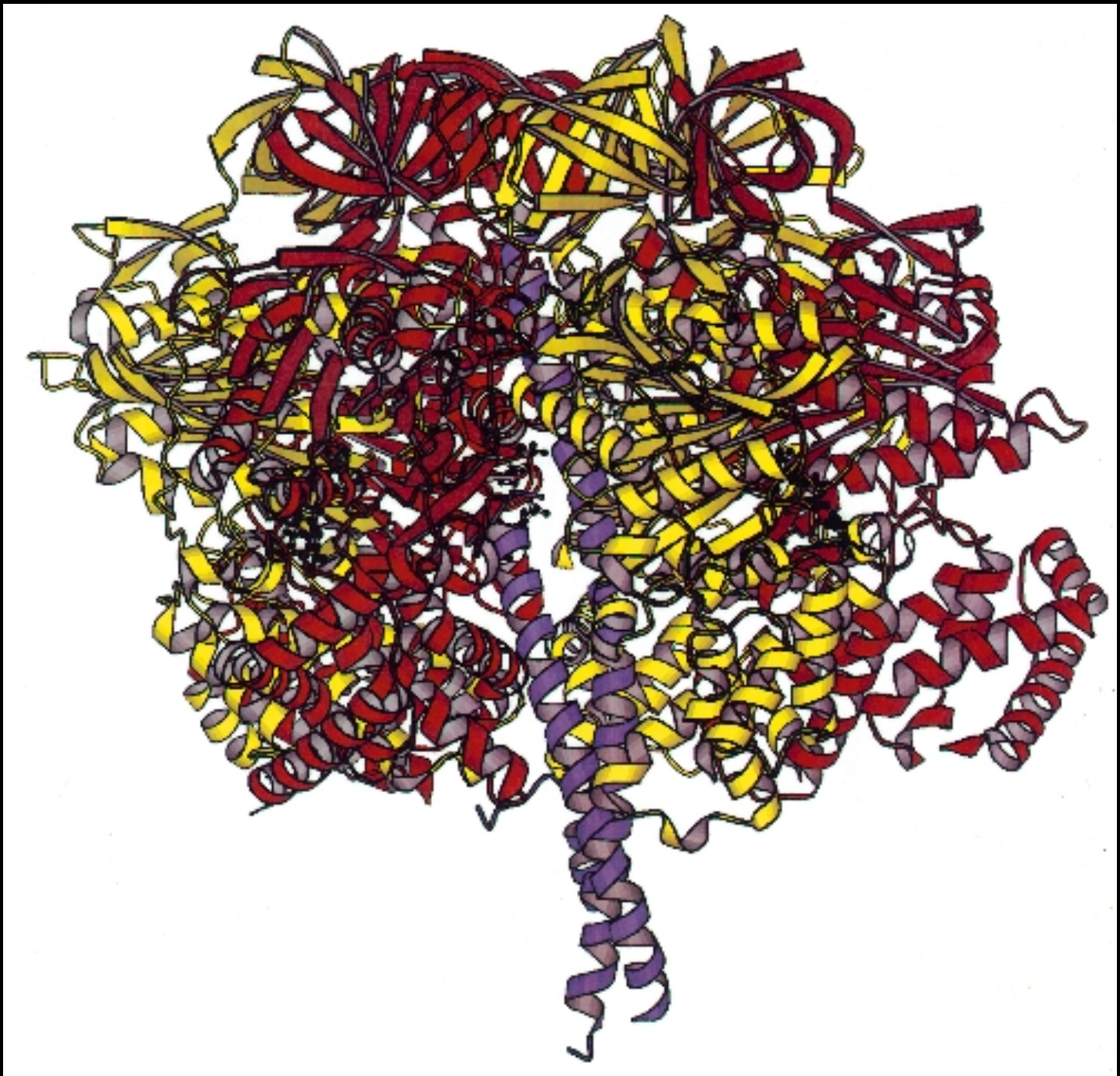
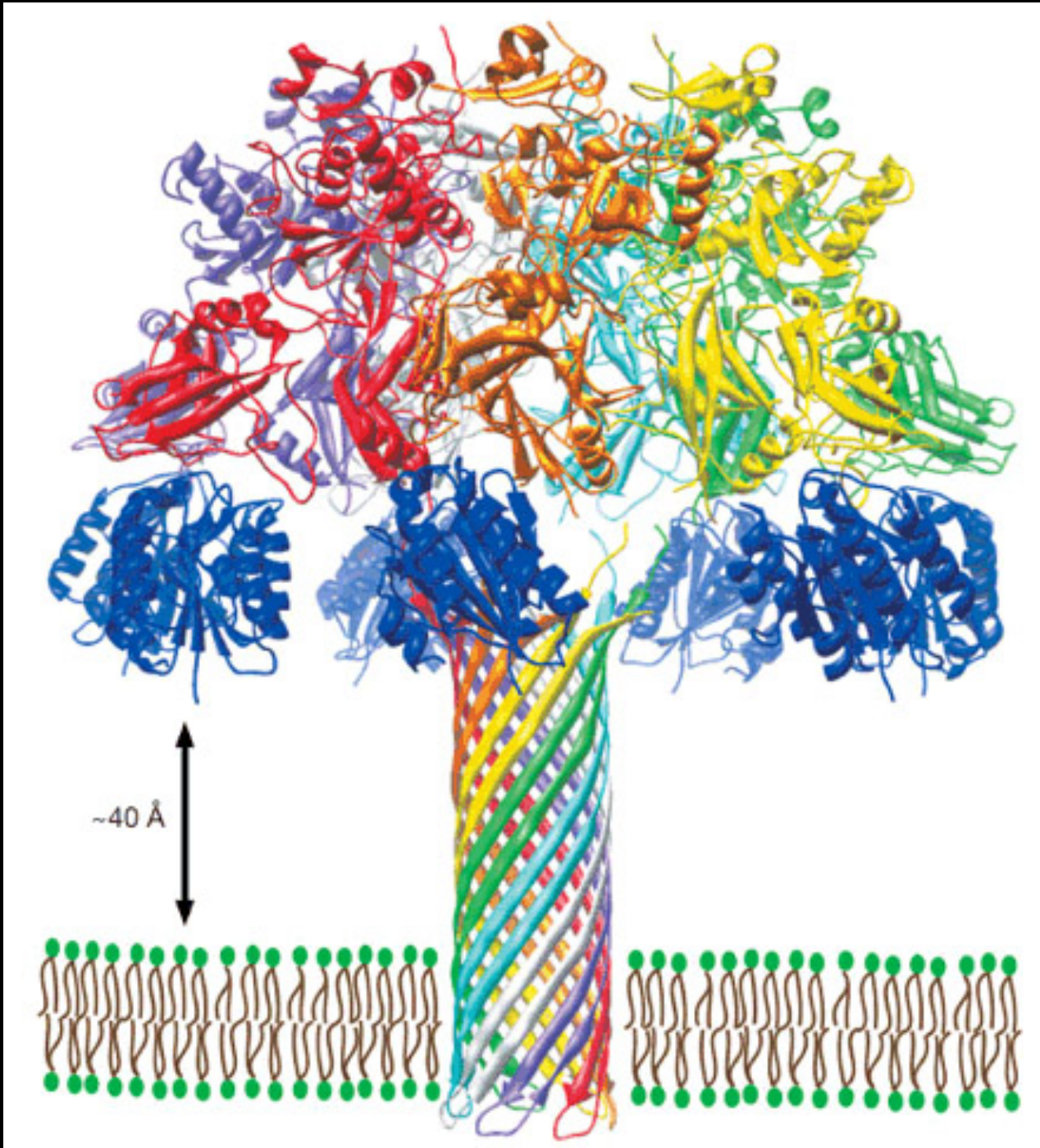


