

Subject Index

A

- A₀, 103, 105
A₁, 103, 105
AAA+ ATPases, 459, 462
AAG-box, 201
aaRSs. *See* Aminoacyl-tRNA synthetases (aaRSs)
ABA. *See* Abscisic acid (ABA)
ABA-insensitive 4 (*abi4*) mutant, 574
Abamine, 182
ABA receptor, 517
ABC-transporter, 161, 378
ABC-type complex, 140
ABI4. *See* Abscisic acid insensitive 4 (ABI4)
Abiotic stress, 364, 378, 394–398, 401, 406–409
Abnormal plastid, 463
ABRE element, 574
Abscisic acid (ABA), 8, 11, 182, 517, 538, 557, 648
Abscisic acid insensitive 4 (ABI4), 486, 509
Absorption at 830 nm, 594
Abutilon mosaic virus, 183
Ac115, 82
Acceptor complex, 84
Acceptor side mechanism, 646
Acclimation responses, 509
Acer negundo Hassk. var. *Odessanum*, 595
Acetyl-CoA, 135
Acidic (A) domain, 246
ACP. *See* Acyl carrier protein thioesters (ACP)
Actin, 174, 178, 179, 252
Actin cytoskeleton, 178
Acyl-ACP, 135, 159
Acyl-ACP thioesterase, 137
Acylation of PG, 161
Acyl carrier protein thioesters (ACP), 135
Acyl-CoA, 157, 159
Acyl-CoA synthetase, 137
Acyltransferases, 135
Adaptation, 649
Adenosine triphosphate (ATP), 22, 26, 29, 302
adg-1, 445
Adjustment loops, 511
ADL1, 143
A-domain, 246, 247, 254, 255
ADP-glucose pyrophosphorylase (AGPase), 554, 555, 562
Aesculus hippocastanum, 620, 623
Aging, 286–288, 290–291
Agroinfection, 177
AIF. *See* Apoptotic inducing factors (AIF)
AKR2A. *See* Ankyrin repeat-containing protein 2A (AKR2A)
ALA. *See* 5-Aminolevulinic acid (ALA)
ALAD. *See* 5-Aminolevulinic acid dehydratase (ALAD)
Albino 3 (ALB3), 88
Albino or *pale-green* (*apg*) mutants, 462
Allene oxide synthase, 521
Allium cepa, 173
Allosteric regulation, 146
 α -Carboxyl group of glutamyl-tRNA (Glu-tRNA), 603
 α -Tocopherol (vitamin E), 313, 339, 340, 343, 346, 355, 372
Alternative oxidase (AOX), 485, 488
Amaranthus lividus, 611
Aminoacyl-tRNA synthetases (aaRSs), 267
5-Aminolevulinic acid (ALA), 56, 57, 205, 364, 603, 606, 607
5-Aminolevulinic acid dehydratase (ALAD), 608, 610–611
Aminopeptidase I (API), 438
Amiprophosmethyl (APM), 178
Amitrole, 572
Amoeboid plastids, 172, 174, 181
Amyloplasts, 9, 191, 352, 354–355
Anabaena variabilis ATCC29413, 104
Anabolism, 555
Anchoring subunits, 82
Anchor protein, 29
Angiosperms, 41, 43, 48, 55, 57, 64
Anionic lipids, 135
Anion radical (O₂^{•-}), 531
Ankyrin repeat-containing protein 2A (AKR2A), 264
Anterograde, 485
Anterograde signaling, 505, 570–572, 585
Antheraxanthin, 341
Anthocyanin, 559
Anthocyanin biosynthesis, 582
Antioxidant systems, 512
Antioxidative potential, 382
Antirrhinum majus, 195
Antisense RNA (asRNA), 193
AOX. *See* Alternative oxidase (AOX)
AOX1a, 486
APETALA2-type transcription factor, 486
API. *See* Aminopeptidase I (API)
APM. *See* Amiprophosmethyl (APM)
Apoptosis, 291–292, 530
Apoptotic inducing factors (AIF), 488
Appearance of plastoglobuli, 350–352
Arabidopsis, 4, 136–138, 147, 162, 171–173, 176–182, 221, 229–231, 243–251, 253–255, 257–260, 262, 263, 266, 267, 297, 303, 552
Arabidopsis fluorescent (*flu*) mutant, 512
Arabidopsis thaliana, 6, 77, 103, 104, 106–108, 144, 156, 171, 200, 243, 244, 535, 573, 606, 609, 611, 613, 617, 624, 626
AraSP, 465

Aristida purpurea, 175
 Arrest of the chloroplast development, 463
 Ascorbate, 485
 Ascorbate peroxidases, 512
 asRNA. *See* Antisense RNA (asRNA)
 ATAB2, 81
AtATG12a, 440
AtATG12b, 440
AtΔ1-137 MGD1, 146
 ATG3, 439, 440
 ATG4, 439
 ATG5, 439, 440
atg5, 443
 ATG7, 439, 440
 ATG8, 439, 441
 ATG10, 439, 440
ATG11, 440
 ATG12, 439
 ATG16, 439
ATG25, 440
ATG26, 440
ATG28, 440
ATG30, 440
ATG32, 440
ATG101, 440
atg4a4b-1, 445, 446
atg mutant, 468
 atHsp93-III (ClpC2), 260
 atHsp93-V (ClpC1), 260
 AtMGD1, 147
 ATP. *See* Adenosine triphosphate (ATP)
 ATP/ADP ratio, 493
 ATPase activity, 180
 ATP synthase, 24, 62
 ATS1, 135
 ATS2, 135, 136
ats2, 136, 146
AtSIG1, 200
AtSIG2, 200
AtSIG3, 200
AtSIG4, 200
AtSIG6, 201
AtTIC40, 447
 atTic20-I, 247, 258
 atTic20-IV, 247, 258
 atToc33, 245–248, 253–255
 atToc34, 245–248, 254
 atToc90, 246–248
 atToc120, 246–248, 254
 atToc132, 246–248, 254, 255
 atToc132/120, 247, 248, 254
 atToc159, 246–248, 253, 254
 atToc75-III, 248, 253, 257, 258
 atToc75-IV, 248
 atToc75-V, 248, 249
AtTPPA, 553
AtTPSI, 553, 557, 560
AtTRE1, 560
Aurea mutants, 310

Aurea mutation influence, on the expression of nuclear *cab* genes, 595
Aurea-type leaves, 595–597
 Autophagosomes, 323, 329, 438, 439, 443–445, 447, 448
 Autophagy, 292, 329, 377, 422, 427, 429, 435–449, 468, 469
 Autophagy related genes (ATG genes), 436–443, 447, 448
Auxenochlorella protothecoides, 366
 Auxiliary proteins, 7
Avena sativa, 221, 223

B

BamA. *See* β -Barrel assembly machinery A (BamA)
 Bananas (*Musa cavendish*), 369
 Barley (*Hordeum vulgare*), 171, 175, 181, 223, 229, 231, 309, 319, 324, 365
 Barley mutant *albostrians*, 506
 β -Barrel, 248, 249, 257, 265
 β -Barrel assembly machinery A (BamA), 248
 Basic leucine zipper (bZIP), 651
 Bcl-2 family, 490
 BDM. *See* 2,3-Butanedione 2-monoxime (BDM)
 Beet, 173, 176, 182
 Bell pepper (*Capsicum annum*), 380
 β -Carotenes, 105, 342
 β -Glucanase, 651
 β -Glucosidase, 651
 β -Glycosidic bond, 142
Beta vulgaris, 173, 195, 219, 221, 223
 Billbergia, 339, 345, 347
 Binding sites for UDP-galactose, 144
 Biogenesis, 508
 Biogenic control, 506–509
 Biostatic(stasis), 286, 289
 Biosynthesis of chloroplast PG, 134
 Biotic stress, 180, 364, 378
 Bipartite leader sequences, 268
 Bipartite targeting signal, 265, 266, 268
 Blebbing, 319–327
 Blot hybridization, 223, 230
 BLRP. *See* Blue light responsive promoter (BLRP)
 Blue-green reversibility response, 514, 516
 Blue light responsive promoter (BLRP), 201
 Blumenol, 518
Brassica oleracea, 177
Brassica rapa, 177
 Breakdown of chlorophylls, 469, 519
 Brefeldin A, 268
 Broccoli (*Brassica oleracea*), 372
Bryopsis, 172
 BS. *See* Bundle sheath (BS)
 BtpA, 108
 Buds, 42, 43, 45, 47
 Bundle sheath (BS), 175, 176, 198
 2,3-Butanedione 2-monoxime (BDM), 179
 bZIP. *See* Basic leucine zipper (bZIP)

