

8. Literatur

Argos P., Rossmann M. G., Grau U. M., Zuber H., Frank G. & Tratschin J. D. (1979) Thermal stability and protein structure. *Biochemistry* **25**, 5698-5703

Auerbach G., Jacob U., Grattinger M., Schurig H. & Jaenicke R. (1997) Crystallographic analysis of phosphoglycerate kinase from the hyperthermophilic bacterium *Thermotoga maritima*. *Biol Chem.* **378**, 327-329

Auerbach G., Ostendorp R., Prade L., Korndörfer I., Dams T., Huber R. & Jaenicke R. (1998) Lactate dehydrogenase from the hyperthermophilic bacterium *Thermotoga maritima*: the crystal structure at 2.1 Å resolution reveals strategies for intrinsic protein stabilization. *Structure* **6**, 769-781

Balzer D., Ziegelin G., Pansegrau W., Kruff V. & Lanka E. (1992) KorB protein of promiscuous plasmid RP4 recognizes inverted sequence repetitions in regions essential for conjugative plasmid transfer. *Nucleic Acids Res.* **20**, 1851-1858.

Bashford D. & Karplus M. (1990) pKa's of ionizable groups in proteins: atomic detail from a continuum electrostatic model. *Biochemistry* **29**, 10219-10225

Baumann H., Knapp S., Lundbäck T., Ladenstein R. & Härd T. (1994) Solution structure and DNA-binding properties of a thermostable protein from the archaeon *Sulfolobus solfataricus*. *Nature Struct. Biol.* **1**, 808-819

Bewley M. C., Boustead C. M., Walker J. H., Waller D. A. & Huber R. (1993) Structure of chicken annexin V at 2.25-Å resolution. *Biochemistry* **32**, 3923-3929.

Bjellqvist B., Hughes G. J., Pasquali Ch., Paquet N., Ravier F., Sanchez J.-Ch., Frutiger S. & Hochstrasser D. F. (1993) The focusing positions of polypeptides in immobilized pH gradients can be predicted from their amino acid sequences. *Electrophoresis* **14**, 1023-1031

Bjellqvist B., Basse B., Olsen E. & Celis J. E. (1994) Reference points for comparisons of two-dimensional maps of proteins from different human cell types defined in a pH scale where isoelectric points correlate with polypeptide compositions. *Electrophoresis* **15**, 529-539

Breyer W. A. & Matthews B. W. (2000) Structure of *Escherichia coli* exonuclease I suggests how processivity is achieved. *Nature Struct. Biol.*, **7**, 1125-1128

Bricogne G. (1974) Geometric sources of redundancy in intensity data and their use for phase determination. *Acta Cryst.* **A30**, 395-405

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

8. Literatur

- CCP4** (1994) The CCP4 suite: Programs for protein crystallography. *Acta Cryst.* **D50**, 760-763
- Chothia C. & Murzin A. G.** (1993) New folds for all-beta proteins. *Structure* **1**, 217-222
- Cohen G. B, Ren R., & Baltimore D.** (1995) Modular binding domains in signal transduction proteins. *Cell* **80**, 237-248
- Cruickshank D. W. J.** (1999) Remarks about protein structure precision. *Acta Cryst. D* **55**, 583-601
- Cudney R., Patel S., Weisgraber K., Newhouse Y. & McPherson, A.** (1994) Screening and optimization strategies for macromolecular crystal-growth. *Acta Cryst.* **D50**, 414-423
- Demchuk E., Genick U. K., Woo T. T., Getzoff E. D. & Bashford D.** (2000) Protonation states and pH titration in the photocycle of photoactive yellow protein. *Biochemistry.* **39**, 1100-1113
- 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
- Eck M. J., Atwell S. K., Shoelson S.E. & Harrison S. C.** (1994) Structure of the regulatory domains of the Src-family tyrosine kinase Lck. *Nature* **368**, 764-769
- Elcock A. H.** (1998) The stability of salt bridges at high temperatures: implications for hyperthermophilic proteins. *J. Mol. Biol.* **284**, 489-502
- Falzone C. J., Kao Y. H., Zhao J., Bryant D. A. & Lecomte J. T.** (1994) Three-dimensional solution structure of PsaE from the cyanobacterium *Synechococcus* sp. strain PCC 7002, a photosystem I protein that shows structural homology with SH3 domains. *Biochemistry* **33**, 6052-6062
- Gill S. C., & von Hippel P.H.** (1989) Calculation of protein extinction coefficients from amino acid sequence data. *Anal Biochem.* **182**, 319-326
- 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. & Marahiel M. A.** (1998) A superfamily of proteins that contain the cold-shock domain. *Trends Biochem Sci.* **8**, 286-90. Review.

