

# Carbohydrate Metabolism

Nov 3, 2011

- Intro to Metabolism
  - ATP, the energy currency of the cell
  - sugar structure
- Glycolysis Phase I
  - gly 1-5
- Glycolysis Phase II
  - gly 6-10
- Control in Glycolysis

# Control of Glycolysis

- Energy Coupling (review phosphorylation potential slide 5)

- Gly 3? driven by ATP hydrolysis

- uphill part is phosphorylation of sugar

Major control point

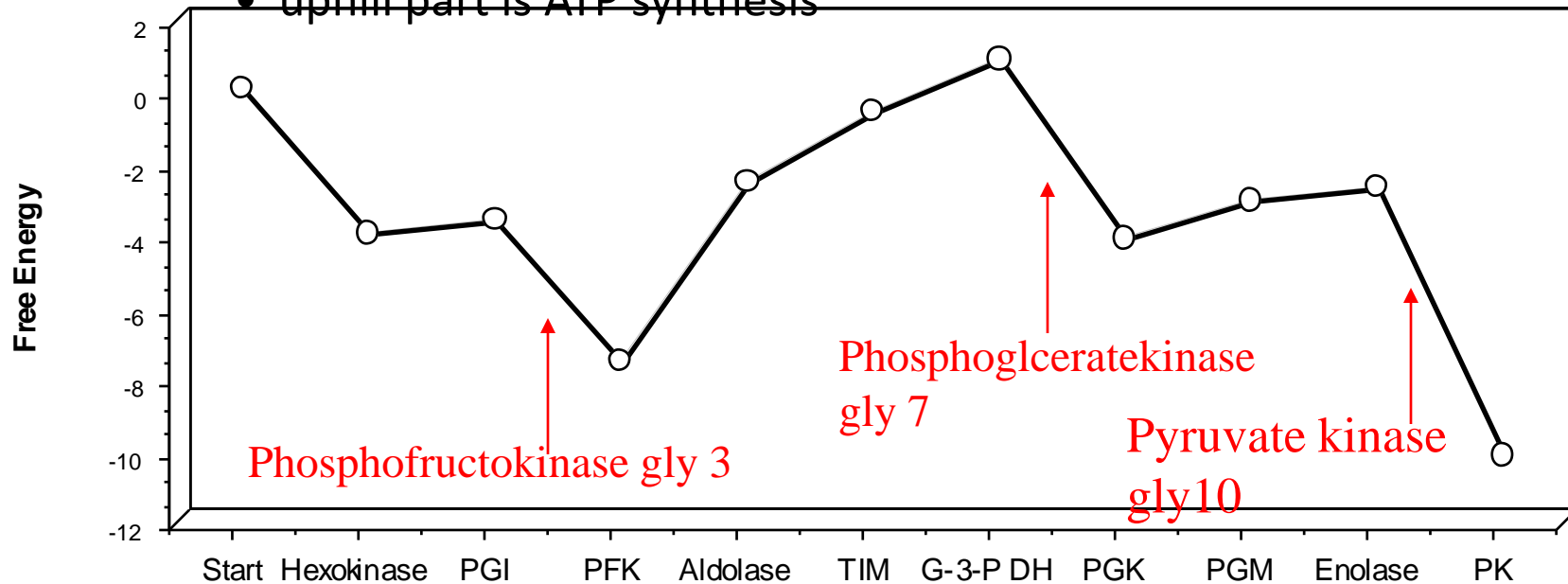
- Gly 7? driven by BPG hydrolysis

- uphill part is ATP synthesis

- Gly 10? driven by PEP hydrolysis

Not likely control since it is the last step in glycolysis

- uphill part is ATP synthesis



# Free Energy of Hydrolysis

Ann. Rev. Physiol. 1985, 47:707-25  
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RESPIRATORY CONTROL AND  
THE INTEGRATION OF HEART  
HIGH-ENERGY PHOSPHATE  
METABOLISM BY  
MITOCHONDRIAL CREATINE  
KINASE

