

This page intentionally left blank

Index

(Page numbers in italics refer to illustrations and tables)

300 Å fiber, nucleosomes coiling into, 139, 144, 145–7
434 repressor protein, 82–3, 84, 177–81, 186, 191

A

A *see* adenine

'A'-form helix

grooves, major and minor, 25, 43–4
phosphates per helical turn, 24–5
right-handedness, 25–6
roll and slide motions, 46, 54, 55, 59
X-ray diffraction studies, 204–10

A–T pairs

hydrogen bonds between adjacent, 30, 31, 43, 44
partial electric charge, 51, 54, 305–7
unwinding at sequence of, 69–70
X-ray diffraction studies, 204, 207

A₆N_x repeat sequences, superhelices, 103–6

AA/TT steps, 43, 48–9, 52, 53, 58, 59, 307, 309

and roll and curvature, 78–9, 80, 81–2, 106, 109

AAA/TTT trimer and DNA curvature, 80, 81, 235

Acetylation of chromosomal proteins, 161–5

Activation, gene, 150, 160–1, 163, 164, 174–7

DNA unwinding as precursor of, 163–4, 165

see also transcription

Activator proteins, 132, 175–6

Adenine, 13, 19, 20, 30, 31, 40
methylation, 270–2

see also A–T pairs

Agarose, gels made from, 220, 273, 274

Ageing, DNA methylation, 284–7

Alpha helix, 176–86

Amino acids

base triplets, coding for, 12, 13, 72
hydrogen bonding with bases, 83–5, 180–96

negatively-charged, in histone carrier proteins, 155

protein production, 11–15, 32–4
RNA polymerase 'tail,' 163, 164

Amplification methods, use in diagnostics, 238–9

Animal models of human disease, 238

Anti-sense oligomers, 313–15

Anticancer drugs, topoisomerases and, 67–8

Antiparallel directionality of DNA nucleotides, 8, 21, 27–8

Arginine, 12, 83–5, 183

Aspartate, 155

Assembly of DNA into chromosomes, 139–65

ATATAT sequence, X-ray diffraction studies, 204

Atomic force microscopy (AFM), 227–8

Azacytosine, 275–6, 289

B

'B'-form helix

grooves, major and minor, 43–4
phosphates per helical turn, 25
right-handedness, 25–6
roll and slide motions, 55, 59
X-ray diffraction studies, 204

Bands, chromosomal, 6, 7, 146–50

Bases

bubble of unpaired bases, 64–8, 70
di-deoxy four-color sequencing, 242–6
hydrogen bonding with amino acids, 83–5, 180–96

Bases (*contd*)

- insolubility in water, 19–22, 34, 50–1, 302–4
- methylation, 249, 270–90
- nucleotide component, 8–9, 19–20
- pairs, 21–3, 28, 30, 31, 32, 33, 34
 - groove sides, major and minor, 40, 42–4, 56
 - helix stability, 32, 69–70
 - mismatches, 34
 - motions, 39–60
 - nanotechnology, 296
 - recombination, 295
 - stacking, 22, 23, 39–60, 70, 87, 301–10
 - unusual, 32–4
- triplets, amino acids coded by, 12, 13, 72

Beads, histone, 141, 144–5

Beta sheet, 176–90

Bisulfite method, 276–7

Brownian movement, 107, 129

Bubble of unpaired bases, 64–8, 70

BZip protein, 182, 183–6

C

C *see* cytosine

C–G pairs, 29, 30, 31, 32–4, 51–2

‘C’ helix, X-ray diffraction studies, 204

CA/TG steps, 49, 52, 53, 59, 307, 309

CAG repeat sequence, 252–7

Cancer

- anticancer drugs, 67–8
- bisulfite-PCR diagnosis, 277
- dinucleotide repeats link, 255
- DNA methylation, 284–7
- GLI protein, 86
- see also* mutations

