

Index

a

aberrant transcript 122
 abundance
 -- quantification 553
 ACE strategy 158f.
 active status 239
 adapter ligation 269ff.
 adaptor sequence
 -- introducing adaptor sequences to the
 genomic DNA by Klenow reaction 222
 adenovirus-associated virus (AAV) 487
 affinity selection
 -- MS2-MBP (maltose-binding protein) affinity
 purification 332ff.
 -- RNA target 223
 agarose gel electrophoresis
 -- analysis of splicing complexes 334
Agrobacterium electrocompetent cell
 -- preparation 458
 -- transformation 458
Agrobacterium-mediated infiltration of *Nicotiana
 benthamiana* leaves 457
 agroinfiltration 459
 Akt 525ff.
 -- pathway 523
 alternative pre-mRNA processing 144
 alternative pre-mRNA splicing 3ff.
 -- application of genetic mosaics 476
 alternative splice site selection 93ff.
 alternative splice variant
 -- quantification 231ff.
 alternative splicing (AS) 575, 583
 -- analysis 575
 -- characterizing novel products 250ff.
 -- cloning of novel alternatively spliced
 transcripts 253
 -- detection using minigenes 383
 -- discovery 255
 -- *Drosophila* genetic mosaics 474ff.
 -- high-throughput analysis by
 RT-PCR 239ff.
 -- in genes of interest by cloning full-length
 cDNA transcripts 255
 -- mutation 142
 -- plant 79ff.
 -- Pol II 403
 -- product 9
 -- reporter minigene 404
 -- structure prediction for alternatively spliced
 protein 583

-- transfection 404
 alternative splicing database 537–538
 -- description 538ff.
 alternative splicing event (ASE) 93ff., 475
 -- computational identification 241
 -- endpoint PCR for detection 239
 -- finding ASE that overlap evolutionarily
 conserved secondary structures 579
 -- identifying ASE in genes of interest 251
 -- *in vivo* analysis 393ff.
 -- monitoring changes in plant 249ff.
 -- quantification 548
 -- variant 549
 alternative splicing factor (ASF) 34, 95
 alternative splicing modulator
 -- screening 496ff.
 Alternative Splicing Mutation Database
 (ASMD) 133
 alternative splicing pattern
 -- visualization with multiple fluorescent
 proteins 299
 amplicon detection 244
 amplification 224
 animal intron
 -- reciprocal system 451
 -- splicing 451
 antagonism 70
 antibody
 -- immunoprecipitation 272
 -- modification state-specific 464ff.
 -- purification 469
 antisense derivatives of U7 snRNA as modulators
 of pre-mRNA splicing 482ff.
 antisense microwalk
 -- identification of splicing *cis*-elements 210ff.
 -- ultra-refined 211
 antisense oligonucleotide (ASO, AON) 211ff.,
 511ff.
 -- chemistry 514
 -- design 513
 -- 2'-*O*-methoxyethyl (MOE) 526
 -- validation of specificity 212
 antisense-mediated exon skipping
 application 512
 antisense-mediated modulation of
 splicing 511ff.
Arabidopsis 453
 -- cell culture 456
 -- genome 81
 -- PEG-mediated transfection of protoplasts 457

-- PTB gene 453
 -- transfection of cell suspension
 protoplasts 456
Arabidopsis thaliana 249
 Argonaute protein 596
 array analysis 261ff.
 ASF/SF2 121, 177
 attachment B (*attB*) site 303, 384f.
 attachment L (*attL*) site 303, 384
 attachment P (*attP*) site 303, 384f.
 attachment R (*attR*) site 303, 384
 automated synthetic lethal analysis by microarray
 (SLAM) 72
 autoradiography 326
 auxiliary splicing regulatory element (SRE) 94

b

B complex
 -- assembly 336
 -- characterization 337
 -- purification 336
 background subtraction
 -- microarray 264
 bacterial artificial chromosome (BAC)
 -- clone 386
 base-pair probability plot 578f.
 binding competition 190
 binding stoichiometry 187
 -- RNA-protein complex 187
 bioinformatics 131, 538ff.
 -- analysis of splicing event 566ff.
 -- computational resources for mRNA-Seq data
 analysis 559
 -- mRNA processing evaluation 131
 BLAT 570
 BP clonase II reaction 305
 BP recombination reaction 305
 branch site (BS, branchpoint) 49
 branchpoint sequence (BPS) 44
tert-butyldimethylsilyl (TBDMS) group 156

c

C complex
 -- assembly 335
 -- characterization 337
 -- purification 335
 Cajal body (CB) 111, 594
 Cajal body-specific RNP (scaRNP) 16
 calcium phosphate-based transfection 394
 cap-binding complex (CBC) 113

