



# Index

- ABC model of flowering, 431–433  
 ABC transporters, 130, 476  
 Abiotic stress, 546  
 abscisic acid (ABA), 491  
 abscission, 531  
 absorption spectrum, 209, 210  
 accessory pigments, 204  
 acclimation, 547  
 acetyl CoA, 271  
 achromic point, 719  
 acid growth hypothesis, 480  
 acoustic detection method, 65  
 action spectrum, 209, 210  
 activation energy, 174  
 active absorption, 58, 59  
 active site, 176  
 active transport, 124, 127  
 acyl carrier protein (ACP), 362  
 adaptation, 547  
 adhesion, 3  
 ADP-glucose, 256  
 aerenchyma, 539, 555–556  
 aerobic respiration, 268  
 aerobic rice technology, 560  
 aeroponics, 102, 103  
 agent orange, 519  
 alcoholic fermentation, 295  
 alkaloids, 602  
 allelopathy, 595  
 allosteric enzymes, 183  
 amides, 320  
 amino acids, 321  
 ammonium assimilation, 316  
 amphibolic pathway, 157, 286  
 amphipathic, 17  
 amphiprotic or Amphoteric compounds, 126  
 amylases, 257, 713  
 amyloplast, 255  
 anabolism, 154  
 anaerobic respiration, 295  
 anaplerotic reaction, 157, 286  
 anion or salt respiration, 125  
 anoxia (or anaerobiosis), 555  
 antagonistic action, 132, 423  
 antennae (or subsidiary) pigments, 220  
 anthocyanins, 599  
 antifreeze proteins, 561  
 antitranspirants, 89–90, 621  
 apical dominance, 416, 480  
 apoenzyme, 169  
 apoplast, 54–56  
 apoptosis, 531  
 apparent free space, 122  
 aquaporins, 26, 28, 551  
*arabidopsis thaliana*, 449–50  
 Asada–Halliwell cycle  
     (ascorbate-glutathione cycle), 559  
 asphyxiation, 57  
 assimilatory power, 223  
 ATP, 164

- ATP synthase, 281–282  
 autolysis, 532  
 autoradiography (radioautography), 229  
 auxins, 468
- bacteriochlorophyll, 209  
 bacteroids, 335  
 beneficial elements, 114  
 bioassays, 474  
 biofortification, 621  
 biogeochemical cycle, 376, 381, 383  
 biological clock, 436  
 biotic stress, 580  
 biotrophs, 539  
 biuret method, 773  
 Blackman's law of limiting factors, 242, 746  
 bleeding, 76  
 blinks effect, 216  
 blue-light responses, 80  
 bolting, 483  
 boundary layer, 91  
 brassinosteroid, 506  
 bud dormancy, 421  
 buffers, 12  
 buffering range, 13  
 bundle-sheath, 236
- caffeine, 602, 814  
 calcium-pumping ATPase, 129  
 calmodulin, 130  
 Calvin–Benson pathway (C3 pathway), 229  
 canola, 367  
 carbohydrate metabolism, 253–263  
 carotenoids, 207  
 carnivore plants, 343  
 carrier proteins, 122  
 catabolism, 154  
 cavitation, 65–66  
 cellulose, 259  
 CF<sub>0</sub>–CF<sub>1</sub> Complex, 221  
 channel proteins, 123  
 chaperones, 562  
 chelating agents, 116  
 chemical potential, 32, 38  
 chemiosmotic mechanism, 225, 280  
 chemosynthesis, 245  
 chlorophyll, 205–206  
 chlorosis, 115  
 Cholodny–Went hypothesis, 442  
 circadian rhythm, 436–439  
 citric acid cycle, 272  
 climacteric, 526  
 climacteric fruits, 499, 528  
 coenzymes, 170–171  
 cofactors, 170, 172  
 cohesion, 3  
 cohesion hypothesis, 63  
 colloids, 13  
 compatible solutes, 549–550  
 compensation points, 243  
 competitive inhibition, 191–192  
 conjugated proteins, 326  
 constitutive enzymes, 173  
 cotransport, 374  
 coumarins, 600  
 coupled reactions, 165  
 covalent modification, 185  
 crassulacean acid metabolism, 240  
 crosstalk, 515  
 cross tolerance, 573  
 cryoprotectants, 561  
 cryptochrome, 462–463  
 cyanide-resistant respiration, 289  
 cyclic photophosphorylation, 222, 224  
 cytochromes, 221, 226  
 cytochrome theory, 125  
 cytokinins, 485
- D1 repair cycle, 564  
 de-etiolation, 249  
 DELLA proteins, 483  
 denaturation, 324  
 dendrograph, 65  
 depolarization, 88  
 development, 411  
 devernialization, 435  
 dialysis, 627  
 differentially or selectively permeable  
   membrane, 16, 682  
 differentiation, 411  
 diffusion, 31  
 diffusion Pressure deficit, 36, 41  
 donnan equilibrium, 121  
 drought-stress inducible genes, 552–553

