(27) **Today**

Chap 13.1: Glycolysis (skip 13.1.3)

Next Class (28)

Chap 13: Glycolysis Energetics and Gluconeogenesis

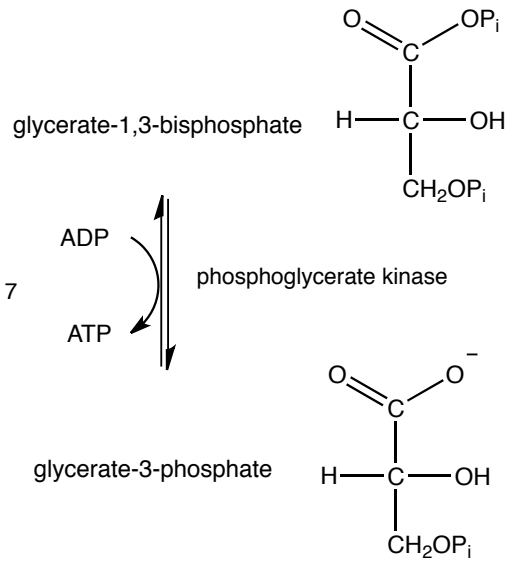
(29) **Second Class from Today**

Chap 13: Glycolysis Energetics and Gluconeogenesis

Third Class from Today (30)

Chap 13: Pentose Phosphate Pathway

Rework test 2 and hand in on Wednesday, April 16


glycerate-1,3-bisphosphate
ADP
ATP
phosphoglycerate kinase
glycerate-3-phosphate

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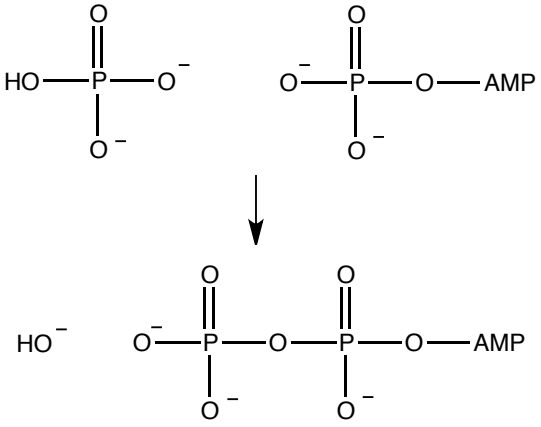
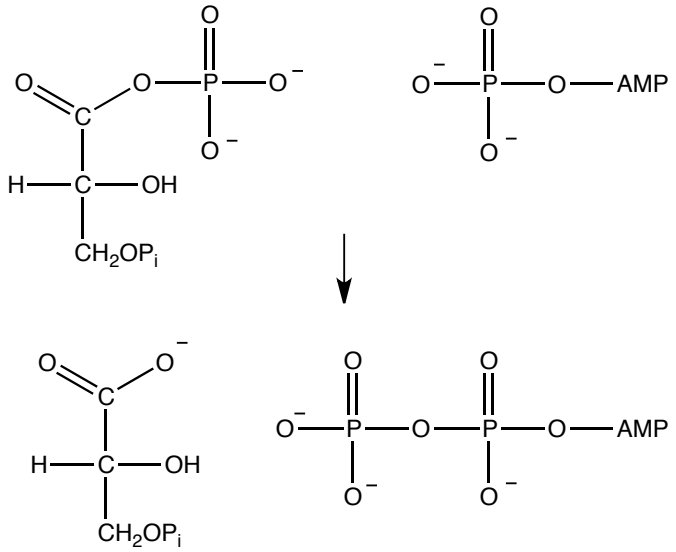

HO
O
P
O
AMP
HO

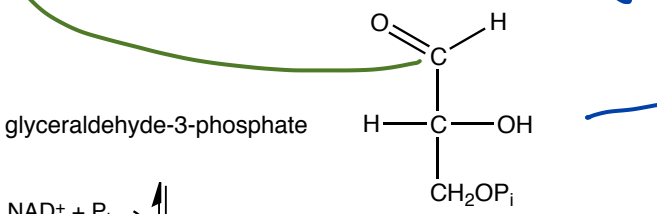

O
C
H
OH
CH2OPi
O
P
AMP

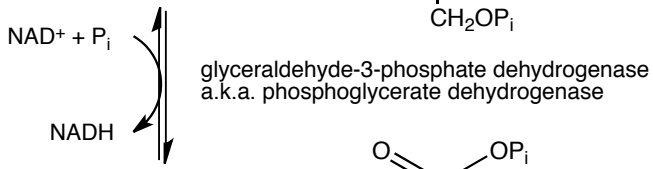
oxidation #

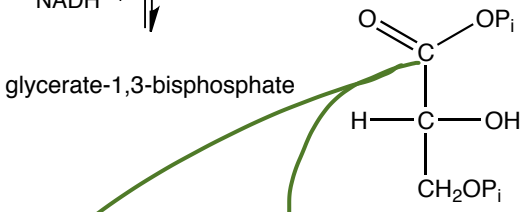
O + -1 +1 +1 = +1 for the aldehyde C atom

C-C C-H C-O C-O

This rxn adds a phosphate, but we are not consuming an ATP





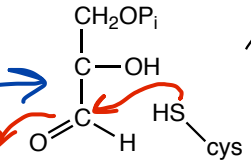


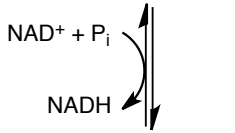
O +1 +1 +1 = 3

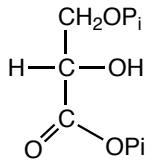
C-C C-O C-O C-O

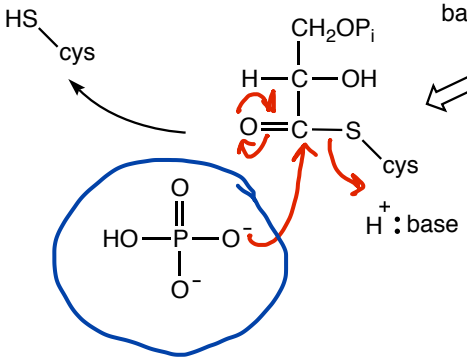
coenzyme - consumed during reaction
- regenerated elsewhere
- returned to the active site

oxidation of the C atom helps make rxn more favorable



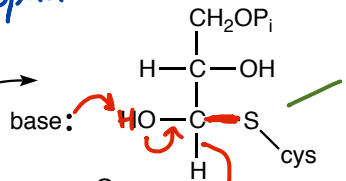


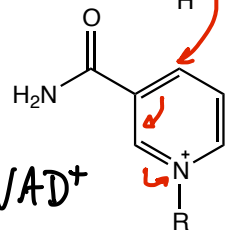




free Pi

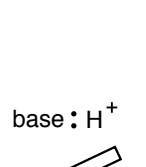
covalent catalysis using a nucleophilic S atom