C

- Ca²⁺, 487, 489
 Cabbage, 177
 Ca²⁺-channels, 487
 Cadmium, 594
 CAH1. *See* Carbonic anhydrase 1 (CAH1)
 Calcium signaling, 261
 Calmodulin (CaM), 242, 261
 Calvin-Benson cycle, 9, 594
 Calvin cycle, 53
 CaM. *See* Calmodulin (CaM)
 Candidate protein, 509
 Canola (*Brassica napus*), 366
Capsicum annuum, 355
 Carbon availability, 557, 560, 561
 Carbonic anhydrase 1 (CAH1), 268
 Carbon signaling, 557
 Carboxyl-terminal processing protease (CtpA), 85
Carex curvula, 181
 Carotenoids, 105, 514, 595
 biosynthesis, 55–56, 507
 cleavage enzymes, 518
 geranylgeraniol diphosphate, 56
 isomerase, 518
 isopentenyl diphosphate, 56
 Caseinolytic protease, subunit C (ClpC), 260
 Ca²⁺ signature, 488
 Caspase, 488
 Caspase (endoprotease) activation, 298
Cassiope tetragona, 173
 Catabolism, 555
 Catabolites, 519
 Catalase, 534
 CDP-DAG, 136
 CDP-DAG synthetase, 142
 Cell death, 329, 376, 520
 Cell leakage, 298
 Cellular energy homeostasis, 651
 Cellular redox status, 487
 ceQORH. *See* Chloroplast envelope quinone
 oxidoreductase homologs (ceQORH)
 Ceramide, 161
Cercidiphyllum japonicum, 366, 382
 Cereal leaf gradient, 58
Cereus, 345
 CERT protein, 161
 CES. *See* Control by epistasy of synthesis (CES)
 CF₁γ subunit of chloroplast ATP synthase, 444
 Chaos, 26
 Chaperones, 242, 250–252, 255–260, 264, 459, 461–462
 Chaperonin, 120–123
 Chemical stressors, 594
 Chilling sensitivity, 111
 Chill-stress, 606, 611
 Chl *a/b* protein, 655
Chlamydomonas, 7, 77, 80, 92, 323, 324, 539
 C. moewusii, 216
 C. reinhardtii, 77, 102–104, 106–110, 134, 191,
 572, 576
 CHLD, 612
 CHLG, 625
 CHLH gene, 612, 613
 Chl-H subunit of Mg-chelatase (CHLH), 517, 612
 CHLI, 612
 CHLI/*Chlorina9*, 612
 Chlide. *See* Chlorophyllide (Chlide)
 CHLI-2 gene, 612
 Chlide(672), 620
 Chlide(684), 620
 Chlide *a*, 623, 625
 Chlide *a* oxygenase (CAO), 371, 623–625
 Chlide *b*, 623, 625
 Chlide dihydrogeranylgeraniol, 624
 Chlide geranylgeraniol, 624
 Chlide-LPOR-NADP⁺, 623
 Chlide-LPOR-NADPH, 623
 Chlide phytol, 624
 Chlide tetrahydrogeranylgeraniol, 624
 CHLI mutant, 612
 CHLM, 613
 CHLM gene, 613
 Chloramphenicol, 572, 574
Chloro-amyloplasts, 354
 Chlorophyll(s), 513, 601–628
 Chlorophyll *a*, 104, 590
 Chlorophyll *a/b* ratio, 61, 62, 314, 371
 Chlorophyllase, 372
 Chlorophyll *b*, 593
 Chlorophyll (Chl) biosynthesis, 41, 43, 44, 46,
 56–62
 Chlorophyll biosynthetic precursors, 572–574
 Chlorophyll *b* reductase, 371, 469, 625
 Chlorophyll *b* reduction, 370–371
 Chlorophyll cycle, 371
 Chlorophyll fluorescence, 594
 Chlorophyllide (Chlide), 491, 614
 chlorophyllide *a*, 57
 chlorophyllide *b*, 57
 3,8-divinyl, 54, 57
 monovinyl, 54, 57
 Chlorophyllide *a* oxygenase (CAO), 371, 623–624
 Chlorophyllin, 374
 Chlorophyll loss, 298
 Chlorophyll (Chl) synthase, 53, 57, 60, 61, 624
 Chlorophyll (Chl) turnover, 365, 382
 Chloroplast, 17–32, 118–126, 176, 179, 504
 biogenesis, 134, 459, 463, 575, 577, 579–585
 breakdown, 345
 derived vesicles, 466
 development, 5, 569–586
 dysfunction, 582, 585
 envelope, 140, 374
 envelope membranes, 180
 morphology, 176
 protein import, 179, 240–244, 248, 249, 251, 255,
 257–259, 262, 268
 proteolytic machineries, 457
 redox signals, 572, 576–577

- Chloroplast envelope quinone oxidoreductase homologs (ceQORH), 267
- Chloroplast import apparatus 2 (CIA2), 255
- Chloroplast import apparatus 5 (CIA5), 258
- Chloroplast lipid desaturation, 143
- Chloroplast-localized kinase FLN1, 511
- Chloroplast-localized sigma factor-binding protein 1 (SIB1), 203
- Chloroplast located LPP ϵ 1, 138
- Chloroplast located LPP ϵ 2, 138
- Chloroplast located LPP γ , 138
- Chloroplast located PAPs, 138
- Chloroplast nucleoid DNA-binding protease 41 kD (CND41), 421, 436, 437, 467
- Chloroplast periphery, 317–319
- Chloroplast secretory (cpSec), 458
- Chloroplast sensor kinase (CSK), 203
- Chloroplast signal recognition particle (cpSRP), 458
- Chloroplast-to-chromoplast conversion, 197
- Chloroplast twin-arginine translocation (cpTat), 458
- Chlororespiratory, 533
- CHLP* antisense, 627
- Chromoplast, 349–350, 352, 355
- CIA2. *See* Chloroplast import apparatus 2 (CIA2)
- CIA5. *See* Chloroplast import apparatus 5 (CIA5)
- Classes of signals, 506
- Class-I genes, 199
- Class-II genes, 199
- Class-III genes, 199
- Cleavage of the D1 protein, 464
- Clonal organisms, 293
- Clones, 293
- Clp, 260, 466
- ClpC. *See* Caseinolytic protease, subunit C (ClpC)
- Clp protease, 459–461, 470
- CLSM. *See* Confocal laser-scanning microscopy (CLSM)
- Cytoplasmic male sterility (*cms*), 486
- CND41, 218
- Co-chaperone, 255–257, 260
- CO₂ fixation, 63
- Com70, 462
- Com44/Cim44, 260
- Commelina communis*, 175
- Computed model, 144
- Concanamycin A, 444
- ‘Condensed’ conformations, 495
- Conditional *aurea* mutants, 595
- Confocal laser-scanning microscopy (CLSM), 170–172
- Confocal microscopy, 182, 183
- Conservative sorting, 264–266
- Conserved hypothetical open reading frames (*ycf*), 192
- Constitutive photomorphogenesis 1 (COP1), 571, 580–582, 585
- Contact sites, 256, 257
- Control by epistasy of synthesis (CES), 29, 83
- COPII vesicular, 143
- Coproporphyrinogen III (Coprogen III), 609, 611
- Coproporphyrinogen oxidase (Coprox, CPO), 609, 611
- Correlative controls, 289
- Co-translational membrane insertion of thylakoid, 89
- Co-translational transport, 250
- Cotyledon epidermal cells, 177
- Cotyledons, 177, 181, 231, 593
- CP43, 82–83, 89
- CP43 (*PsbC*), 75
- CP47, 82–83
- CP47 (*PsbB*), 75
- ^{cp}CK2. *See* Plastid-targeted casein kinase 2 (cpCK2)
- cpHsc70-1, 462
- cpHsp70, 259
- Cpn60, 242, 256, 461, 462
- CPO* gene, 611
- cpSec. *See* Chloroplast secretory (cpSec)
- cpSRP. *See* Chloroplast signal recognition particle (cpSRP)
- cpTat. *See* Chloroplast twin-arginine translocation (cpTat)
- CP47-RC complex, 85
- CRY1 (Cryptochrome 1), 579–583, 585
- CRY1COP1 interaction, 580
- CsA. *See* Cyclosporin A (CsA)
- Csd2* gene, 541
- CSK. *See* Chloroplast sensor kinase (CSK)
- C-terminal processing of D1 precursor, 85 subunit, 91
- CtpA. *See* Carboxyl-terminal processing protease (CtpA)
- Cutins, 137
- Cyanobacteria, 92
- Cyanobacterial PSII assembly machinery, 91
- Cyclic phosphorylation, 484
- Cyclophilin D, 489
- Cyclophilins, 89
- Cyclosporin A (CsA), 489, 492
- Cyperin, 610
- 2-Cysteine-peroxiredoxin (2CPA), 512
- Cysteine protease, 420, 422, 424–427
- Cyt b/f. *See* Cytochrome b/f (Cyt b/f)
- Cyt c. *See* Cytochrome c (Cyt c)
- Cyt f. *See* Cytochrome f (Cyt f)
- Cytochalasin D, 178
- Cytochrome *b6f*, 62
- Cytochrome b/f (Cyt b/f), 24
- Cytochrome c (Cyt c), 488, 490
- Cytochrome f (Cyt f), 489
- Cytochrome oxidase, 483
- Cytokinins, 289
- Cytoplasmic streaming, 178
- Cytoplasm-to-vacuole-targeting pathway (Cvt pathway), 438, 439
- Cytoskeleton, 174, 178, 179
- Cytosolic factors, 243, 250, 251

