This is a free sample of content from The Nucleus, Second Edition. Click here for more information on how to buy the book.

Index

Α

Actin filament action in nucleus assembly, 159-161 cell cycle, 162-163 DNA damage repair, 163-164 long-range chromatin motion, 162 signaling, 161-162 viral replication, 163 monomer action in nucleus allosteric regulation of chromatin remodeling complexes, 157-158 MRTF/SRF-mediated transcription signaling, 155, 157 pools in cytoplasm and nucleus, 154-155 RNA polymerase II functions, 158-159 signaling functions, 156 overview, 153-154 Activin A, 493 ACTN4, 163 AKT, 78 ALPS domains, 31 Alternative polyadenylation (APA), 358 AMPK, 99 ANCHOR, 313 AP-1, 389, 396 AP-2, 389 APA. See Alternative polyadenylation APEX, 284 AR, 373, 379 ARID1A, 158 Arp2/3, 159, 161, 163-164 ASAR, 341-342 ATAD2, 498 ATG11, 35 ATG8, 35 ATRX, 399

В

BAF, 6–7, 74, 78, 157–158, 372–373, 377, 381, 492, 498 BANF1, 17 Barr body, 269 BCR-ABL fusion, 375 BDNF, 358 BMAL1, 77 BPTF, 492 BRD4, 114, 315, 381, 392, 503 Btf, 74

С

CAF-1, 435 Cajal body, 257, 273-274 Calcium flux, mechanotransduction, 98 Cancer chromatin machinery defects cis-regulatory elements aneuploidy, gene expression, and nuclear structure, 379-381 enhancer amplification, 378-379 enhancer hijacking, 378 oncogenes, 379 transcription factor binding, 377-378 deletions RB1, 377 SMARCB1, 377 large-scale alterations, 375-376 mutations chromatin remodeling complexes, 373 DNA methylation genes, 373-374 histone modifiers, 374-375 histones, 372 transcription factors, 372-373 MYC/MYCN gene amplifications, 376-377 overview of machinery, 371-372, 381 prospects for study, 381-382 overview of genetic errors, 369-371 Cbf1, 54 CBP, 238, 276, 374, 395 CCM. See Chromosome copolymer model CD47, 358 CDK, 337, 339 CDK1, 3, 32 CDK5, 3 CDK9, 115, 118, 397 CEC-4, 14 CELF1, 460, 469, 475 CENP-A, 162 CENP-C, 500 CFP1, 431

CHD1, 373, 498 CHM7, 34, 78 Chromatin. See also Nucleosome cancer defects. See Cancer deformation by force, 97 folding in embryogenesis. See Embryogenesis lamina-associated domain geographic organization, 12 mechanical properties and genome organization/ function, 99-101 motion constraints, 177-181 overview, 176-179 organization in nucleus, 175-176 pluripotent cell structure chromosome organization, 500 loops, domains, and interaction hubs, 500 - 502nucleosome organization, 496 open chromatin genome accessibility, 498 remodeling, 498-499 overview, 494-496 prospects for study, 502-503 prospects for study, 181-182 RNA interactions. See RNA-chromatin interactions structure fibers and condensates in vitro, 174-175 overview, 169-171, 173 three-dimensional modeling of genome folding approaches, 211-213 data-driven modeling data deconvolution, 219-221 resample methods, 221–222 mechanistic modeling chromatin loops and topologically associating domains, 214-215 combining loop extrusion and block copolymer models, 216-219 global chromatin compartmentalization, 215-216 overview, 209-211 prospects for study, 222-223 Chromatin subcompartment (CSC) assembly studies, 116 chromocenter features as phase-separated subcompartment, 114 high-resolution structure, 115, 117 liquid-liquid phase separation contribution to structure. 122 - 123

