

7 References

- Aiyar A. (2000). The use of CLUSTAL W and CLUSTAL X for multiple sequence alignment. *Methods Mol Biol* **132**: 221-41.
- Altschul S. F., Gish W., Miller W., Myers E. W., and Lipman D. J. (1990). Basic local alignment search tool. *J Mol Biol* **215**: 403-10.
- Arneodo A., Bacry E., Graves P. V., and Muzy J. F. (1995). Characterizing long-range correlations in DNA sequences from wavelet analysis. *Physical Review Letters* **74**: 3293-3296.
- Arneodo A., D'Aubenton-Carafa Y., Audit B., Bacry E., Muzy J. F., and Thermes C. (1998). What can we learn with wavelets about DNA sequences? *Physica A* **249**: 439 - 448.
- Arnott S., Chandrasekaran R., Hall I. H., and Puigjaner L. C. (1983). Heteronomous DNA. *Nucleic Acids Res* **11**: 4141-55.
- Arnott S., and Selsing E. (1974). Structures for the polynucleotide complexes poly(dA) with poly (dT) and poly(dT) with poly(dA) with poly (dT). *J Mol Biol* **88**: 509-21.
- Audit B., Thermes C., Vaillant C., d'Aubenton-Carafa Y., Muzy J. F., and Arneodo A. (2001). Long-range correlations in genomic DNA: a signature of the nucleosomal structure. *Phys Rev Lett* **86**: 2471-4.
- Audit B., Vaillant C., Arneodo A., d'Aubenton-Carafa Y., and Thermes C. (2002). Long-range correlations between DNA bending sites: relation to the structure and dynamics of nucleosomes. *J Mol Biol* **316**: 903-18.
- Bailey K. A., Marc F., Sandman K., and Reeve J. N. (2002). Both DNA and histone fold sequences contribute to archaeal nucleosome stability. *J Biol Chem* **277**: 9293-301.
- Bailey K. A., Pereira S. L., Widom J., and Reeve J. N. (2000). Archaeal histone selection of nucleosome positioning sequences and the procaryotic origin of histone-dependent genome evolution. *J Mol Biol* **303**: 25-34.
- Baldi P., Brunak S., Chauvin Y., and Krogh A. (1996). Naturally occurring nucleosome positioning signals in human exons and introns. *J Mol Biol* **263**: 503-10.
- Bash R. C., Vargason J. M., Cornejo S., Ho P. S., and Lohr D. (2001). Intrinsically bent DNA in the promoter regions of the yeast GAAL1-10 and GAL80 genes. *J Biol Chem* **276**: 861-6.
- Bateman A., Birney E., Cerruti L., Durbin R., Etwiller L., Eddy S. R., Griffiths-Jones S., Howe K. L., Marshall M., and Sonnhammer E. L. (2002). The Pfam protein families database. *Nucleic Acids Res* **30**: 276-80.
- Batzer M. A., and Deininger P. L. (2002). Alu repeats and human genomic diversity. *Nat Rev Genet* **3**: 370-9.

- Batzer M. A., Deininger P. L., Hellmann-Blumberg U., Jurka J., Labuda D., Rubin C. M., Schmid C. W., Zietkiewicz E., and Zuckerkandl E. (1996). Standardized nomenclature for Alu repeats. *J Mol Evol* **42**: 3-6.
- Bellard M., Dretzen G., Giangrande A., and Romain P. (1989). Nuclease digestion of transcriptionally active chromatin. *Methods Enzymol* **170**: 317-46.
- Blomquist P., Belikov S., and Wrangé O. (1999). Increased nuclear factor 1 binding to its nucleosomal site mediated by sequence-dependent DNA structure. *Nucleic Acids Res* **27**: 517-25.
- Bolshoy A., McNamara P., Harrington R. E., and Trifonov E. N. (1991). Curved DNA without A-A: experimental estimation of all 16 DNA wedge angles. *Proc Natl Acad Sci U S A* **88**: 2312-6.
- Brown N. P., Leroy C., and Sander C. (1998). MView: a web-compatible database search or multiple alignment viewer. *Bioinformatics* **14**: 380-1.
- Brukner I., Sanchez R., Suck D., and Pongor S. (1995). Sequence-dependent bending propensity of DNA as revealed by DNase I: parameters for trinucleotides. *Embo J* **14**: 1812-8.
