

Index

A

α - and β -expansins, 94–95

ABP1, 50

Actin

- binding proteins, 212, 215, 218, 221–226
- bundling protein, 31
- configurations, 35
- cytoskeleton (filaments), 28, 31–33, 35, 36, 106–109, 211–214, 216–220, 223, 224, 226
- depolymerizing factor (ADF/cofilin), 156, 214, 222–224
- dynamics, 29
- expression, 220
- fine filamentous-actin (fine F-actin), 31, 35, 36, 215, 217–220, 223–226
- genes, 220, 224
- interacting protein 1 (AIP1), 223–224
- related protein (ARP) 2/3 complex, 197–198, 224–225
- visualization, 212–215, 223, 226

AFBs/*afb* mutants, 50, 51

Agrobacterium transformation, 234

Allium, 235

Annexin, 157

Apical growth, 36

Appressorium, 320, 322, 323

Arabidopsis thaliana, 28, 30, 234–238, 240–244

Arabinoglycan proteins, 88, 89, 92

Arbuscular mycorrhizas, 317–323

Arbuscules, 318, 320, 321, 325–327, 332, 333

ARF (Auxin Response Factor), 51, 53

ARF-GEF (GNOM), 57

Armadillo repeat-containing kinesin, 32

Ascomycete, 317

Atomic force microscopy, 41–42

AtrbohC, 198, 203

Atrichoblasts, 28

Attachment, 297–302, 304–308

AUX1/*aux1*, 48, 54, 55, 57, 58

Aux/IAAs, 50–54

Auxin, 10–12, 16–17, 45–60 197, 201–204

apoplastic, 55

efflux carrier, 50, 55

gradient (for hair positioning), 58

influx carrier, 55

maximum, 58

receptor, 46, 50, 51

signaling, 46, 47, 50–53

transporter, 46, 48, 50, 54–59

AXL1, 51

axr1/AXR1, 46, 47, 51

axr2/AXR2/IAA7, 46, 47, 51, 53, 57

axr3/AXR3/IAA17, 47, 51, 53

B

Basidiomycete, 317

Biofilm, 297–310

Biomechanical models, 103, 104

Biomechanics, 113–117

Biopolymers, 36

BJ38, 301

Brefeldin A (BFA), 56–59

Brownian motion, 33

Bulge formation, 28, 32

β -Yariv/Æs reagent, 89

C

Ca²⁺, 28, 36, 238, 253–257, 259–263

ATPase, 155

channels, 106, 113, 117–118, 150

gradients, 109, 113

ions, 106, 117

sensitive probes

- Ca²⁺ (*cont.*)
 Cameleon YC2.1, 162
 Cameleon YC3.6, 162
 cytoplasmic, 108, 109, 113, 118
 Fura-2, 161
 Indo-1, 148, 161
 Oregon green, 161
- Callose, 36, 37
 Calmodulin, 158
 Capsular polysaccharide, 302
 Cargo selection, 81
 CaX, 155
 CDPK, 156, 158
 Cell communication, 7
 Cell division, 6, 8, 27, 32
 Cell elongation, 27–31, 34, 36
 Cell expansion, 37
 Cell fate specification, 6–8
 Cell growth, 27, 28, 35, 36, 103–104, 106
 Cellulose, 86–92, 94, 96, 106, 113–116
 microfibrils, 31, 36–41, 299, 302, 304
 synthase complex, 31, 36, 37
 synthases, 29, 31, 36, 88–91
 Cellulose-synthase (CesA)-like (CSL) genes,
 89–91
 Cell wall, 28–40, 85–96, 103, 107,
 109–119, 160
 hardening, 117
 matrix polymers, 28
 orthogonal growth, 105
 texture, 37–39
 Chemical fixations, 213, 223
 Chloride transport
 channels, 135–136
 proton/chloride symport, 135–136
 Chromatin, 6, 8
 Clathrin-coated vesicles, 29
 Clathrin-mediated endocytosis, 34
 Coated pits, 29, 32, 33, 39
 Confocal laser scanning microscope, 34, 215
 COPI coated vesicles, 69
