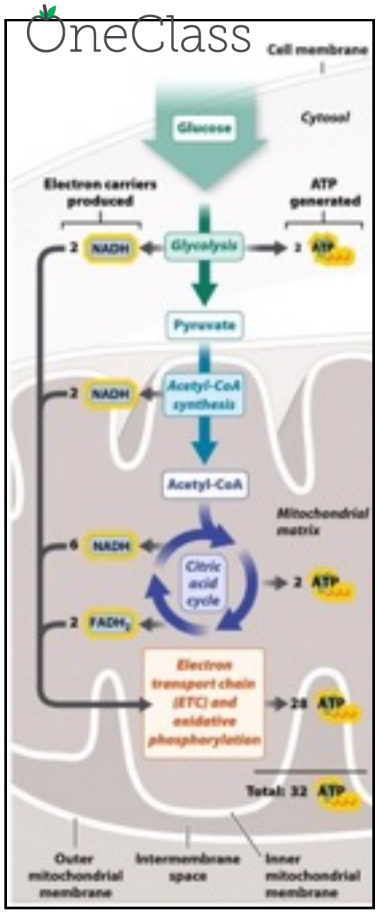


CELLULAR RESPIRATION:
Eukaryotes:
1. Glycolysis (Where? cytoplasm)
   - Input: glucose, 2xATP
   - Output: 2xNADH, 2xpyruvate, 2xATP
2. Acetyl Co-A synthesis (where? matrix)
   - Input: 2xpyruvate
   - Output: 2xNADH, 2xCO2, 2xAcetylCo-A
3. Krebs cycle (where? matix)
   - Input:2xAcetylCo-A
   - Output: 2xCitrate, 4xCO2, 2xATP, 2xFADH2, 6NADH
4. ETC: (where? matrix and inter membrane space)
   - exergonice (-G) redox rxns
   - NADH and FADH2 reduced
   - ^^energy to pump H+ from matrix->intermembrane space
   - ATP synthase (facilitated diff) - endergonic (+G)

Prokaryotes:
Same as eukaryote except in ETC, H+ is pumped out of cytoplasm, in-between cell membrane and wall

- Template strand=Transcribed
- Coding strand=NOT transcribed
- 3' = OH end
- 5' = phosphate
- purine + pyrimidine = same geometry
- DNA more stable than RNA because of stacking interactions
- DNA=negative

CELLULAR RESPIRATION

	Location in Eukaryotes	Location in bacteria
Glycolysis	cytoplasm	cytoplasm
Acetyl-CoA	matrix	cytoplasm
CAC	matrix	cytoplasm
ETC	intermembrane space	cytoplasmic membrane

Anaerobic Respiration
- Uses a TEA that is NOT oxygen (inorganic)
- ETC: involves membrane bound proteins
- large energy production

Lactic Acid Fermentation (cytoplasm)
- Pyruvate oxidizes NADH -> Lactate + NAD+

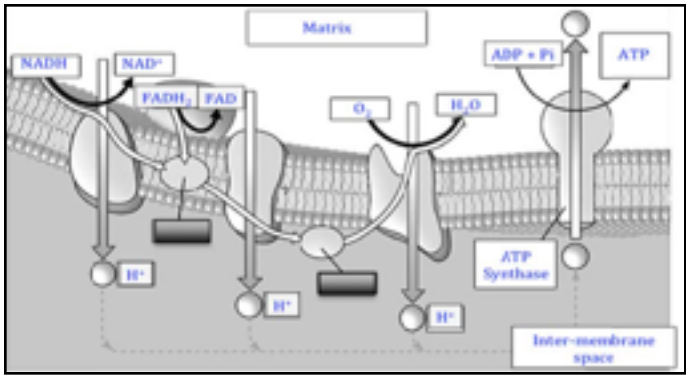
Alcohol Fermentation (cytoplasm)
- Pyruvate -> CO2 + ethanol

*Lactic acid and alcohol fermentation = small ATP yield
*Uses organic molecules as TEA

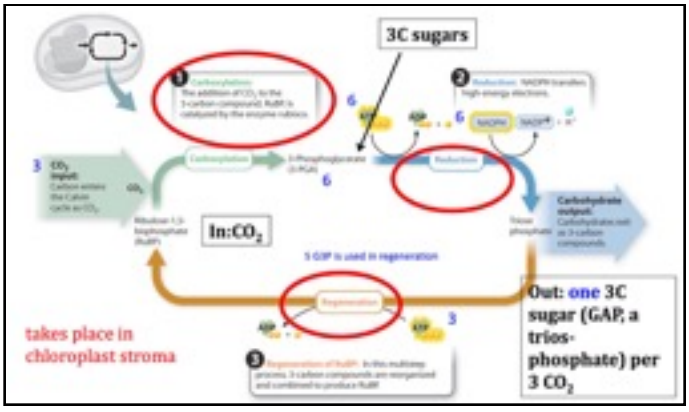
TYPES OF PHOSPHORYLATION:
Oxidative Phosphorylation:
Indirect reduction of ADP (ETC)
Substrate Level Phosphorylation:
Direct reduction of ADP (Glycolysis, CAC/Krebs)
Photophosphorylation:
H2O provides electrons for PSII
Light energy to reduce ADP (pETC)
Oxygenic photophosphorylation:

PHOTOSYNTHESIS:
1.Light dependent rxn: (where? between lumen and stroma)
- Light hits PSII
- hydrolysis -> electron
- electron excited by light
- Electron acceptor oxygen
- provides energy for H+ gradient
- ATP synthase
- Light hits PSI
- electron excited
- electron acceptor NADP
- provides energy for NADPH synthase

