

Index

A

- Aar2, 368
- ABCE1, 299
- ADAR. *See* Adenosine deaminase acting on RNA
- Adenosine deaminase acting on RNA (ADAR)
 - ADAR2, 252
 - high-throughput analysis of edited RNAs
 - editing cluster defining, 145
 - enrichment of edited transcripts, 141–142
 - false-positive exclusion, 144–145
 - overview, 141
 - sequencing and alignment, 142–143
 - tools, 143–144
 - historical perspective of editing site identification, 138–141
 - prospects for study, 146
- AID. *See* Auxin-inducible degnon
- Alb1, 303
- APEX labeling, 46–47
- Aptamer
 - advantages as reagents, 541
 - green fluorescent protein RNA aptamer, 202
 - modification by postselection medicinal chemistry, 541–542
- NELE, 202
- selection
 - modified bases and novel base pairs, 542–544
 - modSELEX, 542
 - X-SELEX, 544–545
- AQR. *See* Aquarius
- Aquarius (AQR), 348, 356
- ARC, 14, 26
- Arx1, 301, 303
- Auxin-inducible degnon (AID), 20

B

- Base pairing, RNA
 - complex structure elucidation, 173–177
 - conservation analysis of structures, 171, 173
 - cross-linking data analysis, 170–171
 - cross-linking with proximity ligation and high-throughput sequencing, 168–170
 - dynamics studies, 173–174
 - history of structure studies, 164–165
 - long-range structures in transcriptome, 171
 - novel RNA–RNA interactions, 174–175
 - psoralen cross-linking studies, 159, 165–168, 175
- BCL11A*, 245

- Bdnf*, 113
- bicoid*, 105
- BioID, 46–47
- BIRC3, 108
- BRR2, 348, 350–351, 358, 360
- Brr2, 331, 334, 338, 340, 368, 375
- bS16, 423
- bS20, 423
- Bud20, 301
- Bud31, 335, 340, 371

C

- Cap binding complex (CBC), 57–58
- CBC. *See* Cap binding complex
- CBP2, 422
- CCDC49, 358
- CCDC94, 358
- CD47, 108–109
- CDC5L, 348
- CDC5L, 351, 353
- Cef1, 335, 338, 340, 371
- Cex2, 335
- CHART, 222, 225, 227
- Chirality. *See* Homochirality
- Chromatin immunoprecipitation.
 - See* RNA splicing
- CIRS-Seq, RNA structure probing, 156
- Clf1, 335, 337–338, 340, 373
- CLIP. *See* Cross-linking and immunoprecipitation
- CLIR-MS/MS. *See* Mass spectrometry
- CMCT, RNA structure probing, 156
- Colocalization single-molecule microscopy.
 - See* Single-molecule fluorescence microscopy
- CPEB, 106
- CRISPR
 - applications
 - base editing, 241
 - CRISPRa, 241, 243
 - CRISPRi, 241
 - Cas types
 - Cas9, 239
 - Cas21, 239
 - Cas13, 239, 241
 - overview, 237–240
- Crm1, 301
- Cross-linking and immunoprecipitation (CLIP)
 - applications, 217–218
 - Chem-CLIP probing of RNA–small molecule interactions, 266–267
 - cTag-CLIP, 214–216
 - data analysis, 213–214

- overview, 93–94, 113, 210
- principles, 210–212
- prospects, 218
- variations, 212–213
- Cryo-electron microscopy. *See* Electron microscopy

- CST, 309
- Cus2p, 421
- Cwc2, 340, 371
- CWC15, 351, 353
- Cwc15, 340
- Cwc21, 340, 366, 375
- CWC22, 360
- Cwc22, 340, 366
- Cwc24, 366, 375, 379
- Cwc25, 338, 366, 375, 379
- CWC27, 353, 356
- Cwc27, 366, 375
- Cwf2, 371
- Cwf3, 373
- Cwf4, 373
- Cwf5, 371
- Cwf19, 340–341
- CXCR4, 108

