Programa Académico de Bachillerato
Universidad de Chile
Curso Biología

Clase: Conceptos generales de termodinámica. Bioenergética.

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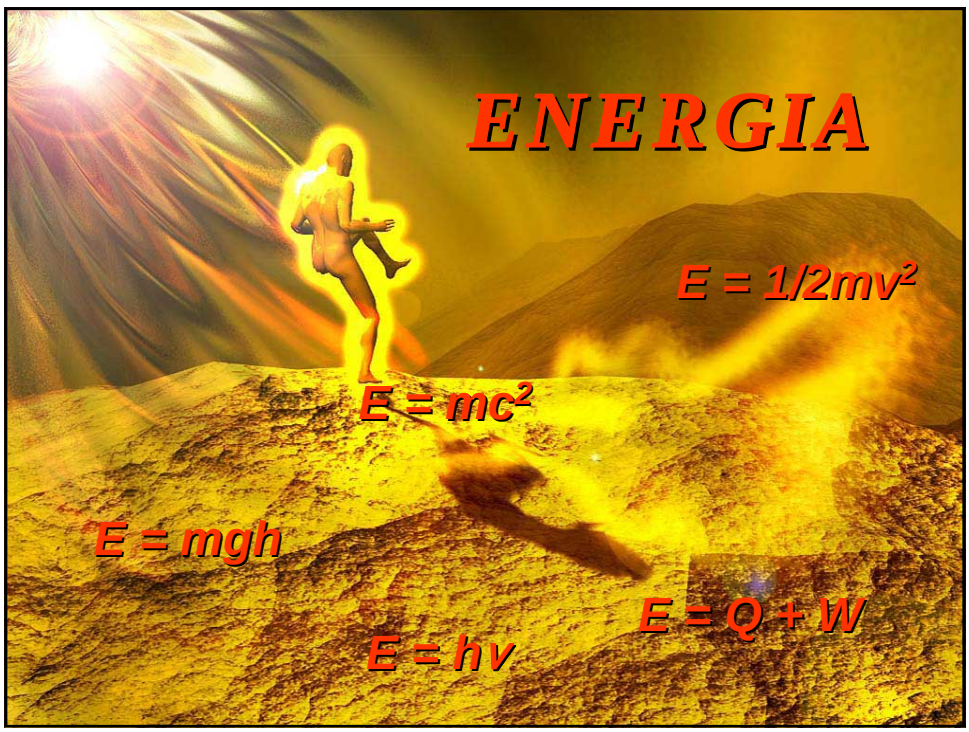
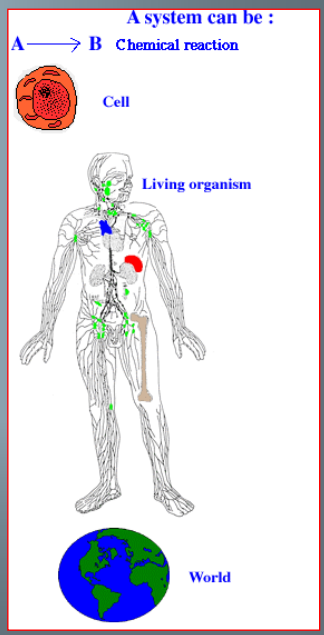


Sistemas y entorno

Hermético (No hay intercambio de energía ni materia)

Cerrado (Hay intercambio de energía pero no de materia)

Abierto (Hay intercambio de energía y materia)

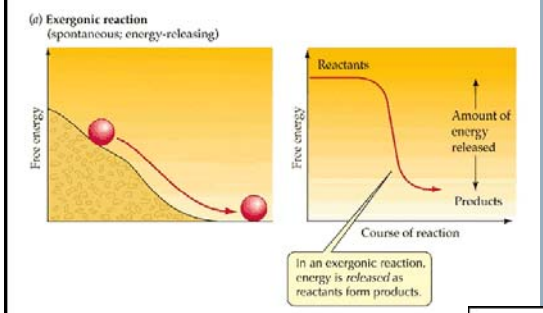


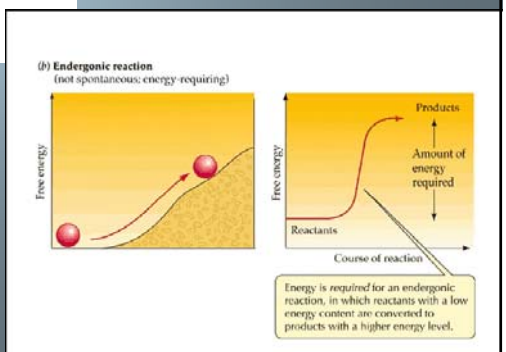
$$\Delta G = \Delta H - T\Delta S$$

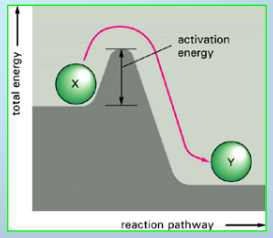
$\Delta G < 0$ Exergónica / Espontánea

$\Delta G > 0$ Endergónica / No Espont.