 COPII coated vesicles, 69
 Cow1 mutant, 30
 Critical point drying, 39
 Cross-linking, 106, 117, 119
 Crystalline cellulose, 40
 Cyclic β -1,2-glucans, 302, 305
 Cytoarchitecture, 30, 33
 Cytochalasin, 35, 36, 217–220
 Cytoplasm, 28–35
 Cytoplasmic Ca²⁺, 146, 148
 Cytoplasmic dense area, 30, 32, 33
 Cytoplasmic strands, 31, 32, 35, 217
 Cytoplasmic streaming, 213, 217, 218, 221
- Cytoskeleton, 11, 12, 28, 29, 31–36, 39, 104,
 109, 156, 211–226, 233–244
- D**
 2,6-Dichlorobenzonitrile, 90, 91
 Differential interference contrast microscope, 30
 Diffuse growth, 85–86
 Diffusion, 106, 107, 109, 112, 117
 Docking, 68, 69, 297, 299–301
 Dry cleaving, 39
 DsRed, 235
- E**
 EB1, 234, 235, 237, 241, 242
 Ectomycorrhizas, 316–318, 321, 331
eir1, 48, 54, 55
 Elastic, 114, 115, 117
 Elasticity, 113, 119
 Electrical properties
 cable properties, 129
 capacitance, 127–128
 coupling, 129
 resistance, 127
 Embedding nodule, 289–290
 Endocytosis, 67, 71, 82
 Endocytotic dye, 34
 Endocytotic machinery, 33
 Endocytotic vesicles, 33
 Endomycorrhizas, 316, 318–321, 323
 Endoplasmic reticulum, 29, 32
 Endosomes, 29, 32
 EPS, 301–303, 305
Equisetum, 233, 235
 Ericoid mycorrhizas, 317–319, 321
 Ethylene, 10–12, 16, 45, 46, 54, 57–59, 197,
 201, 202, 204
Eucalyptus, 243
 Exo70, 199, 204
 Exocyst, 29, 197, 199, 200, 204
 Exocytosis, 28, 29, 33–37, 103, 106–107, 113,
 117–118, 215, 218–220, 222, 238–241
 Exocytotic vesicles, 28, 31
 Exopolysaccharide, 301, 303
 Expansin, 94, 200, 202, 203
 Expansion, 103, 105, 109–111, 114–117
 Extracytoplasmic fracture face, 39
- F**
 Facet, 37
 Fåhrens slide assay, 36
 Farnesylation, 192

FH1 domain, 225
 FH2 domain, 225
 Fibril width, 39
 Fibroblasts, 35
 Fimbriae, 305–306
 Fixation, 212–214, 223
 Flagella, 297, 298, 300, 305, 306
 Fluorescent phalloidin, 35
 FM4–64, 33, 34
 Formin, 225
 Fourier transform infrared
 microscopy, 40
 Freeze etching, 39
 Freeze fixation, 39, 212–214, 233, 234, 236
 Freeze fracturing, 39
 Freeze substitution, 212, 214
 Fungal hyphae, 105, 107, 110, 113, 117

G

Geometrical models, 103–105,
 109–113, 117
 Geranylgeranylation, 192
 Germin, 300
 GFP, 233–237, 241, 242
 GFP:cellulose synthase, 39
 GFP:FABD2, 34, 35, 214–216, 223
 GFP-mTn, 214, 215, 223
 GFP–tubulin, 39
 Glomeromycota, 319, 323
 Glutaraldehyde/osmium tetroxide
 fixation, 33, 40
 Glycoproteins, 28, 32, 37
 GNOM/*gnom*, 49, 57, 58
 Golgi, 65–67, 69–71, 73, 76, 77, 81, 82
 Golgi apparatus, 103, 106
 Golgi bodies, 29, 32–36, 106–107
 Golgi vesicle, 103, 108
 Golgi vesicle membrane insertion, 27, 37
 GPI-anchored proteins, 194
 GTPase, 192–202, 204

H

Helicoidal cell walls, 37, 38
 Hemicelluloses, 37, 87, 88, 91
 Homeostatic process, 28
 Homogalacturonan, 91, 93
 Hydrogen peroxide glacial acetic
 acid, 40
 Hypaphorine, 243
 Hyperpolarization, 151
 Hyphopodium, 322, 328–331

