

The following paragraphs were submitted by students in previous years of this course. They are provided to show you the level of detail you can achieve in this assignment if you apply yourself to learning to look at these structures. The paragraphs have been doctored to maintain some level of anonymity with respect to the proteins involved since they are among the unknowns assigned to the class.

**Example 1:**

**(ENZYME NAME OMITTED)** is a homodimeric enzyme involved in **(PATHWAY NAME OMITTED)**. Its function is to **(REACTION INFORMATION OMITTED)**. 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 a/b 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.

**Example 2:**

The protein **(PROTEIN NAME OMITTED)** 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.