- capillary electrophoresis 242, 504
cationic lipid-mediated transfection 395
cauliflower mosaic virus (CaMV) 35S RNA promoter 452
cDNA (complementary DNA)
-- cloning full-length cDNA 255
-- first strand cDNA synthesis 251, 503
-- gel purification 271
-- QC (quality control) 244
-- synthesis 285, 397, 442
cell
-- adaption of cells to SILAC medium 375
-- CLIP method to study protein–RNA interaction 269
-- harvest 283
-- HeLa cell nuclear extract 312ff.
-- plating 502
-- preparation of RNase-treated cell extract 272
-- single-cell detection of splicing events with fluorescent splicing reporters 298ff.
-- sonication 284
cell culture 202, 212, 528
-- transfection 306, 514
-- UV crosslinking 272
cell line
-- stable cell lines with splicing reporter 408ff.
-- transfection 411
cellular event
-- integration of splicing 109ff.
chemical synthesis
-- RNA 154ff.
chromatin immunoprecipitation (ChIP) 416ff.
chromatin RNA immunoprecipitation (ChRIP) 416ff.
-- cotranscriptional RNA processing 423
chromatin structure
-- splicing 115
cis-acting element 28, 401
cis-element 201ff.
-- 2'-*O*-methoxyethyl (MOE) antisense oligonucleotide 526
cleavable isotope coded affinity tag (cICAT) 370
cleavage and polyadenylation specificity factor (CPSF) 113
Clk 524ff.
-- inhibitor 526
cloning 411
-- fast cloning of splicing reporter minigenes 382ff.
-- full-length cDNA 255
-- generation of overhangs 286
-- identification of positive clones 388
-- novel alternatively spliced transcript 253
coiled coils
-- prediction 586
collision-induced dissociation (CID) 372
-- CID MS/MS 467f.
colony PCR 254
comparative genomics method
-- prediction of small RNA-binding sites 592ff.
comparative modeling 583
compound plate layout 501
consensus sequence
-- splice site 22
conserved tract 208
core pre-mRNA splicing factor 428ff.
core splicing reaction 332
coupled promoter splicing system 400ff.
crosslinking 283
-- UV 268ff., 345
crosslinking and immunoprecipitation (CLIP) 269ff.
-- protein–RNA interaction in intact cells and tissues 269ff.
-- protein–RNA interaction in *Schizosaccharomyces pombe* 281ff.
cryptic splice site activation 122
CUG-BP 39
cytomegalovirus (CMV) promoter 402f.
- d**
data acquisition 499
data analysis 234, 242, 502
-- functional analysis 263ff.
-- microarray 263
-- mRNA-Seq 559
-- normalization of data 263
-- pretreatment 263
-- qPCR 424
-- statistical analysis 263
-- visual inspection 263
-- visualization 265, 562
data processing 499
database 567
decreased abundance by mRNA perturbation (DAmP) strain 72
deletion 587
density gradient 148
dephosphorylation 284
DEXD/H-box protein 56
Dicer/TRBP [human immunodeficiency virus (HIV-1) transactivating response (TAR) RNA-binding protein] complex 596
5'-*O*-(4,4'-dimethoxytrityl (DMT))-2'-*O*-silyl strategy 156
disease
-- prediction of splicing relevance using tissue from mutant or disease states 528
-- splicing 119ff.
-- therapeutic approach 121
disordered region
-- prediction 585
dissociation constant
-- measurement 188
DNA fragment
-- gel-purification 222
-- size selection 222, 286
DNA fragmentation 221
DNA preparation 221
DNA recombination site 384
DNase treatment 233, 284, 442
dosage suppression 70
double-stranded RNA-binding motif (dsRBM) 291
Drosophila genetic mosaics 474ff.
-- analysis of alternative splicing 475
Drosophila genome
-- introduction of splicing reporter 475
Drosophila tissue
-- immunostaining 478
Duchenne muscular dystrophy (DMD) 511
- e**
EASANA analysis system 266
EDI (extra domain I, EDA) 401
-- alternative splicing 406
electron capture dissociation (ECD) 372
electron transfer dissociation (ETD) 372
electrophoretic mobility shift assay (EMSA) 183, 349
-- autoradiography 185
-- chromogenic and chemiluminescent detection method 186
-- detection of RNA–protein complexes 183ff.
-- equipment 191
-- fluorescence 185
-- gel preparation 191
-- imaging 193
-- pre-electrophoresis 192
-- reagent 191
-- sample preparation 192
-- supershift 343ff.
electroporation 394
3' end processing 113
endpoint PCR
-- detection of alternative splicing events 239
enhanced green fluorescent protein (EGFP)-tagged cDNA 389
ENSEMBLE 567
epigenetic chromatin modification 94
Escherichia coli
-- isolation of MS2–MBP-tagged protein 337
-- transformation 286
ESI (electrospray ionization) 367
eukaryotic RNA 6
-- common classes 6
EvoFold 579
excisionase (Xis) protein 385
exon 23
-- kinase regulating an alternative exon 525
-- partially random 204
-- size 94
exon definition 96f.
exon inclusion 532
exon junction complex (EJC) 113, 303
exon probe 262
exon skipping 122, 572
-- antisense-mediated 512
-- determining efficiency 518
exon–exon junction probe 262
exon-junction database 560
exonic sequence
-- functional analysis through iterative *in vivo* selection 201ff.
exonic splicing enhancer (ESE) 24, 51, 94, 322, 568
exonic splicing silencer (ESS) 51, 94, 322, 568
-- element 440
export 113
expression
-- regulated 487
-- RNA 7
extended inhibitory context (Exinct) 208
- f**
FARNA 588
FAST DB 541
fibrillarin 594
first strand cDNA synthesis 251, 503
flip-out study
-- transgene 476
Flp recombinase (flippase) 410
Flp-In™ T-Rex™ system 409
fluorescence energy transfer (FRET) 186

