

Index

- A**
- AACT in brassinosteroid (BR) biosynthesis, 405
 - ABA. *See* Abscisic acid (ABA)
 - ABA1, 276, 280, 281
 - ABA2 (encoding alcohol dehydrogenase), 250, 252–254, 275, 276, 281
 - ABA3 (encoding molybdenum cofactor sulfurase), 252, 254, 273
 - ABA-activated Ca²⁺-permeable channels, 271
 - ABA-activated G-proteins, 267
 - ABA-activated MAPK signaling system, 271
 - ABA-activated protein kinase (AAPK), 263
 - ABA-activated R-type (rapid) anion channel, 267
 - ABA-activated S-type (slow) anion channel, 267
 - ABA-induced activation of CDPKs, 270
 - ABA-induced activation of JA biosynthesis, 278, 288
 - ABA-induced activation of MAPK, 272
 - ABA-induced Ca²⁺ release into cytosol, 269
 - ABA-induced cytosolic Ca²⁺ increases, 271
 - ABA-induced disease resistance, 246, 251, 288
 - ABA-induced NO in stomatal closure, 271, 287
 - ABA-induced ROS production, 263, 267, 270–272
 - ABA-induced stomatal closure immune responses, 271, 287, 292
 - ABA-induced susceptibility, 247, 250
 - ABA-induced virus disease resistance, 287
 - ABA insensitive (ABI) transcription factors
 - ABI1, 259, 260, 264, 265, 281, 285
 - ABI2, 259, 260
 - ABI3, 248, 280
 - ABI4, 248
 - ABI5, 280
 - ABA-mediated Ca²⁺ transients, 268
 - ABA-mediated stomatal closure, 169, 263, 267
 - ABA-modulated JA, SA, and ET signaling pathways, 290
 - ABAR/CHLH as ABA receptor, 256
 - ABA-regulated genes, 276
 - ABA response element-binding factors (ABFs), 6, 252, 265, 270, 272
 - ABA-responsive1 (ABR1), 247
 - ABA-responsive element (ABRE), 6, 245, 270, 272
 - ABA-responsive genes, 250, 259, 262
 - ABA-responsive transcription factors, 264
 - ABA-stimulated calcium-dependent protein kinase1 (ACPK1), 270
 - ABA-suppressed lignin deposition, 291
 - ABA-suppressed PAL activity, 278
 - ABA-suppressed SA biosynthesis, 278
 - ABA-suppressed SA signaling, 290
 - ABA-triggered membrane depolarization, 268
 - ABRE-binding factors. *See* ABA response element-binding factors (ABFs)
 - ABREBs, 6, 265, 272, 273. *See also* ABA response element-binding factors (ABFs)

- Abscisic acid (ABA)
 aldehyde, 252, 254, 284
 biosynthesis genes, 250
 in induced systemic resistance (ISR), 248
 in JA biosynthesis, 168, 275, 276
 receptors, 1, 6, 124, 168, 245, 256
 signal in cytokinin signaling, 375
 signaling system
 conferring resistance, 285
 conferring susceptibility, 289
 triggers callose deposition, 286
 transport, 274
 transporters
 AtABCG25 in ABA transport, 274
 AtABCG40 in intercellular transport of ABA, 274
 as virulence factor, 292
- Abscisic acid oxidase3 (AAO3), 252, 254, 275, 280, 281, 321–323
- Abscisic alcohol, 252
- ACC oxidase (ACO), 159, 196, 198, 201, 204, 205, 207, 208, 282, 283, 285
- ACC synthase (ACS), 195–198, 200–202, 204–208, 282, 333, 334, 436
- ACC synthase inhibitor AVG, 334, 436
- ACGTGGC motif, 245, 272
- ACO gene, 199, 282
- ACPK1. *See* ABA-stimulated calcium-dependent protein kinase1 (ACPK1)
- ACS genes, 199, 206, 230, 283, 333
- Acyl amido synthetase, 319
- Acyl-CoA oxidase (ACX), 126, 127, 129, 137
- Acyl-CoA synthetase, 129
- Adenosine phosphate-isopentenyltransferase (IPT), 360
- AFB1/2/3/4/5 auxin receptors, 323–325, 328, 338
- AHK2/AHK3/AHK4 cytokinin receptors, 362, 363, 371, 373
- AHK sensing and signaling, 363
- AHPs. *See* *Arabidopsis* Hpt (histidine phosphotransfer) proteins (AHPs)
- ALD1 in SAR, 69, 70, 72, 73
- Alkamide, 157
- Allene oxide cyclase (AOC), 126, 127, 130, 137, 138, 164
- Allene oxide synthase (AOS), 126, 127, 135–137, 159, 163, 164, 172, 226, 341
- Allene oxide synthase (AOS) genes, 333, 340
- Alternative oxidase (AOX), 59, 60, 63, 64
- Amidase, 314
- 1-Aminocyclopropane-1-carboxylic acid (ACC), 128, 162, 197, 201–203, 208, 282, 333
- Anion channel, 271, 272
- Anion channel blockers, 267
- Antagonism
 between ABA and ET signaling, 250, 285
 between ABA and JA signaling, 250, 276
 between ABA and SA signaling, 250, 280
 between auxin and ABA signaling, 331
 between GA and BR signaling, 383
 between GA and JA signaling, 383
 between OGs and auxin signaling, 324, 325
 between SA and JA signaling, 81, 96, 162, 163, 331
- Antagonistic regulation of PAMP-triggered immunity by bHLH, 433
- AOC. *See* Allene oxide cyclase (AOC)
- AOS. *See* Allene oxide synthase (AOS)
- AOX. *See* Alternative oxidase (AOX)
- AOX-mediated alternative respiratory pathway, 59
- AOX-mediated redox signaling, 62, 63
- AP2/EREBP transcription factors, 154, 219, 359, 366
- Arabidopsis* histidine kinase (AHK), 364, 365
- Arabidopsis* Hpt (histidine phosphotransfer) proteins (AHPs), 363, 364
 nuclear translocation, 363
 proteins, 365
- Arabidopsis* response regulators (ARRs). *See* ARR-dependent transcriptional activation
- Archetypal defense hormones, 383
- ARF9 enhancing resistance to necrotrophs, 344
- ARF1 suppressing resistance to biotrophs, 344
- ARR7 (Type-A ARR), 366
- ARR-dependent transcriptional activation, 363
- Asp–Glu–Leu–Leu–Leu–Ala (DELLA), 384
 GAI, RGA, RGL1, RGL2, RGL3, 386
 gene, 386, 388, 396
 modulated JA responses, 392, 393
 proteins, 1, 9–11, 383, 384, 386–391, 393, 395
 proteins degradation, 383, 387
 repressing GA-dependent defense responses, 383, 386, 387, 392
- AUX1, 320, 328, 330, 342
- Aux/IAA degradation, 327
- AUX/IAA proteins, 1, 7, 314, 318, 322, 323, 328
- AUX/IAA repressors, 1, 7, 311, 312, 328