D

- Dbr1, 341
- DHX36, 190–191
- Dicer, 267
- Dim1, 303
- Dim2, 303
- Dimethyl sulfate (DMS), RNA structure probing, 154, 157, 188
- DKC. *See* Dyskeratosis congenita
- DMPK, 267–268
- DMS. *See* Dimethyl sulfate
- Double-stranded RNA (dsRNA)
 - adenosine deaminase acting on RNA, historical perspective of editing site identification, 138–141
 - binding proteins, 136–137
 - editing enriching regions, 137–138, 145–146
 - high-throughput analysis of edited RNAs
 - editing cluster defining, 145
 - enrichment of edited transcripts, 141–142
 - false-positive exclusion, 144–145
 - overview, 141
 - sequencing and alignment, 142–143
 - tools, 143–144
 - prospects for study, 145–146
 - viruses, 136

Index

- Drn1, 341
Drug design, RNA targeting
 overview, 260
 prospects, 270–271
 ribosomal RNA, 260–261
 riboswitches, 261
 structure targeting
 advantages and limitations, 261–262
 binding proteins, 262
 Chem-CLIP probing of RNA–small molecule interactions, 266–267
 microRNA protein-binding sites, 264–266
 protein-binding sites in RNA repeat expansions, 267–268
 splicing targeting, 270
 subcellular localization of targeted RNAs, 268
 telomerase RNA protein-binding sites, 268–270
 two-dimensional combinatorial screening, 262–263
- Dscam*, 419
dsRNA. *See* Double-stranded RNA
Dyskeratosis congenita (DKC), 269–270
- E**
Ecm1, 301
Ecm2, 335, 340, 371
eEF1A, 296–297, 299
eEF2, 297
eIF1, 292–294
eIF1A, 292–294
eIF2, 295–296
eIF2 α , 45
eIF3, 292–294, 296, 303
eIF4A, 45, 294
eIF4E, 294
eIF4G, 45, 296
eIF5, 294–295
eIF6, 303
Electron microscopy
 Cryo-electron microscopy
 group II intron ribonucleoprotein complexes, 400, 402–404
 RNA structure probing, 154, 164–165
 single-molecule imaging, 473–474
 spliceosome, 326, 335, 341, 348, 351, 356, 358, 366–371
 telomerase studies
 cryo-electron microscopy
 human telomerase, 317–318
 Tetrahymena telomerase, 316–317, 319
 negative stain, 314–316
 telomerase with telomeric DNA, 318, 320
- EMCV. *See* Encephalomyocarditis virus
Encephalomyocarditis virus (EMCV), 392–393
- Enp1, 301, 303
Epochs, RNA folding
 early observations, RNA World, 434–436
 late epoch
 helix studies, 446–447
 high-throughput characterization of RNA elements, 446
 junction studies, 447
 reconstitution model for folding, 442–446
 structure prediction and design, 442
 tertiary contact motifs, 447–448
 middle epoch
 folding characterization, 436–437
 folding model testing, 437, 439–440