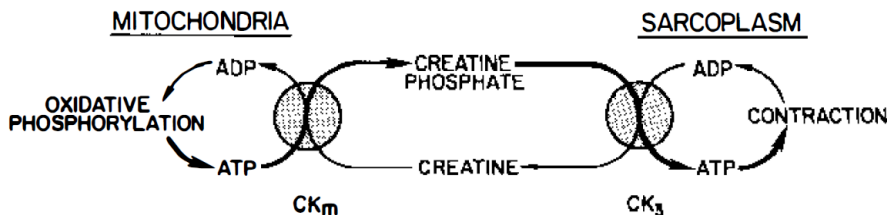
*William E. Jacobus*

20 mM in heart..Phosphocreatine

10 mM in heart... ATP

**Table 13-2. Standard Free Energies of Phosphate Hydrolysis of Some Compounds of Biological Interest**

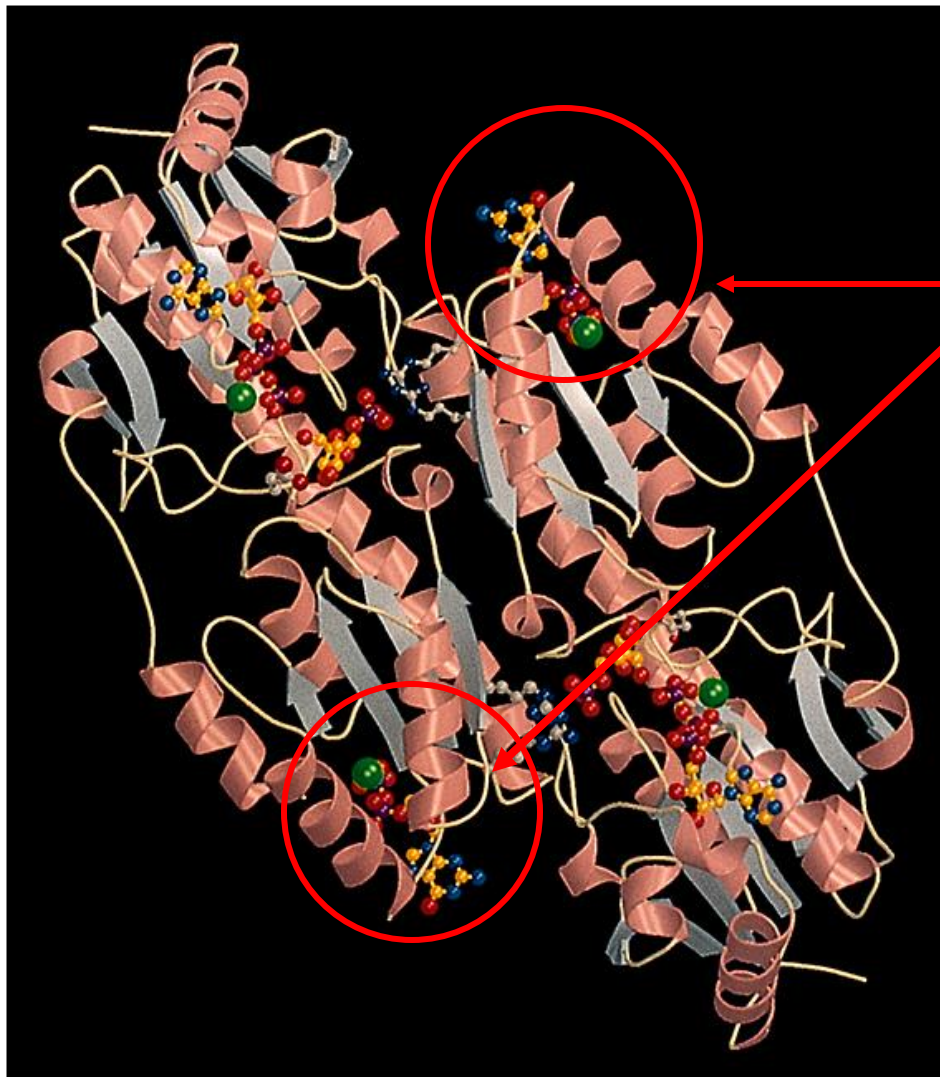
Compound	$\Delta G^{\circ}$ (kJ · mol <sup>-1</sup> )
Phosphoenolpyruvate	-61.9
1,3-Bisphosphoglycerate	-49.4
Acetyl phosphate	-43.1
Phosphocreatine	-43.1
PP <sub>i</sub>	-33.5
ATP (→ AMP + PP <sub>i</sub> )	-32.2
ATP (→ ADP + P <sub>i</sub> )	-30.5
Glucose-1-phosphate	-20.9
Fructose-6-phosphate	-13.8
Glucose-6-phosphate	-13.8
Glycerol-3-phosphate	-9.2



**Figure 6** Model for the integration of heart high-energy phosphate metabolism. *CK<sub>m</sub>* and *CK<sub>s</sub>* are abbreviations for the mitochondrial and sarcoplasmic isoforms of creatine kinase. The flux of high-energy phosphate is indicated by the *dark arrows*.