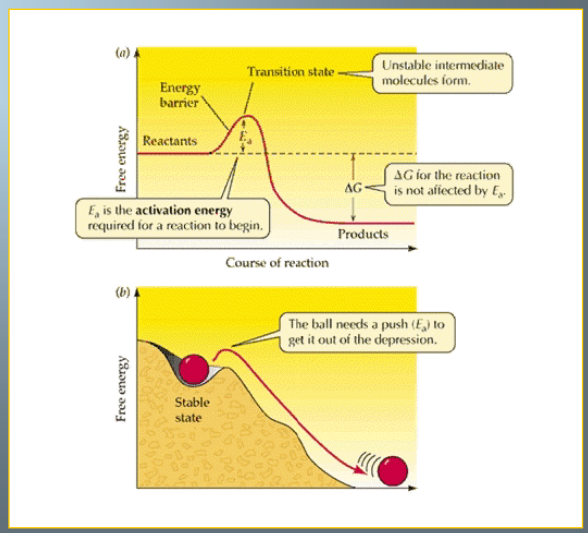
$\Delta G = 0$ Equilibrio termodinámico

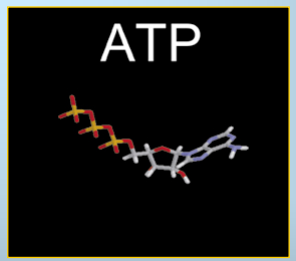


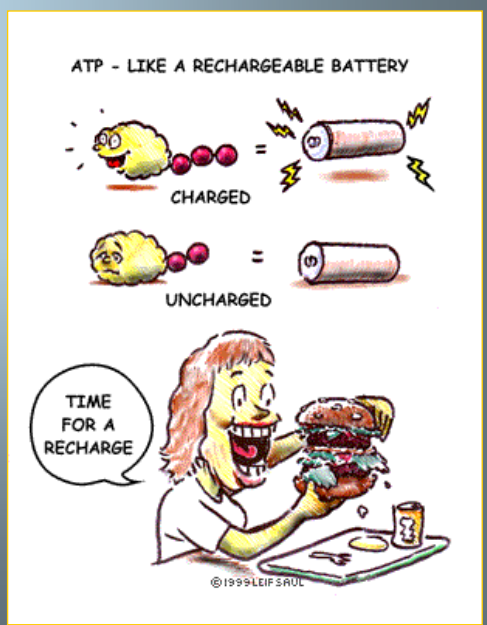


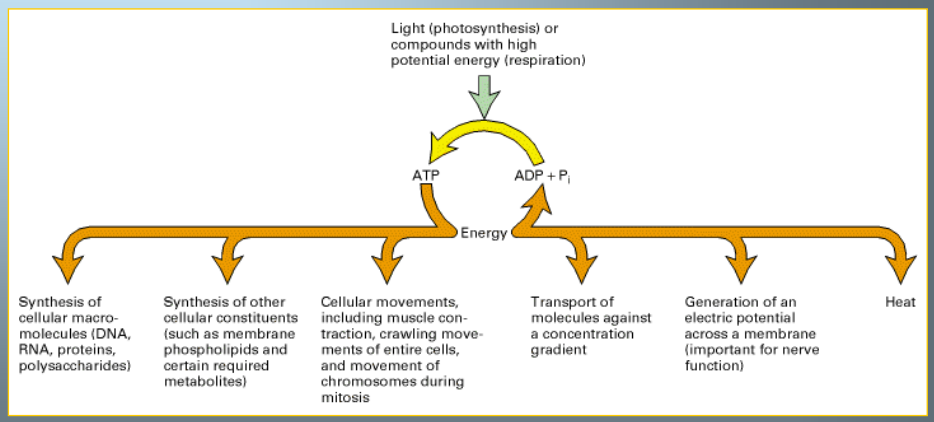

activation energy
X
Y
total energy
reaction pathway

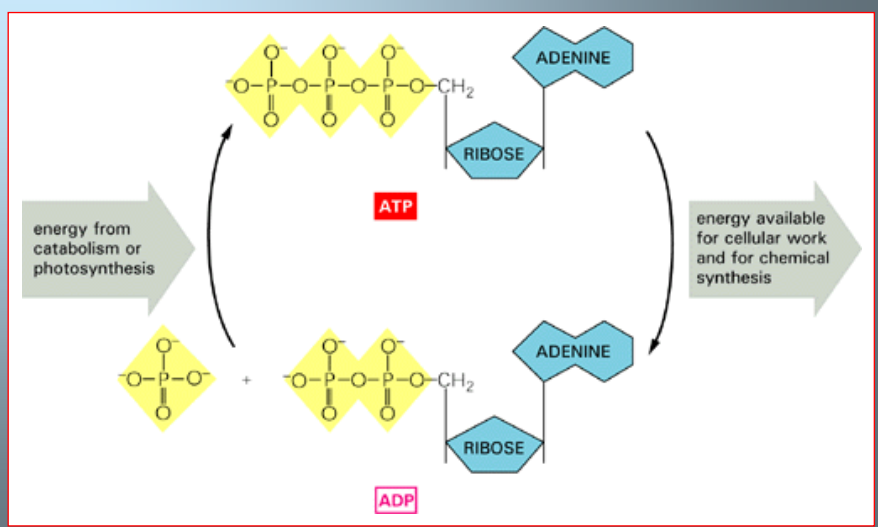
CATALISIS

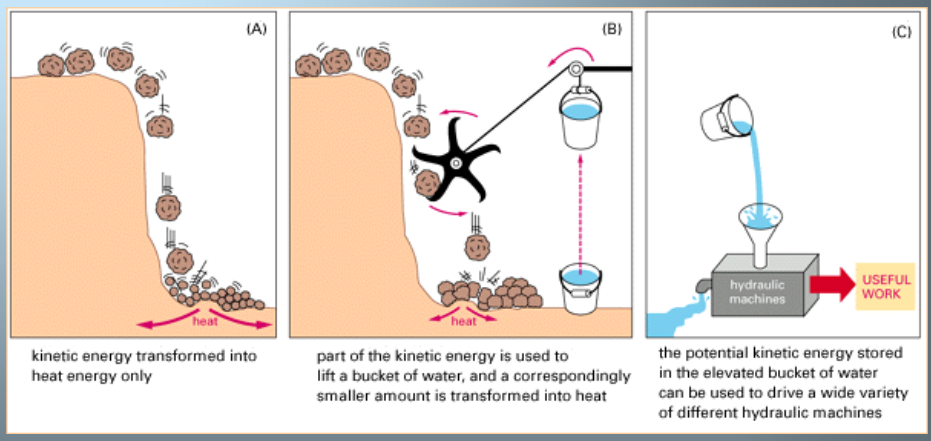

(a)
Transition state
Unstable intermediate molecules form.
Energy barrier
Reactants
E_A
Free energy
ΔG
ΔG for the reaction is not affected by E_a.
E_a is the activation energy required for a reaction to begin.
Products
Course of reaction
(b)
The ball needs a push (E_a) to get it out of the depression.
Free energy
Stable state

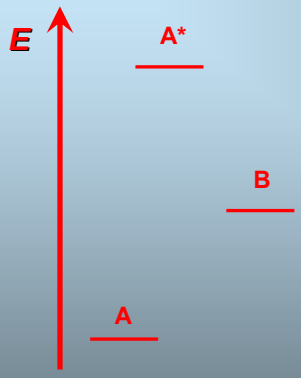

ATP

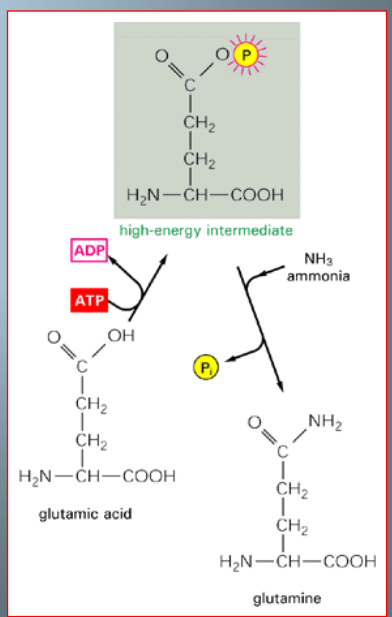

ATP - LIKE A RECHARGEABLE BATTERY
CHARGED
UNCHARGED
TIME FOR A RECHARGE
©1999LEIFSAUL

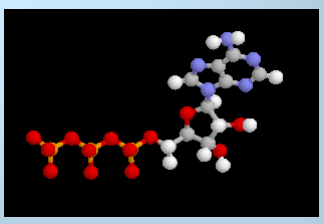

Light (photosynthesis) or compounds with high potential energy (respiration)
ATP
ADP + P_i
Energy
Synthesis of cellular macromolecules (DNA, RNA, proteins, polysaccharides)
Synthesis of other cellular constituents (such as membrane phospholipids and certain required metabolites)
Cellular movements, including muscle contraction, crawling movements of entire cells, and movement of chromosomes during mitosis
Transport of molecules against a concentration gradient
Generation of an electric potential across a membrane (important for nerve function)
Heat

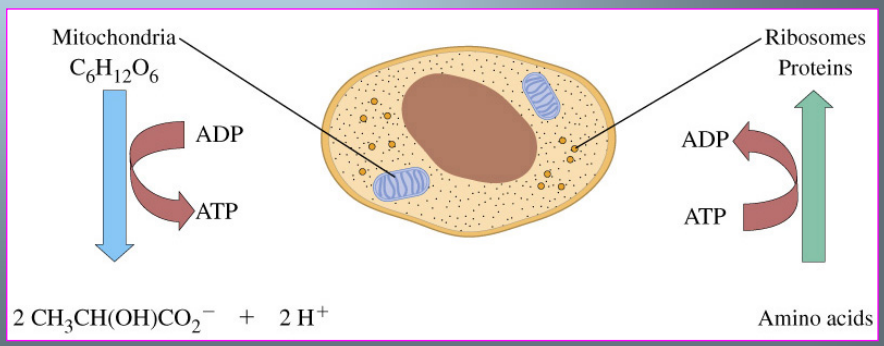

ADENINE
RIBOSE
ATP
energy from catabolism or photosynthesis
energy available for cellular work and for chemical synthesis
ADENINE
RIBOSE
ADP

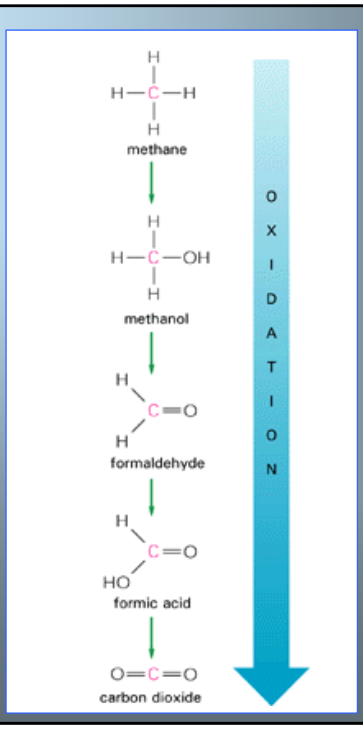

(A)
heat
(B)
heat
(C)
hydraulic machines
USEFUL WORK
kinetic energy transformed into heat energy only
part of the kinetic energy is used to lift a bucket of water, and a correspondingly smaller amount is transformed into heat
the potential kinetic energy stored in the elevated bucket of water can be used to drive a wide variety of different hydraulic machines

