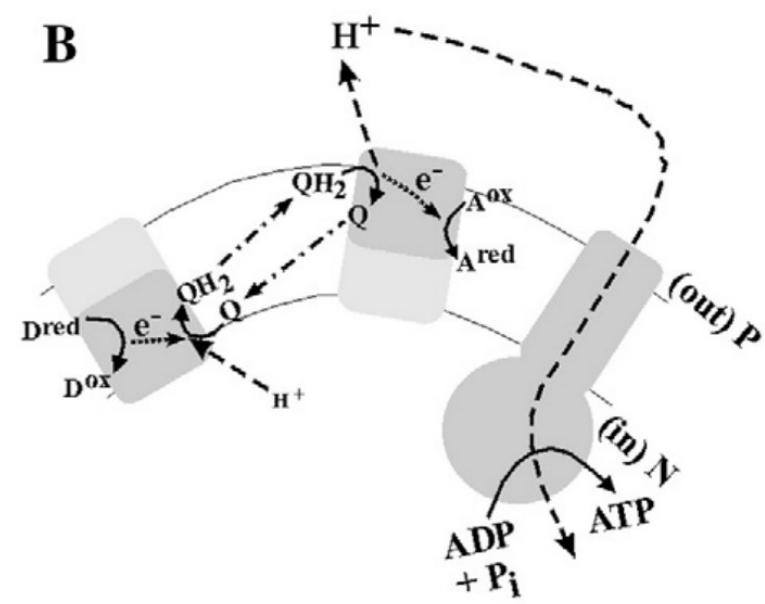
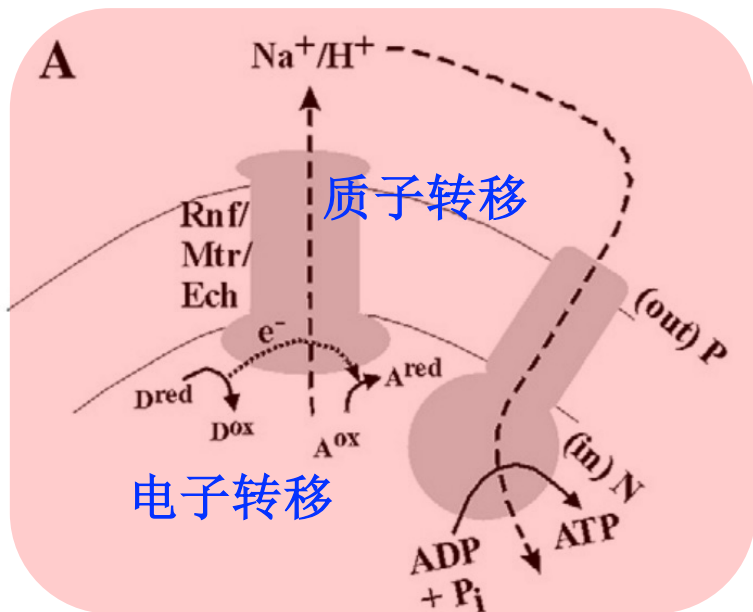
氧化底物

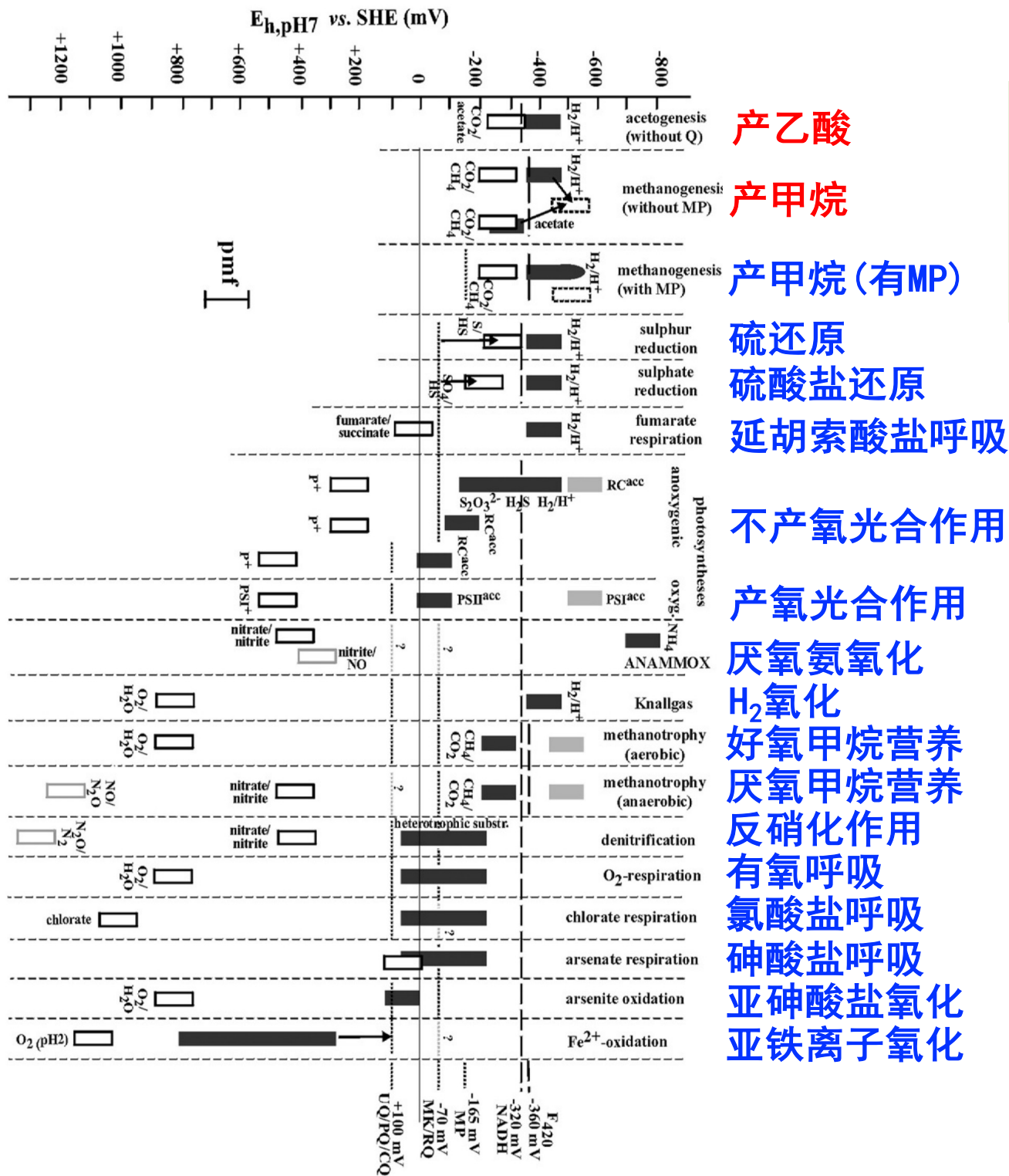




# 电子传递链的复杂程度不同

不涉及脂溶性的膜上电子载体





自然界存在多种多样的基于电子传递链的化学渗透系统

与生物的生存环境和适应机制紧密相关

还原底物

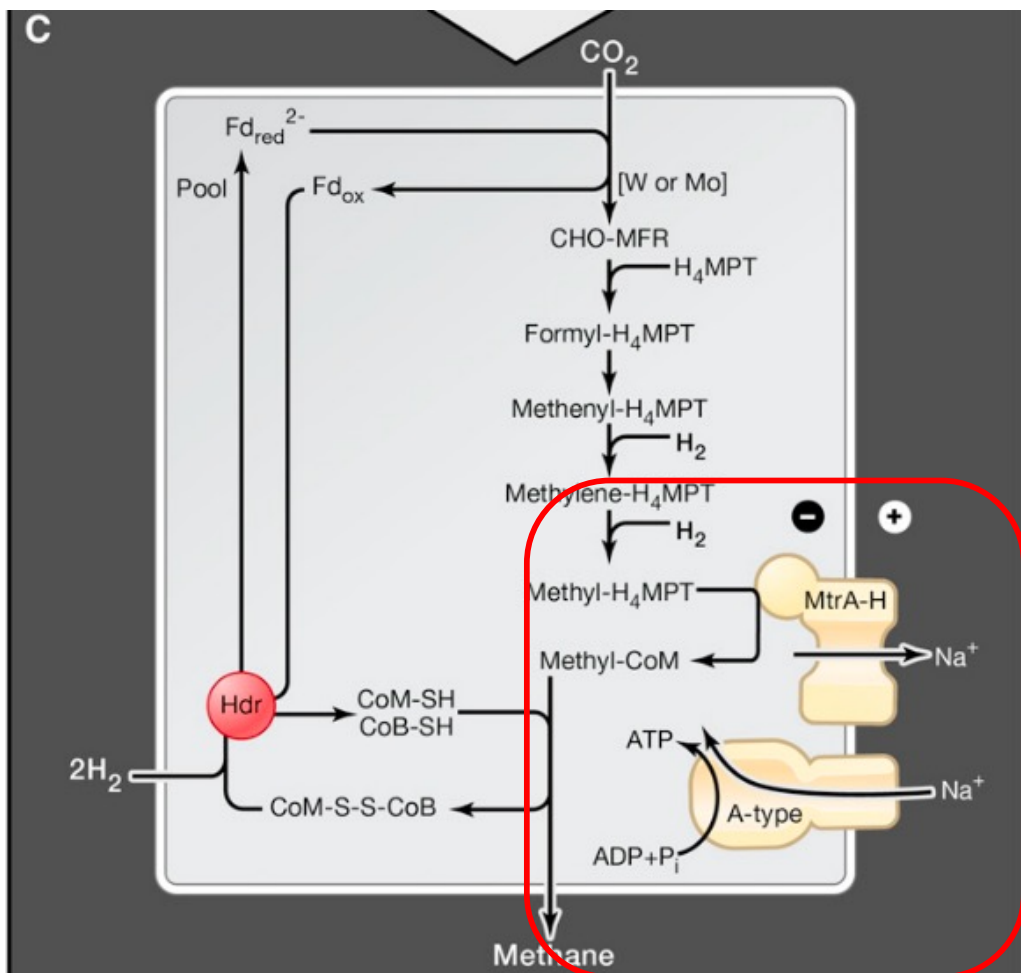
氧化底物

# 超短电子传递链：不涉及脂溶性的膜上电子载体

电子供体与电子受体之间的还原电势差 $\Delta E_m$ 驱动 $\text{Na}^+$ 梯度的建立

## 产甲烷古菌

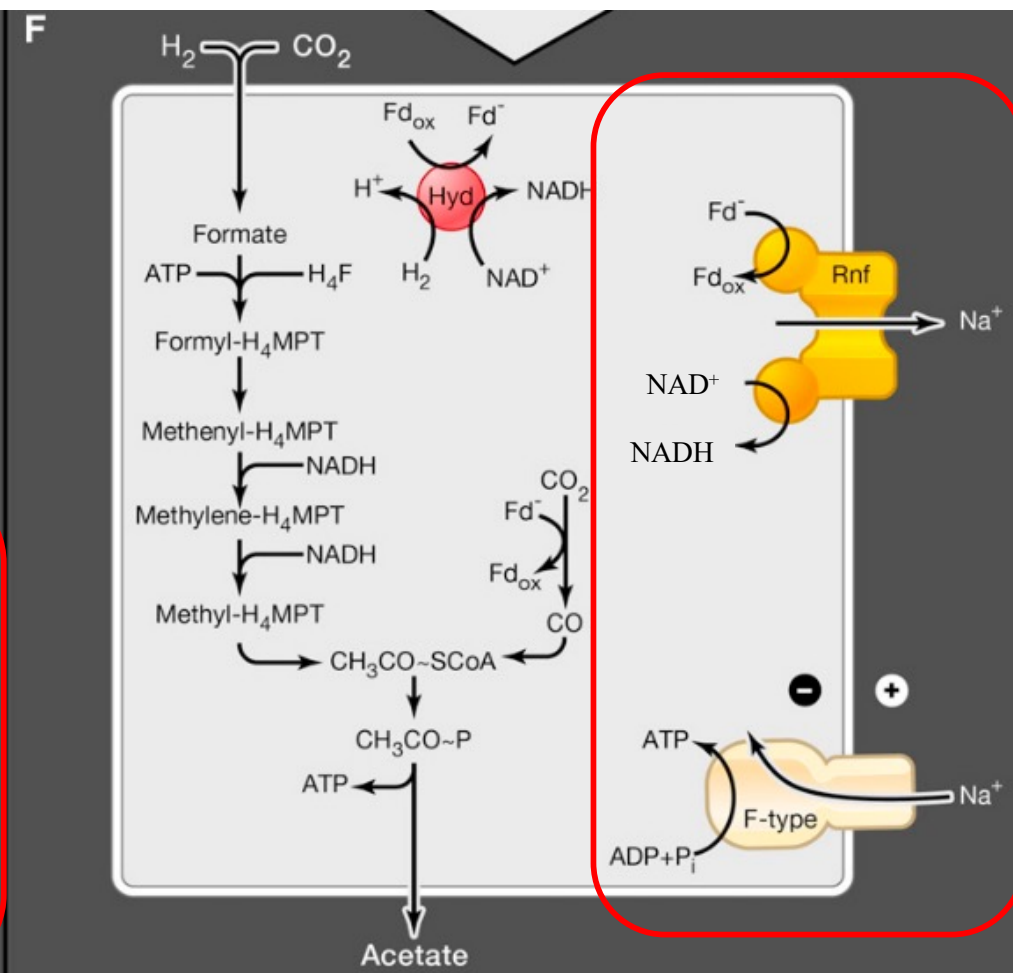
$\text{H}_2/\text{H}^+$  和  $\text{CO}_2/\text{CH}_4$  之间的 $\Delta E_m = 180 \text{ mV}$



跨膜的甲基转移酶MtrA-H

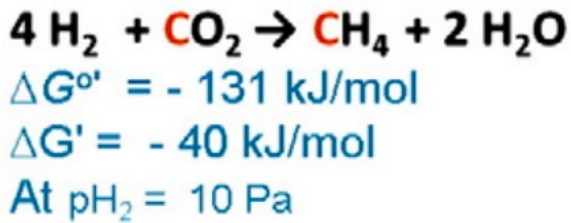
## 产乙酸细菌

$\text{H}_2/\text{H}^+$  和  $\text{CO}_2/\text{acetate}$  之间的 $\Delta E_m = 130 \text{ mV}$



