

Spring 2004 BCHS 3304 Final Exam Review Student Copy-

1). The T→R transition of hemoglobin upon binding of oxygen to the heme has been thoroughly investigated. On a thermodynamic level, this T→R transition can be described as (primarily) an enthalpically driven process. Which of the following phenomena in the T→R transition of hemoglobin is the likely enthalpic driving force?

- a). Movement of the heme iron into the plane of the heme upon oxygen binding.
- b). The binding of oxygen by the distal histidine (E7).
- c). The exclusion of water from the oxygen-binding pocket.
- d). The breaking of pre-existing and making of new C-terminal salt bridges at the  $\alpha/\alpha$  interfaces.
- e). The occlusion of the heme pocket by valine (E11).

2). At a pH more acidic than its isoelectric point, a protein will carry:

- a). no ionic charge
- b). a net positive charge
- c). a net negative charge
- d). a positive charge equal to the negative charge
- e). I have no clue, where am I, who are all of these people

3). Match the following protein with its appropriate characteristic.

- |                        |   |
|------------------------|---|
| a). Collagen           | I). 2 right-handed $\alpha$ -helices forming a left-handed coiled structure                 |
| b). Chymotrypsin       | II). Left-handed proline helices  |
| c). $\alpha$ -Keratin  | III). oxonium intermediate  |
| d). RNase A            | IV). catalyzes $2 \text{ ADP} \leftrightarrow \text{AMP} + \text{ATP}$                      |
| e). Silk Fibroin       | V). stabilizes collagen structure using ascorbic acid                                       |
| f). Creatine Kinase    | VI). catalytic triad  |
| g). Lysozyme           | VII). pair of catalytic histidine residues  |
| h). Prolyl Hydroxylase | VIII). solubilizes $\text{CO}_2$ as bicarbonate anion                                       |
| i). Carbonic Anhydrase | IX). antiparallel $\beta$ -sheet structure comprised of primarily small, aliphatic residues |
| j). Adenylate Kinase   | X). maintains the muscle "energy reserve"   |
| k). IgG Antibody       | XI). Sandwiched $\beta$ -sheet structure with high-affinity ligand binding loops.           |

4). Which of the following statements accurately describes the nature of a biologically active protein?