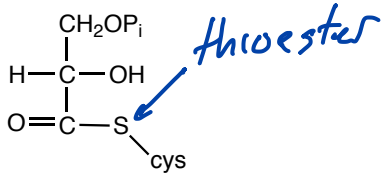


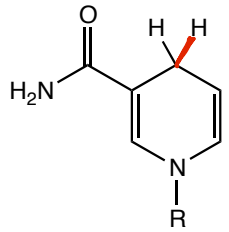
coenzyme

tetrahedral intermediate in an acyl substitution rxn

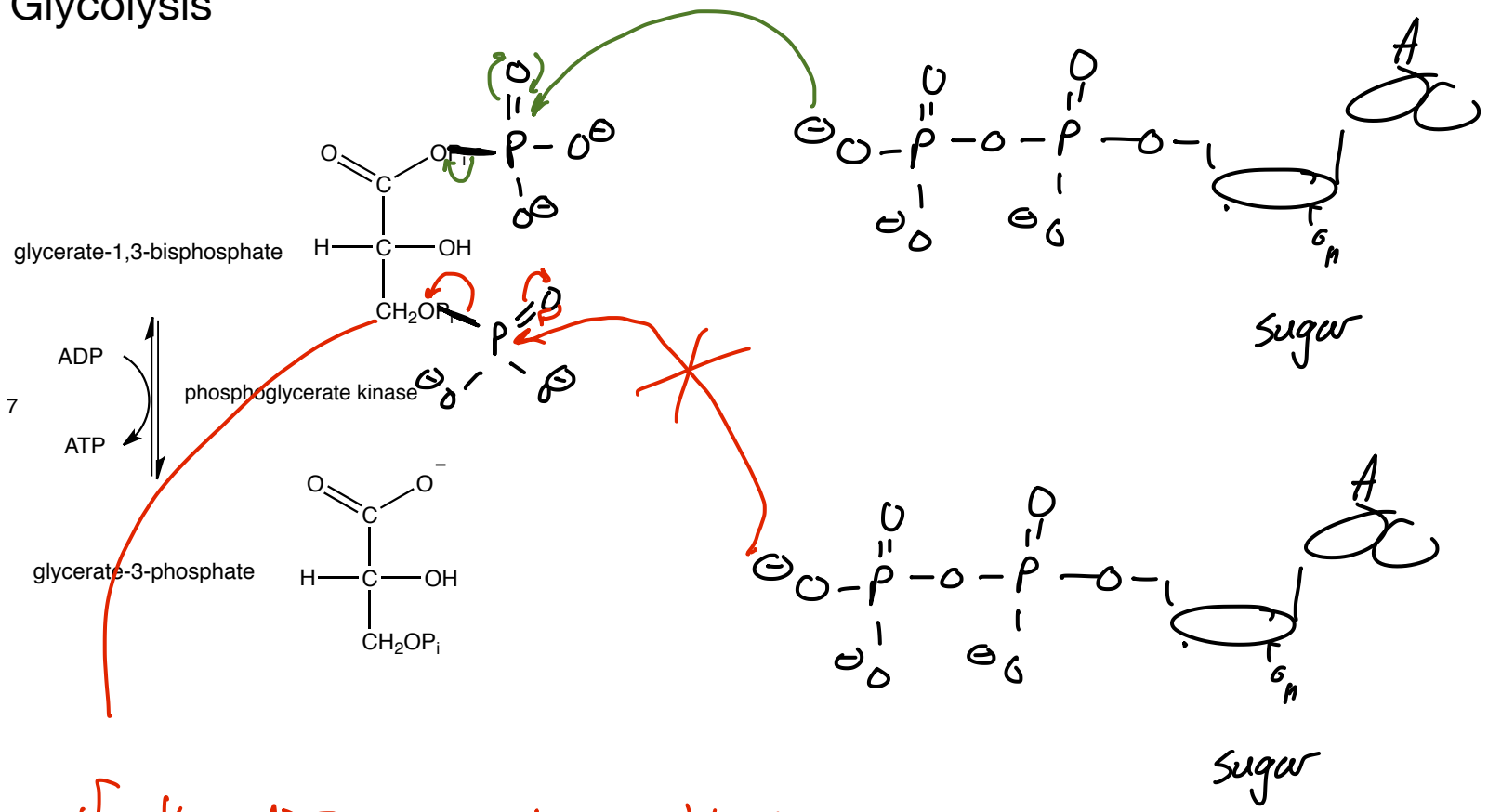


thioester





an H+ and 2e- are transfered to NAD+ to form NADH



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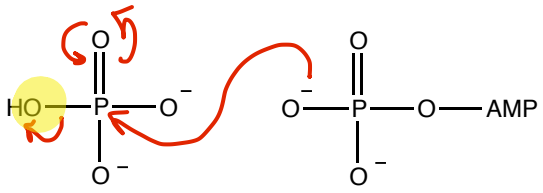
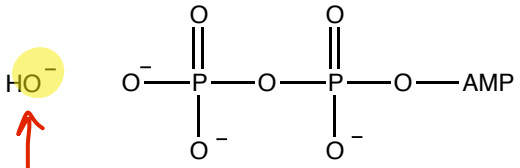
since we get 2 gly-1,3-bis P_i from each glucose we form 2 ATP. We just broke even... 2 ATP in (step 1 or 3) now 2 ATP out

if the ADP reacted with the phosphate on C_3 an alkoxide would form $-CH_2O^{\ominus}$ strongly basic

