

Appendix A - Literature

1. Bernasconi, C.F. (1976) Relaxation kinetics. *Academic Press, New York*.
2. Brunger, A.T. (1993) Assessment of phase accuracy by cross validation: the free R value. Methods and applications. *Acta Cryst D Biol.* **49**: 24-36.
3. Diederichs, K. and Karplus, P.A. (1997) Improved R -factors for diffraction data analysis in macromolecular crystallography. *Nat Struct Biol.* **4**: 269-75.
4. Dill, K.A. and Chan, H.S. (1997) From Levinthal to pathways to funnels. *Nat Struct Biol.* **4**: 10-9.
5. Pande, V.S., Grosberg, A., Tanaka, T., and Rokhsar, D.S. (1998) Pathways for protein folding: is a new view needed? *Curr Opin Struct Biol.* **8**: 68-79.
6. Zhang, J., Peng, X., Jonas, A., and Jonas, J. (1995) NMR study of the cold, heat, and pressure unfolding of ribonuclease A. *Biochemistry.* **34**: 8631-41.
7. Graumann, P.L. and Marahiel, M.A. (1998) A superfamily of proteins that contain the cold-shock domain. *Trends Biochem Sci.* **23**: 286-90.
8. Phadtare, S. and Inouye, M. (2004) Genome-wide transcriptional analysis of the cold shock response in wild-type and cold-sensitive, quadruple-csp-deletion strains of *Escherichia coli*. *J Bacteriol.* **186**: 7007-14.
9. Ermolaeva, M.D., Khalak, H.G., White, O., Smith, H.O., and Salzberg, S.L. (2000) Prediction of transcription terminators in bacterial genomes. *J Mol Biol.* **301**: 27-33.
10. Baker, N.A., Sept, D., Joseph, S., Holst, M.J., and McCammon, J.A. (2001) Electrostatics of nanosystems: application to microtubules and the ribosome. *Proc Natl Acad Sci U S A.* **98**: 10037-41.
11. Wunderlich, M., Martin, A., and Schmid, F.X. (2005) Stabilization of the cold shock protein CspB from *Bacillus subtilis* by evolutionary optimization of Coulombic interactions. *J Mol Biol.* **347**: 1063-76.
12. Lohman, T.M. and Bujalowski, W. (1991) Thermodynamic methods for model-independent determination of equilibrium binding isotherms for protein-DNA interactions: spectroscopic approaches to monitor binding. *Methods Enzymol.* **208**: 258-90.
13. Eftink, M.R. (1997) Fluorescence methods for studying equilibrium macromolecule-ligand interactions. *Methods Enzymol.* **278**: 221-57.
14. Zuker, M., Mathews, D.H., and Turner, D.H. (1999) Algorithms and thermodynamics for RNA secondary structure prediction: A practical guide in RNA biochemistry and biotechnology. *Kluwer Academic Publishers. NATO ASI Series.*
15. Vaguine, A.A., Richelle, J., and Wodak, S.J. (1999) SFCHECK: a unified set of procedures for evaluating the quality of macromolecular structure-factor data and their agreement with the atomic model. *Acta Cryst D Biol.* **55**: 191-205.
16. Schindler, T. and Schmid, F.X. (1996) Thermodynamic properties of an extremely rapid protein folding reaction. *Biochemistry.* **35**: 16833-42.
17. Perl, D., Holtermann, G., and Schmid, F.X. (2001) Role of the chain termini for the folding transition state of the cold shock protein. *Biochemistry.* **40**: 15501-11.
18. Kaan, T., Homuth, G., Mader, U., Bandow, J., and Schweder, T. (2002) Genome-wide transcriptional profiling of the *Bacillus subtilis* cold-shock response. *Microbiology.* **148**: 3441-55.

19. Beckering, C.L., Steil, L., Weber, M.H., Volker, U., and Marahiel, M.A. (2002) Genomewide transcriptional analysis of the cold shock response in *Bacillus subtilis*. *J Bacteriol.* **184**: 6395-402.
20. Graumann, P., Schroder, K., Schmid, R., and Marahiel, M.A. (1996) Cold shock stress-induced proteins in *Bacillus subtilis*. *J Bacteriol.* **178**: 4611-9.