8. Literatur

- 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
- Grimsley G. R., Shaw K. L., Fee L. R., Alston R. W., Huyghues-Despointes B. M., Thurlkill R. L., Scholtz J. M. & Pace C. N.**(1999) Increasing protein stability by altering long-range coulombic interactions. *Protein Sci.* **8**,1843-1849
- Guex N. & Peitsch M. C.**(1997) SWISS-MODEL and the Swiss-PdbViewer: an environment for comparative protein modeling. *Electrophoresis.* **15**, 2714-23.
- Haney P. J., Badger J. H., Buldak G. L., Reich C. I., Woese C. R. & Olsen G. J.** (1999) Thermal adaptation analyzed by comparison of protein sequences from mesophilic and extremely thermophilic *Methanococcus* species.
Proc. Natl. Acad. Sci. U S A. **96**, 3578-3583
- Hennig M., Darimont B., Sterner R., Kirschner K. & Jansonius J. N.** (1995) 2.0 Å structure of indole-3-glycerol phosphate synthase from the hyperthermophile *Sulfolobus solfataricus*: possible determinants of protein stability. *Structure* **3**,1295-1306
- Hennig M., Sterner R., Kirschner K. & Jansonius J. N.**(1997) Crystal structure at 2.0 Å resolution of phosphoribosyl anthranilate isomerase from the hyperthermophile *Thermotoga maritima*:possible determinants of protein stability. *Biochemistry.* **36**, 6009-6016
- Holliger P. & Riechmann L.** (1997)A conserved infection pathway for filamentous bacteriophages is suggested by the structure of the membrane penetration domain of the minor coat protein g3p from phage fd. *Structure* **5**, 265-275
- Holm L. & Sander C.** (1993) Protein structure comparison by alignment of distance matrices. *J. Mol. Biol.* **233**, 123-138
- 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
- Hynes T. R. & Fox, R. O.** (1991) The crystal structure of staphylococcal nuclease refined at 1.7 Å resolution. *Proteins* **10**, 92-105
- Jaenicke R. & Böhm G.** (1998) The stability of proteins in extreme environments. *Curr. Opin. Struct. Biol.* **8**,738-748
- Jagura-Burdzy G., Kostelidou K., Pole J, Khare D., Jones A., Williams D. R. & Thomas C. M.** (1999a) IncC of broad-host-range plasmid RK2 modulates KorB transcriptional repressor activity In vivo and operator binding in vitro *J. Bacteriol.* **181**, 2807-2815

8. Literatur

Jagura-Burdzy G., Macartney D. P., Zatyka M., Cunliffe L., Cooke D., Huggins C., Westblade L., Khanim F. & Thomas C. M. (1999b) Repression at a distance by the global regulator KorB of promiscuous IncP plasmids. *Mol. Microbiol.* **32**, 519-532

Jagura-Burdzy G. & Thomas C.M. (1994) KorA protein of promiscuous plasmid RK2 controls a transcriptional switch between divergent operons for plasmid replication conjugative transfer. *Proc. Natl. Acad. Sci. USA* **91**, 10571-10575

Jagura-Burdzy G. & Thomas C.M. (1997) Dissection of the switch between genes for replication and transfer of promiscuous plasmid RK2: basis of the dominance of trfAp over trbAp and specificity for KorA in controlling the switch. *J. Mol. Biol.* **265**, 507-518

Jameson, G. B. (1982) On structure refinement using data from a twinned crystal. *Acta Cryst.* **A38** 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 S. & Thornton J. M. (1995) Protein-protein interactions: a review of protein dimer structures. *Prog. Biophys. Mol. Biol.* **63**, 31-165

Jones S. & Thornton J. M. (1996) Principles of protein-protein interactions. *Proc. Natl. Acad. Sci. USA* **93**, 13-20

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

Jovin T.M., Geisler N. & Weber K. (1977) Amino-terminal fragments of *Escherichia coli* lac repressor bind to DNA. *Nature.* **269**, 668-672.