## 858 Index

- ebb and flow system, 102–103  
 ectomycorrhizae, 118–119  
 electrical potential, 40  
 electrochemical gradient, 23, 29  
 electrogenic pump, 128  
 electromagnetic spectrum, 212  
 electron transport system (ETS), 275  
 Embden-Meyerhof-Parnas (EMP) pathway, 269  
 embolism, 65–67  
 Emerson effect, 215–16, 220  
 empty ovule technique, 405  
 emulsion, 8  
 endergonic reaction, 161, 164–165  
 endomycorrhizae, 118–119  
 endosmosis, 34  
 enhancers, 616  
 enzymes, 168  
 enzyme inhibition, 190  
 enzyme regulation, 183  
 ethylene, 496  
 etiolation, 115, 439  
 exergonic reaction, 161, 164–165  
 exodermis, 52  
 exosmosis, 35
- facilitated diffusion, 122  
 fatty acid synthase, 182, 362  
 fatty acids:  
    $\beta$ -oxidation, 356  
    $\alpha$ -oxidation, 360  
   synthesis, 362  
 fermentation, 295–296  
 ferredoxin-thioredoxin system, 232–233  
 Fick's law, 33  
 field capacity, 52  
 flavonoids, 597  
 floral meristem identity genes, 431  
 floral organ identity genes, 431  
 florigen, 428  
 FLOWERING LOCUS C (FLC), 430, 434  
 fluid mosaic model, 17, 19  
 fluorescence, 212–213  
 foliar spray, 106  
 free energy, 38  
 free space, 122  
 fructans, 260  
 fruit ripening, 526
- Ganong's potometer, 692  
 gated channel, 123–124  
 gerontoplasts, 536  
 gibberellins, 480  
 girdling, 61, 389  
 gluconeogenesis, 291  
 glutamate-synthase cycle, 319  
 glycolipid, 19, 355  
 glycolysis, 268  
 glycosides, 604  
 glyoxylate cycle, 364  
 golden rice, 619  
 gravitational potential, 40  
 gravitropism, 440  
 growth, 411  
 growth curve, 412  
 growth retardants (or anti-gibberellins), 524–525  
 guttation, 76
- $H^+$ -ATPase, 128  
 haemodialysis, 681  
 halophytes, 565  
 hardening, 547  
 Hatch-Slack pathway (C<sub>4</sub> pathway), 236  
 heat shock elements (HSEs), 563  
 heat shock factors (HSFs), 563  
 heat shock proteins (HSPs), 562  
 heavy metal homeostasis, 134  
 heavy metal stress, 568  
 heliotropic movements, 449  
 herbicides, 519  
 hexokinases, 85, 174  
 Hill's reaction, 215  
 homeostasis, 545  
 hydathode, 76  
 hydration shell, 4  
 hydraulic conductivity, 41  
 hydrogen bond, 4  
 hydrogenase, 338  
 hydrolases (or hydrolytic enzymes), 23, 175  
 hydroponics, 101–103, 617  
 hydrotropism, 445  
 hyperaccumulator, 132  
 hyperpolarization, 88  
 hypersensitive response, 539  
 hypertonic, 34, 663  
 hypotonic, 34, 664, 668, 670

