

# Index

## A

Abscisic acid (ABA), 328  
Actin-based motor proteins, 40–41  
Actin-binding proteins (ABPs), 40–41, 193  
Actin depolymerising factor (ADF), 204, 379  
Actin-interacting protein (AIP), 379  
Actin-interacting protein1 (AIP1), 213  
Actin nucleation  
    formins, 209–211  
    profilins, 211–212  
Activation molecule for response capability (AMOR), 156  
Affymetrix, 260  
Agilent, 260  
Akaike Information Criterion (AIC), 356  
Aldehyde dehydrogenase (ALDH), 304  
Allergomics, 278, 298–300  
Amplified negative feedback loops, 396, 398  
Angiosperm pollen tubes, 136–137  
Aniline blue staining, 159  
Antimycin A, 324  
Aquaporins (AQPs), 21–23  
*Arabidopsis* SCAMP3 (AtSCAMP3), 112, 113, 120  
Arabinogalactan proteins (AGPs), 44, 140, 152  
AtLURE1 peptides, 152  
Atomic force microscopy (AFM), 72–73  
Autoinhibited-type  $\text{Ca}^{2+}$ -ATPases (ACA), 308–309

## B

Ball tonometry, 17, 70  
Basic leucine zipper transcription factor (bZIP TF), 263

Biochemical oscillators, 393

Biological oscillators, 394–402  
    input/output pathways, 395, 396  
    regulatory motifs, 397, 399–400  
        amplified negative feedback loop, 396, 398  
        controlling period/amplitude, 400–401  
        delayed negative feedback loop, 396, 398, 399  
        incoherently amplified negative feedback loops, 396, 399  
        minimal oscillator, 398  
        synchronization, 395–397  
    temporality does not imply causality, 399, 401–402

Biomechanics, 68

Boric acid, 377  
*Brassica napus*, 261, 267  
Brassinosteroids, 310, 322, 328  
BRI1-associated kinase1 (BAK1), 310  
Bryophyta, 249

## C

Calcineurin B-like proteins (CBLs), 196–197  
Calcium-dependent protein kinases (CDPKs), 194–195  
Calcium ions ( $\text{Ca}^{2+}$ ), 40, 41, 55–56, 409  
    calcium signalling, direct targets of, 193–197  
    eukaryotic cells, 181  
    influx oscillations, 184–185  
    RHs and PTs, 183–184  
    signalling, tip-growing cells, 181  
    sources and sinks

