
6. Literaturverzeichnis

- Abola, E., Sussman, J., Prilusky, J., Manning, O. (1997)** Protein Databank archives of three-dimensional macromolecular Structures. *Methods Enzymol.*, **277**, 556-571
- Arnez, J. G., Moras, D. (1997)** Structural and functional considerations of the aminoacylation reaction. *Trends Biochem. Sci.* **22**, 211-216
- Auffinger, P., Westhof, E. (1998)** Hydration of RNA base pairs. *J. Biomol. Struct. Dynam.* **16**, 693-707
- Bae, W., Jones, P. G., Inouye, M. (1997)** CspA, the major cold shock protein of *Escherichia coli*, negatively regulates its own gene expression. *J. Bacteriol.* **179**, 7081-7088
- Berger, I., Kang, C., Sinha, N., Wolters, M., Rich, A. (1996)** A Highly effective 24 condition matrix for the crystallization of nucleic acid fragments. *Acta Cryst.* **D52**, 465-468
- Beuning, P. J., Yang, F., Schimmel, P., Musier-Forsyth, K. (1997)** Specific atomic groups and RNA helix geometry in acceptor stem recognition by a tRNA synthetase. *Proc. Natl. Acad. Sci. U S A* **94**, 10150-10154
- Biswas, R., Wahl, M. C., Ban, C., Sundaralingam, M. (1997)** Crystal structure of an alternating octamer r(GUAUGUA)dC with adjacent G•U wobble pairs. *J. Mol. Biol.* **267**, 1149-1156
- Blundell, T. L., Johnson, L. N. (1976)** Protein Crystallography. Academic Press, London
- Brünger, A. T. (1990)** Extension of molecular replacement: A new search strategy based on the patterson correlation refinement. *Acta Cryst.* **A46**, 46-57
- Brünger, A. T. (1992A)** X-PLOR - A system for xray crystallography and NMR. New Haven, CT
- Brünger, A. T. (1992B)** The free R value: a novel statistical quantity for assessing the accuracy of crystal structures. *Nature* **355**, 472-475
- Cantor, C. R., Tinoco, I. (1965)** . *J. Mol. Biol.* **13**, 65-69
- Cate, J. H., Gooding, A. R., Podell, E., Zhou, K., Golden, B. L., Kundrot, C. E., Cech, T. R., Doudna, J. A. (1996)** Crystal structure of a group I ribozyme domain: principles of RNA packing. *Science* **273**, 1678-1685
- CCP4 (1994)** The CCP4 suite: Programs for protein crystallography. *Acta Cryst.* **D50**, 760-763
- Celander, D. W., Cech, T. R. (1991)** Visualizing the higher order folding of a catalytic RNA molecule. *Science* **251**, 401-407