D

- D1, 80–82
- D1 (*PsbA*), 75
- D2, 81, 82

- D2 (PsbD), 75
DAG. *See* Diacylglycerol (DAG)
DAPI. *See* 4',6-Diamidino-2-phenylindole (DAPI)
DAPI staining, 217, 223, 229, 230
Daucic acid, 370
Dayflower, 175
DCP68, 218
D1 degradation, 464
Decapitation, 594
Deg, 465
Deg protease (DegP), 420, 421, 464–465, 470
Degradation
 of DNA, 229, 232
 of engulfed whole-chloroplasts within
 the vacuole, 469
 of stromal proteins, 466
 of thylakoid proteins, 337–358, 521
Degradational control, 519–521
Dehydrogenases, 483
Delayed greening 1 (DG1), 203
DEPC. *See* Diethylpyrocarbonate (DEPC)
De-repression, 514
Desaturases, 159
Deschampsia antarctica, 175
Desiccoplasts, 351
De-synchronization, 508
Determinate growth, 293
Detoxification, 381, 382
Development of plastids, 337–358, 521
DG1. *See* Delayed greening 1 (DG1)
DGD1, 141
dgd1, 163
DGD2, 141
dgd1dgd2, 134
DGDG. *See* Digalactosyl diacylglycerol (DGDG)
Diacylglycerol (DAG), 135–137, 140, 142,
 144, 156–158
 backbone, 135
 molecular species, 145
4',6-Diamidino-2-phenylindole (DAPI), 196
3-(3,4-Dichlorophenyl)-1,1-dimethylurea (DCMU),
 444, 594
Diethylpyrocarbonate (DEPC), 259, 262
Digalactosyl diacylglycerol (DGDG), 52, 62, 132–134,
 138, 143, 156, 159, 594
 synthase, 141, 148
 synthesis, 141, 159
Dimer, 85
2,2'-Dipyridyl, 371
Disorder, 20, 21, 23, 25, 27, 31, 32
Dissipative structures, 17–32
Dithiothreitol (DTT), 610
Diurnal rhythms, 299
3,8-Divinyl-chlode *a*, 618
divinyl (DV) Chl biosynthesis, 617
Divinyl Pchlode (DV-Pchlode), 613, 615
Divinyl reductase (DVR), 618
DNA cleavage, 302
DNA fiber-based fluorescence in situ hybridization
 (fiber-FISH), 195
DNA gyrases, 218
DnaJ-J8, 249, 257
Dominant negative, 179
Donor side mechanism, 646
Double Rossmann fold, 144
DOXP/MEP, 338
D1 protein, 102
Drosophila, 535
Drought, 517, 556, 557
 stress, 378
DsRed, 444, 445
DTT. *See* Dithiothreitol (DTT)
Dual genetic origin, 76
Dual-targeted(ing), 243, 266–268
DV-Chl. *See* Divinyl (DV) Chl biosynthesis
DV-Pchlode. *See* Divinyl Pchlode (DV-Pchlode)
DVR. *See* Divinyl reductase (DVR)
Dye exclusion, 302
Dynamin-related proteins (DRPs), 495
- E**
E-64, 425
Early import intermediates, 256
Early light-inducible proteins (ELIPS), 579
Early response to dehydration (ERDs), 466
Electrochemical reduction, 376
Electron microscopy, 12, 596
Electron transport, 143
Electron transport inhibitors, 509
Electrostatic interaction, 147
ELIPS. *See* Early light-inducible proteins (ELIPS)
Embryogenesis, 4
Embryo lethality, 461
Empty space, 326
END genes, 584–586
Endolytic protein, 299
Endomembrane system, 317, 324
Endoplasmic reticulum (ER), 7, 10, 137, 317, 318,
 327, 329
 ER network, 140
Endopolyploidization, 221, 230
Endosymbiont, 74
Endosymbiotic origin, 504
Endosymbiotic theory, 570
Energy signaling, 557
Energy status, 484
Entropy, 20–22, 28–32
Envelope, 22, 23, 25, 27–29, 31
Environmental cues, 509, 601–628
Environmental sensors, 487, 505
Environmental stress, 398, 641–660
Epidermal cells, 173, 175–183
Epidermal pavement cells, 175–177
Epimerisation of UDP-glucose, 146
EPR signals, 143
ER. *See* Endoplasmic reticulum (ER)
ERDs. *See* Early response to dehydration (ERDs)
Escherichia coli, 134, 190, 216
Escherichia coli MURG, 144

Ethylene, 182
 Ethylene-dependent gravitropism deficient
 and yellow-green 1 (EGY1), 465
 Etioplasts, 4, 39–64, 191, 223, 342–343, 350,
 352, 354
 differentiation, 41, 50, 51
 natural occurrence, 47
 senescence, 51, 52, 58
 Etioplast-to-chloroplast transition, 43, 55, 59–64, 504
Eucharis, 339
Euglena gracilis, 191
 Eukaryotic galactolipids, 137, 158
Euonymus fortune var. *radicans*, 595
 Excitation pressure, 648
 Exclusion barriers, 303
EXECUTER 1, 512
EXECUTER 2, 512

F

F_A , 105
 FAD2, 143
 FAD2 C18:1 desaturase, 137
 FAD7, 143
 FAD8, 143
 Fatty acid phytol esters, 372
 Fatty acyl units, 135
 F_B , 105
 Feed-back, 543
 Feed-back control, 364
 Feed-back regulation, 371
 Feed-forward, 540, 543
 Feed-forward control, 536–538
 Fenton reaction, 112
 Ferredoxin (Fd), 105, 261, 371, 374, 375
 Ferredoxin-NADP⁺ reductase (FNR), 242, 261
 Ferritin, 259
 Fiber-FISH. *See* DNA fiber-based fluorescence *in situ*
 hybridization (fiber-FISH)
 Fibrillin, 357
Ficus, 345, 347, 348, 356
 Fission and fusion events, 494
 FKBP, 89
 Floral initiation, 560
 Flowering, 560–561
 FLU, 603
 Fluorescence, 58
 Fluorescent chlorophyll catabolite (*pFCC*), 365
fluorescent (flu) mutants, 490, 577
 FNR. *See* Ferredoxin-NADP⁺ reductase (FNR)
 Formation of eukaryotic galactolipids, 139
 14-3-3, 242, 251
Fraxinus angustifolia Vahl, 620
Fraxinus excelsior L. var. *aurea*, 595
 Free energy, 21, 22, 30
 Freezing, 556
 Freezing tolerance, 142
 FtsH protease, 420, 421, 462–464, 466, 470
 Function of plastoglobuli, 355–357

Fuzzy onions-like (FZL), 92
 F_x , 103, 105
 FZL. *See* Fuzzy onions-like (FZL)

G

Gabaculine, 603
 Gaia, 20–22
 Galactolipids, 133, 156, 157, 243, 348, 591
 galactolipid galactosyltransferase, 142
 Galactosylation of DAG, 136
Galanthus nivalis, 175
 Galvestine-1, 141
 GAPs. *See* GTPase activating proteins (GAPs)
 G-box binding factor 1 (*GBF1*), 584
 G-domains, 246, 252, 253
 GEFs. *See* Guanine nucleotide exchange
 factors (GEFs)
 Gene, 19, 22, 27–29, 31
 expression, 555, 558, 560
 expression of these genes, 556
 network, 382
 Genet, 293
 Genetics, 18, 27–28
 Genome, 19, 22–24, 27, 28, 30
 Genomes *uncoupled (gun)* mutants, 507, 573, 574, 578,
 579, 581, 613
 Geranylgeraniol (GG), 54, 57, 61
 Geranyl-geranyl pyrophosphate (GGPP), 624
 Geranyl-geranyl reductase, 626
 Germination in soil, 43, 44
 Gerontoplast, 4, 18, 19, 23, 25, 27, 28, 31, 32, 191, 308,
 310, 317–319, 344–346, 349, 352, 381, 437,
 465, 505, 591
 GFP. *See* Green fluorescent protein (GFP)
 GG. *See* Geranylgeraniol (GG)
 GGPP. *See* Geranyl-geranyl pyrophosphate (GGPP)
 GH1 glycosyltransferase, 142
Ginkgo biloba, 372
GLK1. *See* Golden 2 like 1 (*GLK1*)
 Global (organism) vs. organ failure, 300
 Globular character, 352
 Glucose, 553
 Glucose 6-phosphate (G6P), 553
 Glucosylgalactosyldiacylglycerol, 134
 Glutamate 1-semialdehyde (*GSA*), 603, 607
 Glutamate semialdehyde aminotransferase (*GSA-AT*),
 603, 607, 627
 Glutamine synthetase, 444
 Glutamine synthetase II, 10
 Glutamyl-tRNA reductase (GluTR), 603, 608
 Glutamyl-tRNA synthetase (GluRS), 603
 Glutathione (GSH), 648
 Glutathione synthetase 1 and 2, 513
 GluTR. *See* Glutamyl-tRNA reductase (GluTR)
 Glycerolipid, 133
 Glycerol-3-phosphate, 135
Glycine max, 173, 231
 Golden 2 like 1 (*GLK1*), 575

Golgi, 160, 161, 318
 Grana, 42, 43, 47, 51, 54, 55, 59, 60, 62, 64, 74, 343
 stacks, 465
 thylakoids, 314
 Green fluorescent protein (GFP), 8, 170, 172, 176–178,
 436, 442, 444, 446
 Greening
 chlorophyll synthesis, 53, 59
 development of the photosynthetic
 apparatus, 62, 63
 lipid content, 62
 plant tissues, 590
 GroEL, 462
 Growth rate, 555
 GrpE, 260
 GSA, 606, 607
 GSA-AT. *See* Glutamate semialdehyde aminotransferase
 (GSA-AT)
 GSH. *See* Glutathione (GSH)
 GT28 glycosyltransferases, 140
 GTPase activating proteins (GAPs), 245
 GTPase (G) domain, 245, 246
 Guanine nucleotide exchange factors (GEFs), 245
 Guard cells, 177, 181, 557
 Guidance complex, 242, 250, 251
gun, 486
 Gymnosperms, 54, 57

