

11. References

11.1. Cited References

- Andrade, M. A., Chacon, P., Merelo, J. J. & Moran, F. (1993). Evaluation of secondary structure of proteins from UV circular dichroism spectra using an unsupervised learning neural network. *Protein Eng.* **6**, 383-390.
- Bass, B. L. (1997). RNA editing and hypermutation by adenosine deamination. *Trends Biochem. Sci.* **22**, 157-162.
- Berger, I., Winston, W., Manoharan, R., Schwartz, T., Alfken, J., Kim, Y. G., Lowenhaupt, K., Herbert, A. & Rich, A. (1998). Spectroscopic characterization of a DNA-binding domain, Z α , from the editing enzyme, dsRNA adenosine deaminase: Evidence for left-handed Z-DNA in the Z α -DNA complex. *Biochemistry* **37**, 13313-13321.
- Brusa, R., Zimmermann, F., Koh, D.-S., Feldmeyer, D., Gass, P., Seeburg, P.H. & Sprengel, R. (1995). Early-onset epilepsy and postnatal lethality associated with an editing-deficient GluR-B allele in mice. *Science* **270**, 1677-1680.
- Burley, S. K. & Petsko, G. A. (1988). Weakly polar interactions in proteins. *Adv. Prot. Chem.* **39**, 125-189.
- Burns, C. M., Chu, H., Rueter, S. M., Hutchinson, L. K., Canton, H., Sanders-Bush, E. & Emeson, R. B. (1997). Regulation of serotonin-2C receptor G-protein coupling by RNA editing. *Nature* **387**, 303-308.
- Bragg, W. L., (1913). The diffraction of short electromagnetic waves by a crystal. *Proc. Camb. Phil. Soc.* **17**, 43-57.
- Brünger, A. T. (1992a). *X-PLOR Version 3.1. A System for X-ray Crystallography and NMR*, Yale Univ. Press, New Haven and London.

- Brünger, A. T. (1992b). The free R value: A novel statistical quantity for assessing the accuracy of crystal structures. *Nature* **355**, 472-474.
- Carter, C.W. Jr. & Carter, C. W. (1979). Protein crystallization using incomplete factorial experiments. *J. Biol. Chem.* **254**, 12219-12223.
- Carugo, O. & Bordo, D. (1998). How many water molecules can be detected by protein crystallography? *Acta Cryst. D* **55**, 479-483.
- Cattaneo, R. (1994). Biased (A--->I) hypermutation of animal RNA virus genomes. *Curr. Opin. Genet. Dev.* **4**, 895-900.
- Chan, S. K. & Struhl, G. (1997). Sequence-specific RNA binding by bicoid. *Nature* **388**, 634.
- Chang, H. W. & Jacobs, B. L. (1993). Identification of a conserved motif that is necessary for binding of the *Vaccinia* virus E3L gene products to double-stranded RNA. *Virology* **194**, 537-547.
- Clark, K. L., Halay, E. D., Lai, E. & Burley, S. K. (1993). Co-crystal structure of the HNF-3/fork head DNA-recognition motif resembles histone H5. *Nature* **364**, 412-420.
- Collaborative Computational Project, Number 4 (1994). The CCP4 suite: Programs for protein crystallography. *Acta Cryst. D* **50**, 760-763.
- Conn, G. L., Draper, D. E., Lattman, E. E. & Gittis, A. G. (1999). Crystal structure of a conserved ribosomal protein-RNA complex. *Science* **284**, 1171-1174.
- Cook, W. J., Kar, S. R., Taylor, K. B. & Hall, L. M. (1998). Crystal structure of the cyanobacterial metallothionein repressor SmtB: a model for metalloregulatory proteins. *J. Mol. Biol.* **275**, 337-346.

- Cowtan, K. & Main, P. (1998). Miscellaneous algorithms for density modification. *Acta Cryst. D* **54**, 487-493.
- Draper, D. E. & Reynaldo, L. P. (1999). RNA binding strategies of ribosomal proteins. *Nucleic Acids Res* **27**, 381-388.
- Engh, R. A., Huber, R. (1991). Accurate bond and angle parameters for X-ray protein-structure refinement. *Acta Cryst. A* **47**, 392-400.
- Esnouf, R. M. (1997). An extensively modified version of MolScript that includes greatly enhanced coloring capabilities. *J. Mol. Graphics* **15**, 132-134.
- George, C. X. & Samuel, C. E. (1999). Characterization of the 5'-flanking region of the human RNA-specific adenosine deaminase ADAR1 gene and identification of an interferon-inducible ADAR1 promoter. *Gene* **229**, 203-213.
- Gessner, R. V., Frederick, C. A., Quigley, G. J., Rich, A. & Wang, A. H.-J. (1989). The molecular structure of the left-handed Z-DNA double helix at 1.0-Å atomic resolution. Geometry, conformation, and ionic interactions of d(CGCGCG). *J.Biol. Chem* **264**, 7921-7935.
- Hanahan, D. (1983). Studies on transformation of *Escherichia coli* with plasmids. *J. Mol. Biol.* **166**, 557-580.
- Harrison, S. C. & Aggarwal, A. K. (1990). DNA recognition by proteins with the helix-turn-helix motif. *Annu. Rev. Biochem.* **59**, 933-969.
- Herbert, A. G., Spitzner, J. R., Lowenhaupt, K. & Rich, A. (1993a). Z-DNA binding protein from chicken blood nuclei. *Proc. Natl. Acad. Sci. U. S. A.* **90**, 3339-3342.
- Herbert, A. G. & Rich, A. (1993b). A method to identify and characterize Z-DNA binding proteins using a linear oligodeoxynucleotide. *Nucleic Acids Res.* **21**, 2669-2672.