- Chandrasekaran, R., Arnott, S.** (1989) The structures of DNA and RNA helices in oriented fibres. Springer, Berlin
- Chothia, C., Murzin, A. G.** (1993) New folds for all-beta proteins. *Structure* **1**, 217-222
- Chowrira, B. M., Berzal Herranz, A., Burke, J. M.** (1993) Ionic requirements for RNA binding, cleavage, and ligation by the hairpin ribozyme. *Biochemistry* **32**, 1088-1095
- Clowney, L., Jain, S. C., Srinivasan, A. R., Westbrook, J., Olson, W. K., Berman, H. M.** (1996) Geometric parameters in nucleic acids: Nitrogenous bases. *J. Am. Chem. Soc.* **118**, 509-518
- Condra, J. H., Schleif, W. A., Blahy, O. M., Gabryelski, L. J., Graham, D. J., Quintero, J. C., Rhodes, A., Robbins, H. L., Roth, E., Shivaprakash, M.** (1995) In vivo emergence of HIV-1 variants resistant to multiple protease inhibitors [see comments]. *Nature* **374**, 569-571
- Conner, B. N., Takano, T., Tanaka, S., Itakura, K., Dickerson, R. E.** (1982) The molecular structure of d(ICpCpGpG), a fragment of right-handed double helical A-DNA. *Nature* **295**, 294-299
- Correll, C. C., Freeborn, B., Moore, P. B., Steitz, T. A.** (1997) Metals, motifs, and recognition in the crystal structure of a 5S rRNA domain. *Cell* **91**, 705-712
- Crowther, R. A., Blow, D. M.** (1967) A method of positioning a known molecule in an unknown crystal structure. *Acta Cryst.* **27**, 544-548
- Cruickshank, D. W. J.** (1996) Protein precision re-examined: Luzatti plots do not estimate final errors. *Proceedings of the CCP4 Study Weekend 1996*, 11-23
- Cruse, W. B., Saludjian, P., Biala, E., Strazewski, P., Prange, T., Kennard, O.** (1994) Structure of a mispaired RNA double helix at 1.6-Å resolution and implications for the prediction of RNA secondary structure. *Proc. Natl. Acad. Sci. U S A* **91**, 4160-4164
- Cudney, R., Patel, S., Weisgraber, K., Newhouse, Y., McPherson, A.** (1994) Screening and Optimization Strategies for Macromolecular Crystal-Growth. *Acta Cryst.* **D50**, 414-423
- Dauter, Z.** (1997) Data Collection Strategies. *Methods Enzymol.*, **276**, 326-344
- Dauter, Z., Lamzin, V. S., Wilson, K. S.** (1995) Proteins at atomic resolution. *Curr. Opin. Struct. Biol.* **5**, 784-90
- Di Cera, E., Guinto, E. R., Vindigni, A., Dang, Q. D., Ayala, Y. M., Wuyi, M., Tulinski, A.** (1995) The Na⁺ binding site of Thrombin. *J. Biol. Chem.* **270**, 22089-22092
- Dickerson, R. E., Kendrew, J. C., Strandberg, B. E.** (1961) The crystal structure of myoglobin: phase determination to a resolution of 2 Å by the method of isomorphous replacement. *Acta Cryst.* **14**, 1188-1195

- Drenth, J.** (1994) Principles of Protein X-ray Crystallography. Springer, New York
- Engh, A., Huber, R.** (1991) Accurate bond and angle parameters for X-ray protein structure refinement. *Acta Cryst.* **A47**, 392-400
- Esnouf, R., Ren, J., Ross, C., Jones, Y., Stammers, D., Stuart, D. I.** (1995) Mechanism of inhibition of HIV-1 reverse transcriptase by non- nucleoside inhibitors. *Nature. Struct. Biol.* **2**, 303-308
- Esnouf, R. M.** (1997) *J. Mol. Graph.* **15**, 132-134
- Fedoroff, O. Y., Ge, Y., Reid, B. R.** (1997) Solution structure of r(gaggacug):d(CAGTCCTC) hybrid: implications for the initiation of HIV-1 (+)-strand synthesis. *J. Mol. Biol* **269**, 225-239
- Feske, A.** (1998). Persönliche Kommunikation
- Francklyn, C., Schimmel, P.** (1989) Aminoacylation of RNA minihelices with alanine. *Nature* **337**, 478-481
- Gabriel, K., Schneider, J., McClain, W. H.** (1996) Functional evidence for indirect recognition of G•U in tRNA(Ala) by alanyl-tRNA synthetase. *Science* **271**, 195-197
- Garman, E. F., Schneider, T. R.** (1997) Macromolecular cryocrystallography. *J. Appl. Cryst.* **30**, 211-237
- Gelbin, A., Schneider, B., Clowney, L., Hsieh, S. H., Olson, W. K., Berman, H. M.** (1996) Geometric parameters in nucleic acids: Sugar and phosphate constituents. *J. Am. Chem. Soc.* **118**, 519-529
- Gomis Ruth, F. X., Gomez, M., Ventura, S., Vendrell, J., Aviles, F. X.** (1995) Crystallization and preliminary X-ray analysis of the ternary complex of procarboxypeptidase A from bovine pancreas. *FEBS Lett.* **367**, 211-213
- Götte, M., Fackler, S., Hermann, T., Perola, E., Cellai, L., Gross, H. J., Le Grice, S. F., Heumann, H.** (1995) HIV-1 reverse transcriptase-associated RNase H cleaves RNA/RNA in arrested complexes: implications for the mechanism by which RNase H discriminates between RNA/RNA and RNA/DNA. *EMBO J.* **14**, 833-841
- Graumann, P., Marahiel, M. A.** (1994) The major cold shock protein of *Bacillus subtilis* CspB binds with high affinity to the ATTGG- and CCAAT sequences in single stranded oligonucleotides. *FEBS Lett.* **338**, 157-160
- Graumann, P., Marahiel, M. A.** (1997) Effects of heterologous expression of CspB, the major cold shock protein of *Bacillus subtilis*, on protein synthesis in *Escherichia coli*. *Mol. Gen. Genet.* **253**, 745-752