21. Jaenicke, R. (1987) Folding and association of proteins. *Prog Biophys Mol Biol.* **49**: 117-237.
22. Anfinsen, C.B. (1973) Principles that govern the folding of protein chains. *Science.* **181**: 223-30.
23. Levinthal, C. (1968) Are there pathways for protein folding? *J. Chim. Phys.* **65**: 44-45.
24. Eaton, W.A., Munoz, V., Thompson, P.A., Chan, C.K., and Hofrichter, J. (1997) Sub-millisecond kinetics of protein folding. *Curr Opin Struct Biol.* **7**: 10-4.
25. Fink, A.L. (1999) Chaperone-mediated protein folding. *Physiol Rev.* **79**: 425-49.
26. Macario, A.J. and Conway De Macario, E. (2001) The molecular chaperone system and other anti-stress mechanisms in archaea. *Front Biosci.* **6**: D262-83.
27. Fink, A.L. (2005) Natively unfolded proteins. *Curr Opin Struct Biol.* **15**: 35-41.
28. Uversky, V.N., Gillespie, J.R., and Fink, A.L. (2000) Why are "natively unfolded" proteins unstructured under physiologic conditions? *Proteins.* **41**: 415-27.
29. Tsai, C.J., Maizel, J.V., Jr., and Nussinov, R. (2002) The hydrophobic effect: a new insight from cold denaturation and a two-state water structure. *Crit Rev Biochem Mol Biol.* **37**: 55-69.
30. Dobson, C.M. (1999) Protein misfolding, evolution and disease. *Trends Biochem Sci.* **24**: 329-32.
31. Blake, C. and Serpell, L. (1996) Synchrotron X-ray studies suggest that the core of the transthyretin amyloid fibril is a continuous beta-sheet helix. *Structure.* **4**: 989-98.
32. Blake, C.C., Serpell, L.C., Sunde, M., Sandgren, O., and Lundgren, E. (1996) A molecular model of the amyloid fibril. *Ciba Found Symp.* **199**: 6-15; discussion 15-21, 40-6.
33. Jimenez, J.L., Guijarro, J.I., Orlova, E., Zurdo, J., Dobson, C.M., Sunde, M., and Sambil, H.R. (1999) Cryo-electron microscopy structure of an SH3 amyloid fibril and model of the molecular packing. *EMBO J.* **18**: 815-21.
34. Sambashivan, S., Liu, Y., Sawaya, M.R., Gingery, M., and Eisenberg, D. (2005) Amyloid-like fibrils of ribonuclease A with three-dimensional domain-swapped and native-like structure. *Nature.* **437**: 266-9.
35. Felsenfeld, G. (1985) DNA. *Sci Am.* **253**: 58-67.
36. Darnell, J.E., Jr. (1985) RNA. *Sci Am.* **253**: 68-78.
37. Watson, J.D. and Crick, F.H. (1953) The structure of DNA. *Cold Spring Harb Symp Quant Biol.* **18**: 123-31.
38. Dickerson, R.E., Drew, H.R., Conner, B.N., Wing, R.M., Fratini, A.V., and Kopka, M.L. (1982) The anatomy of A-, B-, and Z-DNA. *Science.* **216**: 475-85.
39. Srinivasan, J., Miller, J., Kollman, P.A., and Case, D.A. (1998) Continuum solvent studies of the stability of RNA hairpin loops and helices. *J Biomol Struct Dyn.* **16**: 671-82.

40. Franklin, S.E. and Gosling, R.G. (1953) Molecular configuration in sodium thymonucleate. *Nature*. **171**: 740-1.
41. Wood, H.A. (1973) Viruses with double-stranded RNA genomes. *J Gen Virol*. **20**: Suppl:61-85.
42. Cech, T.R. (2002) Ribozymes, the first 20 years. *Biochem Soc Trans*. **30**: 1162-6.
43. Deming, J.W. (2002) Psychrophiles and polar regions. *Curr Opin Microbiol*. **5**: 301-9.
44. Kashefi, K. and Lovley, D.R. (2003) Extending the upper temperature limit for life. *Science*. **301**: 934.
45. Mansilla, M.C., Aguilar, P.S., Albanesi, D., Cybulski, L.E., Altabe, S., and de Mendoza, D. (2003) Regulation of fatty acid desaturation in *Bacillus subtilis*. *Prostaglandins Leukot Essent Fatty Acids*. **68**: 187-90.
