

6 Literaturverzeichnis

- Alonso, J.C., Ayora, S., Canosa, I., Weise, F. und Rojo, F. (1996) Site-specific recombination in gram-positive theta-replicating plasmids. *FEMS Microbiol. Lett.*, **142**, 1-10.
- Anderson, W.F., Ohlendorf, D.H., Takeda, Y. und Matthews, B.W. (1981) Structure of the cro repressor from bacteriophage λ and its interaction with DNA. *Nature*, **290**, 754-758.
- Arndt, U.W. und Wonacott, A.J. (1977) The rotation method in crystallography. *Amsterdam:North Holland*.
- Barilla, D. und Hayes, F. (2003) Architecture of the ParF*ParG protein complex involved in prokaryotic DNA segregation. *Mol. Microbiol.*, **49**, 487-499.
- Benoff, B., Yang, H., Lawson, C.L., Parkinson, G., Liu, J., Blatter, E., Ebright, Y.W., Berman, H.M. und Ebright, R.H. (2002) Structural basis of transcription activation: the CAP- α CTD-DNA complex. *Science*, **297**, 1562-1566.
- Beutel, B.A. und Gold, L. (1992) In vitro evolution of intrinsically bent DNA. *J. Mol. Biol.*, **228**, 803-812.
- Bhattacharyya, D. und Bansal, M. (1990) Local variability and base sequence effects in DNA crystal structures. *J. Biomol. Struct. Dyn.*, **8**, 539-572.
- Bignell, C. und Thomas, C.M. (2001) The bacterial ParA-ParB partitioning proteins. *J. Biotechnol.*, **91**, 1-34.
- Bouet, J.Y. und Funnell, B.E. (1999) P1 ParA interacts with the P1 partition complex at *parS* and an ATP-ADP switch controls ParA activities. *EMBO J.*, **18**, 1415-1424.
- Bowie, J.U. und Sauer, R.T. (1990) TraY proteins of F and related episomes are members of the Arc and Mnt repressor family. *J. Mol. Biol.*, **211**, 5-6.
- Bradford, M.M. (1976) A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein-dye binding. *Anal. Biochem.*, **72**, 248-254.
- Brantl, S. (1994) The *copR* gene product of plasmid pIP501 acts as a transcriptional repressor at the essential *repR* promoter. *Mol. Microbiol.*, **14**, 473-483.
- Brantl, S., Birch-Hirschfeld, E. und Behnke, D. (1993) RepR protein expression on plasmid pIP501 is controlled by an antisense RNA-mediated transcription attenuation mechanism. *J. Bacteriol.*, **175**, 4052-4061.
- Brantl, S. und Wagner, E.G. (1997) Dual function of the *copR* gene product of plasmid pIP501. *J. Bacteriol.*, **179**, 7016-7024.
- Breg, J.N., van Opheusden, J.H., Burgering, M.J., Boelens, R. und Kaptein, R. (1990) Structure of Arc repressor in solution: evidence for a family of beta-sheet DNA-binding proteins. *Nature*, **346**, 586-589.
- Brennan, R.G. und Matthews, B.W. (1989a) The helix-turn-helix DNA binding motif. *J. Biol. Chem.*, **264**, 1903-1906.
- Brennan, R.G. und Matthews, B.W. (1989b) Structural basis of DNA-protein recognition. *Trends Biochem. Sci.*, **14**, 286-290.
- Bricogne, G., Vonrhein, C., Flensburg, C., Schiltz, M. und Paciorek, W. (2003) Generation, representation and flow of phase information in structure determination: recent developments in and around SHARP 2.0. *Acta Cryst.*, **D59**, 2023-2030.
- Brunger, A.T. (1992) The free R value: a novel statistical quantity for assessing the accuracy of crystal structures. *Nature*, **355**, 472-474.
- Brunger, A.T., Adams, P.D., Clore, G.M., DeLano, W.L., Gros, P., Grosse-Kunstleve, R.W., Jiang, J.S., Kuszewski, J., Nilges, M., Pannu, N.S., Read, R.J., Rice, L.M., Simonson,

- T. und Warren, G.L. (1998) Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Cryst.*, **D54**, 905-921.