- Graumann, P., Wendrich, T. M., Weber, M. H., Schroder, K., Marahiel, M. A.** (1997) A family of cold shock proteins in *Bacillus subtilis* is essential for cellular growth and for efficient protein synthesis at optimal and low temperatures. *Mol. Microbiol.* **25**, 741-756
- Guex, N., Peitsch, M. C.** (1997) SWISS-MODEL and the Swiss-PdbViewer: An environment for comparative protein modeling. *Electrophoresis* **18**, 2714-2723
- Heinemann, U., Lauble, H., Frank, R., Blöcker, H.** (1987) Crystal structure analysis of an A-DNA fragment at 1.8 Å resolution: d(GCCCGGGC). *Nucleic Acids Res.* **15**, 9531-9550
- Heinemann, U.** (1991) A note on crystal packing and global helix structure in short A-DNA duplexes. *J. Biomol. Struct. Dyn.* **8**, 801-811
- Heinemann, U.** (1995). persönliche Kommunikation
- Helliwell, J. R.** (1998) Synchrotron radiation facilities. *Nature Struct. Biol.*, 614-617
- Henderson, B. S., Beuning, P. J., Shi, J. P., Bald, R., Furste, J. P., Erdmann, V. A., Musier Forsyth, K., Schimmel, P.** (1998) Subtle functional interactions in the RNA minor groove at a nonessential base pair. *J. Am. Chem. Soc.* **120**, 9110-9111
- Hendrickson, W. A.** (1985) Stereochemically Restrained Refinement of Macromolecular Structures. *Methods Enzymol.*, **115**, 252-270
- Herbst-Irmer, R., Sheldrick, G. M.** (1998) Refinement of twinned structures with SHELXL97. *Acta Cryst.* **B40**, 443-449
- Hol, W.** (1978) The α -helix dipole and the properties of proteins. *Nature* **273**, 443-446
- Holbrook, S. R., Cheong, C., Tinoco, I., Jr., Kim, S. H.** (1991) Crystal structure of an RNA double helix incorporating a track of non-Watson-Crick base pairs. *Nature* **353**, 579-581
- Hooft, R. W., Vriend, G., Sander, C., Abola, E. E.** (1996) Errors in protein structures. *Nature* **381**, 272
- Horvath, M. P., Schweiker, V. L., Bevilacqua, J. M., Ruggles, J. A., Schultz, S. C.** (1998) Crystal structure of the *Oxytricha nova* telomere end binding protein complexed with single strand DNA. *Cell* **95**, 963-974
- Hou, Y. M., Francklyn, C., Schimmel, P.** (1989) Molecular dissection of a transfer RNA and the basis for its identity. *Trends Biochem. Sci.* **14**, 233-237
- Hou, Y. M., Schimmel, P.** (1988) A simple structural feature is a major determinant of the identity of a transfer RNA. *Nature* **333**, 140-145