- fluorescent protein
 -- visualization of alternative splicing patterns 300
 fluorescent reporter minigene 302
 -- monitoring splicing patterns 300
 5-fluoroorotic acid (5-FOA) 430ff.
 Flux Capacitor 554
 Flux Simulator 549f.
 footprint experiment 3447
 FOX protein 103
 Fox-2 558f.
 functional analysis
 -- iterative *in vivo* selection 201ff.
 -- microarray data 263ff.
- g**
- GAL4 transcription activator 476
 Gateway® cloning 302, 384
 gene expression
 -- alternative pre-mRNA splicing 8
 -- induction 410
 gene quantification 559
 gene transfer 487
 gene-specific primer (GSP) 304, 405
 Genecards 567
 GENESILICO METASERVER 584ff.
 genetic interaction 70
 -- analysis 433
 -- synthetic 430
 genetic mosaics 476
 -- alternative pre-mRNA splicing 476
 -- *Drosophila* 474ff.
 genetic screen 434
 genome
 -- *Arabidopsis* 81
 -- stable integration 490
 genomic DNA
 -- isolation 221
 -- introducing adaptor sequences by Klenow reaction 222
 genomic DNA fragment cassette 303
 genomic library construction 221
 genomic mapping 559
 GFP (green fluorescent protein)
 -- two-color fluorescent reporter for splicing and translation 498
 GFP expression
 -- visualizing 460
 GFP-based splicing reporter 453
 GFP-tagged protein 300, 359
 -- immunoprecipitation 360
 gradient formation
 -- automatic 149
 -- manual 148
 gradient harvesting 150
 growth condition 283
 GST (glutathione S-transferase) 301
 GST pull-down experiment
 -- nuclear protein 361
- h**
- HBII-52 598
 -- snoRNA 595
 HEK293 cell
 -- transfection with reporter gene construct 389
 HeLa cell
 -- dialysis 315ff.
 -- extract preparation 315ff.
 -- harvesting 314
 -- large-scale growth 314
 -- lysis 315
 -- miniextract 317
 -- nuclear extract 317ff., 323
 -- quality testing 315
 -- small-scale preparation of nuclear extracts 316
 -- storage of extract 317
 heterogeneous nuclear ribonucleoprotein (hnRNP) 25, 51
 -- hnRNPI 96
 -- recognizing polypurine-tract by hnRNP A1 and hnRNP F 40
 HHSEARCH 586
 high-content imager 499
 high-throughput analysis
 -- alternative splicing 239ff.
 -- RT-PCR 239ff.
 high-throughput RNA sequencing 544ff., 557
 -- identification of splicing factor target genes 556ff.
 hit validation 500
 HIV-1 (human immunodeficiency virus 1) minigene 412
 HIV-1 RNA
 -- qRT-PCR analysis of spliced and unspliced species 443
 HIV-1 RNA splicing 440
 -- analysis 439ff.
 HIV-1 transcript 486
 -- primer for analysis 441
 hnRNP K homology (KH) domain 44
 homology 586
 HuD 39
 human disease
 -- wrong splice site selection 9
 Human Gene Mutation Database (HGMD) 133
 Hutchinson–Gilford progeria syndrome (HGPS) 10, 393
 hydrophilic interaction chromatography (HILIC) 369
 hydrophobic interaction chromatography (HIC) 369
- i**
- iFOLDRNA 588
 Illumina paired-end (PE) PCR primer 271
 image processing 502
 imager
 -- high-content 499
 -- laser image scanner 499
 -- PhosphorImager 499
 imaging 502
 immobilized metal ion chromatography (IMAC) 372
 immunization 469
 immunodepletion 469
 -- peptide 470
 immunogen 470
 immunoprecipitation 272ff., 284, 345, 359ff., 530
 -- ChIP, *see* chromatin immunoprecipitation
 -- GFP-tagged protein 360
 -- quantitation of immunoprecipitated nucleic acids 419
 -- Western Blot 259
 immunoselection 345
 -- digested crosslinked product 346
- immunostaining
 -- *Drosophila* tissue 478
in silico analysis, *see* bioinformatics
in vitro splicing 134
 -- nuclear extract 325
 -- pre-mRNA 323
in vitro splicing assay 320ff.
in vitro transcription 223
 -- minigene construction 321
 -- ³²P-labeled pre-mRNA preparation 322
in vivo selection 204
 -- procedure 207
in vivo splicing assay 202, 212
in vivo splicing modulation tool
 -- U7 snRNA 483
in vivo splicing reporter 497
 in-gel hydrolysis 373f.
 -- iTRAQ labeling of in-gel-digested proteins 375
 inhibitor 532
 -- identifying kinases/pathways involved in splicing 527
 input sequence 576
 insertion 587
 insulin 523
 insulin-like growth factor-1 (IGF-1) 523
 integration host factor (IHF) 385
 interactome 72
 intron
 -- plant 80, 451
 intron retention 123
 intron/exon architecture 23
 intron–exon organization
 -- yeast 66
 intronic splicing enhancer (ISE) 24, 94, 568
 intronic splicing processing element (ISPE) 295, 568
 intronic splicing silencer (ISS) 51, 94
 -- N1 (ISS-N1) 211
 ion-exchange chromatography (IEC) 369
 isobaric tags for relative and absolute quantification (iTRAQ) 370ff.
 -- labeling of in-gel-digested proteins 375
 -- sample preparation for labeling 375
 isoform quantification 555, 559
 isotope-coded protein label (ICPL) 370
 iterative *in vivo* selection
 -- functional analysis of large exonic sequences 200ff.
- j**
- junction reads detection 559
- k**
- KH (hnRNP K homology) domain 44
 kinase 525ff.
 -- activation by hormone 525
 -- inhibitor for identifying kinases/pathways involved in splicing 527
 -- role in a splicing event 526
 Klenow reaction
 -- introducing adaptor sequences to the genomic DNA 222
 knockout tissue
 -- prediction of splicing relevance 528
 KRAB/KAP1 transcriptional silencing protein 488