- Buldyrev S. V., Dokholyan N. V., Goldberger A. L., Havlin S., Peng C. K., Stanley H. E., and Viswanathan G. M. (1998). Analysis of DNA sequences using methods of statistical physics. *Physica A* **249**: 430 - 438.
- Burt D. W., Bruley C., Dunn I. C., Jones C. T., Ramage A., Law A. S., Morrice D. R., Paton I. R., Smith J., Windsor D., Sazanov A., Fries R., and Waddington D. (1999). The dynamics of chromosome evolution in birds and mammals. *Nature* **402**: 411-3.
- Calladine C., and Drew H. R. (1992). "Understanding DNA: The Molecule & How it Works," Academic Press.
- Calladine C. R., and Drew H. R. (1986). Principles of sequence-dependent flexure of DNA. *J Mol Biol* **192**: 907-18.
- Calladine C. R., Drew H. R., and McCall M. J. (1988). The intrinsic curvature of DNA in solution. *J Mol Biol* **201**: 127-37.
- Cao H., Widlund H. R., Simonsson T., and Kubista M. (1998). TGGA repeats impair nucleosome formation. *J Mol Biol* **281**: 253-60.
- Chu W. M., Ballard R., Carpick B. W., Williams B. R., and Schmid C. W. (1998). Potential Alu function: regulation of the activity of double-stranded RNA-activated kinase PKR. *Mol Cell Biol* **18**: 58-68.
- Clamp M., Andrews D., Barker D., Bevan P., Cameron G., Chen Y., Clark L., Cox T., Cuff J., Curwen V., Down T., Durbin R., EyraS E., Gilbert J., Hammond M., Hubbard T., Kasprzyk A., Keefe D., Lehvaslaiho H., Iyer V., Melsopp C., Mongin E., Pettett R., Potter S., Rust A., Schmidt E., Searle S., Slater G., Smith J., Spooner W., Stabenau A., Stalker J., Stupka E., Ureta-Vidal A., Vastrik I., and Birney E. (2003). Ensembl 2002: accommodating comparative genomics. *Nucleic Acids Res* **31**: 38-42.

- Clecom (1999). AutoSignal - spectral and time domain signal analysis and processing software, <http://www.clecom.co.uk/science/autosignal/details.html>.
- Cooper D. N., and Gerber-Huber S. (1985). DNA methylation and CpG suppression. *Cell Differ* **17**: 199-205.
- Davey C. A., Sargent D. F., Luger K., Maeder A. W., and Richmond T. J. (2002). Solvent mediated interactions in the structure of the nucleosome core particle at 1.9 Å resolution. *J Mol Biol* **319**: 1097-113.
- Deininger P. L., and Batzer M. A. (1999). Alu repeats and human disease. *Mol Genet Metab* **67**: 183-93.
- Denisov D. A., Shpigelman E. S., and Trifonov E. N. (1997). Protective nucleosome centering at splice sites as suggested by sequence-directed mapping of the nucleosomes. *Gene* **205**: 145-9.
- Dowell R. D., Jokerst R. M., Day A., Eddy S. R., and Stein L. (2001). The Distributed Annotation System. *BMC Bioinformatics* **2**: 7.
- Down T., and Pocock M. (1999). The Biojava Project.
- Down T. A., and Hubbard T. J. (2002). Computational detection and location of transcription start sites in mammalian genomic DNA. *Genome Res* **12**: 458-61.
- Drew H. R., and Travers A. A. (1985). DNA bending and its relation to nucleosome positioning. *J Mol Biol* **186**: 773-90.
- El Hassan MA, and Calladine C. R. (1997). Conformational characteristics of DNA: Empirical classifications and a hypothesis for the conformational behaviour of dinucleotide steps. *PHILOSOPHICAL TRANSACTIONS OF THE ROYAL SOCIETY OF LONDON SERIES A-MATHEMATICAL PHYSICAL AND ENGINEERING SCIENCES* **355**: 43-100.
- Englander E. W., and Howard B. H. (1995). Nucleosome positioning by human Alu elements in chromatin. *J Biol Chem* **270**: 10091-6.
- Englander E. W., Wolffe A. P., and Howard B. H. (1993). Nucleosome interactions with a human Alu element. Transcriptional repression and effects of template methylation. *J Biol Chem* **268**: 19565-73.
