

## Index

### **a**

- active immunoregulatory cytokine  
IL-10 53
- acute liver injury 54
- acyl-homoserine lactone (AHL) 104, 200
- adhesion mechanisms 122–124
- adhesion modulation 125–126
- AHR-mediated type I interferon signaling 98
- Akkermansia muciniphila* 50
- alanine dehydrogenase enzyme (AlaD) 55
- allogenic stem cell transplantation (alloSCT) 227
- altered and aberrant microbiome 155
- anchor-less elongation factor Tu (EF-Tu) 124
- 5'-and 3'-untranslated regions (5'-and 3'-UTRs) 111
- anhydrotetracycline (aTc) 164
- anorexigenic lipids 208
- anti-biofilm enzyme 178
- antibiotics 201
- anti-inflammatory bacterial taxa 223
- anti-inflammatory interleukin-10 (IL-10) 53, 238
- anti-inflammatory molecules 109, 243
- antimicrobials 178, 201
- antimicrobial screening systems 162

- antimicrobial targets 162
- antiseptic 4-hydroxybenzoic acid 164
- aptamer domain 160
- arabinooligosaccharides (AOS) 10
- arabinose 163
- aryl hydrogen carbon receptor (AHR) 97
- autism spectrum disorder (ASD) 22, 63, 228, 243, 250
- auto-phosphorylation reaction 290
- auxotrophies 205

### **b**

- bacterial vaginosis (BV) 7
- bacteriocin Pyocin S5 104
- Bacteroides fragilis* 14, 206, 289
- Bacteroides thetaiotaomicron* 9, 95, 99, 129, 155, 165, 206
- bacteroidetes 97
- Bacteroidetes/Firmicutes* ratio 50
- baker's yeast 168
- bariatric surgery 227
- Barker hypothesis 239, 240
- basal metabolic rate (BMR) 13
- bidirectional interaction 22, 155
- Bifidobacterium longum* 55
- Bifidobacterium*-rich microbiota 245
- Bifidobacterium* spp. 14, 50, 236, 251
- bile-acid metabolism 226
- bile salt hydrolases (BSH) 56
- biofertilization 145

- bioinformatic initiatives 27  
 bioinoculants 145  
 biomarker discovery 159  
 biosensors, types of 159  
     engineering TCS-based sensors 167  
     GPCR 168  
         advances, in yeast 170–171  
         engineered, into yeast 168–170  
         gut microbiome 168  
     riboswitches 159  
         design and selection of, synthetic 160–161  
         molecular detection, of  
             microbiome metabolites 161–162  
         regulatory mechanisms 160  
     TCS systems, for gut diagnostics 166–167  
     testing and utilizing engineered  
         biosensors 171  
         CFPS 171–173  
         *in vitro* testing 173–176  
     transcription factors 163  
         applications 165  
         engineering 164  
         mining 163–164  
     *in vitro* testing 173  
     OOC 174  
     *in vitro* host-microbe  
         characterization 174–176  
     *in vitro* models 174  
 biostimulation 145  
 biosynthesis pathway 200  
 biotherapeutic granulocyte  
     macrophage-colony stimulating factor (GM-CSF) 178  
 bottom-up approach 196  
 brain-gut axis (BGA) 224  
 brain-gut-microbiome (BGM) 22  
 Broad Institute OpenBiome Microbiome Library 159  
 broad-spectrum antibiotics 60, 224
- C**
- Caco2 cells 174  
*Caenorhabditis elegans* intestine 165  
 CAI-1-sensing two-component regulatory system (TCS) 105  
 Canadian Institutes of Health Research (CIHR) 27  
 Canadian Microbiome Initiative (CMI) 27  
 carbapenem-resistant *Enterobacteriaceae* 224  
 carbon catabolite repression 101  
 cardiometabolic risks 236  
 cardiovascular disease (CVD),  
     microbiome engineering 58, 59  
 gut microbiome interventions 59–60  
 microbiome-derived TMAO 60–61  
 cardiovascular diseases 94  
 catecholamines 63  
 cell and mucus-binding protein A (CmbA) 124  
 cell-free protein expression systems (CFPS) 171–173  
 cell-surface protein Spr1345 123  
 central nervous system (CNS) 61  
 cheap paper-based system 173  
 chemotaxis signaling protein (CheZ) 162  
 chenodeoxycholic acid 57  
 Chinese hamster ovary (CHO) cells 172  
 chloramphenicol 201  
 cholera autoinducer 1 (CAI-1) 105  
*Clostridium clostridioforme* 50

