

# Index

## Symbols

- 14-3-3 proteins 12, 16,35, 42–44, 64–66, 218
- inhibition of NR activity 45
- NR complex 65

## A

ABA. *See* abscisic acid

*aba1-1* 18

*aba2-1* 18

*aba3-1* 18

*ABI1* 17

*ABI2* 17

*ABI3-5* 17

*ABI4* 18

*ABI5* 18

abiotic stress 185

abscisic acid 2, 17, 213

synthesis 18

acclimation 266–267

acids *see also*: amino acids

amino 2, 6, 9, 16–17, 183, 249, 251, 25

organic 2

aconitase 13, 199

Actinomycetales 97

active oxygen species (AOS) 162–163, 180–181, 184, 187, 197

adenylate control 179, 182, 183

ADP-glucose (ADP-Glc)

transport 244

translocator 245

ADP-glucose pyrophosphorylase (AGPase) 244

AGPase. *See* ADP-glucose pyrophosphorylase (AGPase)

agroecosystem 269

agronomic manipulation 266

AICAR. *See* 5-aminoimidazole-4-carboxamide 1- $\beta$ -D-ribofuranoside

algae

glycolate metabolism 165

photorespiration 165

unicellular 12, 267

*Alocasia macrorrhiza* 26

alternative oxidase (AOX) 160, 163, 164, 173–188, 200

abiotic stress 185

active oxygen species 180–181, 184, 187

adenylate control 179, 182–183

amino acid pool 183

antimycin A 178, 180

antisense inhibition 182, 186

biochemical regulation 176–177, 179, 182

citrate 180, 181

cysteine residues 177–178

cytochrome pathway 175–176, 180, 185–188

electron transport

in mitochondrial electron transport chain 175

fruit development 186

gene expression 180–182

gene families 175, 180

glycolysis 179, 182

growth 184–186

inhibitors 175

low temperature 185

measurement of activity 175

mitochondrial electron transport chain 174–176

monoclonal antibody (AOA) 175

oxygen isotope discrimination 175, 185–187

phosphate limitation 181–184

physiological function 181–188

pollen development 186

programmed cell death 187–188

pyridine nucleotides 176–177, 179, 182

pyruvate 177–179, 182–183

pyruvate kinase 179, 182–183

root development 186

site-directed mutagenesis 177

sulfhydryl/disulfide regulatory system 177–178

TCA cycle 177, 179, 182

thermogenesis 185–186

tobacco mosaic virus 186–187

transgenic plants 175, 177, 181

alternative pathway 161

for carbon recycling 122

*Amaranthus edulis* 118

amino acids 2, 6, 9, 16–17, 183, 249, 251, 254

diurnal concentrations 250

permeases 255

signaling 17

synthesis 1, 245

transporter 255

aromatic 246

minor 11

total leaf 9

5-aminoimidazole-4-carboxamide 1- $\beta$ -D-ribofuranoside 65

ammonia 2, 36, 50, 53, 54, 57–58, 125, 207, 267

accumulation 125,

assimilation 9, 13, 71, 72–86, 93–109, 270

compensation point 125

incorporation 4

transporter 125

influx 210

permease 93

transport 94

uptake 213, 215

*amt1* 95, 105

*amt2* 95

*amt3* 95

AmtB permease 95

amyloplasts 242

*Anabaena azollae* 97

*Anabaena* sp. PCC 7120 96, 99, 100

*Anabaena variabilis* 95

*Anacystis nidulans* 97, 101

- Anacystis* R2 (*Synechococcus* sp. PCC 7942) 95  
 anaplerosis 16, 135  
   carbon flow 6, 12, 145  
 annual crops 268–269, 272  
   grain crops 268  
