

Index

a

- acetaldehyde 415
- acetone-butanol-ethanol (ABE) fermentation 10, 592
 - application 354
 - genetic tools 346
- acetyl-CoA 676, 681
- Acetyl-CoA carboxylase (ACCase) 621
- Acetyl-CoA synthase I (ACSI) 528
- Acinetobacter baumannii* 611
- actinomycetes 495
- Adenylate energy charge (AEC) 651
- aerobic thermophiles 521
- aetheramides 472
- Agrobacterium tumefaciens* 607
- ajudazols 466
- Alcohol dehydrogenase (ADH) 535
- Alcohol oxidase (AOX) 694
- alcohols 157
- Algae*
 - chloroplast genetic engineering, *see* Chloroplast genetic engineering
 - diversity 605
 - genetic malleability 606
 - nuclear genetic engineering, *see* Nuclear genetic engineering
 - nutraceuticals and nutritional supplements, *see* Nutraceuticals and nutritional supplements
 - protein therapeutics, *see* Protein therapeutics
 - recombinant vaccines, *it see Recombinant vaccines*
 - scalability and growth rate 606
 - transformable species
 - blue-green algae 613
 - dinoflagellates 613
 - alkanes 160

Allochromatium vinosum 590

- ambruticin 465
- Amgen 33
- amino acids 153
- Ammonium (NH_4^+) 655
- anaerobic extreme thermophiles 521
- Anaeromyxobacter dehalogenans* 457, 459, 464
- Anabaena* 586
- anaplerosis 660
- animal feedstocks
 - algal protein extracts 625
- antibodies 677
- antibody-dependent cellular cytotoxicity (ADCC) 662
- AOX1* promoter 694, 695
- Arabidopsis thaliana* 86
- arabinose 680
- archaeal phospholipids 513
- aroma compounds 414
- artemisinin 675
- Arxula adenivorans* 678
- astaxanthin 616
- ATP-citrate lyase (ACL) 679
- autonomously replicating sequences (ARS) 696
- auxotrophies 677
- avermectin 497

b

- B-cell lymphoma (Bcl) 662
- Baby hamster kidney (BHK) 645
- Bacillus subtilis* 88, 97, 243
 - chromosomal modification 239
 - counter-selection strategies 239
 - Cre/loxP site-specific recombination 240
 - crude cell lysates 134
 - gene systems-level models 224

- Bacillus subtilis* (*contd.*)
 - gene target identification 223
 - genetic traits
 - - DNA construct transformation 237
 - - double cross over recombination 232
 - - natural competence 232
 - - plasmid expression systems 234
 - - promoters 233
 - - RBS elements 236
 - - recombineering 241
 - - RSEs 235
 - - transcription terminators 235
 - genome reduction 246
 - industrial application 222, 278
 - lysed protoplast transformation 224, 244
 - mutant diversity 248
 - protein secretion 225
 - - extracellular proteases 229
 - - Sec pathway 227
 - - signal peptides 225
 - - Tat pathway 228
 - safety 258
 - screening platforms 249
 - strain development 222
 - versatile abilities 221
- bacteriocins 407
- bacteriophages 169
- baker's yeast, *see* *Saccharomyces cerevisiae*
- bioethanol 674
- biofuels 433, 507
 - *Caldicellulosiruptor bescii* 548
 - *Escherichia coli* 169
 - extreme thermophiles 511
 - *Saccharomyces cerevisiae* 674
- Biogen S.A. 33
- biomining 511
- biorefinery 681
- biosystems engineering 36
- biotin 271
- biotin–protein ligase (BPL) 528
- Botrytis cinerea* 475
- breast cancer 471
- 2,3-butanediol (2,3-BDO) 140
- butanol 434, 508, 676
- Butyraldehyde dehydrogenase (PduP) 592
- Caenorhabditis elegans* 652