-
- Hsiou, Y., Ding, J., Das, K., Clark, A. D., Jr., Hughes, S. H., Arnold, E.** (1996) Structure of unliganded HIV-1 reverse transcriptase at 2.7 Å resolution: implications of conformational changes for polymerization and inhibition mechanisms. *Structure* **4**, 853-860
- Hunter, W. N., D'Estaintot, B. L., Kennard, O.** (1989) Structural variation in d(CTCTAGAG). Implications for protein-DNA interactions. *Biochemistry* **28**, 2444-2451
- Hutchinson, E. G., Thornton, J. M.** (1996) PROMOTIF a program to identify and analyze structural motifs in proteins. *Protein Sci.* **5**, 212-220
- Hynes, T. R., Fox, R. O.** (1991) The crystal structure of staphylococcal nuclease refined at 1.7 Å resolution. *Proteins: Struct. Funct. Genet.* **10**, 92-105
- Jack, A., Ladner, J. E., Rhodes, D., Brown, R. S., Klug, A.** (1977) A crystallographic study of metal-binding to yeast phenylalanine transfer RNA. *J. Mol. Biol.* **111**, 315-328
- Jack, A., Levitt, M.** (1978) Refinement of large structures by simultaneous minimization of energy and rfactor. *Acta Cryst.* **A34**, 931-935
- Jacobo-Molina, A., Ding, J., Nanni, R. G., Clark, A. D., Jr., Lu, X., Tantillo, C., Williams, R. L., Kamer, G., Ferris, A. L., Clark, P., et al.** (1993) Crystal structure of human immunodeficiency virus type 1 reverse transcriptase complexed with double-stranded DNA at 3.0 Å resolution shows bent DNA. *Proc. Natl. Acad. Sci. U S A* **90**, 6320-6324
- Jameson, G. B.** (1982) . *Acta Cryst.* **A38** On Structure Refinement Using Data from a Twinned Crystal, 817-820
- Jancarik, J., Kim, S. H.** (1991) Sparse matrix sampling: A screening method for crystallization of proteins. *J. Appl. Cryst.* **24**, 409-411
- Jiang, W., Hou, Y., Inouye, M.** (1997) CspA, the major cold-shock protein of *Escherichia coli*, is an RNA chaperone. *J. Biol. Chem.* **272**, 196-202
- Jones, P. G., VanBogelen, R. A., Neidhardt, F. C.** (1987) Induction of proteins in response to low temperature in *Escherichia coli*. *J. Bacteriol.* **169**, 2092-2095
- Jones, T. A., Zou, J.-Y., Cowan, S. W., Kjeldgaard, M.** (1991) Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Cryst.* **A47**, 110-119
- Kauzmann, W.** (1959) Some factors in the interpretation of protein denaturation. *Adv. Prot. Chem.* **14**, 34-41
- Kim, S. H., Suddath, F. L., Quigley, G. J., McPherson, A., Sussman, J. L., Wang, A. H.-J., Seeman, N. C., Rich, A.** (1974) Three-dimensional tertiary structure of yeast phenylalanine transfer RNA. *Science* **185**, 435-440

- Kleywegt, G. J.** (1996) Use of non-crystallographic symmetry in protein structure refinement. *Acta Cryst.* **D52**, 842-857
- Kleywegt, G. J., Jones, T. A.** (1995) Where freedom is given, liberties are taken. *Structure* **3**, 535-540
- Kneale, G., Brown, T., Kennard, O., Rabinovich, D.** (1985) G•T base-pairs in a DNA helix: the crystal structure of d(GGGGTCCC). *J. Mol. Biol.* **186**, 805-814
- Laskowski, R. A., MacArthur, M. W., Moss, D. S., Thornton, J. M.** (1993) PROCHECK: a program to check the stereochemical quality of protein structures. *J. Appl. Cryst.* **26**, 283-291
- Lavery, R., Sklenar, H.** (1989) Defining the structure of irregular nucleic acids: conventions and principles. *J. Biomol. Struct. Dyn.* **6**, 655-667
- Liang, J., Ealick, S., Nielsen, C., Schreiber, S. L., Clardy, J.** (1996) Crystallization and preliminary X-ray analysis of twinned crystals of a chimeric FK506 binding protein 12 and 13 complexed with FK506. *Acta Cryst.* **D51**, 207-210
- Limmer, S.** (1997). persönliche Kommunikation
- Limmer, S., Hofmann, H. P., Ott, G., Sprinzl, M.** (1993) The 3'-terminal end (NCCA) of tRNA determines the structure and stability of the aminoacyl acceptor stem. *Proc. Natl. Acad. Sci. U S A* **90**, 6199-6202
- Limmer, S., Reif, B., Ott, G., Arnold, L., Sprinzl, M.** (1996) NMR evidence for helix geometry modifications by a G•U wobble base pair in the acceptor arm of *E. coli* tRNA(Ala). *FEBS Lett.* **385**, 15-20
- Lu, G. G., Lindqvist, Y., Schneider, G.** (1995) A method for processing diffraction data from twinned protein crystals and its application in the structure determination of an FAD NADH-binding fragment of nitrate reductase. *Acta Cryst.* **D51**, 13-20
- MacArthur, M. W., Thornton, J. M.** (1996) Deviations from planarity of the peptide bond in peptides and proteins. *J. Mol. Biol.* **264**, 1180-1195
- Makhatadze, G. I., Marahiel, M. A.** (1994) Effect of pH and phosphate ions on self-association properties of the major cold-shock protein from *Bacillus subtilis*. *Protein-Sci* **3**, 2144-7
- Matthews, B. W.** (1968) Solvent content of protein crystals. *J. Mol. Biol.* **33**, 491-497
- McClain, W. H., Chen, Y. M., Foss, K., Schneider, J.** (1988) Association of transfer RNA acceptor identity with a helical irregularity. *Science* **242**, 1681-1684
- McRee, D. E.** (1993) Practical Protein Crystallography. Academic Press, San Diego