marker protein internal mixing and nucleoplasm exchange, 118 structure-function relationships in establishment, 121-122 formation mechanisms, 110-112 nucleic acid/protein ratios and local viscosity, 118-119 nucleolus features as phase-separated subcompartment, 113 high-resolution structure, 115 liquid-liquid phase separation contribution to structure, 122-123 marker protein internal mixing and nucleoplasm exchange, 117 structure-function relationships in establishment, 119-120 overview, 109-110, 285-288 prospects for study, 123-124 RNA polymerase II transcription factories features as phase-separated subcompartment, 113-114 high-resolution structure, 115 liquid-liquid phase separation contribution to structure, 122-123 marker protein internal mixing and nucleoplasm exchange, 117-118 structure-function relationships in establishment, 120-121 Chromocenter. See Chromatin subcompartment Chromosome copolymer model (CCM), 218 Chromosome folding cell cycle changes in chromosome shape, 200 - 201cell-type specificity and nuclear organization, 201 - 202compartmentalization, 191-193 interplay between mechanisms compartmentalization versus tethering, 199 extrusion versus compartmentalization, 198-199 transcription, compartmentalization, and loop extruders, 199-200 loop extrusion functional roles, 195-196 mechanics, 194-196 overview, 193-194 mechanisms, 189-191 pluripotent cells. See Pluripotency tethering to subnuclear structures, 196-198 three-dimensional modeling of loop extrusion, 214-219 topological effects, 198

Cis-regulatory elements (CREs) cancer alterations aneuploidy, gene expression, and nuclear structure, 379-381 enhancer amplification, 378-379 enhancer hijacking, 378 oncogenes, 379 transcription factor binding, 377-378 hubs, 309-311 kinetics, 312-313 overview, 303-304 spatial scales in nucleus, 305 transcription-associated nuclear foci, 311 CIZ1, 460 Cleavage body, 276-277 Clk1, 292 CMV. See Cytomegalovirus Cofilin, 154 Cohesin, 51, 307-309 Coilin, 273 Condensin II, 200 Constant timing region (CTR), 328, 330 CREs. See Cis-regulatory elements CRM1, 33-34 CSC. See Chromatin subcompartment CTCF, 10-11, 51-52, 118, 135-136, 142-143, 145, 175, 193-196, 200-202, 214-216, 219, 221, 235, 306-309, 315, 333, 335, 338, 372-374, 381, 395-396, 410, 412, 415-416, 419-420, 437-438, 440, 466, 469-470, 500 CTR. See Constant timing region Cytomegalovirus (CMV), 163, 399-400

D

DAXX, 276 DDK, 337, 339 Development. See Embryogenesis DNA-FISH, 306-307, 317 DNA methylation. See Epigenetics DNA polymerase, 339 DNA replication timing cytological studies, 330-332 genome-wide profiling, 328 Hi-C compartment correlation, 332-333 overview, 327-328 prospects for study, 342-343 regulation early replication control elements, 338-339 initiation, 337-338 trans-acting regulators, 339-341 whole chromosome territory regulation, 341 - 342

single-cell measurements, 328, 330 subnuclear landmarks lamina-associated domains, 335-336 models of nuclear organization, 337 nucleolus-associated domains, 335-336 speckle-associated domains, 336-337 topologically associating domains and replication domain relationship, 333, 335 DNMT1, 377, 429-430 DNMT3A, 429 DNMT3B, 429 DNMT3C, 429 DNMT3L, 429 DPPA2, 433, 436 DPPA4, 433, 436 DUX, 436 DYT1, 79

E

Eaf1, 158 Early replication control element (ERCE), 338-339, 342 - 343EBNA1, 394 EBNA2, 394 EBNA3C, 394 EBNA-LP, 394 EBV. See Epstein-Barr virus EED, 433 Embryogenesis chromatin folding and gene expression CTCF in domain insulation, 415 dynamic versus preformed folding, 413-415 structural variation impact on genome organization, 417-419 topologically associating domains in gene expression, 415-416 transcriptional control mechanisms, 416-417 transposable element functions, 419-420 genome three-dimensional organization early embryogenesis, 412-413 overview, 410-412 prospects for study, 420-421 X chromosome inactivation. See X chromosome inactivation Embryonic stem cell (ESC), 490-491, 494, 498, 502 Emerin, 6, 16, 60, 75-76, 274 ENCODE project, 305, 498 Enhancer cis-regulatory elements and cancer alterations amplification, 378-379 hijacking, 378 enhancer-promoter proximity bursting in single-cell studies, 145-147