- c**
- caffeine 676
- Caldanaerobacter subterraneus* subsp. *tengcongensis*
 - ethanol production 555
 - genetics 555
 - growth substrates 555
- growth temperature 555
- pH range 555
- Caldicellulosiruptor bescii* 513
 - biofuels 548
 - ethanol 550
 - genetics 548
 - growth rate 548
 - growth substrates 548
 - growth temperature 548, 551
 - hydrogen production 550
 - pH range 548
- Calvin-Benson-Bassham (CBB) 589
- Candida boidinii* 678, 692
- Candida curvata* 679
- carbapenems 22
- carbon assimilation 623
- carbon catabolite repression (CCR) 303
- carbonic anhydrase (CA) 528
- carolacton 476
- carotenoids 616
- cas9* gene 492
- cefoxitin 22
- cell penetrating peptides (CPP) 607
- cell-free metabolic engineering (CFME)
 - 126
 - co-factor stability 138
 - fuel cells 135
 - hybrid cell-free systems 134
 - *in vitro* biochemical pathways 130
 - *in vivo* biochemical pathways 132
 - models 139
 - purification challenges 136
 - spatial organization 137
- cell-free protein synthesis (CFPS) 126
- cell–cell communication systems 86
- cellobiose 167
- cephalosporin C 21
- cephamycin C 22
- CFME, *see* cell-free metabolic engineering (CFME)
- cheese 403
- Chinese hamster ovary (CHO) 645
- Chiron Corp. 33
- chivosazoles 466
- Chlamydomonas reinhardtii* 606, 607, 609, 610, 614–618, 621–628
- Chondromyces crocatus* 457, 465
- chloramphenicol 513
- Chlorella ellipsoidea* 615
- Chlorella protothecoides* 628
- Chlorella vulgaris* 630
- Chlorella zoofingensis* 617
- chloroplast genetic engineering
 - gene regulation 611

- reporter genes 612
- selection and reporters 611
- transformation methods 610
- chlorotonal 475
- chondramides 466
- Chondromyces crocatus* 456, 466
- chromosomal modification, extreme thermophiles 518
- citric acid fermentation process 13
- classical strain improvement (CSI) 224
- Clostridium acetobutylicum* 330, 508, 597
 - bacteriophages 335
 - genome sequences 342
 - solvent formation, regulation of 345
- Clostridium beijerinckii* 331
- Clostridium saccharoacetylum* 331
- Clostridium saccharoperbutylacetonicum* 332
- Clostridium thermocellum* 365, 513
- ClosTron system 349
- CO₂ concentrating mechanism (CCM) 589
- cold-methanol quenching 656
- complex/carbon monoxide dehydrogenase (CODH) complex 536
- concatamer cloning 699
- conjugated linoleic acids (CLA) 426
- consolidated bioprocessing (CPB) 548
- Corynebacterium glutamicum* 183, 656
 - biomass synthesis, cellular demand for 192
 - catabolic pathways 184, 185, 186
 - genetic manipulation 192
 - engineering gene expression 195
 - plasmids 193
 - transformation methods 194
 - glyoxylate shunt 187
 - pyruvate node network 189
 - substrate assimilation 186
 - TCA cycle 187, 188
- Cre/lox technique 240
- CRISPR/Cas9 system 492
- crocapeptins 466
- crude cell lysate systems 128, 133, 559
- Customized Optimization of Metabolic Pathways by Combinatorial Transcriptional EngineeRing" (COMPACTER) 98
- Cyanobacteria*
 - bacterial group and metabolisms 582
 - biofuels and chemicals 581
 - circadian clock 584
 - CO₂ direct conversion
 - acetyl-CoA 590
 - biofuels and chemicals 590
 - hydrogen 596
 - keto acids 594
 - TCA cycle 596
 - genetic tools
 - promoters 586
 - ribosome binding site 588
 - terminators 587
 - transformation 585
 - genetic transformation 581
 - light/dark regulation 584
 - nitrogen fixation 583
 - photosynthetic efficiency
 - carbon fixation 589
 - light harvesting 588
 - plants chloroplasts 581
 - cyanophycin 583
 - cyclin-dependent kinases (Cdk) 647
 - Cyclotella cryptica* 621
 - Cylindrotheca fusiformis* 628
 - Cystobacterineae* 457, 459, 460
 - Cystobacter* species 461
- d**
 - Darbepoetin alfa (DA) 663
 - diacetyl 415
 - Dicer and Argonaute proteins 609
 - dihydrofolate reductase (DHFR) 652
 - diols 159
 - disorazoles 465, 475
 - DNA assembler method 97
 - DNA synthesis 87
 - DNA transformation 60
 - double description (DD) method 116
 - double-strand breaks (DSBs) 653
 - Dunaliella salina* 613, 616, 617, 626, 627, 630
 - Dunaliella tertiolecta* 613
 - Dunaliella* genus 613
- e**
 - Earth Microbiome Project 52
 - ecallantide 703
 - EcoCyc (5) 151
 - electrofuels 513
 - electrophoresis 55
 - electroporation 513, 586, 607, 612, 653
 - elementary flux modes (EFMs) 111, 112, 114, 116, 118
 - Embden-Meyerhof-Parnas pathway 650
 - photobioreactors 589, 628
 - endoplasmic reticulum (ER) 648, 701
 - endoplasmic reticulum associated degradation (ERAD) 701
 - enzymes 677, 703