- Burgering, M.J., Boelens, R., Gilbert, D.E., Breg, J.N., Knight, K.L., Sauer, R.T. und Kaptein, R. (1994) Solution structure of dimeric Mnt repressor (1-76). *Biochemistry*, **33**, 15036-15045.
- CCP4. (1994) The CCP4 Suite: Programs for Protein Crystallography. *Acta Cryst.*, **D50**, 760 -763.
- Ceglowski, P. und Alonso, J.C. (1994) Gene organization of the *Streptococcus pyogenes* plasmid pDB101: sequence analysis of the orf eta-copS region. *Gene*, **145**, 33-39.
- Ceglowski, P., Boitsov, A., Chai, S. und Alonso, J.C. (1993a) Analysis of the stabilization system of pSM19035-derived plasmid pBT233 in *Bacillus subtilis*. *Gene*, **136**, 1-12.
- Ceglowski, P., Boitsov, A., Karamyan, N., Chai, S. und Alonso, J.C. (1993b) Characterization of the effectors required for stable inheritance of *Streptococcus pyogenes* pSM19035-derived plasmids in *Bacillus subtilis*. *Mol. Gen. Genet.*, **241**, 579-585.
- Ceglowski, P., Lurz, R. und Alonso, J.C. (1993c) Functional analysis of pSM19035-derived replicons in *Bacillus subtilis*. *FEMS Microbiol. Lett.*, **109**, 145-150.
- Chen, S., Gunasekera, A., Zhang, X., Kunkel, T.A., Ebright, R.H. und Berman, H.M. (2001) Indirect readout of DNA sequence at the primary-kink site in the CAP-DNA complex: alteration of DNA binding specificity through alteration of DNA kinking. *J. Mol. Biol.*, **314**, 75-82.
- Chivers, P.T. und Sauer, R.T. (1999) NikR is a ribbon-helix-helix DNA-binding protein. *Protein Sci.*, **8**, 2494-2500.
- Chothia, C., Lesk, A.M., Tramontano, A., Levitt, M., Smith-Gill, S.J., Air, G., Sheriff, S., Padlan, E.A., Davies, D., Tulip, W.R. et al. (1989) Conformations of immunoglobulin hypervariable regions. *Nature*, **342**, 877-883.
- Costa, M., Sola, M., del Solar, G., Eritja, R., Hernandez-Arriaga, A.M., Espinosa, M., Gomis-Ruth, F.X. und Coll, M. (2001) Plasmid transcriptional repressor CopG oligomerises to render helical superstructures unbound and in complexes with oligonucleotides. *J. Mol. Biol.*, **310**, 403-417.
- Daniels, P., Tamazyan, R., Kuntscher, C.A., Dressel, M., Lichtenberg, F. und van Smaalen, S. (2002) The incommensurate modulation of the structure of Sr₂Nb₂O₇. *Acta Cryst.*, **B58**, 970-976.
- D'Arcy, A. (1994) Crystallizing proteins - a rational approach? *Acta Cryst.*, **D50**, 469-471.
- Davis, M.A., Radnedge, L., Martin, K.A., Hayes, F., Youngren, B. und Austin, S.J. (1996) The P1 ParA protein and its ATPase activity play a direct role in the segregation of plasmid copies to daughter cells. *Mol. Microbiol.*, **21**, 1029-1036.
- de la Hoz, A.B., Ayora, S., Sitkiewicz, I., Fernandez, S., Pankiewicz, R., Alonso, J.C. und Ceglowski, P. (2000) Plasmid copy-number control and better-than-random segregation genes of pSM19035 share a common regulator. *Proc. Natl. Acad. Sci. U S A*, **97**, 728-733.
- de la Hoz, A.B., Pratto, F., Misselwitz, R., Speck, C., Weihofen, W., Welfle, K., Saenger, W., Welfle, H. und Alonso, J.C. (2004) Recognition of DNA by ω protein from the broad-host range *Streptococcus pyogenes* plasmid pSM19035: analysis of binding to operator DNA with one to four heptad repeats. *Nucleic Acids Res.*, **32**, 3136-3147.