2. Light independent rxn: Calvin Cycle (where? stroma)
- 3CO2+3RuBP->3PGA
- 3PGA->GAP
- Input: 9ATP and 6NADPH



	Oxidative phosphorylation	Photophosphorylation
Where does it happen?	In mitochondria (eukaryote) In cytoplasm (bacteria)	In chloroplast (in eukaryote). In cytoplasm (bacteria)
It happens during which metabolic process?	Respiration	Photosynthesis
What are the inputs?	NADH, $FADH_2$, O_2, ADP, Pi	H_2O, $NADP^+$, ADP, Pi
What are the outputs?	NAD^+, FAD, H_2O, ATP	O_2, NADPH, ATP
Is there electron flow?	Yes	Yes
Where are electron carriers located?	On inner membrane of mitochondria in eukaryotic cells, and cell membrane in bacterial cells	On thylakoid membrane
Molecule(s.)that deliver electrons to the ETC	NADH, $FADH_2$	H_2O
Electrons end up with	O_2	$NADP^+$
H^+ gradient is created in both. H^+ is pumped from where to where?	H^+ is pumped from matrix to inter-membrane space	H^+ is pumped from stroma to thylakoid lumen
Enzyme that synthesizes ATP	ATP Synthase	ATP Synthase
Where is ATP synthesized?	Mitochondrial matrix (eukaryotes) Cytoplasm (bacteria)	Stroma (in eukaryote) In cytoplasm (bacteria)



GENOMES&DNA STRUCTURE

PCR:
(Need: DNA, DNA primers, DNA poly (Taq), ATGC)
1. Heated to separate strands
2. Cooled for DNA primers to bind to DNA
3. DNA poly synth DNA

DNA Replication:
(Need: DNA, helicase, topoisomerase, ssb proteins, RNA primers, DNA poly 3&1, ligase, telomerase)
1. Occurs @ origin of repl.
2. Helicase unwinds DNA, topoisomerase relaxes supercoiling
3. ssb proteins bind to keep strands from annealing
4. RNA poly puts primers
5. DNA poly 3 (3'->5') synth DNA (semi conserv)
6. Leading strand=cont. vs lagging=discont
7. DNA poly 1 repl RNA primers with DNA
8. DNA ligase binds Okazaki frags together
9. Lagging strands unable to replicate ends. Telomerase extends end and permits copying of original strand

*Leading strand 3' end towards replication fork

Mutations:
germ-line=reproductive cells, transferrable
somatic=all other cells
point mutation=bp repl by diff bp
- silent: codes for same aa
- missense: codes for diff aa
- nonsense: codes for stop

insertion/deletion=frameshift mutation
chromosome with x2 region=dupl
chromosome w/o region=deletion
inversion=flipped
reciprocal translocation=2 chromosomes exchg parts

Repair

EUKARYOTE:

Transcription: (where? nucleus)
1. Gen transcrip factors bind to TATA(promoter) and recruits RNA poly
2. transcrip activ proteins bind to enhancer and recruit mediator complex
3. RNA poly begins to transcribe @ +1 site
4. Bases are added, high energy PO4 bond broken = energy for phosphodiester bonds
5. Ends at terminator
6. RNA processing: 5' cap+polyA tail+introns spliced out(alt splicing) <prev degr.
7. mRNA->cytoplasm

Translation: (where? cytoplasm)
1. INITIATION: Initiation factors bind to mRNA @ 5'cap
2. recruits small subunit of ribosome
3. moves along mRNA until AUG
4. AUG recruits large ribosomal subunit
5. ELONGATION: tRNA Met moves from A->P site
6. next tRNA Val binds to A site, Met detaches and bonds with Val
7. cont until stop codon

PROKARYOTE: Transl and Transcrip occurs simultaneously

Transcription:(where? cytoplasm)
1. sigma factors bind to promoter (-35, -10) recruits RNA poly
2. at +1 site, RNA poly begins to transcribe
3. Same as eukaryote, no RNA processing

Translation: (where? cytoplasm)
1. initiation complex is formed shine-dalgarno seq
2. Recruits ribosome subunits and starts at AUG
3. Can contain must open reading frames (polycistronic mRNA)

* How do DNA binding proteins (ex. sigma/transcritption factors recog correct binding site on DNA?
  - similar tertiary structure to major/minor groove
  - interact with major and minor grooves

Energy Source	Photo	Chemo
Electron donor	Organo (ex. glycerol)	Litho (inorganic) (ex. H2O,NO2, H2S)
Carbon source	Hetero: obtains carbon from other organisms (ex. glucose, glycerol)	Auto (produces glucose from carbon)

OPERONS:

Prokaryotes:
- **Mal Operon: (+) regul**
  operator (1), promoter (2)
  1. w/o Mal T, RNA binds poorly
  2. Mal T (activator) always present (basal lvls)
  3. Maltose (inducer) binds to Mal T (conformational change)
  4. Mal T binds to operator and recruits RNA poly
  5. RNA poly transcribes Mal P and Q
- **Lac Operon: (-) regul**
  promoter (1), operator (2)
  1. w/o Lac I, RNA binds well
  2. Lac I (repressor) always bound to operator, prevents RNA poly from binding and transcribing
  3. lactose (inducer) binds to Lac I and causes it to fall off operator
  4. RNA poly is free to bind and transcribe Lac Y and Z