跨膜的Fd-NAD氧化还原酶Rnf

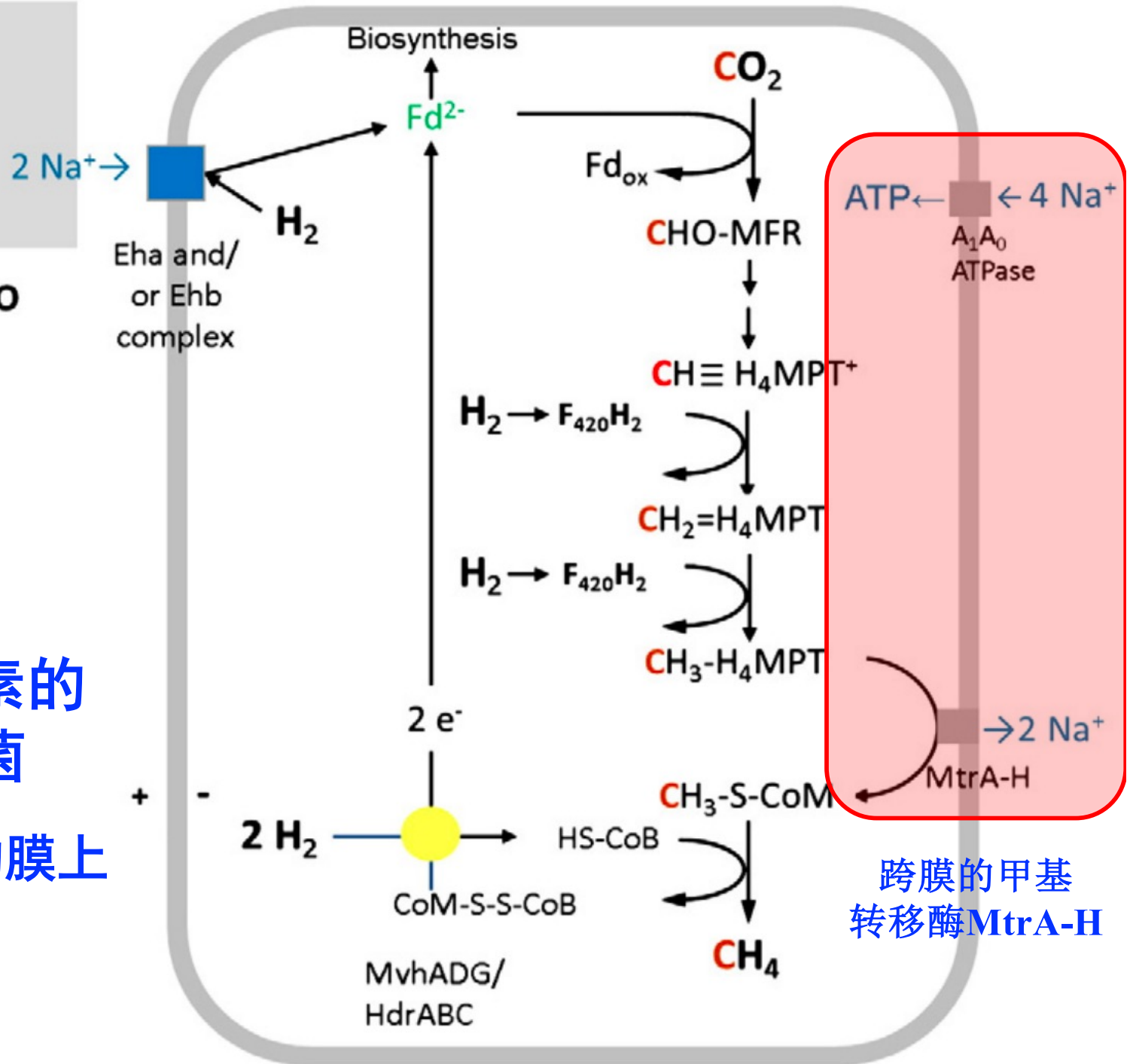
*Methanobacteriales*  
*Methanococcales*  
*Methanopyrales*  
*Methanomicrobiales*  
 (all without cytochromes)



0.5 ATP/CH<sub>4</sub>

不含细胞色素的  
产甲烷古菌

(不涉及脂溶性的膜上  
电子载体)



跨膜的甲基  
转移酶MtrA-H

# 伍氏醋酸杆菌

*Acetobacterium woodii*

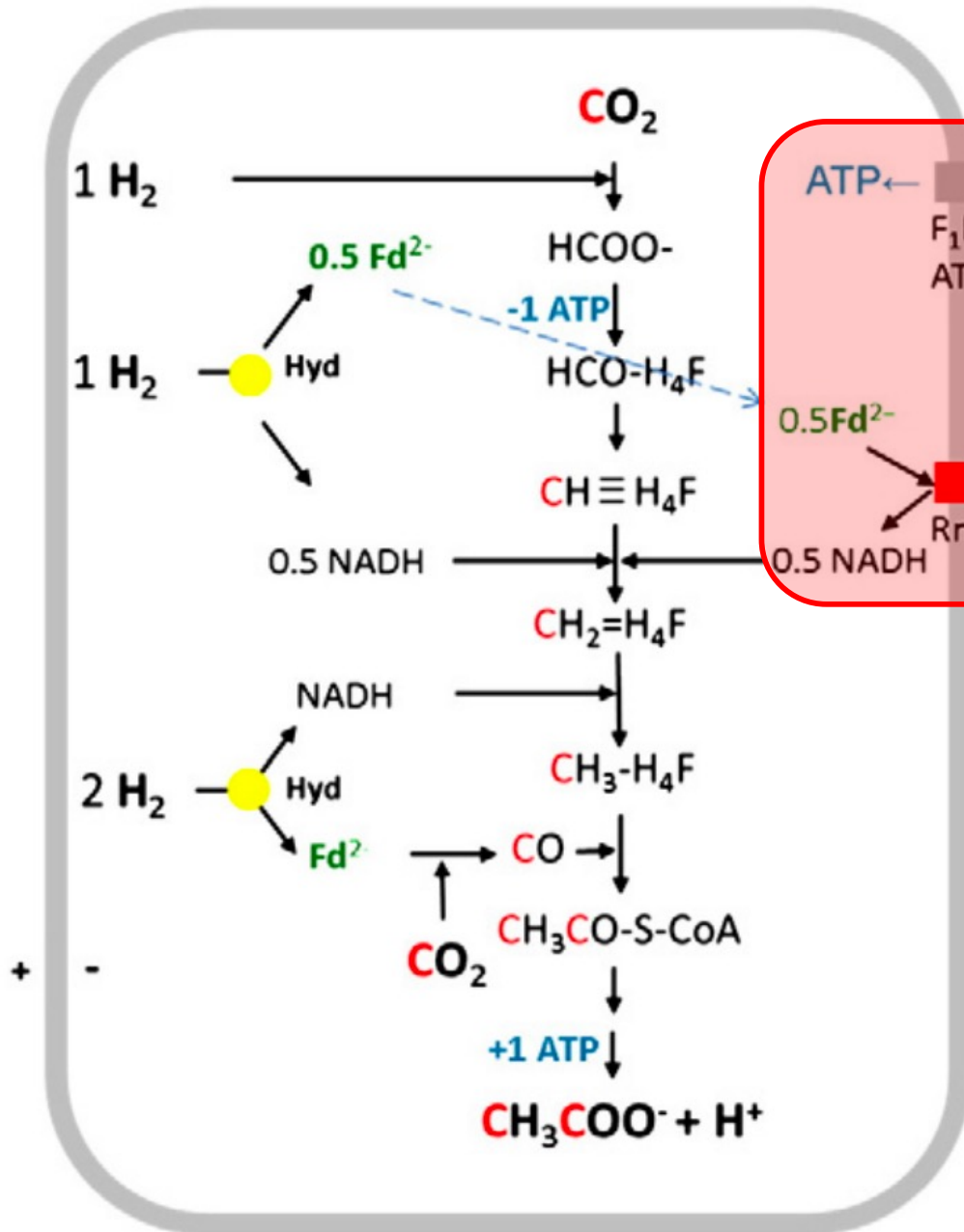
## 不含细胞色素的 产乙酸细菌



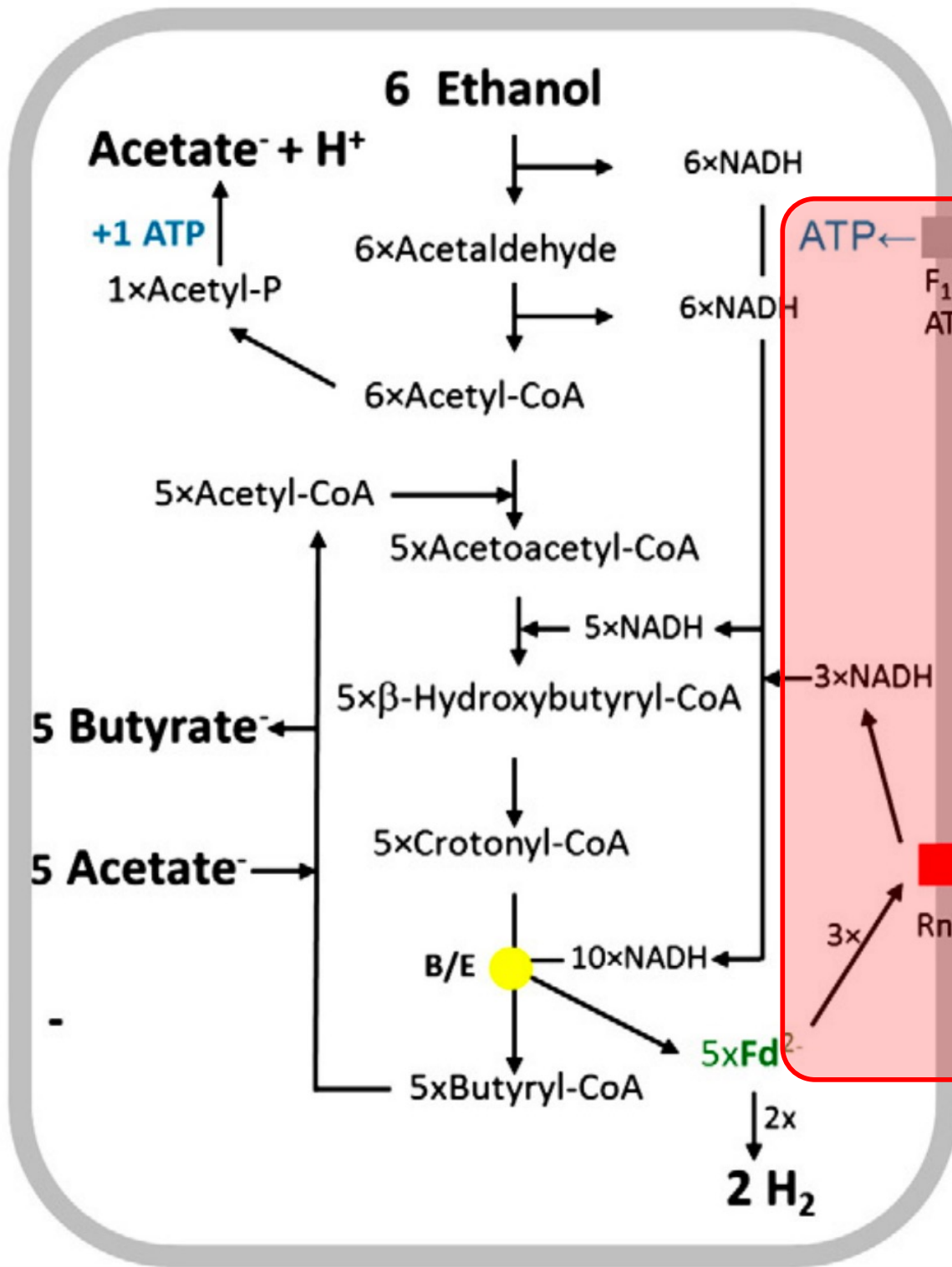
0.25 (?) ATP/Acetate

- 跨膜的Fd-NAD氧化还原酶Rnf

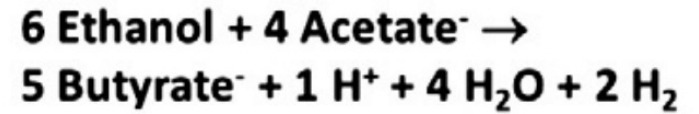
(不涉及脂溶性的膜上  
电子载体)



# 克氏梭菌的乙醇-乙酸发酵



*Clostridium kluyveri*

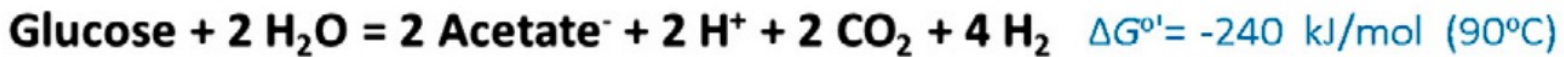
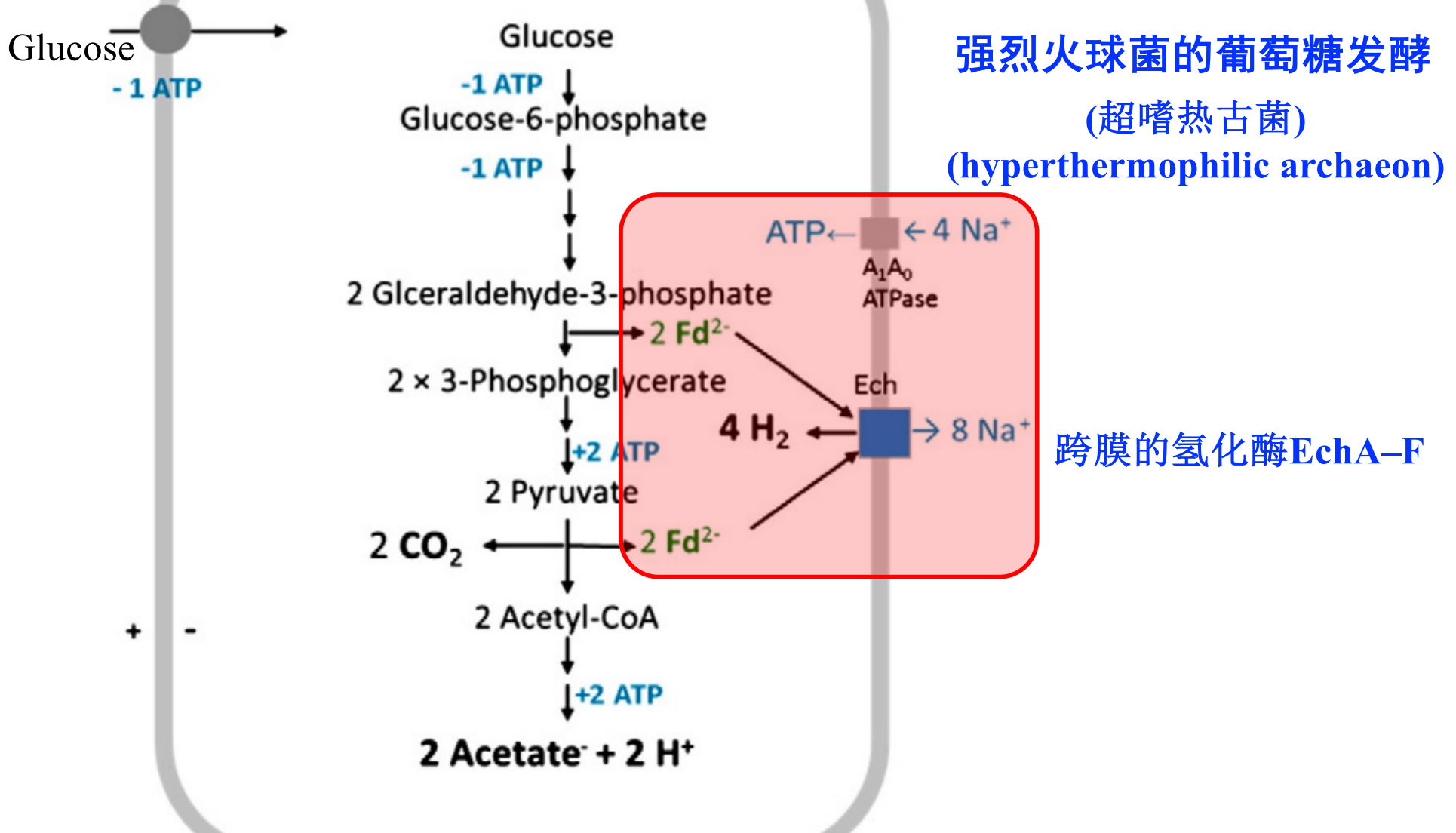