Karshikoff A. & Ladenstein R. (1998) Proteins from thermophilic and mesophilic organisms essentially do not differ in packing. *Protein Eng.* **11**, 867-872.

Kishan K. V., Newcomer M. E., Rhodes T. H. & Guilliot S. D. (2001) Effect of pH and salt bridges on structural assembly: molecular structures of the monomer and intertwined dimer of the Eps8 SH3 domain. *Protein Sci.* **10**, 1046-1055

Kishan K. V., Scita G., Wong W. T., Di Fiore P. P. & Newcomer M. E. (1997) The SH3 domain of Eps8 exists as a novel intertwined dimer. *Nature Struct. Biol.* **4**, 739-743

8. Literatur

- Kissinger C.R., Gehlhaar D.K. & Fogel D.B.** (1999) Rapid automated molecular replacement by evolutionary search. *Acta Cryst.* **D55**, 484-491
- Kleywegt G. J.** (1996) Use of non-crystallographic symmetry in protein structure refinement. *Acta Cryst.* **D52**, 842-857
- Kleywegt G. J.** (1999). Experimental assessment of differences between related protein crystal structures. *Acta Cryst.* **D55**, 1878-1884. *Acta Cryst.* **D55**, 1878-1884 (1999)
- Kleywegt G. J. & Jones T. A.** (1995) Where freedom is given, liberties are taken. *Structure* **3**, 535-540
- Kleywegt, G. J. & Jones, T. A.** (1996). xdlMAPMAN and xdIDATAMAN - Programs for Reformatting, Analysis and Manipulation of Biomacromolecular Electron-Density Maps and Reflection Data Sets. *Acta Cryst.* **D52**, 826-828.
- Kleywegt, G. J. & Jones, T. A.** (1997). Template Convolution to Enhance or Detect Structural Features in Macromolecular Electron-Density Maps. *Acta Cryst.* **D53**, 179-185.
- Kleywegt, G. J. & Jones, T. A.** (1999). Software for handling macromolecular envelopes. *Acta Cryst.* **D55**, 941-944.
- Korndörfer I., Steipe B., Huber R., Tomschy A. & Jaenicke R.** (1995) The crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic bacterium *Thermotoga maritima* at 2.5 Å resolution. *J. Mol. Biol.* **246**, 511-521
- Kostelidou K., Jones A.C. & Thomas C.M.** (1999) Conserved C-terminal region of global repressor KorA of broad-host-range plasmid RK2 is required for co-operativity between KorA and a second RK2 global regulator, KorB. *J. Mol. Biol.* **289**, 211-221
- Kostelidou K. & Thomas C.M.** (2000) The hierarchy of KorB binding at its 12 binding sites on the broad-host-range plasmid RK2 and modulation of this binding by protein. *J. Mol. Biol.* **295**, 411-422
- Kumar S., Ma B., Tsai C.J. & Nussinov R.** (2000a) Electrostatic strengths of salt bridges in thermophilic and mesophilic glutamate dehydrogenase monomers. *Proteins* **38**, 368-383.
- Kumar S., Tsai C. J. & Nussinov R.** (2000b) Factors enhancing protein thermostability. *Protein Eng.* **13**, 179-191
- Kumar S. & Nussinov R.** (1999) Salt bridge stability in monomeric proteins. *J. Mol. Biol.* **293**, 1241-1255.
- Kumar S. & Nussinov R.** (2000) Fluctuations between stabilizing and destabilizing electrostatic contributions of ion pairs in conformers of the c-Myc-Max leucine zipper. *Proteins.* **41**, 4854-97.
- Kuriyan J. & Cowburn D** (1993) *Curr. Opin. Struct. Biol* **3** : 828-837