Auxin

- application inducing disease resistance, 344
- biosynthesis, 323
- causing repression of cytokinin responses, 359
- conjugation, 319
- homeostasis, 8, 319, 320, 327
- involved in modulation
 - of ABA signaling, 312
 - of cytokinin signaling, 312
 - of ET signaling, 312
 - of JA signaling, 312
 - of ROS signaling, 312
 - of SA signaling, 312
- perception, 311
- receptor TIR1 F-box protein, 7, 311, 312, 314
- response factors modulating defense responses, 343
- signaling genes, 316
- signaling promoting disease resistance, 342, 343
- signaling promoting disease susceptibility, 336–338
- signaling repression by SA, 327
- signaling suppression by small RNA signaling, 336
- transport, 320, 395
- transporters, 323
- transport system in promoting susceptibility, 342
- Auxin-activated G-proteins, 312
- Auxin-activated H⁺-ATPases, 312
- Auxin-activated K⁺ channels, 312
- Auxin-induced suppression of SA signaling, 328, 329
- Auxin-inducible genes
 - Aux/IAA genes, 316, 322
 - Gretchen Hagen3 (GH3s), 316, 329
(*see also* GH3 genes)
 - small auxin upregulated RNAs (SAURs), 316, 322
- Auxin-promoted susceptibility, 324, 337
- Auxin-response element (ARE) TGTCTC, 315, 316
- Auxin response factor (ARF), 1, 311, 312, 315, 317–319, 322, 323, 335, 343
- Auxin-responsive genes, 311, 315, 317, 323, 334
- Auxin-responsive genes promoting disease resistance, 342
- Auxin responsive protein (ARP), 328

- AUX–LAX family of amino-acid permease-like proteins, 320
- AVG (ethylene biosynthesis inhibitor), 197
- AXR1, 332, 333, 338, 344
- AXR4, 342
- AXR6, 344
- Azelaic acid, 330

B

- BABA-induced disease resistance, 286
- Backbone of plant immune system, 383
- BAK1, 9, 10, 403, 413–416, 419, 420, 430, 434
- BAK1-activated JA signaling system, 428
- BAK1 in immune signaling, 428
- BAK1-mediated PAMP–PRR signaling, 431
- BAK1-mediated programmed cell death, 432
- BAK1-triggered disease resistance, 427
- BEE transcription factor, 418
- Benzoic acid 2-hydroxylase, 27, 44
- BES1, 410, 415, 416, 419, 421, 422, 436
- β-oxidation, 126, 127, 136
- β-oxidation pathway, 30, 127
- β-thujaplicin, 159, 225
- bHLH transcription factor HB11, 433
- BIG* gene encoding calossin-like protein, 342
- BIK1, 416, 430, 434
- BIM1, 410
- BIN2, 410, 411, 415, 417, 419, 421–423, 434, 436
- Bioactive GAs, 384, 385
- BK11, 415, 417, 418
- Blocking of SAR by ABA, 279
- BOS1 in ABA signaling, 273, 275
- Branches of tryptophan-dependent pathway, 312
- Brassinazole (BRZ), 428, 436
- Brassinolide (BL)
 - biosynthesis pathways, 407, 408
 - promoted susceptibility, 428
- Brassinosteroids (BRs), 9, 383, 403, 404
 - biosynthesis, 405–409, 425
 - biosynthetic gene
 - CPD1, 405, 410, 425
 - DWARF2, 405, 425
 - homeostasis, 408–410, 425, 426
 - in negative regulation of GA-induced immune responses, 383, 429
 - receptors, 9, 403
 - signaling-induced susceptibility, 428
 - signaling pathway, 417

- Brassinosteroids (BRs) (*cont.*)
- signaling regulators
 - BSK1, 403, 415, 416
 - BSU1, 403, 410, 415, 420, 422
 - CDG1, 403, 416
 - PP2A, 403, 415–417
 - signaling-triggered disease resistance responses, 427
 - signal processing genes, 425
- Brassinosteroids-modulated plant immune responses, 404
- BRI1, 9, 10, 403, 410–413, 415–420, 430, 432, 434
- BRI1-activated inhibition of PAMP-triggered immunity, 433
- BRI1–BAK1 interaction, 418
- BRI1–BSK1 interaction, 418
- BRI1–BSK3 interaction, 418
- BR-induced susceptibility, 429
- BR-inducible gene OsBLE2, 405
- BRL1, 412
- BR-mediated negative regulation of GA signaling, 429
- BR-mediated suppression of SA defenses, 429
- BR-responsive genes, 416, 425
- BRs. *See* Brassinosteroids (BRs)
- BR signaling kinases (BSKs), 418
- BR-triggered susceptibility, 429
- BRZ-triggered disease resistance, 429
- BSK1, 416–419, 434
- BSK2, 418
- BSK3, 418, 419
- BSU1 phosphatase, 416, 417, 419, 421, 434
- bZIP transcription factors, 245, 255, 262, 273, 411, 418
- BZR transcription factors, 404, 410, 415–417, 424
- BZR1, 415–419, 421–424, 433, 434
- BZR1-mediated suppression of PAMP–PRR signaling system, 433
- BZR2, 417, 419, 421–423
- C**
- Calcineurin B-like (CBL) protein kinase, 270
- Calcium (Ca²⁺)
- dependent protein kinase, 195, 202, 263, 269, 270
 - influx, 123, 133–135, 201, 202, 224, 225, 260, 261, 266–268
 - mediated ethylene biosynthesis, 201
 - mediated NO signaling, 123
 - ion channel blockers, 201
 - ion channels, 123, 202, 266
 - ion chelator EGTA, 201, 224, 225
 - responsive cis elements, 270
 - sensors, 41, 195, 269
 - signaling, 41, 202, 287
 - signals, 202
 - signature, 27, 40–42, 123, 201, 202, 268
 - signature (triggered) JA biosynthesis, 134
 - wave, 123, 134, 195, 202
- Callose deposition, 7, 58, 249, 368
- Calmodulin (CAM), 41, 42, 225
- Calmodulin-binding protein CBP60g, 27, 41, 42
- Calmodulin-binding protein EICBP, 225
- Calyculin A, 198
- Camalexin, 368
- CAM binding domain, 225
- Campestanol, 407
- Campesterol, 406
- CAMTA transcription factors, 42
- Castasterone, 407, 409, 426
- CDG1 in BR signal transduction, 420
- CDL1, 420
- CDP. *See* *ent*-Copalyl diphosphate (CDP)
- CDR1 gene in SA biosynthesis, 35, 36
- Cell wall fortification, 249, 290
- Chorismate, 32
- Chromatin modification-induced priming, 28, 78
- Chromatin remodeling, 3, 28
- CIPKs, 270
- CKX4/CKX5 cytokinin metabolism genes, 366, 375, 376
- Cofactor of TGA transcription factors, 56
- COI1-dependent pathway, 126
- COI1-independent pathway, 126
- COI1 in JA signal perception, 123, 139, 331, 332
- COI1-JAZ interaction, 143
- COI1-JAZ receptor complex, 140, 164
- COI1 protein, 142, 153, 331
- Conjugated auxin, 341
- Conjugated auxin-promoted susceptibility, 341
- Constitutive triple response1 (CTR1), 160, 195, 209–214, 216, 218, 219, 222, 223
- Cooperative function
 - of JA and ABA signaling systems, 276
 - of JA and ET signaling pathways, 158, 159
- ent*-Copalyl diphosphate (CDP), 384, 385
- ent*-Copalyl diphosphate synthase (CPS), 384, 385
- Copper transporter (RAN1), 210

