

Index

- ABCE1, 22, 62–66
aIF2, 31–33, 44
AKT
 mTORC1 modulation, 126–127
 oncogenic signaling, 262, 267
AMP-dependent protein kinase (AMPK), 128
AMPK. *See* AMP-dependent protein kinase
Antisense inhibition. *See* eIF4E
Argonaute, microRNA-induced silencing complex role,
 238–239, 245
A-site, 2, 56–57, 81, 83
ATF4
 transcript in upstream open reading frame-dependent
 translation initiation, 166–167
 unfolded protein response, 166–167
ATF5
 transcript in upstream open reading frame-dependent
 translation initiation, 167
 unfolded protein response, 167

BACCE501, 152
BDNF. *See* Brain-derived neurotrophic factor
BEZ235, 270
BHQ. *See* Black hole quencher
Biarsenical fluorescent dyes, fluorescence imaging in single
 cells, 232–233
Bicaudal-C, 200
Bicaudal-D, 195
Bicoid, messenger RNA localization in oocyte pattern
 specification
 anterior–posterior protein gradient formation,
 196–197
 anterior targeting, anchoring, and translational
 regulation, 196
 cis-acting elements, 195
 overview, 194–195
BiP, 152
Black hole quencher (BHQ), 81
BNIP3, 128
Brain-derived neurotrophic factor (BDNF), 228, 230, 289

CAF1, 244–245, 248
Calnexin cycle, protein quality control, 152–153
Calreticulin
 calcium binding, 153
 protein quality control, 152–153
 structure, 153
Cancer
 evolutionary considerations, 265–266
 gene defects in translational machinery
 initiation factors, 255, 257–258
 ribosome protein mutations, 258–261
 table, 256–257
 oncogenic signaling and translation perturbation, 261
 therapeutic targeting of translation components
 eIF4E
 antisense oligonucleotides, 334–335
 cap interaction blockers, 333
 eIF4G interaction uncoupling, 334
 helicase inhibitors, 335–336
 phosphorylation inhibitors, 336–337
 eIF4F
 phosphatidylinositol 3-kinase inhibitors, 332
 rapamycin analogs, 329
 target of rapamycin kinase inhibitors,
 330–332
 tumorigenesis role, 328–329
 overview, 270–271, 328
 prospects, 338
 ternary complex formation inhibitors, 337–338
 translational control
 defects by cancer stage
 progression and metastasis, 268–270
 transformation and tumor initiation,
 266–268
 degradation, 253–255
 Cap-independent translation enhancer
 (CITE), 94, 307
 Caprin, neuron function, 289–290
 Cartilage–hair hypoplasia syndrome (CHH), 261
 Caudal, 4EHP in translation repression, 202
 CBP20, 333
 CBP80, 333
 CCR4, 117, 177, 179, 182, 199–201, 241–242,
 244–245, 249
 CDK11, 268
 Cercosporamide, 337
 CHH. *See* Cartilage–hair hypoplasia syndrome
 CHOP
 transcript in upstream open reading frame-dependent
 translation initiation, 167–168
 unfolded protein response, 167
 CITE. *See* Cap-independent translation enhancer
 COPII vesicle, 156, 158
 CPEB. *See* Cytoplasmic polyadenylation element-binding
 protein
 ϵ TAGE5, 156
 Cup, 116, 203