8. Literatur

- 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
- Lobočka M. & Yarmolinsky M** (1996) P1 plasmid partition: a mutational analysis of ParB. *J. Mol. Biol.* **259**, 366-382
- Lodi P. J., Ernst J. A., Kuszewski J., Hickman A. B., Engelman A., Craigie R., Clore G.M. & Gronenborn A. M.** (1995) Solution structure of the DNA binding domain of HIV-1 integrase. *Biochemistry* **34**, 9826-9833
- Loladze V. V., Ibarra-Molero B., Sanchez-Ruiz J. M. & Makhatadze G. I.** (1999) Engineering a thermostable protein via optimization of charge-charge interactions on the protein surface. *Biochemistry*. **38**, 16419-16423.
- Macartney D. P, Williams D. R, Stafford T. & Thomas C. M.** (1997) Divergence and conservation of the partitioning and global regulation functions in the central control region of the IncP plasmids RK2 and R751. *Microbiology* **143**, 2167-2177
- Macedo-Ribeiro S., Darimont B., Sterner R. & Huber R.** (1996) Small structural changes account for the high thermostability of [4Fe-4S] ferredoxin from the hyperthermophilic bacterium *Thermotoga maritima*. *Structure* **4**, 1291-1301
- Maignan S., Guilloteau J. P., Fromage N., Arnoux B., Becquart J. & Ducruix A.** (1995) Crystal structure of the mammalian Grb2 adaptor. *Science* **268**, 291-293
- Matsumoto K., MERIC F. & Wolffe A. P.** (1996) Translational repression dependent on the interaction of the *Xenopus* Y-box protein FRGY2 with mRNA. Role of the cold shock domain, tail domain, and selective RNA sequence recognition. *J Biol Chem.* **271**, 22706-22712
- Matthews B. W.** (1968) Solvent content of protein crystals. *J. Mol. Biol.* **33**, 491-497
- Matthews B. W., Weaver L. H. & Kester W.R.** (1974) The conformation of thermolysin. *J. Biol. Chem.* **249**, 8030-8044
- Mayer K. L., Shen G., Bryant D. A., Lecomte J. T & Falzone C. J.** (1999) The solution structure of photosystem I accessory protein E from the cyanobacterium *Nostoc sp.* strain PCC 8009. *Biochemistry* **38**, 13736-13746
- Mayr B., Kaplan T., Lechner S. & Scherer S.** (1996) Identification and purification of a family of dimeric major cold shock protein homologs from the psychrotrophic *Bacillus cereus* WSBC 10201. *J Bacteriol.* **178**, 2916-25
- Motallebi-Veshareh M., Balzer D., Lanka E., Jagura-Burdzy G. & Thomas C. M.** (1992) Conjugative transfer functions of broad-host-range plasmid RK2 are coregulated with vegetative replication. *Mol. Microbiol.* **6**, 907-920

8. Literatur

- Motallebi-Veshareh M., Rouch D. & Thomas C. M.** (1990) A family of ATPases involved in active partitioning of diverse bacterial plasmids. *Mol. Microbiol.* **4**, 1455-1463
- Mueller U., Perl D., Schmid F. X. & Heinemann U.** (2000) Thermal stability and atomic-resolution crystal structure of *Bacillus caldolyticus* cold-shock protein. *J. Mol. Biol.* **297**, 975-988
- Müller U.** (1999) Makromolekulare Kristallographie bei atomarer Auflösung: Synthetische Nukleinsäurefragmente und bakterielle Kälteschockproteine. *Inaugural-Dissertation* Freie Universität Berlin
- Murshudov G. N., Vagin A. A. & Dodson E. J.** (1997) Refinement of macromolecular structures by the maximum-likelihood method. *Acta Cryst.* **D53**, 240-255
- Murzin, A. G.** (1993) OB(oligonucleotide/oligosaccharide binding)-fold: common structural and functional solution for non-homologous sequences. *EMBO J.* **12**, 861-867
- Musacchio A., Wilmanns M. & Saraste M.** (1994) Structure and function of the SH3 domain. *Prog. Biophys. Mol. Biol.* **61**, 283-297
- Nakagawa N., Masui R., Kato R. & Kuramitsu, S.** (1997). Domain structure of *Thermus thermophilus* UvrB protein. *J. Biol. Chem.* **272**, 22703-22713.
- Narayana N., Matthews D. A., Howell E. E. & Nguyen-huu X.** (1995) A plasmid-encoded dihydrofolate reductase from trimethoprim-resistant bacteria has a novel D2-symmetric active site. *Nature Struct. Biol.* **2**, 1018-1025
- Navazza J.** (1994) AMoRe: an automated package for molecular replacement *Acta Crystallogr* **A50**, 157-163
- 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. USA* **91**, 5114-5118
- Nicholls A., Sharp K. A. & Honig B.** (1991) Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons. *Proteins* **11**, 281-296.
- Nishida M., Nagata K., Hachimori Y., Horiuchi M., Ogura K., Mandiyan V., Schlessinger J. & Inagaki F.** (2001) Novel recognition mode between Vav and Grb2 SH3 domains. *EMBO J.* **20**, 2995-3007
- Otwinowski Z. & Minor, W.** (1997) Processing of x-ray diffraction data collected in oscillation mode. *Methods Enzymol.* **276**, 307-326
- Pace C. N., Alston R. W. & Shaw K. L.** (2000) Charge-charge interactions influence the denatured state ensemble and contribute to protein stability. *Protein Sci.* **9**, 1395-1398.