- Fiorini A., Basso L. R., Jr., Paco-Larson M. L., and Fernandez M. A. (2001). Mapping of intrinsic bent DNA sites in the upstream region of DNA puff BhC4-1 amplified gene. *J Cell Biochem* **83**: 1-13.
- Fox K. R. (1992). Wrapping of genomic polydA.polydT tracts around nucleosome core particles. *Nucleic Acids Res* **20**: 1235-42.
- Gonzalez P. J., and Palacian E. (1989). Interaction of RNA polymerase II with structurally altered nucleosomal particles. Transcription is facilitated by loss of one H2A.H2B dimer. *J Biol Chem* **264**: 18457-62.

- Goodsell D. S., and Dickerson R. E. (1994). Bending and curvature calculations in B-DNA. *Nucleic Acids Res* **22**: 5497-503.
- Grate L., Hughey R., Karplus K., Moeri N, and K H. (1996). Tutorial: Stochastic Modeling Techniques: Understanding and using hidden Markov models.
- Hager G. L., and Fragoso G. (1999). Analysis of nucleosome positioning in mammalian cells. *Methods Enzymol* **304**: 626-38.
- Hamiche A., Sandaltzopoulos R., Gdula D. A., and Wu C. (1999). ATP-dependent histone octamer sliding mediated by the chromatin remodeling complex NURF. *Cell* **97**: 833-42.
- Hartl D. L., and Jones E. W. (1998). Eukaryotic Chromosomes. In "Essential Genetics", pp. 81 - 88, Boston Jones & Bartlett.
- Havlin S., Buldyrev S. V., Bunde A., Goldberger A. L., Ivanov P., Peng C. K., and Stanley H. E. (1999). Scaling in nature: from DNA through heartbeats to weather. *Physica A* **273**: 46-69.
- Hendrich B., and Bickmore W. (2001). Human diseases with underlying defects in chromatin structure and modification. *Hum Mol Genet* **10**: 2233-42.
- HGSC (2001). The International Human Genome Sequencing Consortium, Initial sequencing and analysis of the human genome. *Nature* **409**: 860-921.
- Higgins D. G., Thompson J. D., and Gibson T. J. (1996). Using CLUSTAL for multiple sequence alignments. *Methods Enzymol* **266**: 383-402.
- Hubbard T., Barker D., Birney E., Cameron G., Chen Y., Clark L., Cox T., Cuff J., Curwen V., Down T., Durbin R., Eyraas E., Gilbert J., Hammond M., Huminiecki L., Kasprzyk A., Lehtvaslaiho H., Lijnzaad P., Melsopp C., Mongin E., Pettett R., Pocock M., Potter S., Rust A., Schmidt E., Searle S., Slater G., Smith J., Spooner W., Stabenau A., Stalker J., Stupka E., Ureta-Vidal A., Vastrik I., and Clamp M. (2002). The Ensembl genome database project. *Nucleic Acids Res* **30**: 38-41.
- Hunter C. A., and Lu X. J. (1997). DNA base-stacking interactions: a comparison of theoretical calculations with oligonucleotide X-ray crystal structures. *J Mol Biol* **265**: 603-19.
- IMGSC (2002). The International Mouse Genome Sequencing Consortium, Initial sequencing and comparative analysis of the mouse genome. *Nature* **420**: 520-62.
- Ioshikhes I., Bolshoy A., Derenshteyn K., Borodovsky M., and Trifonov E. N. (1996). Nucleosome DNA sequence pattern revealed by multiple alignment of experimentally mapped sequences. *J Mol Biol* **262**: 129-39.
- Ioshikhes I., and Trifonov E. N. (1993). Nucleosomal DNA sequence database. *Nucleic Acids Res* **21**: 4857-9.
- Jenuwein T., and Allis C. D. (2001). Translating the histone code. *Science* **293**: 1074-80.

- Kang J. G., Hamiche A., and Wu C. (2002). GAL4 directs nucleosome sliding induced by NURF. *Embo J* **21**: 1406-13.
- Karchin R. (1999). Hidden Markov Models and Protein Sequence Analysis.
- Karrer K. M., and VanNuland T. A. (1999). Nucleosome positioning is independent of histone H1 in vivo. *J Biol Chem* **274**: 33020-4.
- Kim C., Rubin C. M., and Schmid C. W. (2001). Genome-wide chromatin remodeling modulates the Alu heat shock response. *Gene* **276**: 127-33.
