

Index

A

- AAA metalloproteases, 238
AAA-protease, 214
Aac2, 91
Abf2, 92
Ace1p, 33
Acetic acid, 35, 111, 113, 139, 166, 179, 195, 211–212, 215, 244, 261, 273–274, 280
ACO1, 86
Aconitase, 19, 62, 72, 90–92, 110, 177, 238
Acridine orange staining, 209
Actin, 5, 15, 40, 71, 81, 170, 211, 218, 220, 259, 331–347
Actin cytoskeleton, 5, 40, 71, 170, 218, 259, 331–347
Actin dynamics, 15, 40, 211, 332, 336–338, 340, 346
Actin/Hsp70/sugar kinase superfamily, 81
Adaptation, 29–32, 34, 66–67, 80, 89, 163–164, 166, 177
Adaptive regrowth, 103, 114, 196–197
Adenine nucleotide translocase, 91
Adenine nucleotide transporter, 61
Adenylate cyclase, 86, 104, 106, 108–109, 261, 336–337
Ad libitum, 9, 165, 237
Afo1, 5, 66, 68–69, 85, 191, 224, 276
Aft1p, 28, 33
Agar plating, 150
AGC family, 92
Ageing/Aging, 1–10, 13–43, 55–73, 79–96, 101–116, 123–140, 146–156, 162–171, 173, 175–178, 187–202, 207–224, 233–246, 251–281, 291–309, 325–328, 331–347
Aif1, 35, 244
Aif1p, 35, 212–213
AifA, 245
AIF (apoptosis-inducing factor), 212–213, 222, 242, 244–245
AKT, 65, 105–106, 108, 114–115, 132, 188, 199, 201, 257, 299, 309
Alpha-tocopherol, 42, 58
Altruistic, 166, 219–220
Ambient temperature, 146
AMID, 212–213
Amino acid, 9, 16, 18–19, 25, 35, 67, 86, 93–94, 108, 111, 148, 161–180, 257, 269, 272–274, 279, 325, 340
Amiodarone, 35, 211
Ammonia, 93–94, 173–175
AMP, 65, 257, 261
Anabolic processes, 85–86, 152, 170
Aneuploid, 217
Annexin V, 211, 216, 218
Antagonistic pleiotropy, 152, 219
Anti-aging, 111–112, 215
Anti-apoptotic, 35, 209, 211, 213–214, 222
Antimycin A, 81
Antioxidant, 18–21, 23, 26–30, 32–34, 36–38, 42, 58, 110, 154
Anti-silencing, 214
Apaf-1 (apoptotic protease activating factor 1), 209
Apoptosis, 35, 66, 207–224, 242–246, 261
Apoptotic
 bodies, 35, 209
 DNA degradation, 149
 execution, 215
Aqueous suspension, 148
Arabidopsis thaliana, 237
Arrest, 31–32, 40, 58, 103, 107, 111, 126, 146–147, 149–150, 162, 168, 198–200, 215, 217, 219, 252
Arsenic, 211, 243
Ascomycete, 239, 242, 245
Asf1p, 214

- Aspartate, 9, 86, 91, 209, 243
Aspergillus fumigatus (*A. fumigatus*), 245
Aspergillus nidulans, 245
 Aspirin, 211
 Asymmetric, 4, 6, 40, 71–73, 89–90, 137, 162–163, 188–190, 194, 219–220, 254–256, 258–259, 261, 299–300, 315–329
 Asymmetric segregation, 4, 10, 40, 71–73, 89–90, 220, 256, 258–259, 316, 320, 324, 327–328
 Asymmetric segregation of damage, 10, 71–73, 316, 324
 ATF4, 223
 ATG1 kinase complex, 88
 ATG8, 172, 240–241
 ATG11, 71, 167, 240, 342–343
 ATG13, 82, 88
 ATG30, 240
 ATG32, 71, 246
 ATO3, 93–94
 ATP, 8, 32, 56, 60–61, 65, 81, 83, 91, 174, 259, 293, 297, 332, 340–342, 346
 ATP2, 89–91, 259, 293, 296, 298, 306
 ATP-binding domain, 81, 83, 91
 ATP sensor, 91
 AUP1, 82, 89, 238–239
 Autolysis, 208
 Autophagic bodies, 241
 Autophagosome, 127, 236–237, 239, 241
 Autophagy, 5, 8, 10, 32, 42, 71–72, 82, 85, 88–89, 92–93, 95, 152, 166–173, 176–178, 234–242, 246, 268–269, 275, 280, 342–343
 Auxotrophic requirements, 148–150
 Auxotrophs, 18, 86, 148, 150, 164, 168
- B**
 Back-signalling, 68–69, 72–73
 Barcode, 151, 304–308
 BAX, 41, 209, 211, 213–214, 236
 BCL-2, 208–209
 BCL-X_L, 209
 BEC-1, 237
 BIM, 209
 Bioscreen, 152, 271, 273
 Biosynthetic intermediates, 84, 86
 Bip/GRP78, 223
 Bir1p, 212, 214
 Bleomycin, 211
 BLM, 113, 200–201
 Bloom's syndrome, 113
 BMH1, 81–83, 85
 BMH2, 81, 83, 85
 Bni1p, 220, 334
 Bre1p, 214
 Bud scars, 2–3, 189, 253, 275
 Buffering cultures, 149
- C**
 Cadmium, 35, 39, 212
C. albicans (*Candida albicans*), 243–244, 325
 Calcineurin, 82, 92
 Calendar time, 2, 218
 Caloric/calorie restriction (CR), 2, 9–10, 42, 67–68, 93–94, 96, 111–112, 148–149, 152, 165–171, 176, 178–180, 192–194, 202, 217, 237, 299–303
 CAMP, 65, 67–68, 70, 85–86, 124, 131, 336–337, 347
 Canavanine resistance/resistant, 62, 155
Candida boidinii, 236, 240
 Carbonylated proteins, 40–41, 220, 256, 259, 316
 Carbonylation, 18–19, 26, 220, 259, 317
 Carbonyl groups, 220
 Cardiolipin, 95
 Caspase, 35, 66, 209, 212, 242–244, 331
 Catabolic processes, 152, 170
 Catalase, 22–26, 32, 39–40, 58, 65, 106, 154, 176, 199, 240, 256
 CBS1, 70
 CCCP (carbonyl cyanide 3-chlorophenyl hydrazine), 41, 92
 CDC48, 35, 211
 Cdc48p, 212, 222
 Ced mutants, 208
C. elegans (*Caenorhabditis elegans*), 2, 13, 60, 67, 89, 94, 101–102, 105, 108, 112, 114, 124, 138, 146, 154, 167, 178, 208, 210, 215, 217, 237, 256, 264, 267–268, 273, 279–280, 298–299, 300, 303, 306
- Cell
 cycle
 arrest, 31–32, 103, 111, 168, 215, 219
 checkpoint, 3
 delay, 31–32, 34, 37–38
 death, 15, 18, 28–29, 35–36, 42, 56, 66, 104, 138, 163, 168, 196, 198, 202, 207–215, 220, 222, 234, 236–237, 241–245, 261, 318, 331–333, 337–340, 347
 markers, 207

