

Index

The index is arranged in letter-by-letter sequence; page numbers in italics refer to figures; page numbers in bold refer to tables.

- A3GT *see* anthocyanin 3-O-glycosyltransferase (A3GT)
- AATs *see* anthocyanin acyltransferases (AATs)
- ABC (adenosine 5'-triphosphate binding cassette), 149
- ACE *see* angiotensin converting enzyme (ACE)
- N*-acetyltransferase 1 (NAT1), polymorphisms, 360
- N*-acetyltransferase 2 (NAT2), polymorphisms, 360
- acibenzolar-S-methyl (ASM), 220
- adenosine 5'-triphosphate (ATP), 78
- adenosine 5'-triphosphate binding cassette (ABC), 149
- A-EpRE genes *see* antioxidant/electrophile-responsive element (A-EpRE) genes
- afzelechins, 187
- aglycons, 20–1, 236–7
 - cellular metabolism, 73–4
 - conjugation, 72
 - diffusion, 8
 - solubility, 2
- AHA10* gene, 120
 - expression, 122
- AHR (aryl hydrocarbon receptor), 359, 360–1
- aldehydes, 124
- aldose reductase, inhibition, 344
- alizarin, 9
- allelochemicals, 7
- allelopathy, use of term, 6–7
- Alliaria petiolata* (garlic mustard), 20
- Allium cepa* (red onion)
 - 5-carboxypyranocyanidin, 178
 - cyanidins, 182
 - UGT73J1, 129
- Allium schoenoprasum* (chive), anthocyanin–flavone pigments, 188
- Alstroemeria* spp. (Peruvian lilies), anthocyanin glycosides, 181–2
- Alternaria alternata* (fungus), infection, 214
- Anemone coronaria* (poppy anemone), anthocyanins, 183
- angiogenesis, phenolic conjugate effects, 345
- angiosperms
 - anthocyanins, 167
 - flavonoid biosynthesis, metabolic engineering, 142–9
 - flavonoid biosynthetic pathways, 139–40
- angiotensin converting enzyme (ACE)
 - inhibitors, 266
 - and pomegranate juice, 265–6
- animals, innate immune response, 203
- animal studies
 - anthocyanin metabolism, 251–2
 - see also* pig studies
- ANR (anthocyanin reductase), 118
- ANR* gene, 118
 - expression, 121–2, 123
- ANS *see* anthocyanin synthase (ANS)
- ANS* gene, 118
 - expression, 121–2
- anthocyanin vacuolar inclusions (AVIs), 139, 149–52, 191–2
 - formation, 149
 - in petals, 150–2
 - occurrence, 150
 - use of term, 150
- anthocyanin 3-O-glycosyltransferase (A3GT), 140
- sequencing, 145
- anthocyanin O-glycosyltransferases (AGTs), clones, 145
- anthocyanin reductase (ANR), 118
- anthocyanidins, 168–78
 - classification, 228–9
 - equilibrium forms, 178–81
 - hydroxylation, 140
 - modification enzymes, 146
 - structure, 180, 181
 - see also* proanthocyanidins (PAs)
- anthocyanin synthase (ANS), 118–20, 140
- recombinant, 120
 - roles, 190
- anthocyanin acylglycosides, 183–6
- anthocyanin acyltransferases (AATs), 147–8
 - aliphatic, 147
 - aromatic, 147
- anthocyanin 3-O-coumaroyltransferases, 148
- anthocyanin–flavone C-glycosides, 187–8
 - structure, 179
- anthocyanin–flavone pigments, 187–8
- anthocyanin galactosides, 128
- anthocyanin glycosides, 181–3
- anthocyanin glycosyltransferase (BpUGAT), 128
- anthocyanin metabolites, 247
 - biosynthesis, 248–9
 - pathways, 248
- anthocyanin-related regulatory proteins, 154
- anthocyanins, 8, 132, 228–62
 - absorption, 72, 236–47, 249
 - analytical methodology, 241–2
 - mechanisms, 243–5
 - variability, 239–42
 - acylation, 145, 147–8
 - antiatherogenic activity, 233–4
 - antibacterial activity, 235

- anticancer activity, 234
 anti-inflammatory activity, 233
 antioxidant activity, 230–1, 232
in vitro, 231
 antiviral activity, 235
 applications, 181
 flower pigments, 140, 144–9, 167, 228
 bioactivity, 229–36
 biosynthesis, 119, 189–91
 regulatory mechanisms, 139, 152–7
 blood concentration, 243
 chromatograms, 250
 color differences, 229
 disaccharides in, 182–3
 dosage variations, 239
 elimination, 242–3, 249
 in flavonoid complexes, 187–8
 in food matrix, 241
 gastric protective activity, 236
 in health, 228
 identification, 140
 localization, in plant cells, 191–2
 metabolism, 247–54
 animal studies, 251–2
 human studies, 247–51
 mechanisms, 252–4
 routes, 249
 methylation, 148
 modification enzymes, 146
 molecular biology, 189–91
 neuroprotective activity, 235
 new, 174
 obesity prevention, 235–6
 occurrence, 169–73, 228
 pharmacokinetics, 238, 242–3
 prooxidant activity, 232
 regulatory genes, 142–3
 research publications, 167, 168
 roles, 228
 sources, 228
 structural transformations, 245–7
in vitro, 246–7
 in water, 246
 structure, 175, 176, 185, 186
 chemical, 240–1
 classification, 228–9
 research developments, 167–201
 transport models, 149
 urine concentration, 243
 and vision improvement, 236
- anthocyanoplasts, 150
Anthonomus grandis (boll weevil), 20
 anthragallol, 9
 anthraquinones, 9
 anti-aging agents, antioxidants as, 263
 antiatherogenic activity, anthocyanins, 233–4
 antibacterial activity, anthocyanins, 235
 antibiotic activity, tannins, 15
 antibiotics, preformed, 11, 14–15
 anticancer activity
 anthocyanins, 234
 cocoa polyphenols, 105–9
 epicatechins, 108–9
 polyphenols, 359–60, 363–9
 proanthocyanidins, 105–9
 antifungal activity, 214–15
 dihydrochalcones, 15
 flavanones, 15
 flavones, 15
 flavonols, 15
 and lipophilicity, 15
 phenolic acids, 15
 phenols, 15, 214–15
 stilbenes, 15
 anti-inflammatory activity, anthocyanins, 233
 antimicrobial activity
in vitro, 211–12
 natural, 211
 antioxidant activity
 anthocyanins, 230–1, 232
 dietary flavonoids, 68, 70–1
 ellagitannins
in vitro, 265
 issues, 266–74
 flavonoids, 263–4
 research publications, 264
 phenolics, 263–4
 and plant defenses, 222
 research publications, 264
 plant food, 263
 polyphenols, *in vitro*, 359
 pomegranate juice, 265
 urolithins, 346
 antioxidant/electrophile-responsive element (A-EpRE) genes, expression, 82–3
 antioxidants
 and anti-aging agents, 263
 marketing claims, 263–4
 studies, *in vitro* vs. *in vivo*, 263–4
antirrhinum majus (snapdragon), aurones, 132
 antiviral activity, anthocyanins, 235
 apigenin, 130, 313
 apigeninidin, 217
 apigenin-xanthine oxidase complex, 75
 apoptosis, 107
 colon cancer cells, 365, 367–9
 induction, 271–3
 apple beverages, oxidation products, liquid chromatography-mass spectrometry analysis, 288–90
 apple juice
 phenolic oxidation products, 278–92
 world production, 278
 apples
 phenolics in, 278–81
 world production, 278
 apple skins, flavonoids, 128
Arabidopsis spp. (cresses), 46–7
 defense modeling, 206
 genomes, 50
 ICS gene, 204
 isoflavone synthase, 115
 mutants, 205
 proanthocyanidins, 121–2
 salicylic acid, 203
Arabidopsis thaliana (thale cress)
 anthocyanidin synthase, 120
 caffeo-3-O-glucoside, 127
 glycosyl hydrolases, 123
 phenylpropanoids, 6
 salicylic-acid-dependent responses, 205–6
 UGT72E1, 130
 uridine diphosphate glycosyltransferases, 124, 130
 arabinoxylans, acylation, 51
 arbutin synthase, 127, 130