Source: Jencks, W.P., in Fasman, G.D. (Ed.), *Handbook of Biochemistry and Molecular Biology* (3rd ed.), Physical and Chemical Data, Vol. 1, pp. 296-304, CRC Press (1976).

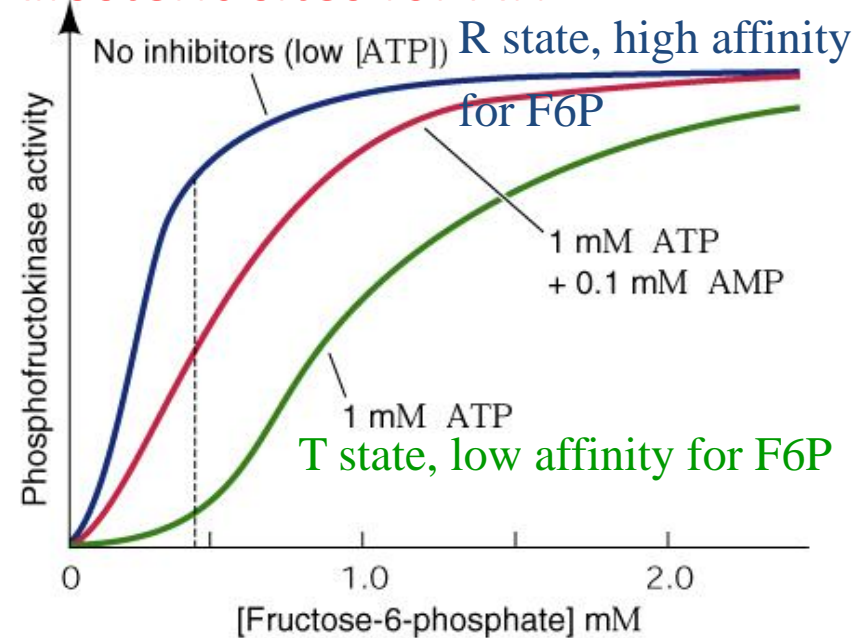
# PFK--Committed Step: Allosteric Control



