

Index

A

ABA. *See* Abscisic acid
Abscisic acid (ABA), 374
ACAP, 223
Acetabularia, 369
Acetobacter pomorum, 33–34
Acromyrmex echinator, 32
Actin
 dynamics
 comparison of prokaryotes and eukaryotes,
 207–208, 211
 cooperation between filaments, 210
 dynamic instability, 208–210
 force generation, 210
 nucleation, polymerization and capping, 208
 treadmilling, 208
 origins, 203–205
Actinobacteria, Neomura relationship, 52–53
Adaptin, 222, 226
ADP-ribosyltransferase (ART), 284–285
African sleeping sickness, 224
Alb3, 241
Algoriphagus machipongonensis, 34
Alp7, 209
Alp7A, 210
 α -Proteobacterial component (APC), mitochondria
 origins, 254, 259–260
Alternative splicing. *See* Spliceosome
Alu, 321
Alveolates. *See* Stramenophiles, alveolates,
 and Rhizaria
Amoeba proteus, 86
Amoebophilus, 288
Amoebozoa, 185
Anaphase promoting complex (APC), 60
AP-1, 226–227
AP-2, 224
AP-3, 226
AP-5, 226–227
APC. *See* α -Proteobacterial component; Anaphase
 promoting complex
Apoptosis, threshold, 92
Arabidopsis, 372
ARAP, 224
ARC6, 268
Archaea. *See also* TACK superphylum
 eukaryome

 cell division and membrane remodeling
 systems, 123
 cytoskeleton, 119, 122–123
 RNA interference system, 123–124
 ubiquitin signaling system, 118–122
microfossil records of eukaryogenesis,
 153–160
phylogenomics study of evolutionary association
 with eukaryotes
 concatenated protein and ribosomal DNA data
 sets, 103–104
 compositional bias effects, 107
 data selection, 101–103
 discordant protein cluster removal, 104–106
 prospects for study, 108–109
 taxon sampling effects, 107
Archaeplastida, 186–187
ArfGAPs, 223–224, 226
Arp2/3, 44, 46, 203, 205
ArsA, 239
ART. *See* ADP-ribosyltransferase
Aspergillus, parasexuality, 345
ATP synthase, 258, 264
ATP/ADP translocase, 144, 258–259
Auxin, rhizobacteria synthesis, 32–33

B

Bacteria, animal origin influences
 biology of first animals, 395–398
 choanoflagellate colony as model, 398–399
 developmental switch regulation, 399–491
 genetic toolkit for animal multicellularity,
 401–403
 overview, 393–395
 prospects for study, 403–404
Bangiomorpha, 264
Bangiomorpha pubescens, 154, 157, 169, 172
Bigelowiella, 288
Bigelowiella natans, 228–229, 309
Bioenergetics
 mitochondria and evolution of basal eukaryotic
 traits
 mitonuclear coadaptation, 90–92
 overview, 89–90
 respiratory function and evolutionary
 trade-offs, 92–93

Index

Bioenergetics (*Continued*)

- proton gradients and constraints on origin of life
 - alkaline hydrothermal vents for harvesting, 82–83
 - evolution of machinery, 83–85
 - overview, 81–82
- transition from prokaryotes to eukaryotes
 - core bioenergetic genome, 87
 - overview, 85
 - prokaryote genomic asymmetry from endosymbiosis, 89
 - scaling of cell volume and genome copy number, 85–87