 anoxia 54, 65, 68  
*ANR1* 18, 208, 217  
 anthocyanin 219  
 antimycin A 178, 180  
*Anthamium* sp. 99  
 AOA *See* monoclonal antibody (AOA)  
 AOS *See* active oxygen species (AOS)  
 AOX *See* alternative oxidase (AOX)  
 AP2 17  
 aphid-stylect-technique 247  
 Apiaceae 249  
 apoplast 50, 52–53, 251  
   nitrate reduction 50–54  
   phloem loading 251  
 aquatic plants 267  
*Arabidopsis* 14, 39, 54, 56–59, 234, 242  
*Arabidopsis thaliana* 117, 140–141, 208, 210, 242  
   histidine biosynthesis 17  
 Arg 11  
*Arum maculatum* 185  
 AS. *See* asparagine synthetase (AS)  
 Asn 9, 11, 15  
 Asp 6  
 Asp aminotransferase 6  
 asparagine synthetase (AS) 234  
 ATP synthetase complex (ATPase) 95, 266  
   CF<sub>0</sub>-CF<sub>1</sub> 26, 28–29  
   H'-ATPase (plasma membrane) 50  
 ATP/ADP 161  
 auxin 17, 18  
 azaserine 214  
*Azospirillum brasilense* 99
- B**
- bacteria 16  
*B. subtilis* 101  
 Bacteroidaceae 98  
*Bacteroides fragilis* 97–98  
 barley 6, 57, 118, 128, 157, 244  
*bifA* 103  
 biomass 266–267  
 birch 57  
 blue light regulation 53  
 brittle-2 244  
 BSC. *See* bundle sheath cells (BSC)  
 bundle sheath cells (BSC) 137  
*Butyrivibrio fibrisolvens* 98
- C**
- C *see* carbon (C)  
 C<sub>3</sub> plants 2, 24, 30, 135, 137, 154, 229, 267, 269–271  
   photosynthesis 6  
 C<sub>4</sub> 24, 30, 135–137, 165, 229, 266  
   aspartate/alanine shuttle 231  
   characteristics 30  
   glycine oxidation 165  
   photorespiration 165  
 calcium 135  
   influx 143  
 calcium-dependent protein kinases 35  
*Calothrix* sp. PCC 7601 97  
 CAM *See* crassulacean acid metabolism (CAM)  
 cAMP receptor protein (CRP) 103  
*Candida utilis* 59  
 CAP family 106  
 carbohydrates 2, 12, 16, 213, 241  
   export 13, 242  
   metabolism 11  
   synthesis 13  
   recycling 120–124  
 carbon  
   acquisition 269  
   assimilatory enzymes 229  
   flow 12, 50, 122  
   inorganic carbon accumulation mechanisms 266  
   inorganic carbon pumps 267  
   metabolism 1, 43, 212, 215  
   sequestration 265  
 carbon dioxide *See* CO<sub>2</sub>  
   anthropogenic increases 267  
   assimilation 5–6, 27  
   carboxylation/decarboxylation cycles 266  
   post-illumination burst 164  
 carbon-nitrogen 1, 93–94, 108, 227, 269  
   budgets 268–269  
   mitochondria 152–167  
   photorespiration 117  
 carbonic anhydrase 26, 229, 270, 272  
 carrier (see transporter)  
 carrot 249  
 catalase 30, 118  
   mutant 120  
 celery 249  
 cereal caryopses 269  
*Chlamydomonas reinhardtii* 54, 57, 118, 230  
 chlorate 57  
*Chlorella* 53  
*Chlorella sorokiniana* 57  
 Chlorophyceae 98  
 chlorophyll 13, 266  
   Chl *a:b* ratio 28  
 chloroplast 50, 55, 271  
   membranes 54  
   stroma 119  
   CO<sub>2</sub> concentration 119  
   O<sub>2</sub> concentration 119  
 circadian control 40, 140  
 citrate 157, 180–181  
   transporter 158  
 citrate synthase 13, 212  
*Clarkia xantiana* 242  
*Clematis vitalba* 59