Hypocotyl, 9
 Hypothesis, 105, 113, 117

I

IAA, 201, 202
 IAA28/*iaa28*, 48, 51
 ICR1, 197, 199, 204
 Immunocytochemistry, 35
 Infection
 cortical cells, 278, 279, 281, 285–287, 289
 crack entry, 278
 lateral roots, 278
 root hairs, 278–281, 283
 thread, 249, 250, 252, 255–260, 264–267,
 269, 297, 303–305, 307
 Infection thread networks
 3-dimensional reconstructions, 282–285
 polarized growth, 281, 285–287
 tip growth, 280, 286, 287, 289
 volume, 283–286
 Initiation, 146
 Inositol-1,4,5-triphosphate, 154
 Intercalary plant cell elongation, 29
 Interface, 320, 329
 Ion channels, 28
 Ion transport, 138–139
 Iron, 16

K

K⁺ channels, 159

L

Lateral inhibition, 7, 8
 Latrunculin, 35, 36, 217, 220
 LAXs, 54
 Lectin, 297, 299, 301, 302, 307, 308
 Lectin-mediated attachment, 301
 Legumes, 28
 LENS, 191, 192, 197–199, 203, 204
 Light microscopically, 28
 Lipid rafts, 194
 Lipopolysaccharide (LPS), 301, 304
 Lockhart equation, 114
 Locking, 297, 299–302, 304–306
Lotus, 28, 235, 237

M

Mechanical properties, 105, 113, 116, 117
 Mechanics, 104, 110, 115, 119

- Medicago*, 28, 31, 233–240, 242
- Membrane, 10, 11, 13, 14
 domain, 28
 protrusions, 35
 trafficking, 34
- Membrane fusion
 calcium trigger
 synaptotagmin, 76
 gating of, 75
 Sec1/SM proteins, SNAREs
Keule, 75
 SNAREs
 cis-SNARE complex, 68
 SNAREpin, 72
 SYP1 family, 74, 75
- 1-methylcyclopropene (1-MCP), 54
- Microcolonies, 298, 300, 303, 304,
 306, 307
- Microelectrodes
 double barrel, 129
 ion-selective, 128–130
- Microscopy, 17
- Microtiter plate, 304, 305, 308, 309
- Microtubules, 28, 29, 31, 32, 36, 37, 39,
 107–110, 157
 alignment, 237
 bundles, 235, 236, 241, 243
 cortical (CMTs), 32, 37, 234–238,
 240, 243
 density, 235–237
 depolymerization, 237, 238, 240
 double-labelling, 235
 dynamic instability, 237
 dynamics, 233, 234, 236–238
 endoplasmic (EMTs), 234–243
 growth rate, 237, 238, 240
 minus-end, 237
 nucleation, 236, 237
 organization, 233–236, 240, 243
 plus-end, 235, 237, 241, 242
 polymerization, 237, 238, 240, 241
- Modeling, 103–105, 107–110, 114
- Models, 103–107, 109–113, 116–118
- Morphogenesis, 103–105, 113, 117
- Mutagenesis, 326
- Mutants, 325–328
- Myc factor, 320, 329
- Mycorrhizal fungi, 315, 319, 332–334
- Mycorrhizas, 316–319, 321–323, 332
- Myosin, 36, 217, 221
- N**
- NADPH oxidase, 152
- Naphthylphthalamic acid (NPA), 56, 57
- NIP* gene, 283
- Nitrogen-fixing nodules, 297, 301, 303
- Nitrogen transport
 ammonium, 136
 nitrate, 137
- NMR analysis, 40
- Nod factor, 36, 219, 220, 239, 240, 249–269,
 277, 279, 280, 286, 287, 301, 302,
 307, 308, 326
- Nodule
 determinate, 278, 279
 development, 278, 281, 283
 embedding, 289–290
 indeterminate, 278, 279, 281, 282, 285
 meristem, 278, 279, 281–283, 286, 288
 staining, 289–290
 zones, 278, 279, 281, 283, 286
- NOX (NADPH oxidase), 196, 198–199,
 203, 204
- Nuclear location, 31
- Nucleus, 28–31, 211, 217, 219, 236, 240, 241,
 243, 320, 322, 328–330
 movement, 238
 positioning, 238
- Nutrient acquisition, 315
- O**
- Optical tweezers, 31, 35
- Orchid mycorrhizas, 18, 317, 319
- Organelle movement, 33
- Oryzalin, 36, 237–239
- P**
- Palmitoylation, 192, 194
- Pectin methyl esterases, 93–94
- Pectins, 37, 88, 93, 160
- PGP4/*pgp4*, 48, 55
- pH, 11
- Phaseolus*, 239
- Phosphate, 316, 318, 321, 324, 328, 333
- Phosphatidic acid (PA), 172, 174, 175, 177,
 179–183, 198–199, 203
- Phosphatidylinositol (PI)
 4,5-bisphosphate (PIP2), 10, 173–175,
 178–183, 199, 203
 4-kinase (PI4K), 172, 178
 (4)P 5-kinase (PIP5K), 178, 181, 182
 transfer protein, 172, 173, 178
- Phosphatidyl inositol signalling
 phosphatidyl inositol 4-OH
 kinase, 70
- Phosphoinositide-dependent kinase (PKD),
 174, 179