Enhancer (Continued) range of action, 144–145 transcription activation dependence, 143-144 EP300, 381 EPHA4, 219, 417 Epigenetics histone modifier defects in cancer, 374 - 375nuclear pore complex in memory regulation, 54-55 pluripotency DNA methylation, 492 histone modification, 492-493 reprogramming in early development DNA methylation, 429-430 histone modification bivalent modifications, 433 H2K119ub, 434 H3K27me3, 431-433 H3K36me2/3, 434-435 H3K4me3, 430-431 H3K9me3, 435-436 overview, 427-429 preimplantation embryo chromatin maturation, 440 prospects for study, 440-445 transposable elements, 436 Epstein-Barr virus (EBV), 390, 393-394 ER, 114, 118 ERCE. See Early replication control element ERVK, 435 ERVL, 435 ESC. See Embryonic stem cell ESCRT-III, 77-78, 80 ETS2, 373 EWS, 375 EZH2, 374

F

FAM208A, 397 FAN-1, 73 FBL. *See* Fibrillarin Fertilization, conserved relaxed chromatin organization, 438–440 FGF2, 493 FGF4, 374 Fibrillarin (FBL), 113, 115, 117, 119 53BP1, 73 FIRRE, 263 FLASH, 262, 276 FLI1, 375 FOXA1, 118 FOXO1, 375–376, 378

G

GAGA, 53 GAL1, 53 GAL4, 235 GAM. See Genome architecture mapping GATA2, 144 GATA3, 378 **GATOR2, 37** GCL, 74 GCN4, 114 Gcn4, 53 Genome architecture mapping (GAM), 285, 309 Genome structure enhancer-dependent transcription activation, 143 - 144enhancer-promoter proximity bursting in single-cell studies, 145-147 range of action, 144-145 ensemble studies, 135-137 ensemble topologically associating domains, 142 - 143single-cell studies, 137-139 techniques for study, 134 topologically associating domains, 142-143 transcription and stochastic genomic structure, 139-142, 147 GFI1, 378, 417 GFI1B, 378, 417 GLI1, 75 GRS1, 54 GRS2, 54 GSK3, 492

Н

H1, 171, 181, 371 H19, 252 H2A, 171, 371 H2B, 171, 371 H3, 171, 181, 201, 371-372 H4, 171, 371 HAND2, 381 HBV. See Hepatitis B virus HDAC3, 14, 74-75, 258, 470, 474 Heh1, 78 Hepatitis B virus (HBV), 390, 395, 400 HERV-H, 420 HHV-6B, 399 Hi-C, 134-138, 191-195, 198-199, 213-222, 282-285, 332-334, 380-381, 393-395, 409-412, 490, 500-501 HIRA, 276 Histone locus body (HLB), 257, 276 Histone modification. See Epigenetics

This is a free sample of content from The Nucleus, Second Edition. Click here for more information on how to buy the book.

Index

HIV. See Human immunodeficiency virus HLB. See Histone locus body HMGB1, 395 HOXA9, 55 HOXD13, 55 HP1, 12, 65, 110, 114-115, 118, 121-123, 181, 216, 241, 260, 287, 416, 497 HPV. See Human papillomavirus HSP70, 357 HSPA1A, 290-291 HSPA1B, 290 HSV-1, 390-391 HSV-2, 390-391 HTLV-1, 390, 395 Human immunodeficiency virus (HIV), 74, 390-393, 396-397, 399-400 Human papillomavirus (HPV), 390, 399 HUSH, 396-397

I

ICM. See Inner cell mass ICP0, 399 IDH1, 373 IDH2, 373 IDRs. See Intrinsically disordered regions IE1, 399 IGF2, 417 IGM. See Integrated Genome Modeling Importin β , 32, 34 INF2, 162 INM. See Inner nuclear membrane Inner cell mass (ICM), 490 Inner nuclear membrane (INM) overview, 59-64 proteins. See also specific proteins diseases, 68-71 emerin, 75-76 LAP1, 79-80 LAP2, 74-75 LBR, 65, 67, 72 LEM domain proteins, 74 LEM2, 77-79 MAN1, 76-77 SAMP1, 79 SUN domain proteins, 72-74 table, 61-63 proteomes, 8 INO1, 54 INO80, 158, 162, 373 Integrated Genome Modeling (IGM), 220 Intrinsically disordered regions (IDRs), transcription factor dynamics evolution, 240

overview, 237–238 phase separation driving, 238–239 sequence determination of transcription factor interactions, 239–240 stoichiometric complexes, 238 target search facilitation, 239 ISWI, 373

