

REFERENCES

4.2 (cont.)

- Pautsch, A. & Schulz, G. E. (1998). Structure of the outer membrane protein: a transmembrane domain. *Nature Struct. Biol.* **5**, 1013–1017.
- Pebay-Peyroula, E., Rummel, G., Rosenbusch, J. P. & Landau, E. M. (1997). X-ray structure of bacteriorhodopsin at 2.5 Å from microcrystals grown in lipidic cubic phases. *Science*, **277**, 1676–1681.
- Picot, D., Loll, P. J. & Garavito, M. (1994). The X-ray crystal structure of the membrane protein prostaglandin H2 synthase-1. *Nature (London)*, **367**, 243–249.
- Roth, M., Lewit-Bentley, A., Michel, H., Deisenhofer, J., Huber, R. & Oesterhelt, D. (1989). Detergent structure in crystals of a bacterial photosynthetic reaction center. *Nature (London)*, **340**, 659–662.
- Schirmer, T., Keller, T. A., Wang, Y. F. & Rosenbusch, J. P. (1995). Structural basis for sugar translocation through maltoporin channels at 3.1 Å resolution. *Science*, **267**, 512–514.
- Song, L., Hobaugh, M. R., Shustak, C., Cheley, S., Bayley, H. & Gouaux, J. E. (1996). Structure of staphylococcal alpha-hemolysin, a heptameric transmembrane pore. *Science*, **274**, 1859–1866.
- Stowell, M. H. B., McPhillips, T. M., Rees, D. C., Soltis, S. M., Abresch, E. & Feher, G. (1997). Light-induced structural changes in photosynthetic reaction center: implications for mechanism of electron-proton transfer. *Science*, **276**, 812–816.
- Timmins, P. A., Hauk, J., Wacker, T. & Welte, W. (1991). The influence of heptane-1,2,3-triol on the size and shape of LDAO micelles. Implications for the crystallization of membrane proteins. *FEBS Lett.* **280**, 115–120.
- Timmins, P. A., Pebay-Peyroula, E. & Welte, W. (1994). Detergent organisation in solutions and in crystals of membrane proteins. *Biophys. Chem.* **53**, 27–36.
- Tsukihara, T., Aoyama, H., Yamashita, E., Tomizaki, T., Yamaguchi, H., Shinzawa-Itoh, K., Nakashima, R., Yaono, R. & Yoshikawa, S. (1995). Structures of metal sites of oxidized bovine heart cytochrome c oxidase at 2.8 Å. *Science*, **269**, 1069–1074.
- Tsukihara, T., Aoyama, H., Yamashita, E., Tomizaki, T., Yamaguchi, H., Shinzawa-Itoh, K., Nakashima, R., Yaono, R. & Yoshikawa, S. (1996). The whole structure of the 13-subunit oxidized cytochrome c oxidase at 2.8 Å. *Science*, **272**, 1136–1144.
- Weiss, M. S., Abele, U., Weckesser, J., Welte, W., Schiltz, E. & Schulz, G. E. (1991). Molecular architecture and electrostatic properties of a bacterial porin. *Science*, **254**, 1627–1630.
- Wendt, K. U., Poralla, K. & Schulz, G. E. (1997). Structure and function of a cyclase. *Science*, **277**, 1811–1815.
- Xia, D., Yu, C. A., Kim, H., Xia, J. Z., Kachurin, A. M., Zhang, L., Yu, L. & Deisenhofer, J. (1997). Crystal structure of the cytochrome bc₁ complex from bovine heart mitochondria. *Science*, **277**, 60–66.
- Yoshikawa, S., Shinzawa-Itoh, K., Nakashima, R., Yaono, R., Yamashita, E., Inoue, N., Yao, M., Fei, M. J., Libeu, C. P., Mizushima, T., Yamaguchi, H., Tomizaki, T. & Tsukihara, T. (1998). Redox-coupled crystal structural changes in bovine heart cytochrome c oxidase. *Science*, **280**, 1723–1729.
- Zhang, Z. L., Huang, L. S., Shulmeister, V. M., Chi, Y. I., Kim, K. K., Hung, L. W., Crofts, A. R., Berry, E. A. & Kim, S. H. (1998). Electron transfer by domain movement in cytochrome bc₁. *Nature (London)*, **392**, 677–684.
- Zulauf, H. (1991). Detergent phenomena in membrane protein crystallization. In *Crystallization of membrane proteins*, edited by H. Michel, ch. 2, pp. 53–72. Boca Raton, Florida: CRC Press.
- Braig, K., Otwinowski, Z., Hegde, R., Boisvert, D. C., Joachimiak, A., Horwich, A. L. & Sigler, P. B. (1994). The crystal structure of the bacterial chaperonin GroEL at 2.8 Å. *Nature (London)*, **371**, 578–586.