(GFP)

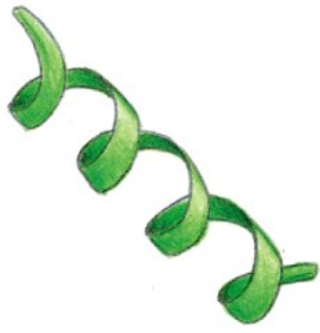




(F1 ATPase)



secondary structures



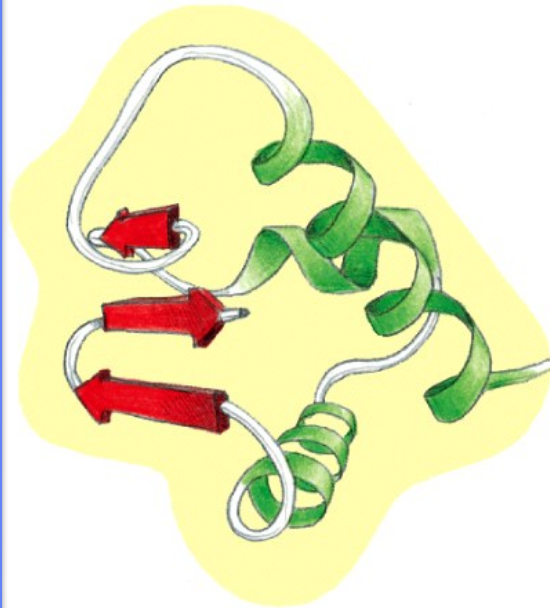
α helix



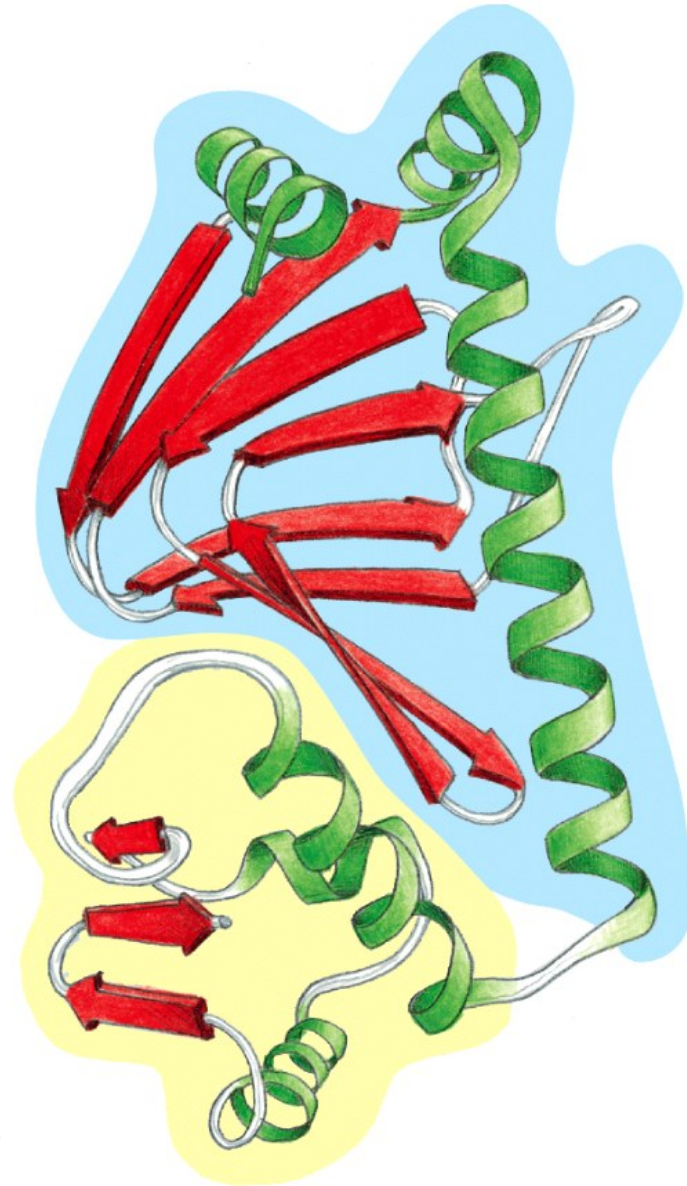
β sheet

secondary structure

tertiary structures



single polypeptide domain

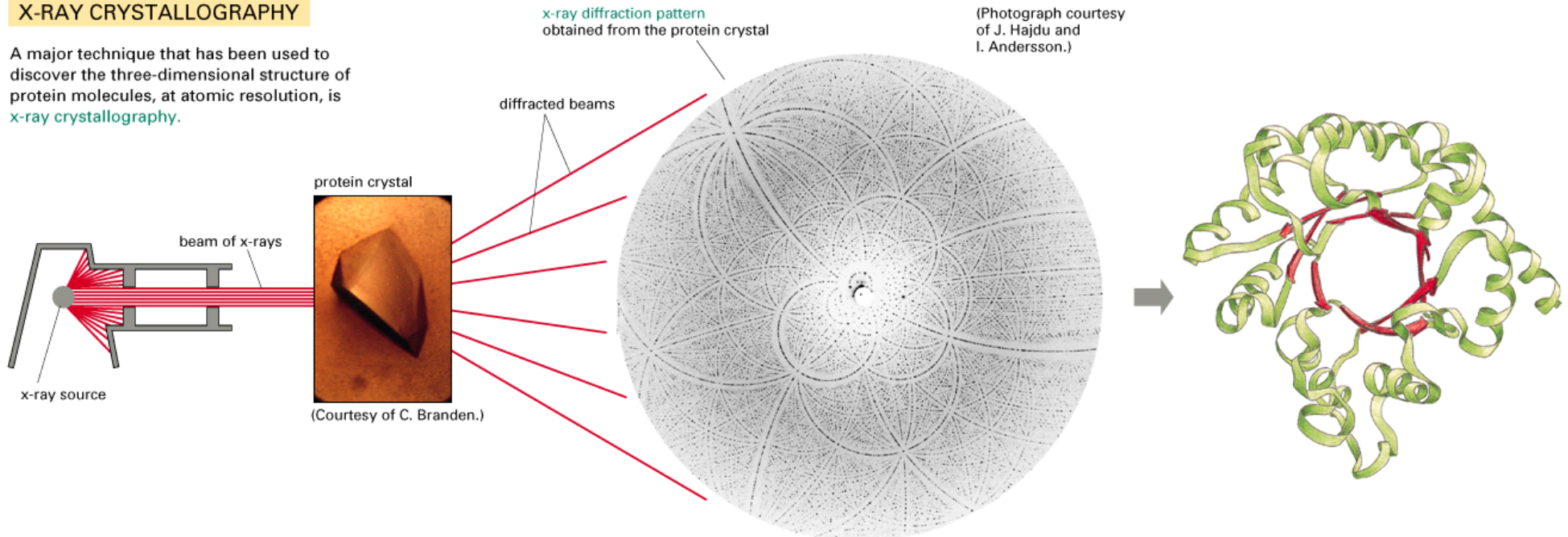


protein molecule made of two different domains

Figure 4-16 Essential Cell Biology 3/e (© Garland Science 2010)

X-RAY CRYSTALLOGRAPHY

A major technique that has been used to discover the three-dimensional structure of protein molecules, at atomic resolution, is **x-ray crystallography**.



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 biphosphate carboxylase, an enzyme that plays a central role in CO_2 fixation during photosynthesis (alpha helices are shown in *green*, and beta strands in *red*).



