

Re-writes of your paragraphs from Problem Set 3.

Learning to write clearly and concisely requires practice and revision. You will be entitled to submit a re-write of your paragraphs if you are not satisfied with the score you received. You will be eligible for up to 10 additional points but the rewrite cannot take your original score above a 20 for these paragraphs). I especially urge those of you who scored below 10 to take this opportunity to improve your writing. I would also suggest that you seek out and talk to the writing tutors about this assignment. Think of it as practice for writing graduate/professional school essays. Many of the factors that contributed to a poor performance on this exercise can easily detract from an admission essay or fellowship application. Below you will find several example paragraphs to see what some of your colleagues came up with.

**Resubmission of your paragraphs are due in class on Monday 10/22.** You must turn in both the revised paragraph as well as the original graded paragraph on which I wrote my comments.

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### **Sample structure paragraphs from C484 – Fall 2001**

#### **Student 1:**

Pyruvate decarboxylase is a homodimeric enzyme involved in glycolysis/gluconeogenesis. Its function in glycolysis is to decarboxylate pyruvate to yield acetaldehyde and carbon dioxide. Each subunit has 563 amino acid residues and a molecular weight of 61.5 kD. The subunits can be broken down into three different domains (figure 1). The N-terminal domain (residues 1-190) architecture can be described as an  $\alpha/\beta$  sandwich with 4 parallel  $\beta$ -strands flanked on both sides by 3 helices. The second domain (residues 200-350) contains 3 helices stacked against a sheet of 5 parallel and 2 anti-parallel  $\beta$ -strands. The C-terminal domain (residues 360-563) consists of another  $\alpha/\beta$  sandwich with 6 parallel  $\beta$ -strands flanked on both sides by 3 helices. The primary positions of interaction between the two subunits exist between the N-terminal and C-terminal domains. The two thiamine pyrophosphate cofactors are nestled in the middle of the interface between the subunits. The active site of the enzyme could exist at a small gap in the subunit interface where a cofactor is partially exposed to the exterior environment.

### **Student 2:**

The protein cytidine deaminase consists of 294 amino acid residues. The N-terminal region of this protein (residues 1-103) consists of four  $\alpha$ -helices in a two-layer sandwich arrangement. The four  $\alpha$ -helices are on one side of two anti-parallel  $\beta$ -strands. On the other side of these  $\beta$ -strands is a fifth short  $\alpha$ -helix followed by a longer sixth  $\alpha$ -helix. These two  $\alpha$ -helices are in one plane. The overall view of this region is a four-layer sandwich: 2- $\alpha$ -helices, 2- $\alpha$ -helices, 2- $\beta$ -strands and two  $\alpha$ -helices (Figure 1). The second region of the protein (residues 104-294) starts with a  $\beta$ -sheet comprised of two parallel  $\beta$ -strands. These  $\beta$ -strands are connected via a short  $\alpha$ -helix and a second longer  $\alpha$ -helix. Following the last  $\beta$ -strand is a long region of two short  $\alpha$ -helices and a long  $\alpha$ -helix interspersed by several residues not arranged into 2° structure. Following this region are two anti-parallel  $\beta$ -strands. The second  $\beta$ -strand connects to a third  $\beta$ -strand via a short then longer  $\alpha$ -helix. This third  $\beta$ -strand is located next to the first  $\beta$ -strand and runs anti-parallel to it. Finally, through a single  $\alpha$ -helix, the third  $\beta$ -strand leads to the fourth  $\beta$ -strand. The two run parallel to one another. Overall, this region is a three-layer sandwich of one  $\alpha$ -helix, a 4-stranded mixed  $\beta$ -sheet and three  $\alpha$ -helices. The C-terminus is located 3 residues after the final  $\beta$ -strand.

### **Student 3:**

Glycerol kinase is a two-domain molecule with the approximate dimensions of 62 x 43 x 46 Å (figure 1). A large beta-sheet from each domain forms an interdomain cleft. The N-terminal domain (residues 1-249) includes a beta sheet sandwich as two five-stranded mixed beta-sheets surround a three-member alpha helical region. This domain also contains an outer, 5-membered alpha-helical region. Several short regions of random coil connect the N- and C-terminal domains. The C-terminal domain (residues 250-501) contains an 8-stranded beta sheet, which helps define the interface of the interdomain cleft. A 5-member alpha-helical region flanks this beta sheet. The interdomain gap allows the substrates, ATP and glycerol, to gain access to the active site of glycerol kinase, which is in the core of the protein. The glycerol 3-phosphate binding site is located in the middle of the cleft. Hydrogen bonds exist between the hydroxyl groups of glycerol 3-phosphate and side chains of Arg83, Glu84, Tyr135, and Asp245 (Figure 2). The ADP binding site is adjacent to the glycerol 3-phosphate binding site. Unlike the glycerol-3-phosphate, however, ADP is found in a mostly hydrophobic environment of the enzyme. Favorable van der Waals interactions exist between the side chains of nonpolar residues such as glycine and alanine and the adenine ring of ADP.