- COP9 signalosome (CSN), 143, 213
 Coronatine, 199, 292, 391
 C-22 oxidation branch in BR biosynthesis pathway, 408
 CPD1, 422
 Crosstalk
 between BR and ABA signaling, 436
 between BR and ET signaling, 436
 between BR and GA signaling, 436
 between BR and JA signaling, 435
 between BR and SA signaling, 435
 between BR biosynthesis pathway and PAMP-PRR signaling, 431
 between JA and small RNA signaling system, 169
 Cryptogein, 135, 199
 CTR1-MKK9-MPK3/MPK6 cascade, 222, 223
 CUL3 E3 ligase, 54
 Cullin RING ligases, 208
 Cuticle in induced SAR, 396
 Cyclase- and HK-associated sensing extracellular (CHASE), 364
 Cytochrome P450, 57, 312
 Cytokinin
 acting as long-range signals, 360
 biosynthesis, 360–362
 concentrations altering immune responses, 360
 conferring resistance against pathogens, 367
 degradation, 362
 homeostasis, 359, 362
 hydroxylases, 374
 in NPR1/TGA3-mediated signaling, 373
 phosphorelay signaling system, 363–365
 phosphoribohydrolase (Lonely Guy), 374
 receptors, 362, 363, 371
 in SA biosynthesis, 36
 synthase, 362
 Cytokinin–auxin antagonism, 376
 Cytokinin-binding CHASE domain, 363
 Cytokinin-induced activation of plant innate immunity, 369
 Cytokinin-induced disease susceptibility, 370
 Cytokinin-induced priming, 368, 369
 Cytokinin-induced TGA3/NPR1, 369
 Cytokinin-modulated redox signaling system, 370, 371
 Cytokinin-modulated SA signaling system, 369
 Cytokinin oxidase/dehydrogenase (CKX), 362, 366, 371, 374
 Cytokinin-responsive genes, 366
 Cytokinin-triggered defense responses, 367
- D**
 DAD1 in JA biosynthesis, 125
 DELLA. *See* Asp–Glu–Leu–Leu–Ala (DELLA)
 DGL1 in JA biosynthesis, 125
 Diacylglycerol kinase (DAG), 222
 Dimethylallyl diphosphate (DMAPP), 360, 361, 375
 Dimethylallyl pyrophosphate (DMPP), 406
 DNA methylation in transgenerational SAR, 28, 80, 81
 Dormant MAPKs in SA-triggered priming, 76
- E**
 Early C6-oxidation pathway, 407, 408
 EAR motif, 123, 141
 EBF1/EBF2 mRNA decay, 217
 EDR1
 in ET signaling, 207, 208
 in JA signaling, 151, 152
 in SA signaling, 43, 49
 EDS1
 in SA biosynthesis, 31–34, 36, 42, 280
 in SA/JA crosstalk, 87
 EDS4 in SA biosynthesis, 31, 33, 34, 36
 EDS5/SID1 in SA biosynthesis, 31, 33, 34, 36
 Effectors suppressing ABA-dependent defenses, 292
 Effectors suppressing SA signaling system, 94
 EIL1
 in JA/ET signaling synergy, 160, 161
 transcription factor, 160, 161, 195, 214, 216, 231, 284
 EIN2 in ET signaling, 160, 195–197, 212–214, 230, 231, 284
 EIN2-targeting protein1 (ETP1), 213, 214
 EIN2-targeting protein2 (ETP2), 213, 214
 EIN3-binding F-box proteins, 160
 EIN3 binding F-box protein 1 (EBF1), 160, 195, 215–217
 EIN3 binding F-box protein 2 (EBF2), 160, 195, 215–217
 EIN3/EIL family of proteins, 215, 227
 EIN3 in ET signaling, 160, 161, 195, 213–217, 221, 224, 284
 EIN3 in JA/ET signaling synergy, 160, 161
 EIN4, 208–211, 217
 EIN5/XRN4, 217
 EIN7, 217
 Endogenous immune signal, 29

