(F1 ATPase)
secondary structures

α helix

β sheet

tertiary structures

single polypeptide domain

protein molecule made of two different domains

Figure 4-16 Essential Cell Biology 3/e (© Garland Science 2010)
X-ray crystallography is a major technique that has been used to discover the three-dimensional structure of protein molecules at atomic resolution. X-rays, like light, are a form of electromagnetic radiation, but with a very small wavelength. If a narrow parallel beam of x-rays is directed at a well-ordered crystal of a pure protein, some of the beam will be scattered by the atoms in the crystal. The scattered waves will reinforce one another at certain points and will appear as a pattern of diffraction spots when the x-rays are recorded by a suitable detector.

The position and intensity of each spot in the x-ray diffraction pattern contains information about the position of the atoms in the protein crystal that gave rise to it. Computers can use this information to provide a three-dimensional electron density map of the protein molecule, which, together with the sequence of the protein, can be used to produce an atomic model. The complete atomic model is often hard to interpret, so simplified versions are derived that show the essential structural features (see Panel 5-2, pp. 142–143). The protein shown here is ribulose bisphosphate carboxylase, an enzyme that plays a central role in CO₂ fixation during photosynthesis (alpha helices are shown in green, and beta strands in red).
HEMOGLOBIN ALPHA CHAIN
HUMAN  142 aa

mvlspadktn vkaawgkvga hageygaeal
ermflsfptt ktyfphfdls hgsaqvkghg
kkvadaltna vahvddmpna lsalsdlhah
klrvdpvnfk llshclllvl aahlpaeftp
avhasldkfl avsstyltsk yr

HEMOGLOBIN BETA CHAIN
HUMAN  147 aa

mvhlttppeeks avtalwgkvn vdevggealg
rllvvpwtpq rffesfgdls tpdavmgnpk
vkahgkkvlg afsdglahld nlkgtfatls
elhcdkhlvd penfrllgnv lvcvlahhfg
keftppvqaa yqkvvagvan alahkyh

(sickle cell hemoglobin has Valine in place of Glutamic Acid as underlined amino acid in the beta chain)
Genetic disorders for which there are gene tests

data from genetests.org
loops that bind antigen

variable domain of light chain (V_L)

constant domain of light chain

antigen-binding site

heavy chain

V_H domain

light chain

V_L domain

disulfide bond

NH_2

COOH

5 nm

(A)

(B)

Figure 4-32 Essential Cell Biology, 2/e. (© 2004 Garland Science)
enzyme binds to two substrate molecules and orients them precisely to encourage a reaction to occur between them.

binding of substrate to enzyme rearranges electrons in the substrate, creating partial negative and positive charges that favor a reaction.

enzyme strains the bound substrate molecule, forcing it toward a transition state to favor a reaction.