H

Haem, 513
 HCF107, 82
 HCF136, 86–88
 HCF145, 106
 HCF173, 81
 hcf phenotype. *See* High chlorophyll fluorescence (hcf)
 phenotype
 Heat, 556
Heat shock protein 70 (HSP70) genes, 572, 573
 Heat-shock proteins (Hsps), 655
 Heat-stress, 606
 HEMA, 603
HEMA1, 606, 607
HEMA3, 606
 Herbicides, 364
 Herbivores, 370
 Heterotrimeric LHCII, 75
 Hexadecatrienoic acid (C16:3), 133
 Hexokinase (HXK), 561, 651
 High chlorophyll fluorescence (hcf) phenotype, 77
 Hip. *See* Hsp70-interacting protein (Hip)
 Hip/Hop, 260
 Histone-like proteins, 218
 Homeostasis, 301, 302, 459
Hordeum vulgare, 171
 Housekeeping protease, 459
Hoya, 345
 HR. *See* Hypersensitive response (HR)
 Hsp70, 242, 249–251, 256, 257, 259, 461

Hsp90, 242, 250–252, 461
 Hsp93, 242, 255, 257, 259–261, 266
 Hsp100, 459, 461
 HSP70B/CDJ2, 144
 Hsp93-III, 462
 Hsp70-interacting protein (Hip), 260
 Hsps. *See* Heat-shock proteins (Hsps)
 Hsp93-V, 462
 HXK. *See* Hexokinase (HXK)
 HY5 (long hypocotyls 5), 571, 580–583, 585
 Hydrogen peroxide (H₂O₂), 512, 531
 Hydrophobic interaction, 147
 Hydroxyl radical (HO•), 112, 531
 7-Hydroxymehtyl Chlide *a*, 625
 Hydroxymethylbilane, 609
 Hydroxymethyl Chl reductase, 371
 3-Hydroxy-3-methylglutaryl-CoA reductase, 555
 Hypersensitive response (HR), 379, 534
 Hypoxia, 487

I

IAP70, 462
ICK1. *See* Inhibitor of cyclin-dependent kinase 1
 IDPs. *See* Intrinsically disordered proteins (IDPs)
 IEP32. *See* Inner envelope protein, 32 kD (IEP32)
 Inhibitor of cyclin-dependent kinase 1, 520
 Immunophilins, 89–90
 Indeterminate growth, 293
 Indole acetic acid, 377
 Inhibition by UDP, 145
 Inner antenna system, 75, 82–83
 Inner envelope membrane, 241, 255–263, 265–268
 Inner envelope protein, 32 kD (IEP32), 267
 Intermembrane space, 242, 249, 250, 256, 257, 261,
 265–266, 268
 Inter-organellar signaling, 13
 Intramembrane proteases, 465
 Intraorganellar protein transport, 263–266
 Intrinsically disordered proteins (IDPs), 255
 Intrinsic degradation, 326
 Intron splicing, 537
 Invertase, 553
 Inverted repeat sequences (IR_A and IR_B), 192
 In vitro reconstitution of transfer, 160
 In vitro transcription assay, 205
 Ion channels, 162
 Ionizing radiation, 290
 Ionomycin, 261
 IPP. *See* Isopentenyl diphosphate (IPP)
Iris unguicularis, 178
Iris versicolor, 175
 Iron homeostasis, 259
 Iron-sulfur center, 262
 Iron-sulfur clusters, 259
 Iron-sulfur proteins, 259
 Iron transport, 259
 Irreversibility, 298–299
 Irreversible journey to death, 542

- Isochorismate, 520
 Isolation membrane, 439
 Isopentenyl diphosphate (IPP), 338
 Isoprenoid biosynthesis, 338
 Isoprenoids, 514
 Iteropary, 287
- J**
- JA. *See* Jasmonic acid (JA)
 Ja, 491
 Jasmonates (JAs), 538
 Jasmonic acid (JA), 11, 182, 377, 584, 586, 651
 J-domain, 249, 257
- K**
- Kinase 10/11, 651
- L**
- LACS, 160
 LACS9, 137
Lactuca sativa, 177
 Large single copy region (LSC), 192
 Lateral heterogeneity, 314
 Latrunculin B, 174, 178
 Leaf chlorosis, 461
 Leaf development, 559
 Leaf senescence, 519, 551–562
 Leaf shape, 558–559
 Leaf-variegation, 463
 Lemon (*Citrus limon*), 373
 Lesion mimic mutants, 379
 Lettuce, 177
Leucocjum aestivum, 175
 Leucoplast, 173, 176, 352, 354–355
 LHC. *See* Light harvesting complex (LHC)
Lhcb, 486
 LHCPs. *See* Light harvesting chlorophyll a/b proteins (LHCPs)
 Light–dark cycles, 44–46, 59
 dark phase of, 44
 Light-dependent protochlorophyllide reductase (LPOR), 109–110, 617
 Light harvesting chlorophyll a/b proteins (LHCPs), 341, 342
 Light-harvesting complex (LHC), 314, 317, 365
 Light-harvesting complex I (LHCI), 102
 Light-harvesting complex II (LHCII), 103, 650
 Light-independent protochlorophyllide reductase (DPOR), 110
 Light intensity
 high light, 47, 62
 low light, 43
 Light microscopy, 592
 Light-regulated genes, 571, 583–585
 Light signaling, 558, 559
Ligustrum ovalifolium Hassk. var. *aureum*, 595
 Lincomycin, 572, 574, 579–584
 Linolenic acid (C18:3), 133
 Lipid composition of plastoglobuli, 346–350
 Lipid homeostasis, 146
 Lipid hydroperoxides, 521
 Lipid peroxidation, 520
 lip1 mutant, 617
 Lipoxygenase (LX), 538
 Liquidambar orientalis, 366
 Lon, 466
 Long chain acyl CoA synthase, 159
 Lon protease, 470
 Low molecular mass intrinsic protein, 75
 Low PSII assembly 1 (LPA1), 88
 Low PSII assembly 2 (LPA2), 89
 Low PSII assembly 3 (LPA3), 89
 LPAT2, 137
 lpat2, 146
 LPAT3, 137
 LPOR. *See* Light-dependent protochlorophyllide reductase (LPOR)
 LPPε1, 138
 LPPε2, 138
 LPPγ, 138
 LSC. *See* Large single copy region (LSC)
 LX. *See* Lipoxygenase (LX)
 Lyso lipids, 157, 160
 Lyso-PA, 135
 Lyso-PC, 157, 160
 Lysophosphatidic acid-acyl CoA acyltransferase, 137
 Lytic vacuoles, 466
- M**
- Macroautophagy, 438, 440, 443, 447, 448
 Magnoglobuli, 345
 Maize (*Zea mays*), 174–176, 366
 Malate valve, 485
 Malonyl-coenzyme A, 377
 Marker of senescence, 313
 Mass spectrometry, 365
 Matrixules, 495, 496
 Maximum entropy production, 21, 26, 29
 Mbb1, 83
 M cells. *See* Mesophyll (M) cells
 MDAR. *See* Monodehydro-ascorbate reductases (MDAR)
 Medicago truncatula, 223, 229
 Mehler reaction, 533
 MeJa, 489, 491, 492
 Membrane bound polysomes, 91
 Membrane contact sites, 140
 Membrane (M) domain, 246, 265
 Membrane protein, 145
 Membranes change, 290
 Membrane transport, 263
 MEP. *See* Methylerythritol phosphate (MEP) pathway
 Meristem, 45, 46, 50, 51, 58
 Mesophyll (M) cells, 172, 173, 175–182, 198, 221, 230, 517
 Mesophyll chloroplasts, 175, 180