24-epibrassinolide (epiBL), 433–435
 Epoxy-carotenoid, 252, 254, 284
 EREBP2/AP2 domain proteins,
 203, 221, 229
ERF
 branch pathway, 165
 in modulation of JA and ET signaling
 pathways, 159, 160
 proteins in ET signaling, 282
 transcription factors, 51, 147–149, 159,
 160, 164, 219, 221, 226, 229, 230,
 282–284
 ERF-regulated JA-responsive gene
 expression, 159
 ERF1, 147–149, 154, 155, 159, 170, 219, 221,
 226, 229
 ERF1 in JA and ET pathways convergence,
 159, 160, 170
 ERS1, 208–211
 ERS2, 208–210
 ET-binding domain (EBD), 209
 Ethephon, 197, 230
 Ethylene (ET)
 biosynthesis, 11, 159, 199
 and JA signaling interdependency,
 225, 226
 in PAMP-triggered immunity, 224
 pathway-induced susceptibility, 230
 receptors, 195, 208
 signaling-triggered ABA
 biosynthesis, 283
 Ethylene enhanced response5 (EER5), 213
 ET-induced calmodulin-binding protein
 (EICBP), 225
 ET-induced disease resistance, 196, 197, 231
 ET-induced JA biosynthesis, 159, 226
 ET-induced susceptibility, 197
 ET-induced transcription of defense genes,
 228, 229
 ET/JA coactions, 226
 ET/JA signaling, 161, 225
 ET-mediated gene expression, 159
 ETR1, 197, 208–211, 213, 218, 219
 ETR2, 208–210, 212, 334
 ETR1 as ROS sensor, 221
 ET-responsive genes, 221
 E3 ubiquitin ligase, 142, 143, 153, 208, 215,
 317, 387, 391
 E3-ubiquitin ligase SCFSLY1/GID2 complex,
 387, 391
 EUI-deactivating biologically active
 Gas, 389, 390
 Exoribonuclease4 (XRN4), 216, 217
 Expansin gene expression, 342, 343

F

Farnesyl pyrophosphate, 406
 Fatty acid desaturase7 (FAD7) in SAR, 69
 Fatty acid hydroperoxides, 125
 F-box proteins, 1, 9, 383, 384
 F-box proteins SLY1 and SNZ in GA
 signaling, 384
 FMO1 gene in SA biosynthesis, 36
 FMO1 in SAR, 64, 70–72
 14-3-3 proteins, 423, 424

G

GA. *See* Gibberellic acid (GA)
 GA12 aldehyde, 384, 385
 GA-degrading enzyme gibberellin
 2- β -dioxygenase, 394
 GA-GID1-DELLA complex, 9, 383, 386
 GA-modulated disease resistance, 383
 GA-modulated disease susceptibility, 383
 GA3 oxidase (GA3ox), 384, 385
 GA13 oxidase, 384, 385
 GA20 oxidase (GA20ox), 384, 385, 388
 G α subunit-accelerating protein (GAP), 253
 G α subunit of heterotrimeric G-protein
 (GPA1), 131, 257, 266
 GATA family transcription factors, 366
 GA-triggered disease resistance, 388
 GA-triggered disease susceptibility, 388
 G-box motif, 164, 411
 GCC-box-mediated transcription, 5, 220
 GCC-box motifs, 5, 51, 88, 124, 160, 164,
 165, 195, 219, 220, 226, 229, 230,
 249, 282
 GCR1, 266
 GCR2, 257
 Geranylgeranyl diphosphate, 384
 GH3 enzymes, 7, 128, 319, 326, 341
 GH3 genes, 325, 326, 329, 340, 342
 GH3-modulated SA signaling, 329
 GH3 in suppression of free IAA
 accumulation, 340
 GH3 in suppression of SA, 340
 GH3.1 gene overexpressing plants, 343
 GH3-2 gene, 343
 GH3-2 gene overexpressing plants, 343
 GH3.5 gene, 34, 329
 GH3-8, 320, 333, 339, 340
 GH3-8 mediated suppression of auxin
 signaling, 340
 GH3-8 overexpressing plants, 340–342
 Gibberellic acid (GA)
 attenuates expression of JA-responsive
 genes, 383

biosynthesis inhibitor uniconazole, 11
 enhancing induction of SAR, 384
 receptor GID1, 1, 9, 383
 relieving repressive activity of DELLAs,
 383, 387
 repressor genes, 395
 repressor protein, 395
 signaling pathway, 8, 384–386
 triggering SAR, 383, 395, 396
 Gibberellin Insensitive Dwarf2 (GID2),
 384, 387
 Gibberellin 20-oxidase3, 394
 GID1, 383–387, 391
 GID1 genes, 384, 385
 Glucosyltransferase, 165
 Glutamate-gated Ca²⁺ channel, 134
 Glutamate receptors, 134, 135
 Glutaredoxin in SA/JA crosstalk,
 85, 86, 167
 Glutathione-S-transferase (GST), 57
 Glyceraldehyde 3-phosphate, 251
 GPCR as ABA receptor, 257
 G-protein-coupled receptors (GPCRs), 253
 G-proteins, 39, 123, 130, 200
 in expression of NADPH oxidase, 130
 involved in ABA biosynthesis, 253
 involved in ABA downstream
 signaling, 265
 switching on calcium ion channels, 123
 switching on Ca²⁺ signaling system, 267
 switching on ET biosynthesis pathway,
 195, 200
 switching on JA biosynthesis pathway, 130
 switching on ROS signaling system, 267
 G-proteins-triggered polyamine
 biosynthesis, 131
 GRAS (GAI1, RGA, SCARECROW), 386
 GTG1/GTG2, 257, 258

H

Heterotrimeric G-proteins, 130, 265
 Hexanoic acid, 5, 172, 174
 Hijacking
 of ABA signaling system
 by pathogens, 291
 of BR signaling machinery
 by pathogens, 435
 of ET signaling, 197
 His phosphotransfer protein (HPT), 365
 Histidine and aspartate phosphorelay, 363
 Histidine kinase receptors, 359, 362, 363
 His to Asp phosphotransfer signal
 transduction, 363

Histone

acetylation, 153
 deacetylases in JA signaling, 123, 153
 memory in SAR, 28
 modifications, 3, 28
 modifications in gene priming, 77
 replacement in priming of SA-responsive
 loci, 79
 HMGR in BR biosynthesis, 405
 HMGS in BR biosynthesis, 405
 H₂O₂. *See* Hydrogen peroxide (H₂O₂)
 Host-associated molecular pattern (HAMP),
 153, 199, 205, 324
 13-HPOT, 126, 127
 Hydrogen peroxide (H₂O₂)
 in Ca²⁺ signaling system, 123
 in ethylene biosynthesis, 203
 production, 203
 in SA biosynthesis, 45
 signaling, 221
N-Hydroxy-TAM (HTAM), 314
 Hyperpolarization-activated Ca²⁺
 channels, 268
 Hypomethylated genes in priming, 28