-
- Merrit, E. A., Bacon, D. J. (1997)** Raster3D: Photorealistic Molecular Graphics. *Methods Enzymol.*, **277**, 505-525
- Morris, A. L., MacArthur, M. W., Hutchinson, E. G., Thornton, J. M. (1992)** Stereochemical quality of protein structure coordinates. *Proteins* **12**, 345-364
- Mueller, U., Maier, G., Mochi Onori, A., Cellai, L., Heumann, H., Heinemann, U. (1998)** Crystal structure of an eight-base pair duplex containing the 3'-DNA- RNA-5' junction formed during initiation of minus-strand synthesis of HIV replication. *Biochemistry* **37**, 12005-12011
- Mueller, U., Schübel, H., Sprinzl, M., Heinemann, U. (1999)** Crystal structure of acceptor stem of tRNA^{Ala} from *Escherichia coli* shows unique G•U wobble base pair at 1.16 Å resolution. *RNA, im Druck*
- Murzin, A. G. (1993)** OB(oligonucleotide/oligosaccharide binding)-fold: common structural and functional solution for non-homologous sequences. *EMBO J.* **12**, 861-867
- Musier Forsyth, K., Usman, N., Scaringe, S., Doudna, J., Green, R., Schimmel, P. (1991)** Specificity for aminoacylation of an RNA helix: an unpaired, exocyclic amino group in the minor groove. *Science* **253**, 784-786
- Neidhart, D. J., Distefano, M. D., Tanizawa, K., Soda, K., Walsh, C. T., Petsko, G. A. (1987)** X-ray crystallographic studies of the alanine-specific racemase from *Bacillus stearothermophilus*. Overproduction, crystallization, and preliminary characterization. *J. Biol. Chem.* **262**, 15323-15326
- Newkirk, K., Feng, W., Jiang, W., Tejero, R., Emerson, S. D., Inouye, M., Montelione, G. T. (1994)** Solution NMR structure of the major cold shock protein (CspA) from *Escherichia coli*: identification of a binding epitope for DNA. *Proc. Natl. Acad. Sci. U S A* **91**, 5114-5118
- Ott, G., Dörfler, S., Sprinzl, M., Müller, U., Heinemann, U. (1996)** Crystals of the Chemically Synthesized Acceptor Stem of tRNA(Ala) From *Escherichia Coli* Diffracting to High Resolution. *Acta Cryst.* **D52**, 871-873
- Otwinowski, Z. (1999)** . *Proceedings of the CCP4 Study Weekend 1999*, im Druck
- Otwinowski, Z., Minor, W. (1997)** Processing of X-Ray Diffraction Data Collected in Oscillation Mode. *Methods Enzymol.*, **276**, 307-326
- Pal, G. P., Jakob, R., Hahn, U., Bowien, B., Saenger, W. (1985)** Single and twinned crystals of ribulose-1,5-bisphosphate carboxylase-oxygenase from *Alcaligenes eutrophus*. *J. Biol. Chem.* **260**, 10768-10770
- Park, S. J., Schimmel, P. (1988)** Evidence for interaction of an aminoacyl transfer RNA synthetase with a region important for the identity of its cognate transfer RNA. *J. Biol. Chem.* **263**, 16527-16530