- Kim J. L., Nikolov D. B., and Burley S. K. (1993). Co-crystal structure of TBP recognizing the minor groove of a TATA element. *Nature* **365**: 520-7.
- Kiyama R., and Trifonov E. N. (2002). What positions nucleosomes?--A model. *FEBS Lett* **523**: 7-11.
- Klug A., Rhodes D., Smith J., Finch J. T., and Thomas J. O. (1980). A low resolution structure for the histone core of the nucleosome. *Nature* **287**: 509-16.
- Koo H. S., Wu H. M., and Crothers D. M. (1986). DNA bending at adenine . thymine tracts. *Nature* **320**: 501-6.
- Kornberg R. D., and Lorch Y. (1999). Twenty-five years of the nucleosome, fundamental particle of the eukaryote chromosome. *Cell* **98**: 285-94.
- Levitsky V. G., Podkolodnaya O. A., Kolchanov N. A., and Podkolodny N. L. (2001a). Nucleosome formation potential of eukaryotic DNA: calculation and promoters analysis. *Bioinformatics* **17**: 998-1010.
- Levitsky V. G., Podkolodnaya O. A., Kolchanov N. A., and Podkolodny N. L. (2001b). Nucleosome formation potential of exons, introns, and Alu repeats. *Bioinformatics* **17**: 1062-4.
- Levitsky V. G., Ponomarenko M. P., Ponomarenko J. V., Frolov A. S., and Kolchanov N. A. (1999). Nucleosomal DNA property database. *Bioinformatics* **15**: 582-92.
- Lewin B. (2000). Chapter 19: Nucleosomes. In "Genes VII", pp. 567-606, Oxford University Press, Cambridge, Massachusetts.
- Li T., Spearow J., Rubin C. M., and Schmid C. W. (1999). Physiological stresses increase mouse short interspersed element (SINE) RNA expression in vivo. *Gene* **239**: 367-72.
- Liu K., and Stein A. (1997). DNA sequence encodes information for nucleosome array formation. *J Mol Biol* **270**: 559-73.
- Liu W. M., Chu W. M., Choudary P. V., and Schmid C. W. (1995). Cell stress and translational inhibitors transiently increase the abundance of mammalian SINE transcripts. *Nucleic Acids Res* **23**: 1758-65.

- Lorch Y., Cairns B. R., Zhang M., and Kornberg R. D. (1998). Activated RSC-nucleosome complex and persistently altered form of the nucleosome. *Cell* **94**: 29-34.
- Lowary P. T., and Widom J. (1997). Nucleosome packaging and nucleosome positioning of genomic DNA. *Proc Natl Acad Sci U S A* **94**: 1183-8.
- Luger K., Mader A. W., Richmond R. K., Sargent D. F., and Richmond T. J. (1997). Crystal structure of the nucleosome core particle at 2.8 Å resolution. *Nature* **389**: 251-60.
- Lustig A. J., and Petes T. D. (1984). Long poly(A) tracts in the human genome are associated with the Alu family of repeated elements. *J Mol Biol* **180**: 753-9.
- MacDonald D., Herbert K., Zhang X., Polgruto T., Lu P., and Polgruto T. (2001). Solution structure of an A-tract DNA bend. *J Mol Biol* **306**: 1081-98.
- Mahadevan M., Tsilfidis C., Sabourin L., Shutler G., Amemiya C., Jansen G., Neville C., Narang M., Barcelo J., O'Hoy K., and et al. (1992). Myotonic dystrophy mutation: an unstable CTG repeat in the 3' untranslated region of the gene. *Science* **255**: 1253-5.
- Marini J. C., Levene S. D., Crothers D. M., and Englund P. T. (1983). A bent helix in kinetoplast DNA. *Cold Spring Harb Symp Quant Biol* **47 Pt 1**: 279-83.
- Meyer I. M., and Durbin R. (2002). Comparative ab initio prediction of gene structures using pair HMMs. *Bioinformatics* **18**: 1309-18.
- Nair T. M. (1998). Evidence for intrinsic DNA bends within the human cdc2 promoter. *FEBS Lett* **422**: 94-8.
- Negri R., Buttinelli M., Panetta G., De Arcangelis V., Di Mauro E., and Travers A. (2001). Sequence dependence of translational positioning of core nucleosomes. *J Mol Biol* **307**: 987-99.
