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Gut Microbiome Analysis

Comprehensive Analysis, 16S rRNA Sequencing

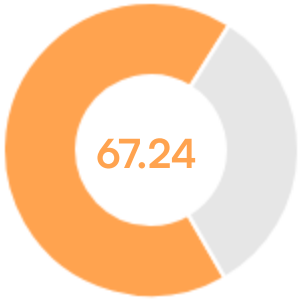
[redacted]

This is your complete gut microbiome analysis containing condition related findings with food and supplements recommendation to optimize your gut health.

SECTION 1: Summary of your results

0-49 represents Poor • 50-79 represents Needs work • 80-100 represents Satisfactory

Gut Health Score

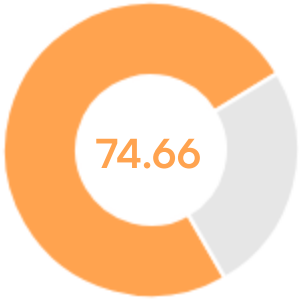


Needs work

Your Gut Health Score

Your Gut Health Score is computed based on all the bacteria & archaea enlisted in section 2. Assuming all your bacterial taxa are within optimal ranges, then your score will be 100. For every taxon that is out of range, your score will decrease accordingly to the degree that it deviates from the optimal range

Diversity Score



Needs work

Your Diversity Score

Your Diversity Score is computed using the Shannon Index, which accounts for the richness and evenness of the species found in your gut. Your score is a percentile value compared to the rest of the people who have taken the Vitract Gut Microbiome Test. Note that apart from diet, other factors such as age, geographical location, genetics, sleep patterns, and antibiotic use, can affect your diversity score

Disclaimer

- This report is not a diagnosis. It is for educational and informational purposes only. 'All associations between your microbiome profile, disease conditions and recommended food suggestions, are based on published peer-reviewed research papers. Note that other factors such as genetics, lifestyle, environment, etc, can contribute to disease or health associations. Always seek the advice of your doctor or healthcare provider for any issues relating to your diagnosis, disease prevention, impairment, symptoms or treatment. This report does not replace the role of your healthcare provider.

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SECTION 2: Bacteria life forms

Health-associated bacteria

Probiotic bacteria

Commensals

Disease-associated bacteria

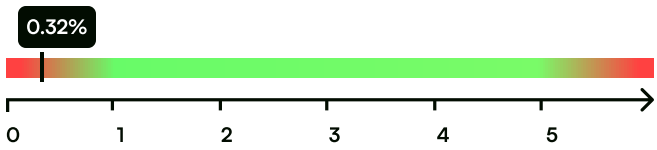
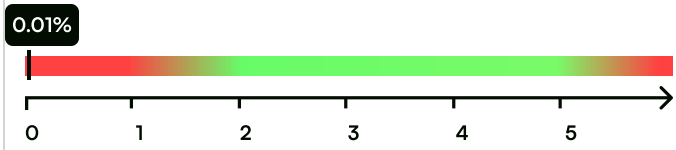
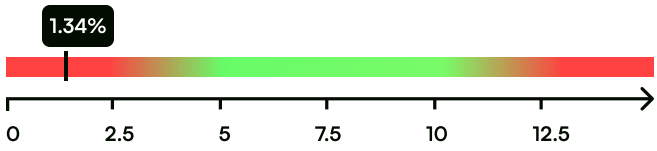
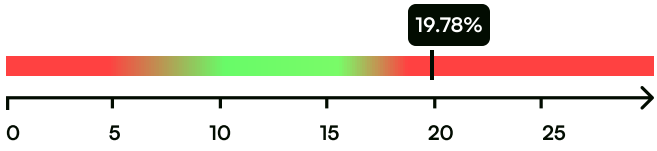
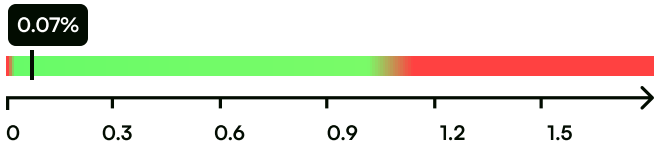
Pathobiont overgrowth

Pathogens

Probiotic bacteria - 52

Probiotic bacteria are live microorganisms that, when consumed in sufficient quantities, provide health benefits by promoting a balanced and healthy gut microbiota.

Low Optimal High represents bacteria levels.

#	Probiotic bacteria	Implication
1	*Akkermansia* - 0.32% Low Optimal Range (1-5%) 	Low Low levels of *Akkermansia* can lead to adisruption in the gut barrier, allowing pathogens toinvade and potentially trigger inflammation. Also,it could lead to reduced activation of the host'simmune system.
2	*Bifidobacterium* - 0.01% Low Optimal Range (2-5%) 	Low Low amounts of Bifidobacterium can lead to dysbiosis, a microbial imbalance associated with various digestive disorders, including IBS, ulcerative colitis and IBD. Additionally, it can weaken the gut's barrier function, making it more susceptible to harmful pathogen invasion.
3	*Blautia* - 1.34% Low Optimal Range (5-10%) 	Low Low levels of Blautia have been reported in adults and children suffering from type 2 diabetes and Inflammatory bowel disease (IBD), including Crohn's disease (CD) and ulcerative colitis and also liver cirrhosis. Also, a reduction in the abundance of Blautia has been associated with colorectal cancer and colitis-related cancer.
4	*Faecalibacterium* - 19.78% Optimal Optimal Range (>=10%) 	Optimal Levels seen are optimal.
5	*Lactobacillus* - 0.07% Optimal Optimal Range (0.01-1%) 	Optimal Levels seen are optimal.