- Clostridium difficile* infection (CDI) 18, 99, 105, 208, 220, 222
- coarse-grained ODE models 202
- colon epithelia 95
- colonizing bacteria 94
- colorectal microbiota 4
- commensals 93
- Commonwealth Scientific and Industrial Research Organisation (CSIRO) 145
- communication molecules 201
- complex macromolecules 199
- complex plant-associated microbiomes 137
- coronary artery disease (CAD) 58
- corticotropin-releasing hormone (CRH) 249
- cortisol 155
- Corynebacterium glutamicum* 162
- CO<sub>2</sub>-supplying butyrate oxidation 95
- COVID-19 pandemic 148, 220
- critical illness, of newborns 250
- Crohn's disease (CD) 20, 178, 223
- Cynomolgus monkeys 56, 292
- cytotoxic T-lymphocyte associated protein-4 (CTLA-4) 177
- d**
- deorphanization 170
- deoxycholic acids (DCA) 56
- design-build-test-learn (DBTL) 112, 138, 202, 209, 278
- dextranomer microspheres (DM) 127
- dextran sodium sulfate (DSS)-colitis mouse model (C57Bl/6) 290
- dextran sulfate sodium (DSS) 21, 98
- dietary lifestyle variation, affecting host microbiome 8
- age groups and dietary-related microbiome changes 13–15
- continental dietary difference Africa 16  
Asia 15  
Australia 16  
Europe 15–16  
North America 17  
South America 16
- dietary role, in shaping microbiome 8
- dietary fibres 9–10
- lipids 10–11
- protein and polypeptides 8–9
- soluble saccharides 9
- diet-related microbiome changes 11–13
- dietary modulation, of microbiome 17
- cancer 21–22
- infection 17
- FMT 17–19
- prebiotic-, diet- and probiotic-mediated prevention 19–20
- inflammatory disease 20–21
- psychological disease 22
- ASD 22
- neurodegenerative diseases 23
- dispersin B (DspB) 178
- distal organs 98
- DNA-editing all-in-one RNA-guided CRISPR-Cas Transposase (DART) method 145
- DNA polymerase (DNAP) 287
- downstream promoter-reporter system 109
- Dynamic Cyan Induction by Functional Integrated Receptors (DCyFIR) 170
- dynamic modelling 203
- dysbiosis 250

**e**

- E. coli* chemotaxis system 162  
 effector domain 166  
 Emulate Bio microfluidic device 175  
 endogenous ethanol 226  
 endometrial microbiota 234–236  
 engineered biosensing probiotics 179  
 engineered microbes 176  
   for disease diagnostics 176, 177  
   cancer 177–178  
   future translation 178–179  
   IBD 178  
   infection 178  
   identifying microbiome changes *in situ* 176  
 engineered probiotics 155, 156  
 engineering microbiome, to treat diseases  
   disease-related perturbations 103, 105, 106, 109, 110  
   strain selection for 102–103  
   therapeutic proteins 110–111  
 engineering population control 206–207  
 engineering synthetic consortia  
   analysis tools 202  
   cell-to-cell communication 200–201  
   computational models 202  
   agent-based models 203  
   dynamic/deterministic models 202–203  
   stoichiometric and genome-scale metabolic models 203–205  
 external and intercellular signal molecules 201  
 genetic manipulation tools 200  
 secretion and exchange, of metabolites 201–202  
 engineering syntrophy 205, 206  
*Enterobacter* 235  
*Enterococcus* 235