I

IAA–alanine, 319
 IAA–amido synthase, 320, 322, 323, 327
 IAA–amino acid hydrolases, 322, 323
 IAA–Asp, 7, 319, 320, 341, 342
 IAA/Aux family genes, 327
 IAA–AUX proteins. *See* AUX/IAA proteins
 IAA/AUX proteins degradation, 344
 IAA–glutamate, 319
 IAA–leucine, 319
ICS1, 371
 Indole-3-acetaldehyde (IAAld), 313, 321
 Indole-3-acetaldoxime (IAOx), 312, 313, 330
 Indole-3-acetamide (IAM) pathway, 311–314
 Indole-3-acetic acid (IAA), 311, 313, 321
 homeostasis, 320, 326
 production, 329, 337
 transport, 8, 334
 Indole-3-acetonitrile (IAN) pathway, 311, 312,
 321, 330
 Indole-3-pyruvic acid (IPA) pathway,
 311–313
 Induced systemic immunity, 171
 Induced systemic resistance (ISR), 1, 4, 124,
 171, 172, 196, 342
 Inositol pentakisphosphate (InsP5), 140
 Interaction between auxin and ET
 signaling system, 333

Interaction between auxin and SA signaling system, 327

Interaction between auxin and small RNA signaling systems, 335

Interaction between cytokinin and ABA signaling systems, 374. *See also* Interplay between cytokinin and ABA signaling

Interaction between JAZ1 and COI1, 140

Interaction between JAZ proteins and DELLAs, 391

Interaction between TIR1 and Aux/IAA protein, 315

Interconnection between ABA and JA signaling pathways, 274

Interplay between ABA and ET signaling systems, 282

Interplay between ABA and SA signaling systems, 278, 280

Interplay between auxin and JA signaling system, 332

Interplay between auxin and MAPK signaling systems, 326

Interplay between BR and PAMP-PRR signaling, 430

Interplay between cytokinin and ABA signaling, 375

Interplay between cytokinin and auxin signaling, 376

Interplay between GA and auxin signaling, 395

Interplay between GA and BR signaling, 394

Interplay between GA and JA signaling, 391

Interplay between GA and SA signaling, 389, 390

Interplay between JA and ABA signaling, 168, 274

Inward-rectifying K⁺ channel, 287

IPT. *See* Isopentenyl transferase (IPT)

Isochorismate, 32, 279

Isochorismate pathway, 29, 31, 279

Isochorismate synthase (ICS), 31, 33, 35–38, 42, 64, 72, 94, 279, 371, 372

Isopentenyladenine (iP), 361

Isopentenyladenine-type cytokinins, 360

Isopentenyl AMP (iAMP), 361

Isopentenyl diphosphate, 251

Isopentenyl pyrophosphate, 406

Isopentenyl transferase (IPT), 360–362, 367, 374–376

Isopentenyl adenosine (iP-Ado), 361

ISR-prime, 5, 174

J

JA-ACC, 128

JA-activated defense genes, 156, 157

JA-amino acid synthetase (JAR1), 128, 143, 332, 333

JA-amino synthetase, 332

JA/ET crosstalk, 10

JA/GA crosstalk, 10

JA-Ile as the mobile signal in ISR, 173

JA-Ile/SCFCOI1 pathway, 144

JA-induced enhanced expression of DELLA genes, 391

JA-Leu, 128

JA-mediated priming, 174

JA-responsive genes, 5, 161–163, 165, 167, 168, 174, 226

Jasmonate (JA)

- biosynthesis blocking by SA, 81
- biosynthesis pathway, 127
- and ET interaction, 159, 225
- and ET signaling system, 162
- in inhibition of SA signaling, 163
- metabolites as signal molecules, 124
- proteasome pathway, 332
- receptor complex
 - COI1, 4, 123, 142, 277
 - inositol pentakisphosphate, 4, 123, 140
 - JAZ proteins, 4, 123, 141
 - and SA interaction, 11, 12, 81–88, 124
 - signaling suppression by JAZ proteins, 141

Jasmonic acid carboxyl methyltransferase (JMT), 127, 128

Jasmonoyl-L-isoleucine (JA-Ile), 4, 123–125, 128, 140, 142, 143, 149, 152, 165, 172–174, 436

JA-Trp, 128

JA-Val, 128

JAZ

- degradation, 4, 142, 144, 147, 227, 392
- degradation signal (degron), 144
- dimerization, 141
- protein JAZ9 inhibits RGA DELLA protein, 391
- proteins, 140–142, 144, 158, 161, 226, 227, 391, 394