- Mesophyll protoplasts, 174
 Metabolic, 19, 23–28, 31, 32
 channeling, 374
 pathways, 519
 Metabolism, 18, 21–23, 25–26
 Metabolites, 506
 Metabolite signature, 519
 Metabolome, 18
 Metal coordination, 145
 Methylerythritol phosphate (MEP) pathway, 514
mex-1, 445, 447
 MGD1. *See* Monogalactosyl diacylglycerol synthase 1 (MGD1)
MGD1, 140
mgd1-2, 141
MGD2, 140
MGD3, 140
 MGD dimerization, 145
 Mg-dechelation, 374
 MGDG. *See* Monogalactosyl diacylglycerol (MGDG)
 MGDG-UDP-galactose galactosyltransferase, 141
 MGD inhibitor, 141
mgd1-1 mutant, 140
 MGD sequences, 144
 Mg-protoporphyrin IX (Mg-PPIX/Mg-ProtoIX), 513, 539, 612, 613
 Mg-protoporphyrin IX monomethyl ester (MPE), 612, 613
 Mg-protoporphyrin IX monomethylester cyclase, 613
 Mg-protoporphyrins, 613
 Mg-tetrapyrrole, 612
 Microarray, 32
 Microautophagy, 438, 439, 447
 Microfilaments, 178, 179
 Microinjection, 177
 Micropexophagy apparatus (MIPA), 439
 microRNA (mRNA), 542
 Microtubules, 179
 Millisecond delayed fluorescence, 594
 Minor antenna proteins, 75
 Minor mistargeting, 266
 MIPA. *See* Micropexophagy apparatus (MIPA)
 Mitochondria, 159, 160, 231
 associated microsomes, 161
 Mitochondrial ATP supply, 484
 Mitochondrial complex I, 535
 Mitochondrial outer membrane, 299
 Mitochondrial translation, 507
 Mitofusin, 162
 Mitophagy (mitochondria specific autophagy), 438, 440
 Mitotic senescence, 292
 Mobile jacket, 172
 Mobile phase, 172
 Monocarpic(y), 287
 organisms, 288
 Monodehydro-ascorbate reductases (MDAR), 488
 Monogalactosyl diacylglycerol (MGDG), 52, 53, 55, 62, 132–134, 137, 143, 157, 256, 594
 synthase, 140, 144, 145, 157
 synthesis, 163
 Monogalactosyl diacylglycerol synthase 1 (MGD1), 144–148, 265
 Monomeric PSII core complex, 85
 Monopyrrole, 370
 Monovinyl Pchl_{ide} (MV-Pchl_{ide}), 615
 Morphology, 495
 Motor complex, 242, 247, 255, 258, 262
 Motor model, 252
 MPE cyclase, 612
 mtHsp70, 259
 Multimeric complexes, 7
 MURG, 144
 Mycorradicin, 518
 Myosin, 179, 180
 Myosin ATPase activity, 179
 Myosin XI, 179, 183
Myrothamnus flabellifolia, 552
- N**
 Nac2, 81
nad7, 486
 NADH dehydrogenase (NDH), 103
 NADPH-Pchl_{ide}, 614
 NADPH:protochlorophyllide oxidoreductase (POR)
 dark-operative NADPH:protochlorophyllide oxidoreductase (DPOR), 54
 import, 53
 light-dependent NADPH:protochlorophyllide oxidoreductase (LPOR), 41, 52
 oligomers, 52, 54, 55, 64
 POR-A, 53, 62, 63
 POR-B, 53
 POR-C, 53
 ternary complexes, 47, 55, 58, 62
 NADP-malic enzyme (NADP-ME), 111
 NADP⁺/NADPH ratio, 261
 Naphthoquinone, 105
 Naproxen, 182
 NCC. *See* Nonfluorescent chlorophyll catabolite (NCC)
 NCED activity, 519
 ncRNAs. *See* Non-coding RNAs (ncRNAs)
ncs, 486
 NDH. *See* NADH dehydrogenase (NDH)
 Ndh complex, 533
ndh gene, 533, 536–538
 Necrogenesis, 287, 289
 Necrosis, 291–292
 Necrotic plastid, 18
 Negative senescence, 293
 Negligible senescence, 293
 Neoxanthin, 347
 NEP-dependent genes, 198
 NEP interacting proteins (NIPs), 206
 NEP promoters, 204
 NEP to PEP switch, 205
 Network, 543
Nicotiana
 N. benthamiana, 172, 177, 179, 182, 183
 N. rustica, 173, 177, 591
 N. tabacum, 170, 229, 625

NIPs. *See* NEP interacting proteins (NIPs)
 Nitrate reductase, 555
 Nitric oxide, 489
 Nitrogen fixation, 482
 Non-canonical protein transport to chloroplasts, 266–268
 Non-coding RNAs (ncRNAs), 193
 Non-equilibrium, 20–22, 31, 32
 Nonfluorescent chlorophyll catabolite (NCC), 365
 Non-mevalonate pathway, 338
 Non-photosynthesis genes, 510
 Non-photosynthetic preproteins, 246, 258
 Non specific lipid transfer proteins (nsLTPs), 160
 Norflurazon, 177, 182, 507, 572–574, 578, 579
 Normalizing data for comparison, 298
 NPC4, 138
 nsLTPs. *See* Non specific lipid transfer proteins (nsLTPs)
 Nuclear encoded phage-type RNA polymerase, 6
 Nuclear-encoded plastid RNA-polymerases, 219
 Nuclear-encoded RNA polymerase, 199
 Nuclear ploidy levels, 219, 221, 232
 Nucleoids, 5, 195
 Nutrients, 381
 NYC1-like (NOL), 469

O

¹⁸O₂, 491
 Octatricopeptide repeat (OPR) motif, 83
 OEC. *See* Oxygen evolving complex (OEC)
Oenothera hookeri, 195
 OEP7/14. *See* Outer envelope protein, 7/14 kDa (OEP7/14)
 OEP61. *See* Outer envelope protein, 61 kDa (OEP61)
 OEP64. *See* Outer envelope protein, 64 kDa (OEP64)
 OEP80. *See* Outer envelope protein, 80 kDa (OEP80)
 (C18:1) oleoyl-ACP, 135
 Oligogalactolipids, 141, 142
 Oncosis, 292
 Onion, 173, 179
 Open system, 20, 30
 Operating efficiency of PSII (Φ PSII), 557
 Operational control, 509–519
 Ophiobolin A, 261
 OPR motif. *See* Octatricopeptide repeat (OPR) motif
 Optical tweezers, 162
 Orange (*Citrus sinensis*), 372
 Order, 20–23, 25, 27–32
 Organellar, 505
 genes, 485
 Organism death, 303
 Organization affects membrane activity, 134
 Orthodox, 495
 Oryzalin, 178
Oryza sativa, 173, 229
OsCAO1, 623
OsCAO2, 624
 Osmiophilic globules, 319
 Osmiophilic plastoglobuli, 338–343
 Osmotic stress, 378
OsSIG1, 200

OTP51, 106
otsA, 556–558
otsB, 556, 557, 559, 561
 Outer envelope membrane, 243–256, 264–266, 268, 317
 Outer envelope protein, 7/14 kDa (OEP7/14), 264
 Outer envelope protein, 61 kDa (OEP61), 252
 Outer envelope protein, 64 kDa (OEP64), 250
 Outer envelope protein, 80 kDa (OEP80), 248, 249, 265
 Oxidative stress, 395–398, 401–403, 406, 407, 595
 Oxygen evolution, 63
 Oxygen evolving complex (OEC), 53, 62, 75
 Oxylipins, 137, 538
Oxyria digyna, 172–174, 176, 178, 179, 181
 Oxysterol binding protein, 161

P

P700, 103, 105, 111
 PA. *See* Phosphatidic acid (PA)
 PAH1, 138
 PAH2, 138
 (C16:0) palmitoyl-ACP, 135
 PAM68, 88
 PAO pathway, 364, 370, 377
 PAP. *See* Phosphatic acid phosphatase (PAP)
 Particle bombardment, 174, 175, 177, 182
 PA synthesis, 146
 Pathfinder kinase, 202
 Pathogen infection, 203, 376, 378
 PC. *See* Phosphatidylcholine (PC)
 PCD. *See* Programed cell death (PCD)
 Pchl_{ide}(650), 620
 Pchl_{ide}(F632/F657), 621
 PCR. *See* Polymerase chain reaction (PCR)
 PC-synthase, 161
 PC synthesis, 157
 PDMs. *See* Prat A defined membranes (PDMs)
 PE. *See* Phosphatidylethanolamine (PE)
 Pea (*Pisum sativum*), 158, 161, 162, 218, 229, 380
 Pear (*Pyrus communis*), 366
 PEG. *See* Polyethylene glycol (PEG)
 PEG-mediated transfection, 174, 176
 PEND. *See* Plastid envelope DNA-binding protein (PEND)
 Pentatricopeptide repeat (PPR) protein, 203, 508, 537
 PEP. *See* Plastid encoded plastid RNA polymerase (PEP)
 Peptidase, 263, 265
 Peptidyl-prolyl isomerases (PPIase), 89
 Peribacteroid, 159
 Periorganellar, 11
 Periplasmic factor, 91
 Periplastic space, 317–319
 Permeability barriers, 303
 Permeability transition pore (PTP), 489
 Permease, 163
 Permease in chloroplasts 1 (PIC1), 259
 Peroxidase (PX), 531
 Peroxisomes, 487, 496
 Peroxules, 496
 PET. *See* Photosynthetic electron transport (PET)