- enteroendocrine L cells 50  
 environmental manipulation 141  
 environmental transformation  
   sequencing (ET-Seq) 145  
 episomal system 110  
 epithelial enterochromaffin cells 63  
 eukaryote riboswitches 160  
 European Society of Microbiology and Infectious Disease (ECMID) 222  
 extracellular polymeric substances (EPS) 127  
 extracytoplasmic function (ECF) sigma factor 101  
 Extreme Science and Engineering Discovery Environment (XSEDE) 159
- f**
- Faecalibacterium prausnitzii* 11, 95, 227  
 farnesoid X receptor (FXR) signaling 226  
 fecal microbiome transplantation (FMT) 17–19, 52  
 fecal microbiota therapy  
   clinical application  
     *C. difficile* infection 222–223  
     IBD 223–224  
     IBS 224–225  
     and liver diseases 225–226  
     and slow-transit constipation 225  
     therapeutic option 224  
 novel indications  
   autoimmune diseases 227  
   chemotherapy-induced diarrhea 226  
   GVHD 227  
   neuropsychiatric disorders 227–228  
   obesity and metabolic syndrome 227

- fecal microbiota transplantation (FMT) 219  
 administration of 220  
 potential donors, recruitment of 220, 221  
 safety 220, 222
- Firmicutes* 97
- Firmicutes/Bacteroides* 24
- Firmicutes/Bacteroidetes* ratio 16
- flavin-containing monooxygenase (FMO) enzyme 60
- 5-fluorouracil (FU) 125
- flux balance analysis (FBA) 144, 203
- FMT donor screening studies 221
- “focal” species *Pantoea* sp. YR343 141
- formula feeding 240
- four-species consortium 206
- fructooligosaccharides (FOS) 10
- fulminant colonic inflammation 222
- fumarate and nitrate reductase (FNR) 282
- functional encapsulations and biofilms 126, 127
- g**
- galactooligosaccharides (GOS) 10, 245
- $\gamma$ -aminobutyric acid (GABA) 59, 63, 155
- gastrointestinal inflammation 103
- gastrointestinal tract (GIT) 2, 122, 223
- genetic enzyme screening system (GESS) 109
- genetic manipulation tools 200
- genome-scale levels 202
- genome-scale metabolic models (GEMs) 143–144, 203
- Gibson assembly 288
- glucagon-like peptide-1 (GLP-1) 50
- glucagon-like peptide-2 (GLP-2) 24
- gluten-and casein-free (GFCF) 22
- GM dysbiosis 219
- Golden Gate assembly system 288
- G protein-coupled receptors (GPCRs) 159, 168
- G protein coupling 169
- graft-versus-host disease (GVHD) 227
- green fluorescent protein (GFP) expression 141
- greenhouse gas emissions (GHGE) 15
- gross domestic product (GDP) per capita 11
- gut-brain axis (GBA) 61
- gut ecosystem 111
- gut-inhabiting bacteria 93
- gut microbiota 219
- gut-on-a-chip *in vitro* models 174
- h**
- heat shock protein 65 (HSP65) 59
- hepatic *de novo* lipogenesis 226
- hepatic encephalopathy (HE) 54, 58, 225
- hepatocellular carcinoma 57
- Herbaspirillum frisingense* 141
- heterologous protein 110, 198, 279, 289
- high-affinity phenylalanine-specific permease (PheP) encoded 110
- hospital-acquired infection 222
- host and microbial metabolites 47
- host-microbe interactions, of host metabolism 97–98
- host-microbial interactions 93, 102
- host-microbiome interactions 98
- host-microbiota interactions 168
- host phenotype modulation 175
- human disorders 94
- human gut 47
- human maternal gut microbiota epigenetic regulation 238–239