Biological species concept (BSC), 3–4

Biomarkers, evolutionary rate calibration estimation, 168–169

Bradyrhizobium, 29

BSC. *See* Biological species concept

BtubA, 205–206

BtubB, 205–206

Bugula, 399

Burkholderia, 32

C

C60-Poisson models, 174–176

Caenorhabditis, 47

Candida albicans, parasexuality, 345–346

Candidatus Caldiarchaeum subterraneum, 116, 118, 120, 122

Candidatus Chloracidobacterium, 64

Candidatus Korarchaeum cryptophylum, 106, 116

Canis familiaris, 4

Carotenoids, biosynthesis, 31, 147

Caulerpa, 369

Cdk8, 281

Cell division, Archaea system, 123

Cell kinds, 41–44

Chagas disease, 224

Chara, 372–374, 376

Chemosynthesis, 30

Chimera, 17–19

Chlamydia, 264–265

Chlamydiae, photosynthetic eukaryogenesis, 144–147

Chlamydomonas reinhardtii, 144, 377–384

Chloroflexi, 64–65, 68

Chloroplast. *See* Plastids

Chromera velia, 143–144

Cilia, phagotrophy-related origin, 57–59

Ciona intestinalis, 399

Cladonia rangifera, 32

Cladophora, 369

CLMP1, 268

Closterium, 376

Coleochaete, 375

Coleochaete orbicularis, 370, 372

Collodictyon, 191

Comparative biology, expectations in eukaryogenesis studies, 151–153

COP coats, 47, 221, 239

CoRR hypothesis, 88

Cryptococcus neoformans, 352

Cyanidoschyzon, 286

Cyanidoschyzon merolae, 143–144

Cytoskeleton

Archaea, 119, 122–123

dynamics

comparison of prokaryotes and eukaryotes, 207–208, 211

cooperation between filaments, 210

dynamic instability, 208–210

filament nucleation, polymerization and capping, 208

force generation, 210

higher-order filament structures, 210–211

treadmilling, 208

eukaryote organelle coevolution, 212–214

functional overview, 200–203

prokaryote homologs

actin origins, 203–205

microtubule origins, 205–206

miscellaneous proteins, 206–207

motor proteins, 206

D

DegP, 238

Deinococcus, 62, 65

Dendroctonus ponderosae, 32

Derlin, 50

Diphylleia, 191

DNA methylation. *See* Epigenetics

Doc, 285

Dot1, 279

DSCR3, 226, 229

E

EGT. *See* Endosymbiotic gene transfer

Elf1, 118

ENCODE project, 321–322

Endoplasmic reticulum (ER)

coevolution of mitochondrial, endoplasmic reticulum, and peroxisomal respiration and segregation, 54–55

origins, 235

Endoplasmic reticulum-associated degradation (ERAD), 235, 239–240

Endoplasmic reticulum-mitochondria encounter structure (ERMES), 133

Endorina, 377

- Endosymbiosis
ATP savings from endosymbiont proteins, 87
photosynthesis
 cryptic Chlamydiae in photosynthetic eukaryogenesis, 144–147
 cryptic green algal endosymbioses in diatoms and chromerids, 142–143
 overview, 141–142
 prospects for study, 147–148
 taxonomic sampling and methods, 143–144
 prokaryote genomic asymmetry, 89
Endosymbiosis. *See also* Mitochondria; Plastids; Symbiosis
 chimeras, 17–19
 order of discovery effect on interpretation, 19–21
 theories, 15–17, 21–23
Endosymbiotic gene transfer (EGT), 142–145, 147, 250, 267
Energetics. *See* Bioenergetics
Enteromorpha, 34
Eocyte model, 98–99, 115
Epigenetics
 bacterial conflict systems, 288–289
 biogeochemical considerations, 289
 DNA modification, 286–287
 encoding, resetting, and reading of marks, 274–278
 eukaryote evolution, 287–288
 overview, 273–274
 prospects for study, 289–290
 protein domains, 276–277, 280
 protein modifications
 acetylation, 279, 281
 acylation, 286
 ADP ribosylation, 284–285
 glycosylation, 285
 methylation, 278–279
 miscellaneous modifications, 285–286
 nucleotidylation, 285
 phosphorylation, 281–282
 ubiquitin system, 282–284
 reactions, 275
Epulopiscium, 86, 88
ER. *See* Endoplasmic reticulum
ERAD. *See* Endoplasmic reticulum–associated degradation
ERMES. *See* Endoplasmic reticulum–mitochondria encounter structure
ESCRT-0, 226
ESCRT-I, 226
ESCRT-III, 45–46, 44, 123
Ethylene, 374
Eubacterium rangifera, 32
Euglena, 86
Eukaryotic tree of life, 166–168, 182–183
Excavata, 185–186
- F**
FECA. *See* First eukaryotic common ancestor
FfH, 237
Fic, 285
Filarcheota, diverse cell biology, 55–57
First eukaryotic common ancestor (FECA), 129, 131, 134, 256
Fossils
 Archaea eukaryogenesis microfossil records, 153–160
 cross-validation for accuracy assessment, 176
 evolutionary rate calibration estimation, 168–169
 molecular clock analysis constraints, 169–170
Frankia, 29
FtsA, 203, 205, 207, 210–211
FtsH, 207
FtsI, 202
FtsW, 202
FtsY, 237
FtsZ, 45, 50, 54, 123, 202, 205, 210, 213, 268
- G**
GA. *See* Gibberellic acid
GAR1, 383
GCN5, 279
Get3, 239
Giardia, 15, 278, 286
Gibberellic acid (GA), 374
GIT, 224
Glycosyltransferases, 285
GOE. *See* Great oxygenation event
Gonium, 380–381
Great oxygenation event (GOE), 289–290
Green algae. *See* Photosynthesis; Plant multicellularity
Grypania, 264
Grypania spiralis, 169
GSM1, 356
GSP1, 356
Guillardia theta, 228–228
- H**
Heliobacterium, 42
HGT. *See* Horizontal gene transfer
Histones, 42, 50, 60
 modification. *See* Epigenetics
Homeostatic property cluster (HPC), 2, 7
Horizontal gene transfer (HGT), 116, 118, 123–124, 147, 191, 205–206, 227, 229, 343
Hotair, 332
HPC. *See* Homeostatic property cluster
Human Microbiome Project, 27
Hydrogen Hypothesis, 10, 98–99
Hydroides elegans, 399