- del Solar, G., Hernandez-Arriaga, A.M., Gomis-Ruth, F.X., Coll, M. und Espinosa, M. (2002) A genetically economical family of plasmid-encoded transcriptional repressors involved in control of plasmid copy number. *J. Bacteriol.*, **184**, 4943-4951.
- Dickerson, R.E. (1998) DNA bending: the prevalence of kinkiness and the virtues of normality. *Nucleic Acids Res.*, **26**, 1906-1926.

- Dickerson, R.E. und Chiu, T.K. (1997) Helix bending as a factor in protein/DNA recognition. *Biopolymers*, **44**, 361-403.
- Ducruix, A. und Giegé, R. (1999) *Crystallization of nucleic acids and proteins : a practical approach*. Oxford University Press, Oxford ; New York.
- Duncan, L.L., Brian, O., Pratt Brock, P. und Pratt Brock, C. (2002) Two Phases of C9H12: why is the structure at 295 K so complicated? *Acta Cryst. B* **58**, 502-511.
- Ebersbach, G. und Gerdes, K. (2004) Bacterial mitosis: partitioning protein ParA oscillates in spiral-shaped structures and positions plasmids at mid-cell. *Mol. Microbiol.*, **52**, 385-398.
- El Hassan, M.A. und Calladine, C.R. (1998) Two distinct modes of protein-induced bending in DNA. *J. Mol. Biol.*, **282**, 331-343.
- Engh, R. und Huber, R. (1991) Accurate Bond and Angle Parameters for X-ray Protein-Structure Refinement. *Acta Cryst. A* **47**, 392-400.
- Fabry, S., Lehrmacher, A., Bode, W. und Hensel, R. (1988) Expression of the glyceraldehyde-3-phosphatase dehydrogenase from the extremely hyperthermophilic archaebacterium *Methanothermus fervidus* in *E. coli*. *FEBS Lett.*, **237**, 213-217.
- Ferre-d'Amare, A.R. und Doudna, J.A. (1997) Establishing suitability of RNA preparations for crystallization. Determination of polydispersity. *Methods Mol. Biol.*, **74**, 371-377.
- Figge, R.M., Easter, J. und Gober, J.W. (2003) Productive interaction between the chromosome partitioning proteins, ParA and ParB, is required for the progression of the cell cycle in *Caulobacter crescentus*. *Mol. Microbiol.*, **47**, 1225-1237.
- Fung, E., Bouet, J.Y. und Funnell, B.E. (2001) Probing the ATP-binding site of P1 ParA: partition and repression have different requirements for ATP binding and hydrolysis. *EMBO J.*, **20**, 4901-4911.
- Gerdes, K. (2000) Toxin-antitoxin modules may regulate synthesis of macromolecules during nutritional stress. *J. Bacteriol.*, **182**, 561-572.
- Gerdes, K., Moller-Jensen, J., Ebersbach, G., Kruse, T. und Nordstrom, K. (2004) Bacterial mitotic machineries. *Cell*, **116**, 359-366.
- Gilson, M., Sharp, K. und Honig, B. (1987) Calculating electrostatic interactions in biomolecules: Method and error assessment. *J. Comput. Chem.*, **9**, 327-335.
- Glass, C.K. (1994) Differential recognition of target genes by nuclear receptor monomers, dimers, and heterodimers. *Endocr. Rev.*, **15**, 391-407.
- Golovanov, A.P., Barilla, D., Golovanova, M., Hayes, F. und Lian, L.Y. (2003) ParG, a protein required for active partition of bacterial plasmids, has a dimeric ribbon-helix-helix structure. *Mol. Microbiol.*, **50**, 1141-1153.
- Gomis-Ruth, F.X., Sola, M., Acebo, P., Parraga, A., Guasch, A., Eritja, R., Gonzalez, A., Espinosa, M., del Solar, G. und Coll, M. (1998) The structure of plasmid-encoded transcriptional repressor CopG unliganded and bound to its operator. *EMBO J.*, **17**, 7404-7415.