- Clostridiaceae* 98
- CO<sub>2</sub>
- <sup>12</sup>CO<sub>2</sub> 120
  - <sup>14</sup>CO<sub>2</sub> 119–122
  - assimilation 5, 6, 27
  - elevated 29, 68
  - compensation point 126
  - concentrating mechanisms 266
  - low inorganic C levels 267
  - limitation 267
  - post-illumination burst 129, 164
- coffee 249
- companion cells 246
- compensation point
- ammonia 125
  - CO<sub>2</sub> 126
- complex I (mitochondrial) 160, 161
- confocal microscopy 141
- constitutive NAD(P)H nitrate reductase (cNR) 50–55, 195
- control strength 119
- cotton 26
- crassulacean acid metabolism (CAM) 135–137, 139, 266–267
- CO<sub>2</sub> concentrating mechanisms 267
- crops 265–272
- environmentally sustainable production 269
  - improvement 266–272
  - perennial 268
- CRP. *See* cAMP receptor protein (CRP)
- crystallography
- X-ray 136
- cucumber 128
- Cucurbitaceae 248, 249, 256
- cyanobacteria 93–94, 99–101, 103, 266
- cyanobacterial NiR 57
- cycD3* 235
- cyclic electron transport 272
- Cymopsis tetragonoloba* 28
- cytochrome *bff* complex 29, 266, 270–271
- cytochrome *c* 51, 53
- cytochrome *c*<sub>6</sub> 266
- reductase activity 38
- cytochrome *c* oxidase (CytOX) 200
- cytochrome *f* 26
- cytochrome pathway 160–161, 175–176, 180, 185–186, 188
- cytokinin 18, 207, 234
- cytosol 50
- ATP/ADP 161
  - NAD(H) pool 65, 68–69, 156–157, 162
  - NADP(H) 154, 158
  - homeostasis 146
  - nitrate 63, 66–68
  - nitrate reductase 49–50
  - pH 66, 146
  - pyruvate kinase 212
- CytOX. *See* cytochrome *c* oxidase (CytOX)
- D**
- D1 protein 270–272
- photodamage 270–272
  - synthesis 270
  - turnover 271
- DBMIB 107
- DCMU (dichlorophenyldimethylurea) 107
- Dehydrogenase (NAD(P)H) external 162
- Deionococcales* 98
- Deionococcus radiodurans* 98
- development 207, 213
- diaphorase 51
- diatoms 98
- dicarboxylate transport 84, 124
- dietary supplements 268
- Digitaria* 141
- Digitaria sanguinalis* 141
- divalent cations 96, 105
- DNA-binding protein 103
- Drosophila melanogaster* 17
- drought 6, 129
- E**
- E4P. *See* erythrose 4-P (E4P)
- eIF-2 17
- electron paramagnetic resonance 199
- electron transport 23, 44, 174–176, 271, 212
- enterobacterial NiR 57
- ER 51
- erythrose 4-P (E4P) 245
- Escherichia coli* 57, 98–99, 136–137
- ethanol formation 68
- Euglena gracilis* 123
- external NAD(P)H dehydrogenase 162
- extracellular nitrate reduction 50–54
- F**
- FAD 37–38, 51–52, 99
- fatty acid biosynthesis 162
- FBPase. *See* fructose 1, 6-bisphosphatase (FBPase)
- Fd. *See* ferredoxin
- Fd-GOGAT *See* ferredoxin-dependent glutamate synthase (Fd-GOGAT)
- Fd:NADP<sup>+</sup> oxidoreductase 55–56, 233
- Fd:NiR 57 *See* nitrite reductase
- ferredoxin 2, 35, 39, 55–56, 233, 266
- ferredoxin NADP<sup>+</sup> reductase 35, 39
- ferredoxin-dependent glutamate synthase (Fd-GOGAT) 5, 14–15, 74–75, 80–83, 93, 99–100, 116, 119, 126–129.
- ferricyanide reductase 38
- flavodoxin 266
- flavonoids 231
- flavoprotein 51
- flow cytometry 142
- FMN 99
- FNR *See* fumarate and nitrate reduction (FNR)
- FOCA 54
- formate transporter 54
- folate 162
- formate 123

formyl-tetrahydrofolate synthase activity 122  
 Fru2,6bP. *See* fructose 2,6-bisphosphate (Fru2,6bP)  
 fructose 1, 6-bisphosphatase (FBPase) 25, 242  
 fructose 2,6-bisphosphate (Fru2,6bP) 242  
 fruit 186, 265, 268  
 fuel 265  
 fumarase 213  
 fumarate 51, 56, 106, 233

**G**

G3PDH. *See* glyceraldehyde-3-phosphate dehydrogenase  
 G6P. *See* glucose 6-phosphate (G6P)  
 galactinol 256  
*Galderia partita* 30  
 GATA 59, 217  
 GCN2. *See* General Control Non-reversible 2  
 GDC glycine decarboxylase (GDC)  
 GDH *See* glutamate dehydrogenase (GDH)  
*gdhA* 102  
 genes 4, 58, 128, 175, 180-182  
   nitrogen-responsive 234  
   nitrogen-responsive 230-231  
 GGAT *See* glutamate-glyoxylate aminotransferase (GGAT)  
*gifA* 106  
*gifB* 106  
*gin6* mutant 17  
 Glc-6P 55  
 Glc1P. *See* glucose 1-phosphate (Glc1P)  
 Glc6P 242. *See* glucose 6-phosphate (Glc6P)  
 Gln 2, 4-6, 9, 12, 14-15, 96, 97, 99, 108, 124  
*glnA* 97  
*glnA* promoters 104  
*glnB* 105, 108  
*glnN* 98, 105  
*glsF* 99  
*glbB* 100  
*gltd* 100  
*gltS* 99  
 Glu 2, 4-6, 11, 96, 100  
 Glu:glyoxylate aminotransferase 6  
 glucose 16, 18, 241-242  
 glucose 1-phosphate (Glc1P) 241  
   transport 243  
 glucose 6-phosphate (Glc6P) 137, 241  
   transport 243  
 glucose-6-phosphate dehydrogenase 39  
 glucose carrier 241  
 glutamate 117  
 glutamate dehydrogenase (GDH) 15, 71, 78, 85-86; 93-94, 99, 102  
 glutamate synthase (GOGAT) 4, 6, 35, 39, 71-73, 79-86; 93, 94,  
   100, 146, 211, 231  
 glutamate-glyoxylate aminotransferase (GGAT) 116, 126-127  
 glutamate-receptors 220  
 glutamine 2, 117  
 glutamine synthetase (GS) 4, 6, 35, 39, 53, 71-79, 81, 85, 93, 94, 211,  
   116, 231. *See also:* GSIII  
   GS2 5, 116, 118, 119, 123, 125-130  
   GS type I 96  
   GS type II 97