- aromatase
catalysis, 293, 294
expression, 294
inhibition, 293–304, 312
by natural phytoestrogens, 295–300
phytoestrogens as lead compounds, 301–4
overexpression, 294
- aromatase inhibitors, development, 294–5
- Arrabidaea chica* (puca panga), carajurin, 177
- aryl hydrocarbon receptor (AHR), 359, 360–1
- ASM (acibenzolar-S-methyl), 220
- atherosclerosis
and polyphenols, 359, 369–73
and pomegranate juice consumption, 266
- ATP (adenosine 5'-triphosphate), 78
- aureusidin, 8
- aureusidin synthase (AUS), 132, 144
- aurones, 8, 132, 140, 143–4
- AUS (aureusidin synthase), 132, 144
- auxin (indole-3-acetic acid), 10, 125
- avenanthramides, 217
- AVIs *see* anthocyanic vacuolar inclusions (AVIs)
- avocado fruit, preformed antifungals, regulatory mechanisms, 214–15
- azoxymethane, 365
- Aztecs, cacao use, 88
- Babiaba stricta* (baboon flower), anthocyanins, 183
- BANYULS gene, 120
- basal resistance *see* induced resistance
- BAs (benzoic acids), 125, 203–4
- basic helix-loop-helix (bHLH), 153, 155
- basic metabolism, use of term, 1
- Bellis perennis* (common daisy), anthocyanin glycosyltransferase, 128
- benzoic acids (BAs), 125, 203–4
- benzoquinones, 9
- benzyl-protected building blocks
and inter-flavan bond formation, 94–7
synthesis, 92–4
- 4-(benzylthio)catechin, 96
- Berberis buxifolia* (calafate), anthocyanins, 181
- bHLH (basic helix-loop-helix), 153, 155
- bilirubinase, 244
- biochanin A, 115, 129
- biphenyls, 50
- Blechnum novae-zelandiae* (fern)
anthocyanin glycosides, 182
anthocyanins, 186
- Bombax malabaricum* (silk cotton tree), aglycones, 168
- Boolean operators, 206
- Botrytis* spp. (fungi), resistance to, 206
- bovine serum albumin (BSA), 345–6
- BpUGAT (anthocyanin glycosyltransferase), 128
- breast cancer, 105, 364
prevalence, 293
protective factors, 293
- breast cancer cells
apoptosis, 107
cell cycle analysis, 106, 107
flow cytometry, 108
necrosis, 107
proliferation, 107
- Broussonetia papyrifera* (paper mulberry), 300
- brown rot, 215
- BSA (bovine serum albumin), 345–6
- C* gene, 121
- C4H (cinnamate 4-hydroxylase), 140
- cacao, early use of, 88
- CA (*trans*-cinnamate), 203–4
- Caco-2 cells, 271–4
model, 72
- caffeic acid, 127, 215, 216
- caffeic acid O-methyltransferase (COMT), deficiency in plants, 41, 44, *Plate 2.3*
- caffeo 3-O-glucoside, 127
- 5-O-caffeoquinic acid *see* chlorogenic acid
- caffeoquinic acid
caffeoquinic acid o-quinone incubation, 282–4
oxidation products, 282–3
total ion current chromatograms, 282, 283
- caffeoquinic acid o-quinone, 279–80
characterization, 281
incubation, 282–7
with caffeoquinic acid, 282–4
with (–)-epicatechin, 285–7
- preparation, 281
total ion current chromatograms, 285
UV spectra, 282–3, 284
- CAGT (coniferyl alcohol glycosyltransferase), 124
- Caladium bicolor* (caladium), transgenics, 143
- Callosobruchus maculatus* (cowpea weevil), 22
- Campanula medium* (Canterbury bells), anthocyanins, 184
- CAN (carbonic anhydrase), 206–7, 220
- cancer
cell proliferation, 105–7
colon, 364, 365
lung, 365
see also anticancer activity; breast cancer; prostate cancer
- capsaicin, 127–8
- carajurin, structure, 177
- carajurone, structure, 177
- carbonic anhydrase (CAN), 206–7, 220
- 5-carboxypyranocyanidin, structure, 178
- 5-carboxypyranopelargonidin, structure, 178
- carnations, fusarium wilt, 214
- caseins, 71
- (–)-catechin, 7
- (+)-catechin
in apples, 278
as starting material, 92
- catechin- β -catechin, synthesis, 103–4
- catechins, 187, 320
in apples, 278
epimerization, 90
oxidation, 281
regiochemistry, 98–9
structure, 90, 187, 279
- catechol, 213
- catechol-O-methyltransferase (COMT), 69–70
cyanidin methylation, 252
- Catharanthus roseus* (Madagascar periwinkle)
anthocyanin glycosides, 181
- CaUGT2, 127–8
- ICS gene, 204
- CaUGT2, 127–8
- CCR (cinnamoyl-CoA reductase), 42–3
- celecoxib, 364
- cell-based assays, phytoestrogens in,
anti-aromatase activity, 298–9
- cell cycle analysis, breast cancer cells, 106, 107

- cells
 phenolic metabolite biosynthesis, 321
see also apoptosis
- cellular transport, phenolic conjugates, 346–8
- Centaurea cyanus* (cornflower)
 flower pigments, 144–5
 protocyanins, 189
- Centaurea maculosa* (spotted knapweed), phytotoxins, 7
- chalcone isomerase (CHI), 140
- chalcones, 8, 140, 143–4
cis-chalcones, 244–5
trans-chalcones, 244–5
 chalcones, anti-aromatase activity, 299–300
 chalcone synthase (CHS), 140, 155
- Charophyceae (algae), 4–5
- CHD *see* coronary heart disease (CHD)
- Cheiranthus cheiri* (wall flower), anthocyanins, 186
- chemoreceptors, insects, 18
- CHI (chalcone isomerase), 140
- chlorogenic acid, 215, 216
 in apples, 278, 279
 UV spectra, 285
- chocolate
 benefits, 88, 89
 early use of, 88
- chorismate, 205
- chromones, anti-aromatase activity, 302
- chrysin, binding, to fungal 17 β -hydroxysteroid dehydrogenase cl, 309
- CHS (chalcone synthase), 140, 155
- CHS gene, expression, 156
- Cicer arietinum* (chickpea)
 isoflavonoids, 20
 uridine diphosphate glycosyltransferase, 128
- cider, phenolic oxidation products, 278–92
- trans*-cinnamate (CA), 203–4
- cinnamate 4-hydroxylase (C4H), 140
- cinnamic acids, structure, 126
- cinnamoyl-CoA reductase (CCR), 42–3
- Citrus aurantium* (bitter orange), tangeretin, 17
- c-Jun N-terminal kinases (JNKs)
 activation, 343
 inhibition, 78–9
- Cladosporium cucumerinum* (fungus), 219, 221–2
 resistance to, 218
- Clitoria ternatea* (butterfly pea), anthocyanins, 184
- Cochliobolus carbonum* (fungus), 216
- Cochliobolus lunatus* (fungus), 17 β -hydroxysteroid dehydrogenase, 308–10
- cocoa, early uses of, 88–9
- cocoa-derived oligomeric epicatechins, synthesis,
 • 88–112
- cocoa polyphenols
 • anticancer activity, 105–9
 research, 88–9
- cocoa procyanidins, chemical properties, 89–91
- Colletotrichum circinans* (fungus), and onion smudge disease, 15, 213
- Colletotrichum gloeosporioides* (fungus), resistance, 214–15
- Colletotrichum lindemuthianum* (fungus), and induced resistance, 220
- Colletotrichum orbiculare* (fungus), resistance to, 221
- Colletotrichum sublineolum* (fungus), 168
- colon, phenolic metabolite biosynthesis, 320
- colon cancer, 364, 365
- colon cancer cells, apoptosis, 365, 367–9
- combinatorial, use of term, 37
- CoMFA (comparative molecular field analysis), 302
- Commelina communis* (Asiatic dayflower), commelinins, 188–9
- commelinins, 188–9
- comparative molecular field analysis (CoMFA), 302
- Compositae (daisy family), 9
- COMT *see* caffeic acid *O*-methyltransferase (COMT); catechol-*O*-methyltransferase (COMT)
- condensed tannins *see* proanthocyanidins (PAs)
- coniferaldehyde, 44–5
- coniferyl alcohol glycosyltransferase (CAGT), 124
- coniferyl alcohols
 biosynthesis, 36
 diffusion, 39
- coniferyl aldehydes, 124
 glycosylation, 125
- 7-*O*-conjugates, antioxidant properties, 341–2
- conjugation, phenolic metabolites, 317, 318
- Convolvulaceae (bindweed family), anthocyanins, 185–6
- Cornus alba* (Siberian dogwood), anthocyanins, 182
- Cornus suecica* (Eurasia dwarf cornel), anthocyanins, 183
- coronary heart disease (CHD)
 reduction, and red wine, 233–4
 risk factors, 234
- p*-coumaric acid, 9, 126
- p*-coumaric acid glucuronides, synthesis, 331
- coumarins, 126
 roles, 10–11
 structure, 125
- p*-coumaroylquinic acid, 278
- p*-coumaroyl alcohols, biosynthesis, 36
- coumestrol, 17 β -hydroxysteroid dehydrogenase type 1 inhibition, 305–7
- COX-2 *see* cyclooxygenase-2 (COX-2)
- cross-coupling, end-wise, 37, 39
- Cruciferae (cabbage family), anthocyanins, 186
- CSLF genes, 52
- cucumbers, salicylic acid, 203–4
- cucumerin A, 217
- curcumin
 anticancer activity, 359–60
 structure, 127
- curcumin metabolites, 344
 biosynthesis, 320
 characterization, 327–8
 structure, 327
- curing, plants, 17
- cyanidin 3-glycoside
 antioxidant activity, 230
 antiviral activity, 235
 metabolism, 248, 252–3
 and obesity prevention, 235–6
 structure, 179
- cyanidins, 128, 140, 168
 anticancer activity, 234
 antioxidant activity, 231
 methylation, 253
 new, 182
- cyanidin 3-sambubioside, 240
- cyanidin sulfate, 253
- cyanodelphin, 182
- cyclin A* gene, 369
- cyclooxygenase-2 (COX-2)
 inhibition, 344, 345
 roles, 343–4
- cyclooxygenase isozymes, COX-2, 233