$$\Delta G^\circ = -180 \text{ kJ/mol H}^+$$

2.5 ATP/H<sup>+</sup>

- 跨膜的Fd-NAD氧化还原酶Rnf
- (乙醇和乙酸)浓度高时起作用

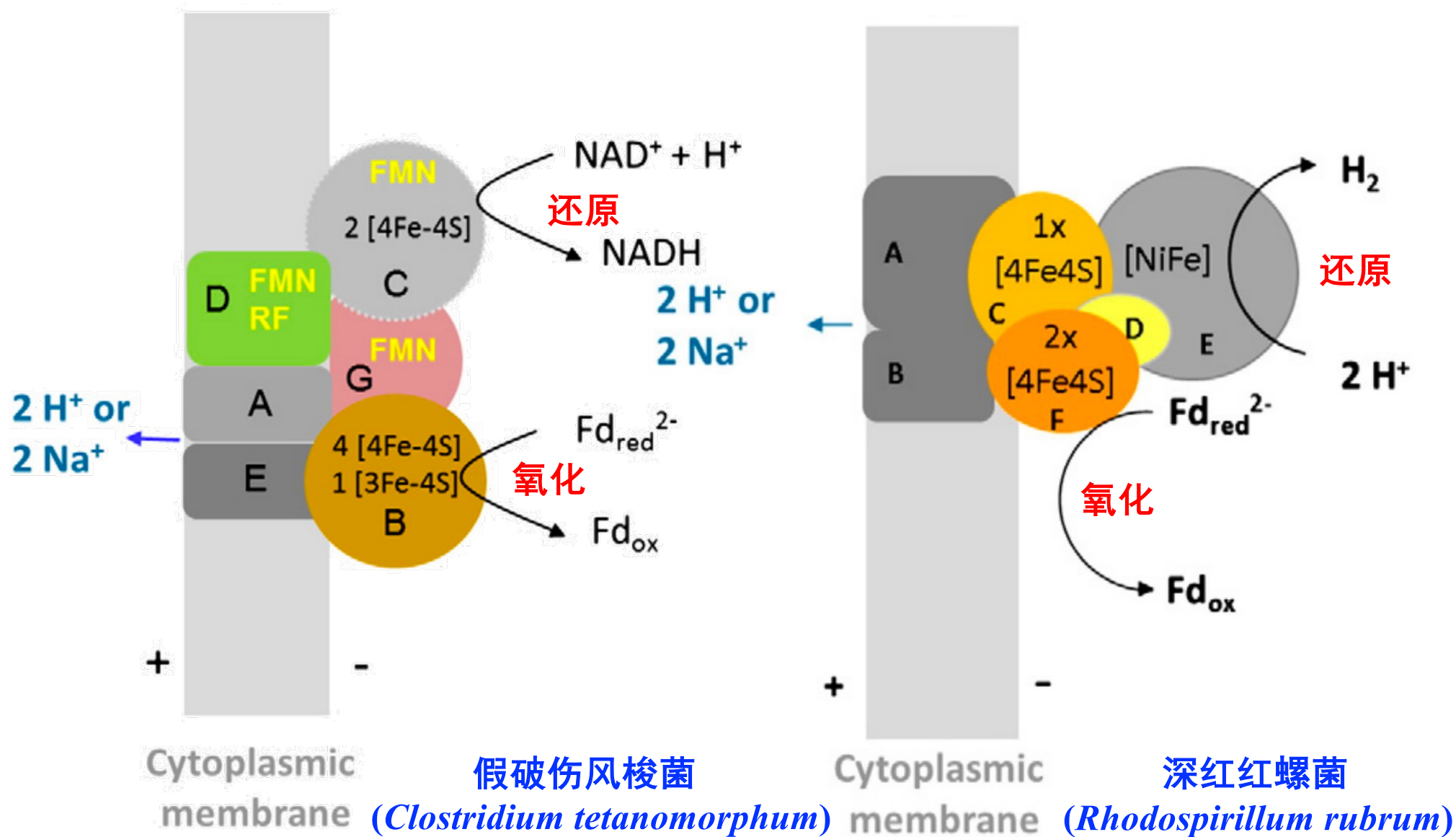
*Pyrococcus furiosus*



3 ATP/glucose



# 超短电子传递链：不涉及脂溶性的膜上电子载体



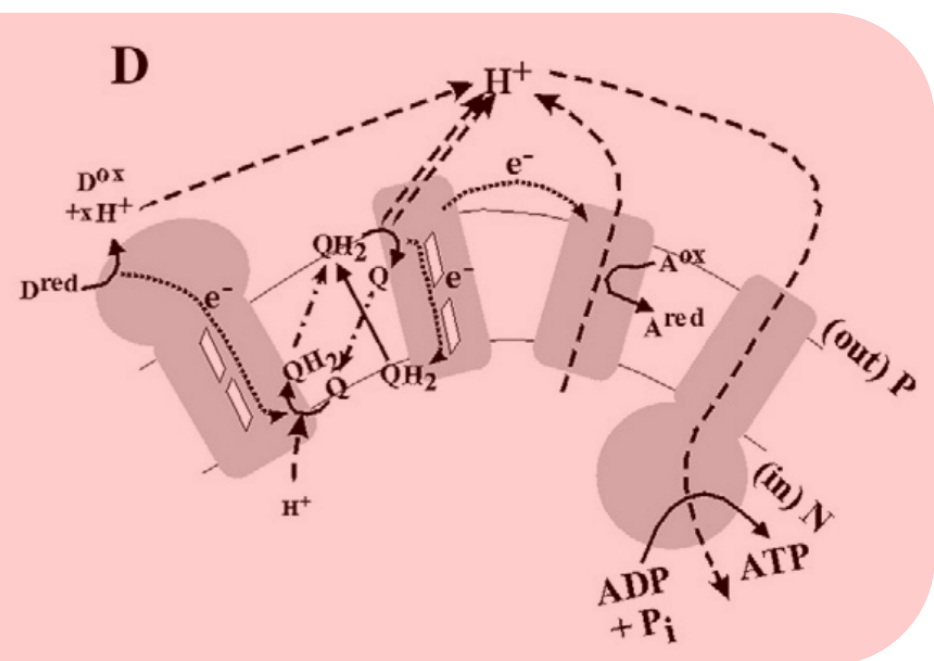
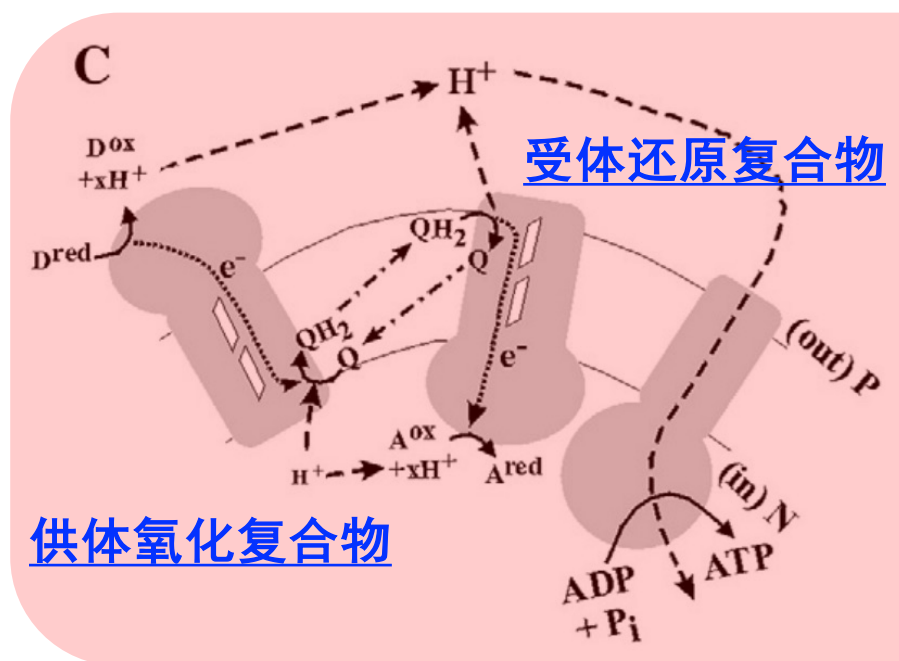
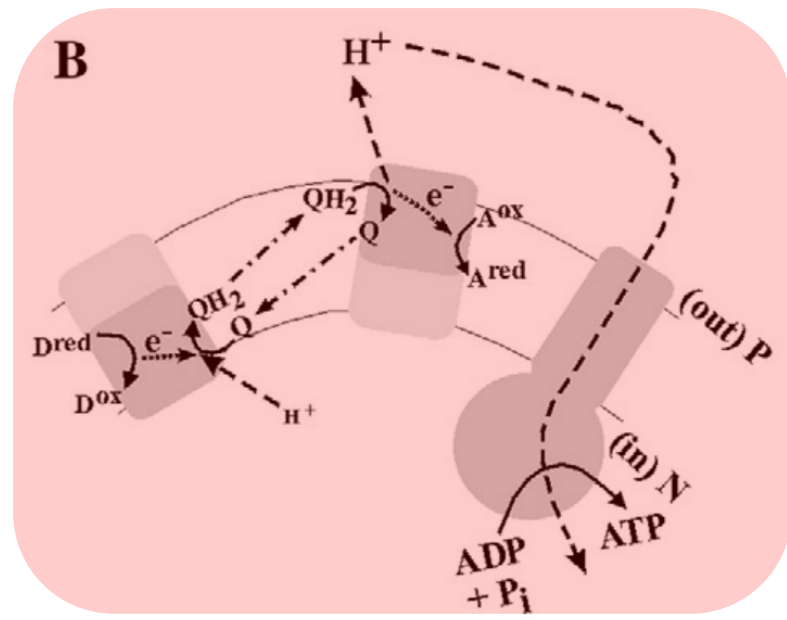
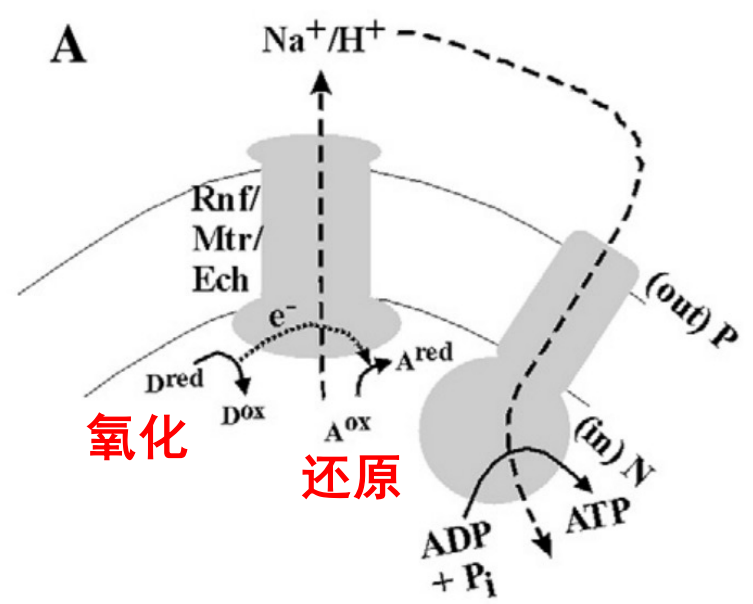
跨膜的Fd-NAD氧化还原酶RnfA-G