Dimer of PFK shown

Substrate binding sites in center

Allosteric sites for ATP



After data from Mansour, T.E. and Ahlfors, C.E., *J. Biol. Chem.* 243, 2523-2533 (1968).  
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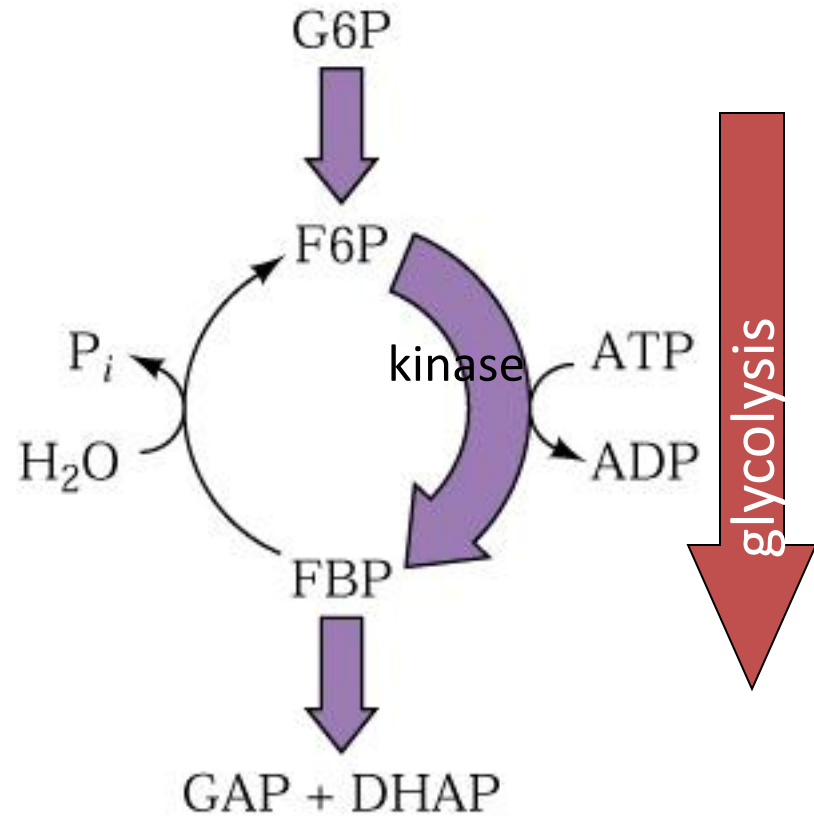
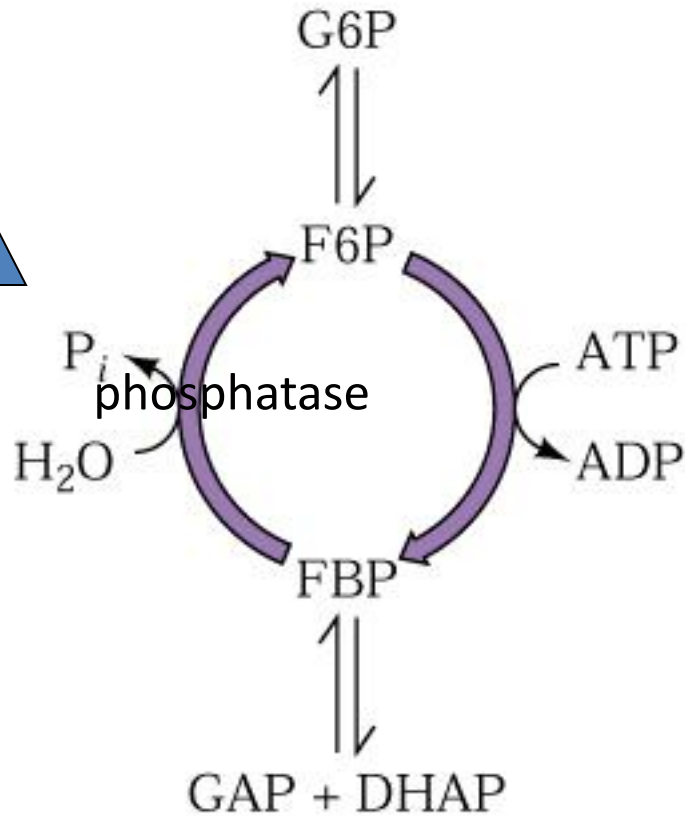


Only T state conformation binds ATP at inhibitor site, high ATP, shift to T, low affinity for f6P

# Substrate Cycling

(a) Different enzymes catalyze the forward and backward reactions

(b)