- Gordon, G.S., Sitnikov, D., Webb, C.D., Teleman, A., Straight, A., Losick, R., Murray, A.W. und Wright, A. (1997) Chromosome and low copy plasmid segregation in *E. coli*: visual evidence for distinct mechanisms. *Cell*, **90**, 1113-1121.
- Hiraga, S. (1992) Chromosome and plasmid partition in *Escherichia coli*. *Annu. Rev. Biochem.*, **61**, 283-306.
- Hol, W.G., van Duijnen, P.T. und Berendsen, H.J. (1978) The alpha-helix dipole and the properties of proteins. *Nature*, **273**, 443-446.
- Honig, B. und Nicholls, A. (1995) Classical electrostatics in biology and chemistry. *Science*, **268**, 1144-1149.
- Hooft, R.W., Vriend, G., Sander, C. und Abola, E.E. (1996) Errors in protein structures. *Nature*, **381**, 272.

- Hunter, C.A. und Lu, X.J. (1997) DNA base-stacking interactions: a comparison of theoretical calculations with oligonucleotide X-ray crystal structures. *J. Mol. Biol.*, **265**, 603-619.
- Jensen, R.B. und Gerdes, K. (1995) Programmed cell death in bacteria: proteic plasmid stabilization systems. *Mol. Microbiol.*, **17**, 205-210.
- Jones, T.A. (1978) A graphics model building and refinement system for macromolecules. *J. Appl. Cryst.*, **11**, 268-272.
- Kabsch, W. (1988) Evaluation of single-crystal X-ray diffraction from a position-sensitive detector. *J. Appl. Cryst.*, **21**, 916.
- Kabsch, W., Kabsch, H. und Eisenberg, D. (1976) Packing in a new crystalline form of glutamine synthetase from *Escherichia coli*. *J. Mol. Biol.*, **100**, 283-291.
- Kabsch, W. und Sander, C. (1983) Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features. *Biopolymers*, **22**, 2577-2637.
- Koonin, E.V. (1993) A superfamily of ATPases with diverse functions containing either classical or deviant ATP-binding motif. *J Mol Biol*, **229**, 1165-1174.
- Kraulis, P.J. (1991) MOLSCRIPT: A Program to Produce Both Detailed and Schematic Plots of Protein Structures. *J. Appl. Cryst.*, **24**, 946-950.
- Laemmli, U.K. (1970) Cleavage of structural proteins during the assembly of the head bacteriophage T4. *Nature*, **227**, 680-685.
- Laskowski, R.A., MacArthur, M.W., Moss, D.S. und Thornton, J.M. (1993) PROCHECK: a program to check the stereochemical quality of protein structures. *J. Appl. Cryst.*, **26**, 283-291.
- Lavery, R. und Sklenar, H. (1988) The definition of generalized helicoidal parameters and of axis curvature for irregular nucleic acids. *J Biomol Struct Dyn*, **6**, 63-91.
- Lavery, R. und Sklenar, H. (1989) Defining the structure of irregular nucleic acids: conventions and principles. *J Biomol Struct Dyn*, **6**, 655-667.
- Le Chatelier, E., Ehrlich, S.D. und Janniere, L. (1994) The pAM β 1 CopF repressor regulates plasmid copy number by controlling transcription of the *repE* gene. *Mol. Microbiol.*, **14**, 463-471.
- Leonard, T.A., Butler, P.J. und Lowe, J. (2004) Structural analysis of the chromosome segregation protein Spo0J from *Thermus thermophilus*. *Mol Microbiol*, **53**, 419-432.
- Leonard, T.A., Butler, P.J. und Lowe, J. (2005) Bacterial chromosome segregation: structure and DNA binding of the Soj dimer - a conserved biological switch. *Embo J*, **24**, 270-282.
- Leslie, A.G.W. (1992) Recent Changes to the MOSFLM package for processing film and image plate data. *Joint CCP4 and ESF-EACBM Newsletter*, **26**.
