

## REFERENCES

## 4.1 (cont.)

- tase: use of phase diagram to improve crystal quality. *Acta Cryst.* **D55**, 149–156.
- Sauter, C., Ng, J. D., Lorber, B., Keith, G., Brion, P., Hosseini, M. W., Lehn, J.-M. & Giegé, R. (1999). Additives for the crystallization of proteins and nucleic acids. *J. Cryst. Growth*, **196**, 365–376.
- Sazaki, G., Yoshida, E., Komatsu, H., Nakada, T., Miyashita, S. & Watanabe, K. (1997). Effects of a magnetic field on the nucleation and growth of protein crystals. *J. Cryst. Growth*, **173**, 231–234.
- Shlichta, P. J. (1986). Feasibility of mapping solution properties during the growth of protein crystals. *J. Cryst. Growth*, **76**, 656–662.
- Shu, Z.-Y., Gong, H.-Y. & Bi, R.-C. (1998). In situ measurements and dynamic control of the evaporation rate in vapor diffusion crystallization of proteins. *J. Cryst. Growth*, **192**, 282–289.
- Skouri, M., Lorber, B., Giegé, R., Munch, J.-P. & Candau, S. J. (1995). Effect of macromolecular impurities on lysozyme solubility and crystallizability. Dynamic light scattering, phase diagram, and crystal growth studies. *J. Cryst. Growth*, **152**, 209–220.
- Snell, E., Helliwell, J. R., Boggon, T. J., Lautenschlager, P. & Potthast, L. (1996). First ground trials of a Mach-Zehnder interferometer for implementation into a microgravity protein crystallization facility – the APCF. *Acta Cryst.* **D52**, 529–533.
- Snell, E. H., Weisgerber, S., Helliwell, J. R., Weckert, E., Hölzer, K. & Schroer, K. (1995). Improvements in lysozyme protein crystal perfection through microgravity growth. *Acta Cryst.* **D51**, 1099–1102.
- Sousa, R., Lafer, E. M. & Wang, B.-C. (1991). Preparation of crystals of T7 RNA polymerase suitable for high resolution X-ray structure analysis. *J. Cryst. Growth*, **110**, 237–246.
- Stojanoff, V., Siddons, D. P., Monaco, L. A., Vekilov, P. & Rosenberger, F. (1997). X-ray topography of tetragonal lysozyme grown by the temperature-controlled technique. *Acta Cryst.* **D53**, 588–595.
- Stojanoff, V., Snell, E. F., Siddons, D. P. & Helliwell, J. R. (1996). An old technique with a new application: X-ray topography of protein crystals. *Synchrotron Radiat. News*, **9**, 25–26.
- Strickland, C. L., Puchalski, R., Savvides, S. N. & Karplus, P. A. (1995). Overexpression of *Crithidia fasciculata* trypanothione reductase and crystallization using a novel geometry. *Acta Cryst.* **D51**, 337–341.
- Stura, E. A. & Wilson, I. A. (1990). Analytical and production seeding techniques. *Methods Companion Methods Enzymol.* **1**, 38–49.
- Suzuki, Y., Miyashita, S., Komatsu, H., Sato, K. & Yagi, T. (1994). Crystal growth of hen egg white lysozyme under high pressure. *Jpn. J. Appl. Phys.* **33**, 1568–1570.
- Syguusch, J., Coulombe, R., Cassanto, J. M., Sportiello, M. G. & Todd, P. (1996). Protein crystallization in low gravity by step gradient diffusion method. *J. Cryst. Growth*, **162**, 167–172.
