



**REFERENZE:** di seguito sono riportate alcune delle referenze alla base del report:

1. Aomatsu *et al.* (2012) **Terminal Restriction Fragment Length Polymorphism Analysis of the Gut Microbiota Profiles of Pediatric Patients with Inflammatory Bowel Disease** // *Digestion*
2. Arumugam *et al.* (2011) **Enterotypes of the human gut microbiome** // *Nature*
3. Barcenilla *et al.* (2000) **Phylogenetic Relationships of Butyrate-Producing Bacteria from the Human Gut** // *Applied and Environmental Microbiology*
4. Belenguer *et al.* (2007) **Impact of pH on Lactate Formation and Utilization by Human Fecal Microbial Communities** // *Applied and Environmental Microbiology*
5. Berry *et al.* (2013) **Intestinal microbiota: a source of novel biomarkers in inflammatory bowel diseases?** // *Best Practice & Research Clinical Gastroenterology*
6. Bhattarai *et al.* (2016) **Irritable bowel syndrome: a gut microbiota-related disorder?** // *American Journal of Physiology-Gastrointestinal and Liver Physiology*
7. Biagi *et al.* (2010) **Through ageing, and beyond: gut microbiota and inflammatory status in seniors and centenarians** // *Plos One*
8. Biagi *et al.* (2012) **Aging of the human metaorganism: the microbial counterpart** // *Age*
9. Biagi *et al.* (2013) **Ageing and gut microbes: perspectives for health maintenance and longevity** // *Pharmacological Research*
10. Biagi *et al.* (2014) **Gut microbiome in Down syndrome** // *PlosOne*
11. Boulangè *et al.* (2016) **Impact of the gut microbiota on inflammation, obesity, and metabolic disease** // *Genome Medicine*
12. Brahe *et al.* (2015) **Specific gut microbiota features and metabolic markers in postmenopausal women with obesity** // *Nutrition & Diabetes*
13. Burger-van Paassen *et al.* (2009) **The regulation of intestinal mucin MUC2 expression by short-chain fatty acids: implications for epithelial protection** // *Biochemical Journal*
14. Cani *et al.* (2007) **Metabolic endotoxemia initiates obesity and insulin resistance** // *Diabetes*
15. Cani *et al.* (2007) **Selective increases of bifidobacteria in gut microflora improve high-fat-diet-induced diabetes in mice through a mechanism associated with endotoxaemia** // *Diabetologia*
16. Cao *et al.* (2014) **Association between Faecalibacterium prausnitzii Reduction and Inflammatory Bowel Disease: A Meta-Analysis and Systematic Review of the Literature** // *Gastroenterology Research and Practice*
17. Charlie *et al.* (2013) **Microbiota-mediated colonization resistance against intestinal pathogens** // *Nature*
18. Chatelier E, *et al.* (2013) **Richness of human gut microbiome correlates with metabolic markers** // *Nature*
19. Chen *et al.* (2016) **An expansion of rare lineage intestinal microbes characterizes rheumatoid arthritis** // *Genome Medicine*
20. Chen *et al.* (2016) **Assessment of Bacterial Communities and Predictive Functional Profiling in Soils Subjected to Short-Term Fumigation-Incubation** // *Microbial Ecology*
21. Clarke *et al.* (2014) **Gut Microbiota: The Neglected Endocrine Organ** // *Molecular Endocrinology*
22. Costea *et al.* (2018) **Enterotypes in the landscape of gut microbial community composition** // *Nature Microbiology*
23. Cotillard A, *et al.* (2013) **Dietary intervention impact on gut microbial gene richness** // *Nature*
24. Crost *et al.* (2013) **Utilisation of Mucin Glycans by the Human Gut Symbiont *Ruminococcus gnavus* Is Strain-Dependent** // *PlosOne*
25. Crost *et al.* (2018) **Mechanistic Insights Into the Cross-Feeding of *Ruminococcus gnavus* and *Ruminococcus bromii* on Host and Dietary Carbohydrates** // *Frontiers in Microbiology*
26. Del Chierico *et al.* (2018) **Gut Microbiota Markers in Obese Adolescent and Adult Patients: Age-Dependent Differential Patterns** // *Frontiers in Microbiology*