HEMOGLOBIN ALPHA CHAIN

HUMAN 142 aa

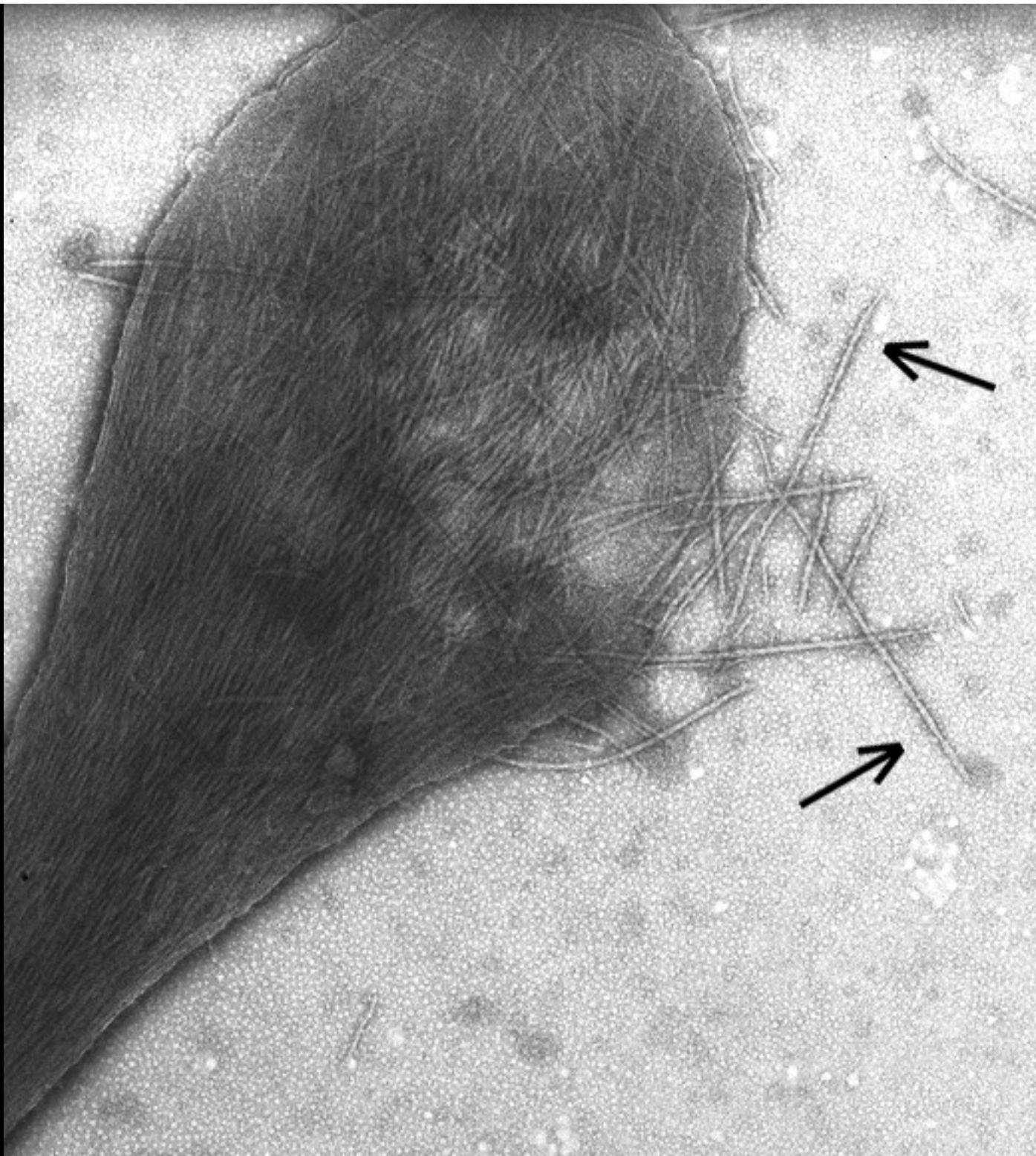
mvlspadktn vkaawgkvga hageygaeal
ermflsfptt ktyfphfdls hgsaqvkgghg
kkvadaltna vahvddmpna lsalsdlhah
klrvdpvnfk llshcllvtl aahlpaeftp
avhasldkfl asvstvltsk yr