- Taleb, M., Didierjean, C., Jelsch, C., Mangeot, J.-P., Capelle, B. & Aubry, A. (1999). Crystallization of biological macromolecules under an external electric field. *J. Cryst. Growth*, **200**, 575–582.
- Thaller, D., Eichele, G., Weaver, L. H., Wilson, E., Karlsson, R. & Jansonius, J. N. (1985). Seed enlargement and repeated seeding. *Methods Enzymol.* **114**, 132–135.
- Thibault, F., Langowski, L. & Leberman, R. (1992). Pre-nucleation crystallization studies on aminoacyl-tRNA synthetases by dynamic light scattering. *J. Mol. Biol.* **225**, 185–191.
- Thiessen, K. J. (1994). The use of two novel methods to grow protein crystals by microdialysis and vapor diffusion in an agarose gel. *Acta Cryst.* **D50**, 491–495.
- Thomas, B. R., Vekilov, P. G. & Rosenberger, F. (1998). Effects of microheterogeneity in hen egg-white lysozyme crystallization. *Acta Cryst.* **D54**, 226–236.
- Thomas, D. H., Rob, A. & Rice, D. W. (1989). A novel dialysis procedure for the crystallization of proteins. *Protein Eng.* **2**, 489–491.
- Timasheff, S. N. & Arakawa, T. (1988). Mechanism of protein precipitation and stabilization by co-solvents. *J. Cryst. Growth*, **90**, 39–46.
- Vaney, M. C., Maignan, S., Riès-Kautt, M. & Ducruix, A. (1996). High-resolution structure (1.33 Å) of a HEW lysozyme tetragonal crystal grown in the APCF apparatus. Data and structural comparison with a crystal grown under microgravity from SpaceHab-01 mission. *Acta Cryst.* **D52**, 505–517.
- Vekilov, P. G., Ataka, M. & Katsura, T. (1992). Laser Michelson interferometry investigation of protein crystal growth. *J. Cryst. Growth*, **130**, 317–320.
- Vekilov, P. G. & Rosenberger, F. (1996). Dependence of lysozyme growth kinetics on step sources and impurities. *J. Cryst. Growth*, **158**, 540–551.
- Vekilov, P. G. & Rosenberger, F. (1998). Protein crystal growth under forced solution flow: experimental setup and general response of lysozyme. *J. Cryst. Growth*, **186**, 251–261.
- Vidal, O., Robert, M.-C. & Boué, F. (1998a). Gel growth of lysozyme crystals studied by small angle neutron scattering: case of agarose gel, a nucleation promotor. *J. Cryst. Growth*, **192**, 257–270.
- Vidal, O., Robert, M.-C. & Boué, F. (1998b). Gel growth of lysozyme crystals studied by small angle neutron scattering: case of silica gel, a nucleation inhibitor. *J. Cryst. Growth*, **192**, 271–281.
- Vuillard, L., Rabilloud, T., Leberman, R., Berthet-Colominas, C. & Cusack, S. (1994). A new additive for protein crystallization. *FEBS Lett.* **353**, 294–296.
- Weber, B. H. & Goodkin, P. E. (1970). A modified microdiffusion procedure for the growth of single protein crystals by concentration-gradient equilibrium dialysis. *Arch. Biochem. Biophys.* **141**, 489–498.
- Yonath, A., Müssig, J. & Wittmann, H. G. (1982). Parameters for crystal growth of ribosomal subunits. *J. Cell. Biochem.* **19**, 145–155.
- Zeppenauer, M. (1971). Formation of large crystals. *Methods Enzymol.* **22**, 253–266.