Index

- Cytoplasmic polyadenylation element-binding protein (CPEB), 268
cognitive function, 287–288
CPEB4, 266
functional overview, 286
isoforms, 287
translation repression, 287
- DAP5, 38
DAPK, 119
DBA. *See* Diamond-Blackfan anemia
DC. *See* Dyskeratosis congenita
DCP1, 181, 245
DCP2, 181, 183, 188, 245
Ddx3, 3–4, 35, 46
Ded1, 35, 38, 46
DENR, 64
Dhh1, 179, 181, 183
Dhx9, 3–4, 46
Diamond-Blackfan anemia (DBA), 259–261
Disulfide bond, formation, 154–156
DOM34, 64–65
Dyskeratosis congenita (DC), X-linked, 258–259, 261
- Edc3, 183–184
EDC4, 245, 247
EDD, 241–242, 246
EDEM1, 152–154
eEF1, 20
recycling, 57
eEF1A, 55–57, 137
eEF2, 20, 32, 56–57, 132, 308
diphthamide modification, 57–58
phosphorylation sites, 137
eEF2K, phosphorylation sites, 137
eEF3, 58–59, 65
EF-G, 23, 57, 60–61, 63, 81, 83–85
EF-P, 59–60
EF-Tu, 22–23, 32, 55–56, 60–61, 64, 81–83
Egalitarian, 195
eIF1, 64
binding site on ribosome, 19–20
phosphorylation sites, 137
start codon recognition role, 39–43
eIF1A, 22, 33, 47–48, 64
start codon recognition role, 39–43
eIF2, 31, 33–34, 36, 47, 93
innate immunity
overview, 310
phosphorylation inhibition by viruses
bypassing, 312–313
combinatorial strategies, 312
inhibitors, 312
Met-tRNA_i; recruitment to small ribosomal subunit
eIF2-GDP recycling, 33–34, 47
overview, 31–32
ternary complex binding promotion factors, 32–33
start codon recognition role, 43
eIF2 α , 136, 164, 172, 312–313, 337
eIF2B, 33, 165–166
eIF2Be, phosphorylation sites, 137
eIF2 β , 32
eIF2D, 64
eIF2 γ , 32, 34, 43
eIF3, 31–33, 38, 63–64, 90, 93, 117, 183, 255, 257–258, 300, 302, 314
messenger RNA recruitment, 37–38
phosphorylation sites, 137
eIF3c, start codon recognition role, 43–44
eIF3e, 36
eIF4A, 4, 31, 34–38, 46, 93, 306, 309, 335–336
eIF4B, 36–37, 131–132, 266, 310
eIF4E, 31, 34–35, 38, 93, 129, 134, 199, 202, 257, 262–265, 268–270, 300, 302, 306, 309–310, 315, 328–330
cancer therapeutic targeting
antisense oligonucleotides, 270, 334–335
cap interaction blockers, 333
eIF4G interaction uncoupling, 334
helicase inhibitors, 335–336
phosphatidylinositol 3-kinase inhibitors, 332
phosphorylation inhibitors, 336–337
rapamycin analogs, 329
target of rapamycin kinase inhibitors, 330–332
tumorigenesis role, 328–329
eIF4F, 37, 46, 94–95, 266, 304, 306, 309, 315, 329
phosphorylation sites, 136
viral DNA replication promotion, 309–310
eIF4G, 6, 31, 34–36, 38, 46, 62, 92–94, 117, 199, 257, 300, 302, 306, 309–310, 315
eIF4GI, 38–39, 96, 136, 181, 269
eIF4GII, 38–39
eIF4H, 37, 46, 131–132, 136
eIF5, 32–33, 36, 47, 90
eIF2-mediated translational control response
role, 165–166
phosphorylation sites, 137
start codon recognition role, 39–44
eIF5A, 59–60, 65, 257, 268
eIF5B, 47–48, 90, 137, 202
eIF5G, 47
eIF6, 3, 137, 265, 267
Elongation, translation
eEF1 recycling, 57
eEF2 diphthamide modification, 57–58
eEF3 function, 58–59
EF-P, 59–60
eIF5A, 59–60
overview in eukaryotes, 55–57
prospects for study, 65–66
single-molecule studies in bacteria
initiation transition to elongation, 76–77
ribosome
conformational changes, 79–81
tracking, 78
Shine-Dalgarno sequence clearing, 78

