

Index

A

Abnormal hydrogenosomes, 95
Acetate/succinate CoA-transferase (ASCT),
117, 290, 292, 294, 296, 300
Adenylate kinase, 141, 142
ADP/ATP carrier (AAC), 45, 54–56, 60, 61
Aerobic mitochondria, 288, 292
Alanine, 190
Alcohol dehydrogenase E (ADHE),
164, 168, 169
Alveolates, 291, 299
Amitochondriate protists, 314, 315
Amitochondriates, 208, 209
Amoebozoa, 291, 300, 301
Anaerobic ciliates
double membrane, 113
evolution, 122–123
methanogenic endosymbionts, 121
Anaerobic energy metabolism, 10, 15, 17–21
Anaerobic enzymes, 122
Anaerobic fungi
bacterial mixed acid fermentations, 164
cellulosomes, 161, 164
diversity, 161
fibre-degrading microorganisms, 161
genera, 160
genome sequencing projects, 162
hydrolysis, cellulose, 164
lignocellulosic biomass, 161
methanogenic bacteria, 161
mitochondria vs. hydrogenosomes, 162–164
monocentric, 160
N. frontalis, 160
phylum *Neocallimastigomycota*, 160

Piromyces and *Neocallimastix*,
hydrogenosomal metabolism,
165–169
Piromyces sp. E2, energy metabolism,
169–170
zoospores, 160
Anaerobic metabolism, 3
Anoxic oceans, 14, 15, 17
Apicoplast, 244–246, 258, 260
Archaeobacteria, 13
Archaic translocase of the outer membrane
(ATOM), 58
Archamoebae, 207
Arginine deiminase (ADI1), 190
Aspartate aminotransferase (AAT), 190
ATP-binding cassette transporter of the
mitochondria (ATM), 290
Autophagic vacuole, 104
Autophagy, 96, 104

B

BLAST, 43, 60
Blastocystis species
adaptations and lateral gene transfer,
269–271
AOX, 273
cell biology and functions, 272, 273
energy metabolism, 275–277
energy-generating organelles, 268
Fe-S clusters, 274
glycolysis, 275
heterokonts, 269
hydrogenosomes, 268, 269

- Blastocystis* species (*cont.*)
 metazoans, 269
 mitochondrial DNA, 270, 272
 mitochondrial protein, 274, 275
 morphology, 276–280
 MROs, 269, 273, 281
 PCD, 280, 281
 stramenopile morphology, 269
- Brain-eating amoeba, 21
- Breviatea, 299, 300
- C**
- Carbohydrate metabolism, 134, 151
 core metabolism, 254
 glycolysis, 255
 PNO, 254, 255
- Carbohydrates, 95, 99
- Cardiolipin, 129
- Cell fractionation analysis, 105
- Cellulosomes, 161, 164
- Chlamydomonas*, 17, 18
- Chromatic granules, 2, 3
- Chytrid hydrogenosomes, 17, 18
- Ciliate hydrogenosomes, 93
- Ciliates
 description, 112
 free-living anaerobic, 113
 hydrogenosomes, 113
 orders, 112
See also Anaerobic ciliates
- Core Eukaryotic Genes Mapping Approach (CEGMA), 311
- Cortical cilia, 112
- CRISPR/Cas9-based strategy, 42
- CRISPRi, 41
- Cristae, 248, 249
- Crypton, 8
- Cryptosporidium* mitochondria, 51
- Cryptosporidium parvum*
 apicomplexan, 212, 220
 ATP/ADP transporter, 229
 and *Encephalitozoon cuniculi*, 231
 and *Entamoeba histolytica*, 230
 Fe-S cluster assembly, 225
 intermembrane space, 216
 IscS, 228
 mitosome, 216
 NADH dehydrogenase, 232
 relict mitochondrion, 209
- Cryptosporidium* species
 apicoplast, 260
 carbohydrate metabolism (*see* Carbohydrate metabolism)
 CB (*see* Crystalloid body (CB))
 in *C. parvum*, 245
 CRISPR-Cas9 system, 261
 cristae, 248, 249
 cytochrome c oxidase, 246
 diverse environments, 244
 energy metabolism, 256, 257
 ETC, 246
 human cryptosporidia, 261
 hydrogenosomes, 245
 in silico information, 261
 intracellular location, 246, 247
 ISC, 250–253
 medical and veterinary importance, 244
 mitochondrial protein, 253, 254
 mitosome, 261
 RER, 250
 subcellular (internal) organization, 249
 subclass, 244
 TCA cycle and glycolysis, 246
 ultrastructural and phylogenetic analyses, 245
 ultrastructure morphology, 246
- Crystalloid body (CB)
C. parvum, 259
 mitochondrial IM, 259
 non-toxic iron, 259
 RER, 257
 sporozoites, 259
 ultrastructural data, 257
- C-tail-anchored proteins (CTAs), 193
- Cyanobacteria, 13, 14, 20
- 5-Cyano-2,3-ditoyl tetrazolium chloride (CTC), 230
- Cysteine, 189
- Cytosol, 10, 17–19
- Cytosolic iron-sulphur cluster assembly (CIA), 274, 310, 313
- D**
- 1,4-Diamino-2-butanone (DAB), 150
- Diplomonads, 207, 226
- Discobids, 291
- DnaK, 63
- Dynammin-related proteins (DRPs), 90, 105
- E**
- Earth history, 9–11
- Ectosymbiotic bacteria, 311
- Electron tomography, 245, 250, 259
- Electron transport chain (ETC), 290, 296–299, 301
- Embden-Meyerhof pathway, 12
- Endomembrane system, 33
- Endoplasmic reticulum (ER), 103–104