- cell wall, 190–191  
 endoplasmic reticulum, 191–192  
 mitochondria, 192–193  
 vacuole, 191  
 vesicles, 192
- spatial and temporal visualization, 181  
 transport and storage systems, 182  
 transporters  
*Arabidopsis* CNGCs, 186, 187  
 calcium-efflux transporters, 189  
 CNGCs, 186  
 GLRs, 188–189  
 HACCs and DACCs, 186–188  
 mechanosensitive calcium channels, 188
- Callose synthases (CalSs), 134–135, 306  
 activity of, 47–48  
 calcium ions, 55–56  
 plasma membrane, insertion in, 47  
 sucrose synthase, 50, 51
- Calmodulin (CaM), 195, 305
- Calmodulin-like proteins (CMLs), 195–197
- Camellia sinensis*, 255, 258, 261
- Cap analysis of gene expression (CAGE), 252
- CBL-interacting protein kinases (CIPKs), 196–197
- CBLs. *See* Calcineurin B-like proteins (CBLs)
- CDPKs. *See* Calcium-dependent protein kinases (CDPKs)
- Cellular force microscopy (CFM)  
 lily pollen tubes  
 cell wall elasticity, 19  
 turgor pressure, 17, 18  
 limitations, 75–76  
 MEMS, 73  
 multichannel LoC devices, 77–78  
 RT-CFM, 73  
 stiffness measurements, 74–75
- Cellulose synthase (CESA), 46, 48–49, 51, 55, 217–218
- Cellulose synthase complexes, 306
- Cellulose synthases A, 135
- Central cell guidance (CCG), 154
- Cephalotaxus*  
*C. koreana*, 278  
*C. sinensis*, 278
- CFM. *See* Cellular force microscopy (CFM)
- Chemical Langevin equation, 348, 355
- Chemical master equation (CME), 348
- Chemotropism, 96–97
- CIPKs. *See* CBL-interacting protein kinases (CIPKs)
- Clathrin-coated pits (CCPs), 118, 119
- ClearSee, 159
- CMLs. *See* Calmodulin-like proteins (CMLs)
- Coarse-grained model, 355
- Cobra-like 10 (COBL10), 154
- COPASI, 349
- Cortical microtubules (CMTs), 215, 216
- Craterostigma plantagineum*, 272
- Crop lodging, 68
- Cryo-field emission scanning electron microscopy, 48
- Cyclic nucleotide-gated channel 18 (CNGC18), 154
- Cyclic nucleotide-gated channels (CNGCs), 186
- Cyclin-dependent protein kinases, 275
- Cysteine-rich polypeptides (CRPs), 152
- Cytochalasin B (CytB), 216
- Cytomechanics  
 cellular force microscopy  
 limitations, 75–76  
 MEMS force sensor, 73  
 RT-CFM, 73  
 stiffness measurements, 74–75  
 dual-axis force sensors, 79–80  
 multichannel LoC devices, 76–78  
 penetration force measurement, 70  
 real-time computer vision, 78  
 stiffness and topography mapping  
 AFM, 72–73  
 microindentation approach, 71–72  
 tip growth, 68  
 turgor pressure measurement  
 ball tonometry, 70  
 incipient plasmolysis, 69–70  
 pressure probe, 70
- Cytoskeleton  
 actin filaments, 37–39  
 apical cell growth, RHs  
 actin bundling, 213  
 actin-depolymerizing factors, 212–213  
 actin-mediated trafficking, 214–215  
 actin nucleation (*see* Actin nucleation)  
 actin polymerization/depolymerization  
 oscillations, 208–209  
 ACT1-specific ABPs, 208  
 AIP1, 213  
 ectopic expression, 207  
 vegetative tissues, 208
- cell wall assembly  
 callose/cellulose synthase, 55–56  
 Golgi bodies, transport of, 52–54  
 PME inhibitor, 53, 55  
 secretory vesicles, accumulation and  
 fusion of, 53–55  
 sucrose synthase, 52, 53

- cell wall synthesis and deposition  
actin-binding proteins and motor proteins, 40–41  
AGPs, 44  
glucan synthases, 47–49  
microtubule-associated proteins, 42–43  
pectins, 43–44  
polysaccharides, local synthesis of, 45–46  
sucrose synthase, 49–51  
intracellular trafficking, control of, 138–140  
microtubules  
and actin interface, 216  
data for, 37  
distribution of, 39, 41  
endocytosis, 41, 42  
immunolocalization techniques, 41  
longitudinal bundles, 41  
longitudinal distribution, 37  
RHs, 215  
root hair morphology, 215–216
- D**  
Delayed negative feedback loop, 396, 398, 399  
DELLA proteins, 327–328  
Depolarization-activated calcium channel (DACCs), 186–188  
Directional memory, 97  
Directional pollen tube growth  
competency control, 155–157  
live-cell imaging, 150, 157–159  
microfluidic device, 150, 159–161  
ovular guidance, 151–153  
AtLURE1, 153, 155  
CCG, 154  
CHX21 and CHX21, 154  
CNGC16, 154  
COBL10, 154  
LIP1 and LIP2, 154, 155  
LURE1 and LURE2, 153, 155  
MDIS1, MDIS2 and MIK1, 155  
MYB 96, 153  
POD1, 154  
PRK6, 155  
ZmEA1, 153–154  
pre-ovular guidance, 150–152  
sporophytic and gametophytic cells, 150  
Domain-negative ROP1 (DN-ROP1), 120  
Drought stress, 28–29  
Dual-axis force sensors, 79–80
- E**  
*E. coli*, 364  
Elastic modulus, 19  
Electrical lab-on-a-chip (ELoC), 99  
Electron transport chain (ETC) activity, 403–404  
Electrospray ionization quadrupole time-of-flight tandem mass spectrometry (ESI Q-TOF MS/MS), 296  
Endoplasmic microtubules (EMTs), 215  
Endoplasmic reticulum (ER), 109, 110, 306, 307  
Endoplasmic reticulum-type  $\text{Ca}^{2+}$ -ATPases (ECA), 308, 309  
Equilibrium statistical mechanics, 346  
ETC activity. *See* Electron transport chain (ETC) activity  
Exocyst-positive organelle (EXPO), 110  
Exocytosis  
polar protein exocytosis  
cell wall extensibility, 111  
GFP-AtSCAMP3, 112, 113, 120  
NtPPME1-GFP (*see* *Nicotiana tabacum* pollen pectin methylesterase 1 (NtPPME1) polar exocytosis)  
post-Golgi exocytic pathway  
ER-Golgi-TGN-PM exocytosis, 109–110  
RLKs, 111  
UPS pathways, 110  
ROP1, 109  
tip growth, PME, 108–109
- F**  
Fick's Laws, 352  
Finite element method (FEM), 75  
Flavonoids, 325–326  
Fluorescence recovery after photobleaching (FRAP), 112, 113, 137  
Flux balance analysis (FBA), 351  
Formins, 209–211  
*Fragaria vesca*, 261  
FRA1 kinesin, 42  
Frequency-less oscillator (FLO), 396
- G**  
Galvano sensing, 98–100  
Gamma-aminobutyric acid (GABA), 152, 322, 324–325  
Gas chromatography–mass spectrometry (GC-MS), 330  
Gaussian distributions, 358