- EMT. *See* Epithelial-to-mesenchymal transition
- Encephalomyocarditis virus. *See* Picornavirus internal ribosome entry sites
- Endoplasmic reticulum (ER)
- calnexin cycle in protein quality control, 152–153
 - disulfide bond formation, 154–156
 - glycosylation of proteins, 150–152, 154
 - inositol-requiring enzyme-1 ribonuclease activity and protein-folding homeostasis, 172
 - protein exit and secretion regulation, 156–158
 - protein targeting, 147–150
 - unfolded protein response. *See* Unfolded protein response
- Endoplasmic reticulum oxidoreductase, 154–155
- Epithelial-to-mesenchymal transition (EMT), cancer, 269
- EPRS, 117–118
- ER. *See* Endoplasmic reticulum
- ERdj5, 152–153
- eRF1, 22, 60–61, 63–66, 314
- eRF3, 22, 60–61, 63–65
- ERGIC53, 157–158
- ES. *See* Expansion segment
- E-site, 57, 81–82
- Expansion segment (ES), ribosomal RNA, 14, 16–17
- FKBP12, 125, 330–331
- FLaSH, 232
- FLuc, small interfering RNA screening for internal ribosome entry site, 100–101
- Fluorescence microscopy. *See* Single-cell imaging; Single-molecule studies
- Fluorescence resonance energy transfer (FRET)
- principles, 73–74
 - single-molecule studies in bacteria
 - ribosome conformational changes during initiation and elongation, 79–81
 - transfer RNA
 - conformational changes, 81
 - dynamics in ribosome, 82–84
 - ribosome interactions, 84–85
- Fluorescent noncanonical amino acid tagging (FUNCAT), global measurement of translation in single cells, 228
- FMRI*. *See* Fragile X syndrome
- FMRP. *See* Fragile X syndrome
- Foot and mouth disease virus. *See* Picornavirus internal ribosome entry sites
- 4E1RCAT, 334
- 4E-BP
- cancer
 - therapeutic targeting, 333–334
 - translational control, 262–264
- 4E-BP1, 95
- mTORC1 signaling to translational machinery, 129–132
- phosphorylation sites, 136
- 4EGI-1, 334
- 4EHP, translation repression of Caudal and Hunchback messenger RNAs, 202
- Fragile X syndrome, FMRP
- function and defects, 282–285
 - messenger RNA target identification, 283–284
 - therapeutic targeting, 291
- FRET. *See* Fluorescence resonance energy transfer
- FUNCAT. *See* Fluorescent noncanonical amino acid tagging
- GADD34, 167–169, 315
- GAIT complex, temporal control of translation, 117–118
- GCN2, 337
- GCN4, 37, 47, 109, 168
- Genome-wide analysis, posttranscriptional gene expression
- cis* and *trans* factor identification, 216–219
 - data analysis, 215–216
 - dynamic regulation, 212
 - techniques for study, 209–211
 - translational activity analysis, 213–215
- Gld2, 286
- Glucosyl transferase (GT), 152
- Glyceraldehyde 3-phosphate dehydrogenase (GPDH), 117–118
- Glycosylation
- endoplasmic reticulum proteins, 150–152
 - protein secretion effects, 154
- GPDH. *See* Glyceraldehyde 3-phosphate dehydrogenase
- GT. *See* Glucosyl transferase
- Gtr1, 127
- Gtr2, 127
- GW182
- domain organization, 240–241
 - microRNA-induced silencing complex
 - plant studies, 246–247
 - protein interactions
 - deadenylase complex, 242
 - plasticity, 242–243
 - poly(A)-binding protein interactions and function, 240, 243–244
 - redundant and combinatorial interactions, 245
 - recruitment, 239
 - proline-rich motif, 242
- Hac1p, 165
- HBS1, 64–65
- HHT. *See* Homoharringtonine
- Hippuristanol, 335–336
- HITS-CLIP, messenger RNA-binding protein target identification, 265, 283–285
- Homoharringtonine (HHT), 328
- HRI, 337–338
- Hrp48, 200
- Hu, neuron function, 290
- Human rhinovirus. *See* Picornavirus internal ribosome entry sites
- Hunchback, 4EHP in translation repression, 202
- ICP6, 308–309
- IF1, 18–19, 74–75

