

Index

- Acinus 259
- Actin-related proteins (Arps) 373
- Activation-induced cytidine deaminase (AID) 39
- Active DNA demethylation, mechanisms for 38
- ADAR enzymes 268, 289, 357
- Adenine methylation 22
- Adf1 factor 125
- ADP-ribose 67
- Affinity mechanism for directing genes to periphery 194–197
- AGO4 317
- Allele-specific expression 15
- Alpha-globin locus 218
- Alternative splicing 257
- Amt1 factor 125
- Aneuploidy 490
- Annotation of genome 4
- Anomalous diffusion, advantage of 178–179
- APOBECs 357
- Architectural chromosomal proteins 147–150
- Asf1 (anti-silencing function 1) 73, 74, 75, 370
- Ash1 289
- Ataxia-telangiectasia mutated (ATM) 400
- ATP-dependent remodeling enzymes Chapter 5
- A-tracts 119
- A-type lamins 202
- AVPR1A regulation 10
- Barrier to autointegration factor (BAF) 186, 191, 456
- Base excision repair (BER) 396–398, 397
- Beta-globin locus 218, 219, 223
- chromatin loops in 219–222
- Bivalent histone modifications at promoters 105
- Boundary activity 190
- Branch point 257
- BRCA2 403
- Break-induced replication 408
- Bromodomains 98
- Cadherin 322
- Cajal bodies (CBs) 260, 428, 429
- Cap binding complex (CBC) 256
- Capping, 3' end formation and polyadenylation 255–257
- CBP20/80 256
- Cdc14 293
- Cell division 449, 450
- Center-mediated pairing 513–514
- Centromeres 489–490
- Centromeric-specific H3 (CenH3) 68, 368, 369, 370, 382
- CFTR 198, 218, 334
- Chaperone-mediated nucleosome assembly and disassembly, mechanism of 75
- Charcot–Marie–Tooth disease type 2B1 201
- Chia-PET 215–216
- ChIP-chip 13, 92
- Chip-loop 215–216
- ChIP-seq 13, 92
- Chp1 315
- Chromatids 471
- Chromatin Chapters 2–9, 15, 17–20
- Chromatin assembly factor 1 (CAF-1) 369, 370
- Chromatin-associated multiprotein complexes 543–548
- Chromatin–chromatin interactions 536, 537

- Chromatin conformation capture (3C)-based studies *see* Chromosome conformation capture
- Chromatin density distributions and accessibility of nuclear space 424–425
- Chromatin domains (CDs) 420
- Chromatin fiber Chapter 6, 150–155, 451–453
- Chromatin immunoprecipitation (ChIP) 12, 36, 91
- Chromatin loci, mobility of 426
- Chromatin looping 536, 537, 542
 - in beta-globin locus 219–222
 - formation of 218–223
 - *Cis* interactions 219–222
 - modeling of 538–539
 - proteins involved in 537–538
 - transcription factories 538
- Chromatin-modifying enzymes Chapter 2, Chapter 4, 192–193, 368
- Chromatin remodeler Chapter 5
 - accessory subunits of 113–114
 - activities of chromatin remodeling factors 114–115
 - ATPase families 112–113
 - nucleosome positioning, in genome 118–124
 - at promoters and enhancers 120–121
 - effects of chromatin remodelers on 122–124
 - gene regulation 124–127
 - nucleosome translocations, mechanisms of 115–118
 - loop-recapture mechanism 115–116
 - targeting to certain site 116–118
- Chromatin states 149–150
- Chromosome architecture
 - nucleosome chain folding Chapter 6
 - macromolecular crowding Chapter 7
 - nuclear lamina Chapter 8
 - as seen in 3C-based assays Chapter 9
 - nuclear organization during interphase Chapter 17
 - mitotic chromosome Chapter 18
 - polymer modeling 225–226, 420–421, Chapter 20
- Chromosome architecture analysis, by 3C-based assays 218–226
 - chromatin loops, formation of 218–223
 - *cis* interactions 219–222
 - *trans* interactions 222–223
 - chromosome compartmentalization 223–224
 - gene associations, in *cis* and *trans* 223
 - polymer aspects of 171–175, 225–226, 420–421, Chapter 20
- Chromosome conformation capture (3C) 212, 213, 217
- Chromosome conformation capture carbon copy (5C) 215
- Chromosome segregation patterns 487–489
- Chromosome territories (CTs) 224–225, 417, 420
- Chromosome territory–interchromatin compartment (CT-IC) model 420, 421
- Chromosomes as polymers 171–175, 225–226, 420–421, Chapter 20
- Chromosome-stretching experiments 459–460
- Circular chromosome conformation capture (4C) 214–215
- Cleavage and polyadenylation specificity factor (CPSF) 256
- Cleavage stimulating factor (CstF) 256
- CNV formation, major mechanisms of 7
- CO interference 521–522
- CO patterning 519, 520, 521
- Cockayne syndrome (CS) 399
- Cockayne syndrome protein B (CSB) 284
- Cohesin 149, 537, Chapter 18, Chapter 19