- Herbert, A., Lowenhaupt, K., Spitzner, J. & Rich, A. (1995). Chicken double-stranded RNA adenosine deaminase has apparent specificity for Z-DNA. *Proc. Natl. Acad. Sci. U.S.A.* **92**, 7550-7554.
- Herbert, A. & Rich, A. (1996). The biology of left-handed Z-DNA. *J. Biol. Chem.* **271**, 11595-11598.
- Herbert, A., Alfken, J., Kim, Y. G., Mian, I. S., Nishikura, K. & Rich, A. (1997). A Z-DNA binding domain present in the human editing enzyme, double-stranded RNA adenosine deaminase. *Proc. Natl. Acad. Sci. U.S.A.* **94**, 8421-8426.
- Herbert, A., Schade, M., Lowenhaupt, K., Alfken, J., Schwartz, T., Shlyakhtenko, L. S., Lyubchenko, Y. L. & Rich, A. (1998). The Z α domain from human ADAR1 binds to the Z-DNA conformer of many different sequences. *Nucleic Acids Res.* **26**, 3486-3493.
- Holm, L. & Sander, C. (1995). Dali: a network tool for protein structure comparison. *Trends Biochem. Sci.* **20**, 478-480.
- Jovin, T. M., Geisler, N. & Weber, K. (1977). Amino-terminal fragments of *Escherichia coli* lac repressor bind to DNA. *Nature* **269**, 668-672.
- Kraulis, P. J. (1991). MOLSCRIPT: A program to produce both detailed and schematic plots of protein structures. *J. Appl. Cryst.* **24**, 946-950.
- Kumar, M. & Carmichael, G. G. (1997). Nuclear antisense RNA induces extensive adenosine modifications and nuclear retention of target transcripts. *Proc. Natl. Acad. Sci. U.S.A.* **94**, 3542-3547.
- Lane, D., Prentki, P. & Chandler, M. (1992). Use of gel retardation to analyze protein-nucleic acid interactions. *Microbiol. Rev.* **56**, 509-528.
- Lilley, D. M. J. (1995). *DNA-Protein: Structural Interactions*, Oxford University Press, Oxford.

- Liu, L. F. & Wang, J. C. (1987). Supercoiling of the DNA template during transcription. *Proc. Natl. Acad. Sci. U. S. A.* **84**, 7024-7027.
- Liu, Y., George, C. X., Patterson, J. B. & Samuel, C.E. (1997). Functionally distinct double-stranded RNA-binding domains associated with alternative splice site variants of the interferon-inducible double-stranded RNA-specific adenosine deaminase. *J. Biol. Chem.* **272**, 4419-4428.
- Lomeli, H., Mosbacher, J., Melcher, T., Hoger, T., Geiger, J. R., Kuner, T., Monyer, H., Higuchi, M., Bach, A. & Seburg, P. H. (1994). Control of kinetic properties of AMPA receptor channels by nuclear RNA editing. *Science* **266**, 1709-1713.
- Maas, S., Melcher, T. & Seburg, P. H. (1997). Mammalian RNA-dependent deaminases and edited mRNAs. *Curr. Opin. Cell Biol.* **9**, 343-349.
- Makrides, S. C. (1996). Strategies for achieving high-level expression in *Escherichia coli*. *Microbiol. Rev.* **60**, 512-538.
- Malfoy, B., Rousseau, N. & Leng, M. (1982). Interaction between antibodies to Z-form deoxyribonucleic acid and double-stranded polynucleotides. *Biochemistry* **21**, 5463-5467.
- Matthews, B. W. (1988). Protein-DNA interaction. No code for recognition. *Nature* **335**, 294-295.
- McPherson, A. (1998). *Crystallization of Biological Macromolecules*. Cold Spring Harbor Laboratory Press, New York.
- Melcher, T., Maas, S., Herb, A., Sprengel, R., Seburg, P. H. & Higuchi, M. (1996a). A mammalian RNA editing enzyme. *Nature* **379**, 460-464.