- human maternal gut microbiota  
(*contd.*)
- gut and brain axis 238
  - maternal gut microbiome and immune functions 236–238
  - placental microbiome and meconium 239
- human maternal microbiota
- endometrial microbiota 234–236
  - gut microbiota 236
  - oral microbiota 233–234
  - vaginal microbiota 234
- human microbiome 173, 207, 208
- current approaches 7
- Human Microbiome Project (HMP) 2, 25
- human microbiota 93, 121, 168, 236
- human milk oligosaccharides (HMO) 245
- human milk microbiota and infant health 245–246
- Human Oral Microbiome Database (HOMD) 2
- hydroxypropyl-methylcellulose (HPMC)-based buccal films 127
- hyperammonemia 54, 55
- hypercholesterolemia 56
- hyperglycemic mice model 24
- hypothalamic-pituitary-adrenal (HPA) 249
- hypoxic tumor microenvironment 177
- i**
- immune cell polarization 237
  - immune impairment 98
  - immunomodulatory molecules 97
  - induced pluripotent stem cells (iPSC) 174
  - inducible promoter 104
- inflammatory bowel disease (IBD) 18, 20, 94, 178, 223, 247
- ingestible micro-bio-electronic device (IMBED) 165
- immune checkpoint inhibitor (ICI)-induced colitis 226
- insulin resistance 18
- interdisciplinary research 142
- interleukin-17 (IL-17) 238
- interleukin-22 (IL-22) 97
- International Diabetes Federation (IDF) 49
- International Human Microbiome Consortium (IHMC) 25
- intestinal indole-3-aldehyde 98
- intestinal metabolic landscape 97
- intestinal mucosal permeability 24
- intratumoral antigen-presenting cells (APC) 177
- in type II diabetes (T2D) patients 24
- in vitro* screening 176
- irritable bowel syndrome (IBS) 224
- isolated microorganisms 157
- isopropyl  $\beta$ -D-thiogalactopyranoside (IPTG) 156
- isopropyl  $\beta$ -D-1-thiogalactopyranoside (IPTG) 279
- isopropyl- $\beta$ -D-thiogalactoside (IPTG) 163
- k**
- Klebsiella* 8, 244, 250
- Kruppel-like factor 4 95
- kynurenic acid 63
- l**
- lactic acid 242
  - lactic acid bacteria (LAB) 121
  - lactic acid-producing *Lactobacillus* species 234
  - Lactobacillus* 50
  - Lactobacillus rhamnosus* 54

- Lactobacillus rhamnosus* GG (LGG) 59
- Lactococcus lactis* 167
- Lactococcus lactis*-based recombinant interleukin-10 expression system 109
- L-amino acid deaminase (LAAD) 56, 110, 285
- layered genetic circuits 285, 286
- L-carnitine 60
- left ventricular ejection fraction 59
- ligand screening 170
- ligase chain reaction (LCR) 287
- limit energy absorption 24
- linear discriminant analysis effect size (LEfSe) 157
- lipopolysaccharide (LPS) 24
- liquid chromatography-mass spectrometry (LC-MS) 157
- liquid nitrogen 158
- live biotherapeutic products (LBP) 65, 74
- liver cirrhosis 54
- low-density lipoprotein receptor-deficient (LDL-RD) murine model 59
- lower limit of quantification (LLOQ) 175
- lysine-OFF riboswitch 162
- m**
- malleable microbiome 155
- Marionette strains 165
- maternal microbiota and gestational age 243, 244 and health 240 and obesity BMI 241 childhood and obesity 241 insulin resistance 241 maternal diet 240–241
- miscarriages and microbiome 242
- obesity 241
- membrane-bound histidine kinase (HK) 283
- metabolic disorders 23, 94 diabetes 24 NAFLD 24–25 obesity 23–24
- metabolic dysfunction 98
- metabolic engineering 128–129
- metabolic endotoxemia 226
- metabolic modelling 196
- metabolomics 156
- metagenome-assembled genomes (MAGs) 157
- metagenome-wide association studies (MGWAS) 49
- metagenomics 156–157
- METAgonomics of the Human Intestinal Tract (MetaHIT) 26
- metatranscriptomics 156–157
- metatranscriptomics studies 142
- methotrexate (MTX) 125
- microbe-microbe interactions 97
- microbes and compositions, host metabolic status 95, 97
- microbial-based diagnostics 168
- microbial-derived riboflavin metabolites, interferon-7 238
- microbial diagnostics 107
- microbial fermentation 10
- microbial fingerprinting 219
- microbially imbalanced intestine 96
- microbial metabolism 102
- microbial residents 93
- microbiome compositions 102
- microbiome development, elements for 5
- diet and nutrition 7
- prebiotics 6