- CYP1A1, 360
inhibition, 79–80
- CYP3A4, 363
- CYP19A1 *see* aromatase
- CYPs *see* cytochromes P450 (CYPs)
- cytochromes P450 (CYPs)
catalysis, 79
inhibition, 79–80
- cytosolic multi-enzyme complexes, 149
- daidzein, 113, 114
incubation, 325
sources, 115
in soy, 369, 372
- daphnetin, 126
- defense compounds
induced, 11, 12
synthesis, 11–12
- defense mechanisms, genetic control, 14
- DEFICIENS protein, 156
- dehydrocatechin A, 280–1, 287
- dehydrocatechin B, 286
- dehydrocatechins, 286–7
- DELILA, 153
- delphinidin 3-rutinoside, 252
- delphinidins, 128, 140, 168
anticancer activity, 234
biosynthesis, 143, 144, 145
occurrence, 182, 188–9
- delphinidin 3-sambubioside, 240
- Dendrobium × superbiens* (orchid), anthocyanins, 184
- 3-deoxyanthocyanidin phytoalexins, synthesis, 12
- 3-deoxyanthocyanins, 190
- Desmodium uncinatum* (silverleaf), leucoanthocyanidin reductase, 118
- desoxyanthocyanidins, 168
- 3-desoxyanthocyanidins, 168–77
- detoxification mechanisms, 359–63
- DFR (dihydroflavonol 4-reductase), 140, 155
- DFR gene, expression, 121–2, 132
- DHCA (dihydroconiferyl alcohol), incorporation, into lignins, 42
- DHF (dihydroflavonols), 140
- Dianthus caryophyllus* (carnation), anthocyanic vacuolar inclusions, 191
- dibenzodioxocins, 50
- dietary flavonoids
absorption, 72–3
antioxidant activity, 68
sites, 70–1
bioavailability, 67–8
binding processes in, 72–4
- catabolism, 70
- cellular metabolism, 73–4
- conjugates, 69–70
- conjugation, 72–3
- gene expression, regulatory mechanisms, 80–3
- interactions
with digestive enzymes, 72
with food proteins, 71
with salivary proteins, 71–2
- research issues, 67–8
- tissue distribution, 73–4
- transport, in plasma, 73
- dietary phytoestrogens, 17 β -hydroxysteroid dehydrogenase type 5 inhibition, 310–11
- diferulate, 9
- digestive enzymes, interactions, with dietary flavonoids, 72
- dihydrochalcones
antifungal activity, 15
in apples, 278
structure, 279
- dihydroconiferyl alcohol (DHCA), incorporation, into lignins, 42
- dihydroflavonol 4-reductase (DFR), 140, 155
- dihydroflavonols (DHF), 140
- dihydroquercetin, 91
- dirigent/replication hypothesis, 36, *Plate 2.2*
criticisms, 40–50, 53–4
issues, 37–8, 50, 52–3
and monomer substitution, 40–5
- disaccharides, in anthocyanins, 182–3
- disease resistance
and phenolics, 15
see also induced resistance
- dormancy, 10–11
- Drosophila melanogaster* (fruit fly), genome, 1–2
- drug discovery, phytoestrogens, for steroid biosynthesis control, 293–316
- EGCG *see* epigallocatechin gallate (EGCG)
- Eichhornia crassipes* (water hyacinth),
anthocyanin–flavone pigments, 188
- electrophilic response element/antioxidant response element (EpRE/ARE), 359, 360–2, 370
activation, 371–2
- ellagic acid
apoptosis induction, 271–3
bioactivity, 264–5
bioavailability, *in vivo*, 267–9
disposition, 270
food, 263–77
future research, 275
metabolism, 270, 271–3
in vivo, 267–9
- ellagic acid metabolites, tissue distribution, 267–9
- ellagic tannin metabolites, characterization, 324
- ellagitannin metabolites
bioactivity, *in vivo*, 269–74
tissue distribution, 267–9
- ellagitanins
antioxidant activity
in vitro, 265
issues, 266–74
- bioactivity, 264–5
clinical studies, 265–6
in vivo, 267
issues, 266–74
- bioavailability, *in vivo*, 267–9
- biosynthesis, 264
- future research, 275
- metabolism, *in vivo*, 267–9
- occurrence, 265
- pig studies, 267–9
- UV spectra, 264
- enterodiol, 325
- enterolactone, 325
anti-aromatase activity, 299
- enzymatic browning, use of term, 279
- epiafzelechins, 187
- (–)-epicatechin
in apples, 278
- caffeoquinic acid *o*-quinone incubation, 285–7
- oxidation products, 285–7

- total ion current chromatograms, 285
 UV spectra, 285
- epicatechin-4 α ,8-epicatechin, synthesis, 102–3
- epicatechin oligomers
 chromatograms, 95
 structure, 90
 synthesis, 104
- epicatechins, 187, 215
 anticancer activity, 108–9
 epimerization, 90
 methylation, 320
 regiochemistry, 98–9
 structure, 90, 324
- epigallocatechin gallate (EGCG), 107
 anticancer activity, 359–60, 363, 365
- EpRE/ARE *see* electrophilic response element/antioxidant response element (EpRE/ARE)
- Erb2 gene, inhibition, 89
- ERBB2-positive tumors, 364
- eriodictyol, 191
 sulfation, 340
- ERK (extracellular signal-related kinase), 78
- Erwinia amylovora* (bacterium), 221
- erythrose-5-phosphate, as intermediate, 13
- Escherichia coli* (bacterium), 191
- esculetin, 126
- estradiol, blocking, 293
- estrogen synthetase *see* aromatase
- estrone, biosynthesis, 293
- ET (ethylene), 205–6
 β -ether frequency anomaly, 39–40
 ethylene (ET), 205–6
- Eustoma* spp. (*lisianthus*), anthocyanic vacuolar inclusions, 150–2
- Eustoma grandiflorum* (*lisianthus*), anthocyanic vacuolar inclusions, 191
- Evolvulus pilosus* (blue daze), anthocyanins, 185–6
- extracellular signal-related kinase (ERK), 78
- F3H (flavone 3-hydroxylase), 140
- F3H gene, 156
 expression, 132
- S-fadrozole, anti-aromatase activity, 302
- ferrlymyoglobin, 71
- ferulic dehydrodimerization, 51
 mechanisms, 52
- ferulic acid, 9
 synthesis, 125
- feruloyl pectin, roles, 9
- flavan-3-ol, 24
- flavan-3-ol conjugates, antioxidant properties, 339
- flavan-3-ol metabolites, characterization, 324
- flavanone conjugates, antioxidant properties, 339
- flavaphones, 73
 antifungal activity, 15
 IC₅₀ values, 295–8
- flavanol metabolites, characterization, 322–4
- flavanone metabolites, characterization, 322–4
- flavanyl acceptors, 91, 96–7
- flavanyl donors, 91, 96–7
 synthesis, 92, 104
- flavone conjugates
 antioxidant properties, 339
 structure, 321–2, 323
- flavone 3-hydroxylase (F3H), 140
- flavone metabolites, characterization, 321–2
- flavones
 anti-aromatase activity, 302–3
- antifungal activity, 15
 binding, 73, 74
- effects on colon cancer cells, 365, 367–9
- in flower pigments, 140
- hydroxylation, 8–9
- IC₅₀ values, 295–8
- localization, 15
- flavonoid biosynthesis
 angiosperms, metabolic engineering, 142–9
 inhibition, 142
 ornamental plants
 metabolic engineering, 139–66
 molecular biology, 139–66
 pathways, 113–14, 139–40, 141
 regulatory mechanisms, 139
- flavonoid complexes, with at least one anthocyanin subunit, 187–8
- flavonoid glucosides, absorption, 319–20
- flavonoid glycosides
 hydrolysis, 318–19
 in saliva, 318
- flavonoid–protein binding
 effects on human health, 74–83
 processes, 67–87
 prior to absorption, 71–2
- flavonoid–protein covalent coupling, 69, 71
- flavonoids, 2, 19
 accumulation, 18–19
 anti-aromatase activity, 300–1
 antioxidant activity, 263–4
 research publications, 264
 antioxidant properties, 68
 in apples, 278
 applications, 5
 flower pigments, 139, 140
 ultraviolet protection, 6
- binding, 67–87
- chemical properties, biologically relevant, 68–71
 gene expression
 redox regulation, 82
 regulatory mechanisms, 80–3
- glycosylation, 128–30
 in host plant selection, 19–20
- 17 β -hydroxysteroid dehydrogenase type 1 inhibition, 307
- 17 β -hydroxysteroid dehydrogenase type 3 inhibition, 310
- IC₅₀ values, 295–8
 pro-oxidant properties, 342–3
 redox, 67
 modulation, 76–7
 roles, in health, 23, 74–83
 structure, 129, 140, 141
 and ultraviolet radiation, 6
see also dietary flavonoids; isoflavonoids
- flavonoid O-sulfates, chemical synthesis, 332–3
- flavonol conjugates
 antioxidant properties, 334–9
 structure, 321–2, 323
- flavonol galactosides, 128
- flavonol metabolites, characterization, 321–2
- flavonol methyl ethers, localization, 15
- flavonols
 antifungal activity, 15
 binding, 73, 74
 in flower pigments, 140
 hydroxylation, 8–9
- flavonol synthase (FLS), 118–20