  GS type III 93, 97  
 glutamine synthetase/glutamate synthase cycle (GS/GOGAT) 9, 13,  
   78, 83-84, 93-94, 99-101, 146, 155-156, 233  
 glutathione 11, 162  
 Gly 2, 6, 9, 11, 117, 121, 124, 164-165  
 Gly decarboxylase (GDC) 116  
 glyceraldehyde-3-phosphate dehydrogenase 14, 25, 154  
 glycerate kinase 121  
 glycerate-3-P 117  
 glycine decarboxylase (GDC) 116, 119-128, 130, 154, 160-161  
 glycolate 165  
 glycolate 2-P 117  
 glycolate dehydrogenase 165, 166  
 glycolate oxidase 116, 120, 122, 128, 129  
 glycolysis 4, 12, 153, 155-157, 179, 182  
 glycosyl-phosphatidylinositol anchor 51  
 glyoxylate 101, 121, 123, 126  
 GOGAT *See* glutamate synthase  
 Golgi apparatus 51  
 GPI. *See* glycosyl-phosphatidylinositol  
 GPT 242-243  
 GS *See* glutamine synthetase (GS)  
 GS/GOGAT *See* glutamine synthetase/glutamate synthase (GS/  
   GOGAT)  
 GS2. *See* glutamine synthetase (GS2)  
 GSI 93, 96, 105  
 GSI-IFs complex 106  
 GSII 97  
 GSIII 93, 97

## H

HATS. *See* high affinity nitrate transport systems (HATS)  
 hemoglobin 199  
*hetC* 105  
 heterocyst 100  
 hexokinase 16, 242  
 high affinity nitrate transport systems (HATS) 37-38, 44, 51, 208  
 His-Asp phosphorelay 16, 148, 227  
 His-containing phosphotransfer (HPt) 234  
 His-protein kinase 234  
 histidine 17  
 HPt. *See* His-containing phosphotransfer (HPt)  
 2-hydroxy-3-butynoic acid 119  
 hydroxypyruvate 117  
 hydroxypyruvate reductase (NADH-HPR) 116  
 hypersensitive response 55, 197  
 hypoxia 55

## I

ICDH *See* isocitrate dehydrogenase (ICDH)  
 IF. *See* inactivating factors (IF)  
 IF-GSI stoichiometry 107  
 IF17 93, 106  
 IF7 93, 106  
 inactivating factors (IF) 105  
 induction of photosynthesis 9, 152, 163-164  
 inositol-1,4,5-trisphosphate 135

iron-regulatory protein (IRP) 199  
 iron-sulfur clusters, 56, 57, 99  
   [3Fe-4S] 99  
   [4Fe-4S] 99  
   [Fe4S4] 56  
   [Fe4S4] 57  
 IRP. *See* iron-regulatory protein (IRP)  
 isocitrate 100  
 isocitrate dehydrogenase (ICDH) 2, 13–14, 16, 85, 93, 100–105,  
 158–159

## K

*Kalanchoe fedtschenkoi* 139–140, 143  
 Kranz anatomy 137

## L

lactate 68  
*Lactuca* 268, 270  
 Lamiaceae 248, 256  
 LATS. *See* low-affinity transport system (LATS)  
 Lb *See* leghemoglobins (Lb)  
 Lb-NO 199  
 leaf 269, 270, 271, 272  
   area 267, 271  
   chlorotic 57  
   drought-stressed 129  
   expansion 267  
   nitrate reduction 64–70  
   nitrogen content 270  
   protein 270  
   vegetables 269  
 LEDR. *See* light-enhanced dark respiration  
 leghemoglobins (Lb) 199  
 legumes 269  
*Lepechinia calycin* 26  
 leukoplasts 242  
 LHC. *See* light-harvesting Chl *a/b* protein complexes  
 light 4  
   enhanced dark respiration 152  
   signal transduction 141–143  
   stress 129  
 light-harvesting Chl *a/b* protein complexes 24, 230, 266  
 lignin 268  
 lipids 231  
 low-affinity transport system (LATS) 208  
 LR. *See* lateral roots  
 luciferase 59  
*Lupinus* 269  
 lysine 17  
*Lysimachia vulgaris* 28

## M

macroalgae 268  
 macroalgal thalli 268  
 MADS-type of transcription factor 40  
 maize 55, 57–58, 137, 139, 144, 229, 234, 244–245