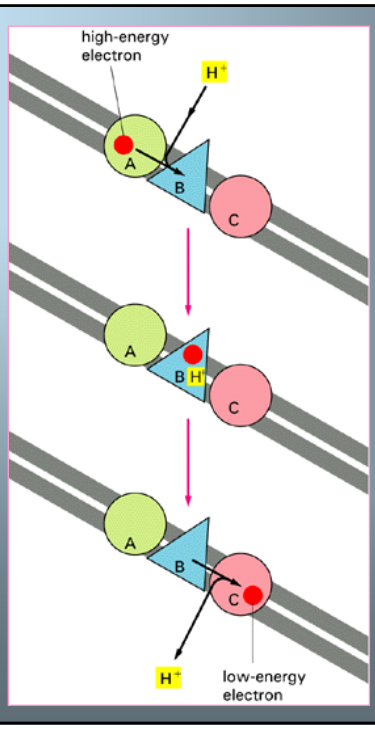

E
A*
B
A

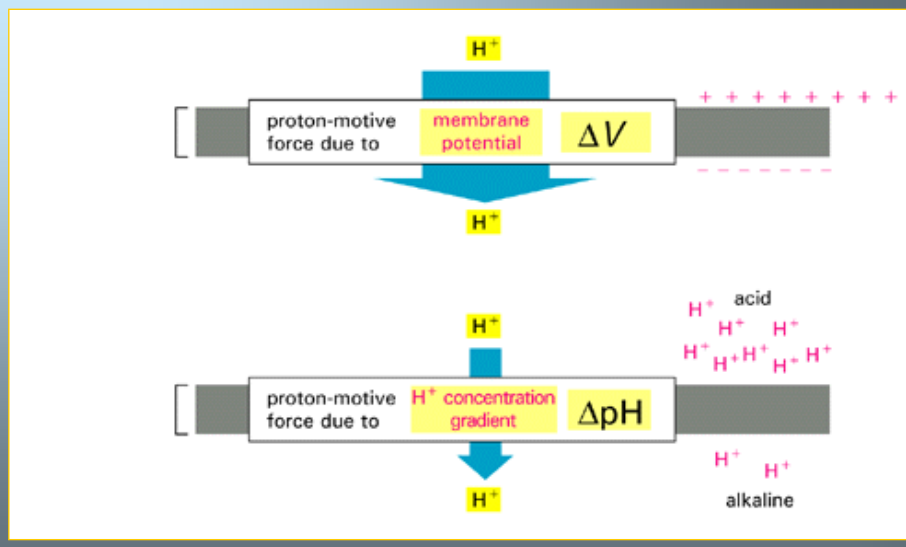

high-energy intermediate
ADP
ATP
NH3
ammonia
glutamic acid
glutamine

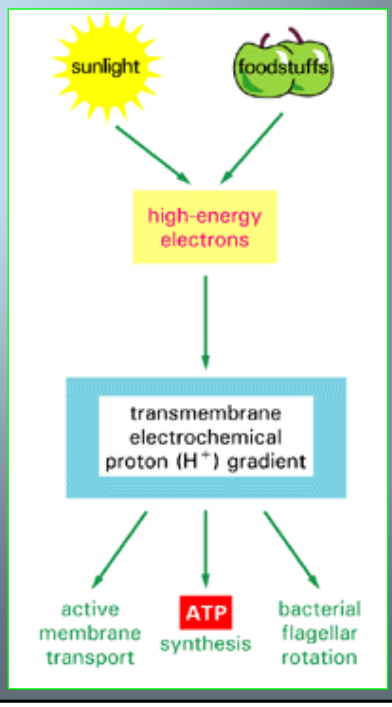


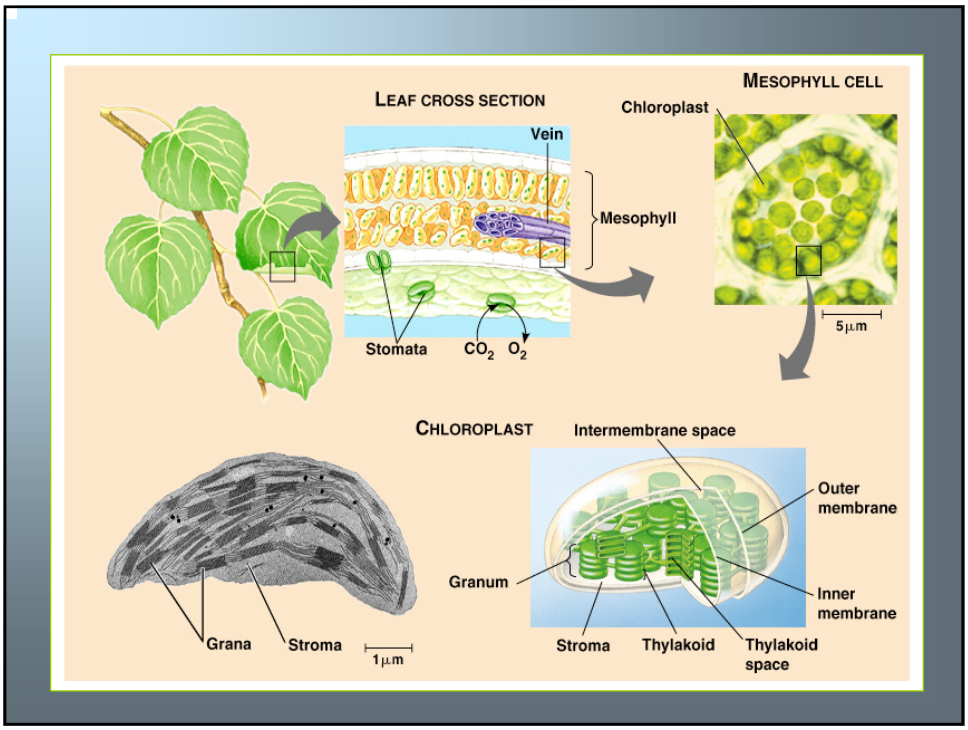

Mitochondria
$C_6H_{12}O_6$
ADP
ATP
Ribosomes
Proteins
ADP
ATP
$2\ CH_3CH(OH)CO_2^-$ + $2\ H^+$
Amino acids

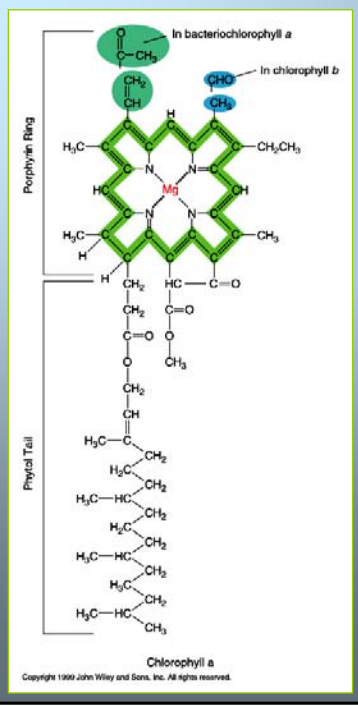

methane
methanol
formaldehyde
formic acid
carbon dioxide
OXIDATION


high-energy
electron
H+
A
B
C
A
B H+
C
A
B
C
H+
low-energy
electron


H+
proton-motive
force due to
membrane
potential
ΔV
H+
H+
acid
H+
H+
H+
H+H+
H+ H+
H+
proton-motive
force due to
H+ concentration
gradient
ΔpH
H+
H+
H+
alkaline


sunlight
foodstuffs
high-energy electrons
transmembrane electrochemical proton (H^+) gradient
active membrane transport
ATP synthesis
bacterial flagellar rotation