- division, 3–6, 29, 31, 40, 56, 59, 65, 89–90, 102–105, 114, 125, 133, 147, 162–163, 188, 190, 194, 196, 199, 219–220, 253–254, 299–300, 317–319, 326, 342
 - preconditioning, 147–150
 - Cellular redox environment, 33
 - Centrifugation, 3, 40, 138, 276
 - Ceramide, 82, 92–93, 95
 - Ceramide synthase, 92–93
 - Chaperone, 18, 26, 32, 82, 90, 151, 167, 239, 293
 - Checkpoint, 3, 31, 155, 196, 214–216
 - Chemostat, 93
 - Chromatin condensation, 35, 211, 218
 - Chromatin-dependent gene regulation, 87–88
 - Chromatin margination, 208, 211
 - Chronological
 - aging, 7–8, 10, 41, 61–62, 72, 101–116, 129, 134–136, 146, 148, 162–169, 171, 173, 175–177, 188–189, 194–200, 215, 218, 221, 224, 243–244, 252, 261, 268, 270, 272–275, 277–280, 299–303
 - life span (CLS), 7, 9–10, 41, 58, 60, 66–67, 85, 101–115, 125, 127, 132–135, 137, 146–155, 162, 164, 167–173, 175–179, 194, 196–199, 219, 222–224, 244, 252–253, 261, 268–275, 277, 280, 299–308
 - assays, 7, 303
 - longevity, 147, 150, 152, 165–169, 171–180, 274
 - Circles, 2, 5, 7, 59, 82, 87, 102, 190, 254, 327
 - CIT1, 86
 - CIT2, 67, 81, 85, 87
 - Clonal aging, 3–5, 71
 - Clonogenicity, 7
 - Coagulation necrosis, 208
 - Collections, 2, 150, 152, 253, 265, 273
 - Colony counting, 150–151
 - Colony forming units (CFU), 103, 126, 129–130, 135, 170, 174, 196, 252, 270–271
 - Colony morphology and differentiation, 94
 - Compensation, 80, 94
 - Complementation, 1, 168, 304
 - Condensation of chromatin, 208
 - Copper zinc superoxide dismutase/copper/zinc SOD (Cu, Zn-Sod), 57, 151, 154–155
 - Counter flow centrifugation elutriation, 276
 - COX2, 238, 293
 - COX4–1, 67
 - COX4–2, 67
 - COX4Δ, 84
 - COX5A, 67
 - COX5B, 67
 - Cpr1p, 213
 - Crabtree effect, 179
 - CRD1, 95
 - Critical oxidative damage targets, 154–156
 - Cross-feeding, 152
 - Cross-talk, 66, 79–80, 82, 85, 95–96
 - CR, *see* Caloric/calorie restriction (CR)
 - Cu, Zn-Sod, *see* Copper zinc superoxide dismutase/copper/zinc SOD (Cu, Zn-Sod)
 - Cyclase/PKA pathways, 104, 108–109
 - Cyclins, 31, 308
 - Cyclophilin A, 213
 - Cysteine residues, 18, 36–37, 343, 345
 - Cytochrome c, 24, 26, 209, 212–215, 238, 337
 - peroxidase, 24, 26
 - Cytoplasm, 13, 20, 26–28, 38, 57, 68, 71, 80–81, 87, 92, 126, 153, 167, 234, 236, 240, 341
 - Cytoplasm-to-vacuole targeting, 240
 - Cytoskeleton, 5, 40, 71, 170, 218, 259, 324, 331–347
- D**
- DAD1 (defender of apoptosis-1), 214
 - DAF-2, 105–106, 237
 - Damage
 - accumulation, 10, 156, 317–318, 320–321, 323–327
 - proteins, 4, 40–41, 71, 152, 192, 258–259, 318, 323–324, 326, 333
 - removal, 8, 10, 177–178
 - Dauer* larva/larvae, 107, 217
 - Daughter cells, 2–4, 6, 40, 60, 71–73, 84, 89–90, 102, 133, 135, 137, 162, 189–192, 216–220, 252, 254, 256, 260, 262, 270, 275–276, 299, 316–319, 321–323, 326, 335, 340–342
 - Degeneration, 33, 91, 146, 208, 280, 340
 - Degradation, 4–5, 10, 15, 18–19, 32, 35, 67, 71–72, 81–83, 90, 131, 166–167, 214, 223, 234, 236–241, 267–268, 280, 317–319, 324, 326–327, 342
 - Deletion mutants, 7, 17, 19, 27, 30, 32, 36, 41, 58, 65–66, 69, 125, 136, 146–147, 151–152, 174, 223, 246, 262–264, 272, 274, 307