**Reciprocal Regulation:** Fructose 2,6 bisphosphate stimulates kinase and inhibits phosphatase

## REVIEW ARTICLE

### Role of fructose 2,6-bisphosphate in the control of glycolysis in mammalian tissues

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# F2,6BP production

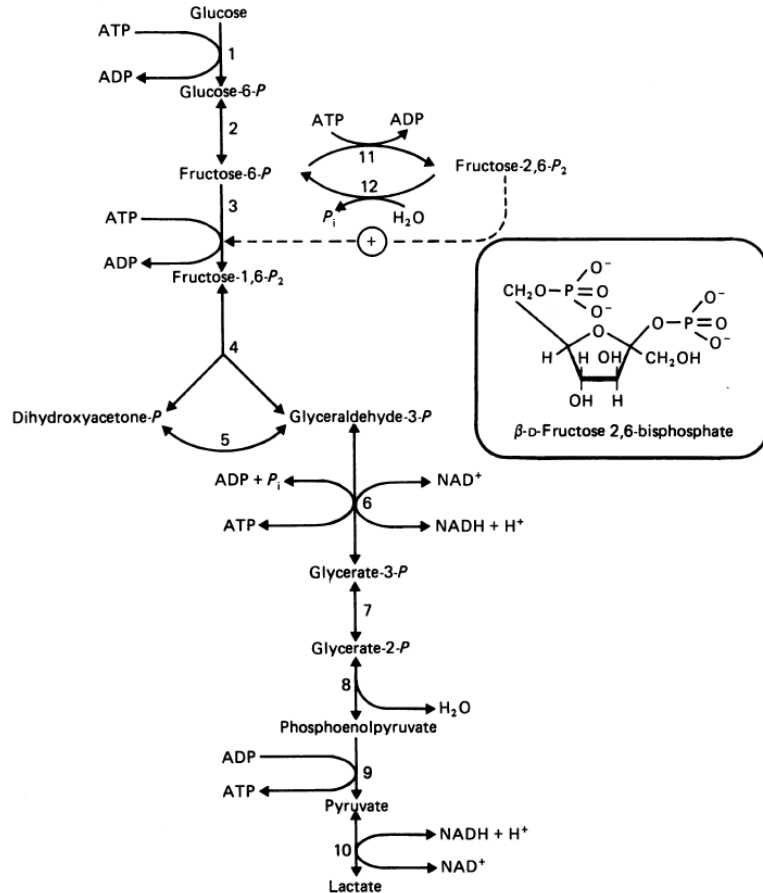


Figure 1. Glycolytic pathway and structure of  $\beta$ -D-fructose 2,6-bisphosphate

The numbers in the Scheme refer to enzymes: 1, hexokinase; 2, phosphoglucose isomerase; 3, 6-phosphofructo-1-kinase; 4, aldolase; 5, triosephosphate isomerase; 6, glyceraldehyde-3-phosphate dehydrogenase; 7, phosphoglycerate mutase; 8, enolase; 9, pyruvate kinase; 10, lactate dehydrogenase; 11, 6-phosphofructo-2-kinase; 12, fructose-2,6-bisphosphatase. The inset shows the structure of  $\beta$ -D-fructose 2,6-bisphosphate which is the natural anomer.

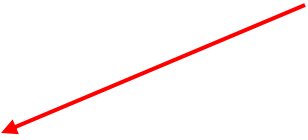
F2,6 BP is made from F6P by PFK-2, a different enzyme that ALSO has a phosphatase activity associated with it.

In the liver, the PFK-2 system (11 and 12 in image at left) is under the control of **glucagon**, a major hormone that signals when glucose is low and glycogen needs to be made (glycolysis inhibited). Glucagon causes (eventually) the phosphorylation of the PFK-2 system and shuts down the production of F2,6BP which shuts down glycolysis.

# Control of Glycolysis (1)

- Velocity =  $\frac{V_{\max} [S_t]}{K_m + [S_t]} = \frac{k_{\text{cat}} [E_t] [S_t]}{K_m + [S_t]}$
- Typical enzyme concentrations, pM- $\mu$ M
- How can Enzyme levels be controlled?
  - Sequestered storage, triggered release
  - Zymogens (inactive precursors)
    - *quick inefficient*
  - Transcriptional activation (small molecule metabolites or hormones bind to the genes)
    - *slow, efficient*
  - mRNA processing activation; (small molecules bind to untranslated nascent mRNA and affect translation)  
riboswitches
    - *quick efficient*

# Control of Glycolysis (2)

- Velocity =  $\frac{V_{\max} [S_t]}{K_m + [S_t]} = \frac{k_{\text{cat}} [E_t] [S_t]}{K_m + [S_t]}$  
- Typical substrate concentrations, 10 $\mu$ M-10 mM
- How can substrate levels be controlled?
  - Sequestered storage (glycogen stores in muscle/liver), hormone triggered release (glucagon)
  - Conversion of related molecule (lactate to pyruvate)
  - Hunger signal to organism (hormone)