LEAF CROSS SECTION
Vein
Mesophyll
Stomata
CO_2
O_2
MESOPHYLL CELL
Chloroplast
5 μm
CHLOROPLAST
Intermembrane space
Outer membrane
Granum
Inner membrane
Stroma
Thylakoid
Thylakoid space
Grana
Stroma
1 μm


In bacteriochlorophyll *a*
In chlorophyll *b*
Porphyrin Ring
Phytol Tail
Chlorophyll a
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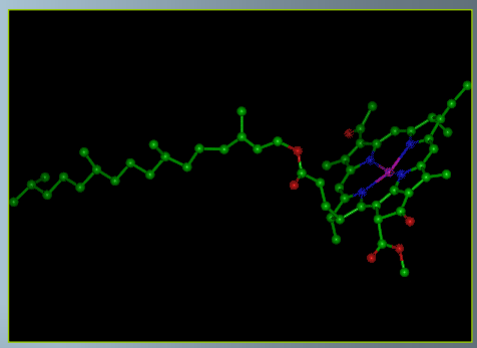
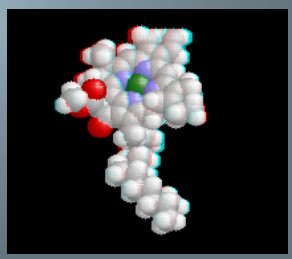
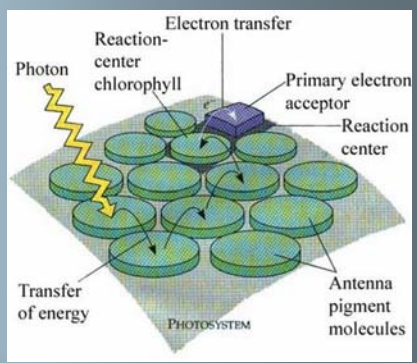
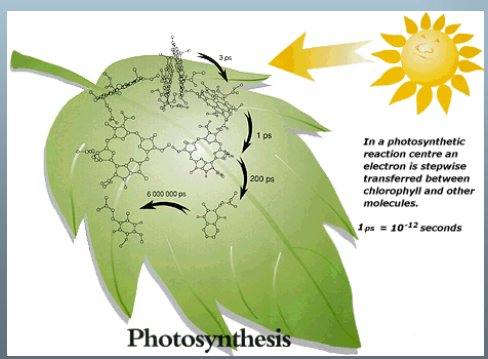
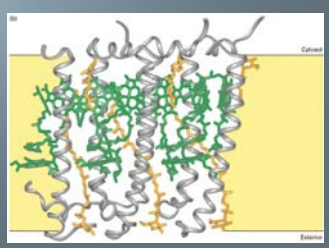
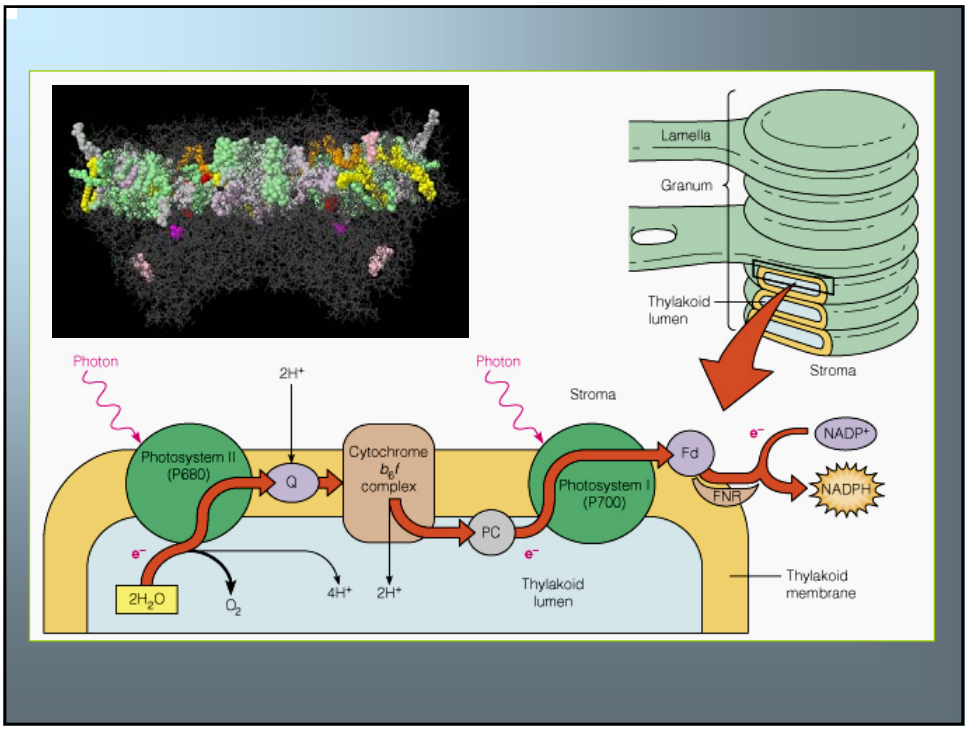