Index

- IF2, 18–19, 74–75, 79
 order of IF2 and transfer RNA arrival in
 bacteria, 75–76
- IF3, 18–19, 63, 75
- Initiation, translation
 bacteria overview, 2–3
 cancer defects in initiation factors, 255, 257–258
 eukaryote overview, 3–5, 29–31
 initiation factor binding sites on ribosome, 18–20
 initiator transfer RNA recruitment, 34
 internal ribosome entry site. *See* Internal
 ribosome entry site
 messenger RNA recruitment to ribosome. *See*
 Messenger RNA
 prospects for study, 48
 ribosomal subunit joining, 47–48
 RNA helicases, 45–46
 single-molecule studies in bacteria
 elongation transition, 76–77
 order of IF2 and transfer RNA arrival, 75–76
 overview, 74–75
 ribosome conformational changes, 79–81
 start codon recognition
 eIF1, 39–43
 eIF1A, 39–43
 eIF2, 43
 eIF3c, 43–44
 eIF5, 39–44
 messenger RNA sequence context, 44
 ribosomal RNA role, 44–45
 transfer RNA role, 44–45
 transfer RNA recruitment to ribosome.
 See Transfer RNA
- INK128, 270
- Inositol-requiring enzyme 1 (IRE1)
 functional overview, 165
 ribonuclease activity and protein folding
 homeostasis, 172
 translational pausing and colocalization of XBP1
 messenger RNA with IRE1 effector domain,
 170–172
- Internal ribosome entry site (IRES)
 cap-independent mechanisms of initiation,
 94–95
- ITAFs, 93–94
 messenger RNA in cells
 bicistronic plasmid test, 96–97
 controls for screening from cryptic promoters or
 splicing, 98–100
 evidence, 95–96
 mapping, 103
 prospects for study, 103–105
 RNA polymerase II transcription dependence,
 97–98
 small interfering RNA screening for FLuc
 expression, 100–101
 transfection and in vitro translation
 assay, 101–102
 overview, 89–90
- picornavirus internal ribosome entry sites
 class III and class IV site mediation, 306–307
 classification, 90–93
 initiation factor requirements, 93–94
 overview, 306
 trans-acting factor requirements, 94–95
 virus distribution, 307
- IRE1. *See* Inositol-requiring enzyme 1
- IRES. *See* Internal ribosome entry site
- ITAFs. *See* Internal ribosome entry site
- K10, 198
- L13a, GAIT complex, 117–119
- L30e, 14
- L41e, 22
- La, 94
- Long-term depression (LTD), translational regulation
 in neurons, 282
- Long-term potentiation (LTP), translational regulation in
 neurons, 282
- LTD. *See* Long-term depression
- LTP. *See* Long-term potentiation
- Mammalian target of rapamycin. *See* Target of rapamycin
- MAPKs. *See* Mitogen-activated protein kinases
- Mass spectrometry, interactome capture, 113
- MCFD2, 157
- MCT-1, 64
- MDM2, 266
- Messenger RNA (mRNA)
 decay
 decapping promotion and translation initiation
 repression, 179–182
 messenger ribonucleoprotein granules
 aggregation, 186
 assembly in cytoplasm, 183–184
 dynamics in cytoplasm, 185–186
 mRNA cycle model, 186–187
 nontranslating messenger RNA assembly into
 RNA–protein granules, 182–183
 pathways, 177–179
 decoding, 22–23
 internal ribosome entry site. *See* Internal ribosome
 entry site
 oogenesis studies in *Drosophila*. *See* Oogenesis,
 Drosophila
 recruitment to ribosome
 eIF3 role, 37–38
 eIF4B role, 36–37
 eIF4F role, 34–36
 initiation factor knockout studies in yeast, 38–39
 overview, 5–6
 single-molecule studies in bacteria, 78
 start codon recognition
 eIF1, 39–43
 eIF1A, 39–43
 eIF2, 43