- Density-gradient separation, 8
D-erythroascorbate, 19
D-erythroascorbic acid, 20
Detoxification, 18, 20, 24, 28, 33, 90, 240, 342
Diamide, 35, 37, 215
Diapause, 107
Diet, 9, 42, 164–166, 178–180, 201
Dietary restriction (DR), 67, 165, 253, 256–258
Diferric-tyrosyl radical, 155
Dihydroethidium (DHE), 15–16, 63, 211, 218
Dihydrorhodamine (DHR), 63, 211, 216, 218
Dinitrophenol, 41, 92, 94
Diploid, 3, 7, 62, 88, 94, 107, 147, 152, 154–155, 163, 253, 260, 271–272
Disposable soma theory, 146, 326
 of aging, 146
Disulphides, 16, 18–19, 26–27
D. melanogaster, 138, 210, 267
DNase II α
 damage/repair, 16, 18, 28, 31, 110, 112–116, 132, 138, 146, 154–156, 171, 187–202, 214–215, 217, 235, 256, 280, 298–299
 fragmentation, 210–211, 218
 “laddering”, 208
 mutations, 64, 112, 114
 replication
 failure, 212
 stress, 187–202
DNase II β , 210
DNM1, 89, 213, 221, 238–239
Dnm1p, 213
Double-strand breaks, 154
Drosophila, 2, 42, 67, 102, 106–108, 110, 138, 146, 154, 165, 178–179, 256, 300, 303
 lifespan, 154
DRP-1, 213, 238
Dynammin, 213
- E**
4E-BP, 223
E. coli, 4, 103, 138, 205, 220
Edelfosine, 211
EIF2, 34, 223
Electron spin resonance (ESR), 15–16, 32
Elutriation, 3, 40, 216, 276
Embryogenesis, 209, 327
Embryonic morphogenic apoptosis, 210
Endonuclease G (EndoG), 212–213, 244
Endonucleases, 36, 193, 196, 208, 212–213, 244
Endoplasmic reticulum (ER), 16, 35, 82, 95, 245, 334
Endosymbiont, 60–61
Energy metabolism, 37, 55, 80, 325
Engulfment, 210, 222, 236, 240, 340
Entry to stationary phase, 153
Environmental stress response, 32, 276
ER, *see* Endoplasmic reticulum (ER)
ERC, *see* Extrachromosomal ribosomal DNA circles (ERC)
ER stress, 16, 223, 245
 response, 222, 269
Ethanol, 41, 61, 63, 67, 111–113, 139, 150, 162, 179, 238, 240, 268, 273
Ethidium bromide, 61
Etoposide, 244
E3 ubiquitin ligase, 67, 82, 339
E3 ubiquitin protein ligase, 214
Eukaryotic evolution, 55–56
Evolution, 7, 15, 20, 42, 55–56, 58, 60–61, 105–106, 108, 116, 124, 133, 146, 162–163, 179, 219–220, 261, 267–268, 279, 296, 298–301, 308–309, 315–329
Externalisation of phosphatidylserine, 208
Extrachromosomal, 2, 82, 87, 102, 190, 254, 327
Extrachromosomal ribosomal DNA circles (ERC), 82, 87–88, 102, 190–193, 200, 254–260, 327
Extramitochondrial, 215
- F**
F-actin, 5, 218, 333–334, 336–338, 341, 343–346
F₁-ATPase, 91
F₁F₀-ATP, 293, 297–299, 309
F₁F₀-ATPase, 298–299, 309
Farnesol, 245
Fas-receptor, 222
Faulty segregation, 210
F-box protein, 213
Fermentation, 61, 179, 244, 273
4Fe/4S, 72
Fibroblasts, 5, 39, 94, 109, 209
Filamentous growth, 86, 163–164, 173
Fis1p, 213
Fission, 72, 89, 101–102, 213, 234, 237–239, 291–309, 316
Flavoprotein, 16, 212

- Formin, 220, 332–334
 Free radical theory of aging, 110, 176, 188, 259
 Fusion, 72, 89, 132, 172, 213, 234, 237, 239–242, 335
- G**
- G1 arrest, 31, 103, 200
 Gamma rays, 56
 Gcn4, 94, 169–171, 258, 269–270
 Gcn4p transcription factor, 35
 Gcn5, 87–88
 Gene
 conversions, 62
 expression, 6, 19, 29–32, 34, 67, 80–83, 93–95, 110, 112, 136–137, 153, 163–164, 173, 175, 193, 198, 222, 259, 277, 294–295, 325
 -regulatory, 9, 81
 General amino acid control, 94, 169–171
 Genetic code, 61
 Genetic instability, 64, 190–191, 196
 Genetic program of aging, 10, 42, 220
 Genetics, 1, 56, 60–62, 80, 103, 105, 109, 153, 253, 299, 303, 308
 Genome
 /genomic instability, 88, 94, 112–116, 133, 188, 191, 194, 200–201
 stability, 87–88, 127, 175, 201
 Genomic screens for altered CLS, 147
 Germ cells, 114, 210
 GFP (green fluorescent protein), 14, 132, 172, 238, 241, 334–335
 G (GTP-binding)-protein, 86
 Gis1, 104, 106, 109, 269
 Gluconeogenesis, 40, 80, 112, 277
 Glucose, 3, 8–9, 23, 25, 32, 40–41, 60–61, 65, 67, 69, 83, 85–86, 92–93, 105, 109–111, 124–127, 130–134, 137, 139, 148–150, 152, 162–164, 166, 168, 170–171, 173, 175, 177, 179, 189, 193–195, 198–199, 201–202, 244, 256–257, 268, 270, 272–274, 277, 300–302, 336–337
 Glucose exhaustion, 8, 125–127, 130–131, 133–134, 137
 Glucose-sensing, 65
 Glucose synthetic complete medium (SC), 148
 Glutamate, 9, 86, 91, 149, 173–175
 Glutamine, 86, 173–174, 257, 339
 Glutaredoxins, 23, 27–28, 30, 32, 36, 346
 Glutathione, 18–19, 23–28, 30, 32–33, 35–36, 42, 58, 154, 176, 344, 346
 Glutathione peroxidase, 18, 24, 28, 30, 176
 Glutathione transferases, 26
 Glutathionylation, 18, 26, 36, 344
 Glycerol, 41, 61, 67, 111–112, 148–149, 238, 244, 270, 298
 Glyceroneogenesis, 112
 Glycogen, 8, 106–107, 127, 219, 272
 Glycolysis, 36, 40, 94, 111–112, 278
 Glyoxylate cycle, 86, 94, 259
 Gompertz law, 3, 218
 GPD1, 111
 GPD2, 111
 Gpx3p, 30, 37
 Growth Advantage in Stationary Phase, 103
 Growth hormone (GH), 106–107, 114, 116
 Grr1, 81–83
 GSH/GSSG, 27, 33, 58
 G₀ state, 163, 219
- H**
- H2B, 213–214
 Haematopoiesis, 210
Hansenula polymorpha (*H. polymorpha*), 236, 240
 HAP1, 33, 66
 Hap1p, 33
 HAP2/3/4/5, 66
 HAP4, 93, 268, 270
 HAP complex, 86
 HAP genes, 66
 Haploid, 1, 3, 107, 129, 147, 151–152, 154–155, 163, 210, 253, 262, 265, 307, 317
 HAP4 overexpression, 149, 274
 Hayflick aging, 6
 Hayflick limit, 6, 209
 Hayflick phenomenon, 6
 Hayflick type aging, 5–6
 HDA1, 87
 Healthspan, 9
 Heat, 23, 27, 29, 109, 116, 211, 274, 301
 Heat shock, 29, 32, 34, 71, 214, 336
 proteins, 28, 32, 71, 106, 324
 Heavy metals, 211
 Hemiascomycetous, 58
 Heterogeneity, 38–39, 134, 137, 146–150
 Heterogeneity in the population of aging cells, 146–150
 Heteroplasmic mitochondrial mutations, 210
 Het loci, 241
 HIF-1, 66–67