- Cohesin SMC complexes 454–455
- COL1A1* gene 189
- Comparative genomic hybridization (CGH) 7, 8
- Condensin I 453, 459
 - in *Drosophila* 454
 - in *Xenopus* 454
 - in yeast 454
- Condensin II 453, 459
- Condensin SMC complexes 453–454
- Constitutive transport element (CTE) 264
- Copy number variants (CNVs) 5, 6
- Core histones 55
- CpG islands Chapter 2
 - and promoter regulation 29–30
- Crossed-linker DNA chromatin fibers 153–154
- Crossover/chiasma Chapter 19
- Crowded environment of genome Chapter 7
 - anomalous diffusion 178–179
 - depletion or entropic forces 170
 - during mitosis 177–178
 - entropic and ionic interactions 179–180
 - entropic forces 175–176
 - finding targets in the genome 179
 - interphase genome 171–175
 - chromosomes and interchromatin compartment 174–175

- chromosomes as polyelectrolyte polymers 171–175
- polynucleosome chains, formation of loops in 174
- macromolecular crowding 169–170
- phase separation 170
- physicochemical parameters 171
- ionic environment 171
- macromolecular environment 171
- transcription and replication factories 176
- Cryptic transcripts 311
- Cryptic unstable transcripts (CUTs) 323
- CTCF 537
- C-terminal domain (CTD) 236, 315
- Cystic fibrosis transmembrane conductance receptor (*CFTR*) 189
- Cytosine methylation 21, 22, 23

- Damaged DNA-binding (DDB) binding proteins complex 399
- Dcp1/Dcp2 complex 265
- DcpS 265
- DEAD-box proteins 260
- Depletion or entropic forces 170
- Dihydrofolate reductase (DHFR) gene 334
- Diplotene 491
- Dis3/Rrp44 265
- Dmc1 497
- DmRrp6 291
- DmTRF4-1 291
- DNA
 - direct DNA/DNA interactions 513
 - junk DNA 309
 - rDNA, transcription of 282
 - rDNA locus, epigenetic mechanisms at 283–285
 - key players in epigenetic regulation of 283–284
 - integration of extracellular signals at 284–285
- DNA adenine methyltransferase 190
- DNA damage mediators/sensors 401
- DNA damage repair mechanisms Chapter 16
 - DNA-damaging agents 395
 - double-strand breaks (DSBs) 400–404
 - homologous recombination (HR) 403–404
 - non-homologous end joining (NHEJ) 401–403
 - signaling 400–401
 - interplay and quality control during 409–410
 - repair pathways 396–400
 - base excision repair 396–398
 - nucleotide excision repair (NER) 398–400
 - replication, repair process in 404–409
 - HR repair 406–408
 - mismatch repair (MMR) 404–406
 - translesion DNA synthesis (TLS) 408–409
- DNA demethylation 37–41
- DNA interactions with histone octamer protein core Chapter 3, 145–147
- DNA methylation Chapter 2
 - control of gene expression by 31–37
 - methyl-CpG binding proteins 32–35
 - transcription factor binding, loss of 32
 - epigenetic control of gene expression 22–24
 - eukaryotic DNA methyltransferases
 - Dnmt1 25–26
 - Dnmt3 family 26–27
 - Dnmts, cooperative function of 27
 - eukaryotic DNA methyltransferases 24–27
 - 5-methylcytosine
 - CpG islands and promoter regulation 29–30
 - in DNA 21–22
 - in mammalian genome 27–31
 - repetitive DNA sequences 30–31
 - spatial distribution of 27–29
 - temporal distribution of 31
 - and higher order chromatin structure and nuclear architecture 36–37
 - interconnection of, with other epigenetic pathways 35–36
- DNA polymerase
 - B-family 409
 - DNA polymerase β 398
 - TLS polymerases 397, 407–409
 - Y-family 409
- DNA rearrangement/elimination, in ciliates involves scanning RNAs 319–321
- DNA repair Chapter 16
- DNA replication Chapter 15
 - in chromatin context 365–368
 - de novo deposition of histones 369–371
 - epigenetic marks and post-translational modifications 375–383
 - fate of parental nucleosomes during 371–372
 - parental nucleosomes, disruption and recycling of 372–375
 - replication, repair process in 404–409
 - HR repair 406–408
 - mismatch repair (MMR) 404–406
 - translesion DNA synthesis (TLS) 408–409
 - replication-dependent *de novo* nucleosome deposition 368
 - replication restart, possible models for 407

- temporal coupling of histone synthesis with 368–369
- DNA sequence and nucleosome positioning 70–73, 121–122
- DNA sequence information Chapter 1
- genes and transcribed regions 1–4
- mapping transcriptional start sites 2–3
- mapping untranslated regions on mRNA 3–4
- open reading frames 2
- individual genetic polymorphisms on gene expression 16