27. Derrien *et al.* (2004) **Akkermansia muciniphila gen. nov., sp. nov., a human intestinal mucin-degrading bacterium** // *International Journal of Systematic and Evolutionary Microbiology*
28. Donaldson *et al.* (2015) **Gut biogeography of the bacterial microbiota** // *Nature Review Microbiology*
29. Duboc *et al.* (2013) **Connecting dysbiosis, bile-acid dysmetabolism and gut inflammation in inflammatory bowel diseases** // *Gut*
30. Duncan *et al.* (2002) **Acetate Utilization and Butyryl Coenzyme A (CoA):Acetate-CoA Transferase in Butyrate-Producing Bacteria from the Human Large Intestine** // *Applied and Environmental Microbiology*

31. Duncan *et al.* (2004) **Lactate-utilizing bacteria, isolated from human feces, that produce butyrate as a major fermentation product** // *Applied and Environmental Microbiology*
32. Duncan *et al.* (2016) **Wheat bran promotes enrichment within the human colonic microbiota of butyrate-producing bacteria that release ferulic acid** // *Environmental Microbiology*
33. Emoto *et al.* (2016) **Analysis of Gut Microbiota in Coronary Artery Disease Patients: a Possible Link between Gut Microbiota and Coronary Artery Disease** // *Journal of Atherosclerosis and Thrombosis*
34. Emoto *et al.* (2017) **Characterization of gut microbiota profiles in coronary artery disease patients using data mining analysis of terminal restriction fragment length polymorphism: gut microbiota could be a diagnostic marker of coronary artery disease** // *Heart Vessels*
35. Erny *et al.* (2015) **Host microbiota constantly control maturation and function of microglia in the CNS** // *Nature*
36. Faith (1992) **Systematics and conservation: on predicting the feature diversity of subsets of taxa** // *Cladistics*
37. Faith (1994) **Phylogenetic pattern and the quantification of organismal biodiversity** // *Philosophical Transactions of the Royal Society B*
38. Ferrer *et al.* (2013) **Microbiota from the distal guts of lean and obese adolescents exhibit partial functional redundancy besides clear differences in community structure** // *Environmental Microbiology*
39. Finnie *et al.* (1995) **Colonic mucin synthesis is increased by sodium butyrate** // *Gut*
40. Fukuda *et al.* (2011) **Bifidobacteria can protect from enteropathogenic infection through production of acetate** // *Nature*
41. Gao *et al.* (2016) **Predictive functional profiling using marker gene sequences and community diversity analyses of microbes in full-scale anaerobic sludge digesters** // *Bioprocess Biosystem Engineering*
42. Geirnaert *et al.* (2017) **Butyrate-producing bacteria supplemented in vitro to Crohn's disease patient microbiota increased butyrate production and enhanced intestinal epithelial barrier integrity** // *Scientific Reports*
43. Gibson *et al.* (1991) **Growth and activities of sulphate-reducing bacteria in gut contents of healthy subjects and patients with ulcerative colitis.** // *FEMS Microbiology Ecology*
44. He *et al.* (2016) **Alterations of the gut microbiome in Chinese patients with systemic lupus erythematosus** // *Gut Pathogens*
45. Hevia *et al.* (2014) **Intestinal Dysbiosis Associated with Systemic Lupus Erythematosus** // *mBio*
46. Hiiipala *et al.* (2018) **The Potential of Gut Commensals in Reinforcing Intestinal Barrier Function and Alleviating Inflammation** // *Nutrients*
47. Hou *et al.* (2017) **Human Gut Microbiota Associated with Obesity in Chinese Children and Adolescents** // *Biomed Research International*
48. Human Microbiome Project Consortium (2012) **Structure, function and diversity of the healthy human microbiome** // *Nature*
49. Human Microbiome Project Consortium, (2012) **A framework for human microbiome research** // *Nature*