- High-throughput methods, 271, 276
 High throughput sequencing, 151
 Histone, 87, 102, 112, 190, 197, 212–214, 254, 256, 293, 297
 Histone acetyltransferase, 87
 Histone deacetylase, 87, 102, 190, 212, 254
 Historical background, 207–210
 H₂O₂ (Hydrogen peroxide), *see* Hydrogen peroxide (H₂O₂)
 Homologous recombination, 154, 255
 Housekeeping genes, 87
 Hsp104, 71, 324
 HtrA2/Omi, 212, 214
 Human cancer, 114–115, 129, 217
 Human stem cells, 219, 299
 HUVEC, 5
 Hydrogen, 27
 Hydrogen peroxide (H₂O₂), 14, 16, 18–20, 22–27, 29–31, 33–39, 58, 65, 110, 116, 199, 212–213, 215–216, 243–245, 256, 343–345
 Hydroperoxides, 18, 22, 25–27, 29–30, 35, 215
 8-Hydroxy-2'-deoxyguanine, 113
 Hydroxylase, 67
 Hydroxyl radicals, 14, 16, 20
 4-Hydroxy-nonenal, 15
 Hydroxyurea, 155, 197–198
 Hypermitogenic, 58
 Hyperosmotic shock, 243
 Hypochlorous acid, 211
 Hypoxia, 16, 66–69
- I**
 IAP, 209, 214
 IDH1, 86, 297
 IDH2, 86
 idi-6, 241
 idi-7, 241
 IGF, 65, 67, 105–107, 114–116, 154, 178–179, 257, 268
 IGF-I, 105, 107, 114–116
 IGFR, 217
 IMF1, 70
 Immortality, 6
 Incompatibility, 241–242
 Increased Cu, Zn-Sod activity, 154
 Inflammation, 208
 Inner membrane complexes, 80
 Inner mitochondrial membrane protein complexes, 90
 Insoluble protein aggregates, 212–213
- Insulin, 105, 107, 114, 124, 138, 217, 237
 Insulin/IGF-I signalling, 154
 Insulin/insulin-like growth factor-I signaling, 105, 178
 Insulin-like growth factor, 65, 105, 178–179
 Intercolony communication, 94
 Intergenomic signaling, 80, 84
 Intermediary metabolism, 9–10
 Internucleosomal DNA fragmentation, 211
 Interorganelle Communication, 79–96
 Ionizing radiation, 56, 154
 Iron-sulfur cluster, 88, 110, 190
- K**
 Karyolysis, 208
 Karyorhexis, 208
 Kinase, 28, 31–32, 34, 38, 65, 67–68, 81–82, 85–86, 88, 92, 104–106, 108, 124–125, 131–132, 146, 152–153, 155, 178, 197, 199, 214, 223, 236, 240, 257, 267, 269, 280, 292–293, 297, 299, 308, 337
 Kinetics of outgrowth, 152
 Knock in, 1, 63
- L**
 LAC1, 82, 93, 95
 Lactate, 61, 67
 LAG1, 82, 92–93, 95, 102, 276
 Large deletions, 61–64
 L-ascorbate, 16, 20
Leishmania major, 243
 Lifespan, 145–156, 298–299, 308–309
 Limitation of auxotrophic requirements, 149
 Linoleic acid hydroperoxide, 29–30
 Lipid hydroperoxides, 18, 21, 25
 Lipid peroxidation, 16–18, 29, 31, 42
 Longevity determining gene, 92
 Lon protease, 5, 240
 Loss of heterozygosity, 3, 62, 88, 260–261
 Low glucose, 9, 166, 171, 179, 273, 301
 LST8, 82–86
- M**
 M-AAA protease, 90
 Macroautophagy, 71, 167, 172, 236, 240
 Macropexophagy, 236, 240
 Maintenance DNA repair, 154–156
 Maintenance in G₀, 153–154
 Maintenance repair of DNA, 153
 Malondialdehyde, 15, 18, 29