- Petunia, 170, 172, 176, 177
Petunia hybrida, 170
 Pexophagy (peroxisome specific autophagy), 438–440
 PG. *See* Phosphatidyl glycerol (PG)
 pgm, 445
 PG synthesis, 142
 Phagocytosis, 302
 Phase contrast, 171
 Phase contrast microscopy, 172, 176, 178
Phaseolus vulgaris, 173, 591
 Phenyltetrazolium chloride (TTC), 302
 Pheophorbide (PPD), 377
 Pheophorbide, 369
 Pheophorbide *a* oxygenase (PAO), 470
 Pheophytinase, 373
 Pheophytin pheophorbide hydrolase (PPH), 470
 Phosphatase Sal 1, 519
 Phosphate limited growth, 159
 Phosphatic acid phosphatase (PAP), 138, 163
 Phosphatidic acid (PA), 135, 138, 146, 158, 163
 Phosphatidylcholine (PC), 133, 137, 157, 158, 160
 Phosphatidylethanolamine (PE), 439
 Phosphatidyl glycerol (PG), 132, 133, 137, 143, 146, 156, 158
 Phosphatidylglycerol-phosphate phosphatase, 142
 Phosphatidylglycerol-phosphate synthase, 142
 Phosphatidylinositol (PI), 133, 158
 Phosphatidylserine residues, 299
 Phospholipase C (PLC), 138
 Phospholipase D (PLD), 138, 157, 163
 Phosphonucleotide 3'-phosphoadenosine 5'-phosphate (PAP), 519
 Phosphorylation, 202
 Phosphorylation cascade, 511
 Photo acoustic, 26
 Photoinhibition, 111
 PSI, 102
 PSII, 532
 Photomorphogenesis, 653
 Photomorphogenic programme, 504
 Photooxidation, 47, 55, 61, 63, 64
 Photooxidation of the plastoquinone-9 pool, 356
 Photooxidative damage, 654
 Photooxidative stress (POS), 507, 531
 Photophosphorylation
 cyclic, 63
 non-cyclic, 63
 Photoprotective function, 517
 Photoreceptor, 653
 Photostasis, 650
 Photosynthetic activity, 40, 55, 60, 62–64
 Photosynthetic electron flow, 506
 Photosynthetic electron transport (PET), 509, 531
 Photosynthetic mutants of higher plants, 77
 Photosynthetic reducing equivalents, 484–485
 Photosystem I (PS I), 8, 24, 29, 63
 Photosystem II (PS II), 8, 24, 26, 29, 53, 61–63, 135
 Photosystem stoichiometry, 110
 Phycobilisome, 103, 109
 Phycoerythrobilin, 375
 Phylloquinone K1, 343
Physalis alkekengi, 355
Physcomitrella patens, 172, 182, 199
 Physiological definition, 284
 Phytochromobilin, 375, 513
 Phytoene, 55, 56
 Phytoene desaturase, 507
 Phytoferritin, 48
 Phytoferritin inclusions, 593
 Phytohormones, 519
 Phytol, 54, 57, 61, 63
 PI. *See* Phosphatidylinositol (PI)
 PIC1. *See* Permease in chloroplasts 1 (PIC1)
 Pigment biosynthesis, 506
 Pigment-protein complex, 102
 PI myo-inositol exchange, 161
Pinus
 P. ponderosa, 173, 174
 P. thunbergii, 192
Pisum sativum, 104, 192
 PLAM. *See* Plastid associated membranes (PLAM)
 Plant growth, 558–559
 Plant homeodomain (PHD) type transcription factor, 509
 16:3 plants, 156, 158
 Plasma membrane, 159
Plasmodiophora brassicae, 554
 Plastid(s), 4, 505
 amyloplast, 41, 50–52
 biogenesis, 4
 chloroplast, 39–64
 chromoplast, 41
 differentiation, 40, 41, 48, 50, 58, 461
 division, 43, 223, 232
 elaioplast, 41
 etio-chloroplast, 42, 43, 45, 47, 52, 54, 59, 63, 64
 genome, 6
 gerontoplast, 41
 leucoplast, 41
 morphology, 171, 173, 181, 182
 nuclei, 195
 nucleoids, 216, 218, 219
 number, 48
 periphery, 317
 pre-granal plastid, 51
 proplastid, 41, 43, 50–52, 58, 64
 proteinoplast, 41
 ribosome, 49
 senescing chloroplast, 41
 signaling, 595
 transcription, 507
 types, 40, 41
 young chloroplast, 43, 44, 59
 Plastid associated membranes (PLAM), 161–162
 Plastid DNA (ptDNA), 195, 536
 Plastid DNA replication, 223
 Plastid encoded plastid RNA polymerase (PEP), 6, 197, 199, 219
 core subunits, 199
 PEP-specific inhibitors, 203

- Plastid-encoded RNA polymerase, 511
 Plastid envelope DNA-binding protein (PEND), 218
 Plastid envelope membranes, 170
 Plastidial translation, 200
 Plastidic type I signal peptidase (Plsp), 459
 Plastid-lipid associated-protein (PAP), 357
Plastid protein import 1 (ppi1), 245, 246, 249, 253, 256
Plastid protein import 2 (ppi2), 246, 248, 253–255
Plastid protein import 3 (ppi3), 246, 254
 Plastid-targeted casein kinase 2 (cpCK2), 202
 Plastid-targeted GFP, 172, 175
 Plastid transcriptionally active chromosome (pTAC), 196
 Plastocyanin, 62, 105
 Plastoglobules, 310, 319, 372
 Plastoglobuli, 9, 23, 25, 41, 48, 49, 51, 52, 59, 337–358, 591
 Plastoglobulin, 357
 Plastoglobulus, 350
 Plastome, 505
 Plastome copies, 219, 221, 223, 229, 230, 232
 Plastome copy numbers, 216, 219, 221, 229, 232
 Plastoquinol-9 (PQ-9H₂), 343, 346, 355, 356
 Plastoquinol PX, 533
 Plastoquinone, 158, 532
 Plastoquinone-9, 339, 340, 343, 355
 Plastoquinone pool, 135, 202, 510
 Plastosomes, 313
 PLB. *See* Prolamellar body (PLB)
 PLC. *See* Phospholipase C (PLC)
 PLD. *See* Phospholipase D (PLD)
 PLD/PAP, 138
 PLD ζ 1, 138
 PLD ζ 2, 138, 148
pld ζ 2 knock out mutant, 148
 PLD ζ s, 138
Plectonema boryanum, 110
 PmgA, 110
Poa alpina, 181
 Points of no return, 296–297
 Pollen tube growth, 141
 POLRMT, 206
 Polycarpic organisms, 287
 Polycarpic plants, 301
 Polycarpy, 287
 Polycistronic pre-RNAs, 190
 Polycistronic transcription units, 77
 Polyethylene glycol (PEG), 181, 182
 Polymerase chain reaction (PCR), 230
 Polypeptide transport associated (POTRA), 248
 Polyribosome, 80
Polytrichum formosum, 173, 182
 Polyunsaturated fatty acid (PUFA), 520
 Poplar, 176
Populus alba, 176
 POR. *See* Protochlorophyllide oxidoreductase (POR)
 PORA, 616
 PORB, 616
PORB mutants, 617
PORB/PORC, 617
PORC gene, 616
POR gene, 616, 617
 POR-Pchl_{ide}-NADPH, 618–621
 (POR-Pchl_{ide}-NADPH)₂, 615
 (POR-Pchl_{ide}-NADPH)_n, 615, 621
 Porphobilinogen (PBG), 608
 Porphobilinogen deaminase (PBGD), 609, 611
 POS. *See* Photooxidative stress (POS)
 Post-harvest, 364, 373
 Post-import pathway, 265, 266
 Post-transcriptional regulation, 191
 Post-transcriptional RNA processing, 191
 Post-translational transport, 250
 POTRA. *See* Polypeptide transport associated (POTRA)
 PPDK. *See* Pyruvate orthophosphate dikinase (PPDK)
ppi1. *See* *Plastid protein import 1 (ppi1)*
 PPIase. *See* Peptidyl-prolyl isomerases (PPIase)
PPOX1 gene, 610
PPOX2 gene, 610
PPOX2 L, 610
PPOX2 S, 610
 PPR protein. *See* Pentatricopeptide repeat (PPR) protein
 PrataA, 91
 Prata A defined membranes (PDMs), 92
 Pre-autophagosomal structure (PAS), 439
 Precursors, 457
 PreP. *See* Presequence protease (PreP)
 Preproteins, 241–248, 250–265, 267, 268
 Presequence protease (PreP), 262, 458
 Primary active transport, 378
Prochlorothrix hollandica, 624
 Programed cell death (PCD), 9, 291–292, 488–491, 493, 530
 Prokaryotic lipids, 135
 Prokaryotic pathway, 156
 Prolamellar body (PLB), 7, 217, 342, 591
 dispersal, 60
 function, 64
 lattice type
 open prolamellar body, 49, 50, 59
 spiral/centric, 49, 50
 square lattice, 48, 50
 wurtzite, 50
 zincblende (diamond), 50
 low-light prolamellar body, 47
 molecular composition
 lipids, 52, 62
 pigments, 53–55
 proteins, 52, 53, 55
 prothylakoid body, 52–55
 structure, 47, 52, 54, 55
 Promoter level, 518
 Proplastids, 4, 18, 22–26, 28–30, 32, 174, 175, 191, 223, 342, 352–354, 504, 593
 Proplastid-to-chloroplast transition, 43, 62
 Proteases, 13, 371, 381, 454
 Proteasome, 460
 Protein(s), 493
 assembly, 120, 122
 degradation, 454, 457–465
 degradation during leaf senescence, 465–470