50. Ijssennagger *et al.* (2016) **Sulfide as a Mucus Barrier-Breaker in Inflammatory Bowel Disease?** // *Trends in Molecular Medicine*
51. Ilhan *et al.* (2017) **pH-Mediated Microbial and Metabolic Interactions in Fecal Enrichment Cultures** // *mSphere*
52. Jalanka *et al.* (2019) **The Effect of Psyllium Husk on Intestinal Microbiota in Constipated Patients and Healthy Controls** // *International Journal of Molecular Science*
53. Jiang *et al.* (2018) **Altered gut microbiota profile in patients with generalized anxiety disorder** // *Journal of Psychiatric Research*
54. Jie *et al.* (2017) **The gut microbiome in atherosclerotic cardiovascular disease** // *Nature Communication*
55. Joossens *et al.* (2011) **Dysbiosis of the faecal microbiota in patients with Crohn's disease and their unaffected relatives** // *Gut*
56. Kampmann *et al.* (2016) **Composition of human faecal microbiota in resistance to Campylobacter infection** // *Clinical Microbiology and Infection*
57. Karlsson *et al.* (2012) **Symptomatic atherosclerosis is associated with an altered gut metagenome** // *Nature Communications*
58. Karlsson *et al.* (2012) **The microbiota of the gut in preschool children with normal and excessive body weight** // *Obesity*
59. Knoll *et al.* (2017) **Gut microbiota differs between children with Inflammatory Bowel Disease and healthy siblings in taxonomic and functional composition: a metagenomic analysis** // *American Journal of Physiology-Gastrointestinal and Liver Physiology*
60. Kolenbrander (2006) **The Genus *Veillonella*** // *Prokaryotes*
61. Lahti *et al.* (2013) **Associations between the human intestinal microbiota, *Lactobacillus rhamnosus* GG and serum lipids indicated by integrated analysis of high-throughput profiling data** // *PeerJ*
62. Langille *et al.* (2013) **Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences** // *Nature*
63. Le Chatelier *et al.* (2013) **Richness of human gut microbiome correlates with metabolic markers** // *Nature*

64. Ley *et al.* (2005) **Obesity alters gut microbial ecology** // *Proceedings of the National Academy of Sciences of the USA*
65. Ley *et al.* (2006) **Microbial ecology. Human gut microbes associated with obesity** // *Nature*
66. Li *et al.* (2019) **Change of intestinal microbiota in cerebral ischemic stroke patients** // *BMC Microbiology*
67. Li *et al.* (2014) **An integrated catalog of reference genes in the human gut microbiome** // *Nature Biotechnology*
68. Louis *et al.* (2010) **Diversity of human colonic butyrate-producing bacteria revealed by analysis of the butyryl-CoA:acetate CoA-transferase gene** // *Environmental Microbiology*
69. Lozupone CA, *et al.* (2012) **Diversity, stability and resilience of the human gut microbiota** // *Nature*
70. Machiels *et al.* (2014) **A decrease of the butyrate-producing species *Roseburia hominis* and *Faecalibacterium prausnitzii* defines dysbiosis in patients with ulcerative colitis** // *Gut*
71. Maji *et al.* (2018) **Gut microbiome contributes to impairment of immunity in pulmonary tuberculosis patients by alteration of butyrate and propionate producers** // *Environmental Microbiology*
72. Mar Rodriguez *et al.* (2015) **Obesity changes the human gut mycobiome** // *Scientific Reports*
73. Mayer *et al.* (2017) **The Gut and Its Microbiome as Related to Central Nervous System Functioning and Psychological Well-being: Introduction to the Special Issue of Psychosomatic Medicine** // *Psychosomatic Medicine*
74. Michielan *et al.* (2015) **Intestinal Permeability in Inflammatory Bowel Disease: Pathogenesis, Clinical Evaluation, and Therapy of Leaky Gut**, // *Mediators of Inflammation*
75. Morgan *et al.* (2012) **Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment** // *Genome Biology*