- Mammalian cells, 24, 31, 58, 102, 155, 167–168, 194–196, 201, 209, 211–212, 223, 238, 339, 343–346
- Manganese SOD, 57
- Manganese superoxide dismutase (Mn-Sod), 22, 151, 154
- Mannosyl-diinositolphosphoryl ceramides, 82
- MAP kinase pathway, 86
- Maximal yeast CLS, 146
- Mdm30p, 213
- MDM38, 71, 238–239
- Mdv1p, 213
- Medium acetic acid, 149
- Meiosis, 163, 210
- Meiotic divisions, 210
- Membrane potential, 71–73, 82, 84, 88–89, 91–92, 94, 215, 238–239, 259, 338, 342
- Menadion, 29, 31, 33, 110, 176, 343
- MET15, 62
- Metabolic equilibrium, 93
- Metabolic regulation, 93–94
- Metabolic stress, 86, 88, 162
- Metabolism, 9–10, 15, 18–19, 24, 27, 30–33, 37, 40, 55, 57, 62, 67, 71, 80, 88, 90, 93, 111, 131–132, 162, 175, 179–180, 201, 219, 240, 253, 259, 261, 265, 267–268, 272–273, 325
- Metabolomics, 14, 277–278
- Metacaspase, 212, 218, 243–245
- Metal ion homeostasis, 16
- Methionine, 9, 18, 22, 27, 178–179, 272
- Methionine sulfoxide reductase, 18
- Microarray DNA hybridization, 151
- Microarrays, 2, 137, 275–278
- Microautophagy, 167, 236
- Micropexophagic membrane apparatus (MIPA), 240
- Micropexophagy, 236, 240
- Microtubules, 214
- M(IP)₂C, 82
- Mitochondrial back-signaling, 80, 85, 259–260
- Mitochondrial biogenesis, 66–67, 83, 90–91, 95, 179, 237, 259
- Mitochondrial catalase, 65
- Mitochondrial code, 61
- Mitochondrial DNA, 61, 63–64, 70, 80, 176, 190–191, 200, 213, 298
- Mitochondrial dysfunction, 72, 80–85, 87–91, 176, 190, 244, 259, 337, 347
- Mitochondrial fission, 89, 213, 238–239
- Mitochondrial fission-fusion equilibrium, 89
- Mitochondrial fragmentation, 212–215
- Mitochondrial fusion, 213, 237
- Mitochondrial genome, 29, 56, 61, 63–65, 69, 80, 176–177, 191, 295–296, 298–299, 307
- Mitochondrial inheritance, 90, 341
- Mitochondrial integrity, 90
- Mitochondrial matrix, 20, 27, 57, 72, 177, 239, 293
- Mitochondrial membrane potential, 82, 84, 88–89, 91–92, 94, 215, 259, 338
- Mitochondrial morphology, 15, 42, 63, 213, 216, 341
- Mitochondrial point mutations, 61–64
- Mitochondrial proteome, 91, 214
- Mitochondrial quality control, 82, 88–91, 235, 239
- Mitochondrial respiration, 9, 61, 67, 111, 149, 340
- Mitochondrial ribosomal protein, 5, 61, 69, 85, 111, 191
- Mitochondrial status, 79
- Mitochondrial superoxide dismutase, 104, 107, 110
- Mitochondrial surveillance, 79
- Mitochondrial theory of aging, 56–58, 176–178
- Mitochondrial translation, 61, 69–71, 177–178
- Mitochondrial translation complex, 69–71
- Mitochondria-to-nucleus signaling, 80, 95, 294–297
- Mitochondrion, 15–16, 20, 26, 28, 30, 55–73, 80–83, 85–86, 88–92, 95, 110, 132–133, 175–178, 213, 235, 237, 239, 245, 294–297, 342
- Mitophagy, 41, 71–72, 82–83, 88–89, 167, 214, 234–240, 246, 342–343
- MKS1, 81–85, 91, 175, 259
- MMII, 214, 221–222
- Mmi1p, 214
- Mn²⁺, 243
- Mn-Sod (Manganese superoxide dismutase), *see* Manganese superoxide dismutase (Mn-Sod)
- Model organism, 1, 101, 105, 110, 114, 124, 135, 165, 188–189, 202, 210–211, 252, 279
- Molecular machinery, 209, 211–215
- Morphogenesis, 209
- Morphogenic, 209–210
- Mortality rate, 3, 103, 219
- Mortification, 208

- Mother
 cell, 2–7, 39–40, 62–63, 66, 71–72, 89–91, 101–102, 104, 125, 132–133, 162–163, 189–193, 216–220, 223–224, 243, 252, 254–256, 258–262, 264, 270, 275–277, 299, 317, 323, 327–329, 333, 335, 342
 cell-specific (replicative) aging, 2–7, 62, 218–219
 Mother Enrichment Program (MEP), 191, 276–277
 Mouse, 1–2, 13, 39, 61, 63–65, 138, 199–200, 209–210, 278
 paw, 209
 mRNA decay, 34
 mRNA stability, 212, 305
 MRPL25, 85, 260, 276
 MSN2/4, 33–34, 38, 70, 104, 106, 109, 257
 MTC (mitochondrial translation complex), 69–71
 mtDNA, 64, 80–81, 83, 88, 91–92, 94, 176, 341
 nucleoid, 91, 341
 MTOR protein kinase, 152
 Multicausal, 10
 Multi-drug resistance genes, 90
 Multifactorial, 10
 Mutagenesis, 18, 56, 113, 155, 293, 297, 307
 Mutations, 1, 3, 7, 19, 28, 61–64, 69–70, 84, 86, 103, 106–107, 110, 112–115, 129, 147, 162, 164, 167, 188, 190, 193, 196–199, 201–202, 210, 217, 219–220, 222, 224, 256, 258–261, 263, 267, 273–274, 278, 293, 295–296, 303–304, 306–309, 317, 326, 338
 MYC, 94
 Myo2p, 220, 334, 341
- N**
 NAD⁺/NADH, 23, 58, 153, 174, 190
 ratio, 149, 153
 NADH dehydrogenase, 213, 238
 NADH/NAD⁺, 58
 NADP⁺, 22–25, 33, 58, 60, 174
 NADPH, 22–25, 27–28, 30, 33–34, 36, 58, 60, 215
 oxidases, 58, 215
 NCA3, 214
 NDE1, 57, 238, 261
 NDE2, 57, 261
 NDII, 57, 212–213, 221
 Ndi1p, 212–213
 Necrobiosis, 208
 Necrosis, 33, 35, 103, 208
 Necrotic yeast cells, 66
 Negative regulation, 66, 85, 174, 199
Neurospora crassa, 245
 Newly-synthesized, 90
 NFκB, 95
 N-glycosylation, 211–212
 Nitrogen assimilation, 173–176
 Nitrogen catabolite repression, 85, 161, 173–174
 Nitrogen starvation, 93, 163, 168
 Nma11p, 212, 214
 Nomenclature, 125, 128
 Non-fermentable carbon source, 61, 92, 125–126, 128, 163, 166, 179, 238, 274, 337
 Nonhomologous end-joining repair, 154
 Non-inflammatory, 208
 Non-quiescent, 123–140, 163, 195, 198–199
 Non-respiring strains, 9
 NOXs, 58
 Nuc1p, 212–213
 Nuclear DNA silencing, 70
 Nuclear fragmentation, 35, 211, 218
 Nuclear genome maintenance, 88
 Nuclear petites, 84
 Nuclease, 212, 214
 Nucleus, 26, 28, 37–38, 65, 67–69, 80–81, 83, 85, 87, 92, 95, 153, 167, 175, 208, 213, 222, 235–236, 244, 260, 294, 296, 309, 334
 Nutrient depletion, 103, 147
 Nutrient limitation, 93–94, 162, 164–166, 169, 237
 Nutritional status, 32, 146–150
- O**
 Old mother cells, 3, 63, 72, 90, 189, 191–193, 217, 219
 Oligomerize, 305
 Oligomycin, 81
 OPA1, 236
 Organelle, 67, 222, 269, 331, 334
 Organic peroxides, 14, 23–24
 Organismic, 2, 10, 13
 Ost2p, 214
 Oxidative
 damage, 28, 37, 39, 84, 90, 94, 110, 112, 146, 154, 176–177, 179, 188, 199–200, 215, 220, 256, 258–259, 261, 331, 343–346