Κ

KAP1, 436, 492 Kaposi's sarcoma-associated herpesvirus (KSHV), 390 KASH domain, 7, 72, 274 KASH5, 72 KAT14, 158 KCNJ12, 415-417 KDM proteins, 374-375 KDMA4, 435 KIT, 374 KLF4, 492, 498, 500 KLF5, 379 KMT2B. See MLL2 KMT5C, 118, 122 KSHV. See Kaposi's sarcoma-associated herpesvirus Ku80, 164

L

LADs. See Lamina-associated domains Lamina laminopathies, 15-17 lamins. See also specific lamins classification, 1-3 lamina interface scaffolding, 6-8 regulation, 3-5 overview, 1-3, 274 prospects for study, 17 proteomes, 8-9 Lamina-associated domains (LADs) binary compartment model, 282-283 cell cycle and dynamic organization, 15 DNA replication timing, 335-336 gene regulation, 12–13 geographic organization and chromatin state, 12 localization, 292 organization and expression programs, 14-15 preimplantation embryo chromatin maturation, 440 techniques for study, 8, 10-11 transcription factors in organization, 13-14 Laminin-111, 154 LAP1, 79-80 LAP2, 6, 8, 14, 60, 74-75, 274

LBR, 6, 16, 60, 65, 67, 72, 197, 199, 274 LEDGF, 397 LEM2, 60, 77-79, 274 LIF, 493 LINC proteins, 6-7, 17, 95-97, 161 LINE1, 436, 465 LMNA, 1-3, 5, 15-17, 95, 274 LMNA $\Delta 10$, 1–2 LMNB1, 1-3, 5, 16, 67 LMNB2, 1-3, 5 LMNB3, 1-2 LMNC, 1-3, 95 LMNC2, 2-3 LMO1, 145 Loop extrusion. See Chromosome folding LULL1, 79-80

Μ

MAJIN1, 72 MALAT1, 284, 287 MaLR, 435 MAN1, 6, 16, 60, 74, 76-77, 274 **MARGI**, 284 MATR3, 460, 469, 475 MAX, 376-377 MCM, 335 MDN1, 357-358 Mechanical force. See also Mechanotransduction chromatin mechanical properties and genome organization/function, 99-101 DNA damage, 101-103 overview in cells and tissues, 93-94 Mechanotransduction force-mediated regulation of transcription and cell state, 97-99 nucleus mechanosensing chromatin deformation by force, 97 cytoskeletal modulation, 97 nuclear deformation sensing, 96 nuclear transport and signaling regulation, 96-97 overview, 94, 96 principles, 95-96 prospects for study, 103-104 MeCP2, 65, 115, 118, 121-123 MED1, 115, 121, 392, 503 Med14, 476 Mediator, 50, 309, 315, 352-353 MEGABASE, 217 MERV-L, 419, 436 MET-2, 197 Mex67, 50 MFAP1, 287

MICAL-2, 154 MINA, 310 MLL1, 55, 373 MLL2, 373, 430, 433 MLLT1, 374 Mlp1, 51 Mlp2, 51 MLV. See Murine leukemia virus MOF, 464 MOZ, 373 MPP8, 397 Mps3, 73 Mre11, 164 MRTE, 95 MRTF/SRF-mediated transcription, actin signaling, 155, 157 MRTF-A, 155, 157 MUC4, 115 Murine leukemia virus (MLV), 390, 396-397 MVM, 393 MX2, 391 MYC, 376-379, 393, 492 MYCN, 376-377 MYOD, 381 MYOD1, 373

Ν

NADs. See Nucleolus-associated domains NANOG, 464-465, 492-493, 498, 500, 503 NCL. See Nucleolin NDP52, 159 NEAT1_2, 275, 287 **NEK**, 32 Nesprin1, 16 Nesprin2, 16 NET5, 60 Neural stem cell (NSC), 501 NIK, 161 NM1, 159 Noncoding RNA. See RNA-chromatin interactions NONO, 275 NP220, 396 NPAT, 262, 276 NPC. See Nuclear pore complex NPM1, 114-115, 117, 119 NR4A3, 378 NRF2, 400 NS1, 395, 400 NSC. See Neural stem cell NSD1, 430, 434 Nsd1, 55 NTC, 355-356 NuA4, 157-158