GDIs. *See* Guanine nucleotide dissociation inhibitors (GDIs)  
 GEFs. *See* Guanine nucleotide exchange factors (GEFs)  
 Gene chip technique, 260  
 Gibberellic acid (GA), 327  
 Gibbs free energy, 345  
 Gillespie algorithm, 348  
 Globular actin (G-actin), 209, 211, 212, 378  
 Glutamate receptor-like channels (GLRs), 152, 188–189  
 Glyoxalase I (GLO1), 151–152  
 Golgi apparatus, 377  
 Golgi-derived secretory vesicles (GDSVs), 116–119, 121–122  
 Growth oscillations  
     asymmetric waveform, 372  
     characteristics of, 372  
     computational modelling, constitutive and kinetic equations, 379–381  
     growth rate, 372  
     ion concentrations (pace keeper), 378–379  
     kinematic descriptors, 370  
     kinematic observations, 374  
     mean elongation rate, 373  
     mechanistic interactions, 373  
     molecular model, pollen tubes two growth mode, 381–382  
     non-pollen systems, 371  
     1D model, analytical treatment  
         cell wall deformation, 382  
         cell wall viscosity, 384  
         growth cycle, 384  
         ion fluxes, 383  
         plant cell growth, 382  
         pollen tube growth rates, 385  
         stretch-activated ion channels, 384  
         timescales, 383  
         toy models, 382  
         ‘triangular’ waveform, 383  
     pollen tube growth models, elements of, 376–378  
     sinusoidal oscillations, 371  
     sinusoidal/triangular waveform, 372  
     symmetric and asymmetric pulsatile cells, 373  
 GTPase-activating proteins (GAPs), 174–175  
 Guanine nucleotide dissociation inhibitors (GDIs), 175–176  
 Guanine nucleotide exchange factors (GEFs), 175–176  
 Gymnosperm pollen tubes, 136, 137

**H**  
*Helianthus annuus*, 267  
 Helmholtz free energy, 345  
 High-osmolarity glycerol (HOG) MAP kinase pathway, 27–28  
 High-pressure freezing and substitution (HPF), 116, 117  
 Hill functions, 346  
 Homogalacturonan (HG), 108–109, 133, 134, 220  
 Hooke’s Law, 353  
 Hydraulic conductivity, 14–16, 18, 19  
 Hyperpolarization-activated calcium channel (HACCs), 186–188

**I**  
 ImageJ, 375  
 Immobilised metal affinity chromatography (IMAC), 272  
 Incipient plasmolysis, 69–70  
 Incoherently amplified negative feedback loops, 396, 399  
 Indole-3-acetic acid (IAA), 72–73  
 Interactors of constitutive active ROPS (ICRs), 177  
 Invertase (Inv) enzymes, 323  
 Inverted microscope (Olympus IX81), 375  
 Ion dynamics oscillator, 406–407  
 Ion intensity, 297  
 Isobaric tags for relative and absolute quantification (iTRAQ), 297, 298  
 Isotope-coded affinity tag (ICAT), 297