- Parkinson, G., Vojtechovsky, J., Clowney, L., Brunger, A. T., Berman, H. M.** (1996) New parameters for the refinement of nucleic acid-containing structures. *Acta Cryst.* **D51**, 57-64
- Perl, D.** (1997) Stabilität und Faltungsmechanismus des Kälteschockproteins aus dem thermophilen Bakterium *Bacillus caldolyticus*. Diplomarbeit, Universität Bayreuth
- Perl, D.** (1999). persönliche Kommunikation
- Perl, D., Welker, C., Schindler, T., Schröder, K., Marahiel, M. A., Jaenicke, R., Schmid, F. X.** (1998) Conservation of rapid two-state folding in mesophilic, thermophilic and hyperthermophilic cold shock proteins. *Nature Struct. Biol.* **5**, 229-235
- Phillips, K., Dauter, Z., Murchie, A. I., Lilley, D. M., Luisi, B.** (1997) The crystal structure of a parallel-stranded guanine tetraplex at 0.95 Å resolution. *J. Mol. Biol.* **273**, 171-182
- Portmann, S., Usman, N., Egli, M.** (1995) The Crystal Structure of R(Ccccgggg) in Two Distinct Lattices. *Biochemistry* **34**, 7569-7575
- Pratt, C. S., Coyle, B. A., Ibers, J. A.** (1971) . *J. Chem. Soc.*, 2146-2151
- Press, W. H., Flannery, B. P., Teukolsky, S. A., Vetterling, T. V.** (1989) The Art of Scientific Computing. Cambridge University Press, Cambridge
- Proudfoot, N. J., Brownlee, G. G.** (1974) Sequence at the 3'-end of globin mRNA shows homology with immunoglobulin light chain mRNA. *Nature* **252**, 359-362
- Rabinovich, D., Haran, T., Eisenstein, M., Shakked, Z.** (1988) Structures of the mismatched duplex d(GGGTGCCC) and one of its Watson- Crick analogues d(GGGCGCCC). *J. Mol. Biol.* **200**, 151-161
- Rabinovich, D., Shakked, Z.** (1984) A New Approach to Structure Determination of Large Molecules by Multi-dimensional Search Methods. *Acta Cryst.* **A40**, 195-200
- Rahn, R. O.** (1992) Photochemistry of halogen pyrimidines: iodine release studies. *Photochem. Photobiol.* **56**, 9-15
- Ramos, A., Varani, G.** (1997) Structure of the acceptor stem of *Escherichia coli* tRNA Ala: role of the G3•U70 base pair in synthetase recognition. *Nucleic Acids Res.* **25**, 2083-2090
- Read, R. J.** (1986) Improved Fourier coefficients for maps using partial structures with errors. *Acta Cryst.* **A42**, 140-149
- Rees, D. C., Lipscomb, W. N.** (1980) Structure of potato inhibitor complex of carboxypeptidase A at 5.5 Å resolution. *Proc. Natl. Acad. Sci. U S A* **77**, 277-280