malate 14–15, 137, 157  
 malate valve 153–154, 159, 163–164  
 malate-OAA exchange 153  
 malonate 51  
 malting barley 272  
 maltose 241  
   transporter 242  
 mannitol 248, 257  
 maricultured invertebrates 268  
 MC. *See* mesophyll cells (MC)  
*Medicago sativa* 99  
 Mehler reaction 163  
 meristems 267  
*Mesembryanthemum crystallinum* 140–141, 143  
 mesophyll cells (MC) 137, 247  
 metabolism  
   arrest 17  
   control 137  
   cross talk 16  
   intermediates 266  
   secondary 246  
 methemoglobin 199  
 methionine-DL-sulphoximine (MSX) 95  
 methyl viologen 53, 68  
 methylammonium 95  
 microalgae 268  
 microarray analysis 39, 211, 213  
 microsomes 53  
 minor amino acids 11  
 mitochondria 152–167  
   carbon-nitrogen reactions 152–167  
   electron transport 14, 174–176  
   function 200  
   NAD(H) 155, 161  
   NAD(P)H 155, 161–162  
   NAD(P)H dehydrogenases 160  
   NO 200  
   respiration 65, 152  
   uncouplers 65  
   thioredoxin 162  
 Mo-MPT 37–38, 40, 44  
 molybdenum-pterin 51  
   cofactor 210  
   enzyme 55  
 MSX. *See* L-methionine-DL-sulphoximine (MSX)  
 Mustard 55  
 mutants  
   catalase 120  
   photorespiratory 116–118  
   starchless 243  
   tobacco 4

## N

$N^{10}$ -formyl-tetrahydrofolate (THF) synthetase 123  
 $N^5,N^{10}$ -methenyl-THF cyclohydrolase 123  
 $N^5,N^{10}$ -methylene THF 116  
 $N^5,N^{10}$ -methylene-THF dehydrogenase 123  
 NADH/NAD 9, 38, 50, 155  
   cytosolic 69, 156–157, 162  
   mitochondrial 155, 161

- NADPH/NADP  
 cytosolic 154, 158  
 mitochondrial 155, 161-162
- NAD(P)H dehydrogenase 160, 270
- NAD-ME. *See* NAD-malic enzyme (NAD-ME)
- NADH-HPR. *See* hydroxypyruvate reductase (NADH-HPR)
- NADP<sup>+</sup> reductase 266
- NADP-dependent isocitrate dehydrogenase (NADP-ICDH) 101, 212
- NADP-dependent malic enzyme (NADP-ME) 137
- NADP-glutamate dehydrogenase (NADP-GDH) 102
- NADP-malate dehydrogenase (NADP-MDH) 163-164
- NADPH-dependent hydroxypyruvate reductase 122
- NAD(P)H nitrate reductase. *See* NR
- Nar 1* 54
- ndhB* 272
- Neurospora crassa* 17
- nia* 12, 58, 228
- Nicotiana plumbaginifolia* 58-59, 208
- Nicotiana* spp 271
- Nicotiana sylvestris* 125
- Nicotiana tabacum* 57, 271
- nicotine 271,
- nifHKD* 105
- nii* 57-59
- NiR *See* nitrite reductase; nitrite reductase (NiR)
- nitrate 2, 4, 9, 12, 18, 35, 36-46, 49, 50, 58, 94, 207, 267, 270  
 accumulation 53  
 acquisition 50  
 assimilation 50, 267, 270  
 regulation 49  
 availability 55  
 concentration 64, 66-68  
 co-ordinate sensing 18  
 cytosolic 63, 67  
 delivery 270  
 detoxification 49  
 efflux, vacuole 67  
 external 52  
 feeding 67  
 fertilization 36, 270  
 induction 59  
 leakage 63, 67  
 pools 64  
 reduction 2, 36, 50-54, 63-70, 94, 156, 206, 267, 270  
 responsive elements 59  
 sensing 53  
 signaling 16, 39, 40, 50, 45  
 transporters 35, 36, 54, 232  
 uptake 36, 53, 108, 208, 213, 232
- nitrate reductase (NR) 1, 2, 16, 35, 42, 49-50, 66, 73, 81, 201, 210, 228  
 activation slate 4, 12, 35, 42, 63-66, 69  
 biosynthesis 41  
 regulation 41-43  
 constitutive 49-55, 195  
 K<sub>M</sub> 66  
 inhibition 44  
 promoters 41  
 turnover 64
- nitric oxide (NO) 46, 49, 53-54, 55, 60, 188, 193-202  
 synthesis 53-54, 194-196
- nitric oxide synthase (NOS) 53, 194-196
- nitrite 49-50, 54, 57, 94  
 accumulation 65  
 detoxification 49, 54, 68  
 metabolism 54-59
- nitrite reductase (NiR) 35, 49, 50, 53, 56-58, 59, 73, 81, 210, 231  
 bacterial 57  
 cytosolic form 55  
 fungal 57  
 gene expression 58-59  
 post-transcriptional control 59  
 overexpression 59  
 reduction 36, 94, 211  
 nitrite transporter 54
- nitrite:NO oxidoreductase 53
- nitrogen 23, 50, 108, 227, 265-266  
<sup>15</sup>N 214  
 assimilation 2, 43, 64, 266, 270  
 cytokinins (nitrogen-responsive accumulation) 234  
 photorespiratory nitrogen cycle 74, 116, 124-127  
 responsive genes 230-231  
 retention time 267  
 signals 16, 101, 108, 206-22, 234  
 translocation rate 249  
 use efficiency 23, 267
- nitrogenase 100
- nitrous acid 54
- NO *See* nitric oxide (NO)
- NO<sub>2</sub> 55
- nodule 196
- non-photochemical quenching 130
- non-photosynthetic plastids 55
- Norflurazon 59
- NOS. *See* nitric oxide synthase (NOS)
- Nothofagus solandri* 28
- NO<sub>x</sub> 54-55
- NR *See* nitrate reductase
- NtcA 93, 103  
 NtcA-activator 106  
 NtcA-repressor 106  
 regulon 96  
 transcription factor 94
- NUE. *See* nitrogen use efficiency
- O**
- OAA *See* oxaloacetate
- 2-OG. *See* 2-oxoglutarate (2-OG)
- OH-pyruvate. *See* hydroxypyruvate
- oil 269
- okadaic acid 218
- Olcaccae 248-249, 256
- oligomycin 161
- oligosaccharides 248, 256
- olive 249
- Onagraceae 248
- Oocytes, *Xenopus* 209
- OPPP *See* oxidative pentose phosphate pathway (OPPP)
- organic acids 2, 52  
 synthesis 4, 13