- Nelson H. C., Finch J. T., Luisi B. F., and Klug A. (1987). The structure of an oligo(dA).oligo(dT) tract and its biological implications. *Nature* **330**: 221-6.
- Olson W. K., Gorin A. A., Lu X. J., Hock L. M., and Zhurkin V. B. (1998). DNA sequence-dependent deformability deduced from protein-DNA crystal complexes. *Proc Natl Acad Sci U S A* **95**: 11163-8.
- Packer M. J., Dauncey M. P., and Hunter C. A. (2000a). Sequence-dependent DNA structure: dinucleotide conformational maps. *J Mol Biol* **295**: 71-83.
- Packer M. J., Dauncey M. P., and Hunter C. A. (2000b). Sequence-dependent DNA structure: tetranucleotide conformational maps. *J Mol Biol* **295**: 85-103.
- Pattini L C. S. (2001). Evaluation of long term correlation in different regions of a gene sequence. *Biosignal Processing*: 394 - 396.
- Pina B., Bruggemeier U., and Beato M. (1990). Nucleosome positioning modulates accessibility of regulatory proteins to the mouse mammary tumor virus promoter. *Cell* **60**: 719-31.

- Pocock MR, Down T, and TJP H. (2000). ISMB 2000 Poster Presentations, <http://ismb2000.sdsc.edu/posters/poster-list.html>.
- Polikar R. (2000). The Wavelet Tutorial.
- Pruss D., Bushman F. D., and Wolffe A. P. (1994). Human immunodeficiency virus integrase directs integration to sites of severe DNA distortion within the nucleosome core. *Proc Natl Acad Sci U S A* **91**: 5913-7.
- Puhl H. L., and Behe M. J. (1993). Structure of nucleosomal DNA at high salt concentration as probed by hydroxyl radical. *J Mol Biol* **229**: 827-32.
- Quentin Y. (1994). A master sequence related to a free left Alu monomer (FLAM) at the origin of the B1 family in rodent genomes. *Nucleic Acids Res* **22**: 2222-7.
- Rhodes D. (1979). Nucleosome cores reconstituted from poly (dA-dT) and the octamer of histones. *Nucleic Acids Res* **6**: 1805-16.
- Rhodes D. (1997). Chromatin structure. The nucleosome core all wrapped up. *Nature* **389**: 231, 233.
- Richmond T. J., Finch J. T., Rushton B., Rhodes D., and Klug A. (1984). Structure of the nucleosome core particle at 7 Å resolution. *Nature* **311**: 532-7.
- Rubin C. M., VandeVoort C. A., Teplitz R. L., and Schmid C. W. (1994). Alu repeated DNAs are differentially methylated in primate germ cells. *Nucleic Acids Res* **22**: 5121-7.
- Satchwell S. C., Drew H. R., and Travers A. A. (1986). Sequence periodicities in chicken nucleosome core DNA. *J Mol Biol* **191**: 659-75.
- Satchwell S. C., and Travers A. A. (1989). Asymmetry and polarity of nucleosomes in chicken erythrocyte chromatin. *Embo J* **8**: 229-38.
- Schmid C. W. (1991). Human Alu subfamilies and their methylation revealed by blot hybridization. *Nucleic Acids Res* **19**: 5613-7.
- Shamir R. (2001). Algorithms for Molecular Biology: Course Archive.
- Simpson R. T., and Shindo H. (1979). Conformation of DNA in chromatin core particles containing poly(dAdT)-poly(dAdT) studied by ³¹P NMR spectroscopy. *Nucleic Acids Res* **7**: 481-92.
- Sinden R. S. (1994). "DNA Structure and Function," Academic Press.
- Smit A., and Green P. (1997). RepeatMasker, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>.
- Smit A. F. (1999). Interspersed repeats and other mementos of transposable elements in mammalian genomes. *Curr Opin Genet Dev* **9**: 657-63.

- Smith M. M. (2002). Centromeres and variant histones: what, where, when and why? *Curr Opin Cell Biol* **14**: 279-85.
- Sprous D. (1996). Force Fields: definition and overview.
- Staynov D. Z. (2000). DNase I digestion reveals alternating asymmetrical protection of the nucleosome by the higher order chromatin structure. *Nucleic Acids Res* **28**: 3092-9.
- Stein A., and Bina M. (1999). A signal encoded in vertebrate DNA that influences nucleosome positioning and alignment. *Nucleic Acids Res* **27**: 848-53.