HEMOGLOBIN BETA CHAIN

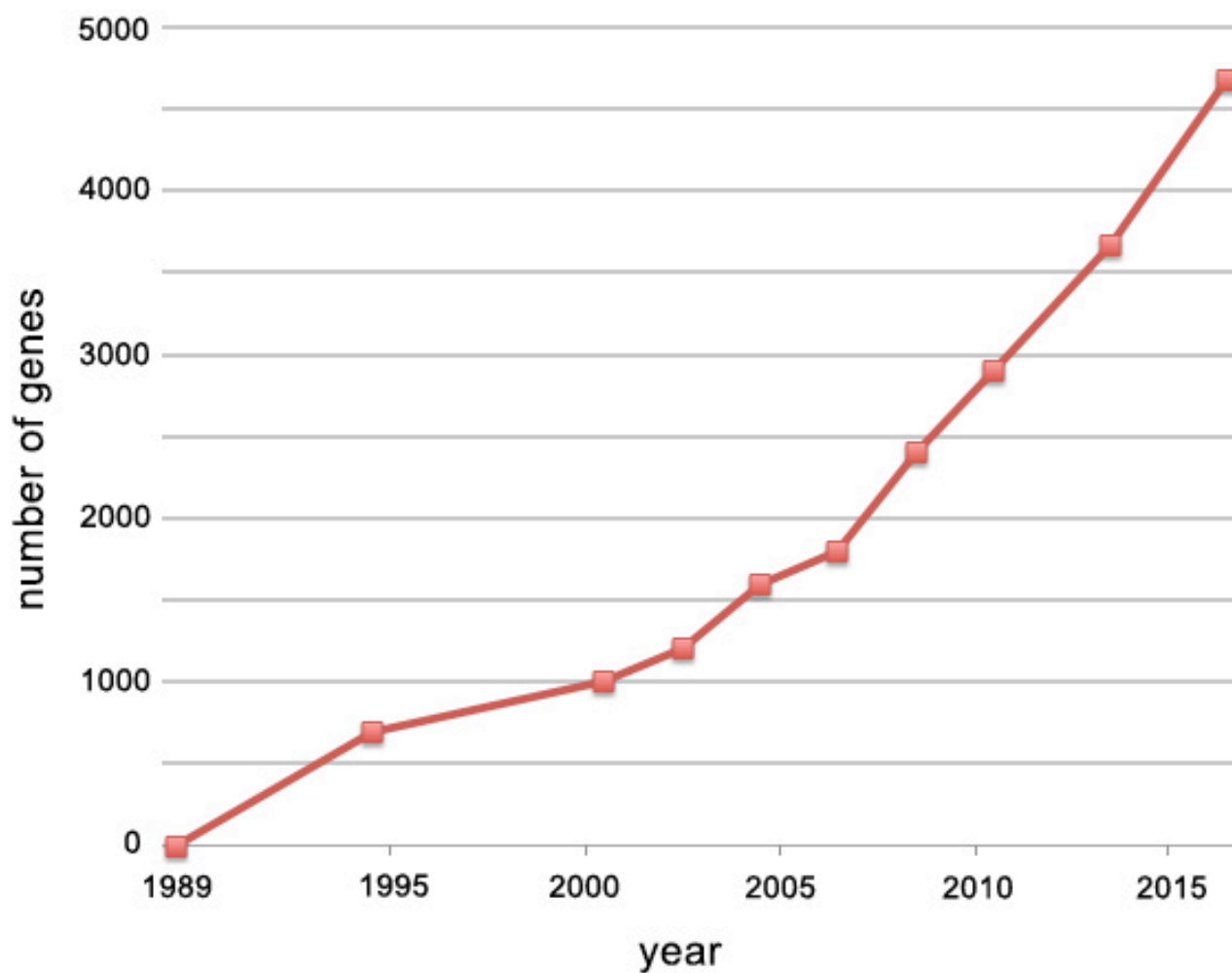
HUMAN 147 aa

mvhltpeeks avtalwgkvn vdevggealg
rllvvypwtq rffesfgdls tpdavmgnpk
vkahgkkvlg afsdglahld nlkgtfatls
elhccklhvd penfrllgnv lvcvlahhfg
keftppvqaa yqkvvagvan alahkyh

(sickle cell hemoglobin has Valine in place of Glutamic Acid as underlined amino acid in the beta chain)