跨膜的氢化酶EchA-F

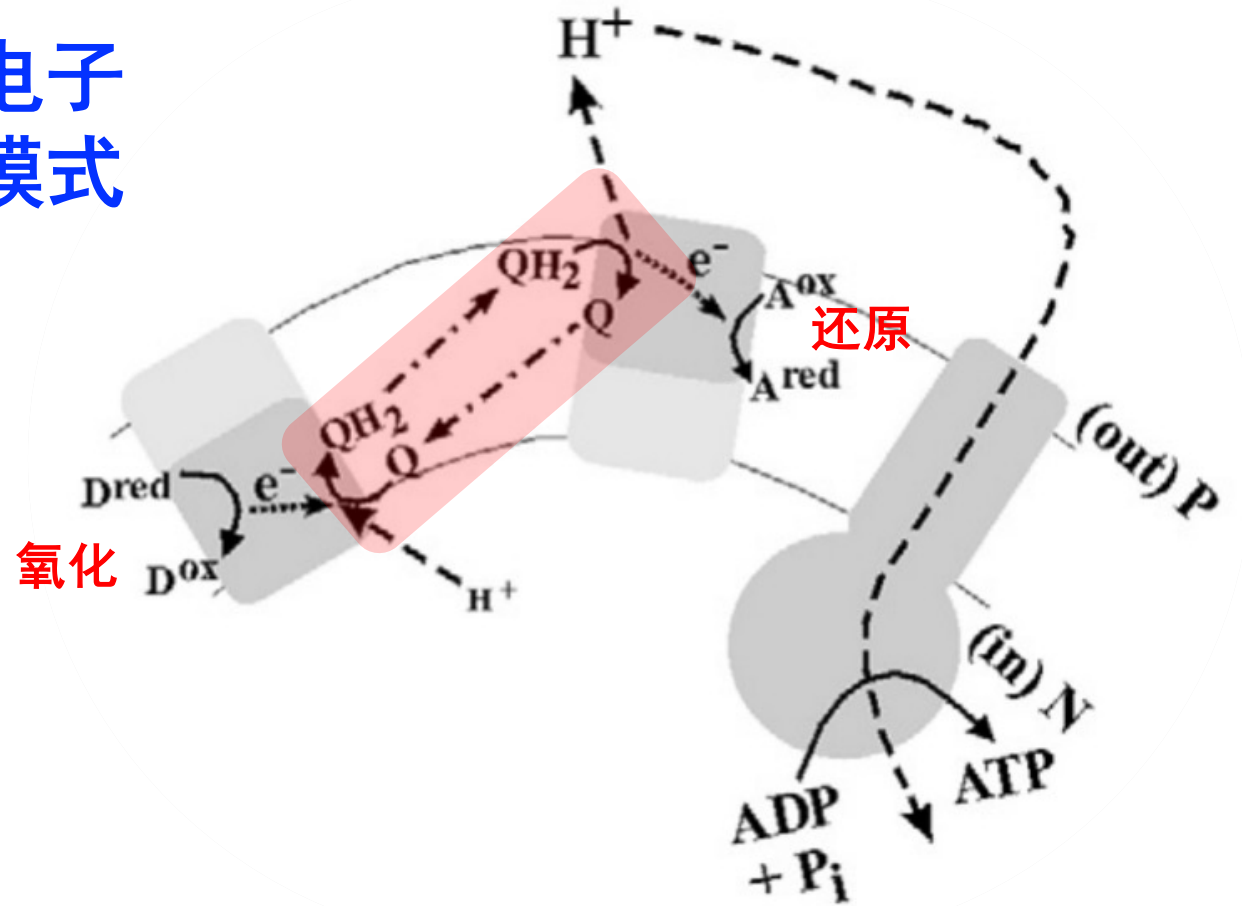


# 电子传递链的复杂程度不同

涉及脂溶性的膜上电子载体



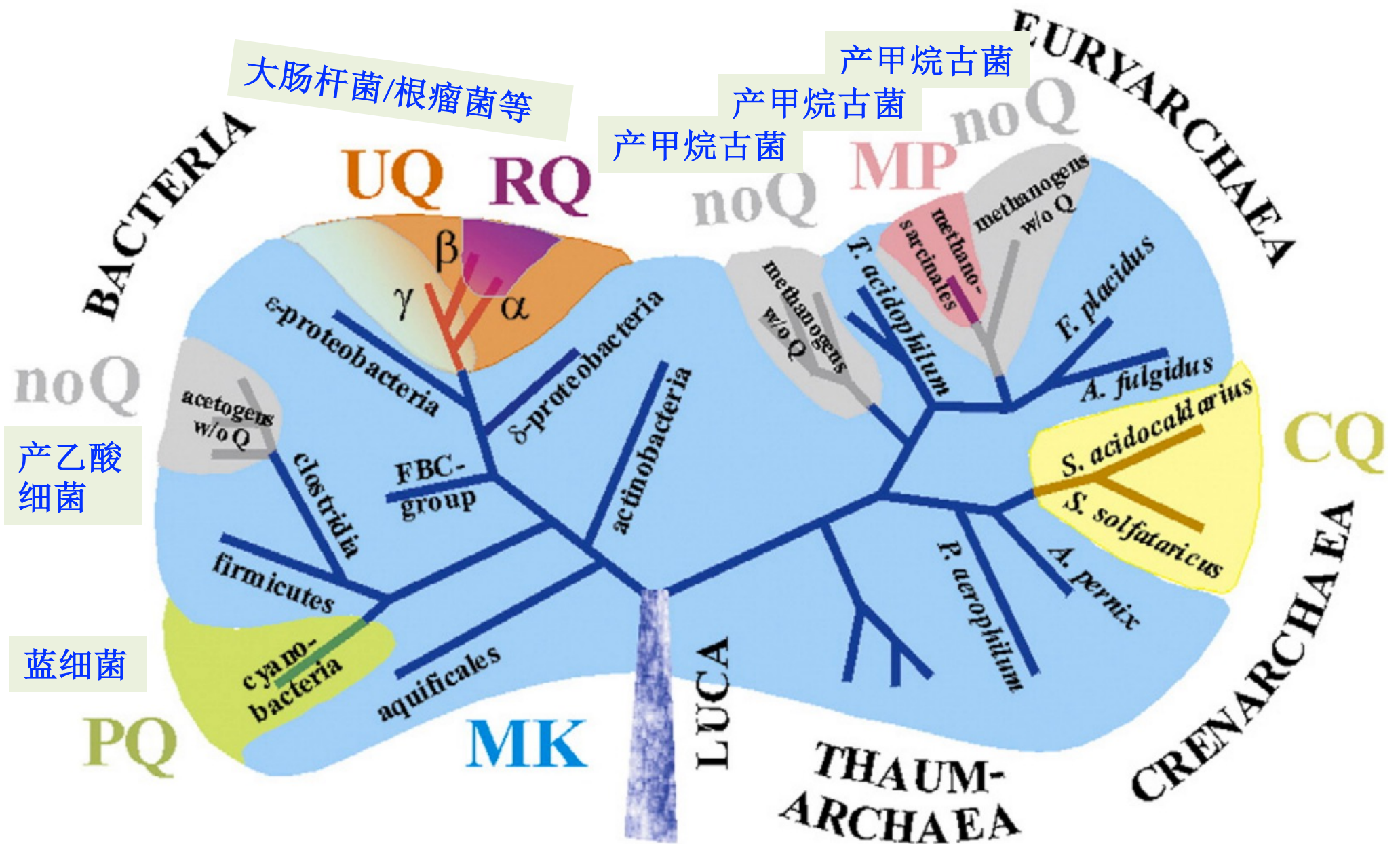
## 醌类和亚甲基吩嗪电子载体在膜上的作用模式



### Q

- Quinones (醌类: 包括mena-, ubi-, plasto-, 和caldariellaquinones)和Methanophenazine (亚甲基吩嗪)
- 这些载体共转移两个电子和两个质子
- 可以在膜内扩散(diffusion):Q的还原位点位于细胞质一侧 (N), QH<sub>2</sub>氧化发生在另一侧(P)
- 注意: 这个模式图中电子供体D和电子受体A的氧化和还原位置为虚拟

# 醌类和亚甲基吩嗪电子载体在细菌和古菌中的分布

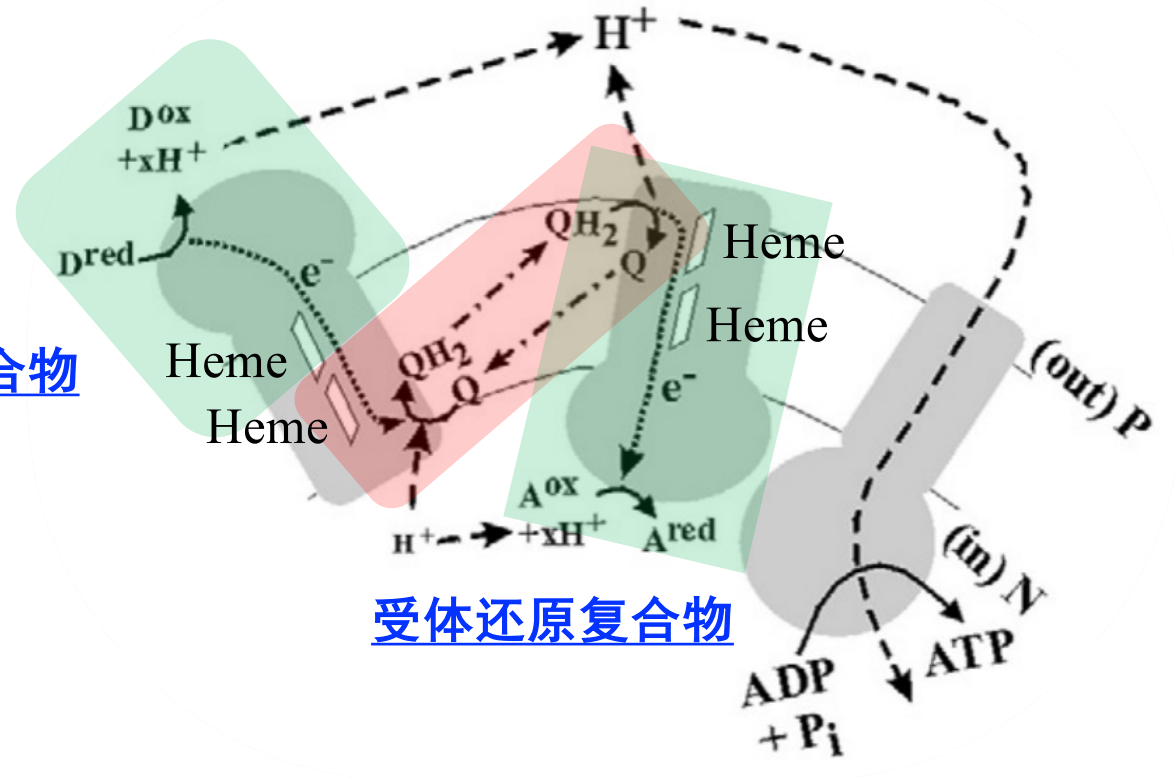


noQ: 没有醌类和亚甲基吩嗪



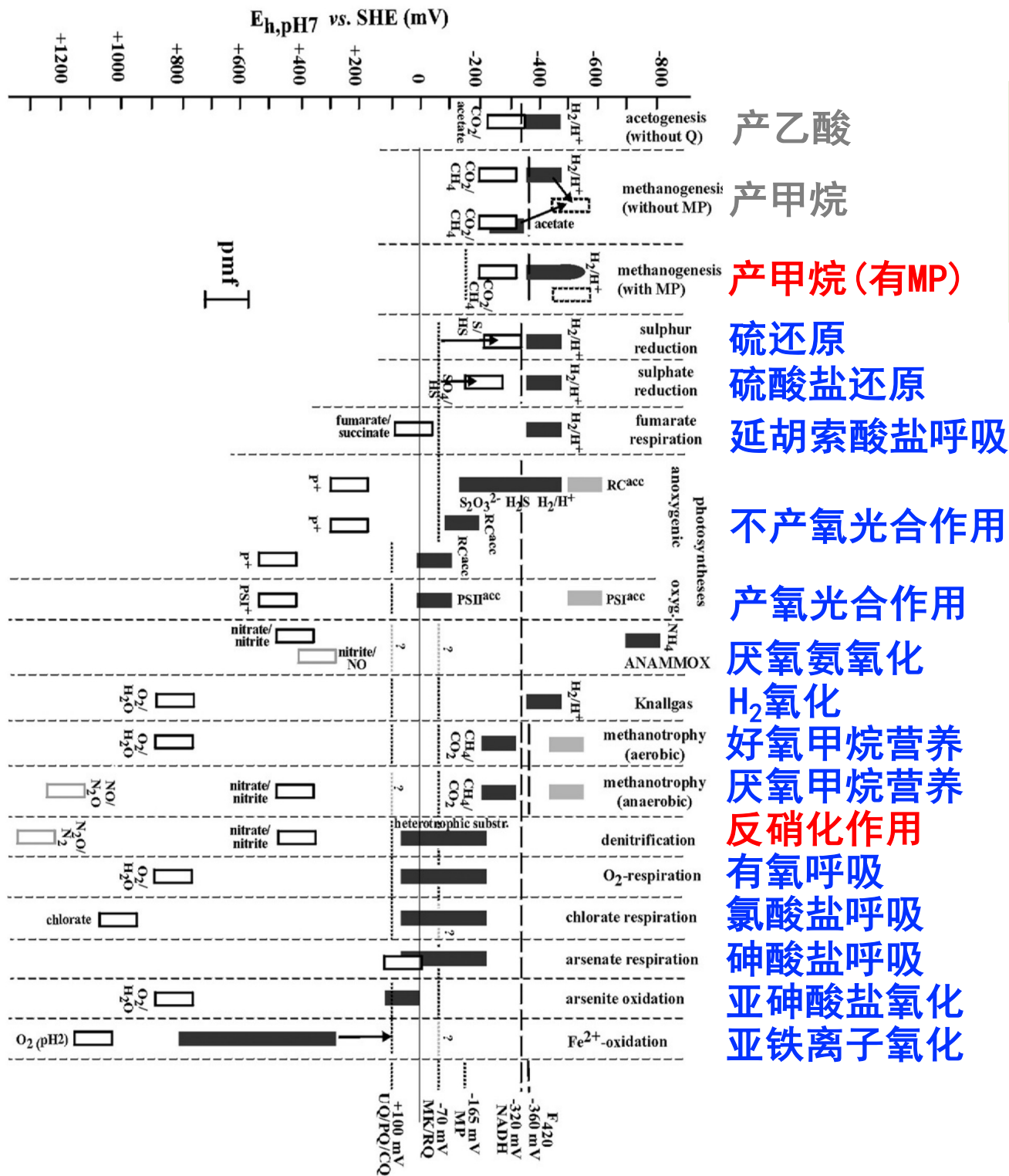
# 醌类和亚甲基吩嗪电子载体在膜上的作用模式

供体氧化复合物



受体还原复合物

- Q可以在膜内扩散(diffusion):Q的还原位点位于细胞质一侧 (N)，QH<sub>2</sub>氧化发生在另一侧(P)
- 电子供体D与Q的各自反应位点不在同一侧，两个血红素(heme)在中间传递电子
- 电子受体A与QH<sub>2</sub>的反应位点不在同一侧，两个血红素(heme)在中间传递电子