nascent luminal proteins, 34
 signal peptidase, 34
 translation and translocation, 34

Endosymbiotic theory, 12

Energetic benefit, 11

Entamoeba mitosomes, 52

ER-mitochondria encounter structures (ERMES), 103, 104

ER signal peptidase, 34

Ethanol, 17

Eukaryotes
 LGT theories, 10
 oxygen role, 10

Eukaryotic anaerobes, 8, 10, 13, 14, 18, 19

Experimental models, 32

F

[FeFe] hydrogenase, 133, 138, 139

Ferredoxins (Fdx), 130, 136, 138

Fe-S clusters
 in bacteria, 221
 biosynthesis, 274
Cryptosporidium spp., 227, 228
Entamoeba histolytica, 228, 229
 in eukaryotes, 221
Giardia intestinalis, 223, 224
 maturation of extramitochondrial, 223
 microsporidia, 226, 227
Mikrocytos mackini, 228
 mitochondrial model, 222
 NIF system, 222
 physiological function, 223
 SUF system, 222

Fe-S proteins, 187, 195

Field emission scanning electron microscopy (FESEM), 92, 95

Flavodiiron (FDP), 145

Fornicata, 289, 290, 293–295
 Diplomonadida, 289
 energy generation, 290–292
 Fe-S clusters, 289, 290
 flagellated eukaryotes, 289
 GCS, 293, 294
 mitochondrial metabolism, 289
 protein import machinery, 293
 pyruvate metabolism, 290–292

Frataxin, 147

Free-living protists
 ATP generation, 288
 Fornicata (*see* Fornicata)
 free-living and endobiotic species, 289
 parabasalid parasites, 288