- microbiome development, elements for (*contd.*)
    - probiotics 6–7
  - microbiome, diagnosing
    - considerations and future 158–159
  - microbiome analyses
    - metagenomics 157
    - metatranscriptomics 157
    - proteomics and metabolomics 157–158
    - small subunit rRNA analysis 156–157
  - microbiome diversity, in human body
    - gastrointestinal microbiome 3–4
    - oral microbiome 2–3
    - respiratory microbiome 5
    - skin microbiome 4–5
    - urogenital microbiome 5
  - microbiome engineering
    - for diabetes and obesity 49–50, 52
    - for immune modulation 52–53
    - modulate gut-brain axis 61–63
      - psychobiotics, development of 64–65
    - for modulate gut-liver axis 54
      - modulate ammonia metabolism 54–56
      - modulate bile salt metabolism 56–58
    - for next-generation precision
      - agriculture 137–138
      - computational tools, for robust microbiome engineering 142–143
      - genome-scale metabolic modeling 143–144
      - systems approach 139–142
  - microbiome-mediated dysregulation 61
  - microbiome project supporting
    - infrastructures 25
    - global foundations 27
  - international and local initiatives 25–27
  - microbiome therapeutics 102
  - microbiota 1
  - microfluidic devices 174
  - Million Microbiome of Humans Project (MMHP) 26
  - mitigation strategies 146
  - mitogen-activated protein kinase (MAPK) 169
  - mixed co-cultures 174
  - mucin glycoproteins 123
  - mucosa-associated invariant T cells (MAIT) 238
  - mucus-associated surface proteins 126
  - mucus-binding factor (MBF) 124
  - mucus-binding (MUB) protein 123
  - multi-drug resistant organisms (MDRO) 224
  - multi-input/multi-output strain 165
  - multi-omics 159
  - multiple drug-resistant organisms (MDRO) 219
  - multiple logic gate circuits 165
  - multiple sclerosis 219
  - multi-species probiotic formulations 52
- n**
- N*-acetyl-D-glucosamine 101
  - N*-acyl homoserine lactone (AHL) 156
  - natural cell-to-cell communication systems 201
  - natural consortia 196
  - neurodegenerative diseases 23
  - neurodevelopment disorder 22
  - neuroendocrine 61
  - neurohumoral signaling 121
  - neuroimmune system 61
  - neuropsychiatric disorders 227, 228
  - nitrate (NO<sub>3</sub><sup>−</sup>) 106