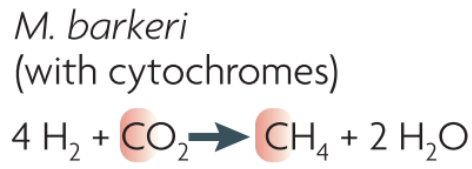


# 自然界存在多种多样的基于电子传递链的化学渗透系统

与生物的生存环境和适应机制紧密相关

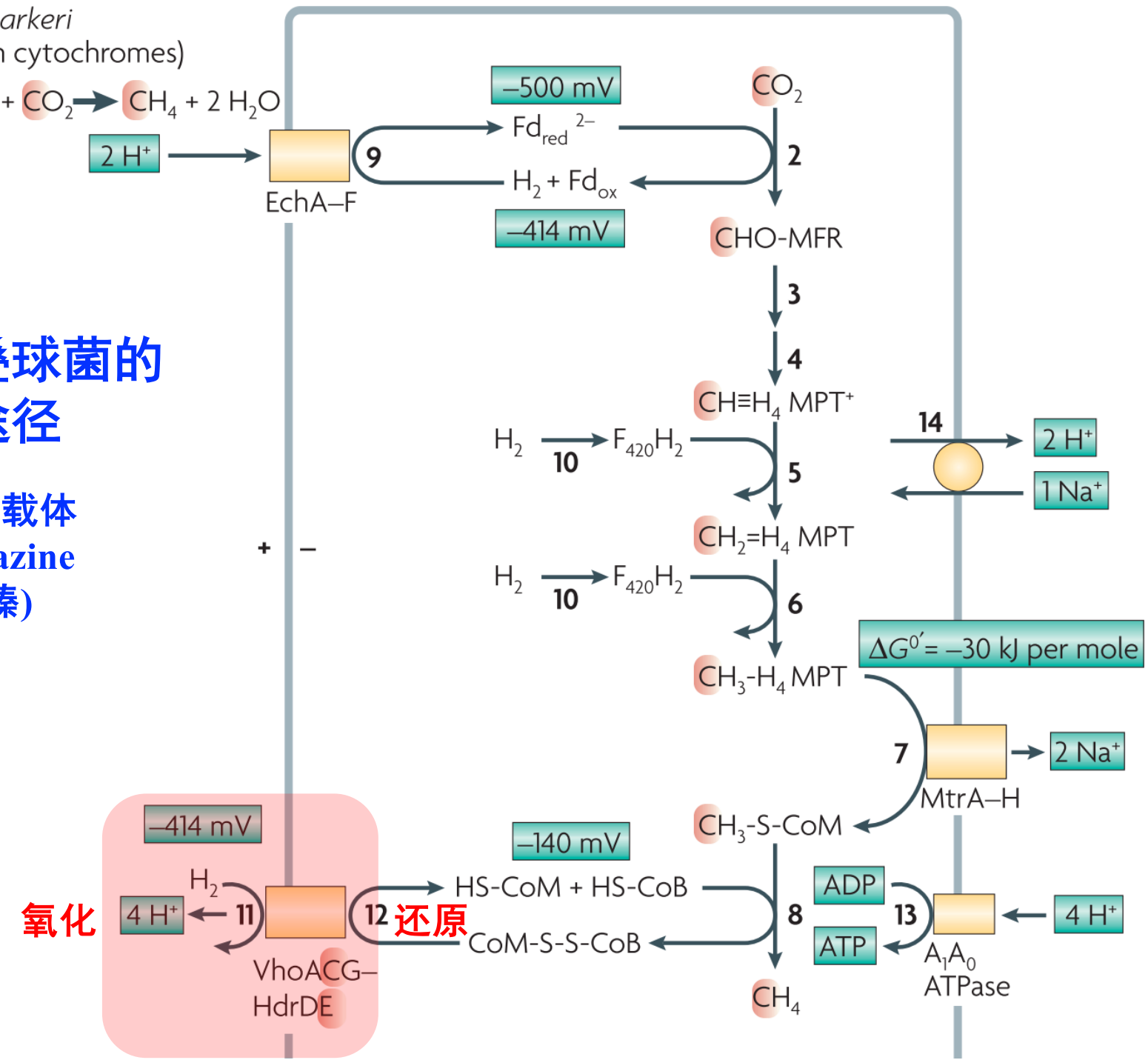
还原底物

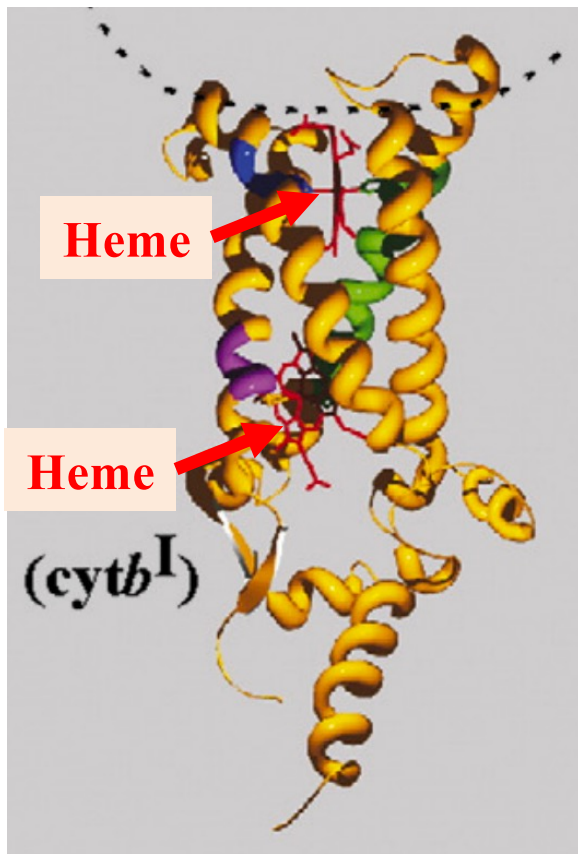
氧化底物



# 巴氏甲烷八叠球菌的 产甲烷途径

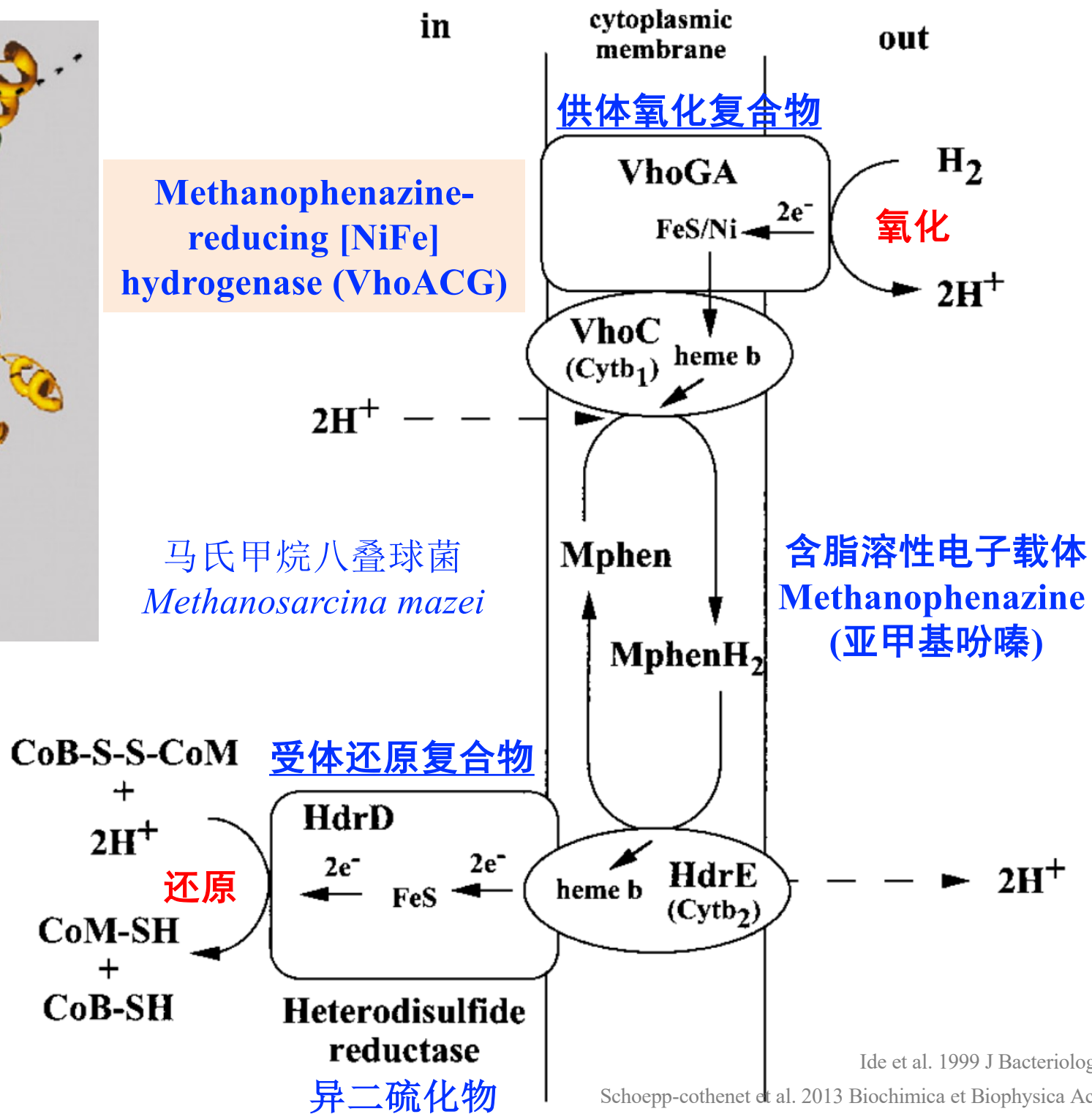
含脂溶性电子载体  
Methanophenazine  
(亚甲基吩嗪)

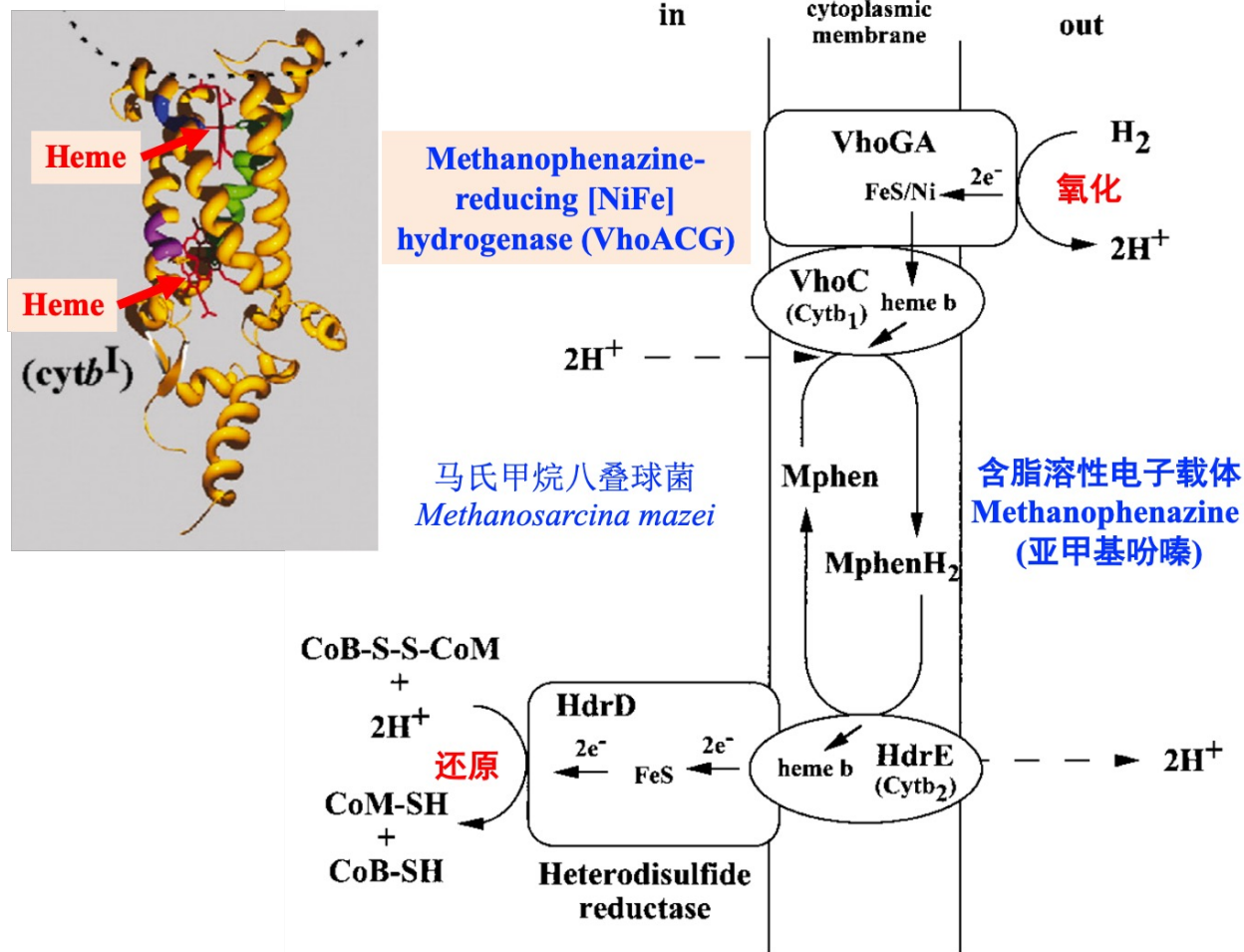




Methanophenazine-reducing [NiFe] hydrogenase (VhoACG)