Fumarate reductase (FRD), 16, 17, 117

Fungal hydrogenosomes, 89, 102

Fungi, 160
 anaerobic (*see also* Anaerobic fungi)
 mycorrhiza, 160

G

Genetic transformation techniques, 41

Giardia intestinalis, 207–210, 214, 215, 218–220, 230, 232

Giardia mitosomes, 52–53

Giardia processing peptidase (GPP), 215

Global oxygen history, 13, 14

Glutamate dehydrogenase (GDH), 190

Glycine cleavage system (GCS), 190, 292–294, 296–298, 300, 313

Glycine decarboxylase complex (GDC), 148, 149, 190

Glycolysis, 275

H

Heart-shaped process, 105

Heterokonts, 269

Heterolobosea, 297

Heteroloboseans, 207

HHpred, 43

Hidden Markov model (HMM), 43, 58, 60, 69

HMMER software, 43

Horizontal gene transfer (HGT), 292, 296, 310, 313, 314

Hybrid cluster protein (HCP), 189

Hydrogenase, 138–139

Hydrogenosomal and mitochondrial protein import
 laboratory techniques and tools, 40–42
 mining genome sequence data, 43

Hydrogenosomal malic enzyme, 139

Hydrogenosomal targeting sequence (HTS), 50

Hydrogenosome components
 envelope, 90–93
 matrix, 99–101
 peripheral vesicles, 93–99

Hydrogenosome matrix
 ammoniacal silver and PTA, 101
 calcium deposits, 101
 description, 99
 electron-dense core, 99
 finely granular and homogeneous, 101
 granular structure, 101

Hydrogenosomes, 207, 208, 210, 213, 214, 217, 221, 231, 268–270, 273, 274, 288, 289, 294, 296, 299

Hydrogenosomes (*cont.*)

- anaerobic ciliates (*see* Anaerobic ciliates)
 - anaerobic fungi (*see also* Anaerobic fungi)
 - autophagy, 96, 104
 - biological nomenclature, 2
 - carbohydrates, 95
 - cell cycle, 106
 - chytrid, 17, 18
 - definition, 128
 - discovery, 8, 178
 - division
 - dynammin, 105
 - furrowing process, 104
 - growth, 104, 105
 - heart-shaped process, 105
 - microscopic and cell fractionation analysis, 105
 - mitochondrial process, 105
 - segmentation process, 104
 - enzymatic activity, 88
 - and ER, 103–104
 - history, 1
 - identification of proteins, 88
 - immunolabeling, 107
 - and microtubules, 106
 - mitotic process, 106
 - morphology, 88
 - new structures and organelles, 86, 87
 - organelles, 4
 - rumen ciliates, 118–120
 - shape, 90
 - sizes, 90
 - trichomonad, 86, 128 (*see also* Trichomonad hydrogenosomes)
 - trichomonad flagellates, 3
 - Trichomonadida order, 88
 - types, 86
- Hydrogen-producing mitochondria, 288

I

- Immunocytochemistry, 102
- Immunolabeling, 107
- Inorganic pyrophosphatase (IPP), 231
- Iron-only hydrogenase ([Fe]-Hyd), 18
- Iron-sulfur cluster (ISC), 139, 146, 221–224, 226–228, 231–233, 250, 252, 253, 258–260

J

- Jakobida, 296, 297
- Jakobids, 207

K

- Karyokinesis, 106

L

- Lactate dehydrogenase (LDH), 255
- Large-scale projects, 178
- Lateral gene transfer (LGT), 9, 10, 15, 19, 222
- Lignocellulosic biomass, 161
- Lysosomes, 2

M

- Malate, 133
- Malic enzyme, 97, 107, 139–140, 150
- Margulis's theory, 12, 13
- Marine invertebrates, 16, 17, 20
- Methanogenic bacteria, 161
- Methanogenic endosymbionts, 121
- Microfibrillar structures, 104
- Microsporidia, 226, 227
- Microtubules, 106
- Mitochondria, 1
 - in anaerobes, 310
 - eukaryote evolution, 8
 - origin, 11
 - oxygen and ATP, 13
- Mitochondrial ATP synthesis, 16
- Mitochondrial carrier family (MCF) proteins, 37, 54, 61, 191, 193
- Mitochondrial division process, 105
- Mitochondrial import (MIM), 36, 41
- Mitochondrial intermediate peptidase (MIP), 37, 64–66
- Mitochondrial loss, 313, 314
- Mitochondrial metabolism, 3
- Mitochondrial outer membrane potential (MOMP), 280, 281
- Mitochondrial processing peptidase (MPP), 35, 37, 44, 50, 53, 64–67, 214, 292, 293
- Mitochondrial protein import machinery
 - endosymbiont transferring, 38
 - endosymbiotic theory, 38
 - mitochondria, 38
 - N-terminal presequence, 39
 - protein import machines, 38
 - in *S. cerevisiae*, 36
 - transferred genes, 39
- Mitochondrial proteins
 - description, 34
 - IMP, 36
 - MCF proteins, 37
 - MPP, 35