- Sved J., and Bird A. (1990). The expected equilibrium of the CpG dinucleotide in vertebrate genomes under a mutation model. *Proc Natl Acad Sci U S A* **87**: 4692-6.
- Thastrom A., Lowary P. T., Widlund H. R., Cao H., Kubista M., and Widom J. (1999). Sequence motifs and free energies of selected natural and non-natural nucleosome positioning DNA sequences. *J Mol Biol* **288**: 213-29.
- Thompson J. D., Higgins D. G., and Gibson T. J. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* **22**: 4673-80.
- Tomaszewski R., and Jerzmanowski A. (1997). The AT-rich flanks of the oocyte-type 5S RNA gene of *Xenopus laevis* act as a strong local signal for histone H1-mediated chromatin reorganization in vitro. *Nucleic Acids Res* **25**: 458-66.
- Tsukiyama T. (2002). The in vivo functions of ATP-dependent chromatin-remodelling factors. *Nat Rev Mol Cell Biol* **3**: 422-9.
- Turner B. M. (2000). Histone acetylation and an epigenetic code. *Bioessays* **22**: 836-45.
- Uberbacher E. C., and Bunick G. J. (1985). X-ray structure of the nucleosome core particle. *J Biomol Struct Dyn* **2**: 1033-55.
- Ulanovsky L., Bodner M., Trifonov E. N., and Choder M. (1986). Curved DNA: design, synthesis, and circularization. *Proc Natl Acad Sci U S A* **83**: 862-6.
- Wada-Kiyama Y., and Kiyama R. (1996). An intrachromosomal repeating unit based on DNA bending. *Mol Cell Biol* **16**: 5664-73.
- Wada-Kiyama Y., Kuwabara K., Sakuma Y., Onishi Y., Trifonov E. N., and Kiyama R. (1999). Localization of curved DNA and its association with nucleosome phasing in the promoter region of the human estrogen receptor alpha gene. *FEBS Lett* **444**: 117-24.
- Wang J. C. (1982). The path of DNA in the nucleosome. *Cell* **29**: 724-6.
- Wang Y. H., Gellibolian R., Shimizu M., Wells R. D., and Griffith J. (1996). Long CCG triplet repeat blocks exclude nucleosomes: a possible mechanism for the nature of fragile sites in chromosomes. *J Mol Biol* **263**: 511-6.

- Wang Y. H., and Griffith J. (1995). Expanded CTG triplet blocks from the myotonic dystrophy gene create the strongest known natural nucleosome positioning elements. *Genomics* **25**: 570-3.
- Widlund H. R., Cao H., Simonsson S., Magnusson E., Simonsson T., Nielsen P. E., Kahn J. D., Crothers D. M., and Kubista M. (1997). Identification and characterization of genomic nucleosome-positioning sequences. *J Mol Biol* **267**: 807-17.
- Widlund H. R., Kuduvalli P. N., Bengtsson M., Cao H., Tullius T. D., and Kubista M. (1999). Nucleosome structural features and intrinsic properties of the TATAAACGCC repeat sequence. *J Biol Chem* **274**: 31847-52.
- Widlund H. R., Vitolo J. M., Thiriet C., and Hayes J. J. (2000). DNA sequence-dependent contributions of core histone tails to nucleosome stability: differential effects of acetylation and proteolytic tail removal. *Biochemistry* **39**: 3835-41.
- Widom J. (1996). Short-range order in two eukaryotic genomes: relation to chromosome structure. *J Mol Biol* **259**: 579-88.
- Wolffe A. (1998). "Chromatin Structure and Function," Academic Press.
- Wolffe A. P., and Guschin D. (2000). Review: chromatin structural features and targets that regulate transcription. *J Struct Biol* **129**: 102-22.
- Wu H. M., and Crothers D. M. (1984). The locus of sequence-directed and protein-induced DNA bending. *Nature* **308**: 509-13.
- Zhou Y., Zheng J. B., Gu X., Li W., and Saunders G. F. (2000). A novel Pax-6 binding site in rodent B1 repetitive elements: coevolution between developmental regulation and repeated elements? *Gene* **245**: 319-28.
- Zhou Y. H., Zheng J. B., Gu X., Saunders G. F., and Yung W. K. (2002). Novel PAX6 Binding Sites in the Human Genome and the Role of Repetitive Elements in the Evolution of Gene Regulation. *Genome Res* **12**: 1716-22.