- non-coding genomic elements 4–10
- pseudogenes 4–5
- repeats 5–6
- structural variant (SV) 6
- transposons and retrotransposons 9–10
- regulatory information 10–16
- allele-specific expression 14–16
- classes of regulatory elements 10–12
- transcription factor binding motifs 12–14
- DNA topoisomerase 411
- DNA topology, entanglement and supercoiling of chromatin in 466–467
- DNA transcription *see* Transcription
- Dnmt1 25–26, 25, 378, 379, 380
- Dnmt2 24
- Dnmt3 26–27
- Dosage compensation complex (DCC) 327
- Double Holliday junction (dHJ) 496
- Double-strand breaks (DSBs) 6, 7, 396, 400–404, 423, 494–495
- homolog bias 498
- homologous partner sequences, identification and interaction with 508
- one-ended 407, 408
- repair by NHEJ and HR 402
- signaling 400–401
- DSB-independent pairing 515
- Dunnigan-type familial partial lipodystrophy (FPLD2) 201
- Dyskerin 288
- eIF4A-III 289
- EKLF transcription factor 221
- Emerin 200, 202
- Emery–Dreifuss muscular dystrophy (EDMD) 201
- Endoribonuclease Swt1 266
- Energy-dependent nucleolar silencing complex (eNoSC) 285
- Entropic forces in the assembly of transcription factories 175–176
- Enzyme guanylyltransferase 256
- Epigenetic code 95
- Epigenetic control of gene expression Chapter 4
- Epigenetic marks Chapter 2, Chapter 4
- crosstalk between 103
- Epsilon gene 219
- ERBB-2* gene 189
- Euchromatin 149, 224, 422, 426–427
- Evolution of genomes 180
- Exon 1–2, 257, 261
- Exon junction complex (EJC) 259–262
- Exonic splice silencer (ESS) 260
- Exonic splicing enhancer (ESE) 260
- Expression quantitative trait loci (eQTLs) 12
- Extrinsic and intrinsic noise 239–240
- FACT 73–75
- Fluorescence *in situ* hybridization (FISH) 211, 536
- Fluorescence recovery after photobleaching (FRAP) 245, 543
- Fork stalling and template switching (FoSTeS) 6, 7
- methylcytosine
- CpG islands and promoter regulation 29–30
- discovery of, in DNA 21–22
- 5-hydroxymethylcytosine (5hmc) 40
- repetitive DNA sequences 30–31
- spatial distribution of 27–29
- temporal distribution of 31
- Fractal globule 226
- Gadd45 proteins 39
- GAGA 125
- γ H2AX 401
- Gal4 125
- GATA-1 transcription factor 125, 220
- G-bands 224
- Gcn5 94
- Gene activation from NE 200–201
- Gene associations in, *cis* and *trans* 223
- Gene deserts 354
- Gene movement and repression/activation, correlations between 197–198
- Gene regulation
- as consequence of peripheral positioning 198–201
- directed gene silencing from NE proteins 199–200
- gene activation from NE 200–201
- general silencing from peripheral environment 199
- epigenetic control of Chapter 2, Chapter 4

- in metazoan genomes 218
- via nucleosome positioning 124–127
- remodeler and nucleosomes as molecular switches 127
- transcription factors and nucleosomes, competitive binding of 124–126
- Genes and transcribed regions 1–4
- mapping transcriptional start sites 2–3
- mapping untranslated regions on mRNA 3–4
- open reading frames 2
- Genome architecture
- macromolecular crowding Chapter 7
- mitotic chromosome Chapter 18
- nuclear lamina Chapter 8
- nuclear organization during interphase Chapter 17
- nucleosome chain folding Chapter 6
- polymer modeling 225–226, 420–421, Chapter 20
- as seen in 3C-based assays Chapter 9
- Genome function, modeling of Chapter 20
- chromatin-associated multiprotein complexes, assembly of 543
- genomic target site, identification of 544–545
- key questions 544
- multiprotein chromatin-associated protein complex 546–548
- large-scale chromatin folding 536
- chromatin looping 536–538
- modelling of 538–542
- Genome organization with respect to nuclear periphery 187–190
- chromosome and gene positioning 187–189
- distinct microenvironment at NPC proteins 190
- epigenetic marks 189–190
- Genomic loci, typical mobilities of 426–428
- Germinal center-associated protein (GANP) 264
- Global genome repair (GG-NER) 398, 399
- Glucocorticoid-remedial aldosteronism (GRA) 10
- GR 125
- Gypsy insulator 197
- H2AX 401
- H3K27 methylation 323, 327, 330
- H3K27 trimethylation 327
- H3K36me3 92
- H3K4-specific methyl-transferase 100
- H3K56 acetylation 375, 376
- H3K9 methylation 319
- H3K79me3 92
- H3S10 453
- HBO1 (histone acetyltransferase binding to ORC1–KAT7) HAT 374
- Hdm2 294