76. Morrison *et al.* (2016) **Formation of short chain fatty acids by the gut microbiota and their impact on human metabolism** // *Gut Microbes*
77. Naseribafrouei *et al.* (2014) **Correlation between the human fecal microbiota and depression** // *Neurogastroenterology and Motility*
78. Neal *et al.* (2006) **Enterocyte TLR4 mediates phagocytosis and translocation of bacteria across the intestinal barrier** // *Journal of Immunology*
79. Olsson *et al.* (2020) **Gut microbiota of obese subjects with Prader-Willi syndrome is linked to metabolic health** // *Gut*
80. Pascal *et al.* (2017) **A microbial signature for Crohn's disease** // *Gut*
81. Peters *et al.* (2018) **A taxonomic signature of obesity in a large study of American adults** // *Scientific Reports*
82. Qin *et al.* (2012) **A metagenome-wide association study of gut microbiota in type 2 diabetes** // *Nature*
83. Ramirez-Farias *et al.* (2008) **Effect of inulin on the human gut microbiota: stimulation of *Bifidobacterium adolescentis* and *Faecalibacterium prausnitzii*** // *British Journal of Nutrition*
84. Rampelli *et al.* (2013) **Functional metagenomic profiling of intestinal microbiome in extreme ageing** // *Aging*
85. Riös-Covian *et al.* (2016) **Intestinal Short Chain Fatty Acids and their Link with Diet and Human Health** // *Frontiers in Microbiology*
86. Rowan *et al.* (2009) **Sulphate-reducing bacteria and hydrogen sulphide in the aetiology of ulcerative colitis** // *British Journal of Surgery*
87. Rowan *et al.* (2010) **Desulfovibrio bacterial species are increased in ulcerative colitis** // *Diseases of the Colon & Rectum*
88. Sato *et al.* (2017) **Prebiotic potential of L-sorbose and xylitol in promoting the growth and metabolic activity of specific butyrate-producing bacteria in human fecal culture** // *FEMS Microbiology Ecology*
89. Scheperjans *et al.* (2015) **Gut microbiota are related to Parkinson's disease and clinical phenotype** // *Movement Disorders*
90. Scher *et al.* (2013) **Expansion of intestinal *Prevotella copri* correlates with enhanced susceptibility to arthritis** // *eLife*
91. Scher *et al.* (2015) **Decreased bacterial diversity characterizes the altered gut microbiota in patients with psoriatic arthritis) resembling dysbiosis in inflammatory bowel disease** // *Arthritis Rheumatology*
92. Schmidt *et al.* (2018) **The Human Gut Microbiome: From Association to Modulation** // *Cell*
93. Schoubert *et al.* (2014) **Microbiome Data Distinguish Patients with *Clostridium difficile* Infection and Non-*C. difficile*-Associated Diarrhea from Healthy Controls** // *Mbio*
94. Schoubert *et al.* (2015) **Antibiotic-Induced Alterations of the Murine Gut Microbiota and Subsequent Effects on Colonization Resistance against *Clostridium difficile*** // *Mbio*
95. Schwiertz *et al.* (2002) ***Anaerostipes caccae* gen. nov., sp. nov., a New Saccharolytic, Acetate-utilising, Butyrate-producing Bacterium from Human Faeces** // *Systematic and Applied Microbiology*
96. Sokol *et al.* (2008) ***Faecalibacterium prausnitzii* is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients** // *Proceedings of the National Academy of Sciences of the United States of America*

97. Stecher *et al.* (2015) **The Roles of Inflammation, Nutrient Availability and the Commensal Microbiota in Enteric Pathogen Infection** // *Microbiology Spectrum*
98. Sun *et al.* (2013) **Regulation of bacterial pathogenesis by intestinal short-chain Fatty acids** // *Advances in Applied Microbiology*
99. Takahashi *et al.* (2016) **Reduced Abundance of Butyrate-Producing Bacteria Species in the Fecal Microbial Community in Crohn's Disease** // *Digestion*