K

ent-Kaurene, 384, 385

ent-Kaurene synthase (KS), 384, 385

ent-Kaurenoic acid, 384, 385

ent-Kaurenoic acid oxidase (KAO), 384, 385

K⁺ current rectifier KAT1, 260, 263

3-Ketoacyl-CoA, 126

- 3-Ketoacyl-CoA thiolase (KAT),
126, 127, 137
- Kinetin, 367
- L**
- Late C6-oxidation pathway, 407, 408
- LAX genes, 322
- Lignin, 249, 290
- Link between Ca²⁺ signaling and ABA
signaling systems, 270
- Link between JA and auxin
signaling, 333
- Linolenic acid, 125–127, 129, 136
- Lipase in JA biosynthesis, 135
- Lipases in synthesis of oxylipins, 125
- Lipid hydroperoxidase (LHP), 173
- Lipid transfer protein (DIR1), 330
- Lipoxygenase (LOX), 125, 126, 129, 130,
133–136, 146, 163, 164, 170,
173, 341
- Lipoxygenase pathway, 173
- L-Methionine, 197
- Lonely Guy, 374
- Long-distance mobile signals in SAR, 65, 66.
See also Systemic mobile signal
molecules involved in SAR
- 13-LOX enzymes, 125
- LOX gene, 333, 340
- Lycopene, 251
- M**
- MADS-box gene family, 425, 426
- Manipulation of signaling network, 12
- MAP kinase (MAPK), 198, 261
- cascade, 27, 43, 48, 123, 137, 138, 195,
 204, 205, 207, 222, 272, 326
- cascade in ethylene biosynthesis, 195, 205
- dormant MAPKs in SA-triggered
 priming, 76
- in JA biosynthesis, 123, 135, 137, 138
- in JA signaling pathway, 150, 151
- MPK4 in ABA-induced stomatal
 closure, 288
- MPK4 in SA/JA crosstalk, 86
- in SA biosynthesis, 43, 44
- signaling module, 43
- signaling system, 39, 41, 48
- MAPK phosphatases (MKPs), 138
- MED8 in JA signaling, 4, 150
- MED15/NRB4 in regulation of SAR, 3, 75
- MED16
 in JA signaling, 4
- in NPR1 function, 3
- in regulation of SAR, 3, 74
- Med16/SFR6 in JA signaling, 150
- MED25
 in ABA and JA signaling interplay, 277
- in ABA signaling, 245, 277
- association with MYC2, 277
- interaction with transcription factors, 277
- in JA signaling, 4, 123, 147–149, 158, 277
- physical association with ABI5, 277
- Mediator complex
 in JA signaling, 147
- in SAR, 73, 74
- Mediators in SA signaling, 28
- Membrane steroid-binding protein 1
(MSBP1), 420
- Methionine in ET biosynthesis pathway, 282
- Methionine synthase, 200
- Methyl esterase1 (MES1) in SAR, 64
- Methyl jasmonate (MeJA), 126, 128, 155, 157,
159, 163, 165, 168, 172, 225, 275
- Mevalonate
 diphosphate decarboxylase, 406
- pathway, 405, 406
- Mevalonate kinase (MVK), 405, 406
- MicroRNA, 170, 335
- miR160a in repression of auxin response
 factor genes, 335
- miR167 in auxin signaling, 324
- miR393 in auxin signaling, 323, 324,
 335, 336
- miR393 targeting auxin receptors, 335
- repression of auxin signaling, 335
- MicroRNA-directed RNA silencing, 124, 170
- Mitochondrial signaling processes, 59
- MKK3–MPK6 cascade in JA
 signaling, 150, 151
- Mobile signaling cue in ISR, 123
- Mobile signal involved in ISR, 172
- Molecular glue, 383, 386
- MPK3/MPK6 in EIN3 protein
 stabilization, 222
- MPK3/MPK6 in ethylene biosynthesis,
 205–207
- MPK4 in ET signaling, 223
- MPK4-mediated ABA signaling, 169
- Multifunctional protein (MFP), 126, 127, 137
- MYB44 in JA/SA crosstalk, 167
- MYB96 as a signaling link in integration of
 ABA and SA signals, 281
- MYB96-induced *SID2* expression, 282
- MYB transcription factors, 36–38, 141, 154,
155, 166, 273, 276, 277,
359, 366

- MYC branch pathway, 165
 MYC-type transcription factors, 164
 MYC2
 in ABA signaling, 168, 273, 276
 in inducing ISR, 146
 induction by ABA, 277
 interaction with JAZ proteins, 144, 145, 161, 392, 393
 as master switch in JA signaling, 146
 regulates JA signaling, 277, 394
 as transcription factor, 4, 95, 123, 141, 142, 144, 145, 147–152, 154, 155, 168, 227, 277, 392, 393
 MYC3, 146, 147, 154, 155, 161, 393, 394
 MYC4, 146, 147, 154, 155, 161, 393, 394
 Myrosinases, 276
- N**
 NAC transcription factors, 96, 154, 155, 247
 NADPH
 in cytosol, 271
 oxidase
 in ABA signaling, 271
 in ROS production, 123, 130, 134, 153, 260, 263, 270
 in SA biosynthesis pathway, 45
 NADPH oxidase-dependent ABA signaling, 270
 NCED. *See* 9-*cis*-epoxycarotenoid dioxygenase (NCED)
 Negative crosstalk between BR and SA signaling systems, 428
 Negative regulation of BR signaling by BIN2, 421
 Neoxanthin, 251, 252
 Next-generation SAR, 1, 3, 28, 80
 9-*cis*-epoxycarotenoid dioxygenase (NCED), 247, 252, 253, 275, 283, 285
 9-*cis*-epoxycarotenoid dioxygenase3, 168
 NINJA, 4, 123, 141, 142
 NINJA-TPL corepressor complex, 123, 141
 Nitrate reductase in NO production, 271
 Nitric oxide (NO)
 in ABA signaling system, 271
 in auxin signaling, 312, 327
 in ethylene biosynthesis enzymes, 204
 in ethylene production, 195, 204
 in JA biosynthesis, 135, 136
 production, 135
 in SA biosynthesis pathway, 45
 in SA signaling system, 46
 signaling, 39, 45, 46, 48
 Nitric oxide synthase (NOS)-like enzyme, 271
 Nitrilase, 312, 313, 321
 Nitrosglutathione as long-distance signal, 48
 NO-induced SAM synthetase, 197
 Non- β -oxidation pathway, 30
 Non-expressor of PR gene1 (NPR1)
 binding with NPR4, 54
 in chromatin modification-induced priming, 78
 as a co-activator in SA signaling, 272
 cytosolic NPR1, 166
 degradation of NPR1, 54
 interacting proteins, 55
 master regulator of SA signaling, 27, 52, 74
 monomeric NPR1, 52, 53
 negative effect over ABA biosynthesis genes, 281
 nuclear localization, 3, 27, 52
 oligomerization, 48, 53
 proteasomal degradation, 53
 regulation by MED16, 3
 regulator of SAR, 48
 in SA/JA crosstalk, 83, 84, 165, 167
 TGA2-NPR1 complex, 3, 52, 372
 transcriptional co-activator, 372
 triggering SAR, 64, 75
 Nonpolar auxin transport, 320
 NPR1-activated transcription factors, 55
 NPR3, 28, 54, 55
 NPR4, 28, 54, 55
- O**
 Oligogalacturonide (OG) elicitor, 200, 205, 324, 325
 OPC-8:0, 126, 127
 OPDA reductase (OPR), 126, 127, 129–131, 135–137, 164, 172
 ORA59 transcription factor, 147–149, 154, 161, 162, 164, 165, 250
OsBLE2, 427, 428
OsCPD1, 427, 428
OsEDR1, 208
OsERF922, 247, 284, 289
OsHK3, 375
OsNCED3,4 in ABA biosynthesis, 284
OsNPR1, 290, 428
OsRac1, 200
OsRAVL1, 425, 426, 428
OsRR4, 375
 Oxalic acid as a virulence factor, 292
 Oxidative burst, 202
 12-Oxo-phytodienoic acid (OPDA), 126, 127, 174, 275, 436
 Oxylipins, 125