- epigenetics 52
 epothilone
 – anti-cancer agents 487
 – ixabepilone, *Sorangium cellulosum* So ce90 474
 – *Myxococcus xanthus* 471
 erythritol 422, 423
 erythropoietin 654
Escherichia coli 88, 89, 90, 92, 99, 460, 507, 586–588, 592, 645, 656, 658, 661
 – biofuels 169
 – bistable gene-regulatory network 99
 – carbon efficiency 165
 – cell–cell communication 103
 – CFME 140
 – crude cell lysates 133
 – genetic transformation 169
 – glycerol 168
 – industrial products 153
 – methanol utilization 166
 – non-oxidative glycolysis 165
 – phage contamination 170
 – products overview 167
 – shikimate pathway 166
 – *Streptomyces* 495
 ethanol 433, 511, 512
 – *Caldicellulosiruptor bescii* 550
 – *Pyrococcus furiosus* 535
 – *Thermoanaerobacter* species 552
 eukaryotic like kinases (ELKs) 464
 exopolysaccharides (EPS) 429
 Exotoxin A 614
 extracellular proteases 229
 extreme thermophiles, metabolic engineering
 – bio-based chemicals and fuels 511
 – bioprocessing advantages 509
 – *Caldanaerobacter subterraneus* subsp. *tengcongensis* 555
 – *Caldicellulosiruptor bescii* 548
 – genetic manipulation 513, 514
 – genetic parts 531, 556
 – host organism, selection of 512
 – limitations 558
 – predictive modeling methods 559
 – promoters 556
 – *Pyrococcus furiosus* 523
 – reporter genes 558
 – ribosomal binding sites 557
 – *Sulfolobus* species 538
 – *Thermoanaerobacter* species 552
 – *Thermococcus* species 537
 – *Thermotoga maritima* 541
 – *Thermus* species 544
- f**
 farnesyl pyrophosphate (FPP) 704
 fast filtration technique 657
 fatty acids 160
 fed batch cultures 661
 fed-batch technology 674
 fermentation process 222, 673
 fermentative and anaplerotic pathways 650
 fermenters 155, 200, 222, 252, 253, 461
 flaviolin 134
FLD1 promoter 694
 flocculants 629
 fluorescence resonance energy transfer (FRET)
 – approach 658
 5-fluorocytosine (5FC) 546
 5-fluoroorotic acid (5FOA) 518
 flux balance analysis (FBA) 659
 fluxomic techniques 166
 folate 424
 formate hydrogen lyase (FHL) 536
 fuel cells 135
 γ -aminobutyric acid (GABA) 427, 428
Gaussia luciferase 609
- g**
 gelonin 614
 gene cloning 60
 gene copy number variation (GCNV) 51
 gene splicing 51
 gene synthesis 88
 Generally Recognized as Safe (GRAS) 151
 genetics
 – *Caldanaerobacter subterraneus* subsp. *tengcongensis* 555
 – *Caldicellulosiruptor bescii* 548
 – *Corynebacterium glutamicum* 192
 – extreme thermophiles 518
 – myxobacteria 462
 – *Pyrococcus furiosus* 523
 – *Sulfolobus* species 539
 – *Thermoanaerobacter* species 552
 – *Thermococcus barophilus* 538
 – *Thermococcus kodakarensis* 537
 – *Thermococcus onnurineus* 538
 – *Thermus* species 545
 – *Yarrowia lipolytica*, lipid production in 679
 Genex Corp. 32
 genome mapping 64
 genome-scale metabolic networks EFMs 116–118
 genomics
 – myxobacteria 462