- Budisa, N., Steipe, B., Demange, P., Eckerskorn, C., Kellermann, J. & Huber, R. (1995). High-level biosynthetic substitution of methionine in proteins by its analogs 2-aminohexanoic acid, selenomethionine, telluromethionine and ethionine in *Escherichia coli*. *Eur. J. Biochem.* **230**, 788–796.
- Bujacz, G., Jaskolski, M., Alexandratos, J., Wlodawer, A., Merkel, G., Katz, R. A. & Skalka, A. M. (1995). High resolution structure of the catalytic domain of avian sarcoma virus integrase. *J. Mol. Biol.* **253**, 333–346.
- Carugo, O. & Argos, P. (1997). Protein-protein crystal-packing contacts. *Protein Sci.* **6**, 2261–2263.
- Cowie, D. B. & Cohen, G. N. (1957). Biosynthesis by *Escherichia coli* of active altered proteins containing selenium instead of sulfur. *Biochim. Biophys. Acta*, **26**, 252–261.
- Dale, G. E., Broger, C., Langen, H., D'Arcy, A. & Stüber, D. (1994). Improving protein solubility through rationally designed amino acid replacements: solubilization of the trimethoprim-resistant type SI dihydrofolate reductase. *Protein Eng.* **7**, 933–939.
- D'Arcy, A. (1994). Crystallizing proteins – a rational approach? *Acta Cryst.* **D50**, 469–471.
- Dasgupta, S., Iyer, G. H., Bryant, S. H., Lawrence, C. E. & Bell, J. A. (1997). Extent and nature of contacts between protein molecules in crystal lattices and between subunits of protein oligomers. *Proteins*, **28**, 494–514.
- Dayhoff, M. O. (1978). *Atlas of protein sequence and structure*, Vol. 5, Suppl. 3, p. 363. Washington DC: National Biomedical Research Foundation.
- Donahue, J. P., Patel, H., Anderson, W. F. & Hawiger, J. (1994). Three-dimensional structure of the platelet integrin recognition segment of the fibrinogen γ chain obtained by carrier protein-driven crystallization. *Proc. Natl Acad. Sci. USA*, **91**, 12178–12182.
- Doublé, S. (1997). Preparation of selenomethionyl proteins for phase determination. *Methods Enzymol.* **276**, 523–530.
- Dyda, F., Hickman, A. B., Jenkins, T. M., Engelman, A., Craigie, R. & Davies, D. R. (1994). Crystal structure of the catalytic domain of HIV-1 integrase: similarity to other polynucleotidyl transferases. *Science*, **266**, 1981–1986.
- Fermi, G. & Perutz, M. F. (1981). *Atlas of molecular structures in biology*, Vol. 2. Oxford: Clarendon Press.
- Golden, B. L., Ramakrishnan, V. & White, S. W. (1993). Ribosomal protein L6: structural evidence of gene duplication from a primitive RNA binding protein. *EMBO J.* **12**, 4901–4908.
- Goldgur, Y., Dyda, F., Hickman, A. B., Jenkins, T. M., Craigie, R. & Davies, D. R. (1998). Three new structures of the core domain of HIV-1 integrase: an active site that binds magnesium. *Proc. Natl Acad. Sci. USA*, **95**, 9150–9154.
- Heinz, D. W. & Matthews, B. W. (1994). Rapid crystallization of T4 lysozyme by intermolecular disulfide cross-linking. *Protein Eng.* **7**, 301–307.
- Hendrickson, W. A. (1991). Determination of macromolecular structures from anomalous diffraction of synchrotron radiation. *Science*, **254**, 51–58.
- Hendrickson, W. A., Horton, J. R. & LeMaster, D. M. (1990). Selenomethionyl proteins produced for analysis by multiwavelength anomalous diffraction (MAD): a vehicle for direct determination of three-dimensional structure. *EMBO J.* **9**, 1665–1672.
- Hendrickson, W. A. & Ogata, C. M. (1997). Phase determination from multiwavelength anomalous diffraction measurements. *Methods Enzymol.* **276**, 494–523.
- Hickman, A. B., Dyda, F. & Craigie, R. (1997). Heterogeneity in recombinant HIV-1 integrase corrected by site-directed mutagenesis: the identification and elimination of a protease cleavage site. *Protein Eng.* **10**, 601–606.
- Hizi, A. & Hughes, S. H. (1988). Expression of the Moloney murine leukemia virus and human immunodeficiency virus integration proteins in *Escherichia coli*. *Virology*, **167**, 634–638.