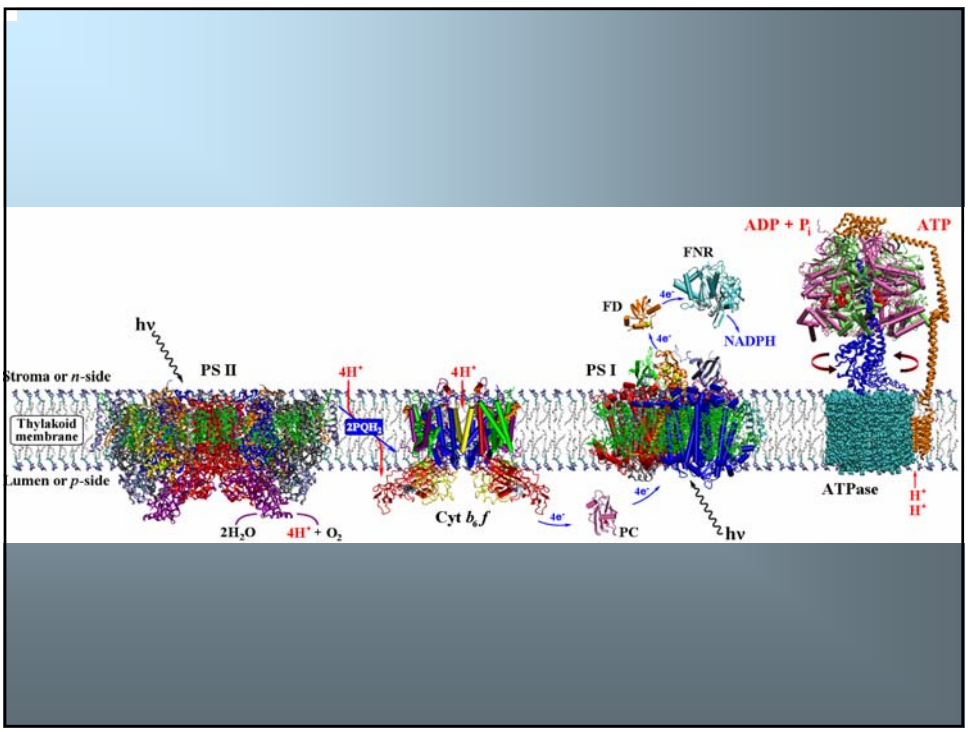


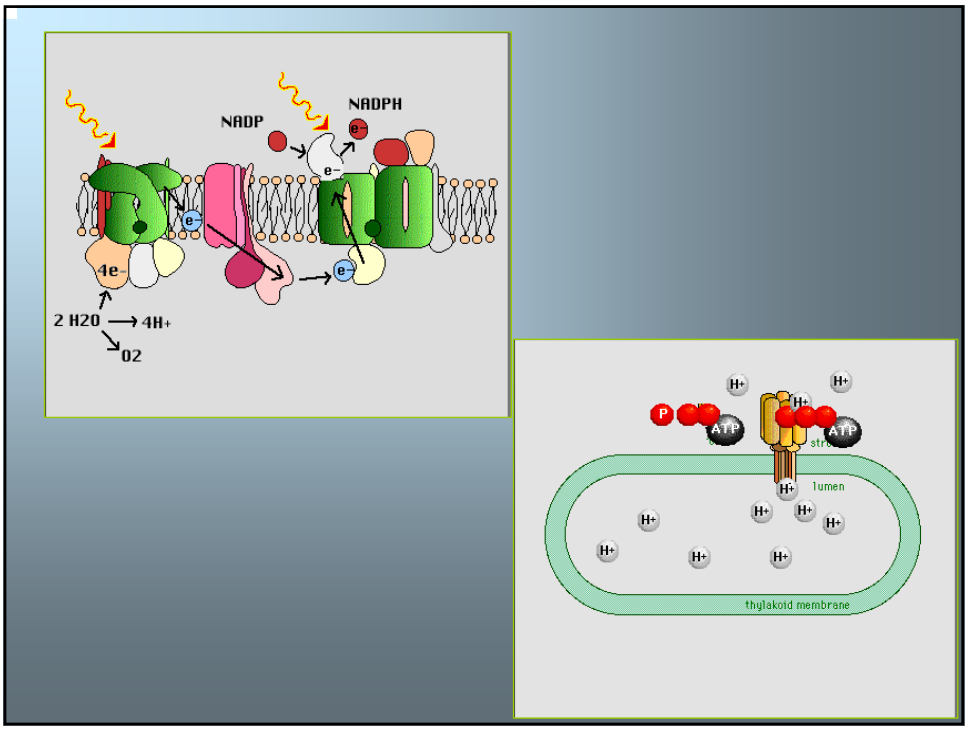

Electron transfer
Reaction-center chlorophyll
Photon
Primary electron acceptor
Reaction center
Transfer of energy
Antenna pigment molecules
PHOTOSYSTEM

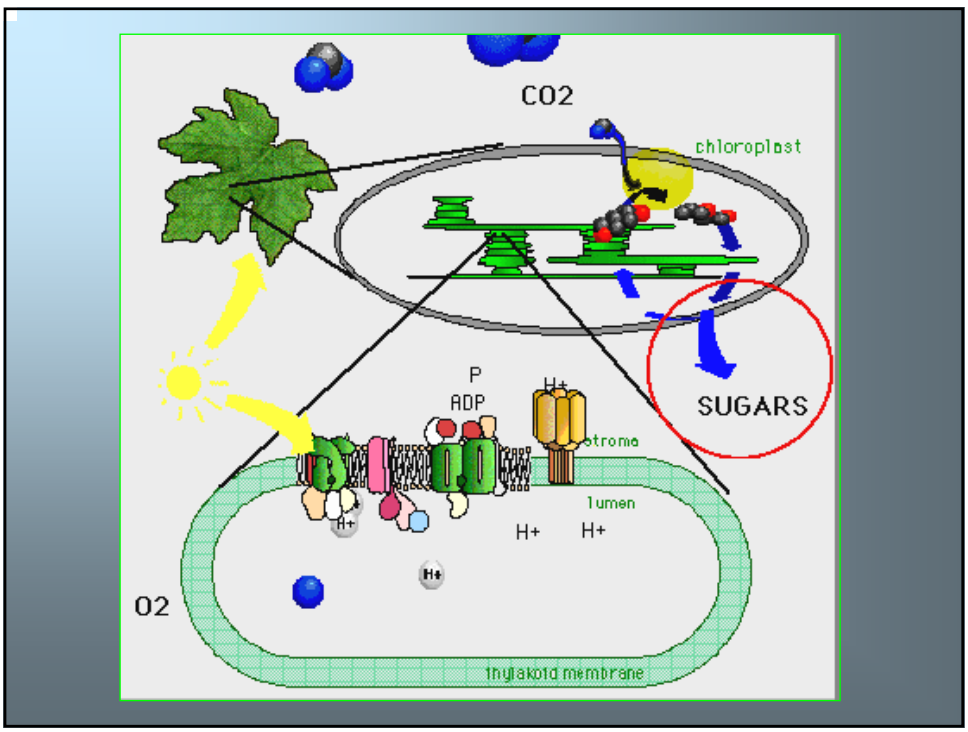

3 ps
1 ps
200 ps
6 000 000 ps
In a photosynthetic reaction centre an electron is stepwise transferred between chlorophyll and other molecules.
1 ps = 10^{-12} seconds
Photosynthesis

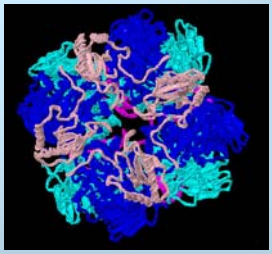


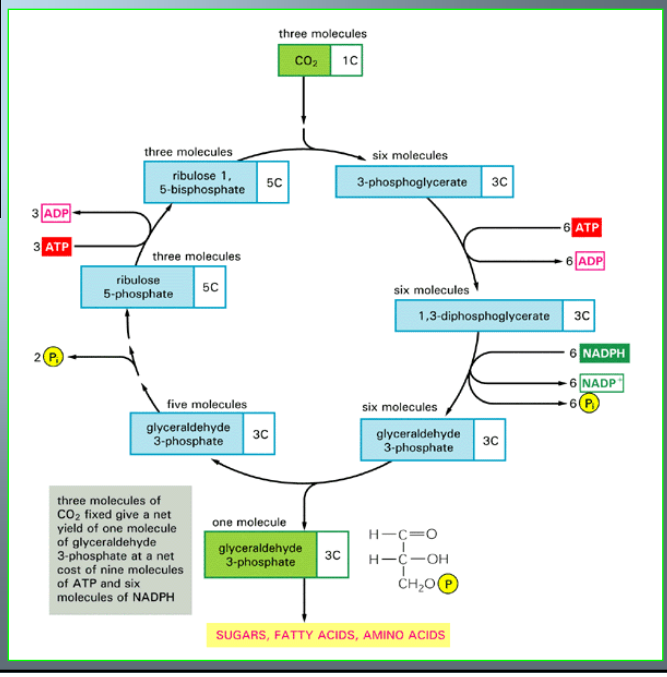

Lamella
Granum
Thylakoid lumen
Stroma
Photon
2H+
Photon
Stroma
Photosystem II (P680)
Q
Cytochrome b_6f complex
PC
Photosystem I (P700)
Fd
FNR
NADP+
NADPH
e−
e−
e−
$2H_2O$
O_2
4H+
2H+
Thylakoid lumen
Thylakoid membrane

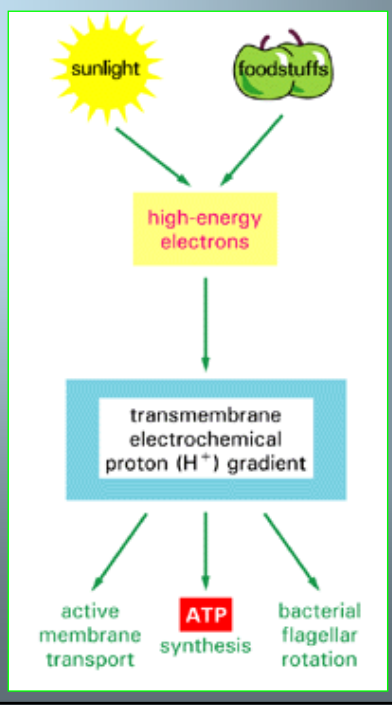

ADP + P_i
ATP
FNR
FD
NADPH
hν
PS II
PS I
Stroma or *n*-side
Thylakoid membrane
Lumen or *p*-side
4H+
4H+
2PQH2
ATPase
H+
H+
$2H_2O$
4H+ + O_2
Cyt b_6f
PC
hν