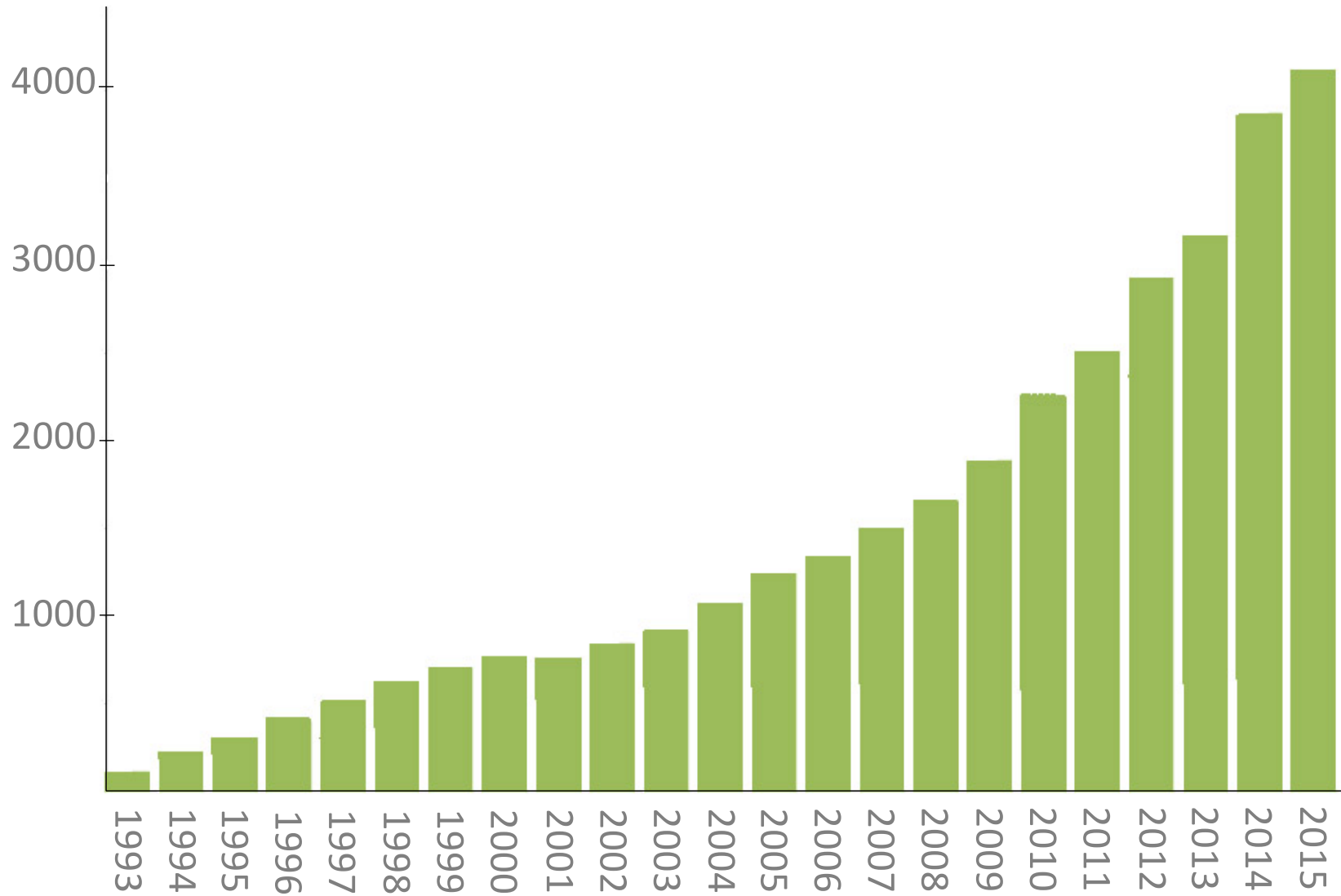


Number of Disease Genes Recognized



disease genes in OMIM database
source: goo.gl/Ddwge3

Genetic disorders for which there are gene tests



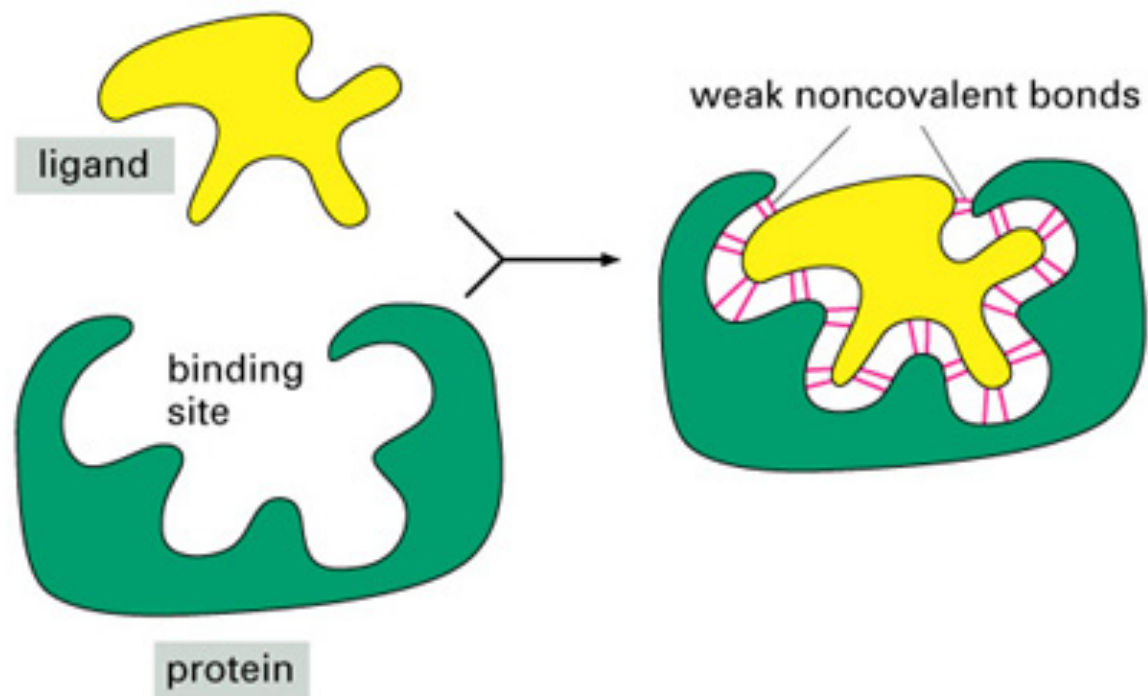