Capillary electrophoresis, 214, 244

Carbon atoms in A–T pair, X-ray diffraction studies, 207

Carrier plasmids, 239–40

Catalysts, 316

CC/GG steps, 51, 53, 305–6, 307

Centromere, 152

CG/CG steps, 49, 51, 307

- de-amination, 285–88
- echinomycin binding, 215–17
- methylation, 272–5, 280

CGCG and CGCGCG sequences, X-ray diffraction studies, 205

CGCGAATTCGCG sequence, NMR studies, 209–10

Chromatin, histone modification, 280–2

Chromosomes, 3–4, 5

assembly of DNA into, 39, 87–8

de-methylation, 282–4

DNA assembly into, 139–65

homologous pairs, 3–4, 5

interphase, 146–7, 150

lampbrush, 147–50, 152

metaphase, 5, 146, 149–54

polytene, 5, 6, 7, 146–7, 149–50

Circular dichroism spectroscopy, 211

Circular DNA

gel electrophoresis, 223

supercoiling, 117–28

Cloning

animals and plants, 238

farm animals, 284

Codons (triplet bases coding for amino acids), 12, 13, 72

Contour length, superhelical N*, 98–103, 106

Crick, Francis, ix, 29

see also Watson–Crick base-pairs

Cruciform configurations, 70, 71

Crystals of DNA, growth, 204–6

Curvature of DNA (*k*), 72–82, 87–8 around histones, 78–81, 109–10, 141–5

nucleosome assembly, 159–60

in promoter regions, 131–2

relevance to gel electrophoresis, 222–3

repression of gene activity, 160

three-dimensional, 94–110

Cytosine, 13, 19–20, 30–1, 32, 40

methylation, 249, 270–90

nitrogen protonation, 31, 32

see also G–C pairs

D

‘D’ helix, 204

De-amination, 285–8

De novo methylases, 279–80, 282–4, 288–9

Degrees of freedom, base-pair motions, 44–45, 46, 47–60

Denaturing gel, 213, 217

Diagnostics, use of DNA, 239–53, 277, 287

Dicer, 318–9

Dinucleotide steps, 39–60

degrees of freedom, 44, 45, 46, 308–9

DNA curvature, 73–8, 107–10

see also specific steps

Dinucleotide repeats, 255

Directionality of DNA nucleotides, 8, 21, 27–8

Disease, use of DNA in, 235–65

Distamycin, 196–8

- DNA polymerase, 240–2
 hairpin loops, 255–6
 replication, 153, 264
 DNAase I, 84, 215–7
 DNAzymes, 316–18
 Dnmt enzymes, 278–83
 Docking, DNA-protein recognition,
 84, 88
 Double helix *see* helix, double
 Doxorubicin, 67
Drosophila (fruit fly) salivary gland
 polytene chromosomes, 5, 6, 7,
 146–7, 149–50
 Dyes *see* fluorescent dyes
- E**
 Echinomycin, binding to DNA,
 215–17
 Eco RI, uses of, 212
 Electric charges
 atomic force microscopy, 228
 base-pair interactions, 30, 301–10
 gel electrophoresis, 211–2, 218–9,
 222–5
 histone carrier protein amino acids,
 155
 partial, base-pairs, 30, 51, 54
 Electron microscopy, 208
 chromosomes, 6, 148
 nucleosomes, 142, 144
 repeating-sequence DNA curvature
 and twist, 101, 102
 Electrophoresis
 capillary, 214, 244
 gel, 101, 156–7, 211–25, 251
 Embryo, methylation in, 282–4, 289
 End restraint, supercoiling, 117
 Endosome, 262
 Enzymes, 11
 DNA cutting, 84, 140, 156, 212,
 277
 HIV insertion, 81
 proofreading, 34
 recombination, 261–3
 repair, 34, 237, 285–6
 used for DNA analysis, 211–18
 Epigenetics, 15, 270–90
 Ethidium bromide, 28, 68, 273, 275
 studies using, 212
 Euler's six degrees of freedom, 44,
 45–6, 52–3, 59, 308
 Evolution
 DNA invasion, 287
 DNA sequencing and, 296
 Expansion of repeated DNA, 251–4
 Expansion or contraction of DNA,
 255–7
- F**
 Fiber, 300 Å, histone spools coiling
 into, 139, 144, 145–7
 First-order influences on DNA
 structure, 19–34, 39
 Flexibility
 DNA, 82–4, 107–8, 159–60
 sugar-phosphate chains, 28–9, 47,
 52, 308
 Fluorescent dyes, four-color
 sequencing, 213, 243–6
 FMR1 protein, 254–5
 'Footprinting' studies, 215–17
 Foreign DNA, 287–9
 transgenic plants and animals,
 154–5
 Four-color method of DNA
 sequencing, 214, 243–6
 Fourier transform of roll angles, 78,
 103–5, 159
 Franklin, Rosalind, 204
 Fruit fly salivary gland polytene
 chromosomes, 5, 6, 7, 146–7,
 149–50
- G**
 G *see* guanine
 G–C pairs, 29, 30, 31, 32–4, 51–2
 partial charge, 305–6
 G–T pairs, 32, 33, 34
 G–U pairs, 32, 33, 34, 285–7
 GC/GC steps, 51, 109–10, 307
 roll and curvature, 80–1
 GG/CC steps, 51, 52, 53, 58–9, 82,
 305–7
 Gel electrophoresis, 101, 156–7,
 211–25, 251
 Gene correction, 261–5, 312–19
 Gene therapy, 261–5, 312–19
 Genes
 activation, 174–6
 expression, 312–19
 protein production, 11–15
 repressors (*see* repression)
 Genetic Code, 12–13, 16–17, 72
 Genetic diseases, diagnosis using
 PCR and sequencing, 250–5
 Genetically modified (GM) foods,
 154–5
 Glutamate, 155
 Grooves
 DNAase binding across, 215
 major and minor, 40, 42–4, 56, 75,
 196–8
 proteins binding in, 177–97
 Guanine, 13, 19, 30, 31, 33, 40, 83, 85
 see also G–C pairs; G–U pairs