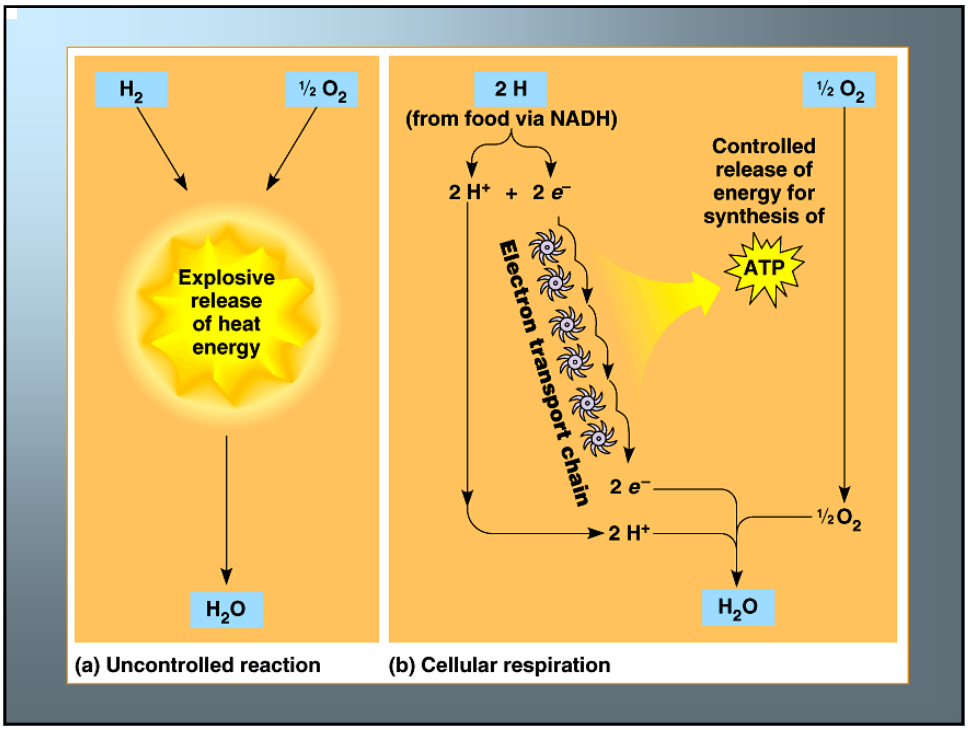

NADP
NADPH
e-
4e-
2 H2O → 4H+
O2
H+
P
ATP
lumen
thylakoid membrane

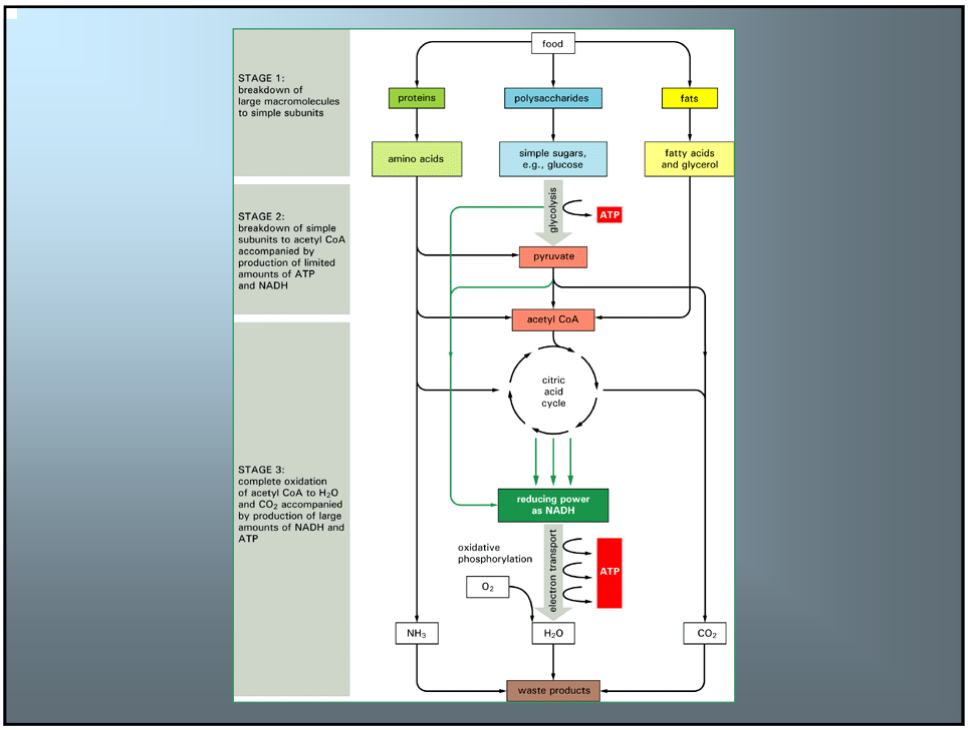

CO2
chloroplast
SUGARS
P
ADP
H+
stroma
lumen
O2
thylakoid membrane

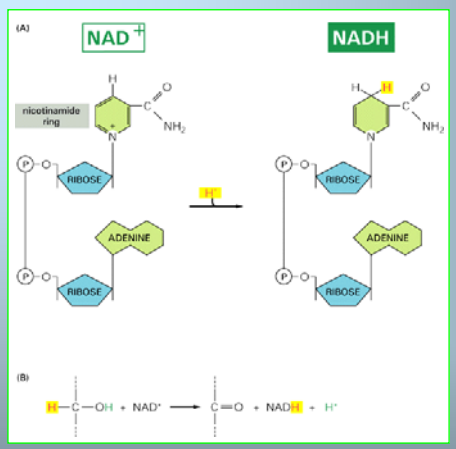


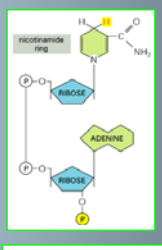

three molecules
CO_2 1C
three molecules
ribulose 1, 5-bisphosphate 5C
six molecules
3-phosphoglycerate 3C
3 ADP
3 ATP
6 ATP
6 ADP
three molecules
ribulose 5-phosphate 5C
six molecules
1,3-diphosphoglycerate 3C
2 P_i
6 NADPH
6 $NADP^+$
6 P_i
five molecules
glyceraldehyde 3-phosphate 3C
six molecules
glyceraldehyde 3-phosphate 3C
three molecules of CO_2 fixed give a net yield of one molecule of glyceraldehyde 3-phosphate at a net cost of nine molecules of ATP and six molecules of NADPH
one molecule
glyceraldehyde 3-phosphate 3C
SUGARS, FATTY ACIDS, AMINO ACIDS

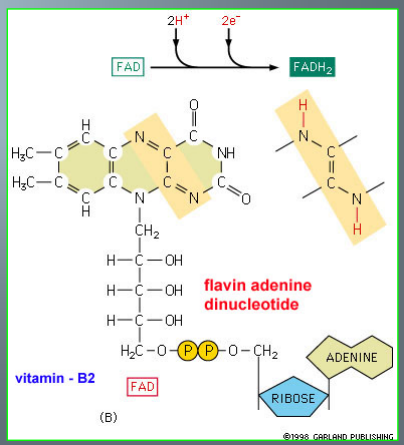

sunlight
foodstuffs
high-energy electrons
transmembrane electrochemical proton (H^+) gradient
active membrane transport
ATP synthesis
bacterial flagellar rotation


H2
½ O2
Explosive release of heat energy
H2O
(a) Uncontrolled reaction
2 H
(from food via NADH)
2 H+ + 2 e−
Electron transport chain
Controlled release of energy for synthesis of
ATP
½ O2
2 e−
2 H+
½ O2
H2O
(b) Cellular respiration


STAGE 1: breakdown of large macromolecules to simple subunits
STAGE 2: breakdown of simple subunits to acetyl CoA accompanied by production of limited amounts of ATP and NADH
STAGE 3: complete oxidation of acetyl CoA to H2O and CO2 accompanied by production of large amounts of NADH and ATP
food
proteins
polysaccharides
fats
amino acids
simple sugars, e.g., glucose
fatty acids and glycerol
glycolysis
ATP
pyruvate
acetyl CoA
citric acid cycle
reducing power as NADH
oxidative phosphorylation
electron transport
ATP
O2
NH3
H2O
CO2
waste products