 integrated folding framework, 440
 rugged landscape model for folding, 440–441
 overview, 434
eRF1, 299
eRF3, 299
Eve crystal, 533
- F**
FAST, 51
FBP21, 351
FCS. *See* Fluorescence correlation spectroscopy
FISH. *See* Fluorescence in situ hybridization
FISSEQ. *See* Fluorescence in situ sequencing
FKBP, 20
Fluorescence correlation spectroscopy (FCS), translation elongation rate studies in living cells, 21–23
Fluorescence in situ hybridization (FISH)
 long noncoding RNA. *See* Long noncoding RNA
 single-molecule studies
 gene expression regulation studies, 3–4
 messenger ribonucleoprotein, 4
 microRNA, 4
 overview, 2–3
 single-nucleotide variants, 5
 throughput, 5
 tissue studies, 6
Fluorescence in situ sequencing (FISSEQ), throughput, 5
Fluorescence recovery after photobleaching (FRAP)
 stress granule protein dynamics, 50
 translation elongation rate studies in living cells, 21–23
Fluorescence resonance energy transfer (FRET), single-molecule studies, 439, 445, 457–459, 474, 476, 484, 491, 500–502
FMRRP, 14
Folding epochs. *See* Epochs, RNA folding
FOXO1, 264
- FRAP. *See* Fluorescence recovery after photobleaching
FRET. *See* Fluorescence resonance energy transfer
Functional nucleic acids, 541, 548
- G**
GADD45B, 75
GAL10, 7
GATA1, 246
G3BP1, 48–49, 51
GCN4, 16, 243
 direct RNA manipulation
 Cas9, 250
 Cas13, 250–252
 posttranscriptional modifications, 252
 RNA interference knockdown, 252
 splicing and localization, 252–253
 long noncoding RNA loci studies, 38, 248–250
 pooled cellular assays
 cell sorting and guide counting, 243, 245
 high-content phenotyping, 245
 prospects, 253
 repeat-epitope tag amplification of single mRNA translation signals, 20–21
 transcription regulation studies, 245–248
 3'-untranslated region studies, 110–112
GFP. *See* Green fluorescent protein
Glycol nucleic acid (GNA), 515
GNA. *See* Glycol nucleic acid
GPD1L, 265–266
G-quadruplex (rG4)
 detection
 computational approaches
 cG/cC skew approach, 184
 G4RNA screener, 185
 predictors, 183–184
 RNAfold tool, 184–185
 in vitro
 biological validation, 187–188
 overview, 185
 reverse transcriptase stalling sequencing, 185–187
 rG4-seq, 185, 187
 in vivo
 biological validation, 190–191
 DMS-seq and reverse transcriptase stop profiling, 188–190
 NAI-seq and reverse transcriptase stop profiling, 188, 190
 history of study, 182
 prospects for study, 1911
Green fluorescent protein (GFP), RNA aptamers, 202
GRIA2, 140