P

PAD4
 in SA biosynthesis, 31–34, 36, 41, 72, 340
 in SA/JA crosstalk, 87

PAMP. *See* Pathogen-associated molecular pattern (PAMP)

PAMP–PRR signaling complex, 1, 10, 124, 137, 223, 224, 430–433, 435

PAMP-triggered ABA biosynthesis, 251

PAMP-triggered expression of small RNAs, 335

PAMP-triggered immunity (PTI), 435

Pathogen-associated molecular pattern (PAMP)
 cues-activated JA biosynthesis, 123, 130
 signals activated G-proteins, 123, 134

Pathogen's signature, 27

Pathogen-triggered BR biosynthesis, 404, 405

Pathogen-triggered BR signaling system, 425

PBS3 (GH3.12) in SA biosynthesis, 38, 47

Pep1 peptide, 153

PEPRs, 153

PG-inhibiting proteins (PGIP), 325

Phenylalanine ammonia lyase (PAL), 27, 37, 45, 249, 270, 278, 289, 291

Phenylalanine pathway, 29, 31, 39

Phenylpropanoid pathway, 290

Phosphatidic acid (PA), 222, 264, 265, 287

Phosphatidylcholine, 264

Phospholipase A1 (PLA1), 125, 127, 138

Phospholipase A enzyme PLA1 γ 1, 125, 126

Phospholipase C, 222

Phospholipase D (PLD), 264, 265, 287

Phytoalexins, 368

Phytoene, 251

PIN genes, 322, 327

PIN proteins, 320, 328, 342, 395

Polar auxin transport (PAT), 8, 320, 342

Polyamines, 131
 biosynthesis, 131, 132
 in ROS production, 133
 spermine, 131, 133
 spermine in JA biosynthesis, 133

PP2A, 9, 276, 422

PP2C. *See* Type 2C protein phosphatase (PP2C)

PP2C–SnRK2 complex, 248, 255, 265

Prenylation, 362

Priming in ISR, 173, 369

Priming in SAR, 369

Priming of defense responses, 1, 28, 29, 330, 368

Priming of JA-dependent responses, 5, 174

Probenazole, 331

Proteasomal degradation, 216, 387

Proteasomal degradation of DELLAs, 387

Proteasome, 54, 208, 316

Proteasome inhibitor MG132, 418, 421

PRR-mediated immune signaling inhibition by BR perception, 435

PYR/PYL/RCAR, 1, 6, 168, 245, 254, 258, 259, 265, 274

R

RBOH-mediated ROS signaling, 131, 249

RCN1 involved in JA and ABA signaling, 276

Reactive nitrogen species (RNS), 221

Reactive oxygen species (ROS)
 in ethylene signaling system, 203
 in JA biosynthesis pathway, 135, 138
 production, 133, 202, 249, 260, 261, 270, 287
 in SA signaling system, 39, 47
 sensor, 221
 signaling downstream of ABA signaling system, 270
 signaling in SA biosynthesis, 44, 53

Reciprocal antagonistic interaction between ABA and SA signaling systems, 280

Regulator of G-protein signaling (RGS), 253, 254

Regulatory proteins in SA biosynthesis, 31–34

Repression of auxin-responsive genes, 318

Respiratory burst oxidase (RBOH), 130

Responsive-to-antagonist1 (RAN1), 210, 211

Reversion-to-ethylene sensitivity1 (RTE1), 218

RNA-binding protein (RBP), 34, 35

RNA-dependent RNA polymerase (RDR/RDRP), 60, 61, 63

RNA polymerase II (RNAPII), 245, 277

RNA silencing, 4, 169

RNA silencing signal, 169

ROS. *See* Reactive oxygen species (ROS)

ROS-mediated ABA signaling, 272

RUB-conjugating enzyme RCE1, 208

RUB protein, 332

RUB1/RUB2, 208

S

SA. *See* Salicylic acid (SA)

SA/ABA crosstalk, 10, 11, 89

SA/auxin crosstalk, 10, 89

SA-binding protein (SABP), 47, 66, 67

SA/BR crosstalk, 90

- SA/cytokinin crosstalk, 11
- S-adenosyl-L-methionine (SAM), 65, 201, 204
- S-adenosyl methionine synthetase, 200, 203, 294
- S-AdoMet, 197, 198
- S-AdoMet (SAM) synthetase, 197, 282
- SA/ET crosstalk, 10, 89
- SA-induced disease resistance, 90–93, 162, 163
- SA-induced transcription of defense genes, 58
- SA-induced virus disease resistance, 93
- SA/JA crosstalk, 10, 81–88, 165
- SA–JA–ET signaling systems as central backbone of innate immunity, 383
- Salicylhydroxamic acid (SHAM), 59, 60
- Salicylic acid (SA)
- analog BTH-induced priming, 76, 77
 - biosynthesis, 32
 - biosynthesis suppression
 - by ABA, 278, 279
 - in inhibition of JA biosynthesis, 83
 - and JA/ET crosstalk, 162
 - signaling inhibition by JA, 88
 - signaling system suppression by ABA, 279
- Salicylic acid carboxyl methyltransferase (SAMT), 66, 67
- Salicylic acid-induced protein kinase (SIPK), 43, 50, 138, 207
- SA-mediated suppression of JA signaling, 82, 87, 88
- SAM synthetase, 203, 204
- SA-O- β -glucoside (SAG), 33, 38, 46, 47
- SAR. *See* Systemic acquired resistance (SAR)
- SAR-definition, 3
- SAR-induced by GA, 383
- SAR priming, 72
- SA-triggered priming, 75, 76
- SAUR genes, 322, 323, 325, 327
- SCFCOII-E3 ubiquitin ligase, 143, 213, 215, 217, 332
- SCFCOII-mediated ubiquitination, 4, 140, 142, 143
- SCFSLY1/GID2 complex. *See* E3-ubiquitin ligase SCFSLY1/GID2 complex
- SCFTIR1-mediated degradation of AUX/IAA proteins, 316, 323
- SCF ubiquitin ligase, 1, 142, 215, 312, 314, 331, 343, 344
- SFD1 in SAR-inducing activity, 69
- SGT1B in auxin signaling, 316, 338, 339
- sgt1b* mutant, 338
- Shikimic acid pathway, 32, 279
- SID2 in SA biosynthesis, 31, 33–35, 37, 40, 41, 280, 281
- SLAC1, 255, 260, 262, 263
- SLEEPY1 (SLY1) in GA signaling, 384
- Slow (S)-type anion channel, 260, 266, 269, 276
- Small-interfering RNAs (siRNAs), 60, 61, 169
- Small monomeric G-proteins, 130, 266
- Small RNA-directed DNA methylation, 335
- Small RNA-directed mRNA cleavage, 335
- Small RNA-directed RNA silencing, 3, 60, 61, 169, 170
- Small RNA-mediated suppression of auxin signaling, 336
- Small RNAs, 63, 169
 - in auxin signaling system, 335
 - molecules as mobile signals, 335
 - signaling system, 170
- Small ubiquitin-like modifier (SUMO). *See* SUMO in SA signaling system
- SNARE in ABA-dependent disease resistance, 286
- Sneezy (SNZ) in GA signaling, 384
- SNF1-related protein kinase (SnRK2), 1, 6, 245, 254, 264, 265. *See also* SnRK2
- S-nitrosoglutathione (GSNO), 52, 53
- S-nitrosothiol (SNO), 327
- S-nitrosylation, 312, 327
- SnRK2, 254, 255, 259, 260, 263–265
- Spermidine synthase, 132, 133
- Spermine, 133
 - biosynthesis, 131, 132
 - synthase, 131, 133
- 26S proteasome, 143, 146, 215, 387, 391
- Staurosporine, 198
- Stomatal closure immune response, 7, 58, 59, 169
- SUMO E3 ligase, 58
- SUMO in SA signaling system, 57, 58
- Suppression
 - of GA signaling by pathogens to cause disease, 396
 - of JA signaling by SA, 163
 - of PAMP-PRR signaling pathway by BZR1, 434
 - of plant immune responses
 - by ABA, 289, 290
 - of SA signaling system by JA, 162
- Synergism between cytokinin and SA signaling, 374
- Synergism between JA and ET signaling systems, 161
- Synergism between SA and JA signaling pathways, 88