马氏甲烷八叠球菌  
*Methanosarcina mazei*

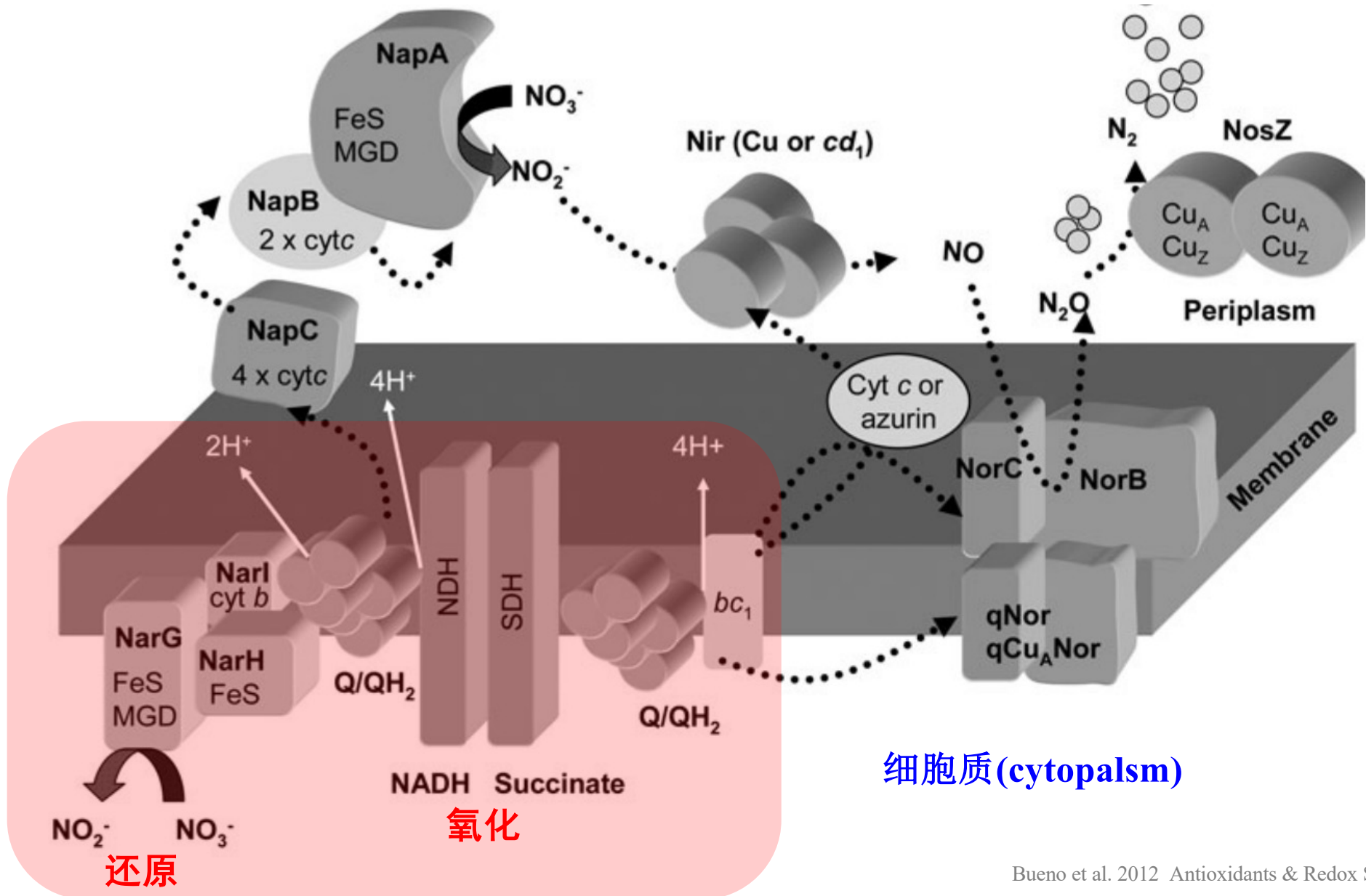




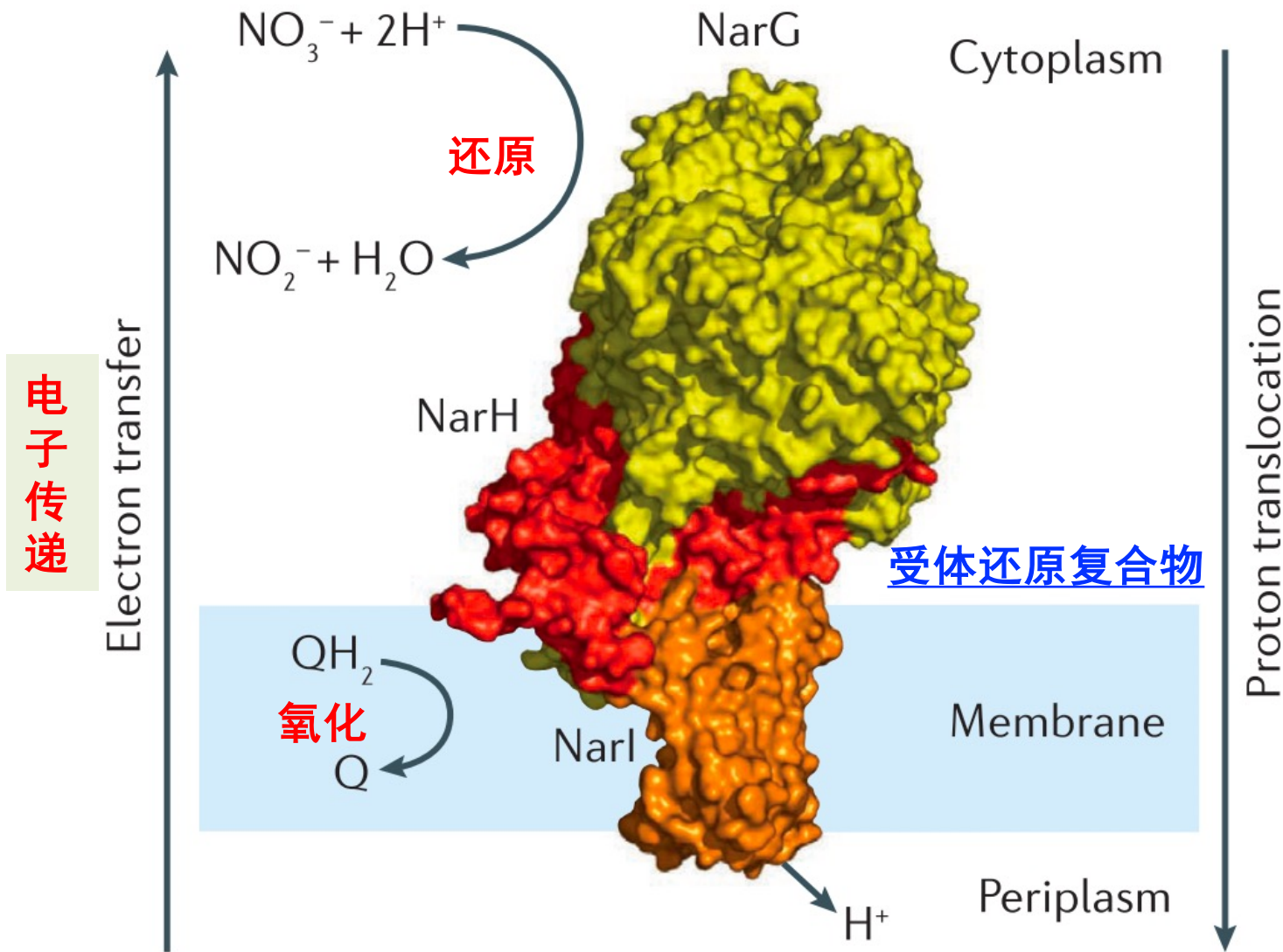
- Q可以在膜内扩散(diffusion):Q的还原位点位于细胞质一侧 (N)，QH<sub>2</sub>氧化发生在另一侧(P)
- 电子供体D与Q的各自反应位点不在同一侧，两个血红素(heme)在中间传递电子
- 电子受体A与QH<sub>2</sub>的反应位点不在同一侧，两个血红素(heme)在中间传递电子

反硝化作用(denitrification): 又称为硝酸盐呼吸, 以 $\text{NO}_3^-$ 代替分子氧作为电子受体的无氧呼吸作用, 完整还原过程的产物为氮气。(在低氧或无氧条件下进行)