- Group II intron
overview, 400–401
retromobility indicator genes, 404–405
reverse transcriptases, 407–411
ribonucleoprotein complexes,
 cryo-electron microscopy, 400,
 402–404
targetron use for bacterial gene targeting,
 405–407
- H**
- HCV. *See* Hepatitis C virus
Helix-junction-helix (HJH), 443–445
Hepatitis C virus (HCV), 261, 296
HIF-1 α , 265–266
High-throughput sequencing
 cross-linking with proximity ligation and
 high-throughput sequencing,
 168–170
 edited RNAs. *See* Double-stranded RNA
 Illumina sequencers, 197–198
 library considerations and requirements,
 199–200
 overview, 196–197
 protein–RNA interaction studies
 interactions across transcriptome
 targets, 202–203
 massively parallel rational design of
 RNA, 203
 sequence and structural determinants
 MS2 binding to mutated RNA
 targets, 200–202
 Puf binding to RNA library, 202
 RNA aptamers, 202
RNA-HiTS
 applications, 204
 prospects, 205
 tertiary structure studies, 203, 205
 total internal reflection fluorescence, 198
 transcription in situ for nascent
 transcripts, 198
HIV. *See* Human immunodeficiency virus
HJH. *See* Helix-junction-helix
Hmga2, 109
Homochirality
 asymmetric autocatalysis, 530–531
 origins in biological systems
 chemical models, 529–532
 chiral amplification, 529
 combining physical and chemical
 models, 534–535
 physical models, 532–534
 symmetry breaking, 529
 overview in biological systems, 528–529
HOXA1, 35
Hrr25, 301, 303
Hsh155, 331
Human immunodeficiency virus (HIV), 158,
 261, 416–421, 472, 480
Human immunodeficiency virus reverse
 transcriptase, 478–484, 492–498
Hybridization capture. *See* Long noncoding
 RNA
5-Hydroxymethylcytosine, overview, 130
- I**
- IGF2BP1, 109
Imaging. *See* Fluorescence in situ
 hybridization; Fluorescence in
 situ sequencing; Live-cell RNA
 imaging; Long noncoding RNA;
 RNA splicing; Stress granule
IMP1, 49, 51
Internal ribosome entry site (IRES), 278, 292,
 295–296, 418
Intracellular single-molecule, high-resolution
 localization, and counting
 (iSHiRLoC), 467–468
Intron. *See* Group II intron
IRES. *See* Internal ribosome entry site
iSHiRLoC. *See* Intracellular single-molecule,
 high-resolution localization,
 and counting
ISY1, 358
Isy1, 338, 379
ITS2, 301
- K**
- KHSRP, 106
- L**
- L1 ligase, 520
LASER. *See* Light-activated structural
 examination of RNA
Lea1, 337, 371, 379
Light-activated structural examination of
 RNA (LASER), RNA structure
 probing, 154–156, 159
Live-cell RNA imaging
 decay studies, 10
 localization studies, 8
 long noncoding RNA, 37–38
 overview of two-color imaging, 6
 ribonucleoproteins
 data analysis, 466
 intracellular delivery of labeled
 components, 465–466
 labeling, 463–465
 overview, 463
 RNA splicing rates, 62–63
 splicing studies, 8
 transcription studies, 6–8
 translation studies
 accessory tags, 20
 heterogeneity of single mRNA
 translation
 efficiency of translation, 24–25
 localization and mobility of
 translation sites, 25–26
 ribosome movement along
 mRNA, 25
historical perspective, 14–16
overview, 8–10
repeat-epitope tag amplification of
 single mRNA translation signals
 advantages, 16
 elongation rate studies, 21–23
 examples, 17–19
 initiation quantification, 23
 limitations, 16, 20
 polysome mobility and shape
 studies, 23–24
 prospects, 24, 26
 ribosome counting on
 polysomes, 21
 tagging with CRISPR editing,
 20–21
lncRNA. *See* Long noncoding RNA
Long noncoding RNA (lncRNA)
 fluorescence in situ hybridization
 complementary probe preparation,
 30, 32
 NEAT RNA-FISH, 32–33
 overview, 30–31
 single-molecule studies
 location tracking, 35–37
 oligo design and conjugation, 33
 probe set validation, 33–35
gene expression regulation
 overview, 86
 posttranscriptional degradation, 87, 89
 prospects for study, 98–99
 sequence-specific mutagenesis
 studies, 87
 transcription initiation inhibition, 87
 transcription termination, 87
hybridization capture studies
 agreement between experiments, 233
 background sources
 capture oligonucleotide
 hybridization to DNA, 231
 hybridization of DNA indirectly via
 captured RNA, 231
 nonspecific binding, 230–231
 off-target RNA hybridization, 231
 overview, 230
 capture oligonucleotide design,
 227–228
ChIP-seq data comparison, 229
controls, 231–233
cross-linking, 227
dosage compensation studies, 229
elution of complexes, 225, 228
extract preparation, 227
global proteomic analysis, 228–229
hybridization conditions, 223–224,
 228
next generation sequencing
 technologies, 225–227
overview, 222–223
washing to remove off-target
 contamination, 224–225, 228