Nuclear compartments. See also Chromatin subcompartment; specific compartments Cajal body, 273-274 cleavage bodies, 276-277 establishment and maintenance, 288-289 functions, 289 genomic analysis of genome nuclear organization, 282-285 histone locus body, 276 imaging early cytology, 277-278 genomics combination studies, 285 radial and binary models of nuclear compartmentalization, 278-279, 281-282 lamina, 274-275 liquid-liquid phase separation, 285-288 nuclear pore, 274-275 nuclear speckles, 272-273, 290-292 nucleolus, 270, 272 paraspeckles, 275-276 perinucleolar compartment, 276 promyelocytic leukemia body, 276 prospects for study, 292-293 virus interactions nuclear speckles, 400-401 promyelocytic leukemia body, 397-400 Nuclear pore complex (NPC) composition, 29 functions, 36-37 life cycle in dividing cells, 32-34 maintenance and turnover, 34-36 overview, 27-28, 274-275 prospects for study, 37 RNA export competence and ribonucleoprotein identity, 359 structure, 28-32 transcriptional regulation epigenetic memory regulation, 54-55 gene silencing, 51 mechanisms of gene interactions, 50-51 overview, 49-50 transcriptional regulation, 51-54 virus entry, 390-393 Nuclear speckles, 255, 257, 272–273, 290–292, 400 - 401Nucleolin (NCL), 113, 115, 117, 119 Nucleolus chromatin subcompartment features as phase-separated subcompartment, 113 high-resolution structure, 115

liquid-liquid phase separation contribution to structure, 122-123 marker protein internal mixing and nucleoplasm exchange, 117 structure-function relationships in establishment, 119-120 history of study, 251 overview, 270, 272 RNA processing, 254-255 Nucleolus-associated domains (NADs), DNA replication timing, 335-336 Nucleosome interactions in chromatin motion restriction, 180 pluripotent cell organization, 496 structure, 171-172 Nup1, 54 Nup2, 50 Nup35, 32 Nup50, 30 Nup53, 32 Nup54, 30 Nup58, 30 Nup60, 51 Nup62, 30, 391 Nup88, 30 Nup93, 30, 33, 51 Nup98, 30, 54-55 Nup100, 54 Nup107, 30, 33-34, 51 Nup145, 51 Nup153, 30, 34, 391 Nup155, 30-32 Nup157, 31 Nup159, 35 Nup160, 30, 33-34, 51 Nup170, 31, 51 Nup188, 31 Nup192, 31 Nup205, 30-31, 33 Nup210, 53 Nup214, 30, 391 Nup358, 30-31, 391

0

OCT4, 114, 464–465, 492–493, 498, 500, 503 Oct4, 98, 160 Oogenesis, genome organization, 438

Р

p53, 159, 291, 373 p300, 374, 395 Paraspeckles, 275–276

PARP, 241 PAX3, 375-376, 378, 417 PAX5, 381 PAX8, 378 PBAF, 377 PCAF, 159 PCGF3, 473 PCGF5, 473 PCNA, 163 PDGFRA, 374 Perinucleolar compartment (PNC), 276 PGC. See Primordial germ cell Phase separation liquid-liquid phase separation chromocenter, 114, 122-123 intrinsically disordered region driving, 238-239 nuclear compartments, 285-288 nuclear structure overview, 311-312 nucleolus, 113, 122-123 RNA polymerase II transcription factories, 113-114, 122-123 polymer-polymer phase separation, 312 Xist RNA compartment, 468-469 PKC, 3 PLK1, 32 Pluripotency chromatin structure chromosome organization, 500 loops, domains, and interaction hubs, 500 - 502nucleosome organization, 496 open chromatin genome accessibility, 498 remodeling, 498-499 overview, 494-496 prospects for study, 502-503 continuum, 494 epigenetics DNA methylation, 492 histone modification, 492-493 history of study, 490-491 overview, 489 regulatory networks, 491-492 states, 493-494 PML, 398-400 PML body. See Promyelocytic leukemia body PNB. See Prenucleolar body PNC. See Perinucleolar compartment Pom121, 31, 34 Population-based genome structure modeling, 219 - 221**PPHLN1**, 397

PRC1, 260, 433, 465, 468, 470–471, 473, 475 PRC2, 372, 374, 431, 433, 465, 470–471, 475 PRDM14, 464–465 Prenucleolar body (PNB), 270, 272 PREP1, 339 Primordial germ cell (PGC), 490 Promyelocytic leukemia (PML) body, 276, 397–400 PRPF38A, 287 PSE, 275 PSPC1, 275 PTBP1, 460, 469, 475 P-TEFb, 396 PTEN, 276 Put3, 54