- I**
- Lamin A protein (LMNA) pre-mRNA 393
 - laser image scanner 499
 - lentiviral infection 170
 - lentiviral vector 490
 - lentiviral-mediated RNAi 167ff.
 - library
 - cleaning and verification 223
 - development 221
 - ligation 253
 - linker 284f.
 - 3' RNA adapter ligation 273
 - 5' RNA adapter ligation 275
 - liquid chromatography-coupled mass spectrometry (LC-MS) 369
 - LC-MS/MS 377ff.
 - low-molecular-weight phosphotyrosine phosphatase (LMPTP) 588
 - LR Clonase® II Plus reaction 306
 - LR recombination reaction 305
 - Lsm (like Sm) 484
- m**
- MALDI (matrix-assisted laser desorption/ionization) 367
 - mammalian cell
 - production and purification of individual SR proteins 179
 - splicing factor ChIP 421
 - mappability 545f.
 - mapping 547
 - read 552
 - short read 558
 - mass spectrometry (MS) 367
 - absolute quantification (AQUA) 371
 - analysis of protein-(RNA) complexes 366ff.
 - quantification 370
 - relative quantification 370
 - sample preparation 368
 - separation 368
 - MBP (maltose-binding protein) affinity purification 332ff.
 - METAMQAP 584ff.
 - MetaMQAPII 589
 - 2'-O-methoxyethyl (MOE) antisense oligonucleotide
 - *cis*-element 526
 - Mfold 576f.
 - microarray 262ff.
 - data treatment 263
 - microarray validation 242
 - PTB-regulated events 234
 - microcapillary electrophoresis (μ CE) 242
 - microRNA (miRNA) 8, 13ff., 593ff.
 - microtubule-associated protein tau (*MAPT*) gene 239
 - minigene 202, 530
 - alternative splicing reporter minigene 404
 - construction 303, 321
 - detection of alternative splicing 383
 - fast cloning of splicing reporter minigenes 383ff.
 - fluorescent reporter minigene 300ff.
 - promoter 402
 - splicing the phenotype of two HIV-1 minigenes 412
 - transfection 389, 404
 - minigene splicing 134
 - assay 134f.
 - minigene-derived mRNA
 - RT-PCR analysis 306
 - splicing pattern 306
 - miRNA-induced silencing complex (miRISC) 596
 - mitogen-activated protein kinase (MEK) family 526
 - model quality assessment 587
 - model quality assessment program (MQAP) 587
 - modeling 582ff.
 - comparative 583
 - template-based 583ff.
 - MODELLER 584ff.
 - MODERNA 588
 - modification
 - chemical 352
 - modification state-specific antibody 465ff.
 - mosaic fly 478
 - motif discovery tool 561
 - mRNA capping 112
 - mRNA processing evaluation
 - bioinformatics 131
 - mRNA-Seq 561ff.
 - computational resources for data analysis 559
 - experiment design 560
 - paired-end (PE) 560
 - single-end 560
 - transcriptome analysis 557
 - MS2-MBP (maltose-binding protein) affinity purification 335ff.
 - MS2-MBP fusion protein 337
 - MultiSite Gateway® System 302
 - muscleblind-like 1 (MBNL1) 42
 - mutagenesis
 - PCR 492
 - plasmid 431
 - mutation 122, 142
 - analysis of splicing mutation 129
 - plasmid shuffle for functional analysis and production of conditional mutations in essential yeast genes 431
 - predicting if a mutation leads to structural changes 578
 - mutation testing 130
 - procedure 133

n

 - next generation sequencing (NGS) technology 547, 557
 - platform 558
 - Nicotiana benthamiana*
 - agroinfiltration 459
 - Nicotiana benthamiana* leaves
 - *Agrobacterium*-mediated infiltration 457
 - NIPU program 570
 - nitrocellulose transfer 274
 - non-protein coding RNA (ncRNA) 7
 - noncoding RNA (ncRNA) 13ff., 292
 - nonsense-mediated decay (NMD) 89, 114, 251, 303
 - normalization
 - microarray 264
 - NOVA protein 103
 - Novo2 (neuro-oncological ventral antigen 2) 44
 - nuclear event
 - integration of splicing 109ff.
 - nuclear extract 313ff., 323
 - *in vitro* splicing reaction 325
 - miniextract 316
 - small-scale preparation 316
 - nuclear protein
 - GST pull-down 361
 - pull-down experiment 359ff.
 - nuclear structure 110

o

 - oligonucleotide design, *see also* primer design 167, 212
 - antisense, *see* antisense oligonucleotide
 - synthesis 212
 - orphan snoRNA 595

p

 - PAGE (polyacrylamide gel electrophoresis)
 - denaturing 326
 - paired-end (PE) mRNA-Seq 560
 - library 560
 - paired-end PCR primer 271
 - paraspeckles 111
 - pathway
 - inhibitor for identifying kinases/pathways involved in splicing 527
 - PCONS method 586
 - PCR 244, 252f., 276, 385, 397
 - amplification 271, 285, 504
 - colony 254
 - endpoint PCR for the detection of alternative splicing events 239
 - forward primer 386
 - introduction of functional sequences into U7 SmOPT 486
 - mutagenesis 490
 - nested primer 386
 - proofreading polymerase 488
 - quantitative (qPCR) 230, 242f., 424
 - radiolabeled 229
 - real-time 230
 - reverse primer 386
 - splice variant quantification 229
 - two-step amplification 304
 - peptide
 - additional separation of generated peptides 368
 - extraction for MS 374f.
 - immunogen design 466
 - synthesis 467
 - peptide immunogen-carrier protein conjugation 469
 - peptidyl-prolyl (*cis/trans*) isomerase (PPIase) 62
 - phenotype
 - HIV-1 minigene 412
 - phosphoinositide-3 kinase (PI3K)
 - PI3Kinase/Akt pathway 523
 - phosphoinositide-dependent kinase 2 (PDK2) 528
 - PhosphorImager 499
 - phosphorylation 372
 - Piwi-interacting RNA (piRNA) 8, 17
 - plant
 - alternative splicing 79ff.
 - genomic SELEX to identify RNA targets of plant RNA-binding proteins 219ff.