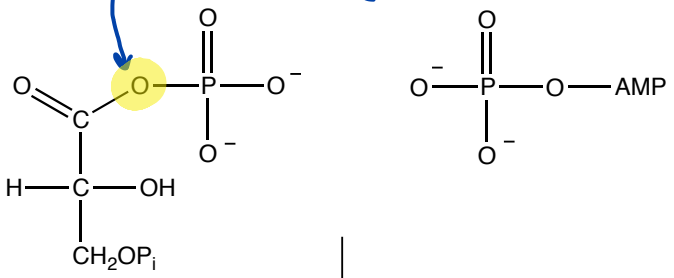
not a good leaving group

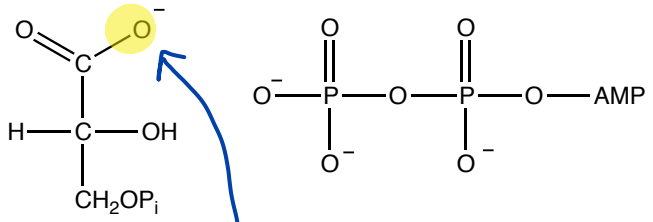
ADP reacts with P_i on C_1 because a $-C(=O)-O^{\ominus}$ carboxylate forms... a good LG





if ADP were to react with P_i the LG would be a $OH^{\ominus}$ ion. $OH^{\ominus}$ is not a good LG.





the O that would have had to leave P_i as $OH^{\ominus}$ can now leave as part of a lower E (less basic) carboxylate ion

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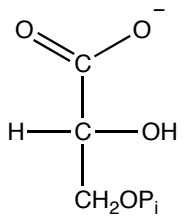
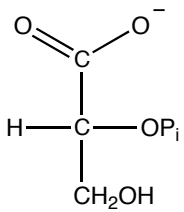
glycerate-3-phosphate



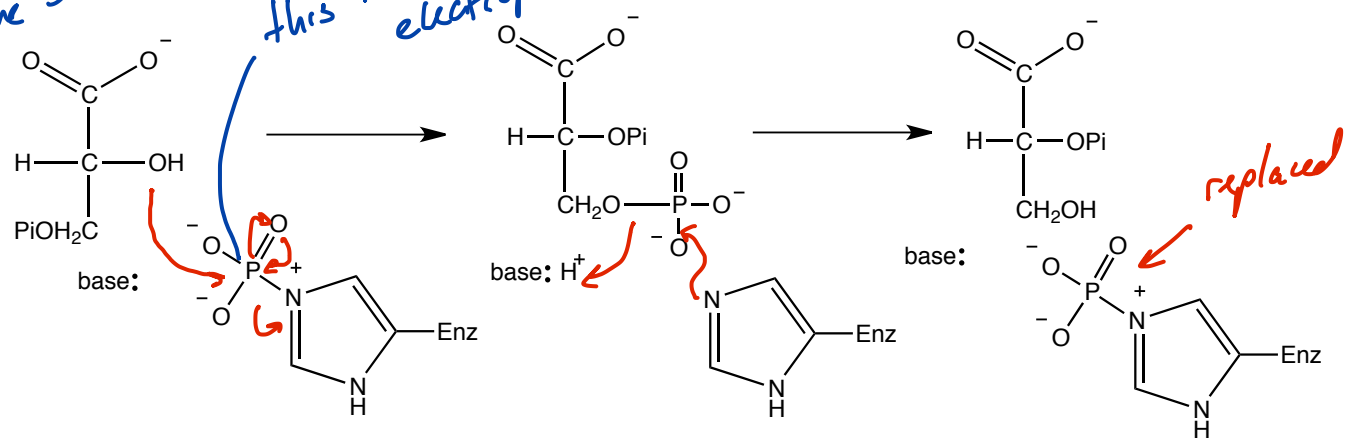
phosphoglycerate mutase

glycerate-2-phosphate



Animals + some bacteria

this P has been made more electrophilic because it is bonded to a +N

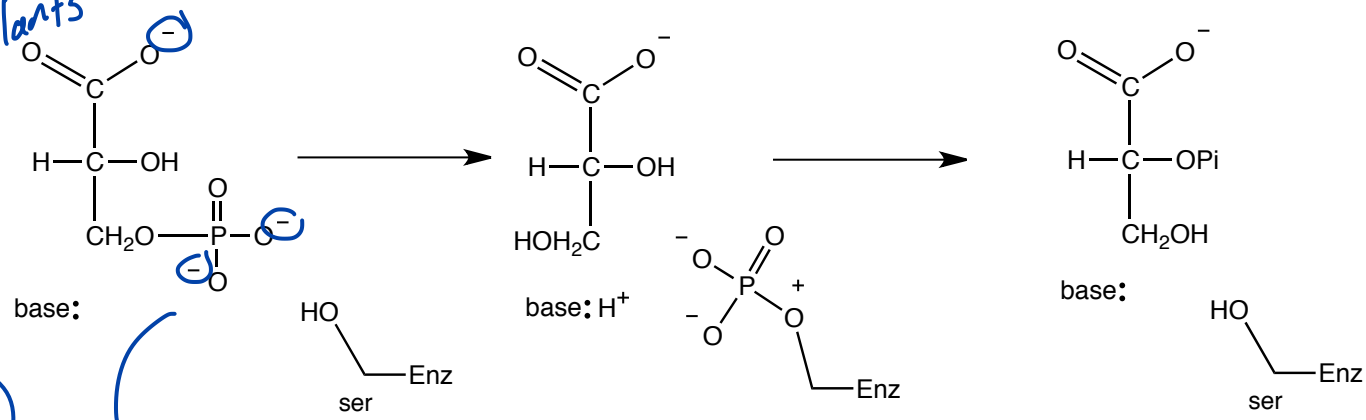


cofactor dependent phosphoglycerate mutase depends on cofactor 2,3-bisphosphoglycerate

phosphorylates enzyme

formed from glycerate-1,3-bisP$_i$

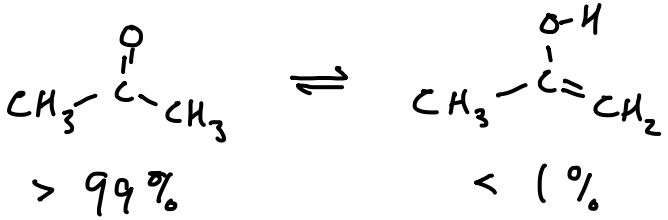
Plants + bacteria



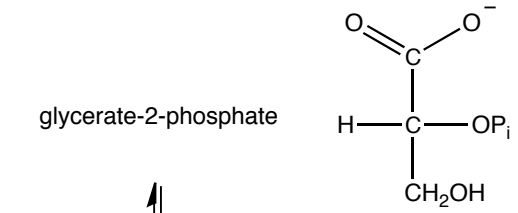
lots of Mg^{2+} in the active site

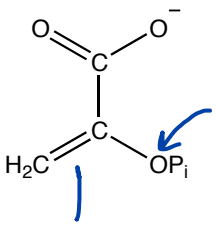
lots of ⊖ charge

positive charge to stabilize the ⊖ and to polarize bonds



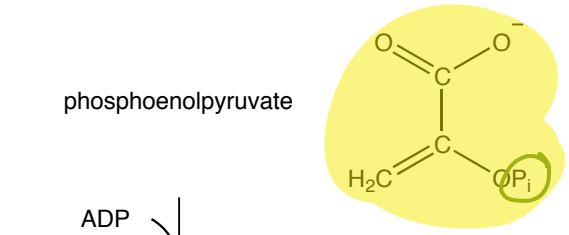
in general carbonyl tautomer is more stable than enol tautomer