**K**  
 KNOLLE antibodies, 119

**L**  
 Lab-on-a-chip (LoC) devices, 7, 76–78, 88, 141, 160  
 Late embryogenesis abundant (LEA) proteins, 304  
 Latin Hypercube sampling method, 358  
 Light sheet microscopy, 7  
 LILIM1 protein, 41  
*Lilium longiflorum* pollen tubes, 16  
     burst pressure, 26  
     cellular force microscopy  
         cell wall elasticity, 19  
         turgor pressure, 18  
     label-free shotgun proteomic workflow, 300–301  
     mercury ions, effect of, 21, 22

- pressure probe technique, 17–19  
protoplast swell assays  
osmotic permeability, 17  
water flux density, 17, 18  
tube elongation, 26, 371, 374–376
- Liquid chromatography–mass spectrometry (LC-MS), 330
- Live-cell imaging, 6, 150, 157–159
- Lycopodiophyta, 249
- M**
- Magnoliales, 249, 250  
Major intrinsic protein (MIP), 21  
Male gametophyte development  
allergomics, 278  
angiosperms, 249, 251  
*Annona cherimola*, 250  
asymmetric DNA methylation, 278  
bi-cellular pollen, 249–251  
methylome sequencing, haploid cell types, 277  
methyloomics, 276  
miRCURY microarray, 277  
miRNAomics, 276  
non-pollinated and pollinated pistils, 279  
phosphoproteomics  
    *Arabidopsis thaliana*, 273  
    cyclin-dependent protein kinases, 275  
    EPP complexes, 272  
    EST sequences, 275  
    mitogen-activated protein kinases, 275  
    phosphorylated peptides, 273  
    phosphorylation motifs, 275  
    tobacco male gametophyte proteome, 274  
    translation regulation, 272  
proteomics  
    energy-related proteins, 270  
    EPP proteins, 271  
    EST/protein sequences, 271  
    gel-free techniques, 269  
    intact proteins, excision of, 267  
    nutrient-specific effects, 270  
    splicing effect, 267  
    2-DE-analysed pollen proteomes, 268  
stigmatic papillary cells, 279  
transcriptomics  
    affymetrix, 260  
    AGP6 and AGP11, 262  
    bryophytes and ferns, 267  
    DNA microarrays, 252  
    DUO1 target genes, 263, 265  
    EST library sequencing, 266  
    gene chip technique, 260  
    MADS-box TF network, 263  
    MADS-domain transcription factors, 262  
    MYB transcription factors, 264  
    overview of, 253–259  
    reverse genetic screen, 265  
    R2R3-MYB transcription factors, 264  
    SAGE, 252  
    Sanger sequencing, 252  
    sperm cell-expressed proteins, 266  
    sporophytic tissue, 261  
    tri-cellular pollen, 249–251  
    triticale stigma development, 278  
*Marchantia polymorpha*, 267  
Massively parallel signature sequencing (MPSS), 252  
Mass spectrometry, 8, 296, 297, 299  
Mathematical modelling, 8  
    biological rates  
        experimental variation, data, 356–357  
        parameter estimation methods, 357–360  
        parameter identifiability problem, 360–361  
    experimentally testable hypotheses, 363  
    model creation  
        binding process, 342  
        biological phenomena, 343  
        biological processes, spatial domain, 352–353  
        cell populations, dynamics in, 349–351  
        degradation process, 342  
        Goodwin oscillator, 343  
        hypothesis test, 343  
        models and model selection,  
            non-uniqueness of, 355–356  
        single cells, small molecule numbers in, 347–348  
        single interaction access, 344–347  
        spatial and temporal scales, biological systems, 344  
        spatio-temporal model, 343  
        tissue growth, mechanical descriptions of, 353–354  
    modern science, 340  
    validation dataset, 362–363  
    variables/parameters, biological phenomena, 364  
Matlab, 375  
Matrix-assisted laser desorption/ionization time-of-flight mass spectrometer (MALDI-TOF MS), 296  
MaxQuant, 8  
Mechanoperception, 98