46. Sajbidor, J. (1997) Effect of some environmental factors on the content and composition of microbial membrane lipids. *Crit Rev Biotechnol*. **17**: 87-103.
47. Chintalapati, S., Kiran, M.D., and Shivaji, S. (2004) Role of membrane lipid fatty acids in cold adaptation. *Cell Mol Biol (Noisy-le-grand)*. **50**: 631-42.
48. Yeagle, P.L. (1985) Cholesterol and the cell membrane. *Biochim Biophys Acta*. **822**: 267-87.
49. Delbruck, H., Mueller, U., Perl, D., Schmid, F.X., and Heinemann, U. (2001) Crystal structures of mutant forms of the *Bacillus caldolyticus* cold shock protein differing in thermal stability. *J Mol Biol*. **313**: 359-69.
50. Li, W.F., Zhou, X.X., and Lu, P. (2005) Structural features of thermozymes. *Biotechnol Adv*. **23**: 271-81.
51. Jaenicke, R. and Bohm, G. (1998) The stability of proteins in extreme environments. *Curr Opin Struct Biol*. **8**: 738-48.
52. D'Amico, S., Claverie, P., Collins, T., Georlette, D., Gratia, E., Hoyoux, A., Meuwis, M.A., Feller, G., and Gerday, C. (2002) Molecular basis of cold adaptation. *Philos Trans R Soc Lond B Biol Sci*. **357**: 917-25.
53. Zecchinon, L., et al. (2001) Did psychrophilic enzymes really win the challenge? *Extremophiles*. **5**: 313-21.
54. Georlette, D., et al. (2004) Some like it cold: biocatalysis at low temperatures. *FEMS Microbiol Rev*. **28**: 25-42.
55. Arsene, F., Tomoyasu, T., and Bukau, B. (2000) The heat shock response of *Escherichia coli*. *Int J Food Microbiol*. **55**: 3-9.
56. Panoff, J.M., Thammavongs, B., Gueguen, M., and Boutibonnes, P. (1998) Cold stress responses in mesophilic bacteria. *Cryobiology*. **36**: 75-83.
57. Jones, P.G., VanBogelen, R.A., and Neidhardt, F.C. (1987) Induction of proteins in response to low temperature in *Escherichia coli*. *J Bacteriol*. **169**: 2092-5.
58. Graumann, P.L. and Marahiel, M.A. (1999) Cold shock response in *Bacillus subtilis*. *J Mol Microbiol Biotechnol*. **1**: 203-9.
59. Jones, P.G. and Inouye, M. (1994) The cold-shock response--a hot topic. *Mol Microbiol*. **11**: 811-8.
60. Somero, G.N. (2004) Adaptation of enzymes to temperature: searching for basic "strategies". *Comp Biochem Physiol B Biochem Mol Biol*. **139**: 321-33.

61. Yancey, P.H. (2005) Organic osmolytes as compatible, metabolic and counteracting cytoprotectants in high osmolarity and other stresses. *J Exp Biol.* **208**: 2819-30.
62. Kaushik, J.K. and Bhat, R. (2003) Why is trehalose an exceptional protein stabilizer? An analysis of the thermal stability of proteins in the presence of the compatible osmolyte trehalose. *J Biol Chem.* **278**: 26458-65.
63. Graumann, P., Wendrich, T.M., Weber, M.H., Schroder, K., and 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**: 741-56.
64. Yamanaka, K., Fang, L., and Inouye, M. (1998) The CspA family in *Escherichia coli*: multiple gene duplication for stress adaptation. *Mol Microbiol.* **27**: 247-55.
65. Graumann, P.L. and Marahiel, M.A. (1999) Cold shock proteins CspB and CspC are major stationary-phase-induced proteins in *Bacillus subtilis*. *Arch Microbiol.* **171**: 135-8.
66. Gualerzi, C.O., Giuliodori, A.M., and Pon, C.L. (2003) Transcriptional and post-transcriptional control of cold-shock genes. *J Mol Biol.* **331**: 527-39.
67. Ermolenko, D.N. and Makhatadze, G.I. (2002) Bacterial cold-shock proteins. *Cell Mol Life Sci.* **59**: 1902-13.
68. Graumann, P. and 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**: 745-52.
69. Lopez, M.M., Yutani, K., and Makhatadze, G.I. (1999) Interactions of the major cold shock protein of *Bacillus subtilis* CspB with single-stranded DNA templates of different base composition. *J Biol Chem.* **274**: 33601-8.