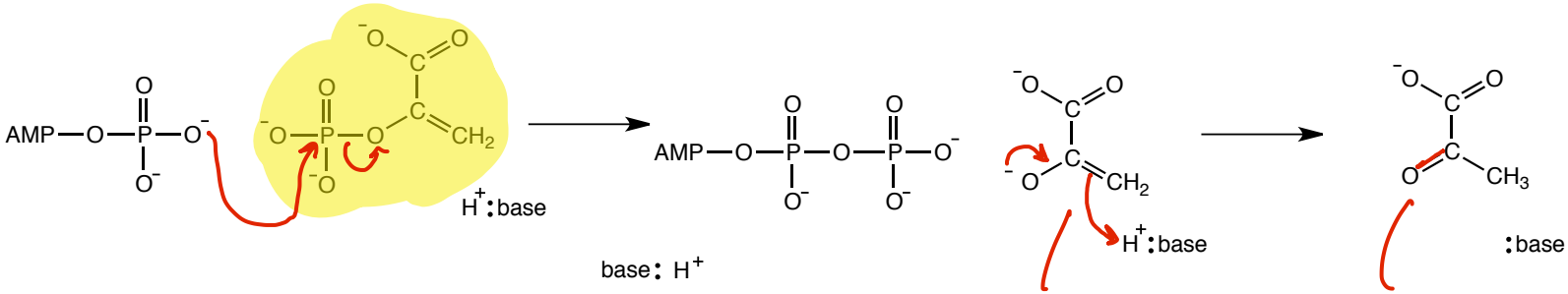




phosphoenol

this is the ene



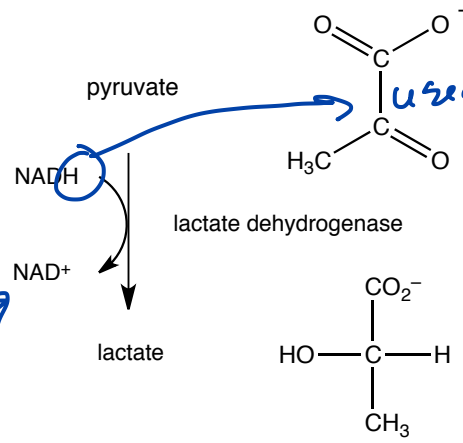


enolate or enol

carbonyl ... more stable than enol drives formation of ATP

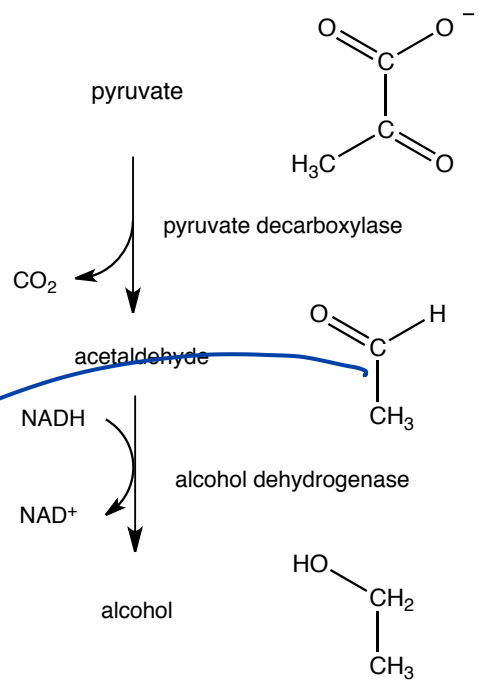
Glycolysis: Regeneration of NAD^+

Section 13.2



used to reduce this 2 atom

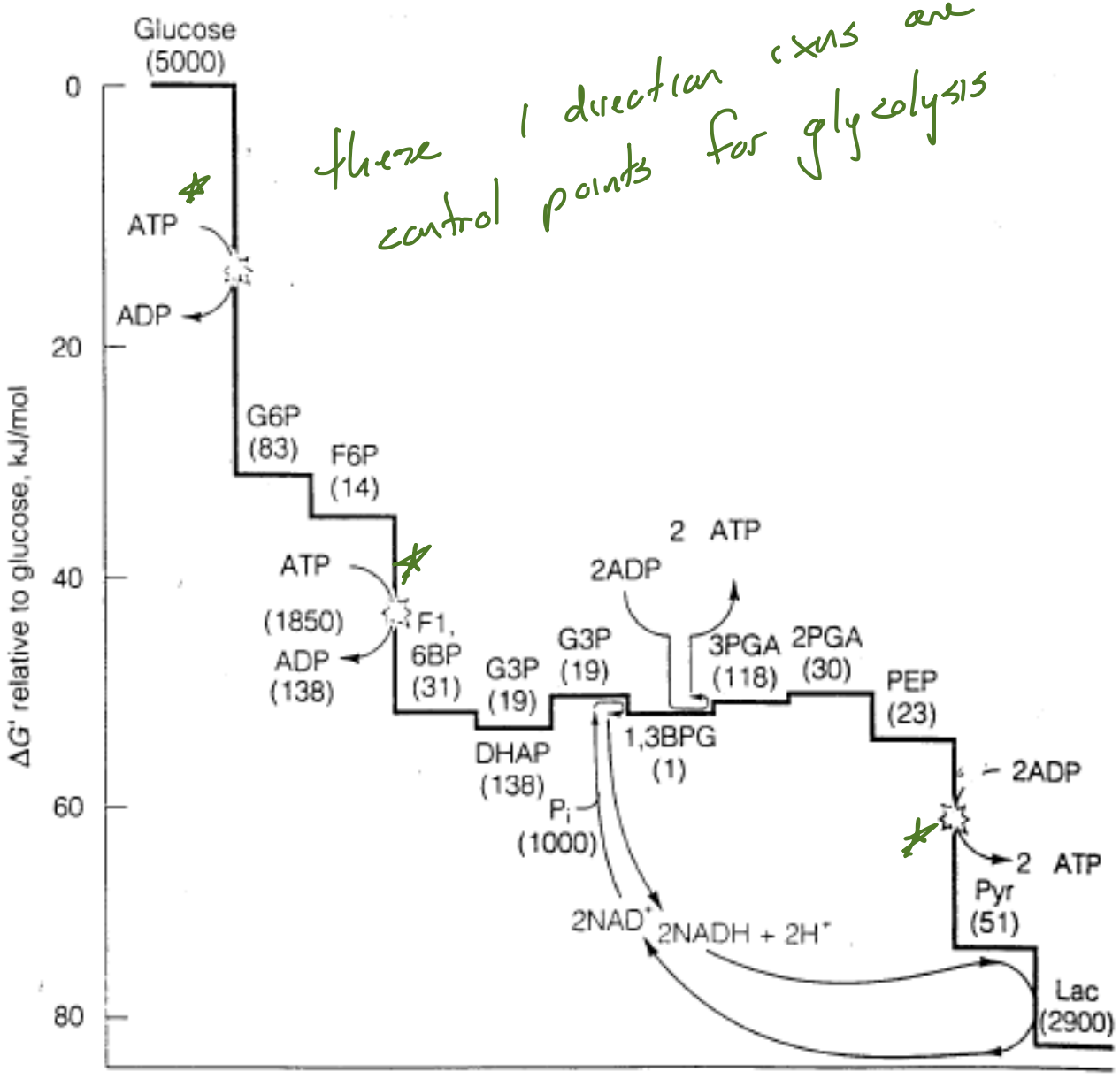
yeast



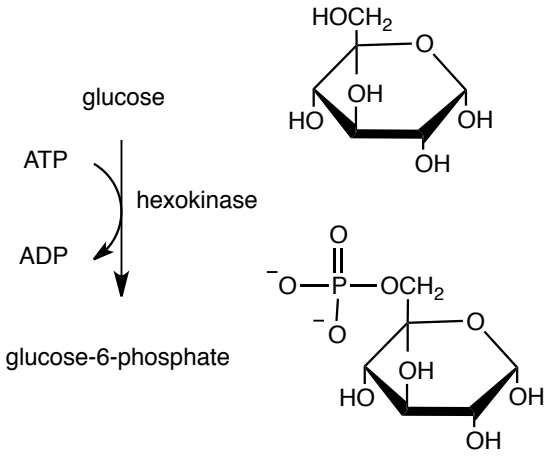
needs to be regenerated for glycolysis to continue