- Mechanosensing, 97–98  
 Mechanosensitive calcium channels, 188  
 MEMS. *See* Microelectromechanical systems (MEMS)  
 Mercury ions, 21, 22  
 Messenger ribonucleoprotein (mRNP), 270  
 Metabolomics  
   experimental analysis, 328–330  
   GC-MS, 330  
   LC-MS, 330  
   phytohormones, 326–328  
   primary metabolism  
     GABA, proline and glutamate metabolism, 324–325  
     polyamines, 325  
     sucrose, 323–324  
   secondary metabolism, 325–326  
 Metal oxide/hydroxide affinity chromatography (MOAC), 272  
 Michaelis–Menten kinetics, 350  
 Microelectromechanical systems (MEMS), 73, 95, 99, 102. *See also* Microfluidic devices  
 Microfluidic chip technique, 19  
 Microfluidic devices, 7  
   cell mechanical properties, measurement of, 100  
   chemotropism, 96–97  
   directional memory, 97  
   galvano sensing, 98–100  
   LoC devices (*see* Lab-on-a-chip (LoC) devices)  
   mechanosensing, 97–98  
   microfluidic network  
     dimensions and features, 91–93  
     electrodes and actuators, components for, 95  
     fluid flow, influence of, 94–95  
     individual pollen grain capture, 89  
     microchannel geometry, influence of, 92, 94  
   PDMS, 95  
   pollinated pistil, placement of, 89  
   TipChip, design principle of, 89–91  
   planar geometry, 89  
   pollen tube guidance, 150, 159–161  
 Micro-indentation approach, 17, 18, 71–72  
 Micromanager software, 375  
 Microtubule-associated proteins, 42–43  
 Minimisation procedure, 359  
 Modeling oscillations, 404  
   ion dynamics oscillator, 406–407  
   limitations, 407  
   mechanical models, 405  
   ROP1 oscillator, 405–406  
   proton (*see* Proton oscillations)  
   self-sustained oscillations, 393  
 ROP1 oscillator, 405–406  
 Monilophyta, 249  
 Myosins, 214–215  
 N  
 Nanosensors, 7  
*Nicotiana tabacum* pollen pectin  
   methyl esterase 1 (NtPPME1)  
   polar exocytosis  
   FRAP analysis, 112, 113  
 GDSVs, cell wall formation, 116–119, 121–122  
 high-pressure freezing and substitution, 116, 117  
 ROP1 signaling, 119–120  
 STORM, 116  
 VEAM imaging, 112–116  
 NimbleGen, 260  
*Nitella axillaris*, 382  
 Non-invasive cellular force microscopy, 6  
 Nonprotein amino acids, 152  
 O  
 Ohm's law, 14  
*Olea europaea*, 264, 278  
 Oligosaccharyltransferase (OST), 307  
 -Omics studies, male gametophyte. *See* Male gametophyte development  
 Ordinary differential equations (ODEs), 349–351, 355  
 Oscillations  
   biochemical oscillators, 393  
   biological oscillators (*see* Biological oscillators)  
   calcium ions (*see* Calcium ions ( $\text{Ca}^{2+}$ ))  
   growth oscillations (*see* Growth oscillations)  
   intrinsic period, amplitude, and phase flow, 392  
   motion-based oscillator, 409  
   oscillatory networks, 393  
   polarity and chemotaxis, 407–409  
   pollen tube apical growth, 393  
   pollen tube tip  
     central pacemaker, 402–403  
     ion dynamics oscillator, 406–407  
     mechanical models, 405  
     modeling limitations, 407  
     multiple oscillators, 403–404  
     ROP1 oscillator, 405–406  
     proton (*see* Proton oscillations)  
     self-sustained oscillations, 393

signaling-based oscillator, 409  
splitting/lumping oscillations, 394  
Osmoregulation, 26–29  
Osmosensing, 26–29  
Osmotic permeability, 16, 17, 20–21  
Osmotic pressure, 15, 16, 24, 25  
OsSCAMP1 antibody, 116–119