- *in vivo* analysis of intron splicing 451ff.
- intron 80
- monitoring changes in alternative splicing events 249ff.
- spliceosomal protein 82ff.
- spliceosome 81
- splicing reporter 452
- transfection of plasmid DNA into protoplasts 453
- plasmid
 - complementing URA3 plasmid 431
 - mutagenesis 431
 - preparation 251
 - shuffle for functional analysis and production of conditional mutations in essential yeast genes 431ff.
 - transfection of plasmid DNA into plant protoplasts 453
- plate reader 499
- Pol II, *see* RNA polymerase II
- poly(A) binding protein 1 (PABPN1) 113
- polyethyleneimine (PEI) 441
- polymerase processivity 94
- polypurine-tract
 - recognizing by hnRNP A1 and hnRNP F 40
- polypyrimidine tract (PPT) 22
- post-transcriptional gene silencing (PTGS) 165
- post-translational modification (PTM) 372, 465
 - modification state-specific antibody 465ff.
- pre-messenger RNA (pre-mRNA) 65
 - analysis of secondary structure 575
 - MS2-MBP- and MS2-tagged 335
 - ³²P-labeled preparation by *in vitro* transcription 322
- pre-mRNA splicing
 - alternative 3ff.
 - antisense derivatives of U7 snRNA as modulators 483ff.
 - *in vitro* 323
 - use of *Saccharomyces cerevisiae* to study the mechanism 65
- pre-mRNA splicing factor
 - core 429
 - yeast genetics 429
- pre-mRNA substrate
 - preparation 321
- pre-processing
 - read 550
- pre-spliceosome 331
- premature termination codon (PTC) 134, 251, 303
- primary structure analysis 585
- primer
 - analysis for HIV-1 transcript 441
 - design 221, 232ff., 241ff., 304, 384, 441, 486
 - forward 386
 - gene-specific (GSP) 304
 - labeling 222
 - nested 386
 - qRT-PCR primer design 441
 - reverse 384
- primer extension analysis 350
- probability of selection pattern 598
- probe 347
 - specificity of the chemical and enzymatic probes 348
- probe design
 - splicing microarray 262
- promoter 401
 - constitutive 402
 - inducible 402
 - minigene 402
- PROQ 584ff.
- protein
 - absolute quantification (AQUA) by MS 371
 - GFP-tagged 360
 - iTRAQ labeling of in-gel-digested proteins 375
 - mass spectrometry-based protein identification of proteins (proteomics) 367
 - MS2-MBP fusion protein 337
 - plant spliceosomal protein 82ff.
 - primary structure analysis 585
 - pull-down experiment 360
 - sample preparation 368
 - separation 368
- protein fold recognition 586
- protein kinase C (PKC) 526
 - PKC β I 532
 - PKC β II 528ff.
- protein structure database (PDB) 583
- protein-RNA complex 183ff., 343ff.
 - binding stoichiometry 187
 - competing nucleic acids and polyanions 187
 - detection of binding 184
 - electrophoretic mobility shift assay (EMSA) 183
 - elution 285
 - footprinting analysis 344
 - measurement of binding activity 187
 - quantitation of binding 184
 - (quantitative) mass spectrometric analysis 367
 - sample preparation 192
 - selection of RNAs bound to the protein of choice 223
 - stability during electrophoresis 186
- protein-RNA interaction
 - analysis of site-specific interactions 343
 - CLIP in intact cells and tissues 269
 - CLIP in *Schizosaccharomyces pombe* 281ff.
 - detection by mass spectrometry 373
 - identification 291ff.
- protein-RRM interactions in splicing regulation 41
 - without RNA binding 41
- proteome analysis 373
- proteomics 367
- protoplast
 - preparation from *Arabidopsis* cell culture 456
- provirus vector DNA
 - transfection into cells 441f.
- Prp28p 430
- pseudoxon 23, 124
 - inclusion 124
- pSpliceExpress 383
- PTB (polypyrimidine-tract binding protein) 36ff., 96ff.
 - *Arabidopsis* PTB gene 453
 - microarray validation of PTB-regulated events 230
- PTB-like protein 86
- PU value
 - computing 577ff.
- pull-down experiment
 - nuclear protein 359ff.
- Pumilio (Puf) homology domain (HD) 291
- purine-pyrimidine tract 39
- putative exonic splicing enhancer (PESE) 24
- putative exonic splicing silencer (PESS) 24, 123
- pyrimidine-tract recognition
 - by sex-lethal, U2AF65, and PTB 37
- pyruvate kinase (PKM) 93
- q**
 - quantitative PCR (qPCR) 230, 240f.
 - data analysis 424
 - quantitative reverse transcription PCR (qRT-PCR) 440
 - analysis 443
 - reaction condition 443
 - spliced and unspliced HIV-1 RNA species 443
 - QUA2 (Quaking homology 2) domain 44
 - quasi-RRM (qRRM) 40
- r**
 - radioimmunoprecipitation assay (RIPA) 359
 - RASMOL 588
 - rate zonal technique 148
 - Raver1 motif 41
 - read 547
 - counting 557
 - deconvolution 546f.
 - mapping 550ff.
 - mapping statistics 554
 - pre-processing 550
 - RPKM (reads per kilobase per million) 561
 - short read mapping 558
 - real-time PCR
 - chemistry and quantification methods 230
 - reciprocal system 451
 - recombination
 - reaction 385
 - site-specific 384
 - recombination protein 383
 - reference indexing 552
 - repeat
 - prediction 586
 - repeat-associated siRNA (rasiRNA) 17
 - repeated segment 586
 - reporter
 - plant splicing reporter construct 452
 - stable cell lines with splicing reporter 409ff.
 - two-color fluorescent reporter for splicing and translation 498
 - reporter gene
 - splicing efficiency 69
 - splicing in living organisms 475
 - transfection of cells 387
 - reporter minigene
 - alternative splicing 404
 - fast cloning of splicing reporter minigenes 383ff.
 - fluorescent 300ff.
 - transfection 404
 - reverse transcriptase (RT) reaction 229, 244, 271ff., 386
 - RFP (red fluorescent protein) 498
 - cDNA 301