- phosphorylation, 41, 67, 80, 176–177, 234, 236, 245, 278, 340
- stress
- resistance, 42, 58, 60, 109–110, 115, 146, 154, 256, 260
 - response, 31, 33, 37–38, 42, 110, 112, 154, 199, 202, 214, 331, 343, 346
- Oxy-blot, 220
- Oxygen sensor, 67
- P**
- p53, 114, 209, 211, 223
- p97/VCP, 222
- PaAtg8, 241
- Paclitaxel, 211
- PaMca1, 243–244
- Paraquat, 18, 22, 26, 31, 59, 110
- Pathways, 2, 5, 14, 18, 23–24, 28, 32–33, 36, 42, 60, 62, 71, 79–96, 104–108, 111, 114–116, 124, 131, 138, 162–163, 166–169, 177–179, 188–189, 195, 199, 201–202, 209–211, 222, 234, 236, 242, 244, 253–255, 257–258, 267, 274, 293, 298, 303, 308–309
- PCA1, 243
- PDR5, 90, 93
- Pentose phosphate pathway, 23, 28, 30, 33, 36
- Permeability transition pore (PTP), 213
- Peroxide, 14, 16–18, 20, 23–26, 58, 65, 110, 199, 212, 215, 243–245, 256
- Peroxynitrite, 16
- Peroxiredoxin, 18–19, 21, 24–27, 37
- Peroxisomal, 22–23, 25, 65, 67, 81, 211–212, 240
- Peroxisomal anaplerotic, 67
- Peroxisome, 16, 20, 25, 65, 68, 81, 167, 235–236, 240, 334
- Peroxynitrite, 14, 16, 57
- Peroxyredoxin, 60
- Petite, 20, 26, 29, 61–62, 68, 84, 91, 94–95, 132–133, 163
- PEX3, 240
- PEX14, 240
- Pexophagosomes, 240
- Pexophagy, 167, 235, 240
- Phagophore, 241
- PHB1, 82, 90
- PHB2, 90
- Phosphatidylserine, 34, 208, 210–211, 216, 218
- Phospholipid, 21, 95
- Phosphorylation status, 81, 292
- Pichia pastoris* (*P. pastoris*), 240
- PKB, 65
- Pkh1, 92
- Pkh2, 92, 267
- Plasma membrane, 21, 86, 90, 93, 208, 333
- PNC1, 70, 257
- Podospora anserina* (*P. anserina*), 239, 241–245
- Polarisome, 71, 220
- Positive regulation, 66
- Post-diauxic phase, 103, 125–126, 132, 137, 162, 179
- Postdiauxic phase, 150
- Postmitotic cells, 7, 10, 194
- PRB1, 241
- Pre-autophagosomal structure, 234, 240, 343
- Preferred nitrogen sources, 149, 173–174
- Prevention of oxidative damage, 154
- Private, 2, 307
- Pro-apoptotic, 213–214, 220–223
- Programmed cell death, 56, 66, 138, 168, 210–211, 220, 243, 245, 340, 347
- Prohibitins, 90–91
- Proline, 67, 173, 337
- Proof-reading, 63
- Prooxidant status, 154
- Pro-survival mechanism, 207
- Proteases, 209, 212, 234–235, 238, 243
- Proteasomal, 5, 10, 71, 211–212, 326
- degradation, 5, 10, 71, 326
- Proteasome, 5, 35, 177, 317
- Protein aggregation, 328, 339–340, 347
- Protein carbonyl, 2, 14–15, 26, 40, 220, 259, 317
- Protein damage, 18, 26, 316–318
- Protein disulphide isomerase, 16, 18
- Protein hydroperoxides, 18
- Protein kinase A, 32, 67, 85–86, 92, 131, 178, 252, 266–267, 332
- Protein kinase C, 32, 82, 108
- Protein thiol, 19, 26–27
- Proteomics, 34, 179, 277–278
- PU.1 null mice, 209–210
- Public, 2, 65, 208, 274, 307–308
- Public mechanisms, 2, 65

Q

- Quality control, 82, 88–91, 210, 237, 239–240, 342
 Quiescent, 123–140, 147, 163, 189, 194–199, 219, 338, 344
 Quiescent (Go) cells, 147