- flavonones, binding, 74
 flavopiridol, 105–6
 flavylum cations, 179
 flavylum compounds, structure, 179–81
floral binding protein2 gene, 156
 flow cytometry, breast cancer cells, 108
 flowering plants *see* angiosperms
 flower pigments
 anthocyanins, 140, 144–9, 167, 228
 blue, engineering, 144–9
 flavonoids, 139
 future research, 157–8
 genetic modification, 139
 patternning, 153–5
 stability, 140
 yellow, engineering, 143–4
FLS (flavonol synthase), 118–20
 food
 ellagic acid, 263–77
 polyphenols, 263–77
 see also plant food
 food matrix, anthocyanins in, 241
 food proteins, interactions, with dietary flavonoids, 71
Fragaria × ananassa (garden strawberry),
 5-carboxypyranopelargonidin, 178
 French Paradox, 369
 Freudenberg concept, 36, 50, 53
 limitations, 53–4
 Friedel–Crafts acylation, 91
 fruit
 post-harvest resistance, 16–17
 post-harvest treatment, 17
 fungal hyphae, 218
 fungal pathogens, 13–17
 furofurans, 22
Fusarium oxysporum f. sp. *dianthi* (fungus), 214,
 220–1
 fusarium wilt, carnations, 214
 fusion protein approach, 117
 GA (gibberelic acid), 125, 156
 galangin, 17 β -hydroxysteroid dehydrogenase type 2
 inhibition, 308
 gastric protective activity, anthocyanins, 236
 gastrointestinal tract (GIT), 237, 244
 anthocyanin transformations, 245
 gene discovery, in phenylpropanoid pathway, 113–38
 gene expression
 flavonoids, regulatory mechanisms, 80–3
 and polyphenols, 359–77
 antiatherosclerosis mechanisms, 359, 369–73
 anticancer mechanisms, 363–9
 detoxification mechanisms, 359–63
 urolithins, studies, 273–4
 genistein, 113, 114, 129, 130
 antioxidant activity, 340–1
 atherosclerosis studies, 371–2
 hydrolysis, 319
 17 β -hydroxysteroid dehydrogenase type 1 inhibition,
 305–7
 incubation, 325–6
 production, 117
 sources, 115
 in soy, 369, 372
 genomes, plants, 1–2
Gerbera spp. (gerbers), pigmentation regulation, 156
Gerbera hybrida (gerbera), anthocyanidin synthase,
 120, 190
 gibberelic acid (GA), 125, 156
 gingerol, 127–8
 GIT *see* gastrointestinal tract (GIT)
 (1 $>$ 3),(1 $>$ 4)- β -glucans, biosynthesis, 51–2
 β -glucuronidase, inhibition, 344
 glucuronides, 268–9
 O-glucuronides, 349
 chemical synthesis, 328–32
 glutathione (GSH), 73–4
 glutathione S-transferases (GSTs), 149, 361–2
 cancer risk studies, 360
 glycerol 3-phosphate dehydrogenase (GPDH),
 inhibition, 345
 glycosidases, 14
 glycosylation, flavonoids, 128–30
 glycosyl hydrolases, 123
 glycosyltransferases (GTs), 140
 in phenylpropanoid modification, 123–31
Glycyrrhiza echinata (Russian liquorice) UGT73F1,
 128
 GPDH (glycerol 3-phosphate dehydrogenase),
 inhibition, 345
 green tea, polyphenols, 363, 369–70
 GSII (glutathione), 73–4
 GSTs *see* glutathione S-transferases (GSTs)
 GTs *see* glycosyltransferases (GTs)
 hardwoods, lignin polymer models, *Plate 2.4*
 HDL (high-density lipoprotein cholesterol), synthesis,
 233–4
 health
 anthocyanins in, 228
 flavonoid–protein binding effects, 74–83
 and plant food, 263
 and plant phenolics, 22–4
Helicoverpa armigera (cotton bollworm), 20
 5-12-cis-heptadecenylresorcinol, 214
 hesperetin, 73, 322
 hesperidin, 322
 anti-aromatase activity, 300
 hexahydroxydiphenic acid, 264
Hibiscus sabdariffa (roselle), anthocyanins, 240
 high-density lipoprotein cholesterol (HDL), synthesis,
 233–4
 hirsutidins, 181
 hormone-dependent diseases, treatment, 293
 horseradish peroxidase, 73
 host plants
 recognition, 19
 selection, 19–20
 HPM (human placental microsome-based) assays,
 phytoestrogens in, anti-aromatase activity,
 295–8
 HRs (hypersensitive responses), 15–16
 HSA (human serum albumin), 73, 345–6
 17 β -HSDs *see* 17 β -hydroxysteroid dehydrogenases
 (17 β -HSDs)
 HT-29 cells, 367–9
 human placental microsome-based (HPM) assays,
 phytoestrogens in, anti-aromatase activity,
 295–8
 human serum albumin (HSA), 73, 345–6
Hydrangea macrophylla (bigleaf hydrangea),
 metalloyanins, 189
 3-hydroxyacetophenone, 214
 3-hydroxyanthocyanins, 140
 hydroxycinnamaldehydes, 44–5
 incorporation, into lignins, 41–2