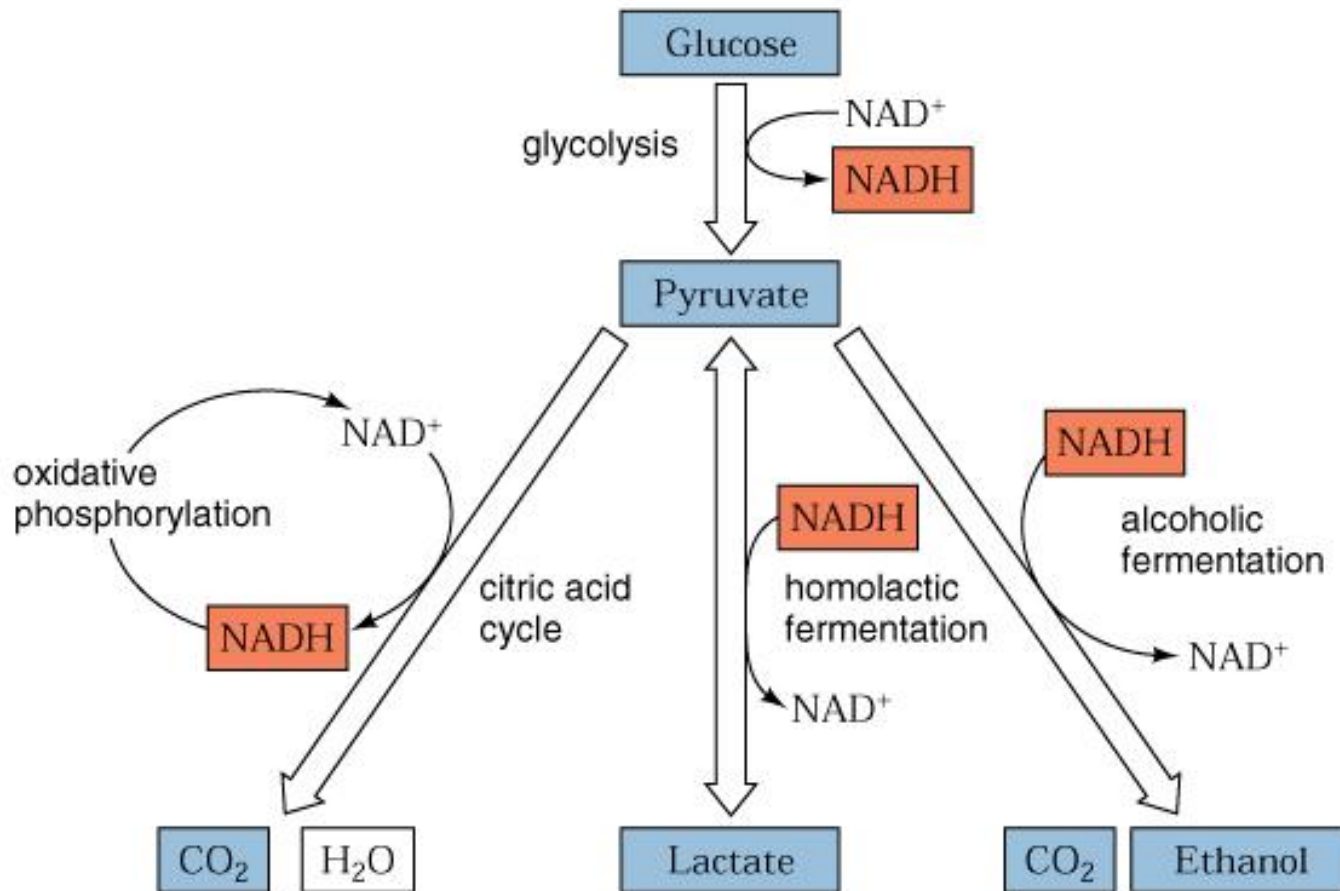
# Control of Glycolysis (3)

- Velocity =  $\frac{V_{\max} [S_t]}{K_m + [S_t]} = \frac{k_{\text{cat}} [E_t] [S_t]}{K_m + [S_t]}$
- Typical  $k_{\text{cat}}$ ,  $10^2$ - $10^6 \text{ s}^{-1}$
- How can  $k_{\text{cat}}$  be increased/decreased?
  - Allosteric effectors (example PFK-gly3)
  - Reversible covalent modification
    - Phosphoryllation, adenylation, methylation, acetyllation, others (example pyruvate dehydrogenase)

# Control of Glycolysis (3b)

- Velocity =  $\frac{V_{\max} [S_t]}{K_m + [S_t]} = \frac{k_{\text{cat}} [E_t] [S_t]}{K_m + [S_t]}$
- $K_m + [S_t]$
- Typical  $K_m$ , 10-1000  $\mu\text{M}$
- How can  $K_m$  be increased/decreased?
  - Self Inhibition