**P**

Pareto fronts, 356, 360  
Partial differential equation (PDE), 352  
Patch-clamp analysis, 202  
PatternLab, 7  
PDMS. *See* Polydimethylsiloxane (PDMS)  
Pectin matrix, 219–220  
Pectin methylesterase (PME), 45, 53–55, 108, 109, 112, 133–134, 220, 377  
Pectin methyl esterase inhibitors (PMEIs), 53, 55, 134  
Pectins, 43–44  
*Phleum pratense*, 278  
Phospholipase D (PLD), 305  
Phosphoproteomics, 7, 8, 272–275  
*Physcomitrella patens*, 267  
Phytohormones, 326–328  
*Picea wilsonii*, 269, 274  
*Pinus*  
    *P. strobus*, 267, 269  
    *P. taeda*, 276  
Pistil cells, 36  
Plant circadian clock, 343, 355, 364  
Plasma membrane intrinsic protein (PIP), 21, 23  
*Plumbago zeylanica*, 266  
PME. *See* Pectin methylesterase (PME)  
PMEIs. *See* Pectin methyl esterase inhibitors (PMEIs)  
PMI. *See* Pollen mitosis I (PMI)  
PMII. *See* Pollen mitosis II (PMII)  
Polar exocytosis  
    cell wall extensibility, 111  
    GFP-AtSCAMP3, 112, 113, 120  
    NtPPME1-GFP  
        FRAP analysis, 112, 113  
        GDSVs, cell wall formation, 116–119, 121–122  
        high-pressure freezing and substitution, 116, 117  
        ROP1 signaling, 119–120  
        STORM, 116  
        VEAM imaging, 112–116  
Polarity-associated model, 405–406  
Pollen allergomics, 298–300

Pollen defective in guidance 1 (POD1), 154  
Pollen development, 261–263, 268–270. *See also* Male gametophyte development  
    gametophytic proteome, 296  
intermediate phase, 296  
metabolomics  
    experimental analysis, 328–330  
    flavonoids, 325–326  
    GABA, proline and glutamate metabolism, 324–325  
    phytohormones, 326–328  
    polyamines, 325  
    sucrose, 323–324  
sporophytic proteome, 296  
stages of, 20  
and tube growth  
    carbohydrate reserves, 320–321  
    dehydration phase, 320  
    exine, 321  
    fatty acids and waxes, 321  
    GABA receptor, 322  
    intine, 321–322  
    lipids, 321  
    microgametogenesis, 320  
    microsporogenesis, 320  
    pollen-stigma interaction, 321  
    pollen tube guidance, 322  
    ripening process, 321  
    starch reserves, 320  
    tryphine, 321  
Pollen membrane proteomics  
    in cell wall biosynthesis, 305–306  
    challenge of, 300  
    ion and nutrient transport, 307–309  
    label-free shotgun proteomic workflow, 300–301  
    organelle marker proteins, distribution of, 302  
    protein abundance, time-dependent changes in, 302–304  
    protein complexes, 309–310  
    protein folding and modification, 307  
    protein trafficking and biosynthesis, 306–307  
    in signalling and stress response, 304–305  
Pollen mitosis I (PMI), 249, 262, 320  
Pollen mitosis II (PMII), 249, 262, 320  
Pollen-specific receptor kinase 6 (PRK6), 155  
Pollen tube growth  
    biophysical interactions, 66, 67  
    cell wall expansion  
        callose synthases, 134–135  
        cellulose, 135