- hydroxycinnamic acid metabolites
characterization, 326–7
structure, 326
- hydroxycinnamic acids
in apples, 278
isomers, 9–10
oxidation, 281
roles, 9–11
structure, 280
- 5-hydroxyconiferyl alcohol
coupling, 44
substitution, *Plate 2.3*
- 4'-hydroxyflavonoids, 73–4
- 2-hydroxyisoflavone synthase, 114
- 17 β -hydroxysteroid dehydrogenases (17 β -HSDs), 293
catalysis, 294
fungal cl, 305, 308–10
phytoestrogen binding, 309–10
inhibition, by phytoestrogens, 304–13
type 1, 305–7
phytoestrogen binding, 307
type 2, 305, 307–8
type 3, 305, 310
type 4, 305, 307–8
type 5, 305, 310–11
- Hypericum calycinum* (great St John's wort), 19
- hypersensitive responses (HRs), 15–16
- IAA (indole-3-acetic acid), 10, 125
- ICS gene, 204
- ICS (isochorismate synthase), 204–5
- IFS see isoflavone synthase (IFS)
- IFS/chalcone isomerase, 116–17
- IFS/CHI fusion gene, 117
- IFS gene, 115–16
- indole-3-acetic acid (IAA), 10, 125
- induced plant defenses
responses, 220–1
and salicylic acid, 202–10
types of, 211
- induced resistance
acibenzolar-S-methyl-mediated, 220
and phenolics, 202–3
and plant growth-promoting rhizobacteria, 220–1
and plant phenols, 219–20
responses, 220–1
and structural phenolics, 221–2
studies, transgenic plants, 205
use of term, 202, 216
- induced systemic resistance (ISR)
mechanisms, 202–3
use of term, 203
see also systemic acquired resistance (SAR)
- innate immune response, animals, 203
- insecticidal activity, lignans, 22
- insecticides, 22
- insects
chemoreceptors, 18
feeding deterrents, 20–1
host plant recognition, 19
host plant selection, 19–20
plant toxin sequestration, 18
see also phytophagous insects
- INTENSIFIER1* gene, 122
- 4,6-inter-flavan bonds, formation, 104–5
- inter-flavan bonds
formation, and benzyl-protected building blocks, 94–7
- future research, 104–5
stereochemistry, 89, 97–102
- IPL (isochorismate pyruvate-lyase), 205
- Ipomoea batatas* (sweet potato), anthocyanic vacuolar inclusions, 150
- Ipomoea batatas* cv Ayamurasaki (purple sweet potato), anthocyanins, 240
- Iris hollandica* (Dutch iris), anthocyanin 3-*O*-coumaroyltransferases, 148
- isochorismate pyruvate-lyase (IPL), 205
- isochorismate synthase (ICS), 204–5
- isoeatin, 8–9
- isoflavone conjugates, antioxidant properties, 339–41
- isoflavone glucosides, 72
- isoflavone metabolites, characterization, 325–6
- isoflavones, 23, 73
anticancer activity, 359–60
antioxidant activity, 341
binding, 74
biosynthesis, 113–15
dietary sources, 115
functions, 113–15
metabolic engineering, 115–17
with artificial isoflavone synthase, 116–17
via ectopic expression of isoflavone synthase, 115–16
- metabolism, 321
- as phytoalexins, 115
- phytoestrogenic activity, 114
in soy, 369
- isoflavone synthase (IFS), 117
in isoflavone metabolic engineering, 115–17
- isoflavonoids, 20
anti-aromatase activity, 303–4
biosynthetic pathways, 113–14
- isolicoflavonol, 312
- isorhamnetin glucuronides, synthesis, 329
- isorhamnetins, 21
structure, 321–2
- isosalipurposide, 8
- ISR *see* induced systemic resistance (ISR)
- JA (jasmonic acid), 205–6
- jasmonic acid (JA), 205–6
- JNKs *see* c-Jun N-terminal kinases (JNKs)
- judaicin, 20
- judaicin-7-*O*-glucoside, 20
- kaempferide, 17 β -hydroxysteroid dehydrogenase type 2 inhibition, 308
- kaempferide triglycosides, 214
- kaempferol, 20–1, 128, 130
binding, to fungal 17 β -hydroxysteroid dehydrogenase cl, 309
- 17 β -hydroxysteroid dehydrogenase type 2 inhibition, 308
- Keap 1 protein, 83
- 4-ketones, synthesis, 102
- lacinilene c, 217
- lactase phlorizin hydrolase, 72
- LAR gene, 118
- LAR (leucoanthocyanidin reductase), 118
- Lc gene, 122
- LC-MS *see* liquid chromatography-mass spectrometry (LC-MS)
- LC-MS/MS *see* liquid chromatography-tandem mass spectrometry (LC-MS/MS)

- LDL receptor, 369–70
 lectins, 71
Leguminosae (pea family), isoflavones, 115
Lens culinaris (lentil), anthocyanins, 183
 leptostachyol acetate, 22
 leucoanthocyanidin reductase (LAR), 118
 leucoanthocyanidins, 118
 leukotrienes, levels, 89
 lignan metabolites, characterization, 325
 lignans, 23
 - anti-aromatase activity, 299
 - insecticidal activity, 22
 lignification, 36–66
 - as biochemical anomaly, 38–9, 51–2
 - β -ether frequency anomaly, 39–40
 - malleability, 43–5
 - mechanisms, 36
 - obligatory linkages, 40
 - roles, in defense, 218–19
 lignification theories
 - challenge hypothesis, 38
 - current, 37, *Plate 2.1*
 - criticisms, 38–40, 53–4
 - direct/replication hypothesis, 36
 - criticisms, 40–50, 53–4
 - issues, 37–8, 50, 52–3
 - issues, 36
 lignin chains
 - branching, 50
 - resinol units in, 49
 lignin oligomers, sequencing, 45–6
 lignin polymerization, theories, 36–54
 lignin polymers, 36, 43, 53
 - branching, 50
 - models
 - hardwoods, *Plate 2.4*
 - softwoods, *Plate 2.4*
 - repeating structures, 45
 lignins
 - biosynthesis, 36
 - branching, 49–50
 - dihydroconiferyl alcohol incorporation, 42
 - hydroxycinnamaldehyde incorporation, 41–2
 - monomer-independent sequences, 46–7
 - number of isomers problem, 48
 - polymer branching, 49–50
 - precursors, 127
 - primary structure, 36
 - polysaccharide, 51–2
 - sequencing, 47
 - well-defined, 45–7
 - racemicity, 47–8
 - repeating structures, 45
 - template replication, 38, 48–9
 - tyramine ferulate incorporation, 42–3
 linoleic acid, 73
 lipophilicity, and antifungal activity, 15
 lipoxygenases, 71
 Lippman, Marc, 88
 liquid chromatography-mass spectrometry (LC-MS)
 - advantages, 290
 - apple beverage oxidation products analysis, 288–90
 liquid chromatography-tandem mass spectrometry (LC-MS/MS)
 - advantages, 290
 - apple beverage oxidation products analysis, 288–90
 - caffeylquinic acid studies, 282–4
 liver, phenolic metabolite biosynthesis, 320
Lobelia erinus (edging lobelia), anthocyanins, 183
 Lobelinin B, 183
Lobularia maritima (sweet alyssum), anthocyanins, 186
Lunaria annua (annual honesty), anthocyanins, 186
 lung cancer, 365
 luteolin, 8–9, 130
 - glucuronidation, 320
 luteolin glucuronides
 - antioxidant activity, 340
 - enzyme inhibition, 344
 luteolinidin, 217
 LXR- α , expression, 370
 maackiain, 20
 MADS protein, 156
 malonic acid, 183
 malonylawobanin, 189
 malvidins, 128, 132, 140, 168
 - occurrence, 181, 183–4
 mango fruit, *Alternaria* infection, 214
 MAPKs (mitogen-activated protein kinases), inhibition, 78
 MATE (multidrug and toxic compound extrusion) proteins, 149
Matthiola incana (hoary stock), anthocyanins, 121
 MCT (monocarboxylic acid transporterT), 346–7
Meconopsis grandis (Himalayan blue poppy), metalloacyanins, 189
Medicago sativa (alfalfa), *IFS* gene, 115–16
Medicago truncatula (barrel clover)
 - ANR* gene, 123
 - IFS* gene, 115–16
 - UGT71G1, 129, 130–1
 MeJA (methyl jasmonate), 205–6
 metabolic engineering
 - flavonoid biosynthesis
 - angiosperms, 142–9
 - ornamental plants, 139–66
 - isoflavones, 115–17
 - in phenylpropanoid pathway, 113–38
 - strategies, 131–2
 - proanthocyanidins, in plants, 122–3
 metabolites
 - ellagic acid tissue distribution, 267–9
 - see also* anthocyanin metabolites; curcumin
 - metabolites; ellagitannin metabolites; phenolic metabolites; resveratrol metabolites; secondary metabolites
 - metalanthocyanins, 188–9
 - metallothioneins, 273–4
 - 2-methoxyjudaicin, 20
 - 7-O-methylapigeninidin, 168
 - O-methylcyanidin, 168
 - 7-O-methylcyanidin 3-galactopyranoside, 168, 181
 - methyl jasmonate (MeJA), 205–6
 - 5-O-methyluteolinidin, structure, 177
 - metmyoglobin, 71
 - microarray-based mRNA analysis, 364
 - mitogen-activated protein kinases (MAPKs), inhibition, 78
 - Mitsunobu reactions, 92
 - molecular biology
 - anthocyanins, 189–91
 - flavonoid biosynthesis, ornamental plants, 139–66
 - Montilinia fructicola* (fungus), infection, 215
 - monocarboxylic acid transporter (MCT), 346–7
 - monolignols
 - applications, 125

