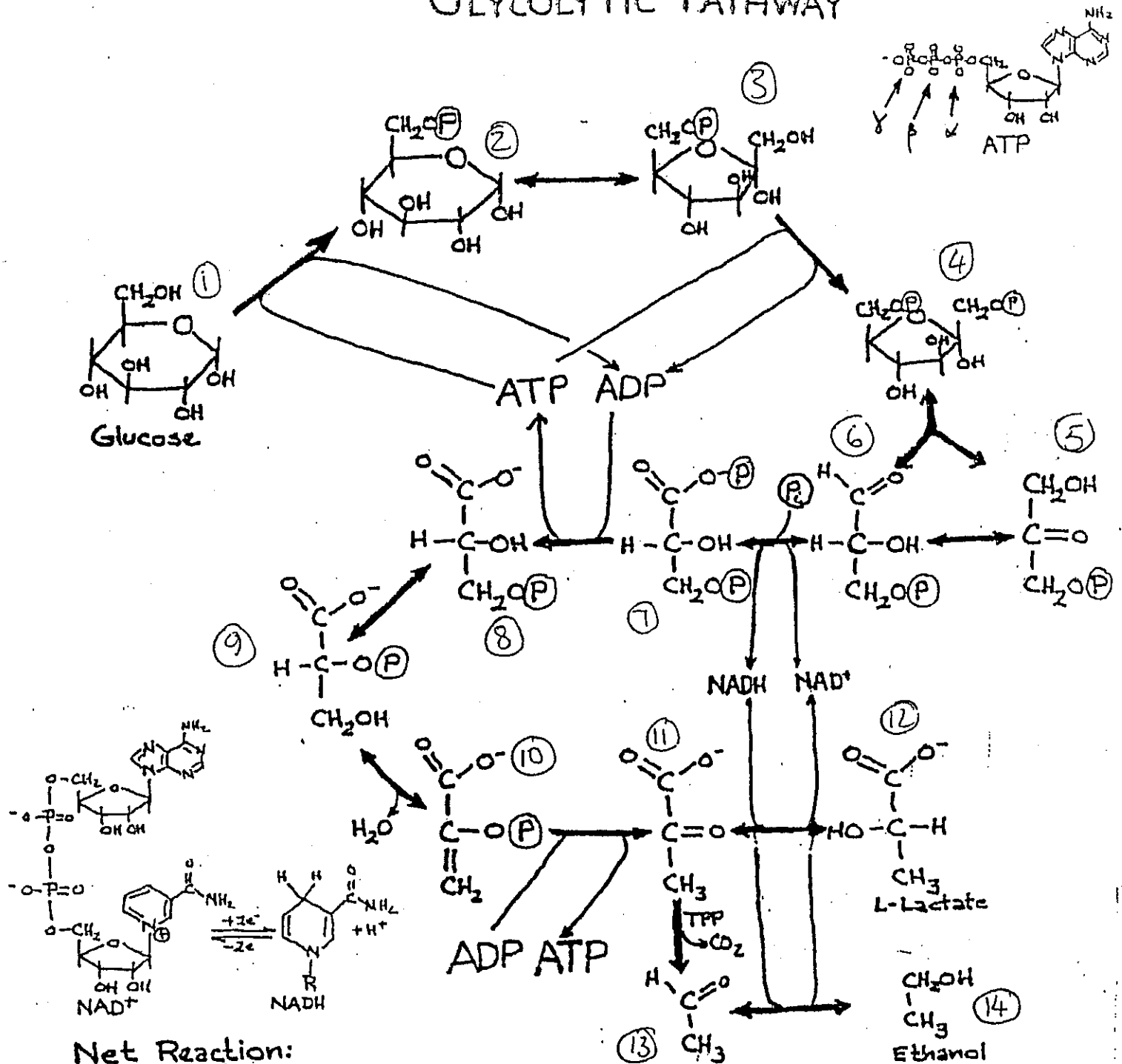
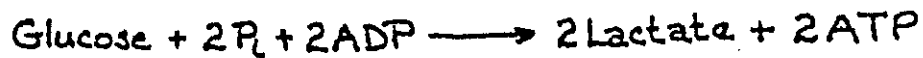