Index

- Long noncoding RNA (lncRNA) (*Continued*)
live-cell imaging, 37–38
localization
CRISPR visualization of loci, 38, 248–250
genome-wide mapping, 95–97
mechanism studies, 97–98
microscopy, 95
prospects for study, 38–40, 233–234
protein interactions
binding site mapping on RNA, 93–94
functional analysis, 94
lncRNA identification, 92–93
protein identification, 89–92
- LtrA, 403–405
Ltv1, 301, 303
- ### M
- m1A. *See* N1-Methyladenosine
m6A. *See* N6-Methyladenosine
MAGOH, 380
MALAT1, 174, 419, 427
Maltose-binding protein (MBP), 21
MAPT, 270
MARIO, RNA structure probing, 168
Mass spectrometry (MS)
CLIR-MS/MS
integrative modeling with nuclear magnetic resonance structure data, 394–396
overview, 392
protein–RNA interaction mapping, 394
RNA labeling, 392–394
cross-linking studies of protein–RNA complexes, 389–390
direct analysis of RNA, 389
overview, 387
RNA-binding protein identification, 389–390
structural methods, 388–389
workflow, 387–388
MBP. *See* Maltose-binding protein
m5C. *See* 5-Methylcytosine
MCP, 87
MCT-1, 296
MDN1, 6–7
N1-Methyladenosine (m1A), antibody
enrichment-based mapping, 127–129
N6-Methyladenosine (m6A)
CLIP analysis, 218
detection in mRNA
advantages and challenges, 122–123
historical perspective, 120–122
m⁶Am mapping in cap, 131–132
mapping
antibody-based enrichment, 123
cross-linking to antibodies, 123
overview, 120
structural dynamics during translation, 475–477
Methylated nucleotides. *See also*,
5-Hydroxymethylcytosine;
N1-Methyladenosine;
N6-Methyladenosine;
5-Methylcytosine;
7-Methylguanosine
detection in mRNA
advantages and challenges, 122–123
historical perspective, 120–122
2'-O-methylated nucleotides
cap mapping, 130–131
metabolic labeling, 129–130
overview, 129
structural dynamics during translation, 477
overview, 120
prospects for study, 132
5-Methylcytosine (m⁵C)
bisulfite mapping, 126–127
enzyme trapping, 127
7-Methylguanosine (m⁷G)
cap mapping, 130–131
overview, 130
METTL4, 142
METTL3, 142
Mex67, 301
m7G. *See*, 7-Methylguanosine
Mhc, 419
MicroRNA, drug targeting, 264–266
MLN51, 380
MLV. *See* Murine leukemia virus
MOV10, 113
MRP, 419
MS. *See* Mass spectrometry
MS2, 6–10, 20, 37–38, 89–90, 200–202
Msl1, 337, 371, 379
Msl5, 329
Mud2, 329
Murine leukemia virus (MLV), 421–422
Muscular dystrophy, 267–268
MYC, 246
MYOD1, 113
- ### N
- Nanotechnology. synthetic genetic polymers, 547
Neat, 32, 36–38, 44, 98
NELE, RNA aptamers, 202
Netrin-1, 15
Nevirapine, 494
Nmd3, 301
NMR. *See* Nuclear magnetic resonance
Nob1, 301, 303
Nog2, 301
NOP10, 316
Ntr1, 340
Ntr2, 340
Nuclear magnetic resonance (NMR)
electron paramagnetic resonance comparison, 387, 391
protein–RNA complexes, 390–392, 394–396
RNA structure probing, 153–154, 164–165, 426–427, 472–473
telomerase RNA studies
p65–TER complex, 312
structure, 311–312
X-ray crystallography combination, 386, 391
oskar, 105, 109
8-Oxoguanine, overview, 130
- ### P
- p65, 312, 314, 316
PAB1, 48, 51
PABP. *See* Poly(A)-binding protein
PAPD4, 106
PARIS, RNA structure probing, 159, 168, 171, 173–174, 427
PARN, 106
PARS, RNA structure probing, 156
PARTE, RNA structure probing, 156
PHD. *See* Prolyl hydroxylase
PHF5A, 355
PKR, 137, 152
PLRG1, 351, 353
Pno1, 303
Poly(A)-binding protein (PABP), 109–110
Polymerase engineering
primer-dependent RNA polymerases, 539
xeno nucleic acids
overview, 538–539
polymerase and reverse transcriptase engineering, 540
Pop1, 308
Pop6, 308
Pop7, 308
POT1, 309
Powner/Sutherland RNA synthesis, 532
PP7, 6–10, 20, 90
PPIE, 356, 358
PPIL1, 358
PPIL2, 356
PRC1, 91
PRC2, 91–92, 233
PRKRIP1, 380
Prolyl hydroxylase (PHD), 265
Protocell
compartmentalization
genetics, 522–523
importance, 509
membrane systems
alternatives, 510–511
pros and cons, 509–510
vesicle division pathways, 511–512
overview of self-assembly, 508–509
RNA
alternatives, 515
chemical replication
cycles, 519
elongation, 517–518