- import, 457–459
 - interaction, 371, 374
 - maturation, 454, 461
 - misfolding, 459
 - quality control, 459
 - quality control in membranes, 462–464
 - synthesis, 118, 120, 125, 461
 - transport, 457
 - Proteolysis, 454
 - Proteolytic cleavage, 509
 - Prothylakoid
 - lipid composition, 52
 - pigment composition, 53–55
 - protein composition, 52
 - Protochlorophyllide (Pchl_{id})
 - divinyl, 57
 - monovinyl, 57
 - photoreduction, 53, 54, 61
 - spectral forms
 - non-photoactive, 51, 58, 61
 - photoactive, 51, 58, 59, 61, 62
 - synthesis, 54
 - Protochlorophyllide oxidoreductase (POR), 590, 614, 652
 - Proto IX. *See* Protoporphyrin IX (PPIX)
 - Protoplasts, 162, 176
 - Protoporphyrin IX (PPIX), 376, 482, 489, 608, 610–612
 - Protoporphyrinogen oxidase (Protox), 610, 611
 - Protubular body, 353
 - Psb27, 90
 - Psb28, 90
 - Psb29, 90
 - psbA*, 232
 - psbA* mRNA translation, 80
 - psbA* translation initiation, 80
 - psbA* 5' UTR, 80
 - psbB-psbT-psbH-petB-petD* transcript, 82
 - psbC*, 83
 - psbD* mRNA, 81–82
 - PsbH*, 82–83
 - Pseudo-cyclic phosphorylation, 484
 - Pseudomonas syringae*, 378
 - PS I. *See* Photosystem I (PS I)
 - PS II. *See* Photosystem II (PS II)
 - PSII assembly, 84
 - PSII assembly factors, 84, 86
 - PSII complex, 8
 - PSII complex assembly, 84–86
 - PSII core complex, 75
 - PSII reaction center-like assembly complex, 84
 - PSII repair, 465
 - PSII repair cycle, 464
 - PSII repair proteins, 90
 - pTAC. *See* Plastid transcriptionally active chromosome (pTAC)
 - PTP. *See* Permeability transition pore (PTP)
 - PUFA. *See* Polyunsaturated fatty acid (PUFA)
 - PX. *See* Peroxidase (PX)
 - Pyrenophora teres*, 318
 - Pyropheophorbide, 369, 377
 - Pyruvate, 56
 - Pyruvate orthophosphate dikinase (PPDK), 111
- Q**
- qPCR. *See* Quantitative real-time PCR (qPCR)
 - QTL analysis, 560
 - Quality control of proteins, 454
 - Quantitative real-time PCR (qPCR), 230
- R**
- RAB75, 447
 - Ramets, 293
 - Ranunculus glacialis*, 172, 173, 181
 - Raphanus sativus*, 347
 - Ratio chlorophyll a/b, 341
 - RB38, 80
 - RB47, 80
 - RB55, 80
 - RB60, 80
 - RbcL, 444
 - RBCS, 8, 444
 - RBP40, 81
 - RBP63, 81
 - RCB/RCV, 323, 324, 329
 - RCBs. *See* Rubisco containing bodies (RCBs)
 - Reaction center, 75
 - Reactive oxygen species (ROS), 11, 291, 364, 393–410, 483, 485, 487, 488, 490–494, 506, 511, 530, 644, 658
 - Red chlorophyll catabolite, 366
 - Redifferentiation of gerontoplasts, 593
 - Redox homeostasis, 12, 649
 - Redox-imbalanced (*rimb*) mutants, 512
 - Redox poisoning, 533
 - Redox potential, 643
 - Redox-regulation, 80–82
 - Redox signals, 510
 - Redox state, 202
 - Redox status, 487
 - Reduced glutathione, 513
 - Regeneration, 293
 - Regreening, 13, 591
 - Release, 509
 - Remobilization, 381, 519
 - Reporter, 521
 - Repressive signal, 508
 - Respiratory chain, 482
 - Retrograde regulation, 485
 - Retrograde signaling, 382, 485–487, 505
 - Reversed-phase HPLC, 366
 - Ribulose-1,5-bisphosphate carboxylase oxygenase (Rubisco), 436–437, 447, 466
 - Rice, 173, 175, 176, 229
 - Ricinosomes, 323, 426, 427
 - Rieske, 262
 - Rieske type oxygenase, 374
 - Rifampicin, 203

- RNA maturation, 461
 RNA(R)TPR proteins, 82
 ROS. *See* Reactive oxygen species (ROS)
 Rosette leaves, 231
 ROS signaling, 379
 RpaB, 111
rpo genes, 199
 RPOT_m, 204
 RPOT_{mp}, 204
 RPOT_p, 204
 Rubisco, 4, 8, 9, 62, 117–126, 170, 231, 317, 319, 323, 331
 Rubisco containing bodies (RCBs), 9, 323, 331
 Run-on assays, 231
 Rye, 229
 Rye grass (*Festuca pratensis*), 371
- S**
- SA. *See* Salicylic acid (SA)
Saccharum officinarum, 175
 S-Adenosyl-L-methionine:Mg-PPIX methyltransferase (SAM-MgProtoMTF), 613
 SAG. *See* Senescence associated genes (SAG)
 SAG12, 420, 424, 427, 428, 468, 561
 Salicylic acid (SA), 11, 182, 651
 Salt, 556
 Salvage nutrients, 466
 SAM-MgProtoMT, 613
 SAR. *See* Systemic acquired resistance (SAR)
Sarothamnus scoparius, 349, 355
 SAVs. *See* Senescence associated vacuoles (SAVs)
 SCABRA3, 204
 Scattered nucleoid type (SN-type), 216
ScTSP1, 558
 SDGs. *See* Senescence down-regulating genes (SDGs)
 SDR superfamily. *See* Short-chain dehydrogenase/reductase (SDR) superfamily
 Secretary (Sec), 263, 266
 Secretary compartment, 160
 Seed aging, 291
 Seed bank, 291
 Seedling growth, 559
 Seedlings, 504
Selaginella lepidophylla, 552
 Self-organization, 20–24, 26, 27, 29–32
 Semelapary, 287
 Semi-autonomous, 505
 Senescence, 4, 284, 286–291, 393–410, 435–449, 492–493, 556, 560–561, 590, 657
 Senescence associated genes (SAG), 534
 Senescence associated vacuoles (SAVs), 9–10, 323, 331, 417–429, 442, 468
 Senescence down-regulating genes (SDGs), 659
 Senescence syndrome, 286, 298
 Sethoxydim, 353
sex-1, 445
 SFDA. *See* Sulfonylfluorescein diacetate (SFDA)
 SFR2, 141
 Shade chloroplasts, 341–342
 Shibata shift, 61, 618–623
 Shikimate-phenylpropanoid pathway, 520
 Short-chain dehydrogenase/reductase (SDR) superfamily, 81, 614
 Short-lived plants, 291
 SIB1. *See* Chloroplast-localized sigma factor-binding protein 1 (SIB1)
 Sigma factor, 199
 Sigma heterogeneity, 200
 Sigma70-type promoter, 199
 Signal recognition particle (SRP), 245, 263
Silene acaulis, 181
 Singlet oxygen (¹O₂), 376, 490–491, 512, 531
 Singlet–singlet transfer, 645
 Sink-source transition, 555
 Small copy region (SSC), 192
 Small non-messenger RNA (snmRNA), 193
 SMP domain, 162
 snmRNA. *See* Small non-messenger RNA (snmRNA)
 Snowdrop, 175
 Snowflake, 175
 SNRK 1. *See* Sucrose non-fermenting 1-related kinase 1 (SNRK 1)
 SOD. *See* Superoxide dismutase (SOD)
Solanum lycopersicum, 170
 Soybean (*Glycine max*), 173, 180, 223, 231, 380, 593
 Spatiotemporal assembly, 13
 Spatiotemporal pathway, 91–93
Spinacia, 221
 S. oleracea (Spinach), 140, 144, 173, 176, 178, 223, 366
 Spontaneous changes, 290
 Spontaneous insertion pathway, 263
 Spontaneous pathway, 263, 458
 SPP. *See* Stromal processing peptidase (SPP)
 SppA protease, 470
 spRNAP-IV, 206
 SQDG. *See* Sulfoquinovosyldiacylglycerol (SQDG)
 Squash (*Cucurbita pepo*), 373
 70S ribosomes, 505
 SRP. *See* Signal recognition particle (SRP)
 SSC. *See* Small copy region (SSC)
 Stacking degree, 341
 Starch, 555, 562
 granule formation, 170
 granules, 327
 synthesis, 554–555
 Starvation, 555, 557, 561
 State transition, 76, 109
 Stay-green mutants, 10, 371, 380, 470
 Stay-green phenotype, 297
 (C18:0) stearoyl-ACP, 135
 Stearoyl-ACP Δ9 desaturase, 135
 Stereospecificity, 375
 Sterol regulatory element binding protein site 2 protease (SREBP S2P protease), 465
 Sti1. *See* Stress-inducible 1 (Sti1)
 Stoichiometric synthesis, 12
 Stoichiometry, 244
 of TOC complex components, 244

Stomatal closure, 517
 Stomatal guard cells, 175–177
 Stromules, 494
 Stop-transfer pathway, 265
 Strawberry (*Fragaria x ananassa*), 374
 Stress, 555–557, 561
 conditions, 512
 protectant, 552, 555
 response, 556
 signaling pathways, 182
 tolerance, 555–557
 Stress-inducible 1 (Sti1), 260
 Strigolactones, 517, 518
 Stroma, 24, 28, 29, 326
 Stroma lamellae, 74
 Stromal jacket, 174
 Stromal processing peptidase (SPP), 200, 242, 256, 262, 263, 457
 Stromal redox components, 510
 Stroma thylakoids, 314
 Stromule (stroma-filled tubule structure), 8, 10, 159, 169–183, 231, 324, 443–444, 448, 468, 495, 496
 Sucrose, 553–555, 560, 562
 Sucrose non-fermenting 1-related kinase 1 (SnRK1), 555, 557, 558, 561, 562, 651
 KIN10, 557, 561
 Sucrose phosphate synthase, 555
 Sucrose synthase, 553
 Sugar cane, 175, 552
 Sugar-limiting condition, 651
 Sugar signaling, 554–555, 559, 561, 659
 Suicide feed-forward, 540
 Sulfonylfluorescein diacetate (SFDA), 301
 Sulfoquinovosyldiacylglycerol (SQDG), 133, 135, 136, 143, 146
 synthesis, 142
 Sun, 341–342
 Sunlight, 43
 Supercomplexes, 85
 Superoxide anion radical, 112
 Superoxide dismutase (SOD), 531
 Surface dilution model, 145
 Survivorship curve, 288, 290
 Synechocystis, 365
Synechocystis sp. PCC 6803, 77, 103, 107–110, 615
 Systemic acquired resistance (SAR), 534
 Systemic signaling, 512
 Systems biology, 13