- nitric oxide (NO) 178  
*N*-methyl-*d*-aspartate (NMDA)  
 receptor 63  
 non-alcoholic fatty liver disease  
 (NAFLD) 23–25, 225  
 norepinephrine 63  
 Novozymes 146
- o**
- OFF switch 160, 162  
 oligonucleotides 287, 288  
 oligosaccharides 14, 245, 247  
 omics 156  
 one-component regulatory systems  
 (OCs) 283, 284  
 oral cavity species 233  
 ordinary differential equations (ODE)  
 202  
 organic incubator 93  
 organoids 174  
 organ-on-a-chip (OOC) platforms  
 174  
 oropharynx microbiota 250  
 outer membrane vesicles (OMV) 99,  
 289  
 output modules, types of 284, 285
- p**
- pancreatic  $\beta$  cell death 53  
 Parkinson's disease 22, 23, 219, 227,  
 238  
 pathogenic bacteria 94, 103, 234,  
 246, 250, 283, 285  
 perinatal antibiotic treatment  
 247–249  
 peripheral regulatory T cells 95  
 personalized nutrition 235  
 personalized probiotics 235  
 pharmacodynamics (PD) 74  
 pharmacokinetics (PK) 74  
 phase-variable surface layers 99  
 phenylalanine ammonia-lyase (PAL)  
 110, 284
- phenylalanine hydroxylase (PAH)  
 55, 110  
 phenylalanine lyase (PAL) 56  
 phenylketonuria (PKU) 56, 284  
 phenylpyruvate (PP) 292  
 phosphotransfer 166  
 phosphotransferase system (PTS)  
 transporter 128  
 phylogenetic lineages 157  
 phytobiomes 146  
*Pimelobacter simplex* 164  
 plant growth-promoting (PGP) traits  
 139  
 point-of-care sensing 172  
 polymerase chain reaction (PCR)  
 287  
 polymerase cycling assembly (PCA)  
 287  
*Populus deltoides* 141  
*Porphyromonadaceae* 54  
 postpartum microbiome  
 mode of delivery 242–243  
 vaginal seeding 243  
 Precigen ActoBio 53  
 probiotic and prebiotic therapies as  
 modulators 250–251  
 probiotic-associated therapeutic curli  
 hybrids (PATCH) system  
 127  
 probiotic engineering 155  
 probiotics, and mechanism of action  
 clinical studies 71–73  
 preclinical studies 66–70  
 programmed cell death protein-ligand  
 1 (PD-L1) 177  
 proinflammatory cytokines 103, 223  
*proteobacteria* 243  
 proteomics 156  
 proton pump inhibitors (PPI) 222  
*Pseudomonas aeruginosa* 104, 165,  
 283  
*Pseudomonas* proliferation 250  
*Pseudomonas syringae* 164

- putative mucoadhesion factors 125  
*pyrimido[4,5-d]pyrimidine-2,4-diamine* (PPDA) 162
- q**  
 quinolinic acid 63  
 quorum-sensing circuit 165, 177  
 quorum-sensing molecules 105, 156, 165, 200, 207
- r**  
 Raman microspectroscopy 141  
 randomized genome-wide disruption 100  
 reactive oxygen species (ROS) 106  
 recommended dietary allowances (RDA) 15  
 respiratory microbiome 5  
 response regulator (RR) 166, 283  
 reverse transcriptase-quantitative PCR (RT-qPCR) measurements 173  
 rhamnose 156  
*Rhodopseudomonas palustris* 206  
 ribosome binding site (RBS) 160, 289  
 riboswitch engineering 160  
 RNA-based regulatory systems 159  
 RNA polymerase (RNAP) 278  
 RNA sequencing approaches 157  
 routine colonoscopy 220
- s**  
 saccharolytic commensal B 101  
 S-adenosylmethionine 161  
*Salmonella typhimurium* 106, 167, 206  
 “self-established, metabolically cooperating yeast community” (SeMeCo) 205  
 semi-synthetic consortia 196  
 sensor histidine kinase (SK) 166  
 sensor optimization approaches 176  
 serotonergic neurotransmission 63  
*Shewanella halifaxensis* 167  
 short-chain fatty acids (SCFAs) 10, 20, 50, 95, 237, 238  
 short-fatty acid metabolism 96  
 Singapore Research, Innovation and Enterprise Council (RIEC) 148  
 skin microbiota 5  
 small intestinal bacterial overgrowth (SIBO) 225  
 small intestinal secretory immunoglobulin A (IgA) 123  
 small subunit rRNA (SSU rRNA) 157  
 smoking 249  
 spatio-temporal pattern generators 207  
 16S rRNA sequencing 105  
 Ste12-responsive genes 170  
 STimulator of INTerferon Genes (STING) 177  
 streptozotocin-induced T1D mice model 53  
 stress under pregnancy 249, 250  
 synthetic biology 195  
   for genome and genetic engineering 144–146  
 synthetic communities (SynComs) 139  
 synthetic microbial consortia 207, 208  
   advantages of, labor division 197  
   metabolic burden 198–199  
   optimal conditions 198  
   reducing crosstalk and competition 199–200  
 synthetic transcription factors (STFs) 170  
 systematic evolution of ligands by exponential enrichment (SELEX) 161