100. Thingholm *et al.* (2019) **Obese Individuals with and without Type 2 Diabetes Show Different Gut Microbial Functional Capacity and Composition** // *Cell Host & Microbe*
101. Tilg *et al.* (2014) **Microbiota and diabetes: an evolving relationship** // *Gut*
102. Turnbaugh (2012) **Microbiology: fat, bile and gut microbes** // *Nature*
103. Turnbaugh *et al.* (2009) **A core gut microbiome in obese and lean twins** // *Nature*
104. Turroni *et al.* (2018) **Microbiota–Host Transgenomic Metabolism, Bioactive Molecules from the Inside** // *Journal of Medicinal Chemistry*
105. Valles-Colomer *et al.* (2019) **The neuroactive potential of the human gut microbiota in quality of life and depression** // *Nature Microbiology*
106. Vieira *et al.* (2013) **The role of probiotics and prebiotics in inducing gut immunity** // *Frontiers in Immunology*
107. Vijay *et al.* (2010) **Metabolic syndrome and altered gut microbiota in mice lacking Toll-like receptor 5** // *Science*
108. Walker *et al.* (2005) **pH and Peptide Supply Can Radically Alter Bacterial Populations and Short-Chain Fatty Acid Ratios within Microbial Communities from the Human Colon** // *Applied and Environmental Microbiology*
109. Wang *et al.* (2013) **Increased abundance of Sutterella spp. and Ruminococcus torques in feces of children with autism spectrum disorder** // *Molecular Autism*
110. Wrzosek *et al.* (2013) **Bacteroides thetaiotaomicron and Faecalibacterium prausnitzii influence the production of mucus glycans and the development of goblet cells in the colonic epithelium of a gnotobiotic model rodent** // *BMC Biology*
111. Wu *et al.* (2011) **Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes** // *Science*
112. Wu *et al.* (2020) **The Gut Microbiota in Prediabetes and Diabetes: A Population-Based Cross-Sectional Study** // *Cell Metabolism*
113. Yatsunenko T, *et al.* (2012) **Human gut microbiome viewed across age and geography** // *Nature*
114. Yurist-Doutsch *et al.* (2014) **Gastrointestinal Microbiota–Mediated Control of Enteric Pathogens** // *Annual Review of Genetics*
115. Zhang *et al.* (2009) **Human gut microbiota in obesity and after gastric bypass** // *Proceedings of the National Academy of Sciences of the United States of America*
116. Hjorth *et al.* (2019) **Prevotella-to-Bacteroides ratio predicts body weight and fat loss success on 24-week diets varying in macronutrient composition and dietary fiber: results from a post-hoc analysis.** // *International Journal of Obesity (London)*
117. Kovatcheva-Datchary *et al.* (2015) **Dietary Fiber-Induced Improvement in Glucose Metabolism Is Associated with Increased Abundance of Prevotella.** // *Cell Metabolism*
118. Gorvitovskaia *et al.* (2016) **Interpreting Prevotella and Bacteroides as biomarkers of diet and lifestyle.** // *Microbiome*
119. Roager *et al.* (2013) **Microbial Enterotypes, Inferred by the Prevotella-to-Bacteroides Ratio, Remained Stable during a 6-Month Randomized Controlled Diet Intervention with the New Nordic Diet.** // *Applied and Environmental Microbiology*
120. Cheng *et al.* (2019) **Stereotypes About Enterotype: the Old and New Ideas.** // *Genomics Proteomics Bioinformatics*
121. Lui *et al.* (2018) **Butyrate: A Double-Edged Sword for Health?** // *American Society of Nutrition*
122. Lee *et al.* (2018) **Microbiota-Derived Lactate Accelerates Intestinal Stem-Cell-Mediated Epithelial Development.** // *Cell Host and Microbe*
123. Tomasova *et al.* (2016) **Gut Bacteria and Hydrogen Sulfide: The New Old Players in Circulatory System Homeostasis.** // *Molecules*
124. d'Hennezel *et al.* (2017) **Total Lipopolysaccharide from the Human Gut Microbiome Silences Toll-Like Receptor Signaling.** // *Msystem*
125. Rathinam *et al.* (2019) **Innate immunity to intracellular LPS.** // *Nature Immunology*