Index

I

IDA. *See* Initial Darwinian ancestor
Importin- β , 239
Initial Darwinian ancestor (IDA), 318
Intron. *See* Spliceosome

J

JAK, 282
JBP, 287, 289
JOR/JmjC, 278, 286–287, 289

K

Katanin, 206–207
Kif proteins, 211
Kinesin, 211

L

LACA. *See* Last archaeal common ancestor
Last archaeal common ancestor (LACA), 116, 123
Last eukaryotic common ancestor (LECA)
 Archaea, 114, 123
 dating, 171–174, 177
 epigenetics, 278–279, 281–287
 membrane trafficking system, 222–223, 226–227,
 234
 mitochondria, 129–134, 136–137
 overview, 7–10, 20
 proteome, 256
 sexual reproduction, 343–344, 348, 355
 spliceosome, 299–308
 tree of life, 166, 168
Last mitochondrial common ancestor (LMCA), 250,
 252
Last universal common ancestor (LUCA), 13, 20, 70, 318
Lateral gene transfer (LGT), 8, 43, 51–52, 63, 65, 69–70,
 80, 256, 259, 401–402
LBA. *See* Long branch attraction
LECA. *See* Last eukaryotic common ancestor
Legionella, 288
Leucaena leucocephala, 32
Leucoprinus gongylophorus, 32
LGT. *See* Lateral gene transfer
LINEs, 321–322
LMCA. *See* Last mitochondrial common ancestor
Lolium, 31
Long branch attraction (LBA), 165, 171
LUCA. *See* Last universal common ancestor

M

MADS, 376
Malawimonas, 191
MamK, 205

Markov chain Monte Carlo (MCMC), 176
MAT, 351
Mating-type determination (MTD), 350–353
MCM, 60
MCMC. *See* Markov chain Monte Carlo
ME. *See* Methylerythritol phosphate
Meiosis. *See* Sexual reproduction
Membrane trafficking. *See also* Protein trafficking
 ancient machinery, 221–223
 complexity, 226–229
 conserved and lineage-specific proteins, 223–225
 nonendosymbiotic organ evolution, 222–223
 overview, 219–221
 patchy proteins, 225–226
 prospects for study, 229–230
Mesoprotozoeric era, eukaryote fossils, 155, 157, 169
Mesotigma, 370
MetaHIT, 27
Methylerythritol phosphate (ME), synthesis, 52
Mevalonate, synthesis, 52
MgIA, 206
MgIB, 206
Micrasterias, 375
Microfossils. *See* Fossils
Microtubule, origins, 205–206
MID, 351, 383
Midichloria mitochondrii, 136
MIR element, 323
Mitochondria
 acquisition models, 135–137
 coevolution of mitochondrial, endoplasmic
 reticulum, and peroxisomal respiration
 and segregation, 54–55
 early versus late eukaryogenesis scenarios, 133–135
 evolution of basal eukaryotic traits
 mitonuclear coadaptation, 90–92
 overview, 89–90
 respiratory function and evolutionary trade-offs,
 92–93
 last eukaryotic common ancestor
 inference of mitochondria in, 131–132
 symbiosis timing, 132–133
 pre-endosymbiont hypothesis
 implications, 258–260
 premitochondrion, 256–258
 proteome studies, 254–256
 Rumsfeldian view of origins
 known knowns, 250–252
 known unknowns, 252
 unknown unknowns, 252–253
 symbiotic models, 253–254
Mitochondrion-related organelle (MRO), 15
MIZ, 283
Monosiga, 224
Monosiga brevicollis, 401
Moranella endobia, 136