70. Lopez, M.M. and Makhatadze, G.I. (2000) Major cold shock proteins, CspA from *Escherichia coli* and CspB from *Bacillus subtilis*, interact differently with single-stranded DNA templates. *Biochim Biophys Acta.* **1479**: 196-202.
71. Lopez, M.M., Yutani, K., and Makhatadze, G.I. (2001) Interactions of the cold shock protein CspB from *Bacillus subtilis* with single-stranded DNA. Importance of the T base content and position within the template. *J Biol Chem.* **276**: 15511-8.
72. Jiang, W., Hou, Y., and Inouye, M. (1997) CspA, the major cold-shock protein of *Escherichia coli*, is an RNA chaperone. *J Biol Chem.* **272**: 196-202.
73. Hofweber, R., Horn, G., Langmann, T., Balbach, J., Kremer, W., Schmitz, G., and Kalbitzer, H.R. (2005) The influence of cold shock proteins on transcription and translation studied in cell-free model systems. *Febs J.* **272**: 4691-702.
74. Bae, W., Xia, B., Inouye, M., and Severinov, K. (2000) *Escherichia coli* CspA-family RNA chaperones are transcription antiterminators. *Proc Natl Acad Sci U S A.* **97**: 7784-9.
75. Schindelin, H., Marahiel, M.A., and Heinemann, U. (1993) Universal nucleic acid-binding domain revealed by crystal structure of the *B. subtilis* major cold-shock protein. *Nature.* **364**: 164-8.
76. Schindelin, H., Jiang, W., Inouye, M., and Heinemann, U. (1994) Crystal structure of CspA, the major cold shock protein of *Escherichia coli*. *Proc Natl Acad Sci U S A.* **91**: 5119-23.

77. Mueller, U., Perl, D., Schmid, F.X., and Heinemann, U. (2000) Thermal stability and atomic-resolution crystal structure of the *Bacillus caldolyticus* cold shock protein. *J Mol Biol.* **297**: 975-88.
78. Schnuchel, A., Wiltscheck, R., Czisch, M., Herrler, M., Willimsky, G., Graumann, P., Marahiel, M.A., and Holak, T.A. (1993) Structure in solution of the major cold-shock protein from *Bacillus subtilis*. *Nature.* **364**: 169-71.
79. Kremer, W., Schuler, B., Harrieder, S., Geyer, M., Gronwald, W., Welker, C., Jaenicke, R., and Kalbitzer, H.R. (2001) Solution NMR structure of the cold-shock protein from the hyperthermophilic bacterium *Thermotoga maritima*. *Eur J Biochem.* **268**: 2527-39.
80. Agrawal, V. and Kishan, K.V. (2003) OB-fold: growing bigger with functional consistency. *Curr Protein Pept Sci.* **4**: 195-206.
81. Schindler, T., Perl, D., Graumann, P., Sieber, V., Marahiel, M.A., and Schmid, F.X. (1998) Surface-exposed phenylalanines in the RNP1/RNP2 motif stabilize the cold-shock protein CspB from *Bacillus subtilis*. *Proteins.* **30**: 401-6.
82. Schroder, K., Graumann, P., Schnuchel, A., Holak, T.A., and 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.
83. Messias, A.C. and Sattler, M. (2004) Structural basis of single-stranded RNA recognition. *Acc Chem Res.* **37**: 279-87.
84. Zeeb, M. and Balbach, J. (2003) Single-stranded DNA binding of the cold-shock protein CspB from *Bacillus subtilis*: NMR mapping and mutational characterization. *Protein Sci.* **12**: 112-23.
85. Wolffe, A.P., Tafuri, S., Ranjan, M., and Familiari, M. (1992) The Y-box factors: a family of nucleic acid binding proteins conserved from *Escherichia coli* to man. *New Biol.* **4**: 290-8.
86. Graumann, P. and 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**: 157-60.
87. Matsumoto, K. and Wolffe, A.P. (1998) Gene regulation by Y-box proteins: coupling control of transcription and translation. *Trends Cell Biol.* **8**: 318-23.
88. Matsumoto, K., Tanaka, K.J., and Tsujimoto, M. (2005) An acidic protein, YBAP1, mediates the release of YB-1 from mRNA and relieves the translational repression activity of YB-1. *Mol Cell Biol.* **25**: 1779-92.