- Helicase superfamily 2, 112
- Hemisomes 68
- Heterochromatin 23, 148–149, 188–194, 204–205, 224, 314–320, 376–381, 426–427
- Heterochromatin protein 1 (HP1) 100, 148, 188, 283, 315, 376–381, 453
- Hi-C 216–217
- High mobility group (HMG) proteins 456
- Higher order chromatin organization 417–438
- from 10-nm thick nucleosome chains to chromosome territories 418–424
- genome accessibility 424
- chromatin density distributions and accessibility of nuclear space 424–425
- mobility of inert molecules and complexes on different scales 425
- genomic loci, typical mobilities of 426–428
- large-scale chromatin dynamics 431–434
- considerations on possible mechanisms of 434–438
- mitosis 429–431
- mobility of nuclear bodies 428–429
- Histone acetylation 93, 96, 374
- Histone acetyl-transferases (HATs) 93, 94, 374
- Histone chaperones 73–76, 366–388
- Histone chaperones and chromatin dynamics 73–75
- chaperone-mediated nucleosome assembly and disassembly, mechanism of 75
- DNA repair 74–75
- DNA replication 74, 366–368
- transcription 73–74
- Histone code hypothesis 95–98
- exploiting complexity of 98–104
- histone 96–97
- predictive 104
- recognizing histone modifications 97–98
- Histone deacetylases (HDACs) 93, 374, 376
- Histone demethylases (HDMs) 93
- Histone fold 55
- Histone methylation 376, 377
- Histone-methyltransferases (HMTs) 93, 283
- recruitment of 102

- Histone modifications Chapter 4
 - in chromatin 93–95
 - “crosstalk” between different modifications 98–104
 - increased code complexity and signal integration 101–104
 - sequential processes on chromatin 101–104
 - complexity of 89–93
 - heritable epigenetic marks 104–106
 - histone code hypothesis 95–98
 - in nucleosome and chromatin structure 68–70
- Histone modification-specific antibodies 90
- Histone-modifying enzymes 93–95, 127
- Histone octamer 56–60
 - DNA interactions 60–63, 145–147
 - DNA sequence-dependent binding affinities of 118–119
- Histone tails Chapter 3, Chapter 4
- Histone variants
 - effect on nucleosome structure and dynamics 66–68
 - location, biological role and homology of 66
- Histones 56–60
 - de novo deposition of 369–371
- HNF3/FoxA 125
- Holliday junction 403
- Holliday junction recognition protein (HJURP) 382
- Homologous chromosome pairing 493, 507–515
- Homologous recombination (HR) 396
 - DSB repair by 402–404
 - models for replication restart by 407
 - repair during replication 406–408
- HOTAIR 329
- Hox clusters
 - non-coding RNAs (ncRNAs) 328–330
- HSF 125
- Hutchison–Gilford Progeria syndrome (HGPS) 201
- IBP160 262
- Igf2 locus 218
- Imitation SWItch (ISWI) 373
- Immunoglobulin H (*IgH*) 189
- Imprint control element (ICE) 336
- Inactive X chromosome 318, 326, 327
- ING5 374
- Inner nuclear membrane (INM) 186
- INO80 373
- Interchromatin compartment (IC) 421
- Interchromatin domain (ICD) model 421
- Interchromatin network (ICN) model 421
- Interferon gamma *IFN-γ* 200
- Interphase genome 171–175
 - chromosomes and interchromatin compartment 174–175
- Interstrand crosslink (ICL) 408, 411
- Intron definition 1, 2, 260
- Intronic ncRNAs 312, 334
- Intronic splicing enhancer (ISE) 260
- Intronic splicing silencer (ISS) 260
- ISWI remodelers 113–114
- Kinetochore assembly 68
- KLF1 transcription 223
- Lac operator (lacO) 194
- LacI–NET fusions 195
- Lamin B receptor (LBR) 191, 202
- Lamins
 - and INM proteins 191
 - and NETs 190
- Large-scale chromatin dynamics 431–434
 - considerations on possible mechanisms of 434–438
- Lengthwise condensation, and chromosome segregation 472
- Leptotene 491
- Limb–girdle muscular dystrophy (LGMD) 201
- Linker histones 55, 148, 452
- LMNA mutations 201
- Lmo7 200
- Locus control region (LCR) 219
- Long interspersed nuclear elements (LINEs) 10
- Long non-coding RNAs (lncRNAs) 354
- Loop–recapture model 115–116
- LSD1/co-Rest 94
- Lymphoblastoid cell line (LCL) transcriptome 12
- Lysine, methylation of 97
- Lytechinus variegatus* 142
- m7-G cap 256
- MacroH2A 66–67
- Macromolecular crowding Chapter 7
- Macronucleus 319
- Male specific lethal (MSL) 327
- MAN1 202
- Mash1* gene 189, 194, 198
- Mason–Pfizer monkey virus (MPMV) 264
- MeCP2 149
- Meiosis Chapter 19

- Meiotic chromosome dynamics 487–523
 - aneuploid gametes, producing 490