H

- H1, 141, 142, 158, 159
 - function, 145
 - phosphorylation, 162
- H2A, H2B, 141, 142, 143, 155, 156, 158, 162, 164–5
- H3, 141, 142, 143, 155, 156, 158
 - acetylation, 162
 - phosphorylation, 162
- H4, 141, 142, 143, 155, 156, 158
 - acetylation, 162
- Hairpin loops, 217–18, 255–9
- Hammerhead ribozyme, 316–7
- Helix
 - alpha helix, 176–86
 - double
 - curvature, 73–82
 - different kinds, 39–60, 304
 - left-handed, 25, 26, 205
 - phosphates per helical turn, 24–5
 - right-handed, 25, 26, 40
 - stability, 32, 69–70
 - untwisting/unwinding, 64–72, 86–8
 - triple, 32, 37
 - see also* superhelices/supercoils
- Histone carrier proteins, 155–6, 159
- Histones, 79, 80, 84, 109–10, 139–41
 - modification, 161–5, 280–2
 - octamer, 141–3, 159, 165
 - see also* specific histones (H1–H4)
- HIV insertion enzyme, 81
- HMGA, 145, 157–8
 - acetylation, methylation and phosphorylation, 162
- HMGB, 145, 157–8
 - acetylation, 162
- HMGN, 145, 157–8
 - phosphorylation, 162
- Hoogsteen, Karst, 31
- Hoogsteen base-pairs, 31, 32
- Hormone receptors, 191, 192
- HP1 protein, 162
- Hydrogen atoms, in NMR studies, 209–11
- Hydrogen bonding
 - between adjacent A–T pairs, 43, 44
 - between bases and amino acids, 83–6, 180–96
 - between water molecules, 302–3
 - and helix stability, 32, 69–70
 - and propellor twist, 43, 44
 - within base-pairs, 30–3, 48–9, 51
 - see also* Watson–Crick base-pairs
- Hydrophobicity of bases, 19–23, 50–1, 302–4

I

- Illegitimate recombination, 237–8
- Imprinting, 257–61, 284
 - protein, 279–81
- Improved animals and plants, 154–5, 238
- Insolubility of bases in water, 19–23, 50–1, 302–4
- Interbands, chromosomal, 6, 7, 146–8
- Interphase chromosomes, 147, 150
- Interwound supercoiling, 116–28

K

- k* *see* curvature of DNA
- Kinases, chromosomal protein
 - phosphorylation, 161–5