- systems biology 102  
 high-throughput data-driven, of gut microbiota 100–101  
 rational design of, gut microbiome editing strategies 98–100
- t**
- T-cells within colonic mucosa 226  
 terminators 111  
 tetracycline 164, 201  
 tetrathionate 106, 167  
 tetrathionate/thiosulfate 109  
 TF-based biosensors  
     chassis 288–289  
     construction of, genetic circuits 286  
     construction of, genetic circuits  
         gene synthesis 287  
         Gibson assembly 288  
         restriction enzyme-based cloning 287–288  
     construction of, genetic circuits  
         Gibson assembly 288  
     strategies, for improvement 293  
 test  
     biocontainment 292–293  
     diagnostics 289–290  
     therapeutics 291–292  
 transcriptional activators 282–283  
 transcriptional repressors 278–279, 282  
 The Environmental Determinants of Diabetes in the Young (TEDDY) 2  
 T-helper cells 97  
 The Microsetta Initiative (TMI) 26  
 thorough-omics profiling 196  
 toehold switches 160, 172  
 toll-like receptors (TLRs) 226, 237, 238  
 top-down approaches 197  
 trans-cinnamic acid 56  
 transcriptional activator 164  
 transcription factor (TF)  
     based biosensors 280  
     based single-cell genetic reporter system 109  
 transepithelial electrical resistance (TEER) measurements 175  
 transposon insertion sequencing (Tn-Seq) 100, 105  
 transposon mutagenesis sequencing (Tn-Seq) 100  
 Transwell dishes 174  
 trimethylamine (TMA) 60  
 trimethylamine N-oxide (TMAO) 60  
 tryptophan-2,3-dioxygenase (TDO) 63  
 tryptophan metabolism 63, 95  
 two-component histidine kinase receptor CqsS 105  
 two-component regulatory systems (TCSs) 283  
 two-component systems (TCSs) 159, 166–167  
 type 1 diabetes (T1D) 49, 227  
 type 2 diabetes (T2D) 49  
 Typhimurium 96  
 tyrosine-kinase inhibitors (TKIs) 226
- u**
- ulcerative colitis (UC) 20, 178, 223  
 undesired downstream gene expression 169  
 unmanned aerial vehicles (UAVs) 147  
 UN Sustainable Development Goals (SDG) 147  
 5'-untranslated region (UTR) 111, 160, 292  
 uric acid 164

urogenital microbiome 5  
US National Institutes of Health  
(NIH) 2

**v**

vaginal microbiota 234, 235, 242  
vancomycin-resistant *Enterococcus*  
(VRE) 224  
very low birth weight (VLBW) infants  
243  
very-low-density lipoprotein (VLDL)  
226  
*Vibrio cholerae* 165, 167  
visual reporter (lycopene) 170

**w**

wastewater treatment 140, 141  
wild type bacteria 52  
Wisconsin Alumni Research  
Foundation (WARF) 27  
World Economic Forum (WEF) 147

**x**

xylooligosaccharides (XOS) 10

**y**

yeast G-protein machinery 169  
yield biochemicals 95