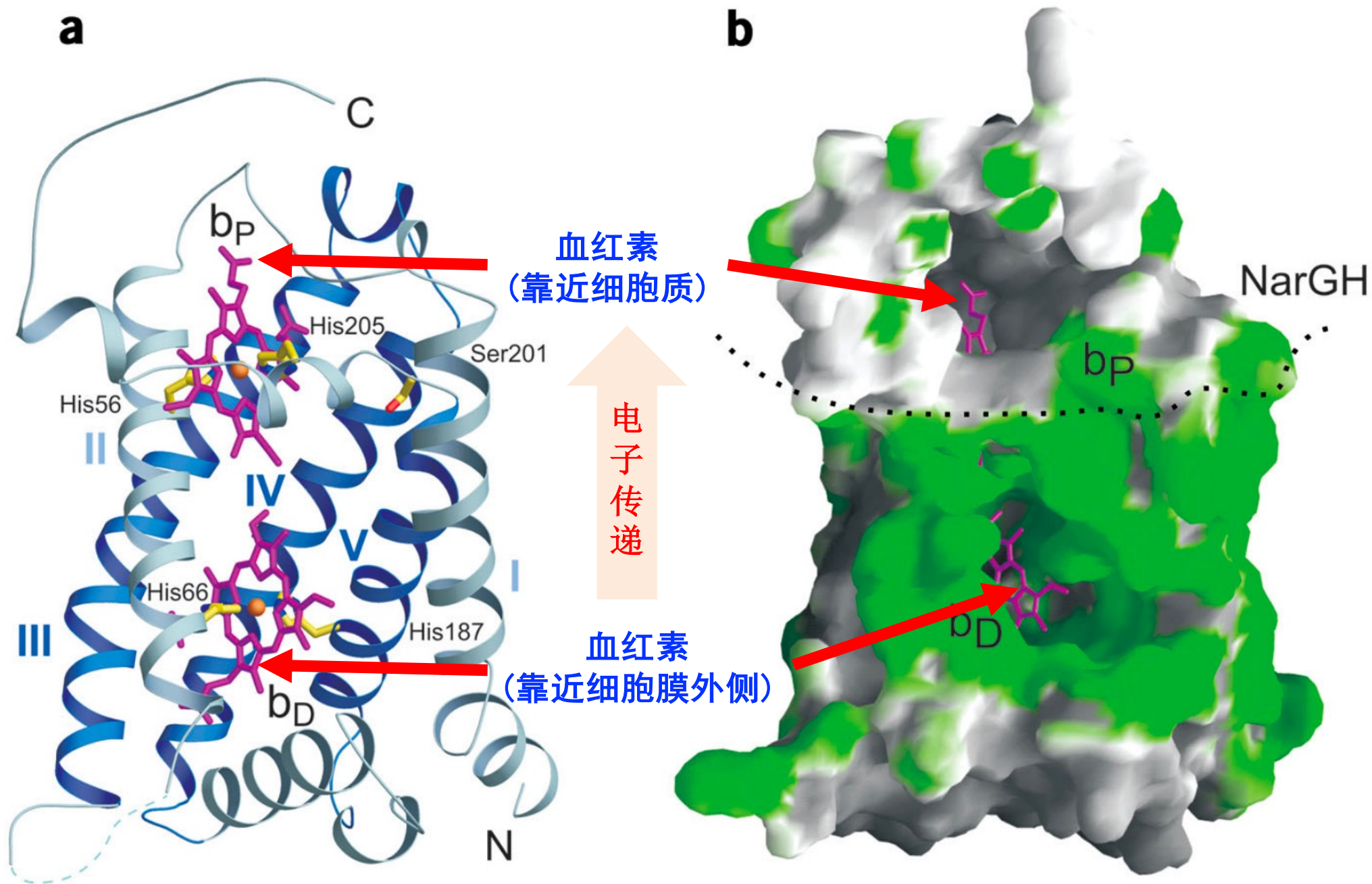
ATP产率降低, 但是可以存活与繁殖。



# (质膜)硝酸盐还原酶 (membrane-bound nitrate reductase; NAR)

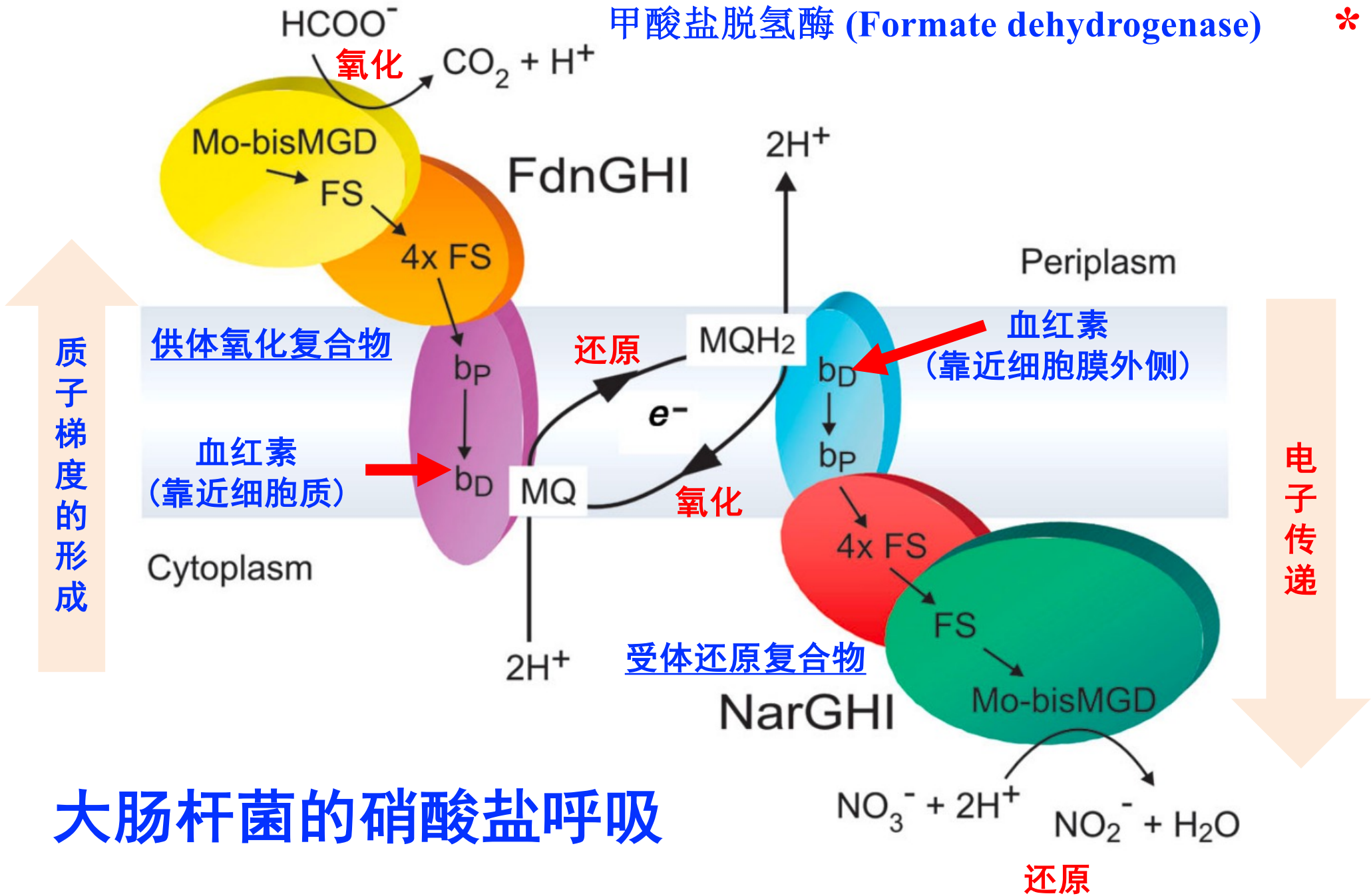


产生质子动力势、ATP合酶合成ATP，实现低氧条件下细胞的生长。

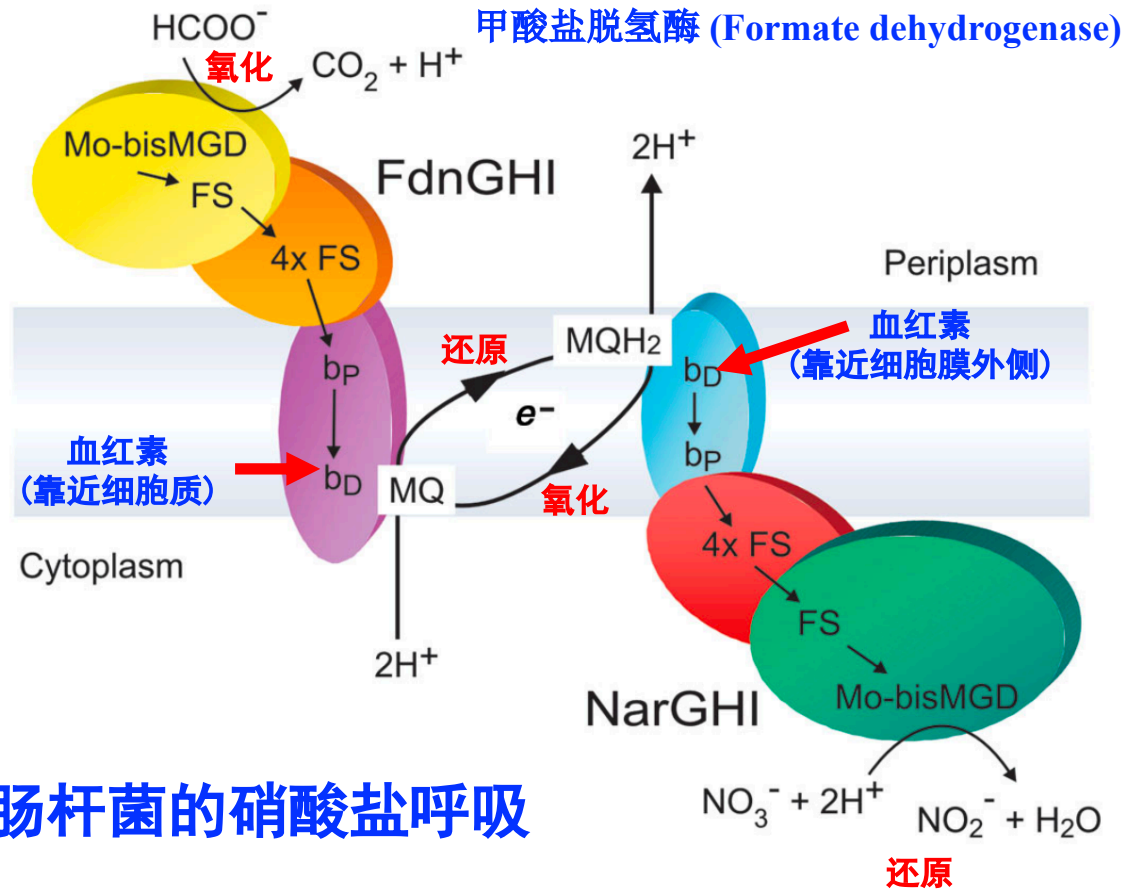


整合在膜上的 Nar I

# 甲酸盐脱氢酶 (Formate dehydrogenase) \*



## 大肠杆菌的硝酸盐呼吸

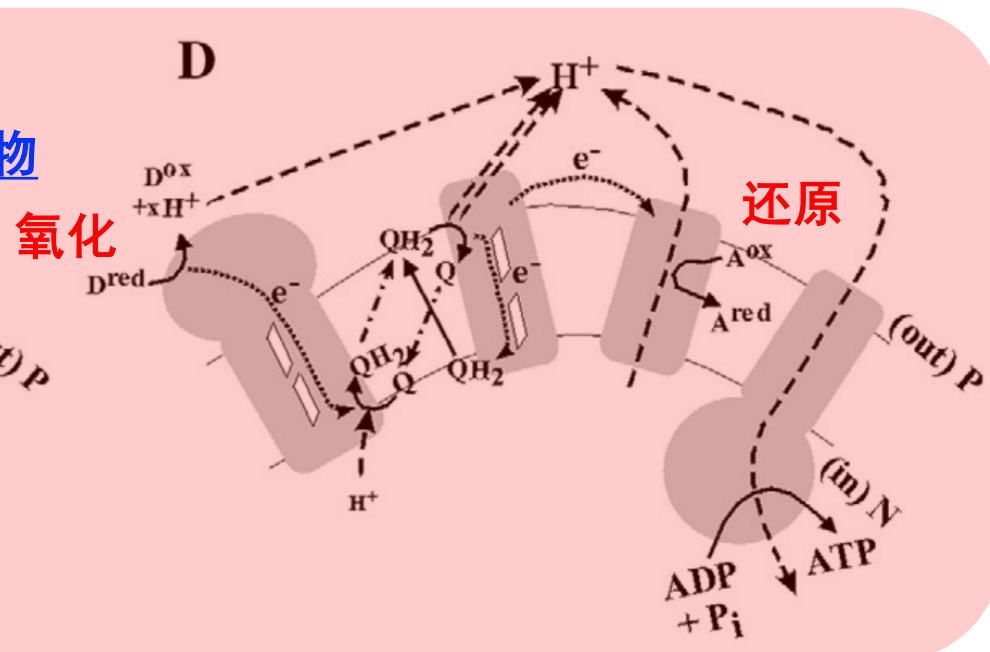
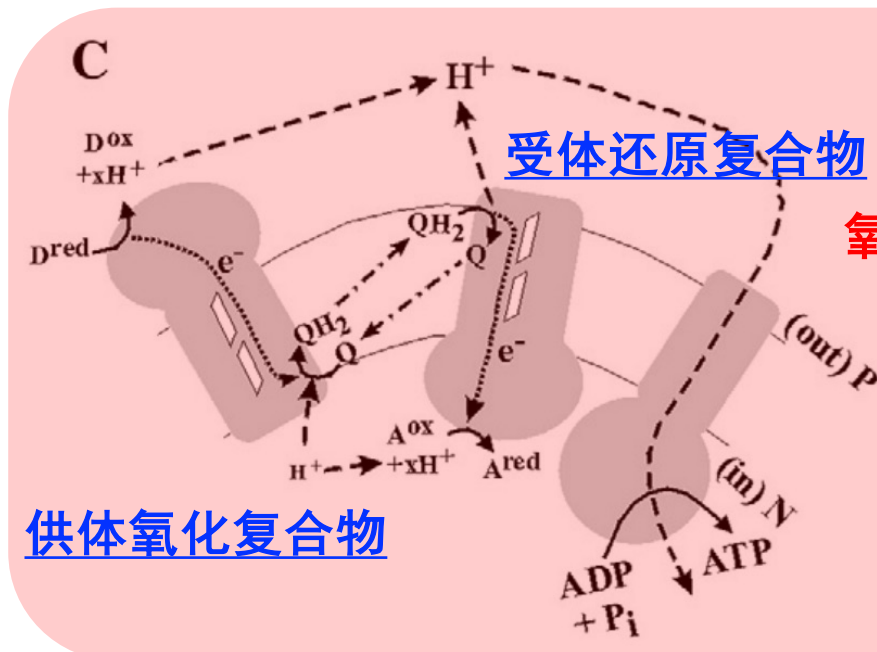
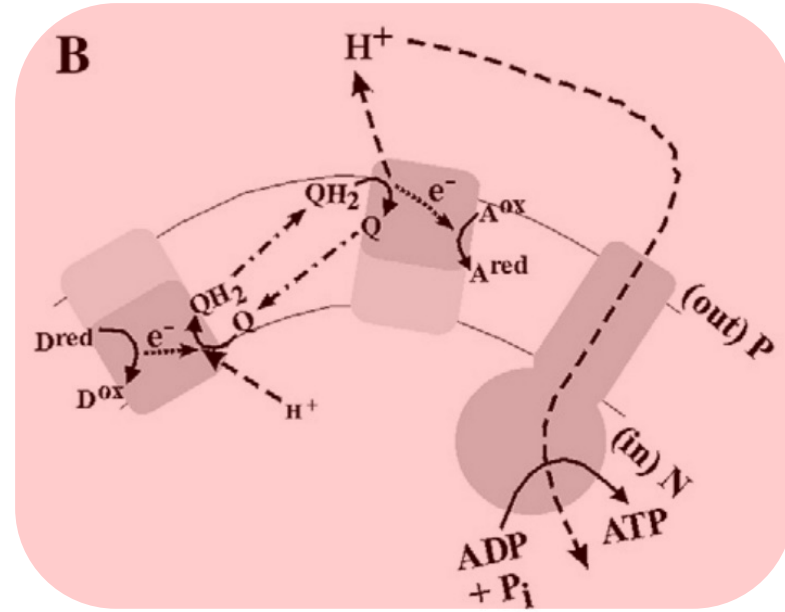
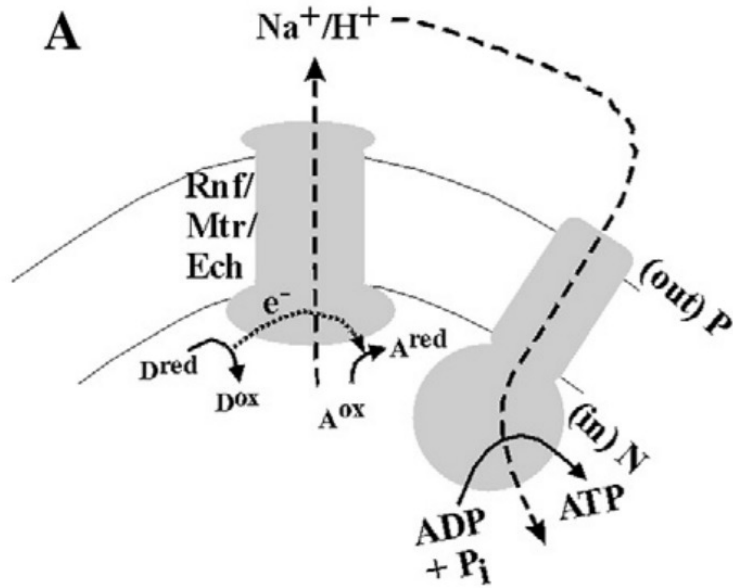


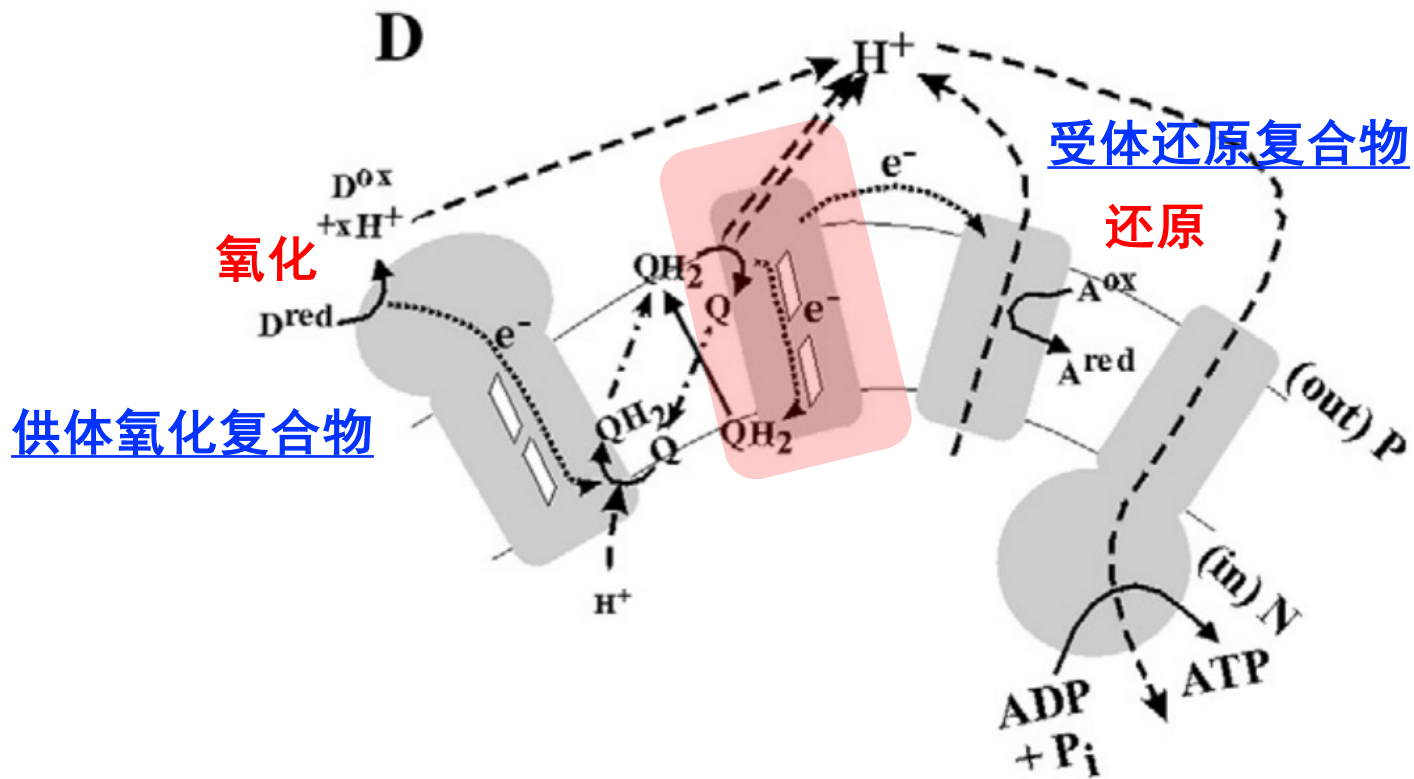
## 大肠杆菌的硝酸盐呼吸

- Q可以在膜内扩散(diffusion):Q的还原位点位于细胞质一侧 (N)，QH<sub>2</sub>氧化发生在另一侧(P)
- 电子供体D与Q的各自反应位点不在同一侧，两个血红素(heme)在中间传递电子
- 电子受体A与QH<sub>2</sub>的反应位点不在同一侧，两个血红素(heme)在中间传递电子

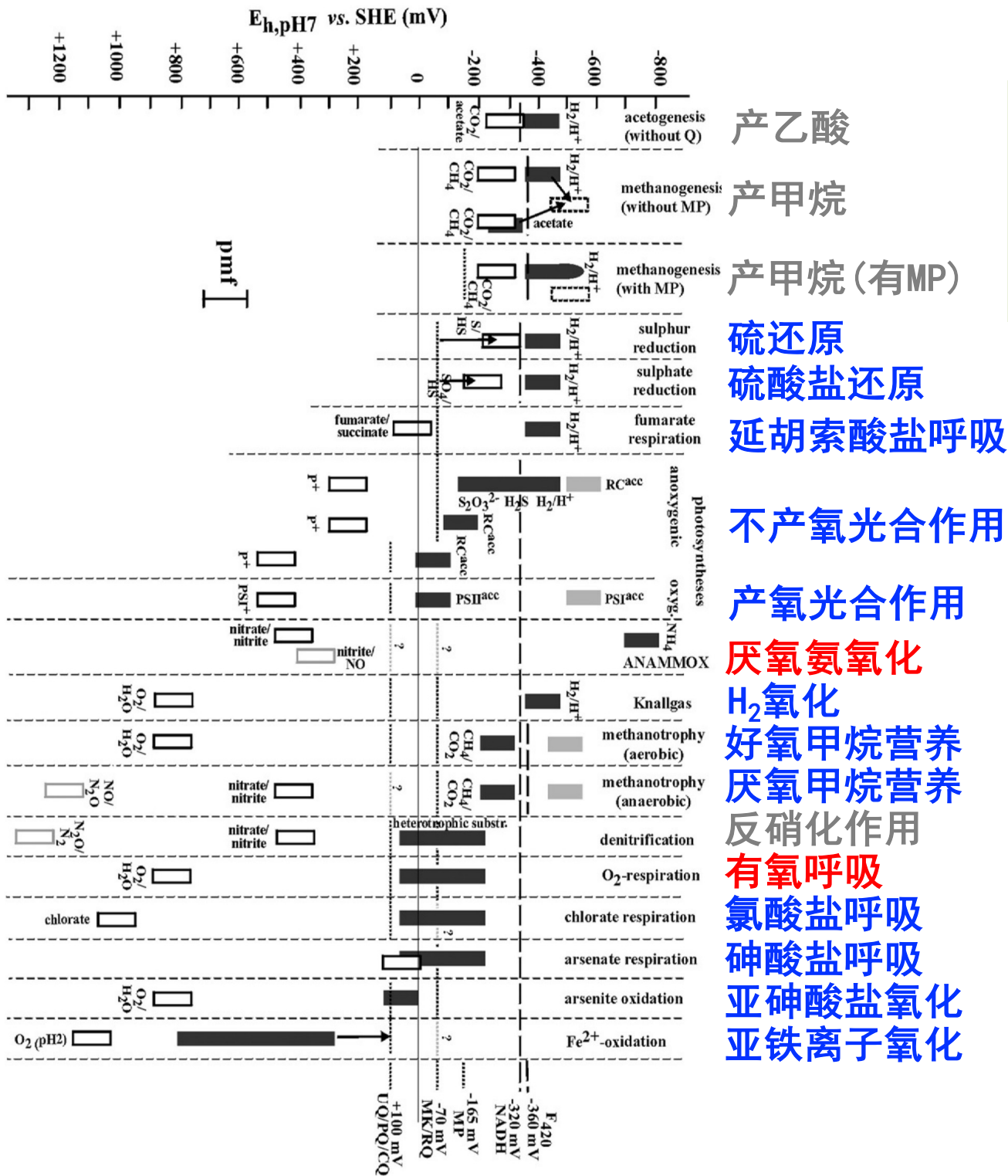
# 电子传递链的复杂程度不同

涉及脂溶性的膜上电子载体



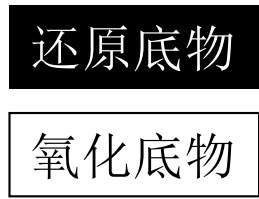


- **通过构象变化泵出更多质子，如：Heme-copper  $O_2$  reductase和线粒体的 Complex I**
- **在供体氧化复合物与受体还原复合物中间加入其他酶，如：Rieske/cytb 复合物 (包括  $bc_1$ -type (complex III) 和  $b_6f$ -type 复合物)**