- MORC, 277
Most recent universal common ancestor (MRUCA),
7–8, 256
MreB, 45, 202–203, 205
MRO. *See* Mitochondrion-related organelle
MRUCA. *See* Most recent universal common ancestor
MT loci, 350–352, 383
MTD. *See* Mating-type-determination
Multicellularity. *See* Bacteria, animal origin influences;
Plant multicellularity
Myo1, 203
- N**
- Naegleria*, 227, 286
Natural kinds
domains, two versus three, 4–6
eukaryote, 6–11
shared history, 2–3
shared properties, 2
species and domains, 3–4
Negibacteria, cell envelope, 62–64
Neomuran revolution
actinobacteria relationship, 52–53
archaeobacterial divergence, 51–52
cell cycle/structure coevolution, 50–51
cell kinds, 41–44
cilia, phagotrophy-related origin, 57–59
coevolution of mitochondrial, endoplasmic
reticulum, and peroxisomal respiration
and segregation, 54–55
coevolutionary theory of eukaryogenesis, 44–50,
234
cotranslational secretion, 53–54
Filarcheota diverse cell biology, 55–57
green bacteria and origin of life, 64–65
methodological bias and molecular clock myths,
67–71
misunderstandings, 61–62
multigene sequence trees and fossil data integration
for real timing of cell megaevolution,
65–67
negibacteria cell envelope, 62–64
Neoprotozoic era, eukaryotic diversification, 156
NigE, 278–279
Nitella, 372–373
Nitrosoarchaeum, 206
Nitrosopumilis maritimus, 123
NMD. *See* Nonsense-mediated decay
Non- α -proteobacterial component (NPC),
mitochondria origins, 252, 254–255,
259–260
Nonparametric rate smoothing (NPRS), 170
Nonsense-mediated decay (NMD), 306, 308
NPC. *See* Non- α -proteobacterial component; Nuclear
pore complex
NPRS. *See* Nonparametric rate smoothing
NTF2, 240
Nuclear envelope, origins, 235
Nuclear pore complex (NPC), 239
- O**
- Odysella*, 288
Omp85, 238, 240–241
OPH. *See* Organelle paralogy hypothesis
Opisthokonta, 185
Organelle paralogy hypothesis (OPH), 222–223
Ostreococcus lucimarinus, 144
Ostreococcus tauri, 144
Oxa1, 241
- P**
- Paederus*, 31
Palmitoyltransferases, 286
Pandorina, 377
ParA, 50, 57, 202–203
Parasexuality. *See* Sexual reproduction
ParB, 50, 57
PARC5, 268
ParM, 202–203, 205, 209
PARP. *See* Poly(ADP-ribose) polymerase
Paulinella, 265–266, 354
Paulinella chromatophora, 29, 244
PDV1, 268
Peroxisome, coevolution of mitochondrial,
endoplasmic reticulum, and
peroxisomal respiration and
segregation, 54–55
Persiciverga, 287
Pex proteins, 239
Phaeodactylum tricorutum, 144
Phagocytosing Archaeon Theory (PhAT), 98–99,
108–109, 136
PhAT. *See* Phagocytosing Archaeon Theory
Photosynthesis. *See also* Plastids
endosymbiosis
cryptic Chlamydiae in photosynthetic
eukaryogenesis, 144–147
cryptic green algal endosymbioses in diatoms
and chromerids, 142–143
overview, 141–142
prospects for study, 147–148
taxonomic sampling and methods, 143–144
overview, 263
Phylogenomics
deep relationships among eukaryotes, 190–191
eukaryotic supergroups
Amoebozoa, 185
Archaeplastida, 186–187
Excavata, 185–186