- Melcher, T., Maas, S., Herb, A., Sprengel, R. & Seeburg, P. H. (1996b). RED2, a brain specific member of the RNA specific adenosine deaminase family. *J. Biol. Chem.* **271**, 31795-31798.
- Merritt, E. A. & Murphy, E. P. (1994). Raster3D version 2.0 – a program for photorealistic molecular graphics. *Acta Cryst. D* **50**, 869-873.
- Nakagawa, N, Masui, R., Kato, R. & Kuramitsu, S. (1997). Domain structure of *Thermus thermophilus* UvrB protein. *J. Biol. Chem.* **272**, 22703-22713.
- 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.
- Otwinowski, Z. & Minor, W. (1997). Denzo/Scalepack. *Meth Enz* **276A**, 307-326.
- Pabo, C. O. & Sauer, R. T. (1984). Protein-DNA recognition. *Annu. Rev. Biochem.* **53**, 293-321.
- Pabo, C. O. & Sauer, R. T. (1992). Transcription factors: structural families and principles of DNA recognition. *Annu. Rev. Biochem.* **61**, 1053-1095.
- Passner, J. M., Ryoo, H. D., Shen, L., Mann, R. S. & Aggarwal, A. K. (1999). Structure of a DNA-bound ultrabithorax-extradenticle homeodomain complex. *Nature* **397**, 714-719.
- Peck, L. J., Nordheim, A., Rich, A. & Wang, J. C. (1982). Flipping of cloned d(pCpG)_n•d(pCpG)_n DNA sequences from right- to left-handed helical structure by salt, Co(III), or negative supercoiling. *Proc. Natl. Acad. Sci. U. S. A.* **79**, 4560-4564.
- Piper, D. E., Batchelor, A. H., Chang, C. P. , Cleary, M. L. & Wolberger, C. (1999). Structure of a HoxB1-Pbx1 heterodimer bound to DNA: role of the hexapeptide and a fourth homeodomain helix in complex formation. *Cell* **96**, 587-597.

- Pohl, F. M. & Jovin, T. M. (1972). Salt-induced co-operative conformational change of a synthetic DNA: Equilibrium and kinetic studies with poly d(G-C). *J. Mol. Biol.* **67**, 375-396.
- Polson, A. G., Bass, B. L. & Casey, J. L. (1996). RNA editing of hepatitis delta virus antigenome by dsRNA-adenosine deaminase. *Nature* **380**, 454-456.
- Porter, R. R. (1973). Structural studies of immunoglobulins. *Science* **180**, 713-716.
- Riazance-Lawrence, J. H. & Johnson, W. C. Jr. (1992). Multivalent ions are necessary for poly[d(AC) • d(GT)] to assume the Z form: a CD study. *Biopolymers* **32**, 271-276.
- Rich, A., Nordheim, A. & Wang, A. H.-J. (1984). The chemistry and biology of left-handed Z-DNA. *Ann. Rev. Biochem.* **53**, 791-846.
- Rich, A. (1993). DNA comes in many forms. *Gene* **135**, 99-109.
- Rost, B., & Sander, C. (1994). Combining evolutionary information and neural networks to predict protein secondary structure. *Proteins* **19**, 55-72.
- 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.
- Sambrook, J., Fritsch, E. F. & Maniatis, T. (1989). *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
- Schade, M., Turner, C. J., Lowenhaupt, K., Rich, A. & Herbert, A. (1999). Structure-function analysis of the Z-DNA-binding domain Z α of dsRNA adenosine deaminase type I reveals similarity to the ($\alpha + \beta$) family of helix-turn-helix proteins. *EMBO J.* **18**, 470-479.

- Schroth, G. P., Kagawa, T. F. & Ho, P. S. (1993). Structure and thermodynamics of non-alternating C/G base pairs in Z-DNA: The 1.3 Ångstroms crystal structure of the asymmetric hexanucleotide d(m(5)CGGGm(5)CG /d(m(5)CGCCm(5)CG). *Biochemistry* **32**, 13381-13392.
- Schulz, G. & Schirmer, R. (1979). *Principles of Protein Structure*. Springer-Verlag New York Inc., New York.
- Schultz, S. C., Shields, G. C. & 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. & Rich, A. (1976). Sequence-specific recognition of double helical nucleic acids by proteins. *Proc. Natl. Acad. Sci. U. S. A.* **73**, 804-808.
- Sommer, B., Köhler, M., Sprengel, R. & Seuberg, P. H. (1991). RNA editing in brain controls a determinant of ion flow in glutamate-gated channels. *Cell* **67**, 11-19.
- Tal, M., Silberstein, A. & Nusser, E. (1985). Why does Coomassie Brilliant Blue R interact differently with different proteins ? A partial answer. *J. Biol. Chem.* **260**, 9976-9980.
- Terwilliger, T. C. & Berendzen, J. (1996). Correlated phasing of multiple isomorphous replacement data. *Acta Cryst. D* **52**, 749-757.
- Wah, D. A., Hirsch, J. A., Dorner, L. F., Schildkraut, I. & Aggarwal, A. K. (1997). Structure of the multimodular endonuclease FokI bound to DNA. *Nature* **388**, 97-100.
- Wang, A. H.-J., Gessner, R. V., van der Marel, G. A., van Boom, J. H. & Rich, A. (1985). Crystal structure of Z-DNA without an alternating purine-pyrimidine sequence. *Proc. Natl. Acad. Sci. U. S. A.* **82**, 3611-3615.