- Synergistic interaction between ABA and ET signaling systems, 285
- Synergistic interaction between ABA and SA signaling systems, 281, 282
- Systemic acquired resistance (SAR), 1–4, 8, 28, 29, 48, 64, 171, 327, 330, 331, 342, 383
- Systemic immunity, 1, 4, 6, 196, 197
- Systemic mobile signal molecules involved in SAR, 2
- azelaic acid, 2, 28, 65, 66, 70
 - dehydroabietinal, 2, 28, 65, 70
 - glycerol-3-phosphate, 2, 23, 65, 66, 68, 69
 - lipid transfer protein (DIR1), 2, 28, 65, 66, 68, 69
 - methyl salicylate, 2, 28, 65, 66, 68
 - methylsalicylate esterase (MSE), 28, 67, 68
 - pipecolic acid, 2, 71–73
- Systemic movement of ABA, 273
- Systemic RNA silencing, 64
- Systemin, 138, 139
- T**
- TAA family of aminotransferases, 312
- TCP transcription factor, 170
- TGA transcription factors, 28, 55–57, 85, 86, 154, 155, 157, 167, 168, 372, 373
- TGA transcription factors in SA/JA crosstalk, 85, 86, 167
- Thioredoxin (TRX), 52, 53
- TIFY motif in ZIM domain, 141
- TIR1, 314, 323–325, 327, 328, 332, 338
- TIR1/AFB nuclear receptors, 1, 7, 311, 312, 315, 317, 318
- TIR1/AFB proteins, 311, 312, 319, 325
- TOPLESS (TPL), 123, 141, 142, 144, 315, 317
- TOPLESS (TPL) as corepressor of JA signaling pathway, 4
- Toxin-mediated suppression of ABA-dependent defenses, 292
- Toxins in suppression of SA signaling system, 94, 95
- Transgenerational SAR, 1, 3, 28, 80
- Trans-zeatin*, 360–362, 375
- tRNA-isopentenyltransferase (tRNA-IPT), 362
- Tryptamine (TAM) pathway, 311, 314
- Tryptophan as the precursor for IAA biosynthesis, 312, 313
- Two-component phosphorelay system, 359
- Type-A AAR in SA-dependent immune responses, 373, 374
- Type-A ARR transcription activators, 359, 360, 365, 366, 372, 374, 376
- Type-B ARR transcription activators, 359, 360, 365, 367, 372, 376
- Type 2C protein phosphatase (PP2C), 1, 6, 245, 246, 254, 255, 258–261, 263, 265, 274
- U**
- Ubiquitination, 320
- Ubiquitin, 316
- Ubiquitin-conjugating enzyme, 220
- Ubiquitin ligase, 54, 317
- Ubiquitin–proteasome in auxin signaling, 316, 318, 344
- Ubiquitin–proteasome pathway in ET biosynthesis, 195, 208
- Ubiquitin–proteasome pathway in GA signaling, 383
- Uniconazole, 11
- V**
- Verapamil, 201
- Violaxanthin, 251, 252
- Viral replicase–Aux/IAA interaction, 339
- Viral suppressor of RNA silencing (VSR), 61–64
- W**
- WIZZ transcription factor, 170
- Wound-induced protein kinase (WIPK), 43, 138, 207
- WRKY transcription factors, 38, 49–51, 57, 58, 77, 78, 84, 96, 150, 153–155, 163, 165, 166, 170, 206, 273, 290
- WRKY18 induced by SA, 50
- WRKY33
- in ABA signaling, 250
 - ethylene biosynthesis, 206, 207
 - in JA/SA crosstalk, 96, 163, 165
- WRKY45 in SA signaling, 290
- WRKY50 in JA/SA crosstalk, 166
- WRKY 51 in JA/SA crosstalk, 166
- WRKY62
- induced by SA, 50
 - in JA/SA crosstalk, 84, 165

WRKY62 (*cont.*)

in suppression of JA-responsive gene
expression, 166

WRKY70

in JA/SA crosstalk, 84, 85,
166, 167

in SA-responsive gene
expression, 50, 84

X

Xanthophylls, 252, 253

Xanthoxin, 252–254, 284

Y

YUCCA family of flavin monooxygenases,
312–314

Z

Zeatin degradation, 375

Zeatin riboside (ZR), 361

Zeatin riboside diphosphate (ZDP), 361, 375

Zeatin riboside monophosphate (ZMP), 361, 375

Zeatin riboside triphosphate (ZTP), 361, 375

Zeaxanthin, 251

ZmPep1, 199