- ornamentation 265
- oscillator
- circadian 140
- oxalate 270
- Oxalis* 270
- oxaloacetate 117, 124, 157-163
- oxidative detoxification 55
- oxidative pentose phosphate pathway 50, 55
- oxidative pentose phosphate pathway (OPPP) 56, 212, 242-243
- 2-oxoglutarate (2-OG) 6, 13-15, 93-94, 101-102, 117
- animation 96
  - anaplerotic 2-OG formation 6
  - transporter 84
    - malate translocator 245
- oxygen isotope discrimination 175, 185, 186, 187
- oxygen sensor 199
- oxygenase activity of Rubisco 116-119
- P**
- P. boryanum* 100
- Panicum miliaceum* 230, 245
- pasture grasses 268
- pathogens 60, 269
- pathways
- alternative 161
  - cytochrome 160, 161, 176, 180
  - reductive pentose phosphate (RPP) 116, 138-139, 212, 213
  - shikimate 245, 246
- PDC. *See* pyruvate dehydrogenase complex (PDC)
- PDH *See* pyruvate dehydrogenase
- pea 118, 243
- PEP (see phosphoenolpyruvate)
- transport 245
- PEP carboxylase (PEPc) 12-14, 16, 30, 136-148, 155-156, 163, 212, 215
- regulation 136-148
- PEP/phosphate translocator (PPT) 245
- PEPc *See* PEP carboxylase (PEPc); phosphoenolpyruvate carboxylase
- PEPc protein kinase (PEPcK) 139
- PEPc-specific protein-serine/threonine kinase (PEPc 135
- PEPcK. *See* PEPc protein kinase (PEPcK.); PEPc-specific protein-serine/threonine kinase (PEPc
- peroxynitrite 46, 55, 195
- petH* 105
- PGA. *See* 3-phosphoglyceric acid (PGA)
- 3-PGA. *See* 3-phosphoglycerate (3-PGA)
- PGI. *See* phosphogluco isomerase (PGI)
- PGM *See* phosphoglucomutase (PGM) 244
- PGP *See* phosphoglycolate phosphatase (PGP)
- Phaseolus vulgaris* 27, 129, 267
- phenylalanine 268
- phenylalanine ammonia lyase 4, 268
- phloem 207, 246-257, 268, 271
- loading 246-257, 251
  - sap 214, 247, 249
  - transport 271
- Phormidium laminosum* 97
- phosphate limitation 181-184
- phosphoenolpyruvate 245
- phosphoenolpyruvate carboxylase 4, 136-148, 229
- phosphorylation 136-148
  - regulation 136-148
- phosphogluco isomerase (PGI) 242
- 6-phosphogluconate dehydrogenase 39
- 3-phosphoglycerate (3-PGA) 138, 240
- phosphoglycolate phosphatase (PGP) 116, 119-120, 128
- phosphoinositide-specific phospholipase C 135
- phosphoenolpyruvate carboxylase 12, 64, 135-148, 231
- photochemical dissipation of excitation energy 271
- photoinhibition 59, 120, 129, 164-165, 269, 271
- photorespiration 1, 2, 6, 9, 11, 15, 23, 30, 74-75, 78, 82, 116-130, 152, 154, 157, 160-62, 164, 166
- carbon and nitrogen metabolism 116-117
  - feedback on other processes 127-129
  - recycling of carbon 120-124
  - recycling of nitrogen 124-127
    - in algae 165
    - in C<sub>4</sub> plants 165
  - stress 129, 129-130
- photosynthesis 4, 6, 9, 24, 27, 50, 55, 93-94, 120, 266-267, 272
- apparatus 26, 265, 266-269
  - efficiency 229
  - induction 152, 163, 164
- Photosystem I 24, 55
- Photosystem II 24, 271
- phycobilins 102, 266
- phycobilisomes 266
- phytochrome 40, 75, 81
- Pi translocator 153, 154
- PII 16, 108, 218
- PK. *See* pyruvate kinase (PK)
- plant hormones 2
- plasma membrane 50, 52, 53
- NO formation 53
  - nitrate reductase 50-53, 60
  - bound nitrite:NO oxidoreductase in 49, 50
  - H<sup>+</sup>-ATPase 50
- plasmodesmata 247, 256
- plastocyanin 266
- plastoquinone 26, 266, 272
- Plectonema boryanum* 99
- PM-NR *See* plasma membrane-bound nitrate reductase
- PNUE. *See* photosynthetic nitrogen use efficiency
- poll* 235
- pollen 186
- polyamines 42, 43
- Porphyra purpurea* 99
- potato 6, 9, 11, 26
- PPT. *See* PEP/phosphate translocator (PPT)
- Prevotella melaninogenica* 98
- privet 249
- Prochlorococcus* 96
- Prochlorococcus marinus* 101
- programmed cell death 187-188
- protein kinase 12, 17, 35, 42, 44-45, 231
- CDPK 44
  - cascade 143
  - inhibitors 218
  - plant 44
  - SNF1-related 44