126. Simpson *et al.* (2019) **Pushing the envelope: LPS modifications and their consequences.** // *Nature Reviews Microbiology*
127. Fei *et al.* (2020) **Endotoxin Producers Overgrowing in Human Gut Microbiota as the Causative Agents for Nonalcoholic Fatty Liver Disease.** // *Mbio*
128. Paone e Cani (2020) **Mucus barrier, mucins and gut microbiota: the expected slimy partners?** // *BMJ*
129. Cornick *et al.* (2019) **VAMP8-mediated MUC2 mucin exocytosis from colonic goblet cells maintains innate intestinal homeostasis.** // *Nature Communications*
130. Lennon *et al.* (2014) **Influences of the colonic microbiome on the mucous gel layer in ulcerative colitis.** // *Gut Microbes*



131. Wang *et al.* (2019) **Prebiotic Supplementation of In Vitro Fecal Fermentations Inhibits Proteolysis by Gut Bacteria, and Host Diet Shapes Gut Bacterial Metabolism and Response to Intervention.** // *Applied and Environmental Microbiology*
132. Wang *et al.* (2020) **Prebiotics Inhibit Proteolysis by Gut Bacteria in a Host Diet-Dependent Manner: a Three-Stage Continuous In Vitro Gut Model Experiment.** // *Applied and Environmental Microbiology*
133. Amaretti *et al.* (2019) **Profiling of Protein Degraders in Cultures of Human Gut Microbiota.** // *Frontiers in Microbiology*
134. Honda e Littman (2016) **The microbiota in adaptive immune homeostasis and disease.** // *Nature*
135. Hua Ho *et al.* (2020) **Gut microbiota changes in children with autism spectrum disorder: a systematic review.** // *Gut Pathogens*
136. Rutsch *et al.* (2020) **The Gut-Brain Axis: How Microbiota and Host Inflammasome Influence Brain Physiology and Pathology.** // *Frontiers in Immunology*
137. Barandouzi *et al.* (2020) **Altered Composition of Gut Microbiota in Depression: A Systematic Review.** // *Frontiers in Psychiatry*
138. Gurung *et al.* (2020) **Role of gut microbiota in type 2 diabetes pathophysiology.** // *Ebio Medicine*
139. Corado Gomes *et al.* (2018) **The human gut microbiota: Metabolism and perspective in obesity.** // *Gut Microbes*
140. Palmas *et al.* (2021) **Gut microbiota markers associated with obesity and overweight in Italian adults.** // *Scientific Reports*
141. Verhaar *et al.* (2020) **Gut Microbiota in Hypertension and Atherosclerosis: A Review.** // *Nutrients*
142. Santoro *et al.* (2018) **Gut microbiota changes in the extreme decades of human life : a focus on centenarians.** // *Cellular and Molecular Life Sciences*
143. Agirbasli *et al.* (2005) **Fecal fungal flora of pediatric healthy volunteers and immunosuppressed patients** // *Mycopathologia*
144. Auchtung *et al.* (2018) **Investigating colonization of the healthy adult gastrointestinal tract by fungi** // *mSphere*
145. Back-Brito *et al.* (2012) **Effects of eating disorders on oral fungal diversity** // *Oral Surgery, Oral Medicine, Oral Pathology and Oral Radiology*
146. Banjara *et al.* (2016) **Killer toxin from several food-derived *Debaryomyces hansenii* strains effective against pathogenic *Candida* yeasts** // *International Journal of Food Microbiology*
147. Bliss *et al.* (2008) **Vertical and horizontal transmission of *Candida albicans* in very low birth weight infants using DNA fingerprinting techniques** // *Pediatric Infectious Disease Journal*
148. Chen *et al.* (2011) **Correlation between gastrointestinal fungi and varying degrees of chronic hepatitis B virus infection** // *Diagnostic Microbiology and Infectious Disease*
149. Diebel *et al.* (1999) **Synergistic effects of *Candida* and *Escherichia coli* on gut barrier function** // *The Journal of Trauma and Acute Care Surgery*
150. Esebelahie *et al.* (2013) ***Candida* colonisation in asymptomatic HIV patients attending a tertiary hospital in Benin City, Nigeria** // *Libyan Journal of Medicine*