- eIF3c, 43–44
- eIF5, 39–44
- messenger RNA sequence context, 44
- ribosomal RNA role, 44–45
- transfer RNA role, 44–45
- MFC. *See* Multifactor complex
- MicroRNA
 - Drosophila* ovary messenger RNA protection from degradation, 199
 - functional overview, 237–238
 - translation regulation, 5–6
- MicroRNA-induced silencing complex (miRISC)
 - Argonaute role, 238–239, 245
 - cytoplasmic deadenylase complexes, 244–245
 - deadenylation interaction with translational repression, 247–248
 - decapping enzymes, 245
 - GW182
 - domain organization, 240–241
 - plant studies, 246–247
 - proline-rich motif, 242
 - protein interactions
 - deadenylase complex, 242
 - plasticity, 242–243
 - poly(A)-binding protein interactions and function, 240, 243–244
 - redundant and combinatorial interactions, 245
 - recruitment, 239
 - mechanism, 238–240, 247
 - prospects for study, 248–249
 - miRISC. *See* MicroRNA-induced silencing complex
- Mitogen-activated protein kinases (MAPKs)
 - interacting kinase inhibitor therapy in cancer, 336–337
 - mTORC1 modulation, 127–128
 - signaling to translational machinery
 - interacting kinases, 132–134
 - overview, 132–133
 - prospects for study, 135–137
 - ribosomal S6 kinase, 134–135
- mRNA. *See* Messenger RNA
- MSL2, translational repression of messenger RNA, 114–115
- mTORC. *See* Target of rapamycin
- Multifactor complex (MFC), 29, 33, 65
- Myc, 267
- Nanos
 - messenger RNA localization in oocyte pattern specification
 - cis*-acting elements, 195
 - overview, 194–195
 - targeting to posterior pole plasm, 198
 - translational control, 200–201
 - temporal and spatial control of translation, 115–117
- Neuroigin, 233
- NOT, 177, 179, 182, 241–242, 244–246, 249
- NSAP1, 117–118
- OAS. *See* Oligoadenylate synthase
- Oligoadenylate synthase (OAS), 303
- Oligosaccharide transferase (OST), 151–152
- Oogenesis, *Drosophila*
 - advantages as model system, 193
 - 4EHP in translation repression of Caudal and Hunchback messenger RNAs, 202
 - messenger RNA localization in pattern specification
 - bicoid
 - anterior–posterior protein gradient formation, 196–197
 - anterior targeting, anchoring, and translational regulation, 196
 - cis*-acting elements, 195
 - gurken localization, 198
 - nanos
 - targeting to posterior pole plasm, 198
 - translational control, 200–201
 - oskar
 - targeting to posterior pole plasm, 197–198
 - translational control, 199–200
 - overview, 194–195
 - protection from degradation, 199
 - Vasa as translational activator, 202–203
- Oskar, messenger RNA localization in oocyte pattern specification
 - cis*-acting elements, 195
 - overview, 194–195
 - targeting to posterior pole plasm, 197–198
 - translational control, 199–200
- OST. *See* Oligosaccharide transferase
- p27, 259
- p53, 259–260, 268
- Pab1, 179
- PABP. *See* Poly(A)-binding protein
- PAN2, 241–242, 244–245
- PAN3, 241–242, 244–246
- PAR-CLIP, 111–113, 218
- PARN, 286
- Pat, 245
- Pat1, 179, 181–182, 185
- Pateamine A, 335
- P-body
 - aggregation, 186
 - assembly in cytoplasm, 183–184
 - dynamics in cytoplasm, 185–18
 - messenger RNA decay
 - decapping promotion and translation initiation repression, 179–182
 - pathways, 177–179
 - mRNA cycle model, 186–187
- PCBP-2, 94
- PDCD4
 - phosphorylation sites, 136
 - translational regulation, 131
- PDI. *See* Protein disulfide isomerase
- PDK1, 131
- PDX1, 155
- Peptidyl transfer center (PTC), 56, 61
- PERK, 164, 168–169, 172, 265–265, 310, 312, 337

Index

- Peroxiredoxin IV, 156
Phosphatidylinositol 3-kinase (PI3K)
 inhibitors for cancer treatments, 332
 mTORC1 modulation, 126, 135
 oncogenic signaling, 262
PI3K. *See* Phosphatidylinositol 3-kinase
PIC. *See* Preinitiation complex
Picornavirus internal ribosome entry sites
 class III and class IV site mediation, 306–307
 classification, 90–93
 initiation factor requirements, 93–94
 overview, 306
 trans-acting factor requirements, 94–95
PIKK, 329, 332
PIM2, 336
PKR. *See* RNA-dependent protein kinase
Poglut, 154
Poly(A)-binding protein (PABP), 6, 31, 34, 62, 66, 117,
 240–244, 286, 302, 309, 314
Polypyrimidine tract-binding protein
 (PTB), 92, 94, 199
POP2, 244–245
Pop2, 177, 179, 182
PP242, 270
PP1R15A, 169–170
PP1R15B, 169–170
PRAS40, 127
Preinitiation complex (PIC), 29–31, 34–42, 77
PRE. *See* Programmed ribosomal frameshifting
Programmed ribosomal frameshifting (PRF), 259
Protein disulfide isomerase (PDI), 152, 154–156
PRTE. *See* Pyrimidine-rich translation element
PSD95, 233
P-site, 2, 18, 39, 44, 56–57, 78, 81, 83–85
PTB. *See* Polypyrimidine tract-binding protein
PTC. *See* Peptidyl transfer center
PTEN, 329, 336
Pumilio
 mechanism of action, 288
 neuron function, 288
Puromycin, fluorescent analogs for global measurement
 of translation, 228–229
Pyrimidine-rich translation element (PRTE), 270