- ribonuclease A 583
 ribonuclease P (RNase P) 14
 ribonucleoprotein (ribonucleoprotein particle, RNP) 13ff., 343, 373
 -- cellular function 15
 -- cellular small 14
 -- complex 291
 -- formation of complexes 346
 -- three-dimensional (3-D) structure 345
 ribonucleoprotein (RNP) domain 35
 ribonucleoside phosphoramidite building block 156
 ribosomal RNA (rRNA) 14
 -- snoRNA-rRNA interaction 595
 ribozyme 5ff.
 RNA
 -- 7SK RNA 18
 -- 7SL RNA 17
 -- alternative pre-mRNA splicing 3ff.
 -- analysis 515
 -- binding by splicing factor 36f.
 -- chemical synthesis 155ff.
 -- common classes of eukaryotic RNA 6
 -- computational prediction of secondary structures 576
 -- DNase treatment 229
 -- dynamics of the spliceosomal RNA-RNA rearrangements 53
 -- enzymatic 5
 -- expression 7
 -- extraction/isolation 229, 243, 251, 270ff., 397, 405, 442, 459, 503, 517
 -- flexible conformation 4
 -- gel purification 275
 -- high-throughput RNA sequencing 545ff.
 -- interaction 35f.
 -- precipitation 270
 -- preparation/purification 229, 243, 251, 270ff., 397, 405, 442, 459, 503, 517
 -- regulatory element 570
 -- secondary structure 26, 94, 347, 570, 575
 -- solid-phase synthesis 155
 -- structure 5
 -- 3-D structure prediction 588
 -- synthesis 349
 3' RNA adapter ligation 273
 5' RNA adapter ligation 275
 RNA binding 36ff.
 -- comparative genomics methods for the prediction of small RNA-binding sites 593ff.
 RNA binding protein
 -- genomic SELEX to identify RNA targets of plant RNA-binding proteins 219ff.
 3' RNA dephosphorylation 273
 RNA element
 -- cis-acting 28
 -- splicing 21ff.
 RNA integrity number (RIN) 244
 RNA interference (RNAi) 165ff.
 -- lentiviral-mediated 167ff.
 RNA modification 158, 270
 -- combined chemical and enzymatic strategies 158
 -- coupling of biophysical probes to aliphatic amino groups on RNA 160
 -- during solid-phase synthesis 158
 -- enzymatic ligation of RNA fragments using T4 RNA or T4 DNA ligase 160
 -- incorporation of modified phosphoramidites during solid-phase synthesis 160
 -- post-synthetic 158
 5' RNA phosphorylation 270ff., 285
 RNA polymerase II (Pol II) 27, 100, 401ff., 526
 -- mutant 406
 RNA processing 27
 -- ChRIP for analysis of cotranscriptional RNA processing 423
 RNA pulldown experiment 291
 RNA structure
 -- *in vitro* probing 349
 -- secondary structure 26, 94, 347, 570, 575
 -- structure 5
 -- 3-D structure prediction 588
 RNA substrate 184
 RNA target
 -- affinity selection 223
 -- genomic SELEX to identify RNA targets of plant RNA-binding proteins 219ff.
 RNA template 292
 RNA transcript
 -- high-throughput RNA sequencing 545ff.
 -- renaturation 349
 RNA world 3ff.
 -- hypothesis 6
 RNA-binding domain (RBD) 35, 453
 RNA-binding protein (RBP) 291
 RNA-induced silencing complex (RISC) 165
 RNA-protein complex 183ff., 343ff.
 -- binding stoichiometry 187
 -- competing nucleic acids and polyanions 187
 -- detection of binding 184
 -- electrophoretic mobility shift assay (EMSA) 183
 -- footprinting analysis 344
 -- measurement of binding activity 187
 -- quantitation of binding 184
 -- (quantitative) mass spectrometric analysis 367
 -- sample preparation 192
 -- selection of RNAs bound to the protein of choice 223
 -- stability during electrophoresis 186
 RNA-protein interaction
 -- analysis of site-specific interactions 343
 -- CLIP in intact cells and tissues 269ff.
 -- CLIP in *Schizosaccharomyces pombe* 281ff.
 -- detection by mass spectrometry 373
 -- identification 291ff.
 RNA-recognition motif (RRM) 34f., 453
 -- RNA binding 36ff.
 -- RRM-protein interactions 41
 -- RRM-protein interactions in splicing regulation 41
 -- RRM-RRM interactions in splicing regulation 40f.
 RNA-seq data 242, 545ff.
 RNA-seq read 553
 RNAfold 576f.
 RNase treatment 284, 346ff.
 ROSETTA 586f.
 RPKM (reads per kilobase per million) 561
 RT-PCR 224, 229, 276, 388, 397, 459, 517, 531
 -- analysis of splice site utilization 445
 -- conventional 230
 -- establishing the conditions 250
 -- high-throughput analysis of alternative splicing 239ff.
 -- minigene-derived mRNA 306
 -- multiple RT-PCR AS panel using 96-well plates 251
 -- purification 253
 -- quantitative (qRT-PCR) 440
 -- validation 503
S
Saccharomyces cerevisiae
 -- mechanism of pre-mRNA splicing 65
 -- model system for studying spliceosomal factors 429ff.
 -- protein composition of spliceosomal complex 59f.
 -- splicing factor ChIP 419
Schizosaccharomyces pombe
 -- cell harvest 283
 -- growth condition 283
 -- RNA-protein crosslinking and immunoprecipitation 281ff.
 SDS PAGE (polyacrylamide gel electrophoresis) 274, 369
 secondary structure
 -- computational prediction 576
 -- RNA 26, 94, 347, 570, 576f.
 secreted alkaline phosphatase (SEAP) assay 442
 sedimentation coefficient 147
 sedimentation marker 150
 selection pattern
 -- probability 598
 SELEX (systematic evolution of ligands through exponential enrichment) 201, 345, 526
 -- genomic SELEX to identify RNA targets of plant RNA-binding proteins 219ff.
 sequence
 -- analysis 204
 sequence alignment 255ff., 561
 sequence database
 -- tissue-specific annotation 243
 sequencing 254ff.
 -- high-throughput RNA sequencing 545ff.
 serine-arginine (SR) protein 112
 sex-lethal 37
 SF1/BBP protein (splicing factor 1/branch binding protein) 55
 SHIP2 525
 short hairpin RNA (shRNA) 165ff.
 short interfering RNA (siRNA) 8, 13ff., 165ff.
 -- role of a kinase and spliceosomal protein in a splicing event 526
 short read mapping 558
 signal recognition particle (SRP) 15
 signaling pathway
 -- extracellular stimulated 523
 signaling system
 -- regulation of splicing 524
 5'-O-silyl-2'-O-bis(2-acetoxyethoxy)methyl orthoester (ACE) strategy 156f.
 single-cell detection
 -- splicing events with fluorescent splicing reporters 299ff.
 single-stranded region
 -- prediction 577
 single-stranded RNA (ssRNA) 35
 site-specific recombination 384
 size-exclusion chromatography (SEC) 369