- hypoxia, 283, 539, 555
- imbibition, 29
- impermeable, 52
- incipient plasmolysis, 664
- indole-3-acetic acid (IAA), 469, 804
- induced fit hypothesis, 179
- inducible enzymes, 173, 367
- integral proteins, 19
- invertase, 255, 528, 710, 713
- ion antagonism, 131
- ion channel, 24, 123
- iron metabolism, 383
- iron stress, 116
- isocitrate lyase, 365–367
- isoelectric point, 15, 45, 345
- isotonic, 34, 667
- isozymes (or isoenzymes), 180–181
- Jagendorf's experiment, 638
- jasmonic acid (jasmonates), 380, 505, 582, 608
- karrikins, 415
- kinetin, 486, 645, 800
- Kranz anatomy, 237, 239
- Krebs cycle, 272–273, 275, 284
- lactic acid fermentation, 296
- laws of thermodynamics, 161
- LEA proteins, 551
- leaf senescence, 534
- lecithin hypothesis, 126
- leghaemoglobin, 333
- light harvesting complexes, 221
- light stress, 563
- lignin, 595, 822
- lipase, 354, 787
- lipid bilayer, 17, 19
- lipids, 352
- lock and key hypothesis, 178, 634
- log phase, 412
- long day plant, 424, 426
- Lowry's method, 776
- lysigeny, 533, 556
- macronutrients, 105, 107
- malate synthase, 365–367
- MAPK cascade, 514
- mass flow hypothesis, 392
- matric potential, 39, 413, 664
- mericlone, 615
- metabolic engineering, 156, 367
- metabolons, 156, 836
- metalloenzymes, 170
- metallothioneins, 531, 537
- metabolome, 571, 836
- metabolism, 153–154
- metabolite pool, 157–158
- Michaelis constant ( $K_m$ ), 186
- micrometry, 689
- micronutrients (trace elements), 105, 109, 115
- micropropagation, 490, 614
- micro RNA, 577
- mid-day stomatal closure, 89
- mineral toxicity, 133
- molal solution, 6, 42
- molar solution, 6, 42
- Moringa oleifera*, 622
- motor cells, 344, 446
- multienzyme complex, 181–182, 272, 362
- Münch mass flow, 392
- mycorrhizae (singular mycorrhiza), 118, 617
- NAD (Nicotinamide adenine dinucleotide), 171, 173, 285
- NADP (Nicotinamide adenine dinucleotide phosphate), 171, 285
- NAM (non apical meristem), 537
- necrotrophs, 539
- necrosis, 111, 531
- neem (*Azadirachta indica*), 594
- nernst equation, 131
- nif genes, 337
- nitrate reductase, 314–315
- nitric oxide, 502
- nitrite reductase, 315
- nitrogen metabolism, 313–351
- nitrogenase (dinitrogenase) complex, 336–337
- nitrogen cycle, 339
- nitrogen-fixation (biological  $N_2$ -fixation):  
   -asymbiotic, 332  
   -symbiotic, 333
- nitrogen use efficiency, 341
- nod (nodulation) factors, 334, 338
- nodules (or tubercles), 26, 333, 335

## 860 Index

- non-competitive inhibition, 191–192  
 non-cyclic photophosphorylation, 223–224  
 normal solution, 6, 42  
 nucleic acids, 329  
 nutrient depletion zone, 118  
 nutrient film technique, 102–103  
 nyctinastic movements, 446
- ocular micrometer, 689  
 oleosomes (or spherosomes), 364, 366, 414  
 opines, 491  
 osmoprotection, 549  
 osmoregulation, 27, 81, 107  
 osmosis, 34–35, 682  
 osmotic potential, 39, 663  
 osmotic pressure, 35  
 osmotin, 565  
 oxidative decarboxylation, 271  
 oxidative phosphorylation, 276, 298  
 ozone stress, 569
- $P_{680}$ , 220–221  
 $P_{700}$ , 220–221  
 pacemaker enzyme, 156  
 paper chromatography, 731  
 passive absorption, 59  
 passive transport, 120, 127  
 Pasteur effect, 302  
 patch-clamp technique, 25  
 pathogenesis-related (PR) proteins, 580  
 pearl millet, 95  
 pentose phosphate pathway, 291  
 peribacteroid membrane, 334–335  
 peripheral proteins, 19  
 perlite, 102  
 permeability, 16  
 pH, 10  
 phenolic compounds, 595  
 pheophytin, 226  
 phloem transport, 388–407  
 phloem loading and unloading, 395  
 phosphoenolpyruvate (PEP) carboxylase, 237  
 phospholipids, 355  
 phosphorescence, 212–213  
 phosphorus metabolism, 380  
 photoblastic seeds, 420  
 photochemical reaction, 212  
 photoinhibition, 548, 563  
 photomorphogenesis, 439  
 photoperiodism, 423  
 photophosphorylation, 222, 298  
 photorespiration, 234  
 photosynthesis, 201–252  
 photosystem I, 220, 221  
 photosystem II, 220, 221  
 phototropins, 464–465  
 phototropism, 444  
 phycobilins, 208  
 phycocyanin, 209  
 phycoerythrin, 209  
 phytoalexins, 376, 598  
 phytochelatins, 134  
 phytochrome, 454–462  
 phytoecdysones, 592  
 phytoremediation, 132  
 phytosiderophore, 117  
 phytotron, 473  
 plant hormones, 468–516  
 plant movements, 440–449  
 plant photoreceptors, 453–466  
 plasmodesmata (singular, plasmodesma), 20–22  
 plasmolysis, 36, 38  
 plastoglobuli, 536  
 plastoquinone, 221, 223  
 pneumatophores, 565–566  
 polar molecule, 4, 9  
 polar transport, 476  
 polyamines, 500  
 porins, 271  
 pressure bomb method, 65  
 pressure potential, 39  
 programmed cell death, 531  
 prosthetic groups, 170  
 proteasome, 200  
 proteins, 323–329  
 proteome, 571, 842  
 proton motive force, 29, 128, 281  
 pumps, 128  
 pyruvate dehydrogenase, 272
- Q cycle:  
     (in photosynthesis), 226  
     (in respiration), 279
- reactive oxygen species (ROS), 557  
 recalcitrant seeds, 418