RACK1, 14, 188, 265
Rapamycin, analogs for cancer treatment, 329
Ras, 135
RCK, 179, 245–246
ReAsH, 232
REDD1, 128
RF1, 22, 61, 63
RF2, 22, 61, 63
RF3, 60, 63
Rft1, 150
Rheb, 127–128
Ribonucleoprotein particles (RNPs)
 cis/trans interactions, 113–114
 cross-linking studies, 111–113
 interactome capture, 113
 messenger particles as templates for translation control,
 110–111
 messenger ribonucleoprotein granules. *See* P-body;
 Stress granule
 prospects for study, 119
 RNA affinity chromatography, 113
Ribosomal recycling factor (RRF), 63, 65
Ribosomal RNA (rRNA)
 expansion segments, 14, 16–17
 features in eukaryotes, 14–16
 start codon recognition role, 44–45
Ribosomal S6 kinase (RSK), mitogen-activated protein
 kinase signaling to translational machinery,
 132, 134–135

Ribosome
 binding sites
 initiation factors, 18–20
 transfer RNA, 17–18
 cancer and protein mutations, 258–261
 messenger RNA recruitment. *See* Messenger RNA
 proteins of eukaryotes, 16–17
 recycling, 22–23, 62–63–65
 single-molecule studies in bacteria
 conformational changes, 79–81
 tracking during elongation, 78
 transfer RNA
 dynamics, 82–84
 interactions, 84–85
 transit, 81–82
 structure
 large subunit, 13
 overview, 11, 13
 small subunit, 12
 subunit interactions, 21–22
 ternary complex binding to small subunit, 32–33
 transfer RNA recruitment. *See* Transfer RNA
 tunnel in eukaryotes, 20–21

RIDD, 172
RISP, 314
RLI1, 64–66
RNA2, 34
RNA3, 35
RNA affinity chromatography, RNA-binding protein
 identification, 113
RNA-dependent protein kinase (PKR), 264, 312, 337
RNA helicase, translation initiation, 45–46
RNA-induced silencing complex. *See* MicroRNA-induced
 silencing complex
RNA polymerase II, transcription dependence for
 messenger RNA internal ribosome
 entry site, 97–98
RNPs. *See* Ribonucleoprotein particles
RPL38, 260
RPS25, 307
RRE. *See* Ribosomal recycling factor
rRNA. *See* Ribosomal RNA
RSK. *See* Ribosomal S6 kinase
Rumi, 154
Rumpelstiltskin, 198

- S6 kinase. *See also* Ribosomal S6 kinase
 - mTORC1 signaling to translational machinery, 132
 - substrates, 131–132
 - target of rapamycin activation, 129, 131
 - therapeutic targeting, 330–332
- Scd6, 181–183
- SDS. *See* Shwachman-Diamond syndrome
- Sec12p, 156
- Sex-lethal (SXL), 114–115
- Shine-Dalgarno sequence, ribosome clearing studies, 78
- Shwachman-Diamond syndrome (SDS), 261
- Signal recognition particle (SRP), 148–149
- Silvestrol, 335–336
- Single-cell imaging
 - global measurement of translation
 - fluorescent noncanonical amino acid tagging, 228
 - overview, 227–228
 - puromycin fluorescent analogs, 228–229
 - prospects for translation studies, 233–234
 - transcript-specific translation imaging
 - biarsenical fluorescent dyes, 232–233
 - overview, 229–230
 - reporter proteins, 230–232
 - TimeSTAMP, 233
 - transfer RNA fluorescent derivatives, 229
- Single-molecule studies, translation dynamics
 - elongation studies in bacteria
 - ribosome tracking, 78
 - Shine-Dalgarno sequence clearing, 78
 - eukaryote study prospects, 85–86
 - fluorescence resonance energy transfer
 - principles, 73–74
 - ribosome conformational changes during initiation and elongation, 79–81
 - transfer RNA conformational changes, 81
 - initiation studies in bacteria
 - elongation transition, 76–77
 - order of IF2 and transfer RNA arrival, 75–76
 - overview, 74–75
 - messenger RNA imaging in gene expression, 225–227
 - rationale, 72–74
 - time scales, 71–72
 - transfer RNA
 - dynamics in ribosome, 82–84
 - ribosome interactions and translocation, 84–85
 - transit through ribosome, 81–82
- siRNA. *See* Small interfering RNA
- SKI2, 172
- Small interfering RNA (siRNA), screening for internal ribosome entry sites, 100–101
- Smaug, 116–117
- SOX, 303
- Squid, 198
- SRP. *See* Signal recognition particle
- Stm1, 181
- Stress granule
 - aggregation, 186
 - assembly in cytoplasm, 183–184
 - caprin induction, 288–289
 - dynamics in cytoplasm, 185–188
 - messenger RNA decay
 - decapping promotion and translation initiation repression, 179–182
 - pathways, 177–179
 - mRNA cycle model, 186–187
- SUO, 246–248
- SXL. *See* Sex-lethal
- TANGO1, 156
- Target of rapamycin (TOR)
 - complexes and functions, 124–126
 - kinase inhibitors for cancer treatment, 330–332
 - mTORC1 signaling to translational machinery
 - 4E-BPs, 129–132
 - overview, 126–126
 - S6 kinase, 132
 - upstream factors
 - growth factors and hormones, 126–127
 - nutrients, oxygen, and energy status, 127–128
 - prospects for study, 128–129
 - oncogenic signaling, 262, 264
 - TAR RNA-binding protein (TRBP), 312
- TDI, 61
- Termination, translation
 - overview, 7
 - prospects for study, 65–66
 - release factors, 60–62
 - structural insights, 65
 - virus regulation, 313–314
- Ternary complex (TC), 29, 31–33, 39, 44–45
 - inhibitors for cancer treatment, 337–338
- TIA-1, 185
- TIA-R, 185
- TimeSTAMP, fluorescence imaging in single cells, 233
- TISU element, 5
- TOR. *See* Target of rapamycin
- Tpa1, 66
- TPI. *See* Triose phosphate isomerase
- TPL. *See* Tripartite leader
- TRAM, 150
- Transfer RNA (tRNA)
 - fluorescent derivatives for global measurement of translation, 229
 - Met-tRNA_i recruitment to small ribosomal subunit
 - eIF2-GDP recycling, 33–34
 - eIF2-independent recruitment, 34
 - eIF2 role, 31–32
 - ternary complex binding promotion
 - factors, 32–33
 - ribosome binding sites in eukaryotes, 17–18
 - single-molecule studies in bacteria
 - conformational changes, 81
 - dynamics in ribosome, 82–84
 - order of IF2 and transfer RNA arrival, 75–76
 - ribosome interactions and translocation, 84–85
 - transit through ribosome, 81–82
 - start codon recognition role, 44–45