In the absence of O_2, a great oxidizing agent, NAD^+ gets regenerated

acetaldehyde reduced to ethanol to regenerate NAD^+



these 1 direction rxns are control points for glycolysis

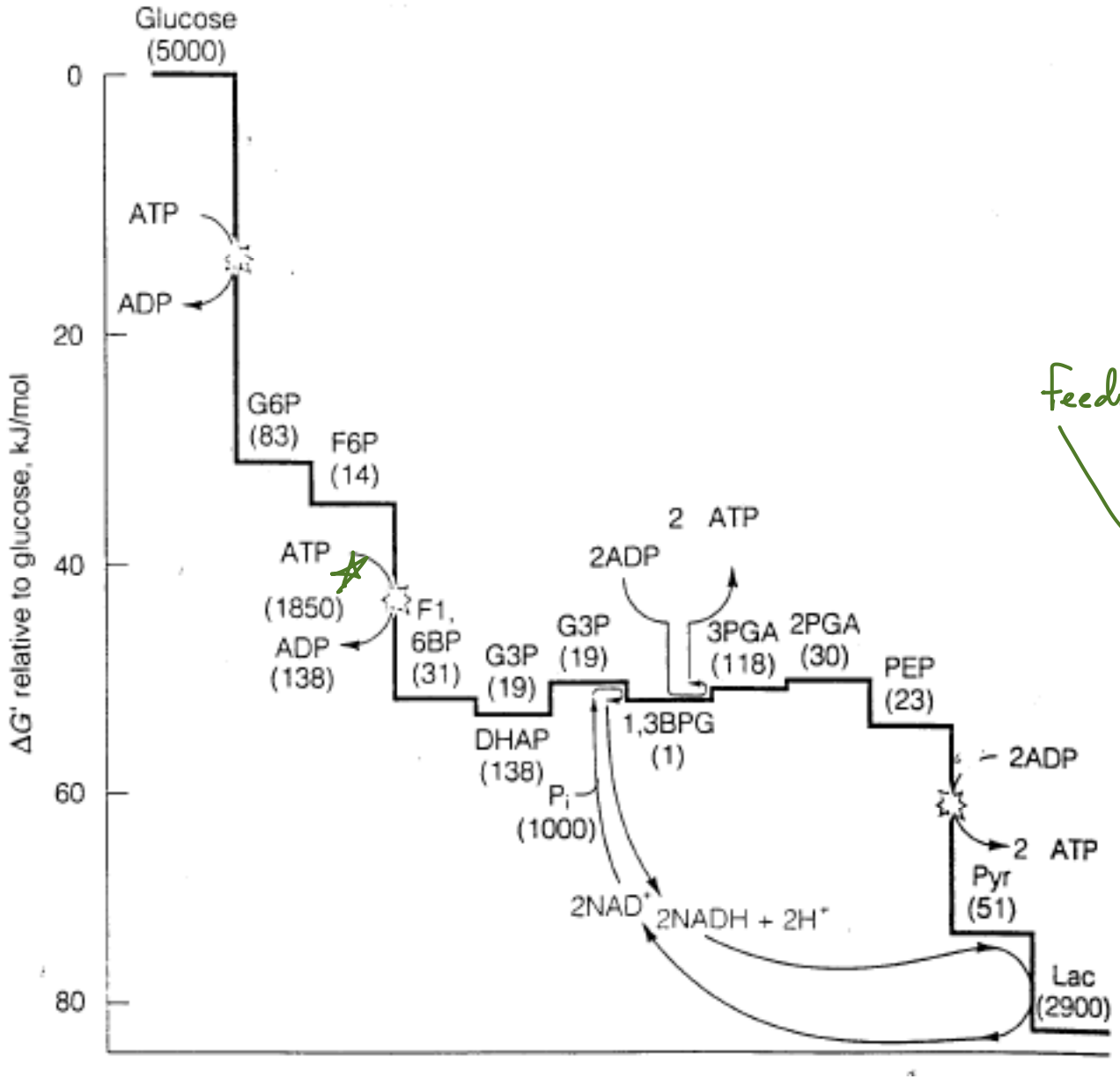


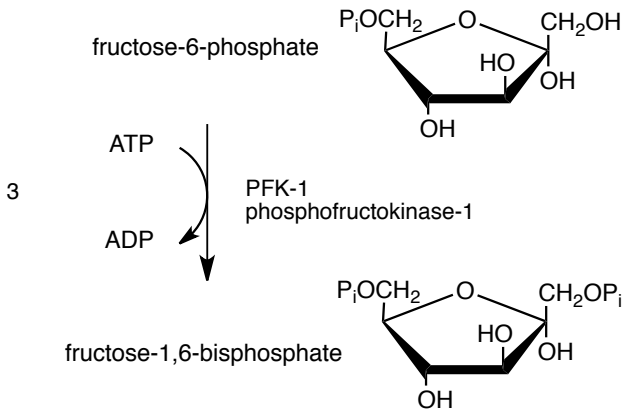
Inhibited by:

- glucose-6-phosphate