- cell wall components, distribution of, 130–131  
 fibrillar outer layer, 133  
 HG synthesis, 133  
 PGs and pectate lyases, 134  
 PME, 133–134  
 PMEIs, 134  
 turgor pressure, 131–132  
 weakly electron-dense inner wall, 133
- cytomechanical measurements (*see* Cytomechanics)  
 directional growth (*see* Directional pollen tube growth)  
 extracellular signals, 36  
 intracellular trafficking  
   cytoskeletal control of, 138–140  
   exocytosis and endocytosis, 136  
   invasive growth, 140–141  
   vesicle motion patterns, 136–137  
 oscillations (*see* Oscillations)  
 pistil cells, 36  
 polarized cell growth, 108  
 turgor pressure, 36  
 water transport (*see* Water transport and pollen tube growth)
- Polyamines, 325
- Polydimethylsiloxane (PDMS), 70, 91, 94, 95, 100
- Polygalacturonases (PGs), 134
- Polysaccharides, 45–46
- Pressure probe technique, 70  
   disadvantage of, 19  
   hydraulic conductivity, 18, 19  
   turgor pressure, 17–19  
   Young's/elastic modulus, 18, 19
- Primary metabolism  
 GABA, proline and glutamate metabolism, 324–325  
 polyamines, 325  
 sucrose, 323–324
- Profilins, 211–212
- Protein–protein interactions, 310
- Proteomics, 8, 310–311  
   male gametophyte development  
     energy-related proteins, 270  
     EPP proteins, 271  
     EST/protein sequences, 271  
     gel-free techniques, 269  
     intact proteins, excision of, 267  
     nutrient-specific effects, 270  
     splicing effect, 267  
   2-DE-analysed pollen proteomes, 268  
 membrane proteomics  
   in cell wall biosynthesis, 305–306
- challenge of, 300  
 ion and nutrient transport, 307–309  
 label-free shotgun proteomic workflow, 300–301  
 organelle marker proteins, distribution of, 302  
 protein abundance, time-dependent changes in, 302–304  
 protein complexes, 309–310  
 protein folding and modification, 307  
 protein trafficking and biosynthesis, 306–307  
 in signalling and stress response, 304–305  
 for model/relevant crop plants, 295–297  
 for non-model organism, 297–298  
 pollen allergens, 298–300
- Proton oscillations  
 H<sup>+</sup> influx  
   cell wall, 200–201  
   proteins, 201–202  
 pH oscillations, signalling downstream of actin remodelling, 204, 206  
   cell wall pectin dynamics, 206  
 proton concentration, 197–198  
 PTs and RHs, 198–200  
 subapical H<sup>+</sup> efflux proteins, 202–204  
 vacuole, H<sup>+</sup> source/sink, 204, 205
- Protoplast swell assays  
 osmotic permeability, 17  
 water flux density, 17, 18
- Pteridium aquilinum*, 267
- Pyrus bretschneideri*, 261
- Q**
- Quercus ilex*, 267
- R**
- Reaction–diffusion systems, 353
- Reactive oxygen species (ROS), 172  
   calcium signalling, 178–179  
   cell wall properties, 179  
   and kinase signalling, 179–180  
   production, 177–178
- Real-time cellular force microscopy (RT-CFM), 73
- Receptor-like kinases (RLKs), 111, 172, 305
- Rho-like GTPases from plants (ROPs)  
   cell wall, dynamic system  
     pectin matrix, 219–220  
     root hair cell walls, cellulose deposition in, 217–218

- second messengers and cell wall sensing/modifying proteins, 220–221  
xyloglucan, 218–219
- control tip growth, 172–173  
effector proteins  
  ICRs/RIPs, 177  
  RICs, 176  
GAPs, 174–175  
guanine nucleotide dissociation inhibitors, 175–176  
guanine nucleotide exchange factors, 174  
Rho-like GTPases from plants 1 (ROP1), 109, 139  
  NtPPME1 exocytosis, 119–120  
  oscillator, 405–406  
Rho of plant guanine nucleotide-exchange factors (ROPGEFs), 155
- Root hair (RH) tip growth  
*Arabidopsis*, pattern and morphology in, 171  
cytoskeleton (*see* Cytoskeleton)  
ion oscillations, extra-and intracellular signalling  
  calcium (*see* Calcium ions ( $\text{Ca}^{2+}$ ))  
  proton oscillations regulation (*see* Proton oscillations)  
ROP GTPases, master regulatory switches  
  control tip growth, 172–173  
  GAPs, 174–175  
  guanine nucleotide dissociation inhibitors, 175–176  
  guanine nucleotide exchange factors, 174  
  ICRs/RIPs, 177  
  RICs, 176  
ROS, diverse signalling molecules  
  calcium signalling, 178–179  
  cell wall properties, 179  
  and kinase signalling, 179–180  
  production, 177–178
- ROP1. *See* Rho-like GTPases from plants 1 (ROP1)
- ROP-interacting partners (RIPs), 139, 177
- ROP-interactive CRIB motif-containing proteins (RICs), 176
- ROPs. *See* Rho-like GTPases from plants (ROPs)
- S**  
Sanger sequencing, 252  
Savitzky-Golay filtering, 376  
Secondary metabolism, 325–326
- Secretory carrier membrane protein (SCAMP), 112
- Semi-in vivo pollen tube growth, 7, 155, 158–160, 264, 276
- Sequential elution from IMAC (SIMAC), 272
- Serial analysis of gene expression (SAGE), 252
- Shear stress, 94, 95
- Shoot apical meristem (SAM), 72
- Signalling pathways, 5
- Simulated Annealing, 359
- Solanum lycopersicum*, 260, 267, 269, 270
- Soluble N-ethylmaleimide-sensitive factor attachment protein receptors (SNAREs), 139, 306
- Spatiotemporal image correlation spectroscopy (STICS), 137
- Spectral counting, 297
- Spinning disk confocal microscopy, 159
- Stable isotope labelling by amino acids in cell culture (SILAC), 297
- Stigma-specific protein1 (STIG1), 151
- Stochastic optical reconstruction microscopy (STORM), 116
- Stochastic simulation algorithm (SSA), 348
- Streptophyta, 249
- Sucrose synthase (SUS), 323  
  anaerobic stress, 50  
cell wall synthesis  
  actin filaments, 50–51  
  callose synthesis, 50, 51  
  cellulose synthase, 51  
  phosphorylation events, 50, 51  
  displacement of, 52, 53  
  invertase, 49–50
- Sugar transport protein (STP), 324
- Systems biology mark-up language (SBML), 349
- T**  
Tensor equation, 354
- TGN. *See* Trans-Golgi network (TGN)
- Thorlabs camera (DCC1545M-GL), 375
- Threshold mechanism, 352
- TipChip, 89–91, 141
- Tonoplast intrinsic protein (TIP), 21, 23
- Total internal reflection fluorescence microscopy (TIRFM), 7, 113, 137
- Transcriptomics, 4  
  affymetrix, 260  
  AGP6 and AGP11, 262  
  bryophytes and ferns, 267  
  DNA microarrays, 252