All bacteria optimal ranges in section 2, with the exception of *Dorea, Coprococcus, Clostridium butyricum, Veillonella, and Enterococcus faecalis*, are based on the recommendations of Dr. Jason Hawrelak of Probiotic Advisor.

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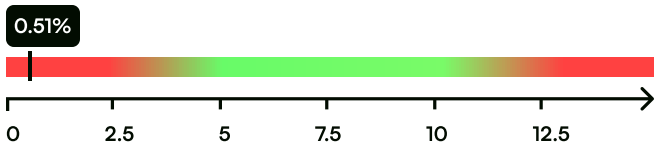
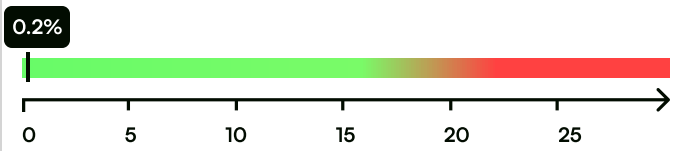
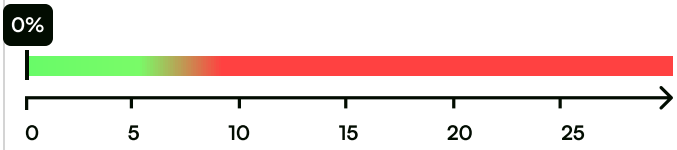
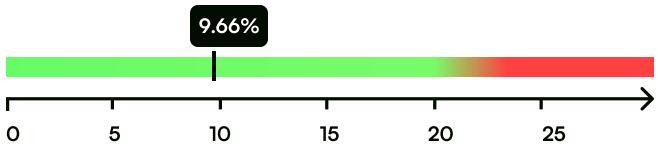
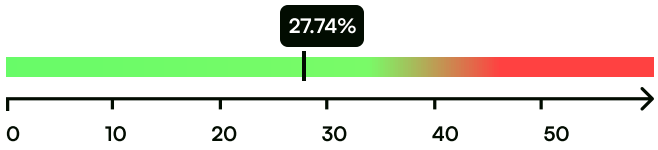
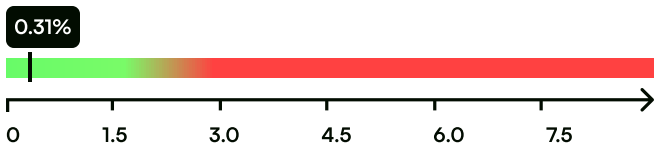
#	Probiotic bacteria	Implication
6	*Roseburia* - 0.51% Low Optimal Range (5-10%) 	Low Low levels of Roseburia can lead to an imbalance in the gut microbiota, which is associated with various gastrointestinal disorders, including irritable bowel syndrome (IBS) and inflammatory bowel diseases (IBD).
7	*Ruminococcus* - 0.2% Optimal Optimal Range (0-15%) 	Optimal Levels seen are optimal.

Commensals - 84

Gut commensals are microorganisms that coexist with the host in the gastrointestinal tract without causing harm. They contribute to host wellbeing and gut homeostasis.

#	Commensals	Implication
1	*Alistipes* - 0% Optimal Optimal Range (0-5%) 	Optimal Levels seen are optimal.
2	*Bacteroides* - 9.66% Optimal Optimal Range (0-20%) 	Optimal Levels seen are optimal.
3	*Bacteroidetes* - 27.74% Optimal Optimal Range (0-35%) 	Optimal Levels seen are optimal.
4	*Coprococcus* - 0.31% Optimal Optimal Range (0-6%) 	Optimal Levels seen are optimal.

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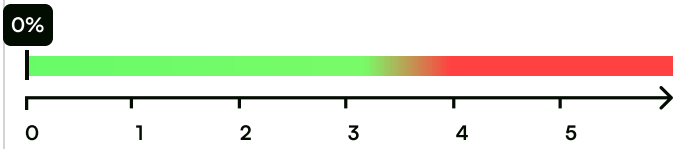
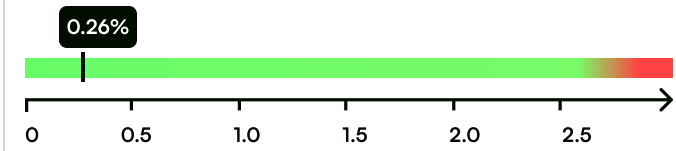