Index

- TRAP, 150
TRBP. *See* TAR RNA-binding protein
Triose phosphate isomerase (TPI), 96
Tripartite leader (TPL), 308
tRNA. *See* Transfer RNA
TSC, 305, 308, 329
- Unfolded protein response (UPR)
 eIF2-mediated translational control response
 eIF5 role, 165–166
 phosphorylation relationship to fitness of stressed cells, 169–170
 transcripts in upstream open reading frame-dependent translation initiation, 166–168
 overview, 164
- UNR, 115
Unr, 94
Upf1, 66
UPR. *See* Unfolded protein response
- Vanishing white matter disease (VWM), 166
Vasa, translational activation in *Drosophila* oogenesis, 202–203
Vascular endothelial growth factor (VEGF), 269
VEGF. *See* Vascular endothelial growth factor
Virus translational control
 balancing translation, replication, and encapsidation, 314
 cap-dependent initiation
 adenoviruses, 307–308
 asfarviruses, 309
 eIF4E phosphorylation and DNA replication promotion, 309–310
 herpesviruses, 308
 megaviruses, 309
 mimiviruses, 309
 papillomaviruses, 307–308
 polyomaviruses, 307–308
 poxviruses, 309
 RNA viruses, 310
 cap-independent translation. *See also* Picornavirus
 internal ribosome entry sites
 internal ribosome entry site virus distribution, 307
 overview, 305–306
 protein-linked 5' ends, 306
 eIF2 in innate immunity
 overview, 310
 phosphorylation inhibition by viruses
 bypassing, 312–313
 combinatorial strategies, 312
 inhibitors, 312
 host translation impairment
 cell translation factors
 direct effects, 300–302
 indirect effects, 302–303
 overview, 304–305
 RNA manipulation, 303–305
 prospects for study, 314–315
 replication strategies, 300
 termination and reinitiation regulation, 313–314
- VP1, 313
VP2, 313
VWM. *See* Vanishing white matter disease
- Wispy, 200
- X-box-binding protein 1 (XBP1)
 functional overview, 165
 translational pausing and colocalization of messenger RNA with IRE1 effector domain, 170–172
XBP1. *See* X-box-binding protein 1
XRN1, 172, 187
- YB-1, 35
- ZBP1. *See* Zip code binding protein 1
Zip code binding protein 1 (ZBP1), neuron function, 288–289
ZIPK, 119