- Lin, D.C. und Grossman, A.D. (1998) Identification and characterization of a bacterial chromosome partitioning site. *Cell*, **92**, 675-685.
- Lovelace, J.J., Narayan, K., Chik, J.K., Bellamy, H.D., Snell, E.H., Lindberg, U., Schutt, C.E. und Borgstahl, G.E.O. (2004) Imaging modulated reflections from a semi-crystalline state of profilin:actin crystals. *J. Appl. Cryst.*, **37**.
- Lu, X.J. und Olson, W.K. (2003) 3DNA: a software package for the analysis, rebuilding and visualization of three-dimensional nucleic acid structures. *Nucleic Acids Res.*, **31**, 5108-5121.
- Lum, P.L., Rodgers, M.E. und Schildbach, J.F. (2002) TraY DNA recognition of its two F factor binding sites. *J. Mol. Biol.*, **321**, 563-578.
- Luscombe, N.M., Austin, S.E., Berman, H.M. und Thornton, J.M. (2000) An overview of the structures of protein-DNA complexes. *Genome Biol.*, **1**, REVIEWS001.

- Lyubchenko, Y.L., Shlyakhtenko, L.S., Appella, E. und Harrington, R.E. (1993) CA runs increase DNA flexibility in the complex of lambda Cro protein with the OR3 site. *Biochemistry*, **32**, 4121-4127.
- McKay, D.B. und Steitz, T.A. (1981) Structure of catabolite gene activator protein at 2.9 Å resolution suggests binding to left-handed B-DNA. *Nature*, **290**, 744-749.
- McNamara, P.T., Bolshoy, A., Trifonov, E.N. und Harrington, R.E. (1990) Sequence-dependent kinks induced in curved DNA. *J. Biomol. Struct. Dyn.*, **8**, 529-538.
- McPherson, A. (1990) Current approaches to macromolecular crystallization. *Eur. J. Biochem.*, **189**, 1-23.
- Meinhart, A., Alonso, J.C., Strater, N. und Saenger, W. (2003) Crystal structure of the plasmid maintenance system epsilon/zeta: functional mechanism of toxin zeta and inactivation by epsilon2zeta2 complex formation. *Proc. Natl. Acad. Sci. U S A*, **100**, 1661-1666.
- Merritt, E.A. und Bacon, D.J. (1997) Raster3D: Photorealistic Molecular Graphics. *Methods Enzymol.*, **277**, 505-524.
- Misselwitz, R., de la Hoz, A.B., Ayora, S., Welfle, K., Behlke, J., Murayama, K., Saenger, W., Alonso, J.C. und Welfle, H. (2001) Stability and DNA-binding properties of the ω regulator protein from the broad-host range *Streptococcus pyogenes* plasmid pSM19035. *FEBS Lett.*, **505**, 436-440.
- Moller-Jensen, J., Borch, J., Dam, M., Jensen, R.B., Roepstorff, P. und Gerdes, K. (2003) Bacterial mitosis: ParM of plasmid R1 moves plasmid DNA by an actin-like insertional polymerization mechanism. *Mol. Cell.*, **12**, 1477-1487.
- Moller-Jensen, J., Jensen, R.B. und Gerdes, K. (2000) Plasmid and chromosome segregation in prokaryotes. *Trends Microbiol.*, **8**, 313-320.
- Moller-Jensen, J., Jensen, R.B., Lowe, J. und Gerdes, K. (2002) Prokaryotic DNA segregation by an actin-like filament. *EMBO J.*, **21**, 3119-3127.
- Motallebi-Veshareh, M., Rouch, D.A. und Thomas, C.M. (1990) A family of ATPases involved in active partitioning of diverse bacterial plasmids. *Mol. Microbiol.*, **4**, 1455-1463.
- Murayama, K., Orth, P., de la Hoz, A.B., Alonso, J.C. und Saenger, W. (2001) Crystal structure of ω transcriptional repressor encoded by *Streptococcus pyogenes* plasmid pSM19035 at 1.5 Å resolution. *J. Mol. Biol.*, **314**, 789-796.