Index

- Phylogenomics (*Continued*)
 Opisthokonta, 185
 stramenophiles, alveolates, and Rhizaria, 187–189
 overview, 183–185
 rooting of eukaryote tree, 189–190
 TACK superphylum study of evolutionary association with eukaryotes
 compositional bias effects, 107
 concatenated protein and ribosomal DNA data sets, 103–104
 data selection, 101–103
 discordant protein cluster removal, 104–106
 prospects for study, 108–109
 taxon sampling effects, 107
Physcomitrella, 374, 376
Plant multicellularity
 cellular diversity in green lineage, 366–368
 green algae evolution
 charophyte algae and origins of land plant multicellularity, 369–376
 embryophyte genetic toolkit origins, 376
 macroscopic complexity
 coenocytic algae, 369
 giant uninucleate algae, 369
 multicellular algae, 369
 overview, 368
 streptophyte transition to multicellularity
 closest unicellular relative of land plants, 370–371
 filamentous growth and cytokinesis, 371–372
 hormone signaling, 373–374
 matrotrophic support of zygote, 375
 oogamous sexual reproduction, 374–375
 regulated division plane, cell differentiation, and polarized growth, 372–373
 symplastic connections and intercellular communication, 373
 volvocine algae
 Chlamydomonas cell biology, 377–379
 multicellular innovations, 379–383
 overview, 376–377
 prospects for study, 384
 innovations rooted in green lineage, 375–376
 overview, 365–366
Plant-growth-promoting rhizobacteria, 32
Plastids. *See also* Photosynthesis
 endosymbiosis hypotheses, 264–268
 gene transfer, 267
 overview of origins, 142, 235–236
 Paulinella studies, 265–266
Pleodorina, 377, 379
Poly(ADP-ribose) polymerase (PARP), 284–285
Prader–Willi syndrome, 324
PRMT. *See* Protein arginine methyltransferase
Profilin, 206
Protein arginine methyltransferase (PRMT), 278
Protein modification. *See* Epigenetics
Protein trafficking
 ancient machinery, 238–240
 bacterial souvenirs, 236–238
 early eukaryogenesis models, 234–236
 endosymbiotic organelles, 240–242
 evolutionary variations of complexity, 244
 overview, 236
 prospects for study, 244
 signal evolution, 242–244
Protochlamydia, 144, 288
Protozoic eon
 eukaryote establishment, 154–156
 Neoprotozoic era and eukaryotic diversification, 156
Prp8, 302
Pseudoalteromonas, 34
Pseudomonas, 31–32
PTEN, 330
PTENP1, 330

R
Rab, 222–224, 226
RAN, 240
Relaxed molecular clock (RMC) analysis
 calibration constraints, 172–173
 CIR model, 175
 comparison with other models, 175–176
 dating deep events in eukaryotic evolution, 171–172
 eukaryote root positioning, 173–174
 last eukaryotic common ancestor dating, 171
 overview, 170–171
 prospects, 176–177
 substitution model combination, 174–175
 UGam, 175
Reproduction. *See* Sexual reproduction
Rhanelia, 32
Rhizaria. *See* Stramenophiles, alveolates, and Rhizaria
Rhizobium, 29
Ribosomal DNA, plastid origin studies, 265
Rickettsiales, 27
RIF-1, 398, 400–401
RING, 283–284
RMC analysis. *See* Relaxed molecular clock analysis
RNA
 chromosomal RNA, 320
 classification, 327–328
 compartmentalization, 319
 competitive RNAs, 330
 history of study, 317–318
 junk RNA as future gene module, 323
 noncoding functional RNA, 326
 novel RNAs, 329–330
 prospects for study, 330–333