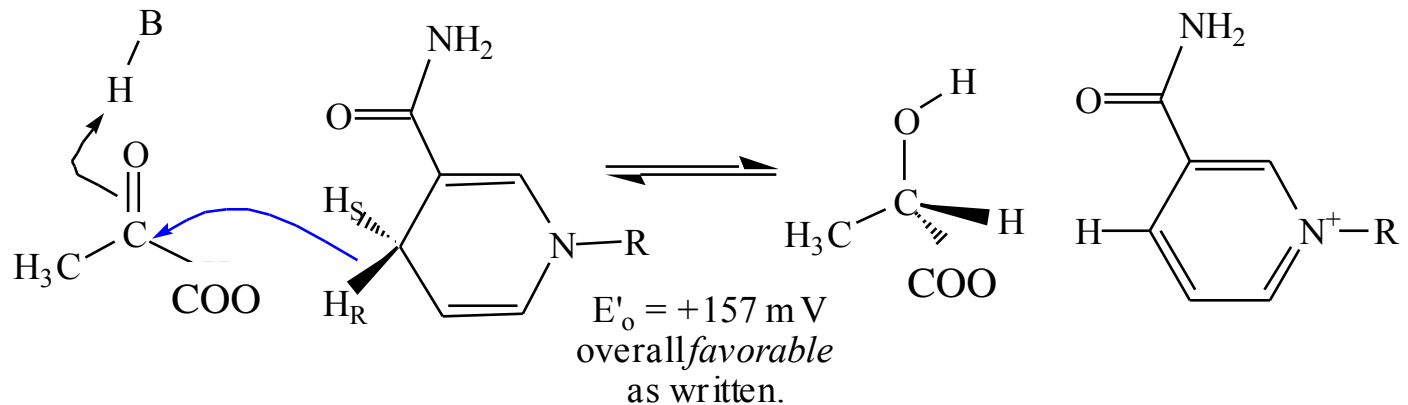
# Fates of Glucose: Fermentation



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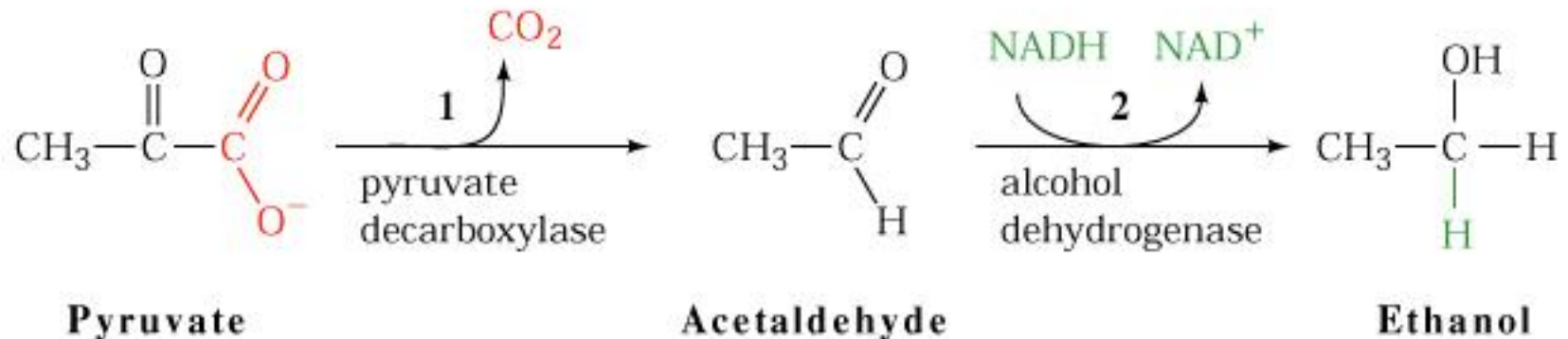
Voet, Voet, and Pratt Fundamentals of Biochemistry

# LDH Mechanism: NADH redox



- redox potential of NADH varies in different enzymes:
- transfer of the  $\text{proH}_R$  or  $\text{proH}_S$  hydride to substrate depends on enzyme class
- binding site selects conformation of the nicotinamide ring and only one stereoselected H is transferred (for reduction) or added (for oxidation).
- His 195 donates a proton to ketone, accepts a proton from alcohol
- Both His 195 and Arg 171 interact electrostatically to orient carboxylic acid of pyruvate in enzyme active site

# Fermentation: Alcohol



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Voet, Voet, and Pratt Fundamentals of Biochemistry

- \* An example of decarboxylation followed by reduction to ethanol.
- \* On Tuesday, we will see how this system has been co-opted in pyruvate dehydrogenase to perform OXIDATIVE decarboxylation

# Pyruvate Decarboxylase Mechanism

Thiamine  
pyrophosphate,  
coenzyme

