BB 422/622						
BB 4 OUTLINE: Introduction and review Transport Glycogenolysis Glycolysis Introduction & overview; 2 phases Phase I Phase II Summary: logic, energetics, labeling studies Other sugars Pasteur: Anaerobic vs Aerobic Fermentations: anaerobic fates of pyruvate Lactate-lactate dehydrogenase Exam-1 material Acetoacetate decarboxylase & alcohol dehydrogenase Pyruvate oxidation: aerobic fates of pyruvate pyruvate dehydrogenase complex Krochs' Cuelo	22/622 See Achieve: Ch19: Case Study: The Narrow Window 8 Steps Citrate Synthase Aconitase Isocitrate dehydrogenase Ketoglutarate dehydrogenase Succinyl-CoA synthetase Succinte dehydrogenase Fumarase Malate dehydrogenase Energetics; Regulation Summary Oxidative Phosphorylation Energetics Mitochondria Transport of protons out Electron transport Discovery Four Complexes Complex II: NADH → CoQH ₂ Complex II: Succinate → CoQH ₂					
How did he figure it out? Overview	Complex IV: Cytochrome C (Fe ²⁺) \rightarrow H ₂ O Chemiosmotic theory ATP synthesis					

Electron Transport							
TABLE The Protein Components of the 19-3 Mitochondrial Respiratory Chain							
Enzyme complex/protein	г (Mass kDa)	Number of subunits ^a	Prosthetic group(s)	Reduction potential (<i>E</i> ູ´ V)	Binding sites for:	Inhibited by:
I NADH dehydroge	enase	850	45 (14)	FMN, Fe-S	-0.36	NADH, CoQ	amytal, rotenone
II Succinate dehydrogenase		140	4	FAD-E, Fe-S	0.09 0.05 (CoQ)	Succinate, CoQ	malonate
III Ubiquinone: cytochrome c oxidoreductase ^b		250	11	Hemes b, c ₁ , Fe-S	0.17	CoQ, Cytochrome c	antimycin a
Cytochrome c ^o	:	13	1	Heme	0.25 (Cyt c)	
IV Cytochrome oxi	dase ^b	204	13 (3–4)	Hemes a, a ₃ ; Cu _A , Cu _B	0.57	Cytochrome c, O ₂	Cyanide, azide, CO
^a Number of subunits in the bacterial complexes in parentheses. ^b Mass and subunit data are for the monomeric form. ^c Cytochrome <i>c</i> is not part of an enzyme complex; it moves between Complexes III and IV as a freely soluble protein.							
" ΔE_{\circ} of ATP synthesis = -0.16 v ΔE_{\circ} of Complex I = -0.41 v ΔE_{\circ} of Complex III = -0.2 v ΔE_{\circ} of Complex IV = -0.25 v " ΔE_{\circ} of Complex IV = -0.25 v							









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Cytochrome c ^c	13	1	Heme				
IV Cytochrome oxidase ^b	204	13 (3–4)	Hemes a, a ₃ ; Cu _A , Cu _B	0.57	Cytochrome c, O ₂	Cyanide, azide, CO	
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Electron Transport							
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Hates e ⁻ +0.05 V +0.077 V -0.1 to +0.3 V							
-		Det	<u>+U.I V</u>		+0.22 V	+0.254 V	
Loves e [_] 2e [_]		em: how does	Reiske Protein([Fe	es]) ectrons into tw	Cytochrome c1	$\rightarrow 2x1e^{-1}$	









Electron Transport

TABLE The Protein Components of the Mitochondrial Respiratory Chain 19-3 Reduction Enzyme Number of Prosthetic **Binding sites** Mass potential (*E*°´V) Inhibted by: complex/protein (kDa) subunits^a group(s) for: I NADH dehydrogenase 850 45 (14) FMN, Fe-S -0.36 NADH, CoQ amytal, rotenone II Succinate Succinate, 140 4 FAD-E, Fe-S 0.09 dehydrogenase CoQ III Ubiquinone: Hemes b, c_1 , CoQ, 0.17 250 11 antimycin a ${\tt cytochrome} \ c$ Fe-S Cytochrome c oxidoreductaseb Cytochrome c^{c} 13 1 Heme Hemes a, a₃; Cytochrome c, Cyanide, azide, 204 0.57 IV Cytochrome oxidase^b 13 (3-4) Cu_A, Cu_B 02 со ^aNumber of subunits in the bacterial complexes in parentheses. ^bMass and subunit data are for the monomeric form. ^cCytochrome c is not part of an enzyme complex; it moves between Complexes III and IV as a freely soluble protein.



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ponents of t espiratory Ch	he nain					
Number of subunits ^a	Prosthetic group(s)	Reduction potential (<i>E</i> 。´V)	Binding sites for:	Inhibted by:		
45 (14)	FMN, Fe-S	-0.36	NADH, CoQ	amytal, rotenone		
4	FAD-E, Fe-S	0.09	Succinate, CoQ			
11	Hemes b, c ₁ , Fe-S	0.17	CoQ, Cytochrome c	antimycin a		
1	Heme					
13 (3–4)	Hemes a, a ₃ ; Cu _A , Cu _B	0.57	Cytochrome c, O ₂	Cyanide, azide, CO		
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	Number of subunits ^a 45 (14) 4 11 13 (3–4) momeric form. e complex; it move	Number of subunitsa Prosthetic group(s) 45 (14) FMN, Fe-S 4 FAD-E, Fe-S 11 Hemes b, c1, Fe-S 1 Heme 13 (3-4) Hemes a, a3; CuA, CuB pomplexes in parentheses. Hemes between Complex; it moves between Complex	Number of subunits ^a Prosthetic group(s) Prosthetic notential (E, V) 45 (14) FMN, Fe-S -0.36 4 FAD-E, Fe-S 0.09 11 Hemes b, c1, Fe-S 0.17 1 Heme 13 (3-4) Hemes a, a3; CuA, CuB 0.57 pomplexes in parentheses. 0.57 pomplexes in parentheses. 0.57	Number of subunits ^a Prosthetic group(s) Prosthetic potential (Es' V) Binding sites for: 45 (14) FMN, Fe-S -0.36 NADH, CoQ 4 FAD-E, Fe-S 0.09 Succinate, CoQ 11 Hemes b, c1, Fe-S 0.17 CoQ, Cytochrome c 1 Heme 0.57 Cytochrome c, O ₂ 13 (3-4) Hemes a, a3; CuA, CuB 0.57 Cytochrome c, O ₂ opplexes in parentheses. Nomeric form. e complex; it moves between Complexes III and IV as a freely soluble pr		









Electron Transport

Multiple Complexes Associate Together to Form a "Respirasome"

Courtesy of Egbert Boekema





Complex III and Complex IV

Clinical Correlations

Hemolytic Anemia: Deficiencies in Glycolytic Enzymes

- Red-blood cells do not have nuclei or mitochondria. They still need to maintain their membrane potential using the Na/K pump and membrane shape using actin microfilaments. Both use glycolysis as the sole source of ATP.
- Any glycolytic enzyme that is impaired sufficiently will affect the efficiency of the entire pathway. Without ATP, the cells swell and lyse, which is a condition called non-spherocytic hemolytic anemia.



- The precise defect in aldolase A that causes hemolytic anemia lead to a deeper understanding of protein stability and cellular function.
- The most common form is from a deficiency in pyruvate kinase. This form is more tolerable than a form from a deficiency of aldolase A. This is likely because there is a buildup of intermediates behind the block at PK, including 2,3,bisphosphoglycerate, the negative heterotropic allosteric effector of Hb. This causes Hb to release more O₂.