- experimental realization, 519
 - fidelity, 518–519
 - monomer activation, 517
 - templated polymerization, 515–516
 - RNA-catalyzed replication
 - ligase ribozyme, 520
 - polymerase ribozyme, 520–522
 - replicase model, 519–520
 - prebiotic synthesis, 512–515
 - PRP2, 348, 355–356
 - Prp2, 337–338, 377
 - Prp3, 331
 - Prp4, 331
 - Prp5, 329, 331
 - PRP8, 350–351, 353, 355, 358, 360
 - Prp8, 331, 334–335, 340–341, 368, 375–377, 379, 403
 - PRP16, 348, 358
 - Prp16, 338, 379, 461–462
 - PRP17, 358, 360
 - Prp17, 338, 375–377
 - PRP18, 360
 - Prp18, 375
 - PRP19, 348, 351, 358
 - PRP22, 348, 360
 - Prp22, 338, 340, 379
 - PRP28, 346, 351
 - PRP38, 351, 351
 - PRP43, 348
 - Prp43, 340, 377, 379
 - Prp45, 340, 373
 - PSD-95, 15
 - Pseudouridine, detection in mRNA, 125–126
 - PTBP1, 392
 - Puf, 202
- R**
- RBFOX2, 113
 - Rbfox2, 176
 - RBM22, 353, 356, 380
 - Rds3, 337
 - RED, 351
 - Rei1, 303
 - Reverse transcriptase. *See also* G-quadruplex; Telomerase
 - evolution, 490–491
 - group II introns, 407–411
 - single-molecule studies
 - human immunodeficiency virus conformational dynamics on nucleic acids, 493–495
 - overview, 492–493
 - prospects for study, 483–484
 - reverse transcriptase interactions with primer–template complex, 481–482
 - reverse transcription initiation, 478–480
 - RNA–tRNA^{Lys} complex structure and heterogeneity, 480
 - sliding, substrate recognition, and strand displacement synthesis, 494, 496–497
 - tertiary structure of initiation complex, 482–483, 497–498
 - telomerase, 498–500
 - tools, 491–492
 - xeno nucleic acids for engineering, 540
- rG4. *See* G-quadruplex
- Ribonuclease P, 308
- Ribonucleoprotein granule. *See* Stress granule
- Ribosome
 - architecture, 288
 - counting on polysomes with repeat-epitope tags, 21
 - eukaryotes
 - biogenesis, 299, 301–303
 - structure, 288–290
 - translation
 - cycle, 290–292
 - elongation, 296–299
 - initiation alternative pathways, 295–296
 - initiation and reinitiation, 292–295
 - termination and recycling, 299–300
 - structural dynamics during translation, 475
- Riboswitch
 - design
 - computational tools, 279–281
 - high-throughput screening, 281–284
 - rules-based approaches, 276–279
 - domains, 423
 - drug targeting, 261
 - overview, 276
 - RNA splicing regulation, 425–426
 - transcription termination control, 423–425
 - translation control, 426
- Ribozyme
 - modified ribozymes, 545–546
 - XNAzymes, 546–547
- RIG-I, 152
- RIG-seq, 404–405
- Rio2, 301, 303
- RIP, 93
- RISC, 110
- RNA folding epochs. *See* Epochs, RNA folding
- RNA-HiTS. *See* High-throughput sequencing
- RNase H, 392, 437
- RNA splicing. *See* Splicing, RNA
- RNF113A, 351, 353, 356
- RocA, 45
- Rrp12, 301
- RsmE, 391
- RsmZ, 392
- S**
- Sad1, 334
 - SAF-A, 95
 - SET, 108–109
 - Severe acute respiratory syndrome coronavirus, 421
 - SF3a, 368, 379
 - SF3A2, 351, 356
 - SF3b, 338, 368, 379
 - SF3B1, 331, 355–356
 - SF3B3, 353
 - SF3B5, 355
 - SHAPE, RNA structure probing, 154–159, 171, 174, 176
 - Single-molecule fluorescence microscopy. *See also* Fluorescence in situ hybridization; Fluorescence resonance energy transfer; Live-cell RNA imaging; Splicing, RNA
 - experimental design, 462–463
 - live-cell imaging of ribonucleoproteins
 - data analysis, 466
 - intracellular delivery of labeled components, 465–466
 - labeling, 463–465
 - overview, 463
 - overview, 474
 - prospects, 467–468
 - RNA–protein interactions
 - illumination and detection, 453
 - immobilization of biomolecules, 456–457
 - labeling
 - dyes, 454
 - protein, 456
 - RNA, 454–457
 - overview, 453
 - RNA silencing studies, 466–467
 - spliceosome studies
 - advanced analysis, 461–462
 - colocalization single-molecule microscopy, 459–461
 - fluorescence resonance energy transfer, 457–459
 - total internal reflection fluorescence microscopy, 453, 463
 - translation structural dynamics studies
 - human immunodeficiency virus studies conformational dynamics on nucleic acids, 493–495
 - overview, 492–493
 - prospects for study, 483–484
 - reverse transcriptase interactions with primer–template complex, 481–482
 - reverse transcription initiation, 478–480
 - RNA–tRNA^{Lys} complex structure and heterogeneity, 480
 - sliding, substrate recognition, and strand displacement synthesis, 494, 496–497
 - tertiary structure of initiation complex, 482–483, 497–498
 - N⁶-methyladenosine effects, 475–477
 - 2'-O-methylation effects, 477
 - ribosome, 475