L

- Ladder, DNA as, 21–3
 - in gel electrophoresis, 213–15
- Lampbrush chromosomes, 147–8, 150, 152
- Latex beads, DNA manipulation, 226–7
- Left-handed helix, 25–6, 205
- Left-handed supercoil, 79, 98, 100, 105
- Leucine zipper, 182, 184
- Linking number (Lk), 122–8
 - in gel electrophoresis, 223
- Liposomes, 155, 261–3
- Looped linear DNA, supercoiling, 118, 119
- Loops, 118, 119, 139, 147–54
 - hairpin, 217–8, 255–9
 - RNA binding, 258–60
- Lysine, modification, 161, 280–2

M

- Major-groove side, 42–4, 56
- Mariner transposons, 287–8
- Medical treatment, limitations of, 236–7, 277
- Messenger-RNA, 14–15, 64, 72, 163
 - anti-sense, 313–15
 - cleavage, 316–19
 - transfer-RNA, base-pairing with, 32–4
 - see also* RNA
- Met repressor protein, 185–7
- MET1 enzymes, 278–9
- Metaphase chromosomes, 5, 146, 148–50, 153–4
- Methionine, 12, 13, 185
- Methylases, 278–81
- Methylation
 - chromosomal proteins, 161–3
 - cytosine, 249, 270–90

- Mica, atomic force microscopy (AFM), 227–8
- Microarrays to sequence DNA, 246–7
- Micropipettes, DNA manipulation, 226–7
- Microtubules, 68, 152
- Minor-groove side, 40, 42–4, 56, 74–5
- Motions, base-pairs, 39–60
see also roll; slide; twist; shift
- Multiple displacement amplification (MDA), 241
- Mutations
in human disease, 245–57, 286–7
see also cancer
- N**
- N1 protein, 155, 156, 158
phosphorylation, 162
- Nanotechnology, 295–6
- Negative electric charge
in amino acids of histone carrier proteins, 155
gel electrophoresis, 219
- Nitrogen
protonation of cytosine, 31, 32
X-ray diffraction studies, 207
- Nogalamycin, X-ray diffraction studies, 205
- Nuclear magnetic resonance (NMR) studies, 209–11
- Nucleoplasmin, 155, 158
phosphorylation, 162
- Nucleosomes, 7, 140–5
assembly, 155–9
and RNA polymerase, 163–5
spacing, 156–9
strings of, 144–5
- Nucleotides, 8, 9, 65, 66
components, 8–9, 19–20, 28–9
see also specific components
- O**
- Oligo-nucleotides
anti-sense therapy, 313–15
in DNA sequencing, 246–7
- Overwound supercoiled DNA, 120–4
- Oxygen atoms in AT pair, X-ray diffraction studies, 207
- P**
- P-element, 149
- Partial electric charges, base-pairs, 51, 54, 305–7
- PCR (polymerase chain reaction), 239–42
- Peptide nucleic acid (PNA), 315
- Persistence length of DNA, 107, 228
- Phosphate
distance to next phosphate, 20–3, 307–8
nucleotide component, 8–9, 19, 27–9, 239–40
see also sugar-phosphate chains
- Phosphorus, radioactive, studies using, 212, 215
- Phosphorylation of chromosomal proteins, 161–5
- Pitch (*p*), superhelical, 98–100
- Plasmid DNA, 239–40
- Point mutation *see* SNPs
- Polyacrylamide, gels from, 220
- Polymerase, RNA *see* RNA polymerase
- Polymerase chain reaction (PCR), 239–42
- Polymerase extension reaction, 247–9
- Polypeptide chains
alpha helix, 176–9
beta sheet, 185–7
- Polytene chromosomes, fruit fly salivary gland, 5, 6, 7, 146–7, 149–50
- Probing, DNA-protein recognition, 84, 173–95
- Promoters, 39, 59, 70–1, 130–2, 173–6
- Proofreading enzymes, 34
- Propeller twist, 39–60, 309
echinomycin binding, 217
- Protein
activator, 132–3
beads on a string, 141, 144–5
chromosomal, 7
(*see also* histones)
DNA binding/recognizing, 68–9, 82–8, 107–10, 129–33, 139–45, 173–99, 236–63
modification, 161–5, 280–2
repressor, 39, 59, 82–3, 133
resolvase, 87
scaffold, 148–9, 153–4
sizes and roles, 10–11
spools, 7–8, 78–9, 84, 126, 127, 139–45
synthesis, 11–15, 32–4, 129–30
(*see also* transcription)
unwinding, 68–9
see also specific proteins and enzymes
- Protonation of cytosine nitrogen, 31, 32
- Purines, 40, 44, 48–50
see also pyrimidines