 - coordination with recombination 500–507
 - organization of meiotic chromosomes 500–504
 - recombinosome–axis association and functional interplay 504–507
 - homologous chromosome pairing 507–515
 - recombination-independent pairing 512
 - recombination-mediated axis juxtaposition 507–512
 - meiosis versus mitosis 487–489
 - recombination and spatial patterning 515–523
 - recombination at DNA level 494–500
 - completion 495–497
 - initiation 494–495
 - modulation 497–499
 - temporal coordination with basic meiotic stages 499–500
 - segregation via tension-mediated sensing of connectedness 487–489
 - sister connectedness, modulation of 489–490
 - two divisions 490–494
- Meiotic recombination and spatial patterning 515–523
 - chromosomal events 516–518
 - crossover/chiasma patterning 516
 - basic logic of 518–519
 - models and mechanisms 519–523
 - crossover interference 523
 - interference and even spacing, mathematical descriptions of 522–523
 - nucleation and spreading, molecular basis for 520–522
 - stress and stress relief 519–520
- Meiotic stages and pachytene chromosomes
 - cytological views of 492
- Messenger RNA (mRNA) Chapter 11
 - biosynthesis of 255–265
 - capping, 3' end formation and polyadenylation 255–257
 - exon junction complex (EJC) 261–262
 - mRNA degradation pathways 264–265
 - nuclear export of mRNA 262–264
 - pre-mRNA splicing 257–261
 - cytoplasmic mRNA quality control
 - processing bodies 268–269
 - mapping untranslated regions on 3–4
 - mRNA-containing RNPs (mRNPs) 289, 289
 - mRNA degradation pathways 264–265
 - nonsense-mediated decay 268–274
 - NMD in mammalian cells 271–272
 - pioneering round of translation 271
 - recognition of premature stop codons 270–271
 - and nuclear quality control 265–268
 - nucleoplasmic retention 265–268
- Methylcytosine 22
- Methyl transfer reaction, mechanism of 25
- Methyl-CpG binding proteins 32–35, 104, 380
 - domain structures of 33
- MicroRNA-containing RNPs 289–290
- Micrococcal nuclease (MNase) 119, 140
- Micronucleus 319
- Mini-chromosome maintenance (MCM) 371
- Minisatellites 5
- Mismatch repair (MMR) 396, 404–406, 405
- Mitosis 429–431
 - crowded environment of genome during 177–178
- Mitotic cell cycle, phases of 491
- Mitotic chromosome Chapter 18
 - large-scale organization of 457–459
 - mechanics of 459–465
 - bending stiffness 463–464, 473
 - chromosome-stretching experiments 459–460
 - reversible folding and unfolding, by salt 464–465
 - stretching elasticity 460–463, 472–473
 - molecular connectivity of 465–468
 - DNA topology, entanglement and supercoiling of chromatin in 466–467
 - interchromosome linkers 467–468
 - nucleases disintegrate mitotic chromosomes 465–466
 - proteases, expanding 466
 - structural components of 450–457
 - chromatin fiber 451–453
 - chromosomal proteins 456–457
 - cohesin SMC complexes 454–455
 - condensin SMC complexes 453–454
 - topoisomerase II 455–456
 - structure and function 468–474
 - as chromatin networks 468
 - crosslinking elements 468–469
 - lengthwise condensation and chromosome segregation 472
 - molecules, cutting and removing effects of 473–474
 - SMC-crosslinked chromatin network model 469–472
- MLL 100
- Molecular copy-number counting (MCC) 9
- Mouse beta-globin locus 220
- MTA2 gene 34

- MukBEF complex 455
- Multiloop subcompartment (MLS)
 - model 541
- Native chromatin fragments 140–142
- NER proteins 546, 547
- Nesprin 202
- Neuronal cells 354
- NMD pathway 270
- No-go decay (NGD) 268, 272
- Non-allelic homologous recombination (NAHR) 6, 7
- Non-coding genomic elements 4–10
 - pseudogenes 1–17
 - repeats 5–6
 - structural variants 6
 - SV detection, methods for 6–9
 - transposons and retrotransposons 9–10
- Non-coding RNAs (ncRNAs) Chapter 13, Chapter 14
 - classification of 311–314
 - definition of 311
 - in dosage compensation 324–328
 - gene regulation mechanisms 332
 - and Hox clusters 328–330
 - regulation *in trans* 329–330
 - transcription leads to altered DNA accessibility 328–329
 - transcription through Hox gene promoters interferes with their expression 329
 - transcripts bind regulatory factors 329
 - long ncRNAs, mechanisms of transcriptional regulation by 330–338
 - directly regulating transcription and RNA processing 334–335