4.3

- Bell, J. A., Wilson, K. P., Zhang, X.-J., Faber, H. R., Nicholson, H. & Matthews, B. W. (1991). Comparison of the crystal structure of bacteriophage T4 lysozyme at low, medium, and high ionic strengths. *Proteins*, **10**, 10–21.

4. CRYSTALLIZATION

4.3 (cont.)

- Hoffman, D. W., Davies, C., Gerchman, S. E., Kycia, J. H., Porter, S. J., White, S. W. & Ramakrishnan, V. (1994). *Crystal structure of prokaryotic ribosomal protein L9: a bi-lobed RNA-binding protein*. *EMBO J.* **13**, 205–212.
- Huang, H., Chopra, R., Verdine, G. L. & Harrison, S. C. (1998). *Structure of a covalently trapped catalytic complex of HIV-1 reverse transcriptase: implications for drug resistance*. *Science*, **282**, 1669–1675.
- Jenkins, T. M., Hickman, A. B., Dyda, F., Ghirlando, R., Davies, D. R. & Craigie, R. (1995). *Catalytic domain of human immunodeficiency virus type 1 integrase: identification of a soluble mutant by systematic replacement of hydrophobic residues*. *Proc. Natl Acad. Sci. USA*, **92**, 6057–6061.
- Karle, J. (1980). *Some developments in anomalous dispersion for the structural investigation of macromolecular systems in biology*. *Int. J. Quantum Chem. Symp.* **7**, 357–367.
- Kuge, M., Fujii, Y., Shimizu, T., Hirose, F., Matsukage, A. & Hakoshima, T. (1997). *Use of a fusion protein to obtain crystals suitable for X-ray analysis: crystallization of a GST-fused protein containing the DNA-binding domain of DNA replication-related element-binding factor, DREF*. *Protein Sci.* **6**, 1783–1786.
- Kwong, P. D., Wyatt, R., Robinson, J., Sweet, R. W., Sodroski, J. & Hendrickson, W. A. (1998). *Structure of an HIV gp120 envelope glycoprotein in complex with the CD4 receptor and a neutralizing human antibody*. *Nature (London)*, **393**, 648–659.
- Lawson, D. M., Artymiuk, P. J., Yewdall, S. J., Smith, J. M. A., Livingstone, J. C., Treffry, A., Luzzago, A., Levi, S., Arosio, P., Cesareni, G., Thomas, C. D., Shaw, W. V. & Harrison, P. M. (1991). *Solving the structure of human H ferritin by genetically engineering intermolecular crystal contacts*. *Nature (London)*, **349**, 541–544.
- Leahy, D. J., Erickson, H. P., Aukhil, I., Joshi, P. & Hendrickson, W. A. (1994). *Crystallization of a fragment of human fibronectin: introduction of methionine by site-directed mutagenesis to allow phasing via selenomethionine*. *Proteins*, **19**, 48–54.
- McElroy, H. E., Sisson, G. W., Schoettlin, W. E., Aust, R. M. & Villafranca, J. E. (1992). *Studies on engineering crystallizability by mutation of surface residues of human thymidylate synthase*. *J. Cryst. Growth*, **122**, 265–272.
- Martinez, C., De Geus, P., Lauwereys, M., Matthysens, G. & Cambillau, C. (1992). *Fusarium solani cutinase is a lipolytic enzyme with a catalytic serine accessible to solvent*. *Nature (London)*, **356**, 615–618.
- Martínez-Hackert, E., Harlocker, S., Inouye, M., Berman, H. M. & Stock, A. M. (1996). *Crystallization, X-ray studies, and site-directed cysteine mutagenesis of the DNA-binding domain of OmpR*. *Protein Sci.* **5**, 1429–1433.
- Matthews, B. W. (1993). *Structural and genetic analysis of protein stability*. *Annu. Rev. Biochem.* **62**, 139–160.
- Mazzoni, M. R., Malinski, J. A. & Hamm, H. E. (1991). *Structural analysis of rod GTP-binding protein*. *Gt. J. Biol. Chem.* **266**, 14072–14081.