89. Schindler, T., Herrler, M., Marahiel, M.A., and Schmid, F.X. (1995) Extremely rapid protein folding in the absence of intermediates. *Nat Struct Biol.* **2**: 663-73.
90. Magg, C. and Schmid, F.X. (2004) Rapid collapse precedes the fast two-state folding of the cold shock protein. *J Mol Biol.* **335**: 1309-23.
91. Perl, D., Mueller, U., Heinemann, U., and Schmid, F.X. (2000) Two exposed amino acid residues confer thermostability on a cold shock protein. *Nat Struct Biol.* **7**: 380-3.
92. Perl, D. and Schmid, F.X. (2001) Electrostatic stabilization of a thermophilic cold shock protein. *J Mol Biol.* **313**: 343-57.
93. Alexandrescu, A.T. and Rathgeb-Szabo, K. (1999) An NMR investigation of solution aggregation reactions preceding the misassembly of acid-denatured cold shock protein A into fibrils. *J Mol Biol.* **291**: 1191-206.

94. Garcia-Mira, M.M., Boehringer, D., and Schmid, F.X. (2004) The folding transition state of the cold shock protein is strongly polarized. *J Mol Biol.* **339**: 555-69.
95. Sambrook, J. and Russell, D.W. (2001) Molecular Cloning. *Cold Spring Harbor, New York.*
96. Schagger, H. and von Jagow, G. (1987) Tricine-sodium dodecyl sulfate-polyacrylamide gel electrophoresis for the separation of proteins in the range from 1 to 100 kDa. *Anal Biochem.* **166**: 368-79.
97. Laemmli, U.K. (1970) Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature.* **227**: 680-5.
98. Nesterenko, M.V., Tilley, M., and Upton, S.J. (1994) A simple modification of Blum's silver stain method allows for 30 minute detection of proteins in polyacrylamide gels. *J Biochem Biophys Methods.* **28**: 239-42.
99. Wang, W. and Malcolm, B.A. (1999) Two-stage PCR protocol allowing introduction of multiple mutations, deletions and insertions using QuikChange Site-Directed Mutagenesis. *Biotechniques.* **26**: 680-2.
100. 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**: 248-54.
101. Wilkins, M.R., Gasteiger, E., Bairoch, A., Sanchez, J.C., Williams, K.L., Appel, R.D., and Hochstrasser, D.F. (1999) Protein identification and analysis tools in the ExPASy server. *Methods Mol Biol.* **112**: 531-52.
102. Gill, S.C. and von Hippel, P.H. (1989) Calculation of protein extinction coefficients from amino acid sequence data. *Anal Biochem.* **182**: 319-26.
103. Pace, C.N., Vajdos, F., Fee, L., Grimsley, G., and Gray, T. (1995) How to measure and predict the molar absorption coefficient of a protein. *Protein Sci.* **4**: 2411-23.
104. Wallace, R.B. and Miyada, C.G. (1987) Oligonucleotide probes for the screening of recombinant DNA libraries. *Methods Enzymol.* **152**: 432-42.
105. Behlke, J., Ristau, O., and Schonfeld, H.J. (1997) Nucleotide-dependent complex formation between the Escherichia coli chaperonins GroEL and GroES studied under equilibrium conditions. *Biochemistry.* **36**: 5149-56.
106. Drenth, J. (1999) Principles of X-ray crystallography. *Springer Press.* **second edition.**
107. Rhodes, G. (2006) Crystallography made crystal clear. *Academic Press.* **third edition.**
108. Carter, C.W., Jr. and Carter, C.W. (1979) Protein crystallization using incomplete factorial experiments. *J Biol Chem.* **254**: 12219-23.
109. Jancarik, J., Scott, W.G., Milligan, D.L., Koshland, D.E., Jr., and Kim, S.H. (1991) Crystallization and preliminary X-ray diffraction study of the ligand-binding domain of the bacterial chemotaxis-mediating aspartate receptor of *Salmonella typhimurium*. *J Mol Biol.* **221**: 31-4.
110. Heinemann, U., Bussow, K., Mueller, U., and Umbach, P. (2003) Facilities and methods for the high-throughput crystal structural analysis of human proteins. *Acc Chem Res.* **36**: 157-63.