Pyrimidines, 40, 44, 48–50
 pyrimidine-purine steps, 48, 49–52,
 53
 unwinding in sequence of, 69–70

R

R *see* roll, base-pair motions
 Radioactive phosphorus, studies
 using, 212–5
 Raman spectroscopy, 211
 Random-sieve gel, 220–2
 Recognition code, 189–90, 194–5, 197
 Recombination, 295
 illegitimate, 237–8
 Recombination enzymes, 261
 Repair enzymes, 34, 237, 285–6
 Repeating-sequence DNA,
 curvature and twist of, 101–8
 Replication
 DNA, 64, 65, 129, 153, 252–3, 263–4
 untwisting at origin of, 116
 Repression
 DNA curvature causing, 160
 proteins causing, 173–6
 proteins causing viral, 82–3, 179–83
 Repressor proteins, 39, 59, 133
 viral, 82–3, 179–83
 Resolvase proteins, 87
 Restriction enzyme, uses of, 213, 228,
 278
 Ribosomal RNA, 14–15, 315–18
 Right-handed helices, 25–6
 Right-handed superhelices, 98, 106,
 163–4
 RNA, 312–13
 base pairing, 32–4
 based imprinting, 260–1
 binding to loops, 258–60
 synthesis from DNA, 64–72, 82–5,
 116–9, 117, 129–33, 152
 types, 14–15
 RNA polymerase, 65–8, 71, 83, 116,
 129–33, 165, 173–4
 amino acid ‘tail,’ 163, 164
 lampbrush chromosomes, 148
 loops, 148, 151–2
 and nucleosomes, 163–5
 RNAase, 66
 Roll, base-pair motions, 41–60, 143
 curvature of DNA, 73–82, 86–7,
 108–10
 helices varying due to, 54–60
 repeating-sequence DNA, 103–7
 sign convention, 46, 60
 slide and twist, relationship, 53–5,
 307
 Roll-slide-twist model, 46, 47–60

S

S *see* slide, base-pair motions
 S1 nuclease, uses of, 217–8
 Salivary gland polytene
 chromosomes, fruit fly, 5, 6, 7,
 146–7, 149–50
 Salt solutions, in gel electrophoresis,
 219
 SatB1 protein, 150
 Scaffold
 DNA looping, 119, 139, 147–54
 protein, 148–9, 153–4
 Scattering power of an atom, 207
 Screwing of DNA through
 polymerase, 66–7
 Second-order influences on DNA
 structure, 39–60, 301–10
 Selective breeding, 154
 Sequence(s) (base-pair order in DNA)
 determination of, 213–15, 242–9
 direct repeats, 255–9
 DNA, repeating, curvature and
 twist of, 101–8
 proteins and DNA binding/
 recognizing, 68–9, 82–8, 107–10,
 130–3, 173–96
 Sequencing, di-deoxy, four-color
 method, 242–6
 Shapes
 DNA
 from gel electrophoresis, 217–25
 in solution, 107–10, 129, 132
 metaphase chromosomes, 5, 153–4
 protein, 10–11, 173–96
 Shift, dinucleotide steps, 308–9
 Si-RNA, 318–9
 Size of DNA
 effect on gel electrophoresis, 211–25
 persistence length, 107, 228
 relative, 1–4, 7
 Skew ladder, DNA as, 22
 Slide, base-pair motions, 45–60, 143,
 308–9
 DNA-protein recognition and,
 85–6
 helices varying due to, 54–60
 partial charge, 305–7
 sign convention, 46, 60
 twist, relationship, 53–5, 70
 Small interfering RNA, 318–19
 SNPs, 246–8
 Solution, DNA in
 curvature, 107–8
 thermal vibration, 110, 124, 131
 Southern blot, 273
 Spectral studies of DNA, 209–11
 Sperm de-methylases, 282–3