Figure 4-30 Essential Cell Biology, 2/e. (© 2004 Garland Science)

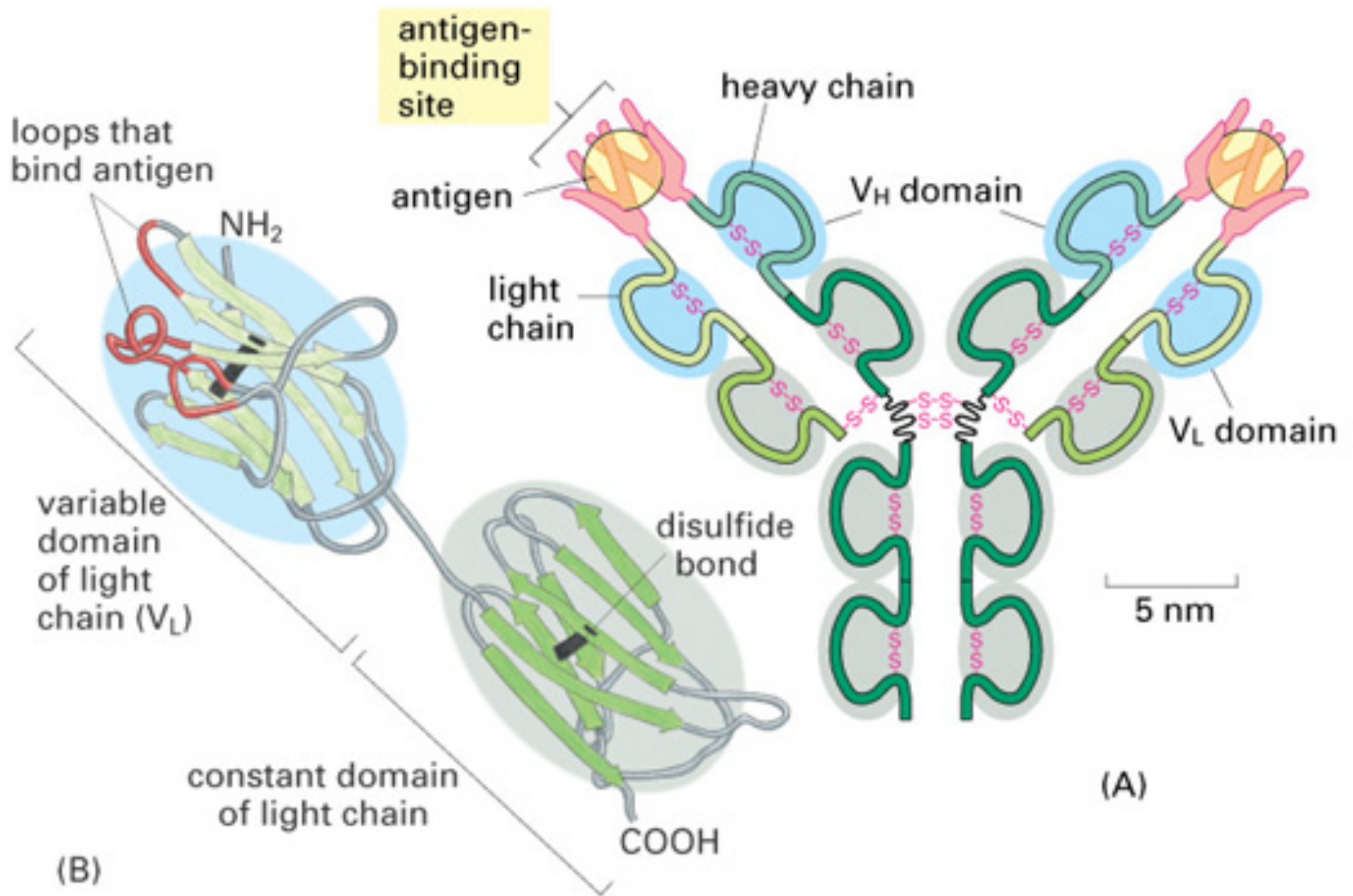
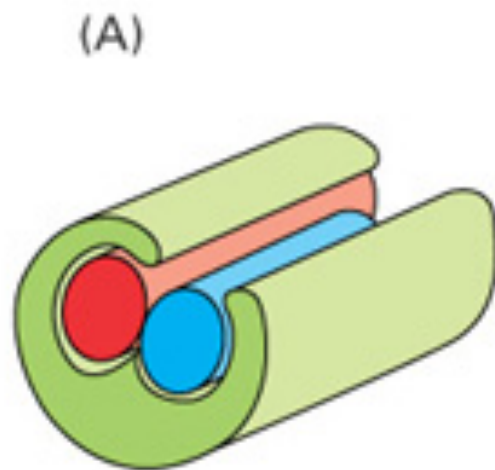
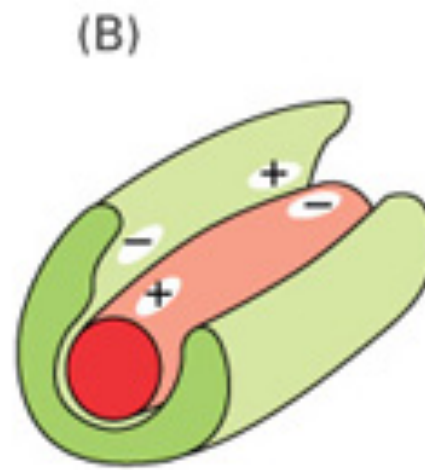