- N-terminal cleavable presequences, 35
 - PAM complex, 37
 - protein import, 34
 - SAM complex, 35
 - TIM23, 37
 - TOM complex, 35
- Mitochondrial tail-anchored (TA) proteins, 55
- Mitochondrial targeting signals, 44–45
- Mitochondria-related organelles (MROs), 86, 170, 178, 199, 269–271, 273–281
- Mitosomes, 1, 288, 289, 294
 - aerobic/anaerobic respiration, 206
 - amitochondrial groups, 208
 - anaerobes, 312
 - Archaea concept, 210
 - ATP, membrane potential and electron transport, 229–231
 - biochemical capabilities, 206
 - biogenesis
 - genome, 213
 - protein targeting, translocation and maturation, 214–217
 - canonical mitochondrial pathways, 208
 - CPN60, 209
 - discovery, 8
 - E. histolytica*, 310
 - Encephalitozoon cuniculi* genome
 - sequence, 209
 - endosymbiotic ancestor, 208
 - eukaryotes, 314
 - evolutionary relationship, 9
 - F₀F₁-ATPase, 206
 - Fe-S clusters, 207, 209, 210 (*see also* Fe-S clusters)
 - Giardia intestinalis*, 211
 - history, 2
 - hydrogenosomes, 207
 - metabolic pathways, 207
 - mitochondrial origin, 209
 - mitochondrion-harboring protists, 208
 - morphology, 207, 210–212
 - oxygen-independent ATP synthesis, 8
 - parasitic protists, 208
 - perspectives, 225, 232, 233
 - physiological functions, 221
 - relict mitochondrion, 209
 - replication
 - division, 217–219
 - structures, 217
 - segregation, 219, 220
 - sulfate activation, 231, 232
 - TCA, 206
 - trypanosome, 206
 - Vavraia culicis*, 212
- Molecular hydrogen, 3
- Monocentric anaerobic fungi, 160
- Monocercomonoides exilis*, 311–315
- N**
- NADH dehydrogenase, 140
- Neocallimastix frontalis*, 160, 168
- Neocallimastix* hydrogenosomes, 51
- [NiFe] hydrogenase, 138
- Nitrogen-fixing (NIF) system, 221, 222, 228, 231, 232
- Noncanonical genetic codes, 311
- N-terminal targeting sequences (NTS), 88, 180, 181
- Nucleoid, 99, 102
- Nucleotide transporters (NTT), 229
- Nucleus, 33
- Nyctotherus ovalis*
 - anaerobic mitochondrion, 113
 - description, 113
 - energy metabolism, 116–117
 - in silico reconstruction, 117–118
 - mitochondrial genome, 113
 - MROs, 115
- O**
- Opisthokonts, 291
- Organellar membranes
 - inner membrane
 - TIM22 complex, 61
 - TIM23 complex, 62
 - outer membrane
 - SAM complex, 59–60
 - TOM complex, 56–59
 - small TIM chaperones, 60–61
- Organellar targeting signals, *see* Targeting signals
- Origin of eukaryotes, 12, 13
- OsmC system, 188, 189
- Oxic environments, 11, 16, 19
- Oxidative phosphorylation, 8, 11, 12
- Oxygen (O₂)
 - accumulation, 14
 - atmospheric levels, 10
 - biochemical, 16
 - endosymbiotic theory, 14
 - eukaryotes, 11
 - global oxygen history, 13
 - O₂-producing algae, 21
 - oxidative phosphorylation, 11
- Oxygen accumulation, earth
 - history, 9, 11