Index

- SKIP, 348, 351, 353, 358
SLU7, 360
Slu7, 338, 375, 379
SMU1, 351
Snca, 113
Snu13, 331
SNU17, 356
SNU23, 351
Snu23, 335
SNU114, 350, 353
Snu114, 334, 340, 371
SPLASH, RNA structure probing, 168, 173
Splicing, RNA
 choreography of spliceosome RNA and protein components, 379
 co-transcriptional splicing
 chromatin immunoprecipitation
 detection of spliceosome assembly and splicing within gene bodies, 57–59
 coordination studies, 63–64
 overview, 56–57
 single-molecule nascent RNA-seq, 59
 CRISPR studies, 252–253
 drug targeting, 270
 exon ligation, 338–340
 historical perspective of spliceosome structure studies, 366–368
 human spliceosome
 hB^{act} conformational dynamics, 358
 helicases, 360
 large-scale movements, 360–362
 overview, 346–348, 379–380
 PPIases and IBC proteins, 356, 358
 prospects for study, 362
 PRP2-mediated catalytic activation, 355–356
 SF3B1 mutations and cancer, 356
 structure
 activated spliceosome, 351–355, 357
 C and C* complexes, 358–360
 precatalytic B complex, 350–351
 snRNPs, 348–350
 kinetics studies
 live-cell fluorescence imaging, 62–63
 RNA metabolic labeling, 60–62
 lariat formation, 337–338
 live-cell RNA imaging, 8
 metalloribozymes, 371–373
 overview, 326–329
 prospects for study, 64–65
 protein components of spliceosome.
 See also specific proteins
 helicases, 376–377
 Prp8 catalytic motifs, 375–376
 splicing factors, 374
 structural proteins, 373–374
 quality assessment of spliceosome structure studies, 368–369
 riboswitch regulation, 425–426
 RNA element recognition, 377, 379
 shared structural features of spliceosomes, 369–371
 single-molecule fluorescence microscopy
 of spliceosome studies
 advanced analysis, 461–462
 colocalization single-molecule microscopy, 459–461
 fluorescence resonance energy transfer, 457–459
 site recognition and prespliceosome formation, 329–331
 spliceosome
 activation, 335–337
 assembly, 334–335
 disassembly and recycling, 340–341
 remodeling, 338
 U4/U6.U5 complex, 331–334
 Spp31, 335
 Strecker amino acid synthesis, 531–532
 Stress granule
 functional overview and diseases, 44–45
 imaging
 assembly and disassembly, 49–50
 internal ultrastructure, 48–49
 prospects, 52
 protein dynamics, 50–51
 RNA dynamics, 51–52
 protein components, 45, 47
 ribonucleoprotein granule overview, 44
 RNA components, 47–48
 techniques for study, 46
 Sub2, 329
 SunTag, 16, 20
 SYF1, 356, 358
 Syf1, 337, 338, 340, 373
 SYF2, 348, 353
 Syf2, 335, 340, 371
 SYF3, 348, 351, 353, 356, 358, 360
- T**
TALEN, 6
TALM. *See* Tracking and localization microscopy
Targaprimir-210, 266–267
Targaprimir-96, 264
Targetron. *See* Group II intron
TDP-1, 142
TDP-43, 142
Telescripting. *See* U1
Telomerase
 electron microscopy
 cryo-electron microscopy
 human telomerase, 317–318
 Tetrahymena telomerase, 316–317, 319
 negative stain, 314–316
 telomerase with telomeric DNA, 318, 320
 overview, 308–310
 reverse transcriptase single-molecule studies, 498–504
 RNA
 nuclear magnetic resonance studies
 p65–TER complex, 312
 structure, 311–312
 protein-binding site drug targeting, 268–270
 X-ray crystallography, 312, 314
 TERC, 173
 Tetrahymena ribozyme, 436–439
 Tetrahymena thermophila telomerase, 500–502
 TGA. *See* Transcribed genome array
 TGIRT, 128
 Thiamine pyrophosphate riboswitch, 423–426
 Threose nucleotide analog (TNA), 515
 TIS11B, 108
 TNA. *See* Threose nucleotide analog
 TPPI, 309
 Tracking and localization microscopy (TALM), 51
 Transcribed genome array (TGA), 202–203
 Translating ribosome affinity purification (TRAP), 112
 Translation. *See* Ribosome
 Translation RNA imaging by coat protein knockoff (TRICK), overview, 9–10, 15–16, 26
 TRAP. *See* Translating ribosome affinity purification
 TREAT, messenger RNA decay imaging, 10
 TRICK. *See* Translation RNA imaging by coat protein knockoff
 Tristetraprolin (TTP), 106
 Tsr1, 301, 303
 TTP. *See* Tristetraprolin
 TUBB, 427
- U**
U1
 antisense morpholino oligonucleotides
 functional knockdown studies, 70–73
 RNA polymerase II elongation
 termination in gene bodies, 73–74
 functional overview, 70
 polyadenylation signal suppression in nascent transcripts, 70–73
 premature cleavage and polyadenylation, 72–80
 spliceosome function, 326, 329, 334, 346, 366
 synthesis, 79–80
 telescripting
 dependence of long genes, 74–77
 mechanism, 78–79
 transcriptome shaping, 77–78
 U2, 326, 329, 331, 334–335, 337, 346, 355, 360, 366, 371, 373, 376
 U4, 326, 329, 331, 334–335, 346, 350–351, 366, 368, 375–377, 380