## 4.2

- Allen, J. P., Feher, G., Yeates, T. O., Komiya, H. & Rees, D. C. (1987). Structure of the reaction center from *Rhodobacter sphaeroides* R-26: the protein subunits. *Proc. Natl Acad. Sci. USA*, **84**, 6162–6166.
- Bordier, C. (1981). Phase separation of integral membrane proteins in Triton X-114 solution. *J. Biol. Chem.* **256**, 1604–1607.
- Buchanan, S. K., Fritsch, G., Ermler, U. & Michel, H. (1993). New crystal form of the photosynthetic reaction centre from *Rhodobacter sphaeroides* of improved diffraction quality. *J. Mol. Biol.* **230**, 1311–1314.
- Buchanan, S. K., Smith, B. S., Venkatrami, L., Xia, D., Esser, L., Palnitkar, M., Chakraborty, R., van der Helm, D. & Deisenhofer, J. (1999). Crystal structure of the outer membrane active transporter *FepA* from *Escherichia coli*. *Nature Struct. Biol.* **6**, 56–63.
- Chang, C. H., El-Kabbani, D., Tiede, D., Norris, J. & Schiffer, M. (1991). Structure of the membrane-bound protein photosynthetic reaction center from *Rhodobacter sphaeroides*. *Biochemistry*, **30**, 5352–5360.
- Chang, G., Spencer, R. H., Lee, A. T., Barclay, M. T. & Rees, D. C. (1998). Structure of the *MscL* homolog from *Mycobacterium tuberculosis*: a gated mechanosensitive ion channel. *Science*, **282**, 2220–2226.
- Cowan, S. W., Garavito, R. M., Jansonius, J. N., Jenkins, J. A., Karlsson, R., König, N., Pai, E. F., Pauptit, R. A., Rizkallah, P. J., Rosenbusch, J. P., Rummel, G. & Schirmer, T. (1995). The structure of *OmpF* porin in a tetragonal crystal form. *Structure*, **3**, 1041–1050.
- Cowan, S. W., Schirmer, T., Rummel, G., Steiert, M., Gosh, R., Pauptit, R. A., Jansonius, J. N. & Rosenbusch, J. P. (1992). Crystal structures explain functional properties of two *E. coli* porins. *Nature (London)*, **358**, 727–733.
- Deisenhofer, J., Epp, O., Miki, K., Huber, R. & Michel, H. (1985). Structure of the protein subunits in the photosynthetic reaction