(A)
NAD+
NADH
nicotinamide ring
RIBOSE
ADENINE
(B)


nicotinamide ring
RIBOSE
ADENINE


2H+
2e−
FAD
FADH2
flavin adenine dinucleotide
vitamin - B2
ADENINE
RIBOSE
(B)
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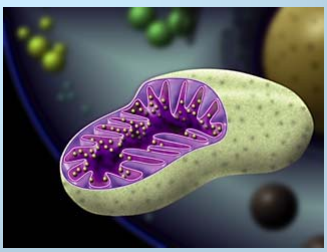
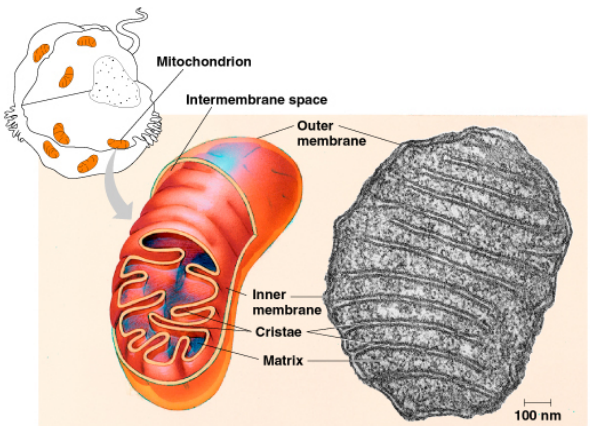
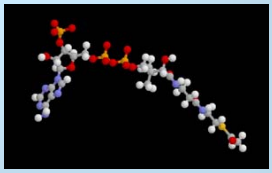
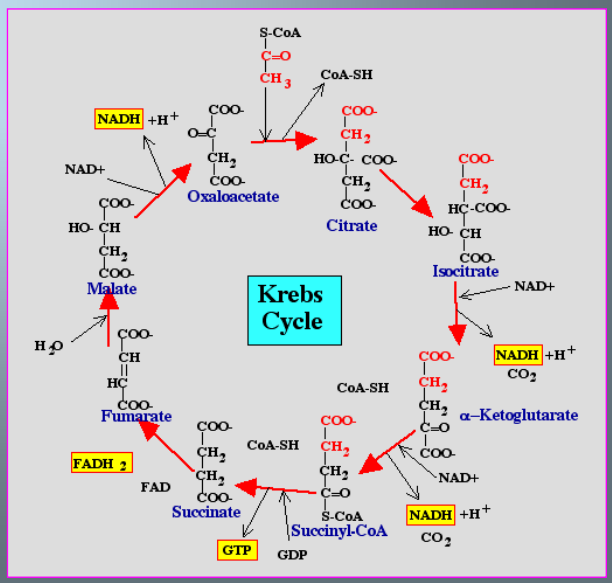
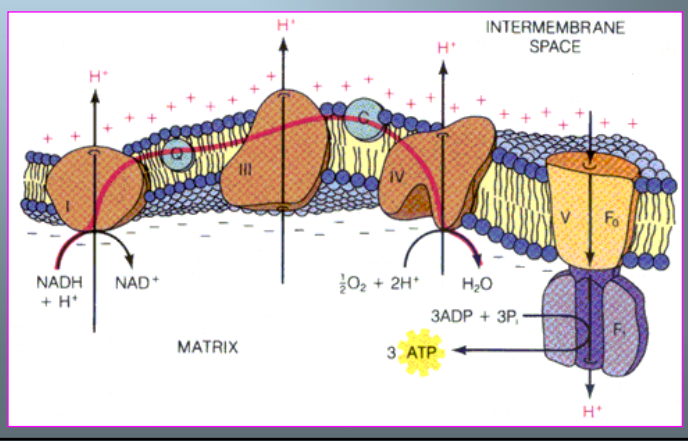
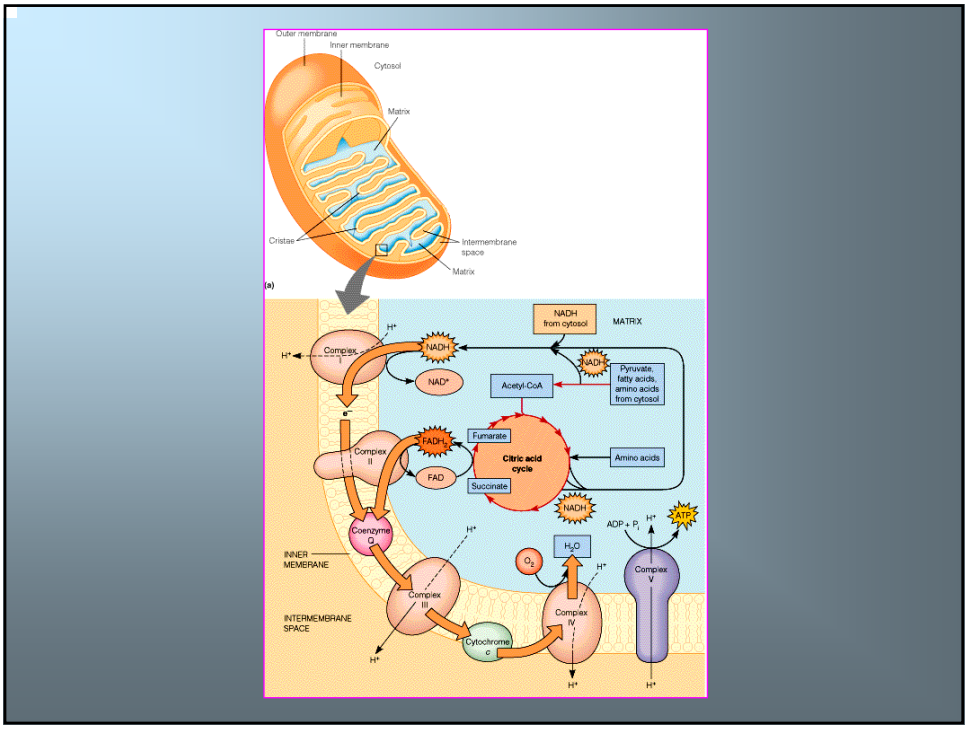


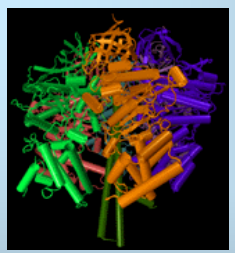

Mitochondrion
Intermembrane space
Outer membrane
Inner membrane
Cristae
Matrix
100 nm