 - gene regulation, expression via ncRNA-induced epigenetic modifications 335–337
 - large-scale chromatin structure 337–338
 - RNA processing 335
 - transcriptional read through leading to activation or silencing 333–334
 - as regulators of transcription and genome organization 309–338
 - small regulatory RNAs, their diverse nuclear functions 314–324
 - DNA rearrangement/elimination, in ciliates involves scanning RNAs 319–321
 - piRNAs, in animals 317–319
 - promoter- and gene-derived transcripts, in yeast and animals 323–324
 - siRNA-mediated activation 322–323
 - siRNAs and miRNAs, transcriptional repression mediated by 321–322
 - siRNAs in animals 317–319
 - siRNAs in yeast and plants 314–317
- Non-homologous end joining (NHEJ) 6, 7, 401–403
 - DSB repair by 402
- Nonsense-altered splicing (NAS) 267
- Nonsense-mediated decay (NMD) 291, 268
- Non-stop decay (NSD) 268, 273
- NoRC remodeling complex 127
- Nuclear autoantigenic sperm protein (NASP) 370
- Nuclear bodies (NBs) 426
 - mobility of 428–429
- Nuclear corepressor (N-CoR) 34
- Nucleolar dominance 281
- Nuclear envelope (NE) proteins
 - and chromatin proteins/chromatin regulatory proteins 191–193
- chromatin-modifying enzymes 192–193
- epigenetically marked chromatin interactions 192
- directed gene silencing from 199–200
- gene activation from 200–201
- linked diseases 201–202
- Nuclear envelope breakdown (NEB) 453
- Nuclear lamina Chapter 8
 - gene regulation
 - as consequence of peripheral positioning 198–201
 - directed gene silencing from NE proteins 199–200
 - gene activation from NE 200–201
 - general silencing from peripheral environment 199
 - genome organization with respect to nuclear periphery 187–190
 - chromosome and gene positioning 187–189
 - distinct microenvironment at NPC 190
 - epigenetic marks 189–190
 - mechanisms directing changes, in genome organization during development 193–198
 - affinity mechanism for directing genes to periphery 194–197
 - correlations between gene movement and repression/activation 197–198
 - dynamic changes in 193–194
 - NE proteins
 - and chromatin proteins/chromatin regulatory proteins 190–193
 - chromatin and DNA 191–192
 - NE proteins and chromatin proteins/chromatin regulatory proteins

- chromatin-modifying enzymes 192–193
- epigenetically marked chromatin interactions 192
- peripheral chromatin organization and disease 201–203
- heterochromatin organization in disease, changes in 202–203
- NE-linked diseases 201–202
- Nuclear pore complexes (NPCs) 186
- Nuclear RNAi defective-2 (NRDE-2) protein 322
- Nucleolar associated domains (NADs) 285
- Nucleolar organizer regions (NORs) 280–282
- Nucleolar proteome 292
 - cell cycle and cell fate 293–294
 - dynamic dimensions of 292–294
 - nucleolus as stress sensor 294
- Nucleolar remodeling complex (NoRC) 283, 284
- Nucleolus Chapter 12
 - and its DNA 279
 - additional implications of chromatin in nucleolus 285
 - epigenetic mechanisms at rDNA locus 283–285
 - nucleolar organizer regions (NORs) 280–282
 - rDNA, transcription of 282–283
 - nucleolar proteome 292
 - cell cycle and cell fate 293–294
 - dynamic dimensions of 292–294
 - nucleolus as stress sensor 294
 - and RNPs 285
 - micro RNA-containing RNPs 289–290
 - mRNA-containing RNPs (mRNPs) 289
 - quality control centre, nucleolus as 291–292
 - ribosome 286–288
 - RNase MRP and RNase P 291
 - signal recognition particle 288
 - small nucleolar RNPs (snoRNPs) 290–291
 - telomerase 288
 - U6 small nuclear RNP 288–289
- Nucleoplasm Chapter 7
- Nucleoporins 262, 265
- Nucleosome chain Chapter 6
 - architectural chromosomal proteins and chromatin states 147–150
 - cohesin and condensin protein complexes 149
 - Heterochromatin protein 1 (HP1) 148
 - high mobility group (HMG), proteins with 148
 - linker histones 148
 - MeCP2 148–149
 - chromatin fiber conformations 150
 - crossed-linker DNA chromatin fibers 153–154
 - solenoid chromatin fiber models 151–153
 - DNA interactions with the histone octamer protein core 145–147
 - experimental systems 140–142
 - native chromatin fragments 140–142
 - reconstituted nucleosome chains 142
 - nucleosome–nucleosome interactions 142–145
 - contributions of histone tails to 145
 - of globular part of histone octamer core 144
