

- Harrison, R.K., and Stein, R.L. (1990b). Substrate specificities of the peptidyl prolyl *cis-trans* isomerase activities of cyclophilin and FK-506 binding protein: evidence for the existence of a family of distinct enzymes. *Biochemistry* 29, 3813–3816.
- Hunter, E. (1994). Macromolecular interactions in the assembly of HIV and other retroviruses. *Sem. Virol.* 5, 71–83.
- Hutchinson, E.G., and Thornton, J.M. (1996). PROMOTIF-A program to identify and analyse structural motifs in proteins. *Prot. Sci.* 5, 212–220.
- Janin, J., and Chothia, C. (1990). The structure of protein-protein recognition sites. *J. Biol. Chem.* 265, 16027–16030.
- Jones, T.A., Zou, J. Y., Cowan, S.W., and Kjeldgaard, M. (1991). Improved methods for building protein models in electron density maps and location of errors in these models. *Acta Cryst. A47*, 110–119.
- Jowett, J.B.M., Hockley, D.J., Nermut, M.V., and Jones, I.M. (1992). Distinct signals in human immunodeficiency virus type 1 Pr55 necessary for RNA binding and particle formation. *J. Gen. Virol.* 73, 3079–3086.
- Kakalis, L.T., and Armitage, I.M. (1994). Solution conformation of a cyclophilin-bound proline isomerase substrate. *Biochemistry* 33, 1495–1501.
- Kallen, J., Spitzfaden, C., Zurini, M.G.M., Wider, G., Widmer, H., Wüthrich, K., and Walkinshaw, M.D. (1991). Structure of human cyclophilin and its binding site for cyclosporin A determined by X-ray crystallography and NMR spectroscopy. *Nature* 353, 276–279.
- Kallen, J., and Walkinshaw, M.D. (1992). The X-ray structure of a tetrapeptide bound to the active site of human cyclophilin A. *FEBS Lett.* 300, 286–290.
- Ke, H., Mayrose, D., and Cao, W. (1993). Crystal structure of cyclophilin A complexed with substrate Ala-Pro suggests a solvent-assisted mechanism of *cis-trans* isomerization. *Proc. Natl. Acad. Sci. USA* 90, 3324–3328.
- Koletsy, A.J., Harding, M.W., and Handschumacher, R.E. (1986). Cyclophilin: distribution and variant properties in normal and neoplastic tissues. *J. Immunol.* 137, 1054–1059.
- Kraulis, P.J. (1991). "Molscript": a program to produce both detailed and schematic plots of protein structures. *J. Appl. Cryst.* 24, 946–950.
- Laskowski, R.A., MacArthur, M.W., Moss, D.S., and Thornton, J.M. (1993). PROCHECK: a program to check the stereochemical quality of protein structures. *J. Appl. Cryst.* 26, 283–291.
- Liu, J., Albers, M.W., Chen, C.-M., Schreiber, S.L., and Walsh, C.T. (1990). Cloning, expression, and purification of human cyclophilin in *Escherichia coli* and assessment of the catalytic role of cysteines by site-directed mutagenesis. *Proc. Natl. Acad. Sci. USA* 1990, 2304–2308.
- Luban, J., Bossolt, K.L., Franke, E.K., Kalpana, G.V., and Goff, S.P. (1993). Human immunodeficiency virus type 1 gag protein binds to cyclophilins A and B. *Cell* 73, 1067–1078.
- McClure, M.A. (1991). Evolution of retroposons by acquisition or deletion of retrovirus-like genes. *Mol. Biol. Evol.* 8, 835–856.
- Momany, C., Kovari, L.C., Prongay, A.J., Keller, W., Gitti, R.K., Lee, B.M., Gorbalenya, A.E., Tong, L., McClure, J., Ehrlich, L.S., et al. (1996). Crystal structure of dimeric HIV-1 capsid protein. *Nat. Struct. Biol.* 3, 763–770.
- Myers, G., Korber, B., Hahn, B.H., Jeang, K.-T., Mellors, J.W., McCutchan, F.E., Henderson, L.E., and Pavlakis, G.N. Human Retroviruses and AIDS, 1995. (Los Alamos, New Mexico: Los Alamos National Library).
- Navaza, J. (1994). AMoRe: an automated package for molecular replacement. *Acta Cryst. A50*, 157–163.
- Otwinowski, Z. (1993). Oscillation data reduction program. In *Data Collection and Processing*, L. Sawyer, N. Isaacs, and S. Bailey, eds. (Warrington, England: SERC Daresbury Laboratory), pp. 56–62.