– *Pichia pastoris* 689, 698
 – *Sorangium cellulosum* So ce56 473
 Gibson assembly technology 97, 238
 global transcription machinery engineering (gTME) 98
 glucoglutaminolysis 654, 660
 gluconic acid 13
 glutamine 651
 glutamine synthetase (GS) 652
 glutaminolysis glutamine 651
 glyceraldehyde 3-phosphate dehydrogenase (GAP) promoter 694
 glycerol 12, 168
 glycoengineering 662
 – *Pichia pastoris* 678, 703
 – *Saccharomyces cerevisiae* 678
 glycosylation 615, 663
 Golgi apparatus 649
 green fluorescent protein (GFP) 493, 558
gusA reporter gene 493
Haematococcus pluvialis 616, 617
Haematococcus 613
Hansenula polymorpha 674, 678

h

heat shock factor 1 (*HSF1*) 608
 heat shock method 523
 heterocystous cyanobacteria 583
 heterologous expression
 – epothilone gene cluster, *Myxococcus xanthus* 471
 – *Escherichia coli* 495
 – *Streptomyces albus* 497
 – *Streptomyces avermitilis* 497
 – *Streptomyces coelicolor* 496
 hexose transporter (*HUP1*) 628
 hexoses 680
 high mobility group protein B1 (HMGB1) 615
 homologous recombination 653
 human embryonic kidney (HEK) 646
 hybrid cell-free systems 134
 hybrid promoter approach 93
 hybridoma cells 656, 661
 hybridoma cultures 659
 hydrocodone 676
 hydrogen 511
 – *Caldicellulosiruptor bescii* 550
 – *Thermococcus kodakarensis* 538
 – *Thermococcus onnurineus* 538
 – *Thermotoga maritima* 542
 3-hydroxypropionate (3HP) 512, 528, 593

i

I-SceI endonuclease 492
 industrial enzymes
 – cellulosic biofuels 626
 – food processing 626
 industrial-scale biosynthesis 125, 126
 isobutanol 594, 595
 isobutyraldehyde 594
 isopentenyl diphosphate (IPP) pathway 94
 isoprenoids 161
 isopycnic density centrifugation 54
 iterative marker excision system (IMES) 490
 ixabepilone 474

k

kanamycin 513, 544
 keto acids 594
kai gene cluster 584
Kluyveromyces lactis 678
Komagataella 688
 l-(–)-ephedrine 12
 l-glutamate 183

l

LAB, *see* lactic acid bacteria (LAB)
 lactic acid (LA) 430
 – fermentation process 12
 lactic acid bacteria (LAB) 395
Lactobacillus plantarum 92
Lactococcus lactis 91
 light-harvesting complexes (LHCs) 622
 lignocellulose 675, 680, 681
 lipids 678, 679
 lipofection 653
 luciferases 493
 lysine 14, 19, 153, 157, 196–200, 273
 lysosomes 649

m

Madin-Darby canine kidney (MDCK) 658
 malolactic enzyme 419
 mammalian cells
 – biopharmaceuticals 645
 – cellular structure 646
 – CHO cells 651
 – compartmentalization of 647
 – genetic and metabolic engineering 662
 – glycosylation patterns 645
 – growth and product formation 654
 – intracellular metabolome analysis 656
 – mABs and fusion proteins 645
 – metabolism 650
 – molecular biology tools 652