-
- Ribas de Pouplana, L., Buechter, D., Sardesai, N. Y., Schimmel, P.** (1998) Functional analysis of peptide motif for RNA microhelix binding suggests new family of RNA-binding domains. *EMBO J.* **17**, 5449-5457
- Riboldi-Tunicliffe, A., Hilgenfeld, R.** (1999) . *J. Appl. Cryst.*, eingereicht
- Ridky, T., Leis, J.** (1995) Development of drug resistance to HIV-1 protease inhibitors. *J. Biol. Chem.* **270**, 29621-29623
- Rogers, K. C., Söll, D.** (1995) Divergence of glutamate and glutamine aminoacylation pathways: providing the evolutionary rationale for mischarging. *J. Mol. Evol.* **40**, 476-481
- Rollett, J. S.** (1970) Least-squares procedures in crystal structure analysis. *Cryst. Comp.*, 167-181
- Rossmann, M. G., Blow, D. M.** (1962) The Detection of Sub-Units within the Crystallographic Asymmetric Unit. *Acta Cryst.* **15**, 24-31
- Ruff, M., Krishnaswamy, S., Boeglin, M., Poterszman, A., Mitschler, A., Podjarny, A., Rees, B., Thierry, J. C., Moras, D.** (1991) Class II aminoacyl transfer RNA synthetases: crystal structure of yeast aspartyl-tRNA synthetase complexed with tRNA(Asp). *Science* **252**, 1682-9
- Saenger, W.** (1984) Series, Principles of Nucleic Acid Structure, Springer, New York.
- Salazar, M., Fedoroff, O. Y., Reid, B. R.** (1996) Structure of chimeric duplex junctions: solution conformation of the retroviral Okazaki-like fragment r(ccca)d(AATGA).d(TCATTGGG) from *Moloney murine leukemia virus*. *Biochemistry* **35**, 8126-8135
- Scaringe, S. A., Francklyn, C., Usman, N.** (1990) Chemical synthesis of biologically active oligoribonucleotides using beta-cyanoethyl protected ribonucleoside phosphoramidites. *Nucleic Acids Res.* **18**, 5433-5441
- Schäfer, M., Sheldrick, G. M., Schneider, T. R., Vertesy, L.** (1998) Structure of balhimycin and its complex with solvent molecules. *Acta Cryst.* **D52**, 175-183
- Schimmel, P.** (1990) Alanine transfer RNA synthetase: structure-function relationships and molecular recognition of transfer RNA. *Adv. Enzym. Relat. Areas. Mol. Biol.* **63**, 233-270
- Schimmel, P., Giege, R., Moras, D., Yokoyama, S.** (1993) An operational RNA code for amino acids and possible relationship to genetic code. *Proc. Natl. Acad. Sci. U S A* **90**, 8763-8768
- Schindelin, H., Jiang, W., Inouye, M., Heinemann, U.** (1994) Crystal structure of CspA, the major cold shock protein of *Escherichia coli*. *Proc. Natl. Acad. Sci. U S A* **91**, 5119-51123
- Schindelin, H., Marahiel, M. A., Heinemann, U.** (1993) Universal nucleic acid-binding domain revealed by crystal structure of the *B. subtilis* major cold-shock protein. *Nature* **364**, 164-168

Schindler, T. (1994) Diplomarbeit, Universität Bayreuth

Schindler, T., Perl, D., Graumann, P., Sieber, V., Marahiel, M. A., Schmid, F. X. (1998) Surface-exposed phenylalanines in the RNP1/RNP2 motif stabilize the cold-shock protein CspB from *Bacillus subtilis*. *Proteins* **30**, 401-406

Schneider, T. (1996) What we can learn from anisotropic temperature factors. *Proceedings of the CCP4 Study Weekend 1996*, 133-145

Schnuchel, A., Wiltscheck, R., Czisch, M., Herrler, M., Willmsky, G., Graumann, P., Marahiel, M. A., Holak, T. A. (1993) Structure in solution of the major cold-shock protein from *Bacillus subtilis*. *Nature* **364**, 169-171

Schock, H. B., Garsky, V. M., Kuo, L. C. (1996) Mutational anatomy of an HIV-1 protease variant conferring cross-resistance to protease inhibitors in clinical trials. Compensatory modulations of binding and activity. *J. Biol. Chem.* **271**, 31957-31963

Schröder, K., Graumann, P., Schnuchel, A., Holak, T. A., Marahiel, M. A. (1995) Mutational analysis of the putative nucleic acid-binding surface of the cold-shock domain, CspB, revealed an essential role of aromatic and basic residues in binding of single-stranded DNA containing the Y-box motif. *Mol. Microbiol.* **16**, 699-708

Schübel, H. (1997) persönliche Kommunikation.