- Ski oncogene interacting protein (SKIP) 332
- Sm binding site 18
- Sm (Stephanie Smith) protein 52, 84
- SMAD2 protein C-terminal domain
- human 470
- small Cajal body RNA (scaRNA) 594
- small nuclear ribonucleoprotein 51, 331, 483
- small nuclear RNA (snRNA) 7, 21, 483, 595
- small nucleolar ribonucleoprotein (snoRNP) 111
- small nucleolar RNA (snoRNA) 7, 15, 593
- box C/D 15, 594
 - box H/ACA 15, 594
 - snoRNA-rRNA interaction 595
- small regulatory RNA 13ff.
- small ribonucleoprotein (snRNP) 21, 52
- small RNA 13, 593
- comparative genomics methods for the prediction of small RNA-binding sites 592ff.
- SNORD115 595
- snoTARGET 595
- solid-phase synthesis
- RNA 155
 - RNA modification 158
- sonication
- cell 284
- spatial proximity effect 94
- spinal muscular atrophy (SMA) 10, 26, 202
- splice site
- analysis 568
 - programs used for analysis 568
- 3' splice site (3'SS) 119, 485, 568
- 5' splice site (5'SS) 119, 485, 568
- splice site activation
- cryptic 122
- splice site (consensus) sequence 22, 94
- splice site definition 23
- splice site pairing 55
- splice site recognition 55
- splice site selection
- wrong 9
- splice site utilization 445
- analysis 444
- splice variant function
- physiological readout 528
- spliced product
- separation and analysis 252
- spliceosomal B complex
- purification 151
- spliceosomal complex
- assembly and isolation *in vitro* 330ff.
 - MS2-MBP-tagged 335
- spliceosomal factor
- yeast as model system for studying 429ff.
- spliceosomal protein
- extracellular stimulated signaling pathway 523
 - role in a splicing event 526
- spliceosome 49ff., 331
- activation 55
 - analysis and purification 147
 - catalytic center 56
 - changing signals 523
 - compositional dynamics and complexity 57f.
 - constitutive splicing 49ff.
 - dynamics of the spliceosomal RNA-RNA rearrangements 53
 - evolutionarily conserved blueprint for yeast and human 61f.
 - plant 81
 - plant spliceosomal protein 82ff.
 - protein composition of *Saccharomyces cerevisiae* spliceosomal complex 59f.
 - stepwise assembly pathway 51
 - ultracentrifugation 147
 - yeast 67
- splicing 110ff.
- aberrant 393
 - alternative pre-mRNA splicing 3ff.
 - analysis 250, 459
 - analysis of common splicing problems 141ff.
 - analysis of splicing products 325f.
 - animal intron 451
 - basics 65
 - cellular event 109ff.
 - constitutive 49ff.
 - core splicing reaction 332
 - cotranscriptional 417
 - database 539
 - detection by chromatin immunoprecipitation 416ff.
 - disease 119ff.
 - 3' end processing 113
 - export 113
 - *in vitro* 134
 - *in vivo* analysis of plant intron splicing 450ff.
 - inhibitors for identifying kinases/ pathways 527
 - mechanism 49
 - minigene 134
 - nuclear event 109ff.
 - oligonucleotides to change splicing 511
 - phenotype of two HIV-1 minigenes 412
 - plant splicing analysis *in vivo* 451ff.
 - reaction 324
 - regulatory element 569
 - reporter genes for splicing in living organisms 475
 - RNA element 21ff.
 - transcription 112
 - translation 114
 - two-color fluorescent reporter for splicing and translation 498
- splicing assay
- *in vivo* analysis 393ff.
- splicing cassette
- generating the initial pool 206
- splicing *cis*-element
- identification through an ultra-refined antisense microwalk 210ff.
- splicing code 28f., 103
- splicing complex
- analysis by agarose gel electrophoresis 334
 - assembly 96
- splicing efficiency 69
- splicing element
- combinatorial effect 28
- splicing event
- bioinformatic analysis 567ff.
 - role of a kinase and spliceosomal protein 526
 - single-cell detection with fluorescent splicing reporters 299ff.
- splicing factor 33, 82, 175, 575
- detection by chromatin immunoprecipitation 416ff.
 - distribution 110
 - identification of target genes by high-throughput sequencing 557ff.
 - RNA binding 36f.
 - SF2/ASF 95, 121, 177
 - yeast 68
- splicing factor ChIP (SF-ChIP) 416ff.
- mammalian cell 421
 - *Saccharomyces cerevisiae* 419
- splicing factor compartment (SFC)/speckles 111
- splicing index 239
- splicing microarray 262
- probe design 262
- splicing modulation
- antisense-mediated 511ff.
 - U7 snRNA 483
- splicing mutation
- analysis 129ff.
- splicing pattern 99
- minigene-derived mRNA 306
- splicing protein
- expression and purification 174ff.
- splicing regulation 143
- combinatorial 101
 - manipulation 143
 - programs used to determine regulatory splicing elements 569
 - regulatory splicing element 569
 - RRM-RNA interaction 35
 - signaling system 524
 - structural biology perspective of proteins 33ff.
- splicing regulator 95
- splicing regulatory element (SRE) 24, 120
- auxiliary 94
- splicing reporter
- fast cloning of splicing reporter minigenes 382ff.
 - gene 477
 - green fluorescent protein (GFP)-based 453
 - *in vivo* 497
 - introduction into the *Drosophila* genome 475
 - plant 452
 - plasmid-based site-specific integration 410
 - single-cell detection of splicing events 298ff.
 - stable cell line 408ff.
- splicing sequence
- unexpected splicing outcomes following the disruption of classical splicing sequence 124
- splicing system 401
- sporulation
- yeast 432
- SR protein 175, 569
- expression in *Escherichia coli* and purification 177
 - preparation of total HeLa SR proteins 175
 - preparation using a baculovirus system 178
 - purification of individual SR proteins 177ff.
- SR protein-specific kinase (SRPK1) 177
- SR-like protein 175