- mammalian cells (*contd.*)
 - proteome and gene expression analysis 661
 - recombinant protein therapeutics 646
 - tissue derivatives 645
 - mannanase 627
 - marine myxobacteria (MMC) 455
 - mechanical disruption technique 657
 - metabolic engineering 620, 662
 - extreme thermophiles, metabolic engineering, *see* extreme thermophiles, metabolic engineering
 - *Pichia pastoris* 700
 - *Saccharomyces cerevisiae* 675
 - metabolic flux analysis (MFA) 166, 659
 - metabolic profiling 658
 - Metabolic Tinker tool 140
 - metabolomics 38, 166, 656
 - metagenomic sequencing 455
 - methanol 687, 688
 - assimilation 691, 692
 - co-feeding strategies 693
 - dissimilation 692
 - oxidation 691, 693
 - oxygen supply, limitation of 693
 - utilization 166
 - methionine sulphoximine (MSX) 653
 - methotrexate (MTX) 653
 - 2-methyl-butanol (2MB) 594, 595
 - methylotrophic yeast 688
 - 6-methylpurine (6MP) 527
 - Micrococcus luteus* 460
 - minicellulosomes 677
 - Minkowski-Weyl Theorem 114
 - MIT Registry of Standard Biological Parts 101
 - Mitochondrial DNA (mtDNA) 651
 - mixed-integer linear program (MILP)
 - approach 118
 - Monoclonal antibodies (mAB) 645
 - Mouse Tumor Necrosis Factor- α (mTNF- α) 487
 - mRNA stabilization elements (RSEs) 235
 - multiple cloning regions (MCS) 95
 - multiplex automated genome engineering (MAGE) 559
 - Mycoplasma genitalium* 88
 - myxobacteria
 - characteristics 463
 - classification 457, 458
 - cooperative morphogenesis 455, 456
 - definition 487
 - epithilones 487
 - genetics and genomics 462
 - growth/nutrient requirements 460
 - marine myxobacteria 455
 - micropredators 455
 - *Myxococcus virescens* 472
 - *Myxococcus xanthus*, *see* *Myxococcus xanthus*
 - phylogeny 457
 - physiology 459
 - prokaryotes 455
 - secondary metabolites 464
 - soil organisms 455
 - *Sorangium cellulosum*, *see* *Sorangium cellulosum*
 - Myxococcales* 457
 - *Anaeromyxobacter dehalogenans* 457, 459
 - Myxococcus xanthus*
 - carbohydrate metabolism 459
 - epithilone, *Sorangium cellulosum* 471
 - expression host 470
 - genome sequence 468
 - prokaryotic development 468
 - protein secretion 460
 - secondary metabolites 469, 470
 - Myxococcus*
 - compounds 468
 - genome sizes 468
 - Myxococcus virescens* 472
 - myxoprincomides 469
 - myxothiazol 465
 - myxovirescin 472
- n**
- N-terminal signal peptides 227
 - Nannocystineae* 457
 - natural products 163
 - next generation sequencing 59
 - next generation synthetic circuits 102
 - nisin 408
 - non-dairy alternative foods 404
 - non-oxidative glycolysis (NOG) 165
 - non-photochemical quenching (NPQ) 588
 - nonribosomal peptide synthetases (NRPS) 466, 469
 - Nostoc* 586
 - nuclear genetic engineering
 - gene targeting and genome editing 609
 - increased nuclear gene expression 608
 - nuclear transformation methods 607
 - selection and screening methods 608
 - transgene expression 607
 - nucleic acid Sequencing 56
 - nucleofection 653

nutraceuticals and nutritional supplements
 – carotenoids 616
 – omega-3 fatty acids 616
 – organic selenium 616
 nutraceutics 420
 nutritional markers 513, 521
Ogataea minuta 678