- Murshudov, G.N., Vagin, A.A. und Dodson, E.J. (1997) Refinement of macromolecular structures by the maximum-likelihood method. *Acta Cryst.*, **D53**, 240-255.
- Naar, A.M., Boutin, J.M., Lipkin, S.M., Yu, V.C., Holloway, J.M., Glass, C.K. und Rosenfeld, M.G. (1991) The orientation and spacing of core DNA-binding motifs dictate selective transcriptional responses to three nuclear receptors. *Cell*, **65**, 1267-1279.
- Niki, H. und Hiraga, S. (1997) Subcellular distribution of actively partitioning F plasmid during the cell division cycle in *E. coli*. *Cell*, **90**, 951-957.
- Nooren, I.M., Kaptein, R., Sauer, R.T. und Boelens, R. (1999) The tetramerization domain of the Mnt repressor consists of two right-handed coiled coils. *Nat. Struct. Biol.*, **6**, 755-759.
- Nordstrom, K. und Austin, S.J. (1989) Mechanisms that contribute to the stable segregation of plasmids. *Annu. Rev. Genet.*, **23**, 37-69.
- Nunn, C.M., Garman, E. und Neidle, S. (1997) Crystal structure of the DNA decamer d(CGCAATTGCG) complexed with the minor groove binding drug netropsin. *Biochemistry*, **36**, 4792-4799.
- Olson, W.K., Gorin, A.A., Lu, X.J., Hock, L.M. und Zhurkin, V.B. (1998) DNA sequence-dependent deformability deduced from protein-DNA crystal complexes. *Proc. Natl. Acad. Sci. U S A*, **95**, 11163-11168.

- Otwinowski, Z. und Minor, W. (1997) Processing of X-Ray Diffraction Data Collected in Oscillation Mode. In Carter C.W.Jr, S.R.M. (ed.), *Macromolecular Crystallography Part A*. Academic Press, Vol. 276, pp. 307-326.
- Pabo, C.O. und Sauer, R.T. (1992) Transcription factors: structural families and principles of DNA recognition. *Annu. Rev. Biochem.*, **61**, 1053-1095.
- Packer, M.J., Dauncey, M.P. und Hunter, C.A. (2000) Sequence-dependent DNA structure: dinucleotide conformational maps. *J. Mol. Biol.*, **295**, 71-83.
- Parkinson, G., Vojtechovsky, J., Clowney, L., Brunger, A.T. und Berman, H.M. (1996) New parameters for the refinement of nucleic acid-containing structures. *Acta Cryst.*, **D52**, 57-64.
- Pavlov, N.A., Cherny, D.I., Nazimov, I.V., Slesarev, A.I. und Subramaniam, V. (2002) Identification, cloning and characterization of a new DNA-binding protein from the hyperthermophilic methanogen *Methanopyrus kandleri*. *Nucleic Acids Res.*, **30**, 685-694.
- Phillips, S.E. (1994) The β-ribbon DNA recognition motif. *Annu. Rev. Biophys. Biomol. Struct.*, **23**, 671-701.
- Phillips, S.E., Manfield, I., Parsons, I., Davidson, B.E., Rafferty, J.B., Somers, W.S., Margarita, D., Cohen, G.N., Saint-Girons, I. und Stockley, P.G. (1989) Cooperative tandem binding of met repressor of *Escherichia coli*. *Nature*, **341**, 711-715.
- Potter, H. (1988) Electroporation in biology: methods, applications, and instrumentation. *Anal. Biochem.*, **174**, 361-373.
- Pujol, C., Chedin, F., Ehrlich, S.D. und Janniere, L. (1998) Inhibition of a naturally occurring rolling-circle replicon in derivatives of the τ-replicating plasmid pIP501. *Mol. Microbiol.*, **29**, 709-718.
- Rafferty, J.B., Somers, W.S., Saint-Girons, I. und Phillips, S.E. (1989) Three-dimensional crystal structures of *Escherichia coli* met repressor with and without corepressor. *Nature*, **341**, 705-710.