- ATP

high conc means pathway is saturated ... don't need more ATP

feedback inhibition





Feedback inhibition

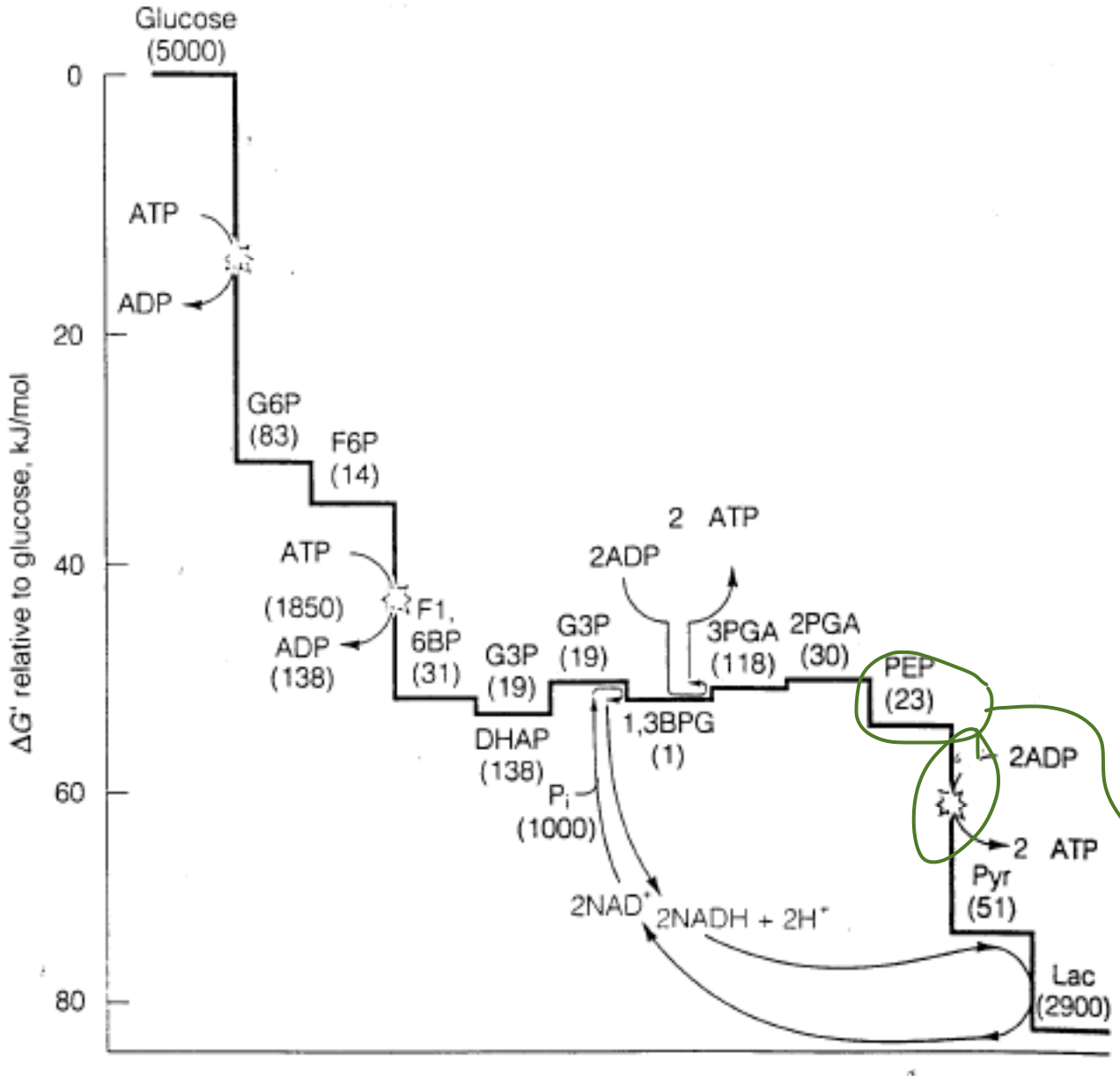
Inhibited by:
- Citrate – reactant in the Krebs cycle
- ATP

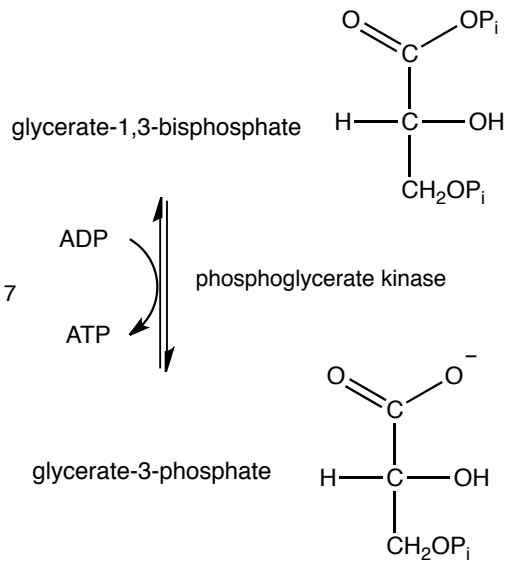
Activated by:
- fructose-2,6-bisphosphate
- AMP