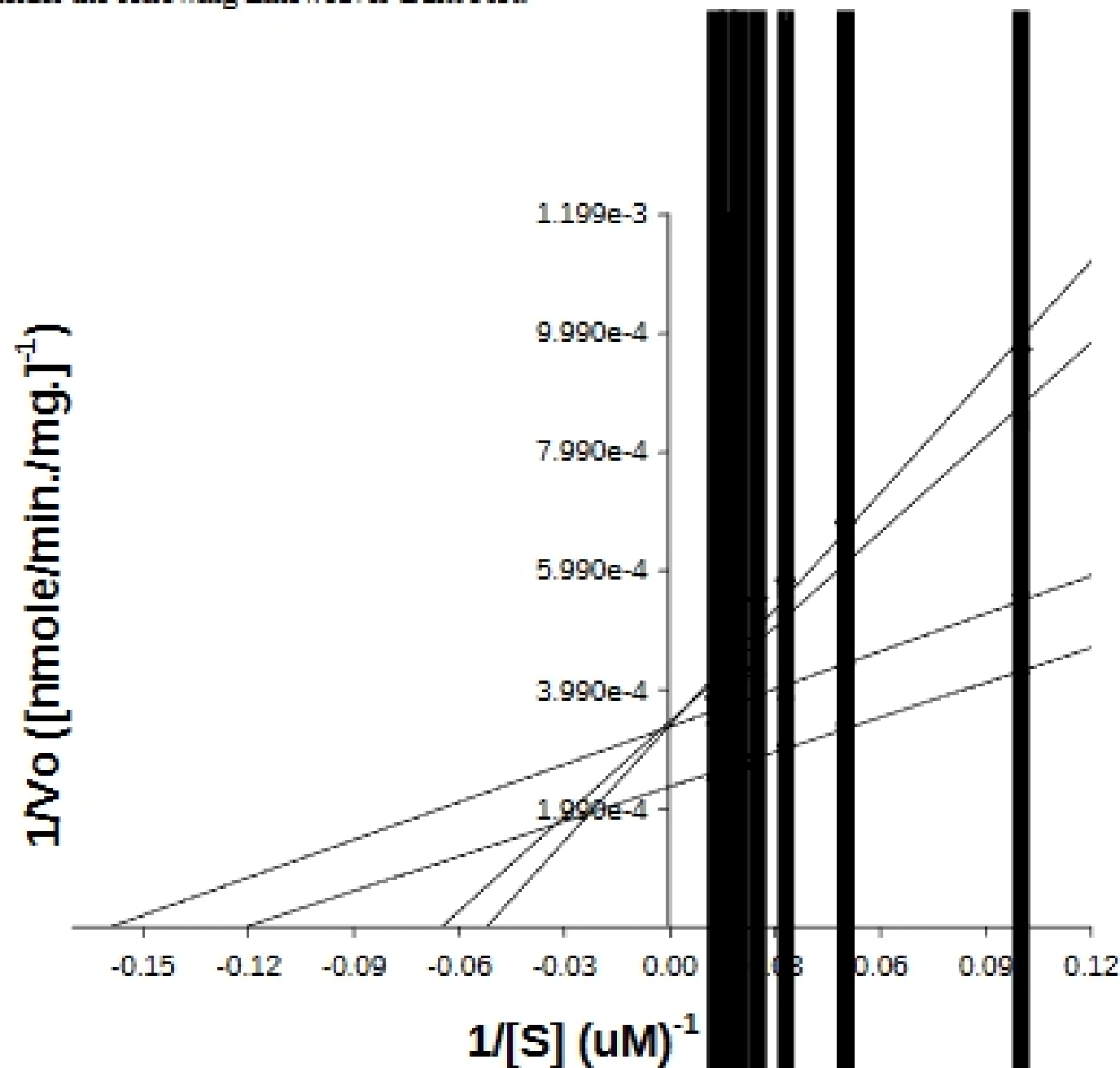
- a). A biologically active protein is composed of a branching sequence of amphoteric, L-amino acids joined together by resonant amide bonds between neighboring residues, each exhibiting free rotation.
- b). A biologically active protein is composed of a non-branching sequence of amphipathic, D-amino acids joined together by resonant amide bonds between neighboring residues, with each exhibiting no free rotation.
- c). A biologically active protein is composed of a non-branching sequence of amphoteric, L-amino acids joined together by resonant amide bonds between neighboring residues, with each exhibiting no free rotation.
- d). A biologically active protein is composed of a branching sequence of amphipathic, D-amino acids joined together by non-resonant amide bonds between neighboring residues, each exhibiting free rotation.
- e). A biologically active proteins is composed of a non-branching sequence of amphoteric, L-amino acids joined together by non-resonant amide bonds between neighboring residues, with each exhibiting no free rotation.

5). Consider the following proteins of the TCA cycle:

<u>Protein-</u>	<u>Mass (kDa)-</u>	<u>pI-</u>	<u>Solubility Limit (% Salt)-</u>
Pyruvate Dehydrogenase	1,100	8.3	25
Aconitase	15	5.0	35
$\alpha$ -ketoglutarate Dehydrogenase	1,080	6.0	27
Succinyl-CoA Thiokinase	357	7.5	20
Fumarase	353	7.3	40
Malate Dehydrogenase	14	7.7	15

Outline a procedure to separate all of the enzymes of the TCA cycle from a crude mitochondrial homogenate, paying specific attention to separating Pyruvate Dehydrogenase from  $\alpha$ -ketoglutarate Dehydrogenase, Aconitase from Malate Dehydrogenase, and Succinyl-CoA Thiokinase from Fumarase in their native states, using affinity chromatography only as a last resort.

6). Consider the following Lineweaver-Burk Plot:



● = no inhibitor. ▼ = 300 nM inhibitor. ■ = 650 nM inhibitor. ◆ = 900 nM inhibitor.

- What type of inhibition is seen at low inhibitor concentrations?
- What type of inhibition is seen at higher inhibitor concentrations?
- Going from the absence of inhibitor to 300 nM inhibitor, is the apparent  $K_m$  increasing or decreasing? Is the presence of the inhibitor making the substrate bind tighter or looser?
- Going from 300 nM inhibitor to 650 nM and 900 nM inhibitor, is the apparent  $K_m$  increasing or decreasing? Is the presence of the inhibitor making the substrate bind tighter or looser?
- Going from the absence of inhibitor to the presence of inhibitor (300-900 nM inhibitor), is the apparent  $V_{max}$  of the reaction increasing or decreasing?