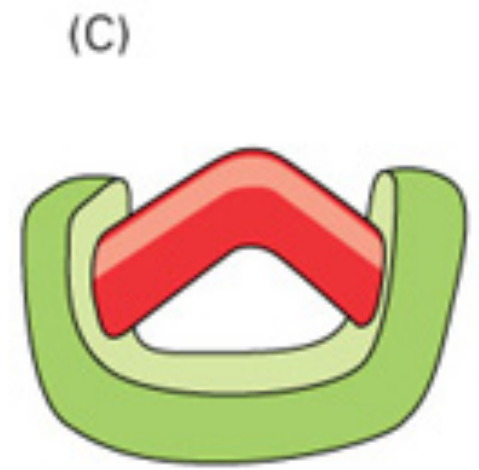
Figure 4-32 Essential Cell Biology, 2/e. (© 2004 Garland Science)



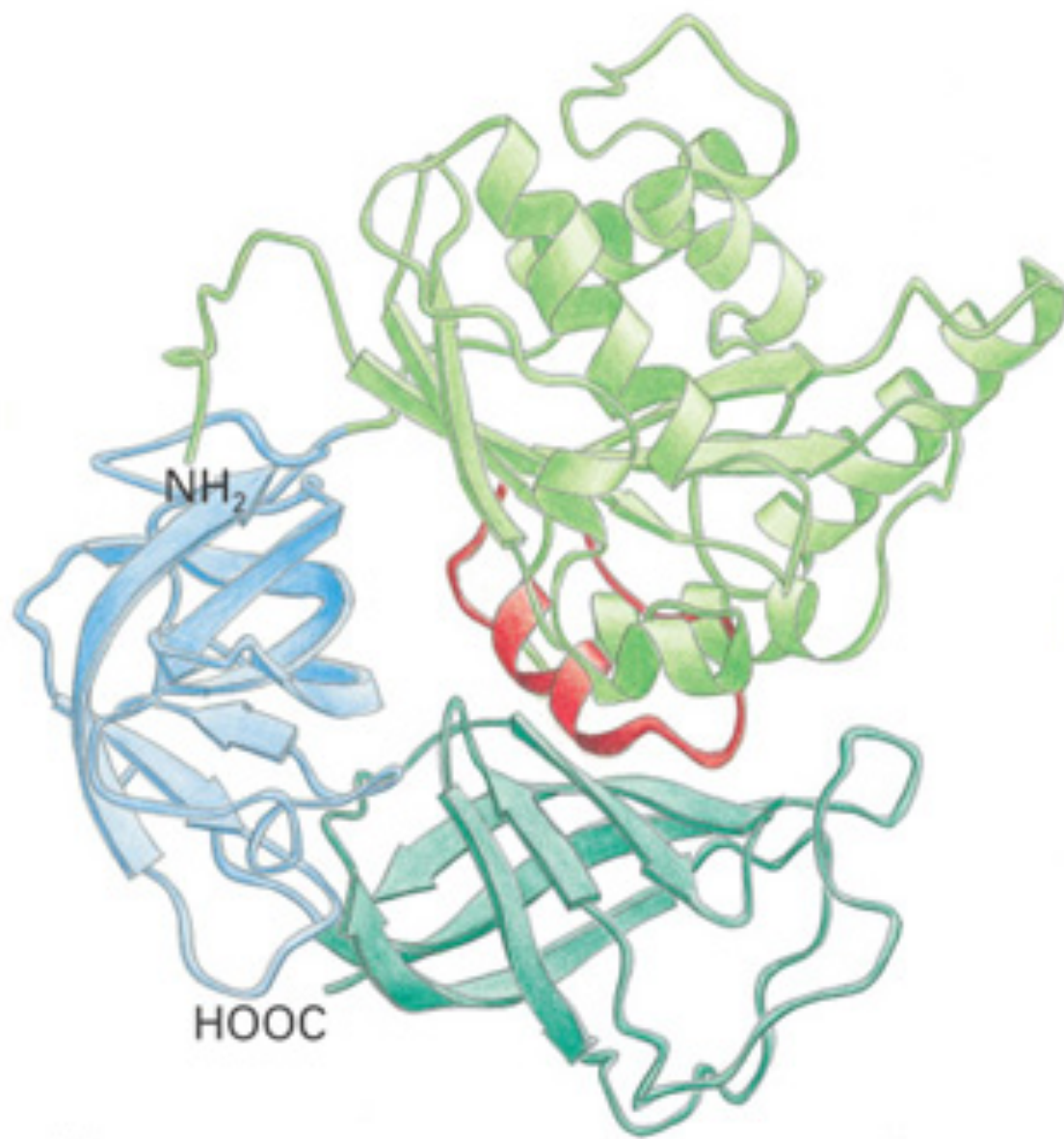
enzyme binds to two substrate molecules and orients them precisely to encourage a reaction to occur between them