- Wang, A. H.-J., Quigley, G. J., Kolpak, F. J., Crawford, J. L., van Boom, J. H., van der Marel, G. & Rich, A. (1979). Molecular structure of a left-handed double helical DNA fragment at atomic resolution. *Nature* **282**, 680-686.
- Wang, A. H.-J., Quigley, G. J., Kolpak, F. J., van der Marel, G., van Boom, J. H. & Rich, A. (1981). Left-handed double helical DNA: variations in the backbone conformation. *Science* **211**, 171-176.
- Watson, J. D. & Crick, F. H. C. (1953). A structure for deoxyribose nucleic acids. *Nature* **171**, 727-738.
- Wilkinson, D. L. & Harrison, R. G. (1991). Predicting the solubility of recombinant proteins in *Escherichia coli*. *Biotechnology* **9**, 443-448.
- Wimberly, B. T., Guymon, R., Cutcheon, J. P., White, S. W. & Ramakrishnan, V. (1999). A detailed view of a ribosomal active site: The structure of the L11-RNA complex. *Cell* **97**, 491-502.
- Wintjens, R. & Rooman, M. (1996). Structural classification of HTH DNA-binding domains and protein-DNA interaction modes. *J. Mol. Biol.* **62**, 294-313.
- Wittig, B., Wolf, S., Dörbic, T., Vahrson, W. & Rich, A. (1992). Transcription of human c-myc in permeabilized nuclei is associated with formation of Z-DNA in three discrete regions of the gene. *EMBO J.* **11**, 4653-4663.
- Xu, H. E., Rould, M. A., Xu, W., Epstein, J. A., Maas, R. L., & Pabo, C. O. (1999). Crystal structure of the human Pax6 paired domain-DNA complex reveals specific roles for the linker region and carboxy-terminal subdomain in DNA binding, *Genes Dev.* **13**, 1263-1275.
- Zheng, N., Fraenkel, F. E., Pabo, C. O. & Pavletich, N. P. (1999). Structural basis of DNA recognition by the heterodimeric cell cycle transcription factor E2F-DP, *Genes Dev.* **13**, 666-674.

11.2. List of Publications

Schwartz, T., Rould, M. A., Lowenhaupt, K., Herbert, A. & Rich, A. (1999). Crystal Structure of the Z α Domain of the Human Editing Enzyme ADAR1 Bound to Left-Handed Z-DNA. *Science* **284**, 1841-1845.

Schwartz, T., Shafer, K., Lowenhaupt, K., Hanlon, E., Herbert, A. & Rich, A. (1999). Crystallization and preliminary studies of the DNA-binding domain Za from ADAR1 complexed to left-handed DNA, *Acta Cryst. D55*, 1362-1364.

Schwartz, T., Lowenhaupt, K., Kim, Y.-G., Li, L., Brown, B. A. 2nd, Herbert, A. & Rich, A. (1999). Proteolytic dissection of Zab, the Z-DNA binding domain of human ADAR1. *J. Biol. Chem.* **274**, 2899-2906.

Kim, Y.-G., Lowenhaupt, K., Schwartz, T. & Rich, A. (1999). The interaction between Z-DNA and the Zab domain of dsRNA adenosine deaminase characterized using fusion nucleases. *J. Biol. Chem.* **274**, 19081-19086.

Berger, I., Winston, W., Manoharan, R., Schwartz, T., Alfken, J., Kim, Y.-G., Lowenhaupt, K., Herbert, A. & Rich, A. (1998). Spectroscopic characterization of a DNA-binding domain, Z α , from the editing enzyme, dsRNA adenosine deaminase: Evidence for left-handed Z-DNA in the Z α -DNA complex. *Biochemistry*, **37**, 13313-13321.

Herbert, A., Schade, M., Lowenhaupt, K., Alfken, J., Schwartz, T., Shylakhtenko, L. S., Lyubchenko, Y. L. & Rich, A. (1998). The Z α domain from human ADAR1 binds to the Z-DNA conformer of many different sequences. *Nucleic Acids Res.* **26**, 3483-3493.