indicator of low energy state

Glycolysis: Energetics and notable steps

Section 13.1, 3





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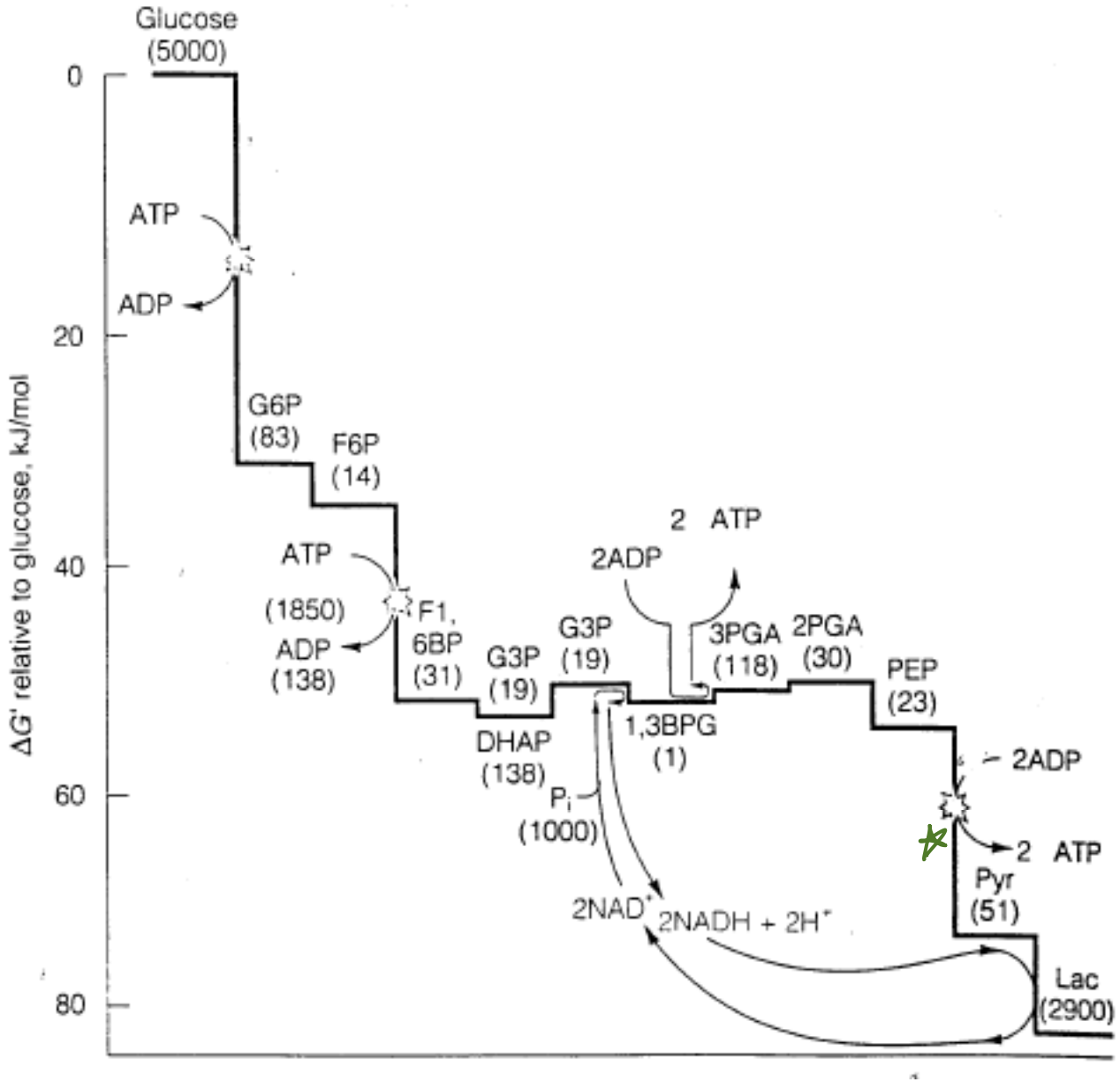
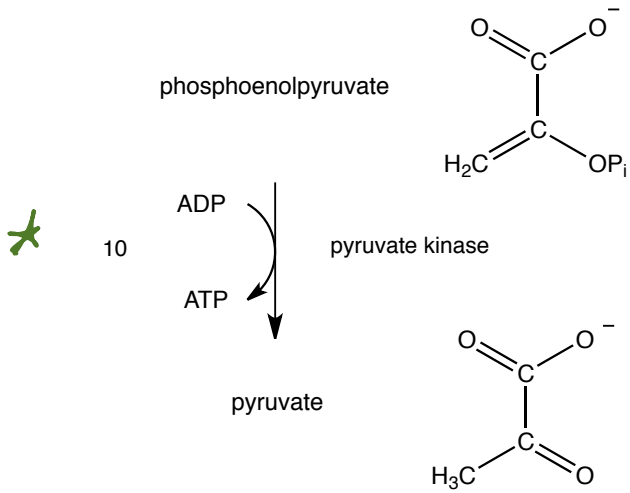
equilibrium rxn with slightly unfavorable ΔG... so it must be driven by linking it to other rxns drive the creation of ATP