 - strength of 143
- Nucleosome positioning Chapter 5
 - effects of chromatin remodelers on 122–124
 - gene regulation 124
 - remodeler and nucleosomes as molecular switches 127
 - transcription factors and nucleosomes, competitive binding of 124–126
 - genome-wide analysis of 119–120
 - histone octamer, DNA sequence-dependent binding affinities of 118–119
 - prediction from DNA sequence 121–122
 - at promoters and enhancers 120–121
- Nucleosome repeat length (NRL) 119, 140, 418
- Nucleosome translocations, mechanisms of 115, 117
- Nucleosome, modular assembly of 59
- Nucleosome-depleted regions (NDRs) 70
- Nucleosome-free regions (NFRs) 120
- Nucleosome–nucleosome interactions 142–145
 - orientation dependence of 144
 - strength of 143
- Nucleosome Chapter 3
 - basic terminology 55–56
 - DNA sequence and nucleosome positioning 70–73
 - dynamic macromolecular assemblies 63–66
 - histone chaperones and chromatin dynamics 73–75
 - histone modifications 68–70
 - histone variants, role of 66–68
 - histones 56–60
 - mechanisms to promote histone exchange in vivo 63–64

- Nucleosome (*Continued*)
 - nucleosomal DNA, structure of 61–63
 - protein DNA interactions, in nucleosome 60–61
 - stability, in vitro determination of 64–66
- Nucleotide excision repair (NER) 396, 397, 398–400, 544, 545
- kinetic model of 545
- NXF1-p15 heterodimers 264
- Open reading frames (ORFs) 2, 271, 314
- Opposing classes of enzymes 93, 100
- Oscar gene 314
- p21 322, 323
- p53 stability 294
- Pachytene 491
- Paired-end mapping (PEM) 8, 9
- Paraspeckles 268
- Parental histone segregation 368
- PCNA-interacting protein box (PIP box) 381
- Perichromatin region (PR) 421
- Perinucleolar compartment (PNC) 286
- PHD finger 98
- Physicochemical parameters of the genome's environment
 - ionic environment 171
 - macromolecular environment 171
- Pinin 259
- Pioneering protein factors
 - in chromatin remodeling and nucleosome positioning 125–126
- Plant homeodomain (PHD) 34
- PML nuclear bodies (PML-NBs) 428
- Poly (dA : dT) DNA sequences 71, 119, 122
- Poly(A) polymerase (PAP) 256
- Poly(A)-binding protein (PABPN) 256, 271
- Polyadenylated mRNA 255–256, 266
- Polycomb (Pc) 326
- Polycomb repressive complex 1 (PRC1) 381
- Polycomb repressive complex 2 (PRC2) 35, 381
- Preinitiation complex (PIC) 282
- Premature termination codons (PTCs) 259, 262
- Progesterone receptor (PR) 125, 322
- Proliferating cell nuclear antigen (PCNA) 26, 366, 398, 409
- Promoter associated small RNAs (PASRs) 281, 313, 323–324
- Protein phosphatase 1 (PP1) 293
- Proteolipid protein (PLP) 191, 202
- prp19/CDC5L complex 260
- Pr-Set7 381
- Pseudogenes 4–5
- PseudoNORs 282
- Rabl configuration 197
- Rad51 403, 497
- Rad54 403
- Random loop (RL) model 421, 540
- Random-walk giant loop (RWGL) model 540
- R-bands 224
 - transcription and chromatin 282–283
 - transcription initiation 282
- Recombination, meiotic 494–500
 - completion 495–497
 - -independent pairing 512
 - initiation 494–495
 - modulation of 497–499
 - temporal coordination with basic meiotic stages 499–500
- Recombinosome–axis association 504–510
- Regulatory DNA elements 11
- Repeat A (RepA) 327
- Replication factor C (RFC) 374
- Replication fork barriers (RFBs) 280
- Replication protein A (RPA) 399, 403
- Restrictive dermopathy 201
- Retinoblastoma protein (Rb) 200
- Retrotransposons 9–10
- Ribonucleoprotein particles (RNPs) 261, 285
- Ribosomal DNA (rDNA) 279, 280
 - active 281, 283
 - epigenetic mechanisms at 283–285
 - key players in epigenetic regulation of 283–284
 - integration of extracellular signals at 284–285
 - inactive 281
- Ribosome 284–288
- RNA *see also* Messenger RNA (mRNA); Non-coding RNAs (ncRNAs); Small interfering RNAs (siRNAs)
 - double-stranded RNA (dsRNA) 2
 - dsRNA mapping 317
 - eRNAs 337
 - mapping untranslated regions on 3–4
 - microRNAs (miRNAs) 2, 257, 311, 313–314, 354
 - mRNA-containing RNPs (mRNPs) 260–261, 266, 272
 - nuclear mRNA 264
 - piRNAs, in animals 317–319
 - piwi-interacting RNAs (piRNAs) 311, 312, 317–319, 354
 - pre-messenger RNA (pre-mRNA) 256

- splicing 257–261, 258
- promoter RNAs (pRNAs) 281
- promoter-associated small RNAs (PASRs) 313, 323
- ribosomal RNAs (rRNAs) 2, 311
- scn RNAs 319, 320
- small nuclear RNAs (snRNAs) 313