8. Literatur

- Pansegrau W., Lanka E., Barth P. T., Figurski D. H., Guiney D. G., Haas D., Helinski D. R., Schwab H., Stanisich V. A. & Thomas C. M.** (1994) Complete nucleotide sequence of Birmingham IncP alpha plasmids. Compilation and comparative analysis. *J. Mol. Biol.* **239**, 623-663
- Pearson W. R.** (1990) Rapid and Sensitive Sequence Comparison with FASTP and FASTA. *Methods in Enzymology* **183**, 63- 98).
- Perl D., Holtermann G. & Schmid F. X.** (2001) Role of the chain termini for the folding transition state of the cold shock protein. *Biochemistry.* **40** 15501-11.
- Perl D., Mueller U., Heinemann U. & Schmid F. X.** (2000) Two exposed amino acid residues confer thermostability on a cold shock protein. *Nature Struct. Biol.* **7**, 380-383
- 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
- Perl D. & Schmid F. X.** (2001) Electrostatic stabilization of a thermophilic cold shock protein. *J. Mol. Biol.* **313**, 343-357
- Perutz M. F. & Raidt H.** (1975) Stereochemical basis of heat stability in bacterial ferredoxins and in haemoglobin A2. *Nature* **255**, 256-259
- Pfeil W., Gesierich U., Kleemann G. R. & Sterner R.** (1997) Ferredoxin from the hyperthermophile *Thermotoga maritima* is stable beyond the boiling point of water. *J. Mol. Biol.* **272**, 591-596
- Pohl E., Holmes R. K. & Hol W. G.** (1999) Crystal structure of a cobalt-activated diphtheria toxin repressor-DNA complex reveals a metal-binding SH3-like domain. *J. Mol. Biol.* **292**, 653-667
- Porter R. R.** (1973). Structural studies of immunoglobulins. *Science.* **180**, 713-716.
- Pratt C. S., Coyle B. A. & Ibers, J. A.** (1971) Redetermination of the Structure of Nitrosylpentaamminecobalt(III) Dichloride. *J. Chem. Soc.*, 2146-2151
- Rosche T. M., Siddique A., Larsen M. H. & Figurski D. H.** (2000) Incompatibility protein IncC and global regulator KorB interact in active partition of promiscuous plasmid RK2. *J. Bacteriol.* **182**, 6014-6026
- Roy R., Kumar A., Lee J. C. & Mitra S.** (1996). The domains of mammalian base excision repair enzyme N-methylpurine-DNA glycosylase. *J. Biol. Chem.* **271**, 23690-23697.
- 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* **25**, 1682-1689