- Phospholipase C (PLC), 154, 173, 175, 179, 180
- Phospholipase D (PLD), 8, 13, 154, 172, 174, 179–182, 240
- Phospholipases, 198, 203
- Phosphorus, 16, 316, 324
- Pili, 297, 298, 305–307
- PINOID, 49, 56
- PINs/pins, 54, 56–58
- PIP kinase, 197–199, 203
- Pisolithus*, 243
- Planar polarity, 57–58
- Plasma membrane, 28, 29, 32–40
- Plasmatic fracture face, 39
- Plasticity, 105, 113, 116–119
- Plastic properties, 115
- Polarity
 - cell, 238, 241, 242
 - cytoplasmic, 238
 - marker, 241, 242, 244
- Polarization, 28, 39
- Polarized secretion, cellular polarity, 85
 - auxin, 77–79, 81
 - intrinsic positional cue, 77–79
 - lipid rafts
 - sterol methyl transferase (*smt1* or *ccp*), 70
 - sterol synthesis, 70
 - ROP GTPase
 - AtRAC10, 70
- Pollen tube, 149
- Polymers, 103, 110, 113–117, 119
 - cross links, 106, 117
- Polysaccharides, 28, 29, 40
- Polysomes, 29, 31
- Potassium transport
 - channels, 133–135
 - osmotic balance, 135
 - permease, 134
- Pre-infection threads (PITs), 281, 286, 287
- Prepenetration apparatus, 320, 328, 330
- Primary cell wall, 37, 38
- Profilin, 222, 225
- Proline-rich proteins, 95
- PRONE GEF, 202
- Properties, 103–107, 109, 113–117
- Protein
 - kinase, 56, 57
 - phosphorylation, 56
- Proton ATPase
 - electrical properties, 132, 135
 - regulation, 132–133
- Pyrolysis mass spectrometry, 40
- R**
- RABA4B, 87, 158
- Rac, 193, 194, 196, 198
- Random wall texture, 38
- Raphanus*, 235
- Ratio analysis, 163
- Reactive oxygen species (ROS), 151, 163, 172, 179, 182, 183
- Receptor, 7–9, 11
- RGD hexapeptide, 300
- Rhamnogalacturonan I, 89, 92, 93
- Rhamnogalacturonan II, 92, 93
- RHD2*, 198, 203
- RHD3*, 66, 67
- RHD6*, 46, 54
- Rhcadhesin, 297, 299, 300, 302, 308
- Rhcadhesin receptor, 300, 308
- Rhizobia, 34, 36, 239, 240
 - Sinorhizobium*, 240
- Rhizobial nodulation factors, 36
- Rhizobium/rhizobia, 211, 219, 249–253, 257, 263, 264, 267
- Rhizosphere, 296, 297
- Rho GTPase, 152
- RIC (ROP-interactive CRIB-motif), 197, 203, 204
- RLK (receptor like kinase), 196, 202, 203
- Root architecture, 323, 324
- Roothairless, 204
- Root hairs
 - curling, 108, 109, 113, 118, 252, 253, 255–259, 264, 269
 - deformation, 253, 256–260
 - development, 28, 34
 - initiation, 10–11
 - length measurement, 59–60
 - plasticity (in development), 59
 - positioning, 57–58
 - and protein kinases, 13
 - specific promoter (AtEXPA7 promoter), 55, 56
 - system (to study auxin transport), 58–59
 - tube, 31, 38
- ROP, 152, 191–205, 225, 242
 - effectors, 193, 195, 197, 198, 200, 204
 - GAP (GTPase-activating protein), 192–196, 203
 - GDF (GDP displacement factor), 195
 - GDI (GDP dissociation inhibitor), 192–195, 198, 201–203
 - GEF (guanine nucleotide exchange factor), 192, 193, 195–198, 201–203
 - of plants, 172, 180–182