o

oligonucleotide sequencing 57
 Open ponds 629
 opioids 676
 OptCircuit framework 101
 oral immunization 619
 organic acids 156
 OROPON® 15, 278
 2-oxoglutarate dehydrogenase complex
 (2-OGDH) 596
 oxygenic photosynthesis 582
 β -oxidation 650
 2-oxoglutarate decarboxylase (2-OGDC) 596
 (R)-pantothenic acid 267

p

pediocin 412
Pelagibaca bermudensis 96
Pelagibacter ubique 52
 penicillin 16
Penicillium chrysogenum NRRL-1951 17, 19
Penicillium notatum 16
 pentose phosphate pathway (PPP) 655, 660,
 692, 700
 pentose, yeasts 680, 681
 pentose-phosphate pathway 650, 660
 peptide vascular endothelial cadherin (pVEC)
 607
 peptidolytic enzymes 419
 peroxisomes 649
 petroleum-based precursors 125
Phaeodactylum tricornutum 613, 618, 621,
 628, 630
 phage contamination 170
 phosphoenolpyruvate carboxylase (PPC) 590
 3-phosphoglycerate (3PG) 589
 phosphoketolase 165
 phosphotransferase transport system (PTS)
 300
 photosynthetic efficiency
 – improvement 622
 – light utilization 622
 – photosynthetically active spectrum 623
 photosynthetically active radiation (PAR)
 623
Pichia methanolica 692

Pichia pastoris

- ARS vectors 696
- biopharmaceuticals 703
- carotenoid lycopene 704
- ecallantide 703
- enzymes 703
- fatty acid synthesis 704
- genomics 689
- glycoengineering 678, 703
- hyaluronic acid production 704
- integration site 697
- metabolic engineering 700
- methylotrophic metabolism 691
- methylotrophy 687
- multiple gene copies, integration of 698
- promoters 694
- protein folding and secretion 701
- protein production 674, 677
- physiology 689
- protein glycosylation 703
- protein secretion 695
- riboflavin synthesis 704
- SAM 704
- selection markers 697
- self-replicating plasmid vectors 696
- taxonomy and natural isolates 688
- xylitol production 704
- plaque assay method 170
- plasmid-based expression method 169
- Plasmodium berghei* 618, 619
- Plasmodium falciparum* 618
- Plasmodium* 618
- polyketide synthases (PKS) 466, 469
- polymerase chain reaction (PCR) 509
- polymers 162
- polyunsaturated fatty acids (PUFAs) 472
- Porphyridium* spp. 613
- Prochlorococcus* 88
- 'Prokaryote-like' approach 660
- promoters
 - extreme thermophiles 556
 - *Pichia pastoris* 694
 - *Streptomyces* 493
 - *Sulfolobus* species 541
- proteases 418
- protein sequencing 55
- protein therapeutics
 - HMGB1 615
 - human antibodies and antibody-drug conjugates 614
 - human metallothionein protein 615
 - molecular pharming 614
 - nuclear-expressed protein therapeutics 615