## 4. CRYSTALLIZATION

### 4.2 (cont.)

- center of Rhodospseudomonas viridis at 3 Å. *Nature (London)*, **318**, 618–642.
- Deisenhofer, J., Epp, O., Sinning, I. & Michel, H. (1995). *Crystallographic refinement at 2.3 Å resolution and refined model of the photosynthetic reaction centre from Rhodospseudomonas viridis*. *J. Mol. Biol.* **246**, 429–457.
- Doyle, D. A., Cabral, J. M., Pfuetzner, R. A., Kuo, A. L., Gulbis, J. M., Cohen, S. L., Chait, B. T. & MacKinnon, R. (1998). *The structure of the potassium channel: molecular basis of K<sup>+</sup> conduction and selectivity*. *Science*, **280**, 69–77.
- Ermler, U., Fritzsche, G., Buchanan, S. K. & Michel, H. (1994). *Structure of the photosynthetic reaction centre from Rhodospseudomonas sphaeroides at 2.65 Å resolution: cofactors and protein-cofactor interactions*. *Structure*, **2**, 925–936.
- Essen, L. O., Siegert, R., Lehmann, W. D. & Oesterhelt, D. (1998). *Lipid patches in membrane protein oligomers – crystal structure of the bacteriorhodopsin–lipid complex*. *Proc. Natl Acad. Sci. USA*, **95**, 11673–11678.
- Ferguson, A. D., Hofmann, E., Coulton, J. W., Diederichs, K. & Welte, W. (1998). *Siderophore mediated iron transport: crystal structure of FhuA with bound lipopolysaccharide*. *Science*, **282**, 2215–2220.
- Forst, D., Welte, W., Wacker, T. & Diederichs, K. (1998). *Structure of the sucrose-specific porin ScrY from Salmonella typhimurium and its complex with sucrose*. *Nature Struct. Biol.* **5**, 37–46.
- Fromme, P. & Witt, H. T. (1998). *Improved isolation and crystallization of photosystem I for structural analysis*. *Biochim. Biophys. Acta*, **1365**, 175–184.
- Gast, P., Hemelrijk, P. & Hoff, A. J. (1994). *Determination of the number of detergent molecules associated with the reaction center protein isolated from the photosynthetic bacterium Rhodospseudomonas viridis. Effects of the amphiphilic molecule, 1,2,3-heptanetriol*. *FEBS Lett.* **337**, 39–42.
- Gerstein, M. (1998). *Patterns of protein-fold usage in eight microbial genomes: a comprehensive structural census*. *Proteins*, **33**, 518–534.
- Grigorieff, N., Ceska, T. A., Downing, K. H., Baldwin, J. M. & Henderson, R. (1996). *Electron crystallographic refinement of the structure of bacteriorhodopsin*. *J. Mol. Biol.* **259**, 393–421.
- Henderson, R., Baldwin, J. M., Ceska, T. A., Zemlin, F., Beckmann, E. & Downing, K. H. (1990). *Model for the structure of bacteriorhodopsin based on high-resolution electron cryo-microscopy*. *J. Mol. Biol.* **213**, 899–929.
- Henderson, R. & Shotton, D. (1980). *Crystallization of purple membrane in three dimensions*. *J. Mol. Biol.* **139**, 99–109.
- Hirsch, A., Breed, J., Saxena, K., Richter, O. M. H., Ludwig, B., Diederichs, K. & Welte, W. (1997). *The structure of porin from Paracoccus denitrificans at 3.1 Å resolution*. *FEBS Lett.* **404**, 208–210.
- Hjelmeland, L. M. (1990). *Solubilization of native membrane proteins*. *Methods Enzymol.* **182**, 253–264.
- Hunte, C., Lange, C., Koepke, J., Rossmann, T. & Michel, H. (2000). *Structure at 2.3 Å resolution of the cytochrome bc<sub>1</sub> complex from the yeast Saccharomyces cerevisiae co-crystallized with an antibody Fv fragment*. *Structure*, **8**, 669–684.
- Iwata, S., Lee, J. W., Okada, K., Lee, J. K., Iwata, M., Rasmussen, B., Link, T. A., Ramaswamy, S. & Jap, B. K. (1998). *Complete structure of the 11-subunit bovine mitochondrial cytochrome bc<sub>1</sub> complex*. *Science*, **281**, 64–71.
- Iwata, S., Ostermeier, C., Ludwig, B. & Michel, H. (1995). *Structure at 2.8 Å resolution of cytochrome c oxidase from Paracoccus denitrificans*. *Nature (London)*, **376**, 660–669.
- Kim, H., Xia, D., Yu, C. A., Xia, J. Z., Kachurin, A. M., Li, Z., Yu, L. & Deisenhofer, J. (1998). *Inhibitor binding changes domain mobility in the iron-sulfur protein of the mitochondrial bc<sub>1</sub> complex from bovine heart*. *Proc. Natl Acad. Sci. USA*, **95**, 8026–8033.
- Kimura, Y., Vassilyev, D. G., Miyazawa, A., Kidera, A., Matsushima, M., Mitsuoaka, K., Murata, K., Hirai, T. & Fujiyoshi, Y. (1997). *Surface of bacteriorhodopsin revealed by high-resolution electron crystallography*. *Nature (London)*, **389**, 206–211.
- Kleymann, G., Ostermeier, C., Ludwig, B., Skerra, A. & Michel, H. (1995). *Engineered Fv fragments as a tool for the one-step purification of integral multisubunit membrane protein complexes*. *Biotechnology*, **13**, 155–160.