R

RAD21, 333, 335 Rad51, 164 RanGTP, 33-34 RanGTPase, 154 RASSF1A, 154 RB1, 377 RBM15, 471 RCC1, 33 Replication timing. See DNA replication timing REX1, 464-465 RIF1, 341 **RING1B**, 473 RMB14, 275 RNA polymerase I, chromatin motion restriction, 181 RNA polymerase II, 73, 143-144, 229, 277, 285, 315, 355-358, 394-396, 467, 469 actin functions, 158-159 chromatin motion restriction, 180-181 RNA processing coupling, 359-360 transcription factor clustering, 241 transcription factory as chromatin subcompartment features as phase-separated subcompartment, 113-114 high-resolution structure, 115 liquid-liquid phase separation contribution to structure, 122-123 marker protein internal mixing and nucleoplasm exchange, 117-118 structure-function relationships in establishment, 120-121 RNA-chromatin interactions chromatin regulation and gene expression functional roles of RNA-mediated nuclear compartments, 260

nuclear compartment organization by RNA, 258, 260 X chromosome inactivation, 258 global RNA disruption and morphological changes in nucleus, 253 history of study, 251-252 mechanisms of RNA-mediated nuclear organization overview, 260-262 phase separation, 262-264 noncoding RNA in nuclear processes, 252-253 prospects for study, 264 RNA processing Cajal body, 257 histone locus body, 257 nuclear bodies in promotion of cotranscriptional RNA processing, 257 - 258nuclear speckles, 255, 257 nucleolus, 254-255 **RNA** splicing overview, 355-356 RNA imaging techniques, 350–352 spliceosome assembly, 356 timing relative to transcription, 356-357 RNF12, 465 rRNA, 254-255 RSX, 462, 465 **RYBP**, 473

S

SAF-A, 176, 258, 460 SAGA, 50 SAHF. See Senescence-associated heterochromatin foci SAMP1, 79 SC35, 272, 400 scaRNA, 257 SCNT. See Somatic cell nuclear transfer SCPP, 378 Sec13, 37, 53 Seh1, 37, 54 **SELEX**, 230 Senescence-associated heterochromatin foci (SAHF), 51 Set1, 159 SET-25, 197 SETD2, 429-430, 434, 475 SHARP, 258-260, 262-263 SHREC, 77 Sir2, 51 Sir3, 51 Sir4, 51

SMAD1, 76-77 SMAD2, 76 SMAD3, 76 SMAD5, 76-77 SMAD8, 77 SMARCA4, 381 SMARCB1, 377 SMCHD1, 469-470, 475 SMN, 273 snoRNA, 252 snRNA, 252-253, 255, 257 Somatic cell nuclear transfer (SCNT), 430, 433, 435, 440 SON, 220, 272-273, 287, 290, 400 SOX2, 118, 464-465, 492-493, 498, 503 SOX9, 415-417 SP1, 114 SP-1, 389 Sp100, 399 SPAD. See Speckle-associated domain Spatial position inference of the nuclear genome (SPIN), 284, 337 Speckle-associated domain (SPAD), 284, 336-337 SPEN, 473-474, 476 Spermatogenesis, genome organization, 437-438 SPIN. See Spatial position inference of the nuclear genome Spliceosome. See RNA splicing SPRITE, 283, 310 SRF. See MRTF/SRF-mediated transcription SRRM2, 272-273, 287, 290 SS1, 375 SS2, 375 SS4, 375 STAT3, 114 STELLA, 429, 492 Stem cell. See Pluripotency SUN1, 6, 17, 60, 72-73 SUN2, 6, 60, 73 SUZ12, 433 SV40, 389 SWR1, 157-158, 162

Т

TADs. *See* Topologically associating domains TAF15, 114, 121 TAL1, 378 TAZ, 158 TBP, 235, 352 TCR, 161–162, 378 TDP. *See* Timing decision point TDP-43, 460, 469, 475 TEAD, 158