- Mittl, P. R. E., Berry, A., Scrutton, N. S., Perham, R. N. & Schulz, G. E. (1994). *A designed mutant of the enzyme glutathione reductase shortens the crystallization time by a factor of forty*. *Acta Cryst. D50*, 228–231.
- Nagai, K., Oubridge, C., Jessen, T. H., Li, J. & Evans, P. R. (1990). *Crystal structure of the RNA-binding domain of the U1 small nuclear ribonucleoprotein A*. *Nature (London)*, **348**, 515–520.
- Nilsson, B., Forsberg, G., Moks, T., Hartmanis, M. & Uhlén, M. (1992). *Fusion proteins in biotechnology and structural biology*. *Curr. Opin. Struct. Biol.* **2**, 569–575.
- Noel, J. P., Hamm, H. E. & Sigler, P. B. (1993). *The 2.2 Å crystal structure of transducin- α complexed with GTP γ S*. *Nature (London)*, **366**, 654–663.
- Oubridge, C., Ito, N., Teo, C.-H., Fearnley, I. & Nagai, K. (1995). *Crystallisation of RNA-protein complexes II. The application of protein engineering for crystallisation of the U1A protein-RNA complex*. *J. Mol. Biol.* **249**, 409–423.
- Peat, T. S., Frank, E. G., Woodgate, R. & Hendrickson, W. A. (1996). *Production and crystallization of a selenomethionyl variant of UmuD', an Escherichia coli SOS response protein*. *Proteins*, **25**, 506–509.
- Price, S. R. & Nagai, K. (1995). *Protein engineering as a tool for crystallography*. *Curr. Opin. Biotech.* **6**, 425–430.
- Privé, G. G., Verner, G. E., Weitzman, C., Zen, K. H., Eisenberg, D. & Kaback, H. R. (1994). *Fusion proteins as tools for crystallization: the lactose permease from Escherichia coli*. *Acta Cryst. D50*, 375–379.
- Scott, C. A., Garcia, K. C., Stura, E. A., Peterson, P. A., Wilson, I. A. & Teyton, L. (1998). *Engineering protein for X-ray crystallography: the murine major histocompatibility complex class II molecule I-A*. *Protein Sci.* **7**, 413–418.
- Stoll, V. S., Manohar, A. V., Gillon, W., Macfarlane, E. L. A., Hynes, R. C. & Pai, E. F. (1998). *A thioredoxin fusion protein of VanH, a D-lactate dehydrogenase from Enterococcus faecium: cloning, expression, purification, kinetic analysis, and crystallization*. *Protein Sci.* **7**, 1147–1155.
- Sun, D.-P., Alber, T., Bell, J. A., Weaver, L. H. & Matthews, B. W. (1987). *Use of site-directed mutagenesis to obtain isomorphous heavy-atom derivatives for protein crystallography: cysteine-containing mutants of phage T4 lysozyme*. *Protein Eng.* **1**, 115–123.
- Windsor, W. T., Walter, L. J., Syto, R., Fossetta, J., Cook, W. J., Nagabhushan, T. L. & Walter, M. R. (1996). *Purification and crystallization of a complex between human interferon γ receptor (extracellular domain) and human interferon γ* . *Proteins*, **26**, 108–114.
- Yang, W., Hendrickson, W. A., Crouch, R. J. & Satow, Y. (1990). *Structure of ribonuclease H phased at 2 Å resolution by MAD analysis of the selenomethionyl protein*. *Science*, **249**, 1398–1405.
- Yang, W., Hendrickson, W. A., Kalman, E. T. & Crouch, R. J. (1990). *Expression, purification, and crystallization of natural and selenomethionyl recombinant ribonuclease H from Escherichia coli*. *J. Biol. Chem.* **265**, 13553–13559.
- Zhang, G., Liu, Y., Qin, J., Vo, B., Tang, W.-J., Ruoho, A. E. & Hurley, J. H. (1997). *Characterization and crystallization of a minimal catalytic core domain from mammalian type II adenylyl cyclase*. *Protein Sci.* **6**, 903–908.
- Zhang, X., Wozniak, J. A. & Matthews, B. W. (1995). *Protein flexibility and adaptability seen in 25 crystal forms of T4 lysozyme*. *J. Mol. Biol.* **250**, 527–552.