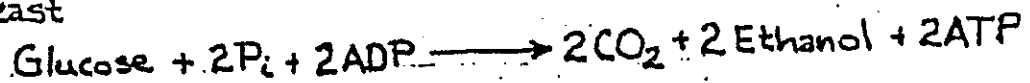
# GLYCOLYTIC PATHWAY



Net Reaction:  
in vertebrates



in yeast

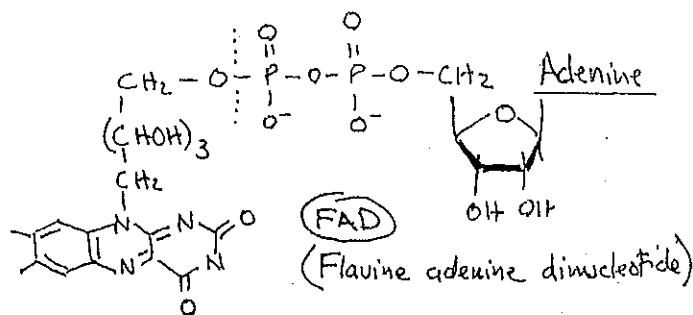
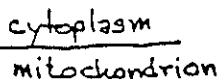


- 1/2 hexokinase
- 2/3 phosphoglucisomerase
- 3/4 phosphofructokinase
- 4/5+6 aldolase
- 5/6 triosephosphate isomerase
- 6/7 glyceraldehyde 3P dehydrogenase