8. Literatur

- Russell R. J., Ferguson J. M., Hough D. W., Danson M. J. & Taylor G.L.** (1997) The crystal structure of citrate synthase from the hyperthermophilic archaeon *Pyrococcus furiosus* at 1.9 Å resolution. *Biochemistry* **36**, 9983-9994.
- Safro M. & Mosyak L.** (1995) Structural similarities in the noncatalytic domains of phenylalanyl-tRNA and biotin synthetases. *Protein Sci.* **4**, 2429-2432
- 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. USA* **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., 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
- Schnuchel A., Wiltschek R., Czisch M., Herrler M., Willimsky 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
- Schuller D.** (1996) MAGICQUASH: More Versatile Non-crystallographic Averaging with Multiple Constraints *Acta Cryst.* **D52**, 425-434
- Scott W. G., Finch J.T., Grenfell R., Fogg J., Smith T., Gait M.J. & Klug A.** (1995) Rapid crystallization of chemically synthesized hammerhead RNAs using a double screening procedure. *J. Mol. Biol.* **250**, 327-332
- Sheldrick G. M. & Schneider T. R.** (1997) SHELXL: High-resolution refinement. *Methods Enzymol.* **277**, 319-343
- Sommerville J. & Ladomery M.** (1996) Masking of mRNA by Y-box proteins. *FASEB J.* **10**, 435-43
- Spassov V. Z., Karshikoff A. D. & Ladenstein R.** (1994) Optimization of the electrostatic interactions in proteins of different functional and folding type. *Protein Sci.* **3**, 1556-1569.
- Spassov V. Z., Karshikoff A. D. & Ladenstein R.** (1995) The optimization of protein-solvent interactions: thermostability and the role of hydrophobic and electrostatic interactions. *Protein Sci.* **4**, 1516-1527
- Spassov V. Z., Ladenstein R. & Karshikoff A. D.** (1997) Optimization of the electrostatic interactions between ionized groups and peptide dipoles in proteins. *Protein Sci.* **6**, 1190-1196.
- Spector S., Wang M., Carp S. A., Robblee J., Hendsch Z. S., Fairman R., Tidor B. & Raleigh D. P.** (2000) Rational modification of protein stability by the mutation of charged surface residues. *Biochemistry* **39**, 872-879
- Terwilliger T. C & Berendzen J.** (1999) Automated MAD and MIR structure solution. *Acta Cryst.* **D55**, 849-861

8. Literatur

- Thomas C. M. & Smith C. A.** (1986) The trfB region of broad host range plasmid RK2: the nucleotide sequence reveals incC and key regulatory gene trfB/korA/korD as overlapping genes. *Nucleic Acids Res.* **14**, 4453-4469
- Thomson V. J., Jovanovic O. S., Pohlman R. F., Chang C. H. & Figurski D. H.** (1993) Structure, function, and regulation of the kilB locus of promiscuous plasmid RK2. *J. Bacteriol.* **175**, 2423-2435
- Thorsted P. B., Macartney D.P., Akhtar P., Haines A. S., Ali N., Davidson P., Stafford T., Pocklington M. J., Pansegrau W., Wilkins B. M., Lanka E. & Thomas C. M.** (1998) Complete sequence of the IncPbeta plasmid R751: implications for evolution and organisation of the IncP backbone. *J. Mol. Biol.* **282**, 969-990
- Wang B. C.** (1985) Resolution of phase ambiguity in macromolecular crystallography. *Methods in Enzymology* **115**, 90-112
- 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
- Williams D. R., Macartney D. P. & Thomas C. M.** (1998) The partitioning activity of the RK2 central control region requires only incC, korB and KorB-binding site O_B3 but other KorB-binding sites form destabilizing complexes in the absence of O_B3. *Microbiology* **144**, 3369-3378
- Williams D. R., Motallebi-Veshareh M. & Thomas C. M.** (1993) Multifunctional repressor KorB can block transcription by preventing isomerization of RNA polymerase-promoter complexes. *Nucleic Acids Res.* **21**, 1141-1148
- Williams D.R. & Thomas C. M.** (1992) Active partitioning of bacterial plasmids. *J. Gen. Microbiol.* **138**, 1-16
- Willmsky G., Bang H., Fischer G. & Marahiel M. A.** (1992) Characterization of cspB, a *Bacillus subtilis* inducible cold shock gene affecting cell viability at low temperatures. *J. Bacteriol.* **174**, 6326-6335.
- Wilkins M. R., Gasteiger E., Bairoch A., Sanchez J.-C., Williams K. L., Appel R. D. & Hochstrasser D. F.** (1998) Protein Identification and Analysis Tools in the ExPASy Server in: 2-D Proteome Analysis Protocols. Editor A.J. Link. Humana Press, New Jersey
- Whisstock J. C & Lesk A. M.** (1999) SH3 domains in prokaryotes. *Trends Biochem Sci.* 132-133
- Wilson K. P., Shewchuk L. M., Brennan R. G., Otsuka A. J. & Matthews B. W.** (1992) *Escherichia coli* biotin holoenzyme synthetase/bio repressor crystal structure delineates the biotin- and DNA-binding domains. *Proc. Natl. Acad. Sci. USA* **89**, 9257-9261
- Wu X., Knudsen B., Feller S. M., Zheng J., Šali A., Cowburn D., Hanafusa H. & Kuriyan J.** (1995) Structural basis for the specific interaction of lysine-containing proline-rich peptides with the N-terminal SH3 domain of c-Crk. *Structure* **3**, 215-226
- Xiao L. & Honig B.** (1999) Electrostatic contributions to the stability of hyperthermophilic proteins. *J. Mol. Biol.* **289**, 1435-44