- Pfütz, G., Kallen, J., Schirmer, T., Jansonius, J.N., Zurini, M.G.M., and Walkinshaw, M.D. (1993). X-ray structure of a decameric cyclophilin-cyclosporin crystal complex. *Nature* 361, 91–94.
- Read, R.J. (1986). Improved Fourier coefficients for maps using phases from partial structures with errors. *Acta Cryst. A42*, 140–149.
- Reicin, A.S., Paik, S., Berkowitz, R.D., Luban, J., Lowy, I., and Goff, S.P. (1995). Linker insertion mutations in the human immunodeficiency virus type 1 gag gene: effects on virion particle assembly, release, and infectivity. *J. Virol.* 69, 642–650.
- Schmid, F.X. (1993). Prolyl isomerase: enzymatic catalysis of slow protein-folding reactions. *Annu. Rev. Biophys. Biomolec. Struct.* 22, 123–142.
- Schreiber, S.L., and Crabtree, G.R. (1992). The mechanism of action of cyclosporin A and FK506. *Immunol. Today* 13, 136–142.
- Schutkowski, M., Wöllner, S., and Fischer, G. (1995). Inhibition of peptidyl-prolyl *cis/trans* isomerase activity by substrate analog structures: thioxo tetrapeptide-4-nitroanilides. *Biochemistry* 34, 13016–13026.
- Stammes, M.A., Rutherford, S.L., and Zuker, C.S. (1992). Cyclophilins: a new family of proteins involved in intracellular folding. *Trend. Cell Biol.* 2, 272–276.
- Steinkasserer, A., Harrison, R., Billich, A., Hammerschmid, F., Werner, G., Wolff, B., Peichl, P., Palfi, G., Schnitzel, W., Mlynar, E., et al. (1995). Mode of action of SDZ NIM 811, a nonimmunosuppressive cyclosporin A analog with activity against human immunodeficiency virus type 1 (HIV-1): interference with early and late events in HIV-1 replication. *J. Virol.* 69, 814–824.
- Sykes, K., Gething, M.-J., and Sambrook, J. (1993). Proline isomerases function during heat shock. *Proc. Natl. Acad. Sci. USA* 90, 5853–5857.
- Thali, M., Bukovsky, A., Kondo, E., Rosenwirth, B., Walsh, C.T., Sodroski, J., and Göttlinger, H.G. (1994). Functional association of cyclophilin A with HIV-1 virions. *Nature* 372, 363–365.
- Thériault, Y., Logan, T.M., Meadows, R., Yu, L., Olejniczak, E.T., Holzman, T.F., Simmer, R.L., and Fesik, S.W. (1993). Solution structure of the cyclosporin A/cyclophilin complex by NMR. *Nature* 361, 88–91.
- Traber, R., Kobel, H., Loosli, H.R., Senn, H., Rosenwirth, B., and Lawen, A. (1994). [Melle(4)] cyclosporin, a novel natural cyclosporin with anti-HIV activity: structural elucidation, biosynthesis, and biological properties. *Antiviral Chem. Chemother.* 5, 331–339.
- Von Pöbltzki, A., Wagner, R., Niedrig, M., Wanner, G., Wolf, H., and Modrow, S. (1993). Identification of a region in the Pr55gag polyprotein essential for HIV-1 particle formation. *Virology* 193, 981–985.
- Wallace, A.C., Laskowski, R.A., and Thornton, J.M. (1995). LIGPLOT: a program to generate schematic diagrams of protein-ligand interactions. *Prot. Eng.* 8, 127–134.
- Wang, C.-T., and Barklis, E. (1993). Assembly, processing, and infectivity of human immunodeficiency virus type 1 gag mutants. *J. Virol.* 67, 4264–4273.
- Weisman, R., Creanor, J., and Fantes, P. (1996). A multicopy suppressor of a cell cycle defect in *S. pombe* encodes a heat-shock inducible 40 kDa cyclophilin-like protein. *EMBO J.* 15, 447–456.
- Wolfenden, R., and Radzicka, A. (1991). Purification of human cyclophilin in *Escherichia coli* and assessment of the catalytic role of cysteines by site-directed mutagenesis. *Chemtracts: Biochem. Mol. Biol.* 2, 52–54.
- Zhao, Y., and Ke, H. (1996a). Crystal structure implies that cyclophilin predominantly catalyzes the *trans* to *cis* isomerization. *Biochemistry* 35, 7356–7361.
- Zhao, Y., and Ke, H. (1996b). Mechanistic implications of crystal structures of the cyclophilin-dipeptide complexes. *Biochemistry* 35, 7362–7368.