- Koepke, J., Hu, X., Muenke, C., Schulten, K. & Michel, H. (1996). *The crystal structure of the light-harvesting complex II (B800–850) from Rhodospirillum rubrum*. *Structure*, **4**, 581–597.
- Kreusch, A., Neubüser, A., Schiltz, E., Weckesser, J. & Schulz, G. E. (1994). *Structure of the membrane channel porin from Rhodospseudomonas blastica at 2.0 Å resolution*. *Protein Sci.* **3**, 58–63.
- Kühlbrandt, W., Wang, D. N. & Fujiyoshi, Y. (1994). *Atomic model of plant light-harvesting complex by electron crystallography*. *Nature (London)*, **367**, 614–621.
- Kurumbail, R. G., Stevens, A. M., Gierse, J. K., McDonald, J. J., Stegeman, R. A., Pak, J. Y., Gildehaus, D., Miyashiro, J. M., Penning, T. D., Seibert, K., Isakson, P. C. & Stallings, W. C. (1996). *Structural basis for selective inhibition of cyclooxygenase-2 by anti-inflammatory agents*. *Nature (London)*, **384**, 644–648.
- Lancaster, C. R. D. & Michel, H. (1997). *The coupling of light-induced electron transfer and proton uptake as derived from crystal structures of reaction centres from Rhodospseudomonas viridis modified at the binding site of the secondary quinone, Q<sub>B</sub>*. *Structure*, **5**, 1339–1359.
- Lancaster, C. R. D. & Michel, H. (1999). *Refined crystal structures of reaction centres from Rhodospseudomonas viridis in complexes with the herbicide atrazine and two chiral atrazine derivatives also lead to a new model of the bound carotenoid*. *J. Mol. Biol.* **286**, 883–898.
- Landau, E. M. & Rosenbusch, J. P. (1996). *Lipidic cubic phases: a novel concept for the crystallization of membrane proteins*. *Proc. Natl Acad. Sci. USA*, **93**, 14532–14535.
- Lindblom, G. & Rilfors, L. (1989). *Cubic phases and isotropic structures formed by membrane lipids – possible biological relevance*. *Biochim. Biophys. Acta*, **988**, 221–256.
- Locher, K. P., Rees, B., Koebnik, R., Mitschler, A., Moulinier, L., Rosenbusch, J. P. & Moras, D. (1998). *Transmembrane signaling across the ligand-gated FhuA receptor: crystal structures of free and ferrichrome-bound states reveal allosteric changes*. *Cell*, **98**, 771–778.
- Luecke, H., Richter, H. T. & Lamy, J. K. (1998). *Proton transfer pathways in bacteriorhodopsin at 2.3 Å resolution*. *Science*, **280**, 1934–1937.
- Luong, C., Miller, A., Barnett, J., Chow, J., Ramesha, C. & Browner, M. F. (1996). *Flexibility of the NSAID binding site in the structure of human cyclooxygenase-2*. *Nature Struct. Biol.* **3**, 927–933.
- McDermott, G., Prince, S. M., Freer, A. A., Hawthornthwaite-Lawless, A. M., Papiz, M. Z., Cogdell, R. J. & Isaacs, N. W. (1995). *Crystal-structure of an integral membrane light-harvesting complex from photosynthetic bacteria*. *Nature (London)*, **374**, 517–521.
- Meyer, J. E. W., Hofnung, M. & Schulz, G. E. (1997). *Structure of maltoporin from Salmonella typhimurium ligated with a nitrophenyl-maltotrioxide*. *J. Mol. Biol.* **266**, 761–775.
- Michel, H. (1982). *Three-dimensional crystals of a membrane protein complex. The photosynthetic reaction centre from Rhodospseudomonas viridis*. *J. Mol. Biol.* **158**, 567–572.
- Michel, H. (1983). *Crystallization of membrane proteins*. *Trends Biochem. Sci.* **8**, 56–59.
- Michel, H. (1991). *Editor. Crystallization of membrane proteins*. Boca Raton, Florida: CRC Press.
- Midura, R. J. & Yanagishita, M. (1995). *Chaotropic solvents increase the critical micellar concentrations of detergents*. *Anal. Biochem.* **228**, 318–322.
- Neugebauer, J. M. (1990). *Detergents: an overview*. *Methods Enzymol.* **182**, 239–253.
- Ostermeier, C., Harrenga, A., Ermler, U. & Michel, H. (1997). *Structure at 2.7 Å resolution of the Paracoccus denitrificans two-subunit cytochrome c oxidase complexed with an antibody Fv fragment*. *Proc. Natl Acad. Sci. USA*, **94**, 10547–10553.
- Ostermeier, C., Iwata, S., Ludwig, B. & Michel, H. (1995). *Fv fragment-mediated crystallization of the membrane protein bacterial cytochrome c oxidase*. *Nature Struct. Biol.* **2**, 842–846.

## 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-I. *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 bc<sub>1</sub> 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 bc<sub>1</sub>. *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  $\gamma$  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.