151. Fidel *et al.* (2004) **History and new insights into host defense against vaginal candidiasis** // *Trends in Microbiology*
152. Frykman *et al.* (2015) **Characterization of bacterial and fungal microbiome in children with Hirschsprung disease with and without a history of enterocolitis: A multicenter study** // *PLoS One*
153. Fujimura *et al.* (2016) **Neonatal gut microbiota associates with childhood multisensitized atopy and T cell differentiation** // *Nature Medicine*
154. García *et al.* (2017) **The human gut microbial metabolome modulates fungal growth via the TOR signaling pathway** // *mSphere*
155. Gunsalus *et al.* (2015) **Manipulation of host diet to reduce gastrointestinal colonization by the opportunistic pathogen *Candida albicans*** // *mSphere*
156. Huseyin *et al.* (2017) **Forgotten fungi-the gut mycobiome in human health and disease** // *FEMS Microbiology Reviews*
157. Iliev *et al.* (2017) **Fungal dysbiosis: immunity and interactions at mucosal barriers** // *Nature Reviews Immunology*
158. Kowalewska *et al.* (2016) **Higher diversity in fungal species discriminates children with type 1 diabetes mellitus from healthy control** // *Patient Preference and Adherence*
159. Kühbacher *et al.* (2006) **Bacterial and fungal microbiota in relation to probiotic therapy (VSL#3) in pouchitis** // *Gut*
160. LaTuga *et al.* (2011) **Beyond bacteria: a study of the enteric microbial consortium in extremely low birth weight infants** // *PLoS One*
161. Luan *et al.* (2015) **Dysbiosis of fungal microbiota in the intestinal mucosa of patients with colorectal adenomas** // *Scientific Reports*
162. Nash *et al.* (2017) **The gut mycobiome of the Human Microbiome Project healthy cohort** // *Microbiome*
163. Park *et al.* (2012) **Characterization of the fungal microbiota (mycobiome) in healthy and dandruff-afflicted human scalps** // *PLoS One*
164. Shuford *et al.* (2005) **Effects of fresh garlic extract on *Candida albicans* biofilms** // *Antimicrobial Agents and Chemotherapy*
165. Sokol *et al.* (2017) **Fungal microbiota dysbiosis in IBD** // *Gut*

166. Strati *et al.* (2016) **Altered gut microbiota in Rett syndrome** // *Microbiome*
167. Van der Velden *et al.* (2013) **Role of the mycobiome in human acute graft-versus-host disease** // *Biology of Blood and Marrow Transplantation*
168. Yang *et al.* (2016) **Enterohemorrhagic *Escherichia coli* promotes the invasion and tissue damage of enterocytes infected with *Candida albicans* in vitro** // *Scientific Reports*
169. Zhang *et al.* (2011) **Characterization of the skin fungal microbiota in patients with atopic dermatitis and in healthy subjects** // *Microbiology and Immunology*
170. Zheng *et al.* (2021) **Depletion of acetate-producing bacteria from the gut microbiota facilitates cognitive impairment through the gut-brain neural mechanism in diabetic mice** // *Microbiome*
171. Fernandez-Veledo *et al.* (2019) **Gut microbiota-derived succinate - Friend or foe in human metabolic diseases?** // *Reviews in Endocrine and Metabolic Disorders*
172. Monfort-Ferré *et al.* (2022) **The Gut Microbiota Metabolite Succinate Promotes Adipose Tissue Browning in Crohn's Disease** // *Journal of Chronic Disease*
173. Strandwitz *et al.* (2019) **GABA-modulating bacteria of the human gut microbiota** // *Nature Microbiology*
174. Mazzoli *et al.* (2016) **GABA/Glutamate\_ The Neuro-endocrinological Role of Microbial Glutamate and GABA Signaling** // *Frontiers in Microbiology*
175. Rutsch *et al.* (2020) **The Gut-Brain Axis-How Microbiota and Host Inflammasome Influence Brain Physiology and Pathology** // *Frontiers in Immunology*