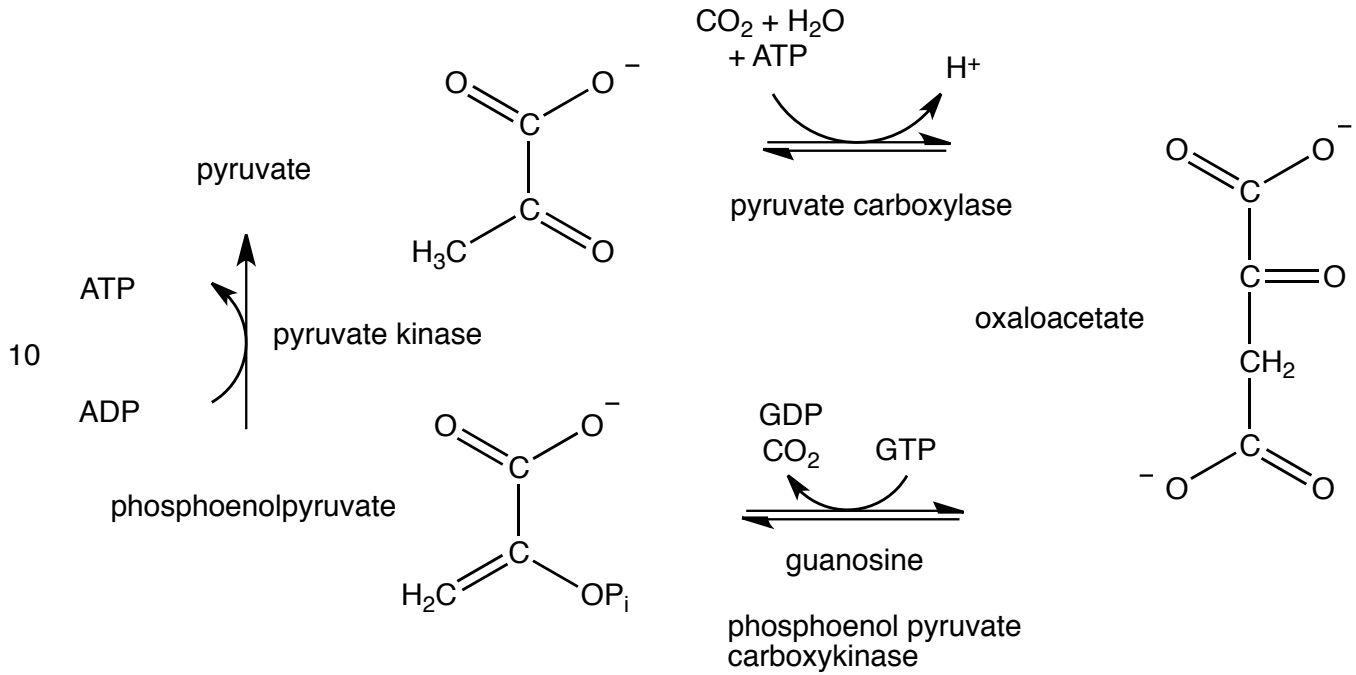




Inhibited by:
- acetyl-CoA – formed from pyruvate to get Krebs cycle going
- ATP

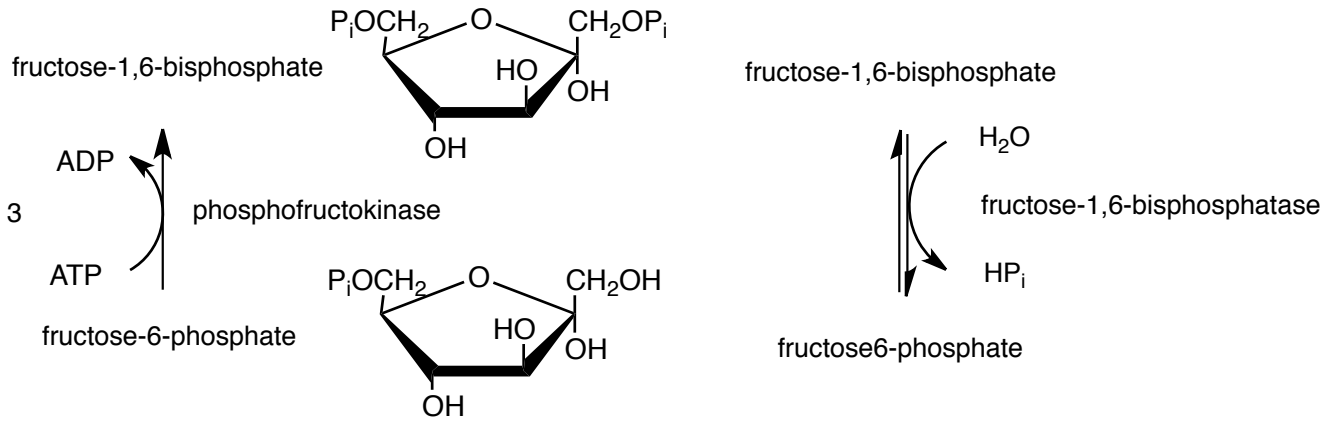
Activated by:
- fructose-1,6-bisphosphate
- AMP

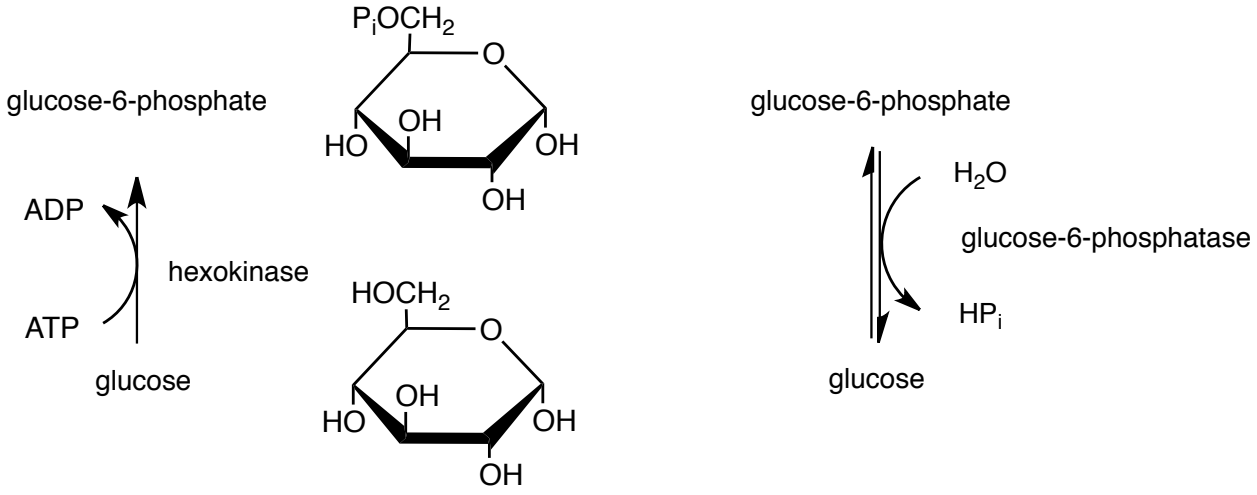
low E


$CO_2 + H_2O$
+ ATP
H^+
pyruvate carboxylase
pyruvate
oxaloacetate
ATP
10
pyruvate kinase
ADP
GDP
CO_2
GTP
guanosine
phosphoenolpyruvate
phosphoenol pyruvate
carboxykinase

Gluconeogenesis: “Reversing” Step 3

Section 13.1, 3




glucose-6-phosphate
ADP
ATP
hexokinase
glucose
P_iOCH_2
O
OH
HO
OH
OH
$HOCH_2$
O
OH
HO
OH
OH
glucose-6-phosphate
H_2O
glucose-6-phosphatase
HP_i
glucose