T

Tab2, 81
 Tachyplants, 291
 Tagetin, 203
 Tail-anchored protein, 264
 Tandem MS-MS, 32
 Targeted induced local lesions in genomes (TILLING), 560, 561
 Targeting model, 252
 Tat. *See* Twin-arginine translocase (Tat)
 Tba1, 80
TBC1, 83
TBC2, 83
TBC3, 83
 TCA cycle, 482, 483
 TCP transcriptional factor, 542
 Temperature-stress, 255
 Terpenoids, 158
 Tethering complexes, 162
 TetraGDG, 142
 Tetrapyrroles, 482, 485, 625
 Tetrapyrrole synthesis, 200
 Tetratricopeptide repeats (TPR), 79, 106, 250, 252, 260
 domain, 250, 260
 proteins, 82
 TGD1, 163
 TGD1 permease, 163
tgdl, 158
 TGD2, 140
tgdl2, 158
 TGD3, 163
 TGD4, 163
 TGD proteins, 140
 Thermal ratchet, 257
 Thermodynamics, 5, 19–23, 26, 28–32
 Thermolysin, 243
Thermosynechococcus elongatus, 75
Thermosynechococcus elongatus BP-1, 104
 THF 1. *See* Thylakoid formation 1 (THF 1)
 Thioredoxin, 262, 374, 554
 Threshold model of leaf variegation, 463
 Thylakoid, 24, 25, 27, 29, 41, 47–49, 52–55, 59, 60, 62–64, 74, 319, 338–341
 centers, 108
 formation, 343, 463
 lumen proteome, 89
 membrane biogenesis, 75
 Thylakoidal processing peptidase (TPP), 263, 265, 459, 561
 Thylakoid formation 1 (THF 1), 143
 Thylakoid rhodanese-like protein (TROL), 261
 TIC. *See* Translocon at the outer/inner envelope membrane of chloroplasts (TIC)
 Tic20, 242, 247, 255, 257, 258
 Tic21, 242
 Tic22, 242, 247, 255–257, 265
 Tic32, 242, 255, 256, 261
 Tic40, 242, 247, 255–262, 266
 Tic55, 242, 255, 256, 262
 Tic62, 242, 255, 256, 261
 Tic110, 242, 244, 247, 255–262, 266
 TIC channel, 256, 257, 265, 268
 TIC complex, 241, 242, 244, 247, 256, 261
 Tilia, 348
 TILLING. *See* Targeted induced local lesions in genomes (TILLING)
 TIM. *See* Translocase of the inner mitochondrial membrane (TIM)

- Tip-shedding, 170
 TMV. *See* Tobacco mosaic virus (TMV)
 Tobacco (*Nicotiana rustica*), 170, 172, 176–182, 218, 229, 366, 373
 Tobacco BY-2 cells, 197
 Tobacco mosaic virus (TMV), 176, 182
Tobacco rattle virus, 179
 TOC. *See* Translocon at the outer envelope membrane of chloroplasts (TOC)
 Toc12, 242, 249, 250, 257
 Toc34, 242, 244–247, 251–254, 256, 262, 264
 Toc64, 249–252
 Toc75, 242, 244, 248–249, 252, 253, 255, 256, 262–265
 Toc86, 244
 Toc159, 242, 244–248, 252, 253, 255, 262, 264
 TOC channel, 257
 TOC complex, 242–250, 252–253, 255, 256, 265
 TOC-TIC complex, 179, 180
 TOC/TIC protein import apparatus, 457
 TOC/TIC supercomplex, 256, 258
 Tomato, 170, 172, 173, 176–178, 182
 Tomato trichomes, 178
 Tonoplast, 138, 159
 marker, 331
 rupture, 466
 T6P. *See* Trehalose 6-phosphate (T6P)
 TPP. *See* Thylakoidal processing peptidase (TPP)
 TPR. *See* Tetratricopeptide repeats (TPR)
 TPR protein. *See* Tetratricopeptide repeat (TPR) protein
Tradescantia, 339
 Transcription, 230
 Transcriptional compensation system, 204
 Transcriptionally active chromosome, 216
 Transcriptional regulation, 191
 Transcription factors, 297, 382
 Transcription rates, 231
trans $\Delta 3$ -hexadecenoic fatty acid, 134
 Transit peptide, 241–243, 249, 254, 256, 260, 262–268, 457
 Translation elongation, 82
 Translation inhibitors, 506
 Translation initiation, 80
 Translation intermediates, 82
 Translocase/insertase, 88
 Translocase of the inner mitochondrial membrane (TIM), 240
 Translocase of the outer mitochondrial membrane (TOM), 240, 243, 250, 264
 Translocation channel, 248, 257
 Translocon, 6
 Translocon at the outer envelope membrane of chloroplasts (TOC), 6, 240–250, 252–257, 264, 265, 267, 268
 Translocon at the outer/inner envelope membrane of chloroplasts (TIC), 6, 241, 242, 244, 247, 253, 255–259, 265, 268
 Translucent plastoglobuli, 351
 Transport of lipid, 139
 Trans-splicing, 191
 Trehalase, 554
 AtTRE1, 553, 561
 TreF, 561
 Trehalose, 551–562
 Trehalose 6-phosphate (T6P), 12, 552–562
 Trehalose 6-phosphate phosphatase (TPP), 552–554, 557, 560
 AtTPPA, 553
 AtTPPB, 553
 OsTPP1, 556
 otsB, 556
 ScTPS2, 556
 Trehalose 6-phosphate synthase (TPS), 552–554, 556
 AtTPS1, 553
 otsA, 556
 ScTPS1, 556
 Trichomes, 172, 175–178
 TriGDG, 141
Triticum
 T. aestivum, 171, 221
 T. dicoccum, 219
 T. monococcum, 219
 tRNA-Glu, 200
trmE-reductase, 513
 TROL. *See* Thylakoid rhodanese-like protein (TROL)
 Trypan blue, 301
 TTC. *See* Phenyltetrazolium chloride (TTC)
 T3/T7 phage-type single-subunit RNA polymerase (RPOT), 203
 Tubulin, 178
 Turnip, 177
 Twin-arginine translocase (Tat), 263
 Two alternative models, 514
 Type II NAD(P)H, 483
 Type-II promoters, 204
 Type I signal peptidase (SPase I), 459
 T Zone, 92
- U**
 UDP-galactose, 137, 141, 145, 146
 DAG galactosyltransferase, 140
 UDP-galactose concentration, 146
 UDP-glucose, 553
 UDP-sulfoquinovose, 143
 UDP-sulfoquinovosyl, 142
 Ultrastructural analyses, 309
 Ultrastructural studies, 161
 Ultrastructure of chloroplasts, 594
 Undifferentiated plastids, 463
 Unitary, 293
 Unitary organisms, 293
 Un-pigmented cotyledons, 506
 3'-Untranslated region (UTR), 193
 Uroporphyrinogen I (Urogen I), 609
 Uroporphyrinogen III (Urogen III), 609
 Uroporphyrinogen III decarboxylase (UROD), 609, 611, 612

Uroporphyrinogen III synthase (UROS), 609
uros mutant, 609
UTR. *See* 3'-Untranslated region (UTR)

V

Vacuolar cysteine proteases, 469
Vacuoles, 324, 327–331, 369, 468
Variegated phenotype, 462
Vesicle budding, 144
Vesicle-inducing protein, 143
Vesicle inducing protein in plastid 1 (VIPP1),
92, 143, 252
Vesicles, 319–327, 331
Vesicle traffic, 268
Vesicular trafficking, 143
Vesicular transport system, 92
Vicia faba, 340, 591
VIGS. *See* Virus-induced gene silencing (VIGS)
Violaxanthin, 341, 343, 532
Violaxanthin de-epoxidase (VDE), 516
VIPP1. *See* Vesicle inducing protein in plastid 1 (VIPP1)
Viridis-115, 82
Virus-induced gene silencing (VIGS), 179
Virus-induced stress, 182

W

ω 3, 143
 ω 6, 143
Water stress, 181–182
Wheat, 174, 175, 181, 182, 223, 229, 372

Whirly, 6, 218, 219, 540
White goosefoot (*Chenopodium album*),
372, 374
Wilting, 298
WRKY53, 297, 298
WRKY transcription factors, 541

X

Xanthophyll(s), 55, 56, 62, 514
Xanthophyll cycle, 356, 533
carotenoids, 341
xanthophylls/ β -carotene, 342
X-ray crystallography, 75
Xylem, 517
Xyloglucan endotransglycosylase/hydrolases, 520

Y

Ycf3, 106–107
Ycf4, 106
Ycf37, 107
Ycf48, 88
Yellow variegated 1 (var1), 463
Yellow variegated 2 (var2), 463
YRTA motif, 204

Z

Zea mays, 77, 174, 229
Zeaxanthin, 341, 514, 532
ZmSIG1, 202