Oxygen late, 15, 18
 Oxygen/ATP, 12, 13
 Oxymonads, 311–313

P

Parasitic protists, 207, 208, 218
Paratrimastix pyriformis, 312, 314
 Percoll-sucrose density centrifugation, 93
 Periodic acid-thiosemicarbazide-silver
 proteinate technique, 95
 Peripheral vesicles, 93, 95, 97, 99
 Peroxiredoxin, 144
 Peroxisomes, 33, 55
 chromatic granules, 2
 marker enzyme, 3
 origin, 2
 Petites, 162
 Phosphoenolpyruvate (PEP), 132
 Phosphofructokinase (PFK), 194, 312
 Phosphotungstic acid (PTA), 101, 102
Piromyces sp. E2, 162, 163, 165, 170
 ADHE activity, 168
 energy metabolism, 166, 169–170
 epifluorescence micrograph, 163
 growth, 165
Plasmodium falciparum, 19
 Polyamines, 150
 Preaxostyla, 314, 315
 Preproteins
 hydrogenosomal, 58
 hydrophobic, 56
 inner membrane, 66–67
 mitochondrial inner membrane, 61
 MPP, 65–66
 soluble matrix-destined, 37
 TIM23 complex, 37
 Presequence translocase-associated motor
 (PAM), 37, 63, 214, 253
 Programmed cell death (PCD), 279–281
 Prokaryote-to-eukaryote transition, 13
 Protein, 107
 DRP, 90
 dynamin, 105
 ERMES, 103, 104
 hydrogenosome matrix, 101
 malic enzyme, 107
 SDS-PAGE, 97
 T. vaginalis hydrogenosome, 88
 Protein family (PFAM), 43
 Protein folding, 63, 67, 68
 Protein import motor, 63–64
 Protein precursors, 46

Protein trafficking
 fungi and mammals, 32
 in eukaryotes
 ER, 34
 mitochondrion, 34
 nucleus, 33
 proteins travelling, 33
 Proteome, *Pentatrichomonas hominis*
 hydrogenosome, 198
 Proteome, *T. vaginalis* hydrogenosomes
 amino acid metabolism, 189–190
 analysis, 179
 carriers, hydrogenosomal inner membrane,
 193
 contaminants/surface-associated proteins, 194
 CTAs, 193–194
 energy metabolism, 182–187
 Fe-S cluster assembly, 187–188
 oxygen metabolism, 181
 protein import, 190–192
 protein sequences, 179
 proteins, 181
 putative pore-forming Hmp35, 181
 quantitative analysis, iron-induced changes,
 195
 ROS defense, 188–189
 silico identification, genes coding, 180
 Proteomic studies, 179, 181, 183, 191, 194
 Protists, 88, 89, 105
 Proton motive force (PMF), 118
 Protons, 117
 Pyridine-nucleotide transhydrogenase (PNT),
 209, 230, 256
 Pyroantimonate, 101
 Pyruvate dehydrogenase complex (PDH), 117,
 118, 121, 135, 270
 Pyruvate ferredoxin oxidoreductase (PFO), 18,
 19, 117, 119, 121, 122, 168, 169,
 171, 181, 182, 187, 188, 195, 198,
 290, 292, 296–298, 300
 Pyruvate formate-lyase (PFL), 17–19, 117, 121,
 290, 292
 Pyruvate NADP+ oxidoreductase (PNO), 254,
 255, 270, 290, 292, 298–300
 Pyruvate phosphate dikinase (PPDK), 276

R

Reactive oxygen species (ROS)
 enzymes and molecules, 188
 peroxide, 188
 SOD, 188
 in *Trichomonas* hydrogenosomes, 188, 189