# 自然界存在多种多样的基于电子传递链的化学渗透系统

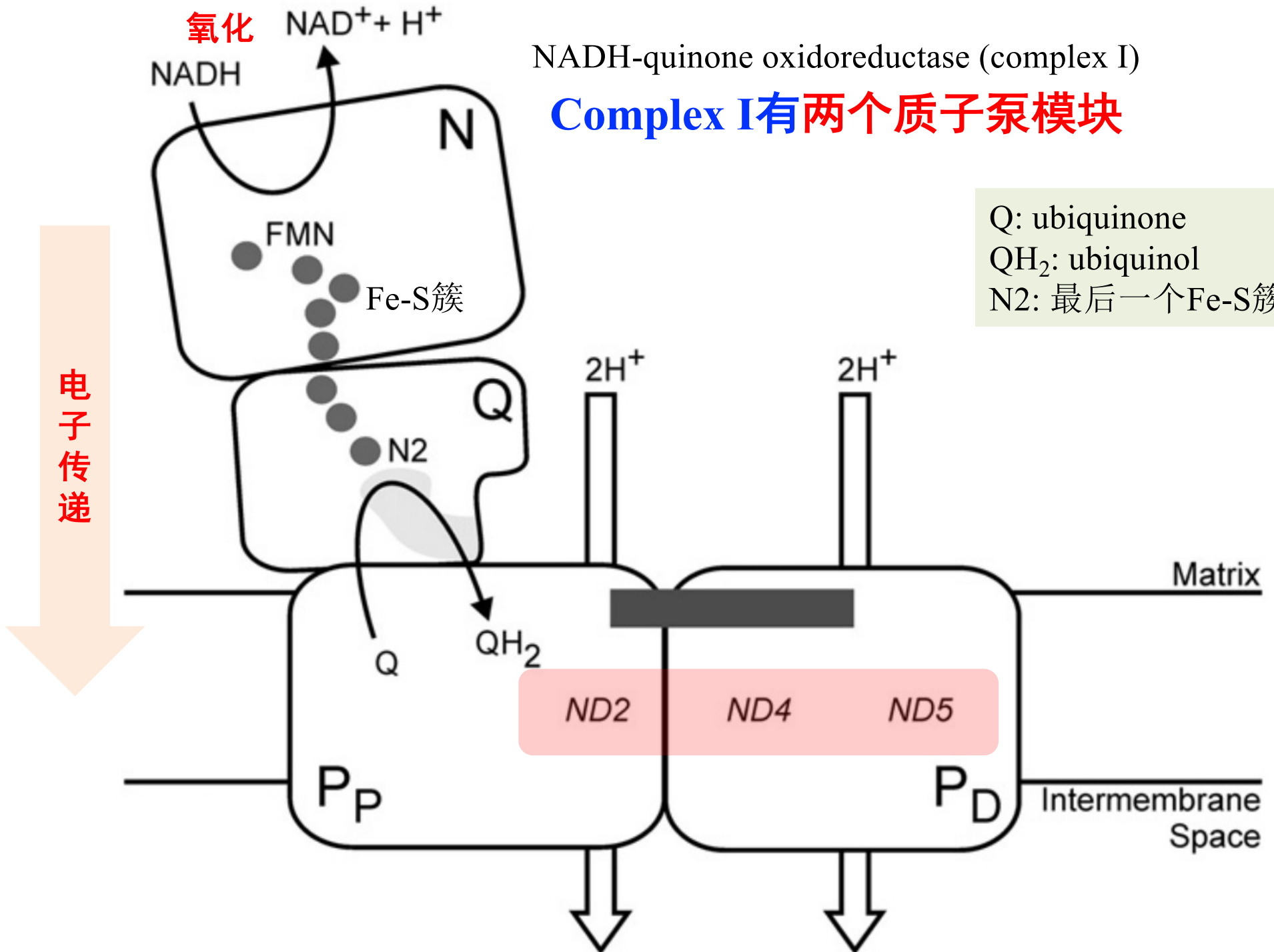
与生物的生存环境和适应机制紧密相关





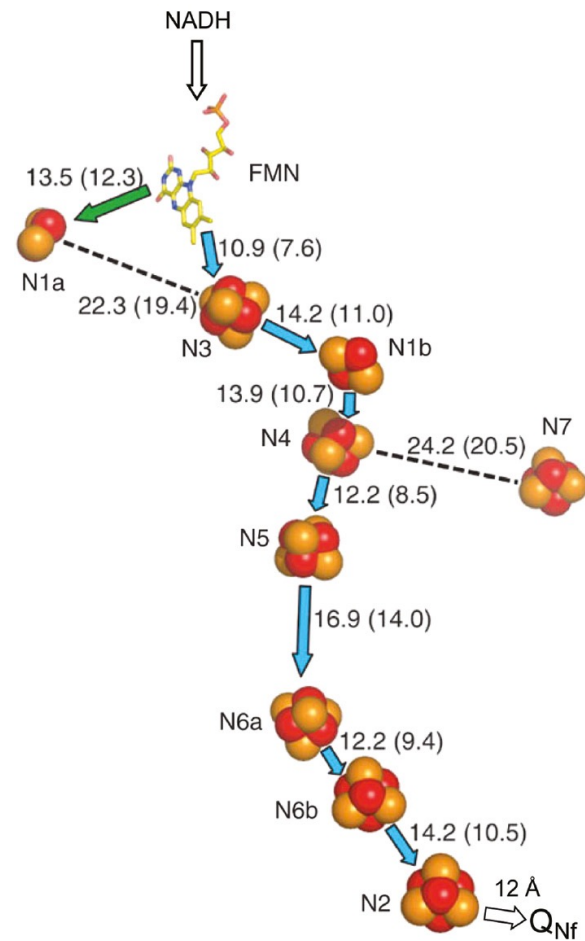
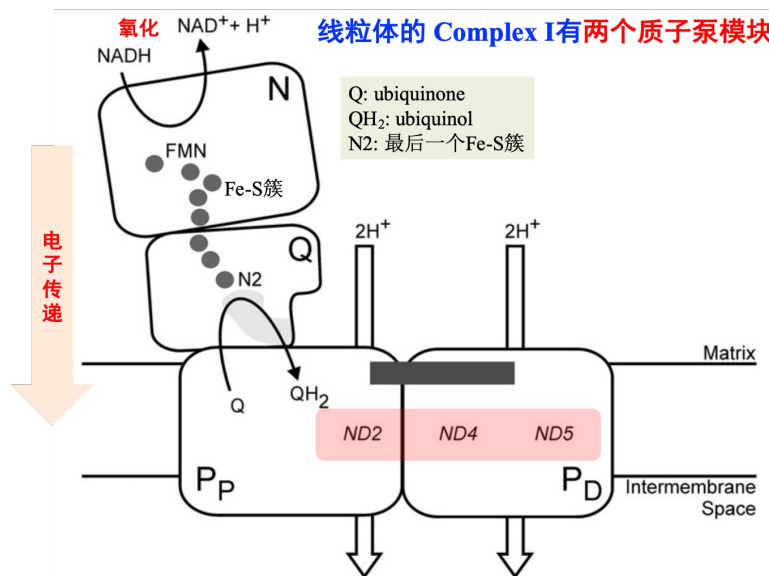
NADH-quinone oxidoreductase (complex I)

## Complex I有两个质子泵模块



Q: ubiquinone  
QH<sub>2</sub>: ubiquinol  
N2: 最后一个Fe-S簇

线粒体的 Complex I 有两个质子泵模块

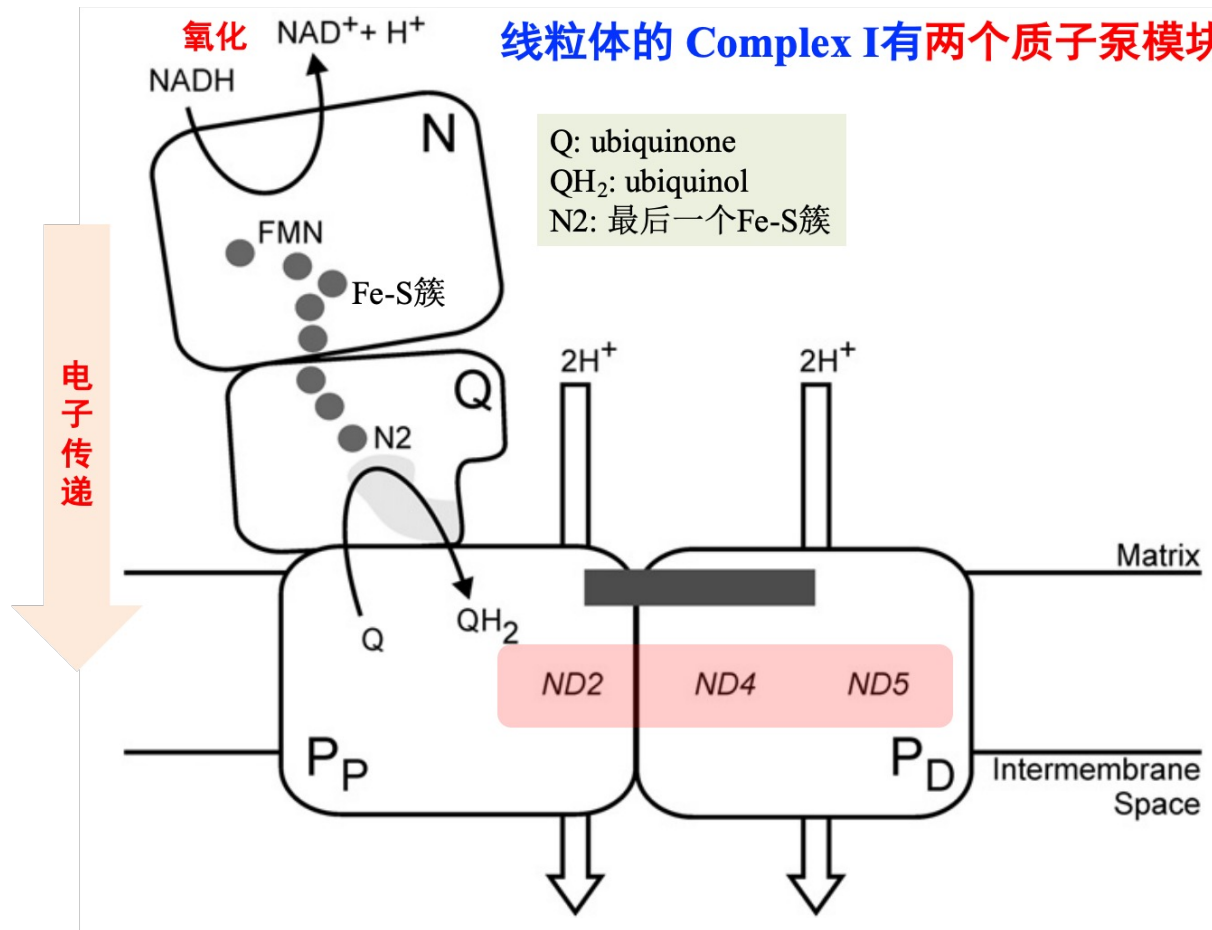


	NADH	FMN	[2Fe-2S] <sub>N1a</sub>	[2Fe-2S] <sub>N1b</sub>	[4Fe-4S] <sub>N3</sub>	[4Fe-4S] <sub>N4</sub>	[4Fe-4S] <sub>N5</sub>	[4Fe-4S] <sub>N6a/b</sub>	[4Fe-4S] <sub>N2</sub>	Q <sub>Nf</sub>	Q <sub>Ns</sub>	Q-pool
$E_{m7.0}$ (mV)	-320	-340	-370	-250	-150~0	-50	?	+90				

- 模块N: NADH氧化
- FeS簇: Fe<sub>2</sub>S<sub>2</sub> 与 Fe<sub>4</sub>S<sub>4</sub>(FeS簇数量在部分原核生物有区别); 连接NADH氧化位点与ubiquinone还原位点
- 模块Q: ubiquinone还原
- 模块P: 质子泵



## 线粒体的 Complex I有两个质子泵模块



Q, ubiquinone;

Q<sup>•-</sup>, ubisemiquinone anion;

QH<sup>•</sup>, protonated semiquinone;

QH<sup>-</sup>, ubiquinol anion;

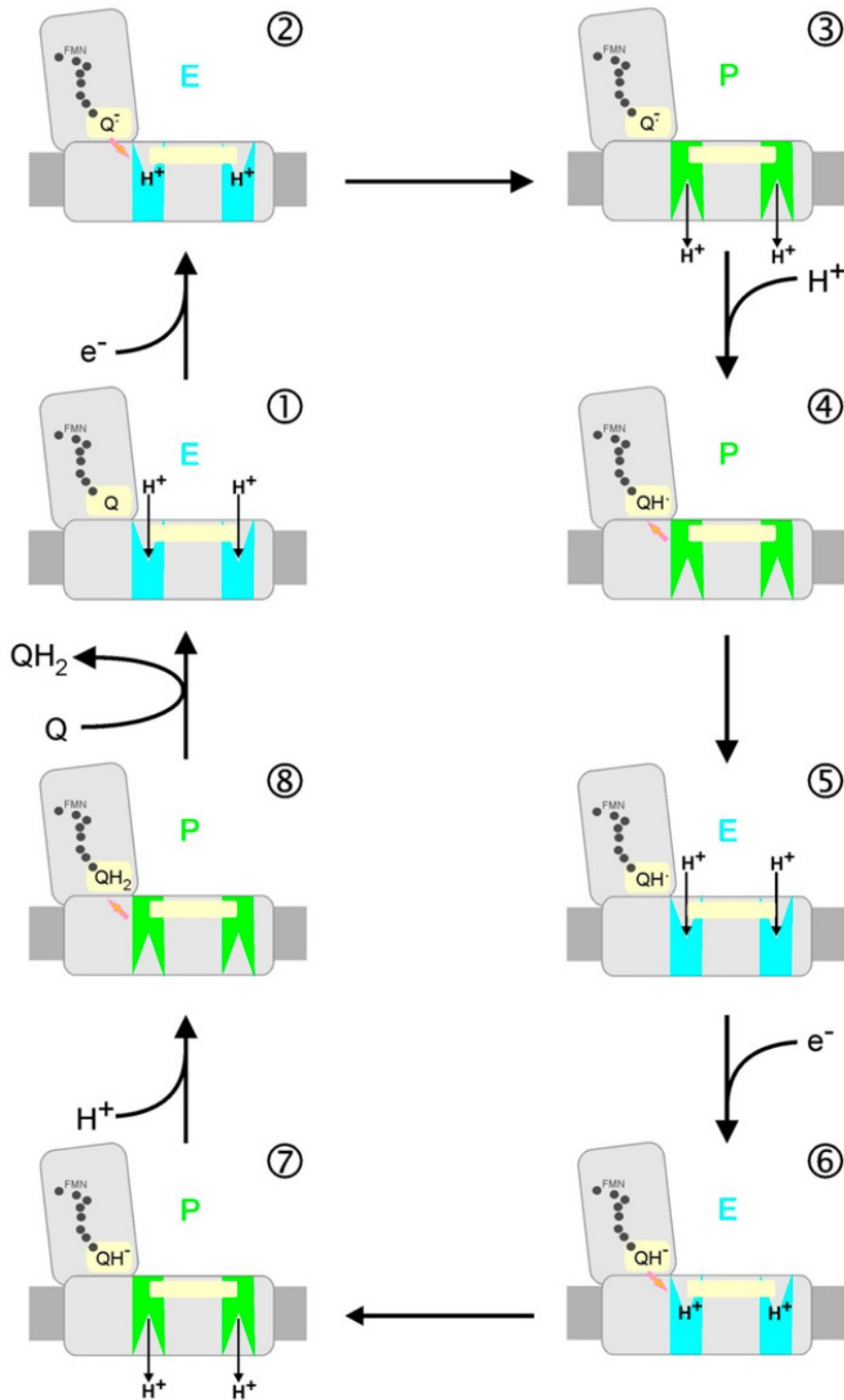
QH<sub>2</sub>, ubiquinol.

- 模块N: NADH氧化
- FeS簇: Fe<sub>2</sub>S<sub>2</sub> 与 Fe<sub>4</sub>S<sub>4</sub>; 连接NADH氧化位点与ubiquinone还原位点
- 模块Q: ubiquinone还原
- 模块P: 质子泵





# 线粒体Complex I的E/P状态



	E-state	P-state
Stabilization of anionic quinone	No	Yes
Electron transfer cluster N2 → quinone	Yes	No
Proton access to quinone	No	Yes
Mode of pump sites	Input	Output

(electron transfer) (protonation)  
电子传递 质子化