R

- Rad53 checkpoint kinase, 155
 Radiation biology, 56
 Radicals, 14, 16–18, 20, 39, 56–58, 65, 217–219
 Rapamycin, 68–69, 82, 85, 88, 93, 108, 146, 152–153, 155, 170–171, 173, 223, 236, 238, 257, 260, 267–268, 272
 RAS2, 42, 67, 82, 85–86, 90–91, 109–110
 RAS2^{ala18, val19}, 67
 Ras2-cAMP pathway, 85
 Ras/adenylate, 104, 108–109
 Ras/cAMP pathway, 65, 67, 85
 Ras/cAMP/PKA, 336–337, 347
 Rate of mutation, 26, 132, 155
 Rats, 9, 179, 237
 R box, 81, 83
 Reactive cysteine, 18, 32, 38
 Reactive oxygen species (ROS), 2, 5, 13–20, 23–37, 39–42, 56–58, 62–63, 65–67, 72–73, 84, 91–92, 110, 114, 127, 131, 137–138, 147, 153–155, 163, 167, 176–179, 188, 199–200, 202, 211–212, 215–218, 234, 236–237, 240, 244–245, 259, 261, 278, 280, 337–338, 340, 342–347
 Recombination, 1, 18, 44, 102, 113, 132, 138–139, 154–155, 190–191, 193, 254–256, 258, 276, 305
 Redox homeostasis, 21, 56, 222
 Redox potential, 13–14, 33
 Redox status, 154
 Reducing potential, 20, 27
 Rejuvenation, 3–4, 72, 329
 Repair, 14, 18–20, 24, 26–29, 31–34, 42, 62, 64, 71, 112–115, 132, 138–139, 146, 154–156, 178, 188, 192–194, 197–198, 200, 215, 235, 256, 299, 315–317, 326–327, 345–346
 Replication stress, 187–202, 215
 Replicative
 aging, 2–7, 40, 62, 68, 72, 79–96, 124, 131, 175, 188–194, 196, 216, 218, 224, 242, 252–254, 256, 258–262, 264, 267–268, 270, 272, 275–277, 279–280
 life span (RLS), 3, 40–42, 58, 60, 69–71, 189–193, 196, 198, 201, 221–222, 224, 236, 243, 245, 273, 292, 295, 299, 300, 338
 senescence, 102, 209, 254
 Respiration, 8–9, 15, 20, 41, 56, 61, 65, 67, 70, 84, 88, 94, 111, 131–132, 149, 162–163, 175–177, 179, 180, 244, 257, 261, 268, 337, 340, 345
 Respiratory
 activity, 153, 268
 carbon source, 41, 149
 chain, 15, 33, 41, 57, 65, 91, 236–238
 complex, 61–62, 69
 deficient, 5, 41, 61–62, 68–69
 metabolism, 33, 67, 149, 268
 Restriction, 2, 9–10, 42, 67, 93–94, 111, 148–149, 152, 165–166, 178–180, 193–194, 202, 237, 253, 256–257, 299–303
 Retrograde regulation, 81, 90, 294
 Retrograde response, 9, 41, 61, 67–70, 72–73, 79–96, 175, 190, 251, 259–260
 Rev1-Pol ζ DNA polymerase complex, 112
 Reverse, 1, 84, 278, 346
 Rhesus monkeys, 9
 Rho⁺ (Rho-plus), 41, 69, 83–84, 87, 190
 Rho⁰ (Rho-zero), 61, 69, 81, 84–85, 87, 90–91, 93–95
 Rho⁻ (Rho-minus), 41, 61, 69, 81, 334
 Ribonucleotide reductase, 27, 155, 197
 Ribosomal
 DNA, 2, 82, 87, 102, 190, 254, 265
 proteins, 61, 69, 111, 222–223, 265, 269, 280
 S6 kinase, 153, 257, 269, 280
 Ribosome, 26, 34, 61, 69, 85, 152, 218, 222–223, 258, 260, 265–267, 270, 280
 Ribosome biogenesis, 85, 152, 280
 Rim15, 104, 153–154, 269
 RNAi, 67, 94, 234, 237, 264, 279, 298–299, 306
 RNAs, 34, 36, 61, 80, 126–127, 131–132, 136–139, 169, 223, 258
 Rodents, 9, 42, 237, 300–301
 ROS sens, 91
 Roundish mitochondria, 72
 ROX1, 30, 66
 RP, 223
 RPD3, 87
 RTG1/2, 68
 RTG1, 81, 295

- RTG2, 81, 84, 86–87, 93, 95, 102, 175, 259, 295–297
- RTG3, 81, 84, 89, 93, 95, 295
- S**
- Saccharomyces cerevisiae* (*S. cerevisiae*),
1, 20, 24, 27–28, 30, 39, 42, 58,
81, 101–102, 105, 107, 114–115,
124, 146–147, 169–170, 173–174,
179, 188–189, 191, 202, 236,
239, 241–242, 244, 246, 252,
292, 298–301, 303, 306–307, 325,
334–335, 338–339, 345
- SAGA histone acetyltransferase, 87
- Salt, 32, 164, 211, 215
stress, 32, 215
- Sch9, 7, 42, 65, 68, 91–92, 103–106, 108,
110–116, 132, 153, 193, 199, 257,
261, 265, 267, 269, 278, 280
- Schizosaccharomyces pombe* (*S. Pombe*), 4, 58,
102, 243, 299–309, 316, 324–325
- SC Hopkins mix, 148
- Screening the deletion mutant collections, 152
- Segregation, 4, 40, 65, 71–73, 89–90, 210, 220,
239, 255–256, 258–259, 315–329,
334, 342
- Selection, 128, 191, 219, 292, 299, 303,
305–308, 319, 324–326, 345
- Self-digestion, 208
- Senescence/Senescent, 2, 4–5, 39–40, 66, 71,
89–90, 94, 102, 105, 115, 124, 129,
132, 134, 146, 152, 163, 189–190,
192, 194–196, 200–202, 209,
216–220, 223, 237, 242, 244–245,
252, 254–255, 276, 292, 299, 325,
347
- Sgs1, 113, 193, 196
- Shock protein, 28, 32, 71, 106, 324
- SICD, 215
- Signaling
pathway, 65, 152, 335
protein kinase A (PKA), 32
retrograde, 81, 83–86, 88–95, 174–175,
259, 294–297
TORC1, 85, 149, 152–153, 155, 171, 269
- Silencing, 70
- SIM1, 214
- Singlet oxygen $^1\text{O}_2$, 16
- SIR2, 41
- Sir2p, 70, 220, 292
- Sirtuins, 104, 253–254, 256–258, 309
- S6 kinase, 65, 106, 108, 153, 223, 257, 269,
280
- Skn7p, 26, 30–31, 33–34, 38
- SLIK complex, 87–88, 93, 95
- SOD1, 18, 20, 22–23, 31, 37, 57, 151,
176–177, 261
- SOD2, 18, 20, 22, 42, 57, 62, 65, 104, 113,
116, 151, 176–177, 261
- Softening, 208
- Somatic maintenance, 146
- Somatic mutation theory of aging, 57, 219
- SOV1, 69–70
- Spent medium, 7, 148, 150, 224
- Spermidine, 89, 268
- Sphingolipids, 92
- Spore, 7, 107
- SPS amino acid sensor, 86
- Starvation, 7, 25–26, 32, 42, 93, 103, 105, 107,
139, 146–147, 149–150, 152, 163,
168, 218, 223, 237, 268–269, 272
- Starvation for an essential auxotrophic
requirement, 150
- Starvation stress, 223
- Stationary
phase, 8, 24, 27, 41, 89, 103, 107, 123–140,
146–150, 153, 162–164, 167,
176–177, 179, 189, 194–201, 218,
238, 270, 272–273, 292, 299–300,
308
survival, 148
yeast cells, 7–8, 218
- Ste20p, 214
- Stem cell, 6–7, 10, 73, 129, 137–139, 156,
188–189, 194, 196, 201, 219, 299,
326
therapy, 6
- S-thiolation, 27, 36
- Stress
granules, 73
resistance, 39–40, 42, 58, 60, 90, 92, 104,
106, 107, 109–110, 115, 146, 154,
175, 254, 256, 260–261, 267, 278,
300–301, 308–309
response, 10, 28, 30–33, 36–38, 42, 81, 88,
106, 110, 112, 154, 170, 178, 199,
202, 214, 220, 222, 259, 268–269,
273, 276, 331, 337, 343, 346
- Succinate dehydrogenase, 110
- Sugar, 81, 179, 211, 215
- Suicide, 209, 261
- Sulfenic, 18, 26–27, 32, 37–38
acid, 18, 26–27, 32, 37–38
- Sulfonic, 27
- Sulphinic, 18
- Sulphonic acids, 18