- protein therapeutics (*contd.*)
 - terrestrial plant-derived vaccines 614
 - VEGF 615
- proteins 165
- proteolytic enzymes 419
- proteomic techniques 166
- Pseudomonas aeruginosa* 103
- Pseudomonas putida*
 - bio-based polymers 312
 - biocatalysis applications 314
 - catabolic pathways 301
 - CCR system 303
 - fluxomics 310
 - genetic manipulation 304
 - genomics 308
 - metabolomics 310
 - multi-omics studies 311
 - proteomics 309
 - substrate uptake 300
 - transcriptomics 308
 - xenobiotic degradation 302
- purified enzyme systems 128, 130
 - advanced production pathways 140
- pyridoxal-5'-phosphate biosynthesis 276
- Pyrococcus furiosus*
 - *n*-butanol production 535
 - 3HP production 528
 - CODH complex 536
 - COM1 strain 527
 - crude cell lysates 134
 - doubling time 523
 - ethanol production 535
 - FHL, heterologous expression of 536
 - growth conditions 523
 - growth temperature 523, 535
 - heat shock method 523
 - lactate production 535
 - metabolism 523
 - temperature-controlled metabolic shift 535
- q**
 - Qualified Presumption of Safety (RBS) 255
 - quinoa (*Chenopodium quinoa*) 406
- r**
 - recombinant DNA technology 71
 - recombinant human erythropoietin (rHuEPO) 663
 - recombinant protein production
 - *Pichia pastoris*, see *Pichia pastoris*
 - *Saccharomyces cerevisiae* 677
 - recombinant vaccines
 - animal efficacy studies 618
 - oral vaccines 619
 - vaccine antigens, algae 617
 - replicating shuttle vectors 518
 - reporter genes
 - extreme thermophiles 558
 - *Streptomyces* 492
 - riboflavin 222
 - biosynthesis 264
 - riboregulated transcriptional cascade (RTC) counters 100
 - ribosomal binding sites (RBS) 495, 588
 - extreme thermophiles 557
 - ribosomal RNAs (rRNAs) 648
 - ribulose-1,5-biphosphate (RuBP) 623
 - ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) 589
 - Riesling-Silvaner infection 475
 - RNA polymerase (RNAP) 89, 587
 - RNA-induced silencing complex (RISC) 652
- s**
 - S-adenosyl-L-methionine (SAM) 704
 - Saccharomyces cerevisiae* 86, 92, 93, 460, 507, 645
 - biorefinery applications 674
 - fed-batch technology 674
 - fermentative capacity 674
 - gene expression 95
 - hybrid promoter approach 93
 - lipids 679
 - metabolic engineering 675
 - pentose 680
 - positive feedback gene circuit 101
 - recombinant protein production 674, 677
 - sakacin 412
 - Schizosaccharomyces pombe* 678
 - secretory proteins 701
 - Selenium 616
 - seleno-proteins 429
 - shikimates 166
 - Shine-Dalgarno (SD) sequence 588
 - signal peptidase (SPase) 225
 - signal peptides 225
 - simultaneous saccharification and fermentation (SSF) process 681
 - simvastatin 523
 - single-nucleotide polymorphisms (SNPs) 652
 - site-specific recombination (SSR) systems 490
 - SMRT sequencing technology 522
 - ixabepilone 474
 - sorangicins 466
 - Sorangineae* 457
 - sorangioides 466

- Sorangium cellulosum*
 – bioactive compounds 465, 475
 – ixabepilone 474
 – *Myxococcus xanthus*, epothilone 471
soraphen 475
sorbitol 423
Spirulina 629
Splicing process 648
 Standard European Vector Architecture (SEVA) 306
Staphylococcus aureus 618, 619
 starch-modifying enzymes 416
 steroid transformations 13
Stigmatella aurantiaca 459
 stimulants 676
Streptomyces
 – antibiotics 487
 – biosynthetic gene clusters 488, 489
 – carbon dioxide 487
 – carbon monoxide 487
 – chassis strain 496
 – chemoheterotrophic 487
 – CRISPR/Cas9 system 492
 – ermEp1 and ermEp2 promoter 494
 – Gram-positive saprophytic bacteria 487
 – I-SceI endonuclease 492
 – industrial application 487
 – mTNF- α 487
 – PA3 promoter 495
 – RBS flanking regions 495
 – reporter genes 492
 – site-specific recombinases 490
 – *Streptomyces albus* 497, 498
 – *Streptomyces avermitilis* 491, 495, 497
 – *Streptomyces coelicolor* 496
 – tcp830p 494
 – *tipAp* promoter 494
 – transposon mutagenesis 491
 streptomycetes 476
 succinic acid 512
 succinic semialdehyde dehydrogenase (SSADH) 596
 sugar alcohols 161
 sulfangolides 466
Sulfolobus species
 – genetic manipulation 539
 – growth substrates 538
 – growth temperature 538
 – metabolic engineering 541
 – pH range 538
 – selection strategies 539
 – thermoacidophilic archaea 538
 surfactins 256
 suspension cultures 654
Synechococcus sp. PCC 7942, 623
Synechococcus elongatus 584, 585, 590
Synechococcus 7942, 587, 590
Synechococcus PCC 7002, 585
Synechococcus PCC 7942, 586, 587, 592, 596
Synechocystis sp. 585
Synechocystis PCC 6803, 585–588
 synthetic biology 676
 – engineering targets 86
 – expression vectors 95
 – functional and robust modules
 – – gene circuit design 100
 – – pathway module design 96
 – promoters 89
 – technological driving forces 85
 Synthetic Biology Software Suite (SynBioSS) 101
 “Takamine” process 15
- t**
- TargeTron system 349
TEF1 promoter 92
Thalassiosira weissflogii 613
 thebaine 676
 theobromine 676
Thermoanaerobacter mathranii 513
Thermoanaerobacterium saccharolyticum 365
Thermoanaerobacter species
 – ethanol production and tolerance 552, 553
 – genetics 552
 – growth conditions 552
 – growth rate 552
 – growth temperature 552
 – pH range 552
Thermococcus species
 – genetics 537
 – growth substrates 537
 – hydrogen production 538
 – optimum growth temperatures 537
 – sugar metabolism 537
 thermostable antibiotics 513
Thermotoga maritima
 – chemoorganoheterotroph 541
 – electroporation 543
 – fermentative metabolism 542
 – growth rate 542
 – growth temperature 541
 – hydrogen production 542
 – liposome-mediated transformation 542
 – metabolic engineering 544
 – pH range 541
 – toga 541
 – transformation efficiencies 543