- ROS (reactive oxygen species), 191, 197–199, 204
- Rough endoplasmic reticulum (RER), 66, 67
- RUB1 & 2, 51
- S**
- SAXS, 40
- Scanning electron microscope, 40
- Scanning probe microscopy, 41
- Schizosaccharomyces*, 241
- scn1*, 195, 198, 201, 203
- SEC3, 199, 204
- sec8*, 199, 204
- Secondary cell wall, 38, 89–90, 93
- Sec14p-nodulin, 153
- Secretory pathway, 66–67, 71, 80
- Secretory vesicles, 86–88
- Shadow casting, 40
- shy2* or SHY2/IAA3, 47, 48, 53
- Signaling, 6–8, 10, 12, 14–17
- Simulations, 109
- slr-1* or SLR-1/IAA14, 48, 51, 53, 54
- Soft spot hypothesis, 105, 113, 117
- Speed of root hair growth, 29
- SPIKE, 196, 198
- Spinning disk confocal microscope, 35, 215, 216
- Spitzenkörper, 107–108, 110, 118
- Staurosporine, 56, 59
- Steady-state, 104, 109–111, 117–118
- Strain, 114, 115
- Stress, 105, 113–117, 119
- Strigolactone, 320
- Subapical cytoplasm, 29, 32, 34
- Sulphate transport, 137
- sur1*, 46, 47
- Surface tension, 115
- T**
- Taxol, 238, 239
- Tethering of vesicles to a target membrane
- Exocyst
- Exo, 70
- exocyst subunit, 80
- Sec3, 80
- Rab GTPase
- Rab1, 1, 73
- RabA4b, 73, 74
- roothairless, 1, 80
- Time-lapse evanescent wave imaging, 33
- tip1*, 194
- Tip-growing cell, 27, 33, 36, 38
- Tip growth, 85–86, 88–90, 92, 93, 95, 103–107, 109–119, 148
- Tip-growth unit, 27–29, 36
- Tip shape, 112, 117–118
- tir1* or TIR1, 47, 50–52
- TobaccoBY2, 237
- Tonoplast, 30
- Touch, 257, 260
- Tpc1, 153
- trans*-Golgi Network (TGN), 66, 67, 69, 71, 73, 74, 87
- Transmission electron microscopy, 31, 40
- TRH1 or *trh1*, 48, 55, 57
- Trichoblasts, 28, 325, 326, 329–331
- Tubulin
- α , 243, 244
- β , 244
- γ , 236, 243, 244
- Turgor pressure, 28–30, 36, 105–106, 109, 114–115
- probe, 129–131
- U**
- UDP-D-glucose 4-epimerase, 92
- UDP-glucose, 31
- Uranyl acetate/lead citrate staining, 33
- V**
- Vacuole, 153
- electrical network, 124, 125
- in situ measurements, 124, 126
- Vesicle budding
- ARF GTPases
- Brefeldin A, 69
- gnom* mutant of, 69
- rpa* mutant of, 69
- Vesicle-rich area, 30, 33, 34, 36
- Vesicles, 14, 103, 105–113, 117–119
- mobility, 33
- supply center, 110
- Vicia*, 28, 233
- Villin, 31, 156
- Viscoelasticity, 114
- Viscoplastic, 113, 116
- Viscoplasticity, 116
- Viscosity, 113, 114
- VSC model, 110–112, 117, 118

W

WAXS, 40

XXET (xyloglucan endotransglycosylase), 200,
202, 203

XFP:cellulose synthase constructs, 37

X-ray analyses, 39

Xylan, 91

Xylogalacturonan, 93

Xyloglucan, 87–89, 91–94

Xyloglucan endotransglycosylases, 92

Xylosyltransferase, 92

Y

YFP, 234, 235, 237, 242

Yucca, 46, 47