- biosynthesis, 36
dimerization, 37
substitution, 43–5
monomers, non-traditional, 44
monomer substitution
and dirigent/replication hypothesis, 40–5
issues, 41–3
MtANR gene, 123
multidrug and toxic compound extrusion (MATE) proteins, 149
Muscari armeniacum (grape hyacinth), anthocyanins, 182
MUTABILIS, 153
MYB factors, 153, 156–7
Myb gene, 155, 156, 190–1
MYC, 153
myricetin, 128
Myrtus caerulea (jaboticaba), anthocyanins, 181
- NADP⁺, reduction, 13
NADPH
oxidation, 13
synthesis, 12–13
NahG (naphthalene hydroxylase), 205
naphthalene hydroxylase (NahG), 205
α-naphthoflavones, 312
anti-aromatase activity, 301
naphthoquinones, 9
naphthylphthalamic acid (NPA), 10
naringenin, 73, 191
naringin, 17
anti-aromatase activity, 300
NAT1 (*N*-acetyltransferase 1), polymorphisms, 360
NAT2 (*N*-acetyltransferase 2), polymorphisms, 360
NCOL-1 colon cells, 369
necrosis, 107
see also apoptosis
neoplasias, 89
neuroprotective activity, anthocyanins, 234
N gene, 219
Nicotiana benthamiana, salicylic acid, 205
nitrobenzene, oxidation, 46–7
NMR (nuclear magnetic resonance), image interpretation, 43
NodD protein, 8
Nod factors, 8
nod genes, 115
expression, 8
non-host resistance, 14
NPA (naphthylphthalamic acid), 10
NPR1 protein, 220
Nrf2 (nuclear factor erythroid-2-related factor), 361–2,
• 370, 372
NtGT1s, 129–30
NtGT3, 129–30
nuclear factor erythroid-2-related factor (Nrf2), 361–2,
• 370, 372
nuclear magnetic resonance (NMR), image interpretation, 43
nyctinasty, 10
Nymphaea caerulea (African water lily), delphinidin, 182
- OAT (organic ion transporter), 347
OATP-B transporter, 348
obesity prevention, anthocyanins, 235–6
olomoucine, 105–6
onion bulbs, resistance, 213
- onion smudge disease, 15, 213
OPDA (12-oxophytodienoic acid), 205–6
Operophtera brumata (winter moth), feeding deterrents, 19
ORAC (oxygen radical absorbance capacity), 230
organic ion transporter (OAT), 348
Origanum vulgare (oregano)
phenolics, 12–13
rosmarinic acid, 12–13
ornamental plants
flavonoid biosynthesis
metabolic engineering, 139–66
molecular biology, 139–66
Orychophragmus violaceus (hanadaikon), anthocyanins, 186
Oxalis triangularis (love plant)
anthocyanin–flavone C-glycosides, 187–8
anthocyanins, 183–4
oxidative pentose phosphate pathway, 12–13
oxidative stress, neutralization, 264
ox-LDL, 372
12-oxophytodienoic acid (OPDA), 205–6
oxygen radical absorbance capacity (ORAC), 230
- p53, phosphorylation, 108
PAHs (polycyclic aromatic hydrocarbons), 360–1
PAL (phenylalanine–ammonia lyase), 203–4
PAMP (pathogen-associated molecular patterns), 15
PAP1 gene, 123
Papilio xuthus (swallowtail butterfly), 20
PAs *see* proanthocyanidins (PAs)
pathogen-associated molecular patterns (PAMP), 15
pathogenesis, mechanisms, 211
pathogen-related (PR) proteins, 202
pelargonidins, 128, 140, 168, 184, 187
absorption, 251–2
biosynthesis, 143
Penicillium digitatum (fungus), 17
5-pentadecylresorcinol, 214
peonidin, 140, 168
Perilla frutescens (green shiso), anthocyanin synthase, 118
Peronospora parasitica (downy mildew), resistance to, 206
peroxidase, induction, 16
peroxisome proliferator-activated receptor- α (PPAR- α), activation, 370
peroxisome proliferator-activated receptor- γ (PPAR- γ), 81
expression, 369–70
petals, anthocyanic vacuolar inclusions, 150–2
petunidins, 140, 168, 181
PGPR (plant growth-promoting rhizobacteria), and induced resistance, 220–1
Phacelia campanularia (California bluebell), anthocyanins, 185–6
Phaseolus vulgaris (common bean), 22
induced resistance, 220
phenolic acids
antifungal activity, 15
roles, 10–11
phenolic conjugates, 317, 318
antioxidant properties, 334–42
biological properties, 334–46
cellular efflux, 346–7
cellular transport, 346–8
cellular uptake, 347–8
chemical synthesis, 328–33

- effects
 on angiogenesis, 345
 on vascular function, 345
 enzyme inhibition, 344–5
 future research, 349
 interactions, with signaling cascades, 343–4
 noncovalent binding, to proteins, 345–6
 pro-oxidant properties, 342–3
 phenolic glycosides, solubility, 2
 phenolic hydroxyls, methylation, 91
 phenolic metabolites
 analytical issues, 317–18
 bioactivity, developments, 317–58
 biological properties, 318
 biosynthesis, sites, 318–21
 characterization, 317, 321–8
 chemical synthesis, developments, 317–58
 detection, 317
 future research, 348–9
 microbial, activity, 346
 tissular, activity, 346
 phenolic oxidation products
 in apple juice, 278–92
 in cider, 278–92
 phenolic phytoalexins, in plant defenses, 216–18
 phenolics, 12–13
 absorption, 3
 antioxidant activity, 263–4
 and plant defenses, 222
 research publications, 264
 in apples, 278–81
 biosynthesis, 3, 13, 16
 chemical induction, and plant resistance, 221–2
 classification, 2
 defense-associated, biosynthetic origins, 212
 and disease resistance, 15
 dissolution, 3
 and induced resistance, 202–3
 as insect feeding barriers, 19
 metabolism, 317
 occurrence, 3
 oxidation, 278–81
 and plant–insect interactions, 17–22
 as preformed defenses, 212–15
 roles
 in fruit post-harvest resistance, 16–17
 in health, 23–4
 structural, and induced resistance, 221–2
 structure, 213, 217
see also plant phenolics
 phenolic structural defenses, 218–19
 phenols
 antifungal activity, 15, 214–15
 bioactivity, 335–8
 definition, 2
 and plant defenses, roles, 222–3
 and plant disease resistance, 211–27
 radical coupling, 36, 37
 phenylalanine, 205
 phenylalanine–ammonia lyase (PAL), 203–4
 phenylpropanoid alcohols, structure, 124
 phenylpropanoid aldehydes, structure, 124
 phenylpropanoid pathways
 angiosperms, 141
 gene discovery, 113–38
 metabolic engineering, 113–38
 strategies, 131–2
 phenylpropanoids
 modification, via glycosyltransferases, 123–31
 mutants, 6
 phloretin xyloglucoside, in apples, 278
 phloridzin
 in apples, 278
 oxidation products, 280–1
 phloroglucinols, 19
Phryma leptostachya (American lopseed), insecticidal activity, 22
 phytoalexins, 14, 17, 202, 217–18
 biosynthesis, 16, 217
 characterization, 216
 isoflavones as, 115
 structure, 177
 phytoanticipins, 14
 use of term, 202
 phytoestrogenic activity, isoflavones, 114
 phytoestrogens, 271
 anti-aromatase activity, 299–300
 in cell-based assays, 298–9
 in human placental microsome-based assays, 295–8
 in recombinant-enzyme assays, 299
 binding
 to fungal 17 β -hydroxysteroid dehydrogenase cl, 309–10
 to 17 β -hydroxysteroid dehydrogenase type 1, 307–8
 17 β -hydroxysteroid dehydrogenase inhibition, 304–12
 as lead compounds
 for aromatase inhibition, 301–4
 for 17 β -hydroxysteroid dehydrogenase inhibition, 311–12
 natural, as aromatase inhibitors, 295–300
 for steroid biosynthesis control, 293–316
 structure, 295
 structure–activity relationships, 300–1
 phytophagous insects, 18
 effects of tannins on, 22
 salivary secretions, 21
Phytophthora infestans (fungus), 216
Phytophthora porri (fungus), resistance to, 206
 phytotoxins, 7
Picea abies (Norway spruce), coniferyl alcohol
 glycosyltransferase, 124
Pieris napi oleracea (mustard white), 20
 pigmentation patterning, 153–5
 pigments
 plant phenolics, 8–9
see also flower pigments
 pig studies
 anthocyanin metabolism, 252
 ellagitannins, 267–69
 pinocembrin, 212
 pinoresinol, coupling, 40
Pinus strobus (eastern white pine)
 aldehydes, 124
 coniferyl alcohol glycosyltransferase, 124
 pisatin, 216
 PKC (protein kinase C), inhibition, 78
 PKC- β (protein kinase C- β), 365–7, 368
 plant cells, anthocyanins in, 191–2
 plant defenses
 active, 215–16
 digital approach, 206
 early studies, 202
 induced resistance, and phenolics, 202–3