- RNA world, 318–320
signatures on extant DNA genomes, 320–323
transcriptional noise, 326, 328–329
transposable elements, 323–325
- RNAi. *See* RNA interference
- RNA interference (RNAi), Archaea system, 123–124
- RNA splicing. *See* Spliceosome
- RPB8, 118
- RPC34, 118
- RPD3, 279, 281
- RUBISCO, 278
- S**
- Salpingoeca rosetta*, 397–398, 400
- SAM. *See* Sorting and assembly machinery
- SAR. *See* Stramenophiles, alveolates, and Rhizaria
- SCOP. *See* Structural Classification of Proteins
- SEC, 237
- Sec systems, 54, 237–238, 240, 243
- Serial Endosymbiosis Theory, 98–99
- Serratia*, 32
- SET, 279
- Sexual reproduction
cell–cell fusion regulation
 recognition/fusion molecule expression,
 349–350
 restricting to self interactions, 349
- LECA, 343–344
- mating type
 coupling of diploidy to resting spore formation,
 352–354
 mating-type-determination system, 350–353
 multiple mating types and homothallism, 352
 organelle genome transmission regulation
 theory, 354–355
 UP systems, 355–356
 origins, 350
- meiosis evolution, 346–349
- parasexuality
 Aspergillus, 345
 Candida albicans, 345–346
- ploidy alteration via cell–cell fusion and meiosis,
 344–345
- sex and speciation, 356–357
- Shuiyousphaeridium macroreticulatum*, 169
- Signal recognition particle (SRP), 53, 237–238, 242
- SINEs, 321–322, 324
- Sir2, 279
- SKL, 54
- Skp, 238
- SMAP, 223
- SNAREs, 221, 239
- SNF2, 277
- Snord116, 331–332
- SopA, 203, 209
- Sorting and assembly machinery (SAM), 241
- Spastin, 206–207
- SPB. *See* Spindle pole body
- Sphingomonas paucimobilis*, 400
- Spindle pole body (SPB), 203
- Spliceosome
 alternative splicing origins, 307–309
 evolution across eukaryotes, 306–307
 history of study, 295–296
 intron classification
 group I self-splicing introns, 298
 group II self-splicing introns, 298
 spliceosomal introns, 296–298
 transfer RNA introns, 298–299
 origin and establishment in eukaryogenesis
 group II intron proliferation in host genome,
 300–301
 group II intron transfer to host genome, 299
 major and minor spliceosome systems, 302–303
 trans-complementation, 301–302
 reconstruction in last eukaryotic common ancestor,
 303–306
- Spo11, 346, 348
- SRP. *See* Signal recognition particle
- SRY, 351
- Stramenophiles, alveolates, and Rhizaria (SAR),
 187–189
- Streptophyte. *See* Plant multicellularity
- Strigolactones, 374
- Structural Classification of Proteins (SCOP), 256
- Stu2, 203
- STY kinases, 281–282
- Substitution, 174–175
- Sulfur Syntrophy, 98–99
- SUMO, 283
- SWI2, 277
- Symbiosis. *See also* Endosymbiosis
 health promotion, 32–35
 metabolism
 ancient evolutionary roots, 28–29
 primary metabolism, 29–31
 secondary metabolism, 31–32
- Synechococcus*, 29
- Synechocystis*, 88
- T**
- TACK superphylum
 eukaryogenesis, 124–125
 evidence for, 103, 116–118
 phylogenomics study of evolutionary association
 with eukaryotes
 compositional bias effects, 107
 concatenated protein and ribosomal DNA data
 sets, 103–104
 data selection, 101–103

Index

- TACK superphylum (*Continued*)
 discordant protein cluster removal, 104–106
 prospects for study, 108–109
 taxon sampling effects, 107
- TAF1, 281
Tappania plana, 169
TAT, 54, 237
TBP, 43
TCA cycle, 259, 265, 289
TE. *See* Transposable element
TEM. *See* Transmission electron microscopy
TET, 289
TFII, 60
TFIIB, 45
TFIID, 281
Thalassiosira pseudomana, 144
Thermoplasma, 18, 115
Thiomargarita, 86, 88
TIC, 241–242, 268
TIM, 244
TIM23, 241
TIR, 395–396
TLS. *See* Trilaminar wall structure
TOC, 240–242, 244, 268
TOM, 240–241
Transmission electron microscopy (TEM), microfossils,
 155
Transposable element (TE), 323–325
Trc40, 239
Tremblaya princeps, 136
Trichomonas vaginalis, 213, 278
Trilaminar wall structure (TLS), chlorophytes, 155
- TTL, 284
TubA, 205
TubZ, 47, 202, 208
- ### U
- U2 intron. *See* Spliceosome
U12 intron. *See* Spliceosome
Ubiquitin
 Archaea signaling system, 118–122
 epigenetics, 282–284
UP systems, 355–356
Urm1, 118
- ### V
- VARL, 382
VDAC, 240
Volvox carteri, 379, 381–384
Vps1, 203
Vps26, 226
Vps29, 239
- ### W
- Walker ATPases, 203, 209
WGA. *See* Wheat germ agglutinin
Wheat germ agglutinin (WGA), 399
- ### Y
- YidC, 237–238, 241