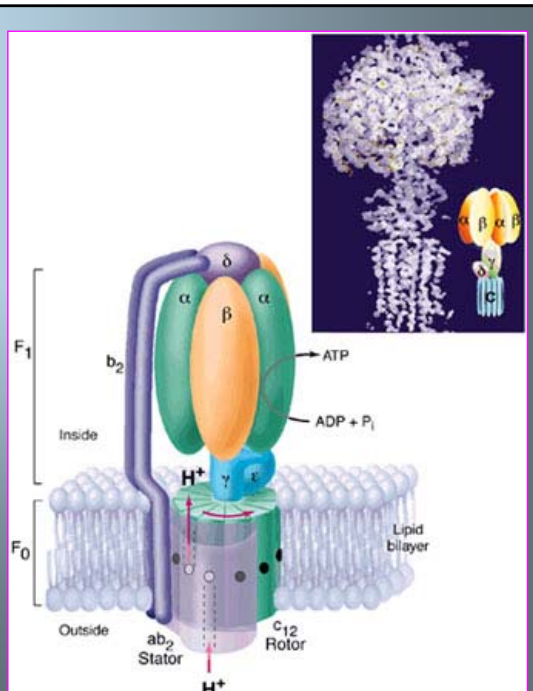


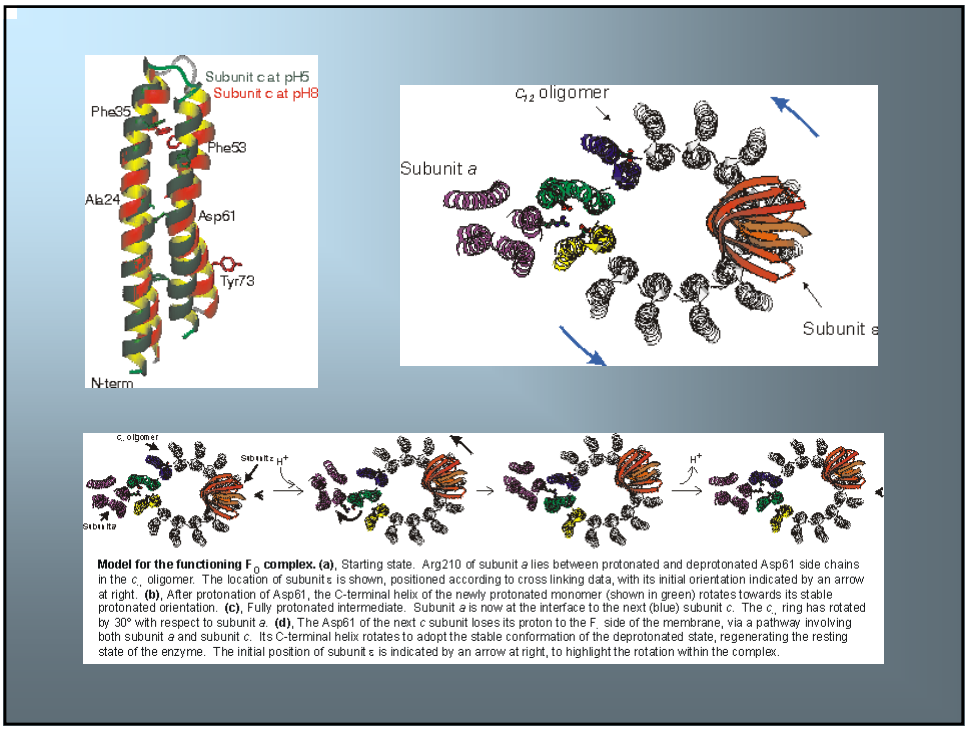

S-CoA
C=O
CH 3
CoA-SH
NADH +H+
COO-
O=C
CH2
COO-
Oxaloacetate
NAD+
COO-
HO- CH
CH2
COO-
Malate
COO-
CH2
HO-C- COO-
CH2
COO-
Citrate
COO-
CH2
HC-COO-
HO- CH
COO-
Isocitrate
NAD+
Krebs Cycle
H2O
COO-
CH
HC
COO-
Fumarate
NADH +H+
CO2
COO-
CH2
CH2
C=O
COO-
α–Ketoglutarate
CoA-SH
FADH 2
FAD
COO-
CH2
CH2
COO-
Succinate
CoA-SH
COO-
CH2
CH2
C=O
S-CoA
Succinyl-CoA
NAD+
NADH +H+
CO2
GTP
GDP


H+
INTERMEMBRANE SPACE
H+
H+
I
II
III
IV
V
F0
F1
NADH + H+
NAD+
½O2 + 2H+
H2O
3ADP + 3Pi
3 ATP
MATRIX
H+

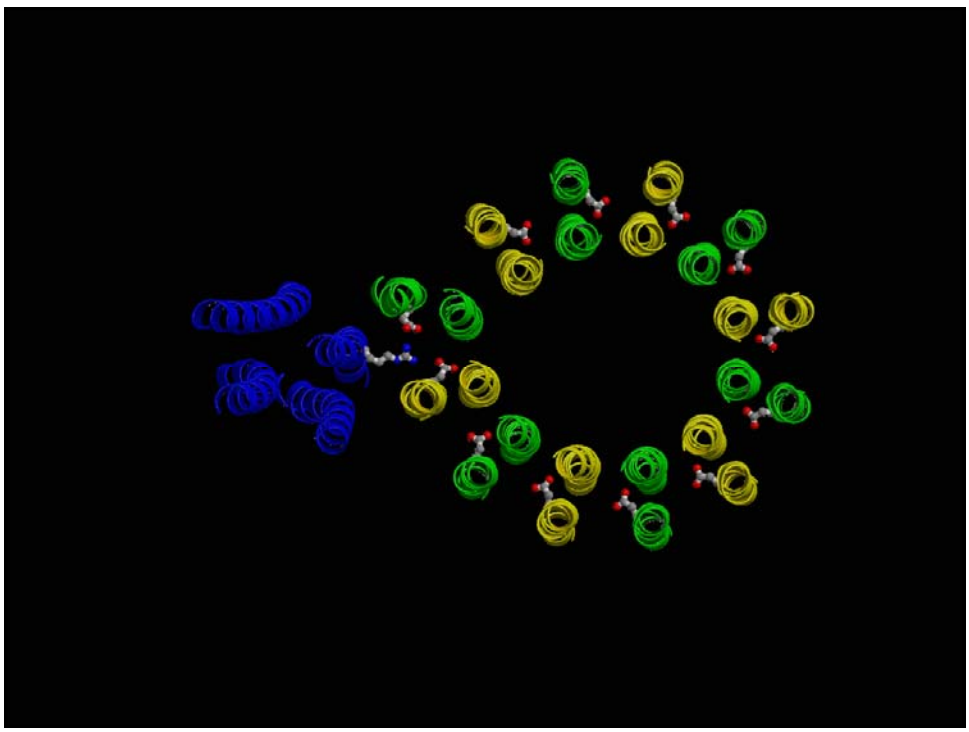

Outer membrane
Inner membrane
Cytosol
Matrix
Cristae
Intermembrane space
Matrix
(a)
NADH from cytosol
MATRIX
Complex I
NADH
NAD+
Acetyl CoA
Pyruvate, fatty acids, amino acids from cytosol
Complex II
FADH2
FAD
Fumarate
Citric acid cycle
Amino acids
Succinate
Coenzyme Q
INNER MEMBRANE
INTERMEMBRANE SPACE
Complex III
Cytochrome c
Complex IV
Complex V
ADP + Pi
ATP
H2O
O2
H+

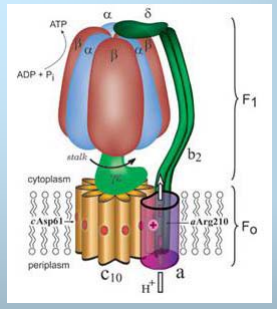


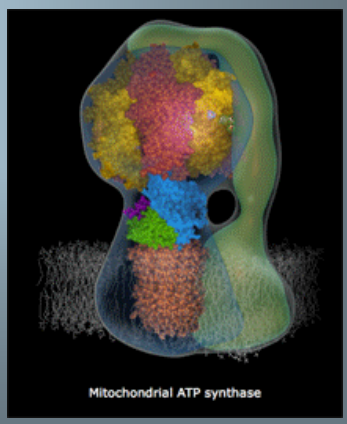

δ
α
β
α
F1
b2
ATP
ADP + Pi
Inside
H+
γ
ε
F0
Lipid bilayer
Outside
ab2 Stator
c12 Rotor
H+
α β α β
δ
γ
ε
c



Model for the functioning F_0 complex. (a), Starting state. Arg210 of subunit *a* lies between protonated and deprotonated Asp61 side chains in the c_{10} oligomer. The location of subunit ε is shown, positioned according to cross linking data, with its initial orientation indicated by an arrow at right. **(b)**, After protonation of Asp61, the C-terminal helix of the newly protonated monomer (shown in green) rotates towards its stable protonated orientation. **(c)**, Fully protonated intermediate. Subunit *a* is now at the interface to the next (blue) subunit *c*. The c_{10} ring has rotated by 30° with respect to subunit *a*. **(d)**, The Asp61 of the next *c* subunit loses its proton to the F. side of the membrane, via a pathway involving both subunit *a* and subunit *c*. Its C-terminal helix rotates to adopt the stable conformation of the deprotonated state, regenerating the resting state of the enzyme. The initial position of subunit ε is indicated by an arrow at right, to highlight the rotation within the complex.




α
δ
ATP
β
α
β
α
β
ADP + Pi
F1
stalk
b2
cytoplasm
cAsp61
aArg210
Fo
periplasm
c10
H+
a


Mitochondrial ATP synthase