8. Literatur

Yip K. S., Stillman T. J., Britton K. L., Artymiuk P. J., Baker P. J., Sedelnikova S. E., Engel P. C., Pasquo A., Chiaraluce R. & Consalvi V.(1995) The structure of *Pyrococcus furiosus* glutamate dehydrogenase reveals a key role for ion-pair networks in maintaining enzyme stability at extreme temperatures. *Structure*. **3**, 1147-1158

Yip K. S., Britton K. L., Stillman T. J., Lebbink J., de Vos W. M., Robb F. T., Vetriani C., Maeder D. & Rice D. W. (1998) Insights into the molecular basis of thermal stability from the analysis of ion-pair networks in the glutamate dehydrogenase family. *Eur. J. Biochem*. **255**, 336-346

Yu H., Rosen M. K., Shin T. B., Seidel-Dugan C., Brugge J. S. & Schreiber S. L. (1992) Solution structure of the SH3 domain of Src and identification of its ligand-binding site. *Science* **258**, 1665-1668

Zatyka M., Bingle L., Jones A. C. & Thomas C. M. (2001) Cooperativity between KorB and TrbA repressors of broad-host-range plasmid RK2. *J. Bacteriol*. **183**, 1022-1031

Zatyka M., Jagura-Burdzy G. & Thomas C. M. (1994) Regulation of transfer genes of promiscuous IncP alpha plasmid RK2: repression of Tra1 region transcription both by relaxosome proteins and by the Tra2 regulator TrbA. *Microbiology* **140**, 2981-2990

Zatyka M., Jagura-Burdzy G. & Thomas C. M. (1997) Transcriptional and translational control of the genes for the mating pair formation apparatus of promiscuous IncP plasmids. *J Bacteriol*. **179**, 7201-7209

Zhang K .Y .J. & Main P.(1990) Histogram Matching as a Density Modification Technique for Phase Refinement and Extension of Protein Molecules. *Acta Cryst*. **A46**, 41-46, 1990

Zhang K .Y .J. & Main P.(1990) The Use of Sayre's Equation with Solvent Flattening and Histogram Matching for Phase Refinement and Extension of Protein Structures. *Acta Cryst*. **A46**, 377-381

8.1. Veröffentlichungen

Publikationsliste

Delbrück H., Mueller U., Perl D., Schmid F. X. & Heinemann U. (2001) Crystal structures of mutant forms of the *Bacillus caldolyticus* cold shock protein differing in thermal stability. *J Mol Biol.* **313**, 359-369

Delbrück H., Ziegelin G., Lanka E. & Heinemann U. (2002) An Src homology 3-like domain is responsible for dimerization of the repressor protein KorB encoded by the promiscuous IncP plasmid RP4. *J Biol Chem.* **277**, 4191-4198.

PDB-Einträge

1IGQ KorB-C in P2₁2₁2₁

1IGU KorB-C in P6₅

1HZ9 *Bc*-Csp E46A

1HZA *Bc*-Csp V64T/L66E/67A

1HZB *Bc*-Csp L66E

1HZC *Bc*-Csp R3E/E46A/L66E

1KQ6 p47phox PX Domäne (in Kooperation mit Wahl M. & Oschkinat H., FMP Berlin)