- U5, 326, 329, 331, 334–335, 337, 346, 351, 366,
368–369, 373, 375–377,
379–380
- U6, 326, 331, 334–335, 346, 350–351, 353,
360, 366, 368–369, 372–373,
375–377, 379–380
- Ubc4, 457, 461
- 3'-Untranslated region
- alternative untranslated regions
 - abundance, 106–107
 - cell type–specific expression, 107
 - isoform-specific translation, 112
 - primary cell regulation of isoforms,
109–110
 - protein–protein interaction
 - regulation, 107–108
 - temporal regulation of translation,
112–113
 - binding proteins
 - effector protein identification,
113–114
 - identification, 113
 - in vivo studies, 110
 - overview, 105–106
 - transfer to binding proteins,
108–109
- CRISPR studies, 110–112
- functional overview, 104
- prospects for study, 114
- regulation of mRNA
- stability regulation by AU-rich
elements, 104–105
 - subcellular localization, 105
 - translation, 105
- repeats and synergistic actions, 109
- UPF1, 113
- UTP-A, 301
- UTP-B, 301
- UTP-C, 301
- V**
- VCP, 51
- Venus, 14–16
- X**
- Xeno nucleic acids (XNAs)
- aptamer selection with X-SELEX,
544–545
 - overview, 538–539
 - polymerase and reverse transcriptase
engineering, 540
 - XNAzymes, 546–547
- XIST, 174, 176, 427
- Xist, 30, 86, 89–98, 229, 231, 233
- XNAs. *See* Xeno nucleic acids
- Y**
- Y14, 380
- Yju2, 338, 366, 375, 379
- Yrb2, 301
- Z**
- ZNF395, 266