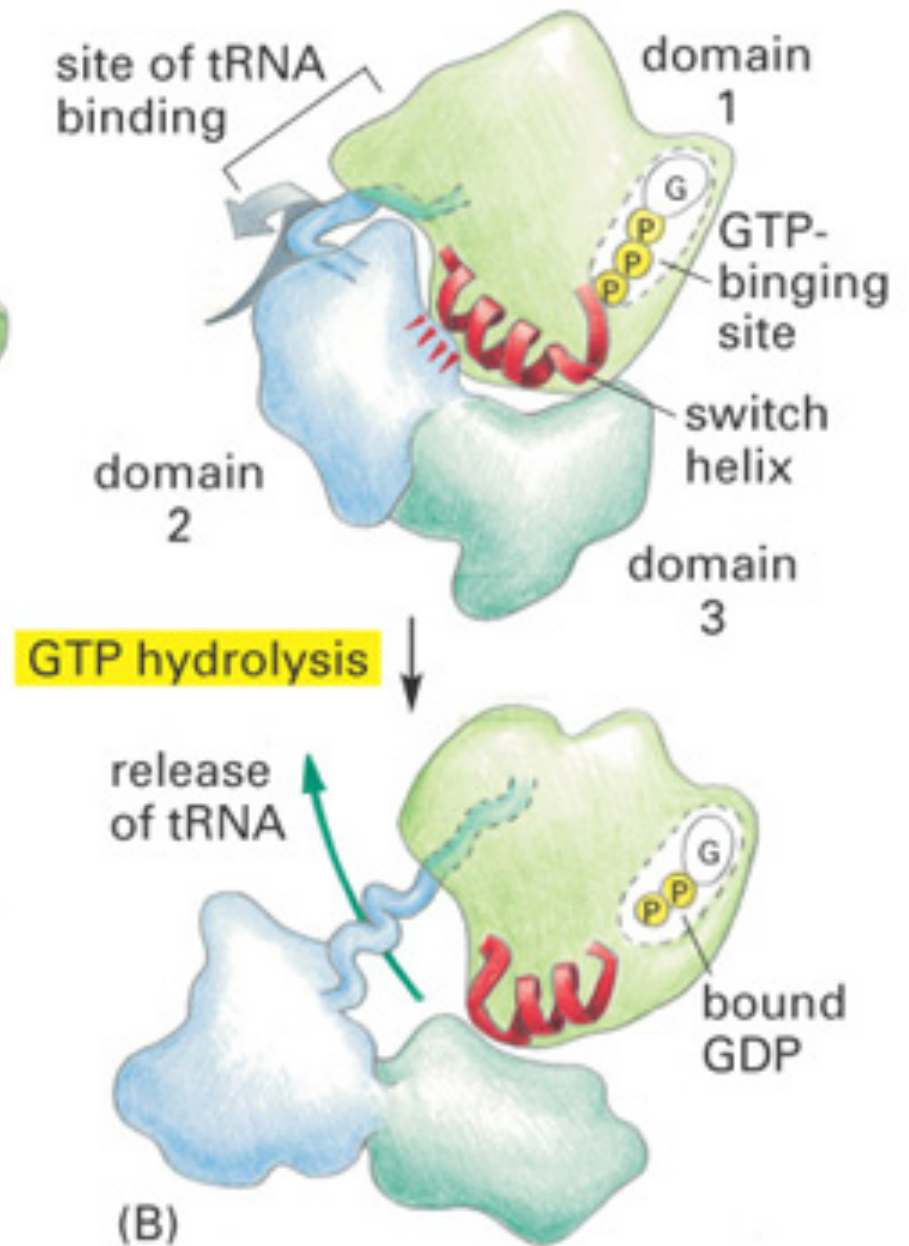
binding of substrate to enzyme rearranges electrons in the substrate, creating partial negative and positive charges that favor a reaction



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



(A)



(B)