111. Deshpande, N., et al. (2005) The RCSB Protein Data Bank: a redesigned query system and relational database based on the mmCIF schema. *Nucleic Acids Res.* **33**: D233-7.

112. Jelsch, C., Teeter, M.M., Lamzin, V., Pichon-Pesme, V., Blessing, R.H., and Lecomte, C. (2000) Accurate protein crystallography at ultra-high resolution: valence electron distribution in crambin. *Proc Natl Acad Sci U S A*. **97**: 3171-6.
113. Kabsch, W. (1993) Automatic processing of rotation diffraction data from crystals of initially unknown symmetry and cell constants. *J Appl Crystallogr*. **26**: 795-800.
114. (1994) The CCP4 suite: programs for protein crystallography. *Acta Cryst D Biol*. **50**: 760-3.
115. Rossmann, M.G. and Blow, D.M. (1962) The detection of sub-units within the crystallographic asymmetric unit. *Acta Cryst*. **15**: 24-31.
116. Navaza, J. (2001) Implementation of molecular replacement in AMoRe. *Acta Cryst D Biol*. **57**: 1367-72.
117. Jones, T.A., Zou, J.Y., Cowan, S.W., and Kjeldgaard (1991) Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Cryst A*. **47**: 110-9.
118. Kleywegt, G.J. and Jones, T.A. (1996) xdlMAPMAN and xdlDATAMAN - programs for reformatting, analysis and manipulation of biomacromolecular electron-density maps and reflection data sets. *Acta Cryst D Biol*. **52**: 826-8.
119. Kini, R.M. and Evans, H.J. (1991) Molecular modeling of proteins: a strategy for energy minimization by molecular mechanics in the AMBER force field. *J Biomol Struct Dyn*. **9**: 475-88.
120. Winn, M.D., Isupov, M.N., and Murshudov, G.N. (2001) Use of TLS parameters to model anisotropic displacements in macromolecular refinement. *Acta Cryst D Biol*. **57**: 122-133.
121. Murshudov, G.N., Vagin, A.A., and Dodson, E.J. (1997) Refinement of macromolecular structures by the maximum-likelihood method. *Acta Cryst D Biol*. **53**: 240-55.
122. Lamzin, V.S., Perrakis, A., and Wilson, K.S. (2001) The ARP/wARP suite for automated construction and refinement of protein models. *International Tables for Crystallography*. **Vol F**: 720 - 722.
123. Luzzati, V. (1952) Traitement statistique des erreurs dans la détermination des structures cristallines. *Acta Cryst*. **5**: 802-810.
124. Branden C. I. and A., J.T. (1990) Between objectivity and subjectivity. *Nature*. **343**: 687-689.
125. Engh, R.A. and Huber, R. (1991) Accurate bond and angle parameters for X-ray protein structure refinement. *Acta Cryst A*. **47**: 392-400.
126. Ramachandran, G.N., Ramakrishnan, C., and Sasisekharan, V. (1963) Stereochemistry of polypeptide chain configurations. *J Mol Biol*. **7**: 95-9.
127. Morris, A.L., MacArthur, M.W., Hutchinson, E.G., and Thornton, J.M. (1992) Stereochemical quality of protein structure coordinates. *Proteins*. **12**: 345-64.
128. Vriend, G. (1990) WHAT IF: a molecular modeling and drug design program. *J Mol Graph*. **8**: 52-6, 29.
129. Laskowski R. A., MacArthur M. W., S., M.D., and M., T.J. (1993) PROCHECK: a program to check the stereochemical quality of protein structures. *J. Appl. Cryst*. **26**: 283-291.
130. Hoof, R.W., Vriend, G., Sander, C., and Abola, E.E. (1996) Errors in protein structures. *Nature*. **381**: 272.

131. DeLano, W.L. (2003) The PyMOL Molecular Graphics System. DeLano Scientific LLC, San Carlos, CA, USA. <http://www.pymol.org>.
132. Zeeb, M., Max, K.E.A., Weininger, U., Löw, C., Sticht, H., and Balbach, J. (2006) Recognition of T-rich single-stranded DNA by the cold shock protein *Bs*-CspB in solution. *Nucl. Acids. Res.* **in press**.
133. Theobald, D.L., Mitton-Fry, R.M., and Wuttke, D.S. (2003) Nucleic acid recognition by OB-fold proteins. *Annu Rev Biophys Biomol Struct.* **32**: 115-33.