- red drop, 216
- redox reactions, 163
- reductive amination, 317
- resonance transfer, 212
- respiration, 267–312
- respiratory quotient (RQ), 298
- reversed stomatal rhythm, 252, 844
- RFOs, 551
- rhizosphere, 333–334
- rhizotron, 103
- ribozymes, 169
- ribulose-1, 5-bisphosphate carboxylase/  
   oxygenase (Rubisco), 231
- Richmond–Lang effect, 490
- RIN (rin) mutation, 615
- root pressure, 58, 63
- rooting hormone, 614
- rubisco activase, 232
  
- salicylic acid, 502
- salt glands, 566
- salt stress, 565
- sand culture, 102
- saturated solution, 7
- scarification, 418, 801
- schizogeny, 533, 556
- secondary messengers, 509, 514
- secondary metabolites, 590–608
- seed dormancy, 416
- seed germination, 413
- seismonastic movements, 446
- semipermeable membrane, 34, 681
- senescence, 530
- senescence associated genes, 537
- shikimic acid pathway, 595–596
- short day plants, 424, 426
- sigmoid growth curve (grand period curve), 412
- signal perception, 509
- signal transduction, 512
- sink organs, 400, 616
- skotomorphogenesis, 439
- skototropism, 444
- solar tracking, 449
- stage micrometer, 414
- standard solution, 8
- starch–statolith hypothesis, 441
- starch biosynthesis, 256
  
- starch catabolism, 258
- statocyte, 441–442
- stomata, 77–80
- stomatal frequency, 688
- stomatal index, 688
- stratification, 418, 802
- strigolactones, 504
- substrate-level phosphorylation, 270, 272
- sucrose biosynthesis, 253
- sucrose catabolism, 254
- sulphur metabolism, 374
- surface tension, 5
- suspension, 8
- symbiotic nitrogen fixation, 333
- symplast, 54–56
- symport, 124, 146
- systemic acquired acclimation (SAA), 572
- systemic acquired resistance (SAR), 583, 608
- systemin, 585, 608
  
- Tanada effect, 461
- tannins, 601
- temperature coefficient ( $Q_{10}$ ), 213
- temperature stress:
  - low temperature stress, 560
  - high temperature stress, 562
- terpenoids, 591
- thermogenesis, 290, 502
- thigmonastic, 448
- thigmotropism, 445
- thin layer chromatography (TLC), 732–733
- transamination, 317
- transcription factors, 554
- transgenics (GM) plants, 621
- transcriptome, 571, 847
- transfer cells, 406–407
- transmembrane potential, 131
- transpiration, 75–99
- transpiration ratio, 92
- transport channels, 24
- transport proteins, 19, 122, 159
- triple response, 496
- turgor pressure, 36
- turnover number, 187, 724
  
- uniport, 128
- ureides, 320
- UVR8, 466

862 Index

- vacuoles, 22–23
- velamen, 57
- vermiculite, 102
- vernalinalin, 434
- vernalization, 433
- vitamins, 171–172
- vivipary, 567
  
- wall pressure, 36
- Warburg effect, 244
- water potential (pronounced *sigh* and has the symbol  $\psi$ ), 38, 41
- water stress:
  - flooding, 555
  - water deficit, 548
  
- water use efficiency, 93
- wilting coefficient, 52
  
- xanthophyll cycle, 209
- xenobiotics, 130, 379
- xerophyte, 587
- xylem vessels, 67
- xylogenesis, 531–532
  
- Yang cycle, 497
  
- Z-scheme (for photosynthesis), 222
  
- ZEITLUPE, 453
- zinc-finger protein, 143, 554
- zwitterion, 345