- Superoxide, 14–16, 18, 20–24, 29, 34–35, 39, 56–57, 65, 104, 106–107, 109–110, 112–114, 138, 154, 176, 199–200, 218, 261
- Superoxide anion $O_2^{\bullet-}$, 15
- Superoxide dismutase (SOD), 16, 18, 20, 22–24, 34, 39, 57, 104, 106–107, 110, 138, 176, 261
- catalase, 23, 106
- Survival/fecundity balance, 146
- Swi6p, 31–32, 37
- Synthetic complete medium, 103, 148, 167, 175
- T**
- Tap42, 153
- Target of rapamycin (TOR), 82, 146, 161, 169, 223, 234, 236, 252, 257, 267
- Tat-D, 214, 221
- TCTP, 214
- Telomere shortening, 6
- Tert-butyl hydroperoxide, 215
- TFIID, 87
- Thiols, 16, 19, 24, 27
- Thioredoxin, 18, 21–28, 30, 32–34, 36–38, 154
- peroxidases (peroxiredoxins), 25
- reductase, 18, 22–23, 26–27, 30, 34, 37
- Throughput, 1, 40, 150–151, 253, 262, 270–271, 275–277, 297, 299
- Thyroxine, 58
- TORC1, 69, 82, 85, 88, 93, 108, 149, 152–156, 170–171, 173–174, 223, 268–269
- kinase, 67
- signaling, 85, 149, 152–153, 155, 171, 269
- TORC2, 85, 92–93, 108, 152, 170, 223, 268
- TOR complex, 85, 152, 170, 268
- Tor/Sch9, 103–108
- TOR protein kinase, 146
- TPK3, 67, 337
- Trace elements, 9, 164, 166
- Trade-off, 316, 321, 326–327
- Transcriptional programme for entry to G_0 , 153
- Transcriptional regulation, 32–33, 66, 93, 172, 294
- Transcription factor, 19, 21, 26–28, 30–38, 66, 68–69, 81–82, 85, 94–95, 104–106, 109, 169–170, 173, 175, 209, 259–260, 268–269, 272, 297
- Translation, 18, 34–35, 61, 69–71, 85, 108, 162, 169, 177–179, 223, 257–258, 265–270, 280, 294
- activators, 69
- Translational control, 34–35, 70
- Translesion synthesis, 62, 112
- Translocation, 35, 81, 83, 87, 108, 209, 238, 260
- Transporters, 30, 90, 92
- Trehalose, 219
- Tricarboxylic acid (TCA), 68, 80, 175
- cycle, 68
- Trinucleotide repeats, 87, 192
- Triose phosphate isomerase, 60
- tRNAs, 61, 169
- Tryptophan, 9, 265
- TSA1, 18, 21, 23, 26–27, 60
- Tumor proliferation, 209
- Tumor suppressor, 67, 202, 209
- TUNEL, 155, 210–211, 216, 218
- assay, 155, 211, 216
- U**
- Ubiquinol, 19–20
- Ubiquinone, 58
- Ubiquitination, 83, 212, 214
- Ubiquitin ligase, 67, 81–82, 339
- Uncouplers, 41, 81
- Unfolded protein response (UPR), 222–223
- UTH1, 41, 83, 88–89, 214, 236–239
- Uth1p, 42, 214
- UV radiation, 211
- V**
- Vacuole, 8, 36, 71, 79–80, 82, 95, 127, 166–167, 236, 238, 240–241, 268, 334, 342–343
- Valproic acid, 212, 243
- VHL, 67
- Vitamins, 9, 166
- Von Hippel-Lindau tumor suppressor, 67
- W**
- WD-repeat protein, 82
- Werner's syndrome, 113
- Woronin bodies, 242
- WRN RecQ helicases, 113
- X**
- X-rays, 56
- Y**
- Yap1p, 27, 30–31, 33–34, 36–38
- YCA1, 35, 66, 212, 218, 243–245
- Yca1p, 35, 212, 218

- Yeast
- aging, [2](#), [9](#), [35](#), [84](#), [87](#), [200–202](#), [207–224](#),
[251–281](#), [309](#)
 - nitrogen base (SD) medium, [148](#)
 - psychrophilic, [146](#)
 - YME1, [214](#), [238–239](#)
 - Yme1p, [214](#)
 - Ypk1, [92](#)
 - Ypk2, [92](#)
 - Ysp1p, [214](#)