- Rastinejad, F., Perlmann, T., Evans, R.M. und Sigler, P.B. (1995) Structural determinants of nuclear receptor assembly on DNA direct repeats. *Nature*, **375**, 203-211.
- Raumann, B.E., Knight, K.L. und Sauer, R.T. (1995) Dramatic changes in DNA-binding specificity caused by single residue substitutions in an Arc/Mnt hybrid repressor. *Nat. Struct. Biol.*, **2**, 1115-1122.
- Raumann, B.E., Rould, M.A., Pabo, C.O. und Sauer, R.T. (1994) DNA recognition by β-sheets in the Arc repressor-operator crystal structure. *Nature*, **367**, 754-757.
- Ravishanker, G., Swaminathan, S., Beveridge, D.L., Lavery, R. und Sklenar, H. (1989) Conformational and helicoidal analysis of 30 PS of molecular dynamics on the d(CGCGAATTCGCG) double helix: "curves", dials and windows. *J. Biomol. Struct. Dyn.*, **6**, 669-699.
- Rhodes, D. und Klug, A. (1986) An underlying repeat in some transcriptional control sequences corresponding to half a double helical turn of DNA. *Cell*, **46**, 123-132.
- Roberts, R.C., Spangler, C. und Helinski, D.R. (1993) Characteristics and significance of DNA binding activity of plasmid stabilization protein ParD from the broad host-range plasmid RK2. *J. Biol. Chem.*, **268**, 27109-27117.
- Rost, B. und Sander, C. (1993) Prediction of protein secondary structure at better than 70% accuracy. *J. Mol. Biol.*, **232**, 584-599.
- Rost, B., Yachdav, G. und Liu, J. (2004) The PredictProtein server. *Nucleic Acids Res.*, **32**, W321-326.
- Saenger, W. (1984) *Principles of nucleic acid structure*. Springer-Verlag, New York.
- Sanger, F., Nicklen, S. und Coulson, A.R. (1977) DNA sequencing with chain-terminating inhibitors. *Proc. Natl. Acad. Sci. U S A*, **74**, 5463-5467.

- Sanner, M.F., Olson, A.J. und Spehner, J.C. (1996a) Reduced surface: an efficient way to compute molecular surfaces. *Biopolymers*, **38**, 305-320.
- Sanner, M.F., Spehner, J.-C. und Olson, A.J. (1996b) Reduced surface: an efficient way to compute molecular surfaces. *Biopolymers*. **38**, 305-320.
- Schildbach, J.F., Karzai, A.W., Raumann, B.E. und Sauer, R.T. (1999) Origins of DNA-binding specificity: role of protein contacts with the DNA backbone. *Proc Natl Acad Sci U S A*, **96**, 811-817.
- Schildbach, J.F., Milla, M.E., Jeffrey, P.D., Raumann, B.E. und Sauer, R.T. (1995) Crystal structure, folding, and operator binding of the hyperstable Arc repressor mutant PL8. *Biochemistry*, **34**, 1405-1412.
- Schneider, T.R. und Sheldrick, G.M. (2002) Substructure solution with SHELXD. *Acta Crystallogr D Biol Crystallogr*, **58**, 1772-1779.
- Schreiter, E.R., Sintchak, M.D., Guo, Y., Chivers, P.T., Sauer, R.T. und Drennan, C.L. (2003) Crystal structure of the nickel-responsive transcription factor NikR. *Nat. Struct. Biol.*, **10**, 794-799.
- Schultz, S.C., Shields, G.C. und Steitz, T.A. (1991) Crystal structure of a CAP-DNA complex: the DNA is bent by 90 degrees. *Science*, **253**, 1001-1007.
- Seeman, N.C., Rosenberg, J.M. und Rich, A. (1976) Sequence-specific recognition of double helical nucleic acids by proteins. *Proc. Natl. Acad. Sci. U S A*, **73**, 804-808.