DUO1 target genes, 263, 265  
 EST library sequencing, 266  
 gene chip technique, 260  
 MADS-box TF network, 263  
 MADS-domain transcription factors, 262  
 MYB transcription factors, 264  
 overview of, 253–259  
 reverse genetic screen, 265  
 R2R3-MYB transcription factors, 264  
 SAGE, 252  
 Sanger sequencing, 252  
 sperm cell-expressed proteins, 266  
 sporophytic tissue, 261  
 Trans-Golgi network (TGN), 109–110, 116,  
   117, 135, 139, 306  
 Translationally controlled tumour protein  
   (TCTP), 280  
 Transmission electron microscopy (TEM), 75,  
   111  
 Transmitting tissue-specific (TTS)  
   arabinogalactan proteins, 152  
 Turgor pressure, 6, 15, 16, 376, 381  
   ball tonometry, 70  
   cellular force microscopy, 17, 18  
   incipient plasmolysis, 69–70  
   pollen grain rehydration, 23, 24  
   pollen tube elongation, 25–26, 132–133  
   pressure probe, 17–19, 70  
 Two-dimensional difference in gel  
   electrophoresis (2D DIGE), 298  
 Two dimensional gel electrophoresis (2-DE),  
   267, 268, 296  
 Two-dimensional polyacrylamide gel  
   electrophoresis (2D-PAGE),  
   296–297  
 Two-photon excitation microscopy (TPE),  
   158–159

**U**

Unconventional protein secretion (UPS), 110

**V**

Variable-angle epifluorescence microscopy  
   (VAEM), 112–116  
 Vesicle trafficking, 138–140  
 Voltage-dependent anion channel (VDAC),  
   309

**W**

Water transport and pollen tube growth, 6  
   aquaporins, 21–23  
   burst pressure, 26  
   flower and pollen development, stages of,  
    20  
   ions and nutrients, cotransport with,  
    20  
   lipid bilayers, permeability of, 20  
   osmosensing and osmoregulation,  
    26–29  
   plants, physiological processes in, 14  
   pollen grain rehydration, 23–25  
   pollen tube elongation, 25–26  
   reproduction and drought stress,  
    28–29  
 water potential  
   ball tonometry, 17  
   cellular force microscopy, 17–19  
   chemical potential of water, 14–15  
   hydraulic conductivity, 14  
   hydrostatic/pressure potential, 15  
   irreversible thermodynamics, theory of,  
    14  
   microfluidic chip technique, 19  
   micro-indentation, 17, 18  
   nonpermeable solutes, water (volume)  
    flow density, 15  
   Ohm's law, 14  
   osmotic pressure, 15  
   pressure probe technique, 17–19  
   protoplast swell assays, 17, 18  
   single cells, useful on, 14  
   water (volume) flow, 14  
   water flux, 15, 16  
   water potential difference, 14

**X**

Xyloglucan (XyG), 218–219

**Y**

Young's modulus, 19, 100, 354

**Z**

*Zea mays*, 260, 261, 266, 272, 274, 278