- small nucleolar RNAs (snoRNAs) 290–291, 312, 313, 354
- small RNAs 354, 355
- snoRNAs 257, 355
- snRNAs 257
- spliRNAs 355
- terminus-associated small RNAs (TASRs) 313, 324
- RNA-dependent RNA polymerase (RDRP) 312, 315
- RNAi-dependent methylation 317
- RNA FISH 240–243
- RNA-induced silencing complexes (RISC) 353, 356
- RNA-induced transcriptional silencing (RITS) 315
- RNA networks 353–358
 - human genome, information content of 353–354
 - non-coding RNAs 354–355
 - RNA as adaptor in digital–analog transactions 356
 - RNA as substrate for environment–epigenome functions 357–358
 - RNA control of nuclear functions 355–356
- RNA polymerase (RNAP) Chapter 10
- RNA processing Chapter 11
- RNA recognition motifs (RRM) 260
- RNase MRP and RNase P 291
- RNF8 401
- Rrp6 265
- Scaffold/matrix-associated region (S/MAR) 537
- Scaffold protein I 456
- Scaffold protein II 453
- Scan RNAs (scn RNAs) 319, 320
- Segmental duplications (SD) 5
- Selfish DNA 354
- SEN3 293
- SEN5 293
- SER3 gene 334
- Serine/threonine kinase 271
- SET- and Ring-associated (SRA) domain 34
- SetDB1 (Set domain bifurcated 1/KMT1E) 377
- Short interspersed nuclear elements (SINEs) 10
- Signal recognition particle (SRP) 288
- Single nucleotide polymorphisms (SNPs) 6
- Single-end invasion (SEI) 496
- Sm protein 257
- Small interfering RNAs (siRNAs) 311, 312, 317–319, 354
 - heterochromatin formation and maintenance, in yeast and plants 314–317
 - and miRNAs
- transcriptional repression mediated by 321–322
- SMC-crosslinked chromatin network model 469–472
- SMC–kleisin complexes 453
- Snf2 family of proteins 112
- Snf2L protein 113
- Solenoid chromatin fiber models 151–153
- SP1 125
- Spliceosome 260
- Splicing factor 1 (SF1) 259
- Spo11 transesterase 494
- Spt6 74
- Ssn6-Tup1 complex 127
- Stable unannotated transcripts (SUTs) 323
- Staufen 289
- Steroid receptor RNA activator (SRA) 314
- Structural maintenance of chromosomes 449
- SURF complex 272
- Synaptonemal complex (SC) 491
- Synthesis-dependent strand annealing (SDSA) 403, 404, 497
- Tandem repeats 5
- Tarsal-less (tal) gene 314
- TATA box binding protein (TBP) 282
- TBP-associated factors (TAF) 282
- Telomerase 288
- Telomere bouquet 510
- Telomere clustering and movement 511
- Tension-mediated sensing of connectedness
 - and chromosome segregation 487–489
- Tethered loop axis complexes 504
- TFIIIA 125
- Tfr4 265
- Th2 locus 218
- THO complex 266
- Thyroid hormone receptor (TR) 126
- TIP5 (TTF-1-interacting protein 5) 283
- Tissue-dependent differentially methylated region (T-DMR) 335

- TLS polymerase 407, 408, 409
- Topoisomerases 455–456, 472
- TRAMP cofactor 266
- TRAMP complex 265, 323
- Transcription Chapter 10
 - bursting 245–250
 - duration of 245–246
 - effects of chromatin remodeling and histone modifications on 247
 - extrinsic and intrinsic noise 239–240
 - histone chaperones and chromatin dynamics 73–74
 - RNA FISH 240–243
- Transcription factor binding, loss of 32
- Transcription factor IIH (TFIIH) 399
- Transcription factory 175–176, 247–250, 432, 538
- Transcription initiation RNAs (tiRNAs) 323, 324, 355
- Transcription start sites (TSSs) 29, 323
- Transcription termination factor 1 (TTF1) 284
- Transcriptional gene silencing (TGS) 322 235–250
- Transcriptional interference (TI) 333
- Transcriptional start sites, mapping 2–3
- Transcription-coupled repair (TC-NER) 398, 399
- Transfer RNAs (tRNAs) 311, 312
- Translesion DNA synthesis (TLS) 396, 408–409
- Transposable elements (TEs) 9–10, 317
- Trf5 292
- Trichothiodystrophy (TTD) 399
- Tsix 327
- TTF-I 126
- U2 auxiliary factor (U2AF) 259
- U6 small nuclear RNP 288–289
- Uhrf1 34
- Untranslated regions' (UTRs) mapping on mRNA 3–4
- Up-frameshift proteins (Upf1–Upf3) 271
- Upstream binding factor (UBF) 282
- Upstream control element (UCE) 282
- Upstream ORF (uORF) 3
- Uridine-rich small nuclear nuclear ribonucleoparticles (U snRNPs) 257
- USF 126
- Variant nucleosome structures 67–68
- Vimentin filaments with nuclear localization 429
- Williams syndrome transcription factor (WSTF) 373
- X chromosome inactivation (XCI) 222, 324, 326
- Xeroderma pigmentosum (XP) 399
- Xist 310, 311, 326
- XPA 399
- XPB 399
- XPC 545
- XPB 399
- Zygotene 491
- Zygotene interlocks 510