- Silbaq, F.S., Ruttenberg, S.E. und Stormo, G.D. (2002) Specificity of Mnt 'master residue' obtained from *in vivo* and *in vitro* selections. *Nucleic Acids Res.*, **30**, 5539-5548.
- Somers, W.S. und Phillips, S.E. (1992) Crystal structure of the met repressor-operator complex at 2.8 Å resolution reveals DNA recognition by β-strands. *Nature*, **359**, 387-393.
- Spink, N., Nunn, C.M., Vojtechovsky, J., Berman, H.M. und Neidle, S. (1995) Crystal structure of a DNA decamer showing a novel pseudo four-way helix-helix junction. *Proc. Natl. Acad. Sci. U S A*, **92**, 10767-10771.
- Storoni, L.C., McCoy, A.J. und Read, R.J. (2004) Likelihood-enhanced fast rotation functions. *Acta Cryst.*, **D60**, 432-438.
- Summers, D. (1998) Timing, self-control and a sense of direction are the secrets of multicopy plasmid stability. *Mol. Microbiol.*, **29**, 1137-1145.
- Surtees, J.A. und Funnell, B.E. (2003) Plasmid and chromosome traffic control: how ParA and ParB drive partition. *Curr. Top. Dev. Biol.*, **56**, 145-180.
- Suzuki, M. (1995) DNA recognition by a β-sheet. *Protein Eng.*, **8**, 1-4.
- Suzuki, M. und Yagi, N. (1995) Stereochemical basis of DNA bending by transcription factors. *Nucleic Acids Res.*, **23**, 2083-2091.
- Terwilliger, T.C. (2000) Maximum-likelihood density modification. *Acta Cryst.*, **D56**, 965-972.
- Terwilliger, T.C. und Berendzen, J. (1999) Automated MAD and MIR structure solution. *Acta Cryst.*, **D55**, 849-861.
- Umesono, K., Murakami, K.K., Thompson, C.C. und Evans, R.M. (1991) Direct repeats as selective response elements for the thyroid hormone, retinoic acid, and vitamin D3 receptors. *Cell*, **65**, 1255-1266.
- Vagin, A. und Teplyakov, A. (1997) MOLREP: an automated program for molecular replacement. *J. Appl. Cryst.*, **30**, 1022-1025.
- van den Ent, F., Moller-Jensen, J., Amos, L.A., Gerdes, K. und Lowe, J. (2002) F-actin-like filaments formed by plasmid segregation protein ParM. *EMBO J.*, **21**, 6935-6943.
- von Hippel, P.H. und Berg, O.G. (1986) On the specificity of DNA-protein interactions. *Proc. Natl. Acad. Sci. U S A*, **83**, 1608-1612.
- Waldburger, C.D., Schildbach, J.F. und Sauer, R.T. (1995) Are buried salt bridges important for protein stability and conformational specificity? *Nat. Struct. Biol.*, **2**, 122-128.

- Weeks, C.M. und Miller, R. (1999) The design and implementation of SnB v2.0. *J. Appl. Cryst.*, **32**, 120-124.
- Wheeler, R.T. und Shapiro, L. (1997) Bacterial chromosome segregation: is there a mitotic apparatus? *Cell*, **88**, 577-579.
- White, B.A. (1993) *PCR protocols : current methods and applications*. Humana Press, Totowa, N.J.
- Williams, D.R. und Thomas, C.M. (1992) Active partitioning of bacterial plasmids. *J. Gen. Microbiol.*, **138**, 1-16.
- Wing, R., Drew, H., Takano, T., Broka, C., Tanaka, S., Itakura, K. und Dickerson, R.E. (1980) Crystal structure analysis of a complete turn of B-DNA. *Nature*, **287**, 755-758.
- Xiao, H., Perisic, O. und Lis, J.T. (1991) Cooperative binding of Drosophila heat shock factor to arrays of a conserved 5 bp unit. *Cell*, **64**, 585-593.
- Xu, X., Sun, Y.L. und Hoey, T. (1996) Cooperative DNA binding and sequence-selective recognition conferred by the STAT amino-terminal domain. *Science*, **273**, 794-797.