- SRC tyrosine kinase gene 101
 SROOGLE 569
 SRPK 525
 stable isotope labeling by amino acids in cell culture (SILAC) 375
 -- adaption of cells 375
 -- quantification 375
 statistical analysis 264f., 561
 -- microarray data 263
 structural biology perspective
 -- proteins involved in splicing regulation 33ff.
 structure prediction
 -- alternatively spliced protein 583ff.
 subcloning strategy 490
 substitution 587
 supershift 344ff.
 suppressor
 -- extragenic 70
 survival of motor neuron (SMN)
 -- pre-mRNA splicing 25
 -- SMN1 201ff., 486
 -- SMN2 202, 211, 486
 SWISS-MODEL 584ff.
 SWISS-PDB-VIEWER 586ff.
 SYBR® Green I 230
 synthetic generic array (SGA) 72
 synthetic lethal analysis by microarray (SLAM)
 -- automated 72
 synthetic lethal screen 71
 synthetic lethality 71
- t**
 T7 promoter 223
 tandem mass tag (TMT) 370
 TaqMan® probe 230
 target prediction 596ff.
 target site
 -- selection 466
 target–template alignment 586
 telomeric RNA (TER) 16
 template-based modeling 583ff.
 tetracycline 403, 410
 tetrad dissection
 -- yeast 432
 tissue
 -- CLIP method to study protein–RNA interaction 268ff.
 -- immunostaining of *Drosophila* tissue 478
 -- prediction of splicing relevance using knockout tissue or tissue from mutant or disease states 528
 -- UV crosslinking 271
 titanium dioxide chromatography 372
 tobacco leaf protoplast
 -- preparation 455
 -- transfection 454
 TOPO TA cloning® 286
 trans-acting factor 143, 569
 -- expression 453
 transactivator
 -- tet-controlled 403
 transcript
 -- aberrant 122
 -- alignment tool 538
 -- assembly 559
 -- cloning of novel alternatively spliced transcripts 253
 -- probing of 5'- or 3' end-labeled transcripts 351
 -- quantification of abundance 553
 transcription 27
 -- *in vitro* 223
 -- splicing 112
 transcriptional gene silencing (TGS) 165
 transcriptome analysis
 -- mRNA-Seq 557
 transfection 202, 212, 306, 388, 394f., 516, 529
 -- adherent cell line 394
 -- alternative splicing reporter minigene 404
 -- *Arabidopsis* cell suspension protoplasts 456
 -- calcium phosphate method 394
 -- cationic lipid-mediated 395
 -- cell line 411
 -- cultured cell 514
 -- electroporation 394
 -- PEG-mediated 455ff.
 -- plasmid DNA into plant protoplasts 453
 -- tobacco leaf protoplast 454f.
 -- virus/provirus vector DNA into cells 441f.
 transformation 254f., 286, 388
 -- *Agrobacterium* electrocompetent cells 458
 -- diploid knockout strain 432
 -- yeast cell 432
 transgene
 -- flip-out study 476
 transgenic animal 306
 translation
 -- splicing 114
 -- two-color fluorescent reporter for splicing and translation 498
 transmembrane helices
 -- prediction 586
 transmembrane region 586
 TREX (TRanscription EXport) complex 114
 2'-O-triisopropylsilyloxymethyl (TOM) group 156
 tumor necrosis factor alpha (TNF α) 523
- u**
 U-rich small nuclear RNP (U snRNP) 14ff.
 U1 small nuclear RNA (snRNA) 51, 595
 U1 snRNP 51, 295, 331
 U2 auxiliary factor (U2AF) 55
 U2 auxiliary factor 35 kDa (U2AF35) 96
 U2 auxiliary factor 65 kDa (U2AF65) 38ff., 82ff.
 U2 snRNA 51, 595
 U2 snRNP 51, 331
 U4 snRNA 51, 595
 U4 snRNP 51, 331
 U5 snRNA 51, 595
 U5 snRNP 51, 331
 U6 ribozyme hypothesis 54
 U6 snRNA 51, 331, 595
 U6 snRNP 51, 331
 U7 Sm OPT (optimized) 484ff.
 U7 snRNA 483ff.
 -- antisense derivatives as modulators of pre-mRNA splicing 483ff.
- U12 snRNA 595
 UBP1-associated protein 1a (UBA1a) 87
 UCSC (University of California Santa Cruz) genome browser 538, 567, 579
 UHM (U2AF homology motif) family 41
 UHM–ULM interaction 38
 ULM (UHM ligand motif) 38
 ultracentrifugation
 -- analysis of spliceosome 147
 -- preparing 150
 -- run 150
 untranslated region (UTR) 596ff.
 UPF (up-frameshift protein) 251
 upstream activator sequence (UAS) 476
 URA3 plasmid 430ff.
 -- construction of complementing URA3 plasmid 431
 -- double-gene 433
 uracil 430
 UV crosslinking 271, 345f.
 -- cell culture 272
 -- tissue 271
 UV-crosslinking and immunoprecipitation (CLIP) method 271ff.
 -- protein–RNA interaction in intact cells and tissues 271ff.
- v**
 validation 500
 -- RT-PCR 503
 virus RNA splicing 439
 virus vector DNA
 -- transfection into cells 441
- w**
 Western Blot 460, 529
 -- immunoprecipitate 259
- y**
 yeast
 -- double-knockout strain 433
 -- GAL4 transcription activator 476
 -- intron–exon organization 66
 -- model system for studying spliceosomal factors 429ff.
 -- plasmid shuffle for functional analysis and production of conditional mutations in essential yeast genes 431ff.
 -- probing of yeast RNAs modified *in vivo* by DMS treatment 352
 -- spliceosome 67
 -- splicing factor 68
 -- sporulation 432
 -- tetrad dissection 432
 -- transformation of cells 432
 -- transformation of diploid knockout strain 432
 yeast genetics 429
 -- function of core pre-mRNA splicing factor 429ff.
- z**
 zinc finger domain 42
 ZRANB2 43