Nucleic Acids in Chemistry and Biology 3rd Edition

Errata List

update January 2008

Contributors

Inadvertently, the chapter assignations were omitted and are now shown below.

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Chapter 2

Page 25, lines 14-15 should read:
The main features of A-, B- and Z-DNA are shown in Figures 2.16, 2.17 and 2.20….

Page 33, line 6 should refer to Section 2.5.3.

Page 71, line 10: should read: "riboswitches".

Reference 85: author 3, should be D. E. Brodersen.

Chapter 6

Figure 6.11 Legend should read:
….(a) The nucleosome. (b) The polynucleosome. (c) The 30 nm fibre.

Chapter 7

Reference 29: author 3, should be D. E. Brodersen

Chapter 8

Page 328, lines 4-8 should be replaced by:
Repair by base excision, BER, identifies minor modifications to the bases of DNA that are removed by either short- or long-patch BER. A **DNA glycosylase**, which has a high affinity for certain forms of base damage, binds to an altered nucleotide and cleaves the *N*-glycosylic bond between the base and the sugar. The resulting abasic site is further processed by **AP lyase**, **AP endonuclease**, [95] and **DNA polymerase** activities that generate intermediates containing a single-base gap, a single-strand nick, or a single- or multiple-nucleotide overhang. A tight coordination of BER enzymes is necessary to prevent the disruption of repair by the binding of other cellular factors to these DNA structures.[116]

New reference 116. S.D. Cline and P.C. Hanawalt, Who's on first in the cellular response to DNA damage? *Nature Rev. Mol. Cell Biol*., 2003, **4**, 361-373.

Page 332, line 5. The sentence should be replaced by
Xeroderma pigmentosum (XP) is an autosomal recessive disease characterized by defective nucleotide excision repair and a severe risk for skin cancer (1000 fold increase). There are seven XP nucleotide excision repair complementation groups (XP-A to XP-G) plus a variant form with normal excision repair. The genes that are defective in XP are involved in the nucleotide excision repair and basal transcription complexes.

Page 337, Reference 75 is incorrect and should be replaced by:
R.J.H. Davies, Purines as targets for DNA photodamage. *Biochem. Soc. Trans*., 1997, **25**, 323-326

Chapter 9

Page 346, lines 16-20 should be replaced by:
The extent of visualization of specific water molecules from crystal structures depends on the resolution of the structure, the quality of the diffraction data and the temperature of the data collection. Typically only a fraction of the possible water molecules are observed in the electron density.

Page 347 (Section 9.5.1)
Several re-determinations of the crystal structure of the Dickerson-Drew dodecamer (DDD; dCGCGAATTCGCG) at high resolution (< 1.4 Å) have indeed revealed a second spine of hydration in the minor groove that leads to formation of a series of fused water hexagons together with the underlying, original spine of hydration (Figure 2.18 in chapter 2). However, unlike stated in section 9.5.1 and in the cited references 11-13 (Chapter 9), the interpretation that minor groove water molecules are partially occupied monovalent metal cations is incorrect. Flaws in the structural analysis and subsequent interpretation by Shui et al. (reference 11) have been discussed in detail (Chiu & Dickerson, 1999). Structural analyses of A-tract DNAs using X-ray crystallography (Tereshko et al., 1999; Howerton et al., 2004) and solution NMR spectroscopy (Stefl et al., 2004) have demonstrated that thymine O-2 keto groups in the minor groove of the ApT step (underlined in the above sequence of the DDD) represent a unique and tight binding site for monovalent ions (reviewed in Egli, 2002). Thus, binding of monovalent ions in the minor groove is highly sequence-dependent (ApT represents a coordination site, but TpA does not) and a bound ion can contribute to narrowing of and bending into the minor groove seen in A-tract DNA.

References

T.K. Chiu, M. Kaczor-Grzeskowiak and R.E. Dickerson, Absence of minor groove monovalent cations in the crosslinked dodecamer C-G-C-G-A-A-T-T-C-G-C-G. *J. Mol. Biol.*, 1999, **292**, 589-608.

M. Egli, DNA-cation interactions: quo vadis? *Chem. Biol.,* 2002, **9**, 277-286.

S.B. Howerton, C.C. Sines, D. VanDerveer and L.D. Williams, Locating monovalent cations in the grooves of B-DNA. *Biochemistry*, 2001, **40**, 10023-10031.

R. Stefl, H. Wu, S. Ravindranathan, V. Sklenar and F. Feigon, DNA A-tract bending in three dimensions: solving the dA_4T_4 vs. dT_4A_4 conundrum. *Proc. Natl. Acad. Sci. U.S.A.*, 2004, **101**, 1177-1182.

V. Tereshko, G. Minasov and M. Egli, A "hydrat-ion" spine in a B-DNA minor groove. *J. Am. Chem. Soc*., 1999, **121**, 3590-3595.

Page 351, line 2 should read: ….Wang and Rich in 1980 and re-refined in 1987 for the complex…
Page 360, line 13 should read: …….laboratory of Neidle (Figure 9.12).[27]
Page 363, Figure 9.14 (b) legend should read:
(b) Exactly the same DNA sequence in a 2:1 drug/DNA complex solved using NMR.
Page 375, line 11 should read: ….**anthraquinones** (Neidle)…
Page 382, Reference 66. This crystal structure has subsequently been found to be incorrect. The correct structure is reported in reference 70.
Page 382, Reference 71 should read:
G.N. Parkinson, M.P.H. Lee M. and S. Neidle, Crystal structure of parallel quadruplexes from human telomeric DNA. *Nature,* 2002, **417**, 876-880.

Chapter 10

The PDB codes should be corrected in the legends for the following Figures

Fig 10.2a : 3HDD not 1YSA
Fig 10.5 : 1TGH not 1IFH
Fig 10.6a : Take out 1TGH reference
Fig 10.11 : 1D3U not 1AKH
Fig 10.19a : 1E0K not 1EOK
Fig 10.22 : 1UN6 not 1VN6
Fig 10.23b : 1ASY not 1JGO

Figures

The following Figures have been corrected in the Powerpoint files available on the Website
2.5 and 2.7
3.79
5.5
6.7
6.23
6.35

8.33

Acknowledgements

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