- Relict mitochondrion, 209, 212
 Revived endosymbiotic theory, 12
 Rhizaria, 298
 RNA silencing, 41
 Rough endoplasmic reticulum (RER), 245
 Rubrerythrin, 144, 188, 189
 Rumen ciliates, 118–120, 122
- S**
- SAM-like pathway, 55
 SecYEG translocon, 34
 Segmentation process, 100, 104, 105
 Serine hydroxymethyltransferase (SHMT), 148, 149
 Small translocase of the inner membrane (small TIMs) chaperone, 36, 55, 60–61
 Sorting and assembly machinery (SAM), 35, 38, 56, 57, 59–60, 69, 214, 274
 Sporozoites, 245–247, 249, 250, 252, 254, 257, 259
 Standard model, 13
 Stramenopila, 297, 298
 Stramenopiles, 291, 298
 Structured illumination microscopy (SIM), 219
 Succinate, 17
 Succinate thiokinase (STK), 18, 133, 141, 181
 Succinyl-CoA synthetase (SCS), 50, 141, 181, 290, 292, 294, 296–300
 Sulfur-mobilization (SUF) system, 221, 222, 228, 232
- T**
- Targeting signals, 38, 39, 41, 44
Cryptosporidium mitochondria, 51
Entamoeba mitochondria, 52
Giardia mitochondria, 52–53
 membrane proteins, hydrogenosomal and mitochondrial, 54–55
 microsporidia mitochondria, 53–54
 mitochondrial, 44–45
Neocallimastix hydrogenosomes, 51
Trichomonas hydrogenosomes, 45–50
 3'-Phosphoadenosine-5'-phosphosulfate (PAPS), 231
 Tom40-like proteins, 58
Trachipleistophora hominis, 207, 209–211, 226, 227, 232
 Transcriptional silencing techniques, 41
 Translocase of the outer membrane (TOM) complex, 35, 37, 56–60
 Transmission electron microscopy (TEM), 245, 247, 250, 252, 254, 259, 276, 289
Trepomonas sp.
 ACS, 296
 GCS, 296
 Tricarboxylic acid (TCA), 206, 227, 290, 292, 296, 298, 299, 301
 Trichomonad ferredoxin, 136
 Trichomonad flagellates, 2, 3
 Trichomonad hydrogenosomes
 amino acid metabolism, 148
 carbohydrate metabolism, 134
 cardiolipin, 129
 energy metabolism
 ADP to ATP, 129
 glycolysis, 132
 SDS-polyacrylamide gels, 132
 GDC, 148, 149
 ISC assembly machinery, 146–148
 malate, 133
 membranes, 128–129
 NADH:ferredoxin, 134
 oxygen and reactive oxygen species, 142–146
 polyamine metabolism, 150
 proteins, core catabolic pathway
 adenylate kinase, 141, 142
 ferredoxin, 136–138
 hydrogenase, 138–139
 malic enzyme, 139–140
 NADH dehydrogenase, 140–141
 PFOR, 135–136
 SCS, 141
 succinyl-CoA:acetate CoA transferase, 141
 pyruvate, 133
 serine, 149
 SHMT, 148, 149
 Trichomonadida, 86, 88
 Trichomonads, 128, 207, 208, 269
Trichomonas hydrogenosomes, 45–50
Trichomonas vaginalis, 178, 207, 208, 215, 217
See also Proteome, *T. vaginalis* hydrogenosomes
Trichomonas vaginalis, 2
 Trichomoniasis, 2
Tritrichomonas foetus
 autophagy, 104
 division, 103
 FESEM, 92
 freeze-fracture images, 98
 interphase, 94
 peripheral vesicle, 95

Tritrichomonas foetus (cont.)

- peripheral vesicles, 93
- plasma membrane, 87
- segmentation process, 105

Trypanosoma brucei

- Excavata group, 220
- kinetoplastid protist, 218
- mitochondrial Fe-S cluster, 223
- mitochondrion, 206
- tubular cristae, 207

U

- Ubiquinone, 129, 134, 140

W

- WGA, 95, 99

Z

- Zoospores, 160