Schulz, G. E., Schirmer, R. H. (1978) Series, Principles of Protein Structure, Springer Verlag New York,

Shah, S. A., Brünger, A. T. (1999) The 1.8 angstrom crystal structure of a statically disordered 17 base-pair RNA duplex: Principles of RNA crystal packing and its effect on nucleic acid structure. *J. Mol. Biol.* **285**, 1577-1588

Shakked, Z. (1991) The influence of the environment on DNA structures determined by X-ray crystallography. *Curr. Opin. Struct. Biol.* **1**, 446-451

Sheldrick, G. M., Schneider, T. R. (1997) SHELXL: High-Resolution Refinement. *Methods Enzymol*, **277**, 319-343

Skalka, A.-M., Goff, S. P. (1993) Reverse Transkriptase. *Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.*

Stanley, E. (1972) . *J. Appl. Cryst.* **5**, 191

Stout, G. H., Jensen, L. H. (1989) X-Ray Structure Determination: A Practical Guide. John Wiley & Sons,

Streicher, B., Westhof, E., Schroeder, R. (1996) The Environment of Two Metal ions surrounding the splice site of a group I intron. *EMBO J.* **15**, 2556-2564

-
- Sussman, J. L., Holbrook, S. R., Warrant, R. W., Church, G. M., Kim, S. H.** (1978) Crystal structure of yeast phenylalanine transfer RNA. I. Crystallographic refinement. *J. Mol. Biol.* **123**, 607-630
- Sweet, R. M., Fuchs, H. E., Fisher, R. G., Glazer, A. N.** (1977) Preliminary crystallographic investigations of two phycobiliproteins. *J. Biol. Chem.* **252**, 8258-8260
- Szyperski, T., Maier, G., Mochi Onori, A., Cellai, L., Heumann, H., Wüthrich, K.** (1999) NMR structure of the chimeric hybrid duplex. *J. Biomol. NMR*, im Druck
- Tronrud, D. E., Ten Eyck, L. F., Matthews, B. W.** (1987) An Efficient General-Purpose Least-Squares Refinement Program for Macromolecular Structures. *Acta Cryst.* **A43**, 489-501
- Valegard, K., Van Scheltinga, A. C. T., Lloyd, M. D., Hara, T., Ramaswamy, S., Perrakis, A., Thompson, A., Lee, H. J., Baldwin, J. E., Schofield, C. J., Hajdu, J., Andersson, I.** (1998) Structure of a cephalosporin synthase. *Nature* **394**, 805-809
- Wahl, M., Sundaralingam, M.** (1997) Crystal structures of A-DNA duplexes. *Biopolymers* **44**, 45-63
- Walsh, M. A., Schneider, T. R., Sieker, L. C., Dauter, Z., Lamzin, V. S., Wilson, K. S.** (1998) Refinement of triclinic hen egg-white lysozyme at atomic resolution. *Acta. Cryst.* **D54**, 522-546
- Wang, B. C.** (1985) Resolution of Phase Ambiguity in Macromolecular Crystallography. *Methods Enzymol.* **115**, 90-112
- Watson, J. D., Crick, F. H. C.** (1953) A structure of deoxyribose nucleic acid. *Nature* **171**, 737-738
- Westhof, E.** (1987) Hydration of oligonucleotides in crystals. *Int. J. Biol. Macromol.* **9**, 186-192
- Wolffe, A. P.** (1995) The cold-shock response in bacteria. *Sci. Prog.* **78**, 301-310
- Yeates, T. O.** (1997) Detecting and Overcoming Crystal Twinning. *Methods Enzymol.* **276**, 344-358
- Zacharias, M.** (1998). persönliche Kommunikation

6.1. Publikationsliste

Mueller, U., Maier, G., Mochi Onori, A., Cellai, L., Heumann, H., Heinemann, U. (1998) Crystal structure of an eight-base pair duplex containing the 3'-DNA-RNA-5' junction formed during initiation of minus-strand synthesis of HIV replication. *Biochemistry* **37**, 12005-12011

Mueller, U., Schübel, H., Sprinzl, M., Heinemann, U. (1999) Crystal structure of acceptor stem of tRNA^{Ala} from *Escherichia coli* shows unique G•U wobble base pair at 1.16 Å resolution. *RNA* **5**, 670-677

Mueller, U., Muller, Y. A., Herbst-Irmer, R., Sprinzl, M., Heinemann, U. (1999) Disorder and Twin Refinement of RNA heptamer double helices. *Acta Cryst., im Druck*

Ott, G., Dörfler, S., Sprinzl, M., Müller, U., Heinemann, U. (1996) Crystals of the Chemically Synthesized Acceptor Stem of tRNA(Ala) From *Escherichia Coli* Diffracting to High Resolution. *Acta Cryst.* **D52**, 871-873