176. Mou *et al.* (2021) **The taxonomic distribution of histamine secreting bacteria in the human gut microbiome** // *BMC Genomics*
177. Dicks (2022) **Gut Bacteria and Neurotransmitters** // *Microorganisms*
178. Lee *et al.* (2010) **Indole as an intercellular signal in microbial communities** // *FEMS Microbiology*
179. Teunis *et al.* (2022) **Interactions between Tryptophan Metabolism, the Gut Microbiome and the Immune System as Potential Drivers of Non-Alcoholic Fatty Liver Disease (NAFLD) and Metabolic Diseases** // *Metabolites*
180. Dong *et al.* (2020) **Intestinal microbiota derived tryptophan metabolites are predictive of Ah receptor activity** // *Gut Microbes*
181. Roager *et al.* (2018) **Microbial tryptophan catabolites in health and disease** // *Nature Communications*
182. Dehghani *et al.* (2019) **Microorganisms, Tryptophan Metabolism, and Kynurenine Pathway- A Complex Interconnected Loop Influencing Human Health Status** // *International Journal of Tryptophan Research*
183. Rath *et al.* (2017) **Uncovering the trimethylamine-producing bacteria of the human gut microbiota** // *Microbiome*
184. Kazemian (2020) **Gut microbiota and cardiovascular disease-opportunities and challenges** // *Microbiome*
185. Wuang *et al.* (2018) **Gut microbiota derived metabolites in cardiovascular health and disease** // *Protein & Cell*
186. Luca *et al.* (2020) **Bioactivity of dietary polyphenols: The role of metabolites** // *Critical Reviews in Food Science and Nutrition*
187. Mayo *et al.* (2019) **Equol-A Bacterial Metabolite from The Daidzein Isoflavone and Its Presumed Beneficial Health Effects** // *Nutrients*
188. Baky *et al.* (2022) **Interactions between dietary flavonoids and the gut microbiome-a comprehensive review** // *British Journal of Nutrition*
189. Rodriguez-Daza *et al.* (2021) **Polyphenol-Mediated Gut Microbiota Modulation-Toward Prebiotics and Further** // *Frontiers in Nutrition*
190. Hossain *et al.* (2022) **B Vitamins and Their Roles in Gut Health** // *Microorganisms*
191. Popescu *et al.* (2021) **Vitamin K2 Holds Promise for Alzheimer's Prevention and Treatment** // *Nutrients*
192. Palmieri *et al.* (2022) **Adherence to Gluten-Free Diet Restores Alpha Diversity in Celiac People but the Microbiome Composition Is Different to Healthy People** // *Nutrients*
193. Cristofori *et al.* (2020) **Bacterial-Based Strategies to Hydrolyze Gluten Peptides and Protect Intestinal Mucosa** // *Frontiers in Immunology*
194. Costante *et al.* (2022) **Biogeographic variation and functional pathways of the gut microbiota in celiac disease** // *Gastroenterology*
195. Verdu *et al.* (2021) **Co-factors, Microbes, and Immunogenetics in Celiac Disease to Guide Novel Approaches for Diagnosis and Treatment** // *Gastroenterology*
196. Kalciak *et al.* (2022) **Influence of Gluten-Free Diet on Gut Microbiota Composition in Patients with Coeliac Disease- A Systematic Review** // *Nutrients*
197. Qu *et al.* (2022) **Gut Microbiota-Mediated Elevated Production of Secondary Bile Acids in Chronic Unpredictable Mild Stress** // *Frontiers in Pharmacology*
198. Yang *et al.* (2022) **Research on Gut Microbiota-Derived Secondary Bile Acids in Cancer Progression** // *Integrative Cancer Therapies*

199. Silva et al. (2021) **Ethanol-striking the cardiovascular system by harming the gut microbiota** // *American Journal of Physiology*
200. Kumpitsch et al. (2021) **Reduced B12 uptake and increased gastrointestinal formate are associated with archaeome-mediated breath methane emission in humans** // *Microbiome*
201. Nava et al. (2012) **Abundance and diversity of mucosa-associated hydrogenotrophic microbes in the healthy human colon** // *ISME Journal*
202. Smith et al. (2019) **Hydrogen cross-feeders of the human gastrointestinal tract** // *Gut Microbes*