## Index

Note: Page numbers followed by f indicate figures, t indicate tables, and b indicate boxes.

A ABO blood group, 29 Absolute abundance, 69-71 Actinomyces odontolyticus, 110 Adhesion, 33-35 Adipose tissue, 63 Aggregatibacter actinomycetemcomitans, 89 Akkermansia muciniphila, 24f, 143-144 Alzheimer's disease, 163 Amplicon sequencing, 59-60 Aryl hydrocarbon receptor (AhR)	Causal reasoning, 133–138 Cell-free DNA (cfDNA), 160 <i>b</i> Cell-free RNA (cfRNA), 160 <i>b</i> Christensenella minuta, 24 <i>f</i> Circadian rhythm, 43 <i>b</i> Circulation, 97 Colonoscopy, 159–160 Colorectal cancer, 175–176 Commensal microbes, 84–88 Commercial deoxyribonucleic acid (DNA) tests, 202 Corynebacterium spp., 10 <i>f</i> COVID-19 pandemic, 83–84	H Habitats, 29–31 Helicobacter pylori, 141–142 Hematogenous spread, 86 Higher-taxonomic resolution, 118–121 Histone deacetylase 3 (HDAC3), 43  I Immunoglobulin A (IgA), 33–35 Indoleamine 2,3-dioxygenase 1(IDO1) inhibitors, 164–165t Infant gut microbiota, 84
agonists, 166–167 <i>t</i> Atherosclerotic cardiovascular disease (ACVD), 94	epidemiology, 83 CPR. See Candidate phyla radiation (CPR)	Interkingdom interactions, 94–96
Atherosclerotic plaque-associated bacteria, 91–93 <i>t</i> Autoantigens, 146–147	Culturomics, 110 Cutibacterium acnes, 29–31	Koch's postulates, 133
B Bacillus anthracis, 134f Bacteria, 119b Bacterial genomes, 111–112f Bacterial species, 120–121f	Dental bacteria, 3b Deoxyribonucleic acid (DNA) extraction, 57–58 metagenomic samples, 67–68	Lachnospiraceae, 33-35 Lactobacillus crispatus, 94 LCT alleles, 29 Liver diseases, 157-159 Low biomass samples, 59-65 Lymphatic drainage, 86
Bacterial strains, 118 Bacteroides fragilis, 2f, 35–37 Bacteroides thetaiotaomicron, 24f Bifidobacterium animalis subsp.,	sequencing amount, 57–58 Diabetes, 144–146 Dietary fibers, 195–200 Drug metabolism, 168f	M Machine learning, 118–119 Macroecology, 21 Mendelian randomization (MR),
24f Biomarkers, 159–160 Branched chain amino acids (BCAAs), 144–146 Bristol's stool score (BSS), 57	E Enterotypes, 38–46 Escherichia coli, 2f F	138–141, 139 <i>b</i> Metabolomics, 97 Metagenome, 6 <i>b</i> Metagenome-assembled genomes
C Cancer screening, 160 Cancer therapy, 168f Candidate phyla radiation (CPR), 113f	Faecalibacterium prausnitzii, 24f, 135–136 Fecal microbiome, 29b Fungal taxonomy, 114f Fusobacterium spp., 175–176	(MAGs), 109 Metagenome-wide association studies (MWAS), 71–73 Metagenomics, 1–5 deoxyribonucleic acid, 67–68 disease screening, 157–161
Cardiometabolic diseases, 89–94 Cardiovascular diseases, 94 Causality, 149	<b>G</b> Gut microbiome, 33–38, 169–170 <i>t</i> circadian rhythm, 43 <i>b</i>	personalized treatment,  161–163  vs. traditional microbiology, 5f

Metagenomic shotgun	Mycobacterium abscessus, 174-175	Probiotics, 200
sequencing, 67	Mycobiota, 87f	Prokaryotic traits, 15f
Methanobrevibacter, 40	Mycoplasma genitalium, 124–126,	R
Methanobrevibacter smithii, 24f, 40b	125-126 <i>f</i>	
Methanogenic archaea, 40b	N	Randomized controlled trials
Microbial cells, 5–12	• •	(RCTs), 139
Microbial counts, 7	Newton's simplicity rule, $135b$	Rheumatoid arthritis (RA), 88–89 prevention, 203 <i>f</i>
Microbial diversity, 46	0	Ribosomal RNA (rRNA), 62f
Microbial genomes, 120–121f	Occult sepsis, 86	Robustness, 26–28
Microbial growth, 65-67	Ockham's razor, 135 <i>b</i>	Ruminococcaceae, 33–35
Microbiology, $5f$	Opportunistic pathogen, 133	Ruminococcaceae, 55-55
Microbiome, 6b	Oral hygiene, 142	S
from ancient times, 13-16	Oral microbiome, 31–33	Sequencing amount, 68-69
cancer therapies, $162-163t$	Organ-specific metabolite	The Serengeti rules, 38-46
causal evidence, 140–141 <i>t</i>	production, 97–98 <i>t</i>	Shotgun metagenomic data, 59t
diseases, 138-143, 175-177	Outer membrane vesicles,	Single-cell sequencing, 202
diversity, 21–26, 27 <i>t</i>	147-149	Skin microbiome, 29-31
female reproductive tract, $11f$		Sparsity, 118
immediate and historical	P	Streptococcus parasanguinis, 139
events, 192–200	Paleogenomics, 13–16	Supra-gingival dental calculus, 15/
interkingdom interactions, 94-96	Pancreatic ductal adenocarcinoma	T
omics, 97-101	(PDAC), 12 <i>f</i>	T
record from birth, 189–192	Path diagrams, 135–136	Treponema spp., 23b
richness, 21–26	Peristalsis, 35–38	Treponema succinifaciens, 24f
species, 13	Permutational analyses of	Trimethylamine (TMA), 40
stability, 21–26	variances (PERMANOVA),	Trimethylamine N-oxide (TMAO),
Microbiota, 6b	72	40 <i>b</i>
de novo assembly, 26-28	Phages, 147–149	Trophic levels, macroecology, 21
Microflora, 21	Placenta microbiome, 62-63	V
Microscopy, 1	Pollution, 201	Viral particles, 12–13
Mucosal lining, 26b	Poly-genetic risk scores (PRS),	Virus-like particles (VLPs), 12
Multiple effective molecules,	200-201	Vitamins, 201
143-144	Polymerase chain reaction (PCR),	
MWAS. See Metagenome-wide	84-88	W
association studies (MWAS)	Prevotella copri, 122f	Whole-cell modeling, 124-127