- localized, 216–20
 and phenolics, antioxidant activity, 222
 and phenols, roles, 222–3
 and plant phenolics, 3, 11–22
see also induced plant defenses
 plant disease resistance, and phenols, 211–27
 plant food
 antioxidant activity, 263
 and health, 263
 plant growth, and plant phenolics, 9–11
 plant growth-promoting rhizobacteria (PGPR), and
 induced resistance, 220–1
 plant-insect interactions, and phenolics, 17–22
 plant pathogens
 diversity, 211
 types of, 211
 plant phenolics
 applications, 3, 5–24
 pigments, 8–9
 signal compounds, 6–8
 ultraviolet sunscreens, 6
 classification, 3
 functions, 3–24
 and health, 22–4
 and plant defenses, 3, 11–22
 and plant growth, 9–11
 secondary metabolites with diverse functions, 1–35
 solubility, 2–3
 structure, 3, 4
 as waste products, 5
 plant phenols, and induced disease resistance, 219–20
 plant polyphenols
 chemical scaffolds, 113
 definition, 2
 physiological properties, 359
 roles, 113
 plant resistance
 and chemical induction of phenolics, 221–2
 mechanisms, 11, 202
 plants
 anthocyanin structures, research developments, 167–201
 caffeic acid *O*-methyltransferase deficiency, 41, 44, *Plate 2.3*
 curing, 17
 genomes, 1–2
 proanthocyanidins, metabolic engineering, 122–3
 secondary metabolism, 1–5
 ultraviolet exposure, 6
see also angiosperms; host plants; ornamental plants;
 tobacco plants
 plant secondary product glycosyltransferase (PSPG), 147
 plant toxins, sequestration, 18
 plumbagin, 9
Plumbago capensis (Cape plumbago), plumbagin, 9
Podosphaera xanthii (fungus), 217–18
 PODs (polyphenol peroxidases), 21
 polycyclic aromatic hydrocarbons (PAHs), 360–1
 polyketide acetate/malonate pathway, 2
 polymer branching, lignins, 49–50
 polymerization, in lignification, 36
Polyommatus icarus (common blue), 18
 polyphenol oxidases (PPOs), 21
 polyphenol peroxidases (PODs), 21
 polyphenol–protein complexes, origins, 7
 polyphenols
 anticancer activity, 359–60
 antioxidant activity, *in vitro*, 359
 definition, 2
 enzymatic oxidation, 279–80
 food, 263–77
 and gene expression, 359–77
 antiatherosclerosis mechanisms, 359, 369–73
 anticancer mechanisms, 363–9
 detoxification mechanisms, 359–63
 protective effects, 359
 use of term, 2
see also cocoa polyphenols; plant polyphenols
 polysaccharides, acylation, 51
 pomegranate juice
 antioxidant activity, 265, 324
 bioavailability, studies, 269
 health effects, 265–6
 metabolism, studies, 269
Populus deltoides (eastern cottonwood), pinocembrin, 212
 post-harvest treatment
 fruit, 17
 vegetables, 17
 potatoes
 defenses, 216
 salicylic acid, 203–4
 PPAR- α (peroxisome proliferator-activated receptor- α), activation, 370
 PPAR- γ (peroxisome proliferator-activated receptor- γ), 81
 expression, 369–70
 PPOs (polyphenol oxidases), 21
 PR-10 protein, 12
 pratinose, 115
 preformed antifungals, regulatory mechanisms, 214–15
 preformed defenses, phenolics as, 212–15
 pregnane \times receptor (PXR), 359
 prevacuolar compartments (PVCs), 192
 primary metabolism, use of term, 1
 primin, 9
Primula obconica (German primrose), primin, 9
 proanthocyanidin biosynthetic pathway
 gene discovery, 117–22
 regulatory genes, 121–2
 structural genes, 118–21
 proanthocyanidins (PAs)
 anticancer activity, 105–9
 biosynthesis, 119
 metabolic engineering, in plants, 122–3
 occurrence, 117–18
 toxicity, 15
 procyanidin B₁, stereochemistry, 97–8, 99–100
 procyanidin B₂
 O-benzylation, 100
 O-methylation, 100
 stereochemistry, 99–100
 structure, 97–8, 99
 procyanidins, 71–2
 activity, 89
 in apples, 278
 cocoa, 89–91
 cytotoxicity, 105, 106
 structure, 279
 synthesis, 89–105
 benzyl-protected building blocks, 92–4
 developments, 102–5
 early studies, 91–2
 prohexadione, 221

- proline biosynthesis, 12–13
 prooxidant activity, anthocyanins, 231
 prostacyclin, levels, 89
 prostaglandin F synthase–NADPH–rutin complex, 68, 70
 prostate cancer
 prevalence, 293
 protective factors, 293
 protein kinase C (PKC), inhibition, 78
 protein kinase C- β (PKC- β), 365–7, 368
 protein kinases, inhibition, 78–9
 proteins, noncovalent binding, to phenolic conjugates, 345–6
 proteome analysis, 364, 365–9
 protocatechuic acid, 213
 protodelphin, 189
 PR (pathogen-related) proteins, 202
Prunus mume (Japanese apricot), anthocyanins, 186
Pseudomonas aeruginosa (bacterium), and salicylic acid biosynthesis, 205
Pseudomonas fluorescens (bacterium), and salicylic acid biosynthesis, 205
Pseudomonas putida (bacterium), 205
Pseudomonas syringae (bacterium), and salicylic acid biosynthesis, 205
Pseudomonas syringae pv. *syringae* (bacterium), 222
 PSPG (plant secondary product glycosyltransferase), 147
Pulsatilla cernua (pasqueflower), anthocyanins, 182–3
 punicalagin, 264, 268
 apoptosis induction, 271–3
 fermentation, 346
 metabolism, 271–3
 structure, 324
 purpurin, 9
 puvalanol B, 105–6
 PVCs (prevacuolar compartments), 192
 PXR (pregnane X receptor), 359
 Pycnogenol, 24
 pyranoanthocyanidin, 168
 pyranoanthocyanins, structure, 177–8
- QSAR (quantitative structure–activity relationship)
 model, 302
 quantitative structure–activity relationship (QSAR)
 model, 302
 quercetin conjugates, metabolism, 320
 quercetin-3-*O*-glucuronide, 78–9
 quercetin glucuronides
 effects on angiogenesis, 345
 enzyme inhibition, 345
 synthesis, 329–30
 quercetins, 9, 20–1, 71, 128, 130
 antioxidant activity, 340–1
 glucuronidation, 72–3, 320
 hydrolysis, 318–19
 oxidation, 76–7
 pro-oxidant properties, 342–3
 structure, 321–2
 toxicity, 343
 quercetin *O*-sulfates
 chemical synthesis, 332–3
 effects on angiogenesis, 345
 quinones, 9
 structure, 126
o-quinones, 281
- RA see rosmarinic acid (RA)
Raphanus sativus (radish), seed germination, 11
 rat studies, anthocyanin metabolism, 251–2
Rauvolfia serpentine (Indian snakeroot), arbutin synthase, 127, 130
Rc gene, 122
 reactive oxygen species (ROS), 6
 increased production, 368
 production, enzyme inhibition, 74–5
 recombinant-enzyme assays, phytoestrogens in, anti-aromatase activity, 299
 red wine
 anthocyanins, 237
 and atherosclerosis, 369
 and coronary heart disease reduction, 233–4
 regulatory genes, for proanthocyanidin biosynthetic pathway, 121–2
 regulatory proteins, anthocyanin-related, 154
 resinols, softwoods, 40
 resinol units, in lignin chains, 49
 resistance
 mechanisms, 11
 species-specific, 14
 see also induced resistance; plant resistance
 resistance genes, 11
 resveratrol, 369
 t-butyldimethylsilylation, 330–2
 resveratrol glucuronides, synthesis, 330, 331
 resveratrol metabolites, 348–9
 characterization, 328
 structure, 328
R gene, 121
 rhamnetin, antioxidant activity, 341–2
 rhizobia, 7
 rhizobia-legume symbiosis, 8
Rhizobium spp. (soil bacteria), genes, 7
Rhizoctonia spp. (fungus), 216
 ribulose-5-phosphate, as intermediate, 13
 robinin, 21
 roots, communication, 7
 ROS see reactive oxygen species (ROS)
 rosacyanin B, structure, 177–8
Rosa hybrida (rose), rosacyanin B, 177–8
 roscovitine, 105–6
Roseal gene, 155
Rosea2 gene, 155
 rosmarinic acid (RA), 12–13
 metabolites, 327
 rubrocampanin, 184
 RUGT-5, 130
 rutin, 318
- SA see salicylic acid (SA)
 SABPs (salicylic acid binding proteins), 206–7, 219–20
 salicylate glucosyltransferase, 125
 salicylates, 19
 salicylic acid binding proteins (SABPs), 206–7, 219–20
 salicylic acid (SA)
 biosynthesis, 203–5
 genetic approach, 204–5
 in plant defenses, 16
 early studies, 203
 induced, 202–10
 mechanisms, 205–7
 synthesis, 125
 saliva, phenolic metabolite biosynthesis, 318–19