TERB1, 72 **TERB2**, 72 **TERT**, 378 TEs. See Transposable elements TET, 429 TET hydroxylases, 371, 374 TET3, 492 TFAP2A, 418 TFIIA, 352-353 TFIID, 352, 355 Timing decision point (TDP), 332-333, 336 Timing transition region (TTR), 328, 330, 335 TM7SF2, 67 TNPO1, 392 Top1, 55 TOP2B, 381 Topologically associating domains (TADs) actin mediation, 164 cancer studies, 380-381 chromatin folding and gene expression in development, 410, 412-416 chromatin subcompartments, 110, 124 ensemble topologically associating domains, 135, 138-139, 142-143, 145, 147 epigenetic reprogramming in early development DNA methylation, 429-430 histone modification bivalent modifications, 433 H2K119ub, 434 H3K27me3, 431-433 H3K36me2/3, 434-435 H3K4me3, 430-431 H3K9me3, 435-436 overview, 427-429 preimplantation embryo chromatin maturation, 440 prospects for study, 440-445 transposable elements, 436 fertilization, 438 formation, 305 insulators, 305 loop extrusion, 193-194, 198 pluripotent cells, 501 replication domain relationship, 333, 335 stochastic genomic structure, 134-135, 138-139, 142-143, 147 three-dimensional modeling of genome folding, 214-215 Xist regulation, 464 Torsin, 79-80, 373 **TPR**, 275 Transcription. See also RNA polymerase II

cotranscriptional loading of factors, 358-359 elongation and end processing dynamics, 357-358 initiation dynamics, 353 overview, 352-353 posttranslational modifications and histone eviction, 355 poly(A) tail isoforms, 358 RNA imaging prospects, 360-362 techniques, 350-352 stability dynamics at promoter, 353, 355 Transcription factor dynamics brief interaction with chromatin residence times, 233-234 search dynamics, 231-233 transcription burst, 236-237 cancer mutations, 372-373 clustering functions in transcription, 241-242 mechanisms without phase separation, 241 overview, 240-241 RNA polymerase II, 241 intrinsically disordered regions evolution, 240 overview, 237-238 phase separation driving, 238-239 sequence determination of transcription factor interactions, 239-240 stoichiometric complexes, 238 target search facilitation, 239 overview, 229-230 prospects for study, 242 techniques for study binding specificity in vitro, 230 in vivo, 230 live-cell kinetics, 230-231 Transcription factory, 277 Transposable elements (TEs) chromatin folding and gene expression in development, 419-420 epigenetic reprogramming in early development, 436 **TREX**, 400 TREX1, 101 **TREX2**, 50 Trichostatin A (TSA), 180 TRIM28, 397, 436 TRIM33, 397 TSA. See Trichostatin A

TTR. See Timing transition region

This is a free sample of content from The Nucleus, Second Edition. Click here for more information on how to buy the book.

Index

U

U2, 274 U7, 257 UBF, 115 UHRF1, 429, 492 UNC-84, 73

V

Virus infection. *See also specific viruses* cell genome interactions, 393–396 genome diversity, 389–390 nuclear compartment interactions nuclear speckles, 400–401 promyelocytic leukemia body, 397–400 nuclear entry, 390–393 retrovirus interactions with chromatin and transcription, 396–397

W

WAPL, 135, 201–202 WASH, 159 WASP, 164 WAVE1, 159 WTAP, 471

Х

X chromosome inactivation (XCI) chromatin changes, 470 early development, 458–460 gene silencing kinetics and escape, 465–466 mechanisms overview, 470–471 polycomb recruitment, 471, 473 RNA methyltransferase recruitment, 471 SPEN role, 473–474 inactive X chromosome nuclear localization, 466–467 structural organization, 469–470 maintenance, 474–476

noncoding RNA role, 253, 258 overview, 457-458 prospects for study, 476-477 reconstitution in vitro, 460 XIST mediation expression regulation cis-regulators, 462-464 imprinted expression in early mouse embryogenesis, 465 trans-regulators, 464-465 history of study, 460-462 modules, 462 RNA compartment, 467-469 XCI. See X chromosome inactivation XIST expression regulation cis-regulators, 462-464 imprinted expression in early mouse embryogenesis, 465 trans-regulators, 464-465 history of study, 460-462 modules, 462 RNA compartment, 467–469 Xist, 253, 258, 460, 462-465, 467-477 XSR, 465

Y

YAP, 95–97, 158 YEATS, 374 YTHDC1, 471 YY1, 465–466

Ζ

ZBTB7B, 14 ZFP57, 492 ZFP809, 397 ZNF410, 229 ZRS, 145 ZSCAN4, 436