- Thermus aquaticus (Taq)* DNA polymerase 509
- Thermus* species
- biotechnology, use in 544
 - genetic engineering 545
 - growth substrates 544
 - growth temperature 544
 - metabolic engineering 547
 - pH values 544
- thebaine 676
- theobromine 676
- THI11* promoter 695
- thiamine 273
- thienamycin 22
- thioredoxins 585
- tipAp promoter 494
- Tissue-plasminogen activator (t-PA) 662
- TLA, *see* Truncated Light-harvesting Antenna (TLA)
- Transcription factor binding sites (TFBS) 587
- transgenic animals 72
- transposon mutagenesis 491
- triacylglycerol (TAG) 620
- tricarboxylic acid (TCA) cycle 135, 187, 648, 650
- Trichodesmium*
- nitrogenase activity 583
- Truncated Light-harvesting Antenna (TLA) 589
- u**
- unfolded protein response (UPR) pathway 699, 702
- untranslated regions (UTRs) 611
- uracil prototrophy 518, 521, 540
- v**
- vascular endothelial growth factor (VEGF) 615
- velocity centrifugation 54
- Vibrio fischeri*
- cell-cell communications 102
- vitamin C fermentation process 11
- vitamins 423
- Volvox carteri* 628
- Vulgaribacter incomptus* 464
- w**
- Warburg-effect 650
- winemaking 419
- x**
- X-box-binding-protein 1 (Xbp1) 662
- X-ray crystallography 55
- xylanase 626
- xylitol 423
- xylose 680
- y**
- Yacon (*Smallanthus sonchifolius*) 404
- Yarrowia lipolytica*
- fatty acid accumulation 508
 - hybrid promoter approach 93
 - lipid production 675, 679
 - recombinant protein production 678
 - yeast 645
 - bioethanol 674
 - biomass production 674
 - crabtree positive phenotype 673
 - fermentative capacity 673
 - in biotechnology 674, 675
 - lipids 675, 678
 - pentose 680, 681
 - *Pichia pastoris*, *see* *Pichia pastoris*
 - process development 674
 - recombinant protein production 677
 - *Saccharomyces cerevisiae*, *see* *Saccharomyces cerevisiae*
 - substrates and products 673, 674
- yeast-based fermentations 14
- YEASTRACT database 89
- z**
- zinc finger nucleases (ZFNs) 653
- Zygosaccharomyces pastori*, *see* *Pichia pastoris*
- zymase 15