- salivary proteins, interactions, with dietary flavonoids, 71–2
- Salix* spp. (willows), salicylates, 19
- Salvia patens* (gentian sage), metalloanthocyanins, 189
- SAR see systemic acquired resistance (SAR)
- Sclerotinia sclerotiorum* (fungus), 221
- scoparone, 17
- scopoletin, 17, 126
- secondary metabolism
- mechanisms, 1
 - plants, 1–5
 - use of term, 1
- secondary metabolites, 211
- bioactivities, 1–2
 - classification, 2
 - with diverse functions, 1–35
 - transport, 5
- seed germination, 10–11
- Ser392, 108
- sex steroids
- biosynthesis, 293
 - blocking, 293
- SGLT1 see sodium-dependent glucose transporter 1 (SGLT1)
- shikimate/phenylpropanoid pathway, 2
- shikimic acid pathway, 13
- signal compounds, plant phenolics, 6–8
- signaling cascades, interactions, with phenolic conjugates, 343–4
- signaling pathways, analysis, 365
- silicon, as defense modulator, 221
- silybin, 323–4
- silybin glucuronides, antioxidant activity, 341
- silymarin, anti-aromatase activity, 300
- sinapaldehyde, 44–5
- sinapic acid, synthesis, 125
- sinapyl alcohols, *Plate 2.3*
- biosynthesis, 36
 - dehydromerization, 39
 - partial substitution, 44
- sinapyl aldehydes, 124
- glycosylation, 125
- Sinningia cardinalis* (sinningia), 3-deoxyanthocyanins, 190
- small intestine, phenolic metabolite biosynthesis, 319–20
- sodium-dependent glucose transporter 1 (SGLT1), 237, 241
- roles, 243–4
- softwoods
- lignin polymer models, *Plate 2.4*
 - resins, 40
- Sorghum bicolor* (sorghum)
- 3-deoxyanthocyanidin phytoalexin synthesis, 12
 - 3-desoxanthocyanidin, 168
- Sorghum caudatum*, 7-O-methylapigeninidin, 168
- soy, polyphenols, 369, 372–3
- soybeans, *IFS* gene, 116
- species-specific resistance, 14
- Sphagnum fallax* (moss), *p*-coumaric acid, 126
- Spodoptera exigua* (beet armyworm), 20
- Spodoptera frugiperda* (fall armyworm), 20
- Spodoptera littoralis* (African cotton leafworm), 20
- SREBP (sterol-response binding protein), 369–70
- steroid biosynthesis control, phytoestrogens for, 293–316
- sterol-response binding protein (SREBP), 369–70
- stilbenes, 23
- antifungal activity, 15
- stomach, phenolic metabolite biosynthesis, 319
- stone fruit, *Monilia* infection, 215
- structural genes, for proanthocyanidin biosynthetic pathway, 118–21
- O-sulfates, 349
- chemical synthesis, 332–3
 - syringaresinol, biosynthesis, 39
 - syringyl oligomers, 46
 - syringyl units, 45–6
 - coupling, 44–5
- systemic acquired resistance (SAR), 16
- mechanisms, 202–3
 - use of term, 203
- see also* induced systemic resistance (ISR)
- tangeretin, 17
- tannins
- antibiotic activity, 15
 - effects on phytophagous insects, 22
 - toxicity, 15
- see also* ellagitannins; proanthocyanidins (PAs)
- TEAC (trolox equivalent antioxidant capacity), 230, 334
- template replication, lignins, 38, 48–9
- ternatin A1, 182
- terpenoids, 2
- testosterone
- biosynthesis, 293
 - blocking, 293
- tetra-*O*-benzylepicatechin
- bromination, 102
 - formation, 92
 - oxidation, 93
- tetrahydrocurcumin (THC), 346
- tetrahydroxydibenzopyranones, 268–9
- tetratrilates, synthesis, 100, 101
- TFs *see* transcription factors (TFs)
- THC (tetrahydrocurcumin), 346
- thioacidolysis, 46–7
- thionocarbonates, synthesis, 100, 101
- thioredoxin reductase, 372
- TIC chromatograms *see* total ion current (TIC) chromatograms
- tissues, phenolic metabolite biosynthesis, 321
- TMV *see* tobacco mosaic virus (TMV)
- tobacco mosaic virus (TMV), 204, 207
- resistance to, 219
- tobacco plants
- coumarins, 126
 - resistance, 219
 - salicylic acid, 203–4
 - transgenic, 117
- TOGT, 126
- tolerance mechanisms, 11
- Torenia hybrida* (snapdragon), malvidin, 132
- total antioxidant potential (TRAP) assays, 230
- total ion current (TIC) chromatograms
- caffeoquinic acid, 282, 283
 - caffeoquinic acid *o*-quinone, 285
 - (–)-epicatechin, 285
- transcription factors (TFs), 81–2, 122–3, 156–7
- activation, 78
 - in anthocyanin biosynthesis, 152–3
- transgenic plants, induced resistance studies, 205
- TRAP (total antioxidant potential) assays, 230
- trichloroacetimidates, 329–30

- Tricyrtis formosana* (toad lily)
 anthocyanins, 184
 cyanidins, 182
 trihydroxydibenzopyranones, 268–9
 trolox equivalent antioxidant capacity (TEAC), 230, 334
- TT2* gene, 121–2
TT8 gene, 121–2
TT12 gene, 120
TT19 gene, 120
TTG1 gene, 121
 tumors, ERBB2-positive, 364
 turgorins, 10
 tyramine ferulate, incorporation, into lignins, 42–3
 tyrosine kinase, inhibition, 89
- UGT71C1, 130
UGT71C1 gene
 expression, 127
 induction, 130–1
 UGT71C4, 130
 UGT71G1, 129, 130–1
 UGT72E1, 124–5, 130
 UGT72E2, 124–5
 UGT73B2, 130
 UGT73F1, 128
 UGT73J1, 129
 UGTs *see* uridine diphosphate glycosyltransferases (UGTs)
 ultraviolet (UV) sunscreens, plant phenolics, 6
 umbel, 182
 umbelliferone, 17 β -hydroxysteroid dehydrogenase type 3 inhibition, 310
 uridine diphosphate glycosyltransferases (UGTs), 129
 active with non-flavonoid phenolics, 124–8
 functional annotation, issues, 130–1
 urolithins, 268, 269, 324
 antioxidant activity, 346
 estrogenic activity, 271
 gene expression studies, 273–4
Uteheisa ornatrix (bella moth), 19
 UV (ultraviolet) sunscreens, plant phenolics, 6
- Vaccinium myrtillus* (bilberry), anthocyanins, 233, 236
 vascular function, phenolic conjugate effects, 345
 vascular smooth muscle cell (VSMC) hypertrophy, 343
 VCEAC (vitamin C equivalent antioxidant capacity), 334
 vegetables, post-harvest treatment, 17
Venosa gene, 155, 156
Viburnum opulus (Guelder-rose), anthocyanins, 183
Vicia villosa (hairy vetch), 18
Vigna spp. (cowpeas), 20–1
Vigna luteola (hairypod cowpea), 21
Vigna marina (beach pea), 21
 VIGS (virus induced gene suppression), 205
Viola cornuta (tufted pansy), pigmentation, 156
 virus induced gene suppression (VIGS), 205
 vision improvement, and anthocyanins, 236
 vitamin C equivalent antioxidant capacity (VCEAC), 334
 vitamin P, 359
 use of term, 233
Vitis vinifera (grape vine)
 anthocyanic vacuolar inclusions, 191
 leucoanthocyanin reductase, 118
VvGT1, 131
 VSMC (vascular smooth muscle cell) hypertrophy, 343
VvGT1, 131
 WD-repeat (WDR) protein, 153, 155
 WDR (WD-repeat) protein, 153, 155
 wine *see* red wine
- xanthine oxidase
 catalysis, 75
 inhibition, 23, 344–5
Xanthomonas spp. (bacterium), 222
 xanthones, anti-aromatase activity, 302
 xenobiotic responsive element (XRE), 360
 xenobiotic transport, 362–3
 XRE (xenobiotic responsive element), 360
- zeatin, 125