- Spirals, geometry of, 23–4, 98–100
see also helices; superhelices
- Spools
 DNA curvature/wrapping, 79, 80, 81, 109–10, 126, 127
 protein, 7–8, 78–9, 84, 126, 127, 139–45
- Stability
 helices, 32, 69–70
 superhelices, 126–7
- Stacking of base-pairs, 22, 23, 39–60, 70, 87, 301–10
- Steps, dinucleotide, 43–60
 DNA curvature, 73–8, 108–9
- Stop-codons, 12, 13, 17, 72
- Strand displacement amplification (SDA), 241
- Structure of DNA
 internal, 19–34, 39–60
 methods of studying, 203–28
- Sugar
 distance to next sugar, 20–3, 307–8
 nucleotide component, 8, 9, 19, 27–9
- Sugar-phosphate chains, 8–9, 20–9, 49, 54, 59–60, 88
 cutting, 84
 DNA sequencing, 242–3
 flexibility, 28–9, 47, 52, 308
 linking number, 122–8
 and topoisomerases, 67
 ‘Z’ helix, 25–7
- Superhelices/supercoils
 end restraint 117–18
 gel electrophoresis, 101, 223
 interwound, 117–29
 left-handed, 78, 98, 100, 106
 right-handed, 98, 106, 163–4
 simple models, 116–17
 stability, 127–8
 topology, 121–28
 toroidal, 116–29, 145
 twist and curvature in, 94–110
- Superoxide dismutase, 251
- Synthesis
 DNA (*see* replication)
 protein, 11–15, 32–4, 129–30
 RNA (*see* transcription)
- T**
T see thymine; twist
 T–A pairs *see* A–T pairs
 T–G pairs, 32, 33, 34, 285–8
 TATA box, 71–2
 TATA sequences, 110, 116, 191, 193
 TA/TA steps, 49, 51, 70, 109, 307
 TATA-type sequences, 69, 70–2, 86–7, 131
- Taxol, 68
- TBP (TATA-binding protein), 71–2, 86–7, 193
- Telomerase, 153
- Telomeres, 152–3
- TG/CA steps, 49, 51, 52, 53, 59, 307
- Thymine, 13, 19, 30, 31, 33, 40
 de-amination of methyl-cytosine, 285–7
see also A–T pairs
- Tilting, base-pairs, 55, 57–9
- Topoisomerases, 67, 118, 149
- Topology of supercoiling, 120–9
- Toroidal supercoiling, 116–29, 145
- Transcription factors, 84, 151, 160, 165, 193
- Transcription of DNA, 64–72, 129–33, 160–1
 lampbrush chromosomes, 147–8
 looped DNA, 147–51
see also activation, gene
- Transfer-RNA, 33
see also RNA
- Transgenic plants and animals, 154–5, 238, 284
 mice, 237–9, 249, 284
- Translations, base-pair motions, 45–8
- Triplet-repeating genetic diseases, 251–7
- TT/AA steps *see* AA/TT steps
- Twist (T), base-pair motions, 45–60, 64
 helices varying due to, 54–60
 low, 70
 propeller twist, 39–50, 60, 309
 sign convention, 46, 60
 slide, relationship, 53–5, 70, 307
 superhelices, 94–110
see also untwisting/unwinding
- Twist (Tw) in supercoils, 121–8
- U**
 U–G pairs, 32, 33, 34
 UAA stop-codon, 12, 72
 Underwound supercoiled DNA, 120–9
- Untwisting/unwinding of DNA, 64–72, 86–8, 116, 129, 131–2, 163–4
- Unwinding protein, 68–9, 174, 175
- Uracil, 14, 19, 30, 33, 276–7, 285–7
see also G–U pairs
- Urea-containing gel, 213, 215
- V**
 Vibration (thermal) of DNA in solution, 107, 110, 129, 131

W

Water, insolubility of bases, 19–23,
50–1, 302–4
Water molecules, 182, 207, 302
Watson, James, 29
Watson–Crick base-pairs, 29–34, 40,
51, 65–6, 69, 116, 129, 217
Writhe (Wr) in supercoils, 121–6, 129–31

X

X chromosome, 4, 5
X-ray diffraction, 203–8
histone octamer, 142
Xist RNA, 260–1

Y

Y chromosome, 4, 5

Z

'Z' helix
left-handedness, 25, 26
phosphates per helical turn, 25
sugar–phosphate chain, 26
Zif268 protein, 84–6, 160, 188–90
Zinc-finger proteins, 84–6, 160,
188–95