protein phosphatase 17, 42  
*Prunus ilicifolia* 26  
*Prunus persica* 28  
 PS I. *See* Photosystem I  
 PS II. *See* Photosystem II  
 PS II function 28  
*Pseudanabaena* sp. PCC 6903 98  
 pumpkin 249  
 purines 17  
 pyridine nucleotides 176, 177, 179, 182  
 pyruvate 177, 178, 179, 182, 183, 245  
 pyruvate dehydrogenase complex (PDC) 13–14, 157  
 pyruvate kinase (PK) 13, 155, 179, 182–183, 212  
 pyruvate, orthophosphate dikinase 229  
 pyruvate translocator 245

**Q**

quenching  
 non-photochemical 130

**R**

R5P. *See* ribose 5-P (R5P)  
 raffinose 247, 248  
 redox 14, 50, 51, 104, 212, 266  
 reductive pentose phosphate (RPP) pathway 116, 138–139, 212, 213  
 resource allocation 207  
 respiration 2, 12–13, 15, 30, 55, 152, 173, 174–188,  
 RFLP markers 57  
*Rheum raponticum* 270  
 Rhizobiaceae 97  
 Rhodophyta 266  
 ribose 5-P (R5P) 245  
 ribulose-1,5-bisphosphate (RuBP) 23, 116–117, 120, 126, 128, 163  
 oxygenation 116–119  
 regeneration 23  
 ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) 16, 23,  
 28–30, 116, 119–122, 125, 126, 127, 128–130, 154, 229, 266,  
 270–272  
 Rubisco activase 26, 270, 272  
 rice 29, 30, 57  
 roots 267  
 architecture 267  
 branching 208  
 development 186  
 fine 267, 269  
 lateral 17, 207, lateral roots  
 pressure 270  
 robust 267  
 -shoot ratio 16, 207  
 Rosaceae 249  
 RPP. *See* reductive pentose phosphate (RPP) pathway  
 Rubiaceae 249  
 Rubisco. *See* ribulose-1,5-bisphosphate carboxylase/oxygenase  
 RuBP. *See* ribulose 1,5-bisphosphate  
 RuBP regeneration 29  
*Ruminococcus flavefaciens* 98

**S**

S-adenosylmethionine-dependent uroporphyrinogen II 232  
*Saccharomyces cerevisiae* 16  
 salicylhydroxamic acid (SHAM) 161  
 salicylic acid 186–187, 201  
*Salmonella typhimurium* 97  
*Sauromatum guttatum* 175  
 SBPase. *See* sedoheptulose-1,7-bisphosphatase  
*Scenedesmus minutum* 212  
*Schizosaccharomyces pombe* 241  
 Scrophulariaceae 248, 249, 256  
 SE-CCC. *See* sieve element-companion cell complex (SE-CCC)  
 seaweed 268  
 sedoheptulose-1,7-bisphosphatase 25  
 seeds 265  
 sensors of carbon-nitrogen status 1  
 Ser 2, 5–6, 9, 124  
 Ser hydroxymethyltransferase (SHMT) 116, 121–124, 127–129, 154  
 Ser-glyoxylate (SGAT) 116, 119, 121–122, 124–128, 130  
 Ser-protein kinases/phosphatases 217  
*sex1* 242  
 SGAT. *See* Ser-glyoxylate (SGAT)  
 SHAM. *See* salicylhydroxamic acid (SHAM)  
 shikimate pathway 245, 246  
 SHMT. *See* Ser hydroxymethyltransferase (SHMT)  
 shrunken-2 244  
 sieve element-companion cell complex (SE-CCC) 246  
 sieve elements 246  
 signal 4  
 nitrate 206  
 nitrogen 206–220  
 signal transduction 1, 4, 18, 45, 49, 135, 146, 196  
 SiR. *See* sulfite reductase  
 siroheme 56–57, 59  
 snapdragon 249  
 SNF1. *See* sucrose non-fermenting  
 SnRKs. *See* SNF1-related protein kinases  
*Solanum dulcamara* 28  
 sorbitol 248–249, 257  
*Sorghum* 137–139, 141, 144–145  
 soybean 29, 55, 161, 195  
 spermidine 42  
 spinach 26, 56–57, 59, 64, 66, 195, 268, 270  
 split root experiments 207, 214  
 SPS. *See* sucrose phosphate synthase (SPS)  
 squash 249  
 slachyose 247, 248  
 starch 2, 11, 13, 231  
 biosynthesis 213  
 degradation 213, 241  
 transitory 241  
 starchless mutant 243  
 stress 4, 18, 129, 185  
 succinate 50–52  
 succinate dehydrogenase 51  
 sucrose 2, 11, 15, 18, 58, 240, 247, 251  
 sucrose non-fermenting (SNF1) SNF1-related protein kinases 16, 44  
 sucrose phosphate synthase (SPS) 16, 218  
 sucrose transporters 253, 254