134. Levitt, M. and Warshel, A. (1978) Extreme conformational flexibility of the furanose ring in DNA and RNA. *J Amer Chem Soc.* **100**: 2607-2613.
135. de Leeuw, H.P.M., Haasnoot, C.A.G., and Altona, C. (1980) Empirical correlations between conformational parameters in β -D-furanoside fragments derived from a statistical survey of crystal structures of nucleic acid constituents. Full description of nucleoside molecular geometries in terms of four parameters. *Isr J Chem.* **20**: 108 - 126.
136. Zeeb, M., Jacob, M.H., Schindler, T., and Balbach, J. (2003) ¹⁵N relaxation study of the cold shock protein CspB at various solvent viscosities. *J Biomol NMR.* **27**: 221-34.
137. Michelson, A.M. (1961) Chemistry of the nucleotides. *Ann Rev Biochem.* **30**: 133-164.
138. Jones, P.G., Krah, R., Tafuri, S.R., and Wolffe, A.P. (1992) DNA gyrase, CS7.4, and the cold shock response in *Escherichia coli*. *J Bacteriol.* **174**: 5798-802.
139. Sands, J.F., Regnier, P., Cummings, H.S., Grunberg-Manago, M., and Hershey, J.W. (1988) The existence of two genes between *infB* and *rpsO* in the *Escherichia coli* genome: DNA sequencing and S1 nuclease mapping. *Nucleic Acids Res.* **16**: 10803-16.
140. Xia, B., Ke, H., and Inouye, M. (2001) Acquisition of cold sensitivity by quadruple deletion of the *cspA* family and its suppression by PNPase S1 domain in *Escherichia coli*. *Mol Microbiol.* **40**: 179-88.
141. Phadtare, S. and Inouye, M. (1999) Sequence-selective interactions with RNA by CspB, CspC and CspE, members of the CspA family of *Escherichia coli*. *Mol Microbiol.* **33**: 1004-14.
142. Gross, M., Wilkins, D.K., Pitkeathly, M.C., Chung, E.W., Higham, C., Clark, A., and Dobson, C.M. (1999) Formation of amyloid fibrils by peptides derived from the bacterial cold shock protein CspB. *Protein Sci.* **8**: 1350-7.
143. Wilkins, D.K., Dobson, C.M., and Gross, M. (2000) Biophysical studies of the development of amyloid fibrils from a peptide fragment of cold shock protein B. *Eur J Biochem.* **267**: 2609-16.
144. Max, K.E.A., Zeeb, M., Bienert, R., Balbach, J., and Heinemann, U. (2006) T-rich DNA single strands bind to a preformed site on the bacterial cold shock protein *Bs*-CspB. *J Mol Biol.* **360**: 702-14.
145. Dominy, B.N., Perl, D., Schmid, F.X., and Brooks, C.L., 3rd (2002) The effects of ionic strength on protein stability: the cold shock protein family. *J Mol Biol.* **319**: 541-54.
146. Zhou, H.X. and Dong, F. (2003) Electrostatic contributions to the stability of a thermophilic cold shock protein. *Biophys J.* **84**: 2216-22.
147. Perez-Jimenez, R., Godoy-Ruiz, R., Ibarra-Molero, B., and Sanchez-Ruiz, J.M. (2004) The efficiency of different salts to screen charge interactions in proteins: a Hofmeister effect? *Biophys J.* **86**: 2414-29.

148. Wassenberg, D., Welker, C., and Jaenicke, R. (1999) Thermodynamics of the unfolding of the cold-shock protein from *Thermotoga maritima*. *J Mol Biol.* **289**: 187-93.
149. Malakauskas, S.M. and Mayo, S.L. (1998) Design, structure and stability of a hyperthermophilic protein variant. *Nat Struct Biol.* **5**: 470-5.
150. Wunderlich, M., Martin, A., Staab, C.A., and Schmid, F.X. (2005) Evolutionary protein stabilization in comparison with computational design. *J Mol Biol.* **351**: 1160-8.
151. Wang, Q., Buckle, A.M., Foster, N.W., Johnson, C.M., and Fersht, A.R. (1999) Design of highly stable functional GroEL minichaperones. *Protein Sci.* **8**: 2186-93.