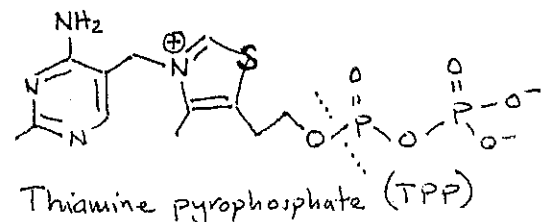
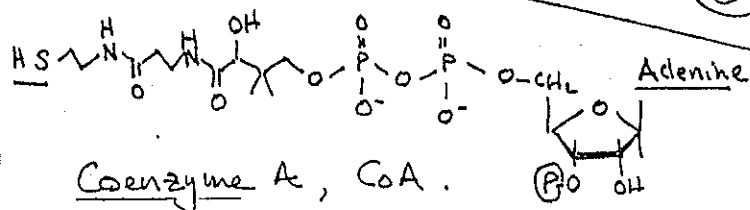
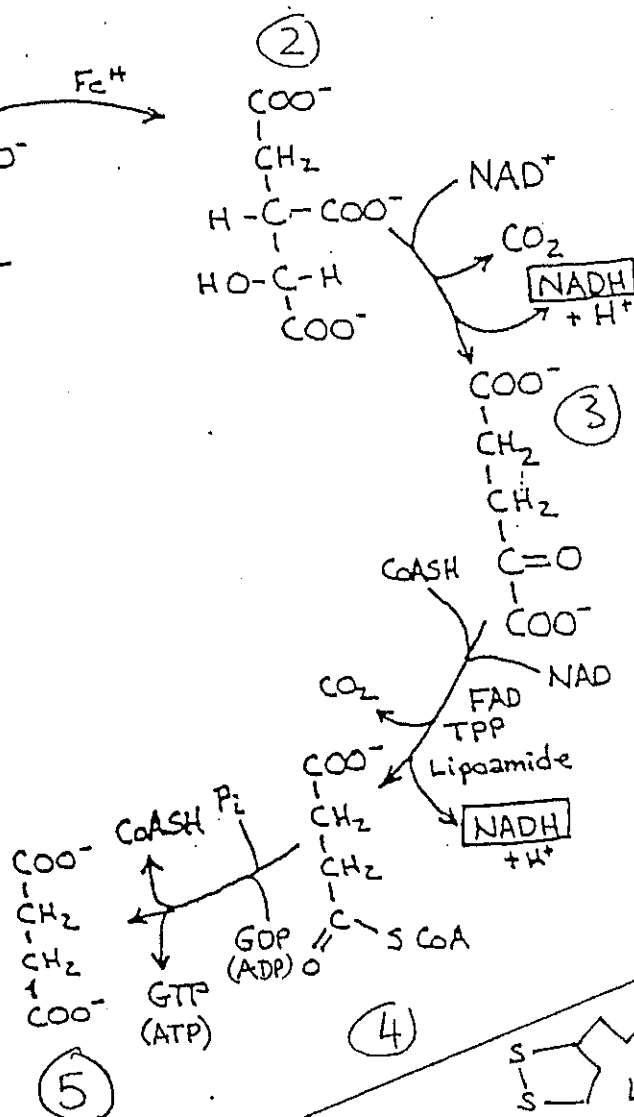
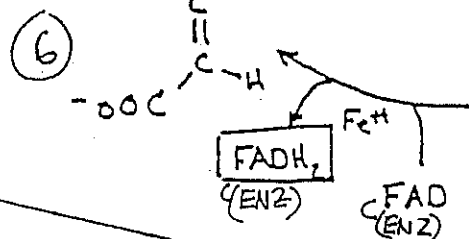
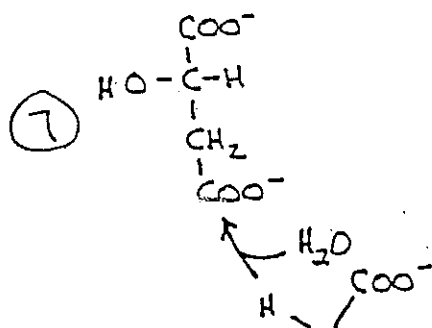
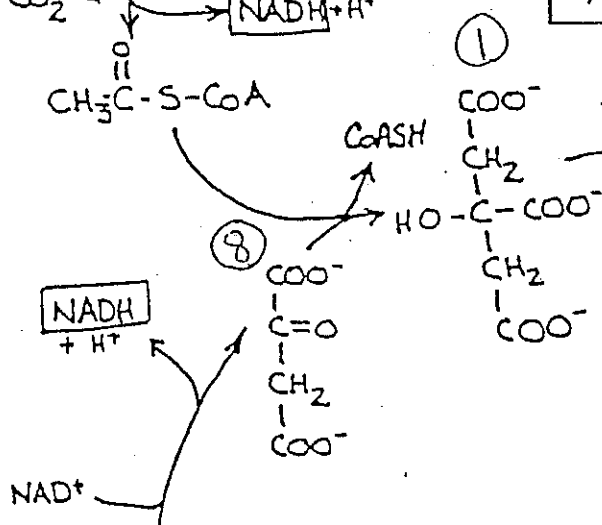
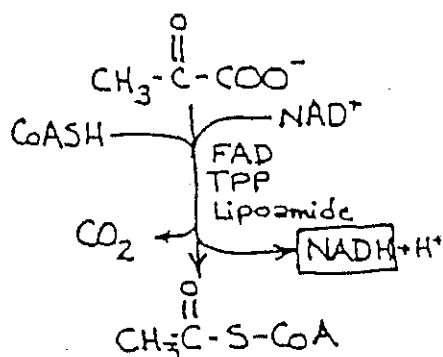
- 7/8 phosphoglycerate kinase
- 8/9 phosphoglyceromutase
- 9/10 enolase
- 10/11 pyruvate kinase
- 11/12 lactate dehydrogenase
- 11/13 pyruvate decarboxylase
- 13/14 alcohol dehydrogenase

HB

glycolysis



8 / 1	citrate synthase
1 / 2	aconitase
2 / 3	isocitrate dehydrogenase
3 / 4	$\alpha$ -ketoglutarate dehydrogenase
	multienzyme complex
4 / 5	thiokinase
5 / 6	succinate dehydrogenase
6 / 7	fumarase
7 / 8	malate dehydrogenase



## FATTY ACID OXIDATION

(This handout provided on the test if required)

- a. Neutral fat (triglycerides) converted to free fatty acids via lipases.
- b. Free fatty acids ( $R\text{-COOH}$ ) enter cell and activated via:



[Note this reaction makes AMP and is equivalent to the consumption of 2 ATP molecules if they were converted to ADP]

- c. Then the CoA thioester ( $R\text{-CO-SCoA}$  above) is degraded via the  $\beta$ -oxidation cycle as shown below. Note each turn releases acetyl-CoA which can enter the TCA cycle. 7 Turns of this pathway releases 8 molecules of acetyl-CoA.

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### MITOCHONDRIAL FATTY ACID OXIDATION (or $\beta$ -oxidation)

E-1 acyl-CoA dehydrogenase

E-2 hydratase

E-3 hydroxyacyl-CoA dehydrogenase

E-4 thiolase