sucrose-phosphate synthase 231  
 sugar alcohols 248  
 sugar beet 51  
 sugar sensing 16, 17  
 sugar-beet 52  
 sugars 12, 16  
 sulfhydryl/disulfide regulatory system 11, 177–178  
 sulfite 57  
 sulfite oxidase 55  
 sulfite reductase 55  
 SUMT. *See* S-adenosylmethionine-dependent uroporphyrinogen II  
*sun6-2* 17  
 sunflower 29, 59  
 symplastic phloem loaders 251, 256  
*Synechococcus* sp. PCC 7942 95–96, 98  
*Synechocystis* sp. PCC 6803 93, 95, 97–98, 100–101

## T

t-zeatin(Z) 235  
 t-zeatin riboside (ZR) 235  
 t-zeatin riboside-5'-monophosphate 235  
 TCA. *See* tricarboxylic acid (TCA)  
 Thioredoxin 162  
 tetrahydrofolate (THF) 116  
 thermogenesis 185, 186  
 THF. *See* tetrahydrofolate (THF)  
 tobacco 4, 11, 12, 14–15, 30, 53, 55, 57, 59, 118, 129, 177, 181, 195, 207, 233  
 tobacco mosaic virus 186–187  
 TP. *See* triose phosphate (TP)  
 TPT. *See* triose phosphate/phosphate translocator (TPT)  
 transaldolase 213  
 transcription  
   cascade 136  
   factors 17, 40, 94, 216  
 transfer cells 251  
 transhydrogenase 155, 162  
 transhydrogenation 155, 162  
 transketolase 213  
 translocation rate 250  
 translocator  
   amino acid 255  
   ADP-Glc 245  
   citrate 158  
   chloroplastic ATP/ADP 154  
   dicarboxylate 124  
   Gln 124  
   Gly 124  
   membrane 118  
   nitrite 54  
   OAA 159  
   oxaloacetate 124  
   oxoglutarate/malate 84, 245  
   PEP/phosphate 245  
   Pi 153, 154  
   pyruvate 245  
   tricarboxylate 158

triose phosphate/phosphate translocator (TPT) 240–242  
 transpiration 267, 270  
 transport  
   ammonia 125  
   dicarboxylate 84  
   maltose 242  
   nitrate 232  
   OAA 157  
   sucrose 253, 254  
   tricarboxylate 158  
 trees 268  
 tricarboxylic acid (TCA) 158  
   TCA cycle 4, 12–13, 101, 157–158, 177, 179, 182  
 triose phosphate (TP) 240, 242  
*Triticum aestivum* 26  
 tryptophan 17  
 tungsten 210  
 type-A response regulator 234  
 Tyr 11

## U

Uncouplers 65  
 unicellular algae 12  
 urea 94  
 uridylylation 108  
 uroporphyrin III methyltransferase 56

## V

Vacuole 67  
 Val 11  
 verbascose 248  
 VF1. *See* NtcA  
*Vibrio* sp. 101

## W

wall (cell) polysaccharides 268  
 water-use efficiency 27  
 wheat 6, 9, 11, 26, 29  
 wind 268  
 wood 265, 268, 269

## X

X-ray crystallography 97, 136  
 xanthine oxidase 55  
 xanthophyll cycle 28, 130  
*Xenopus oocytes* 209  
 xylem 11, 268, 270–271

## Y

yeast 16, 36, 136

**Z**

Z. *See* t-zeatin (Z)

zeaxanthin 28

ZmRR1 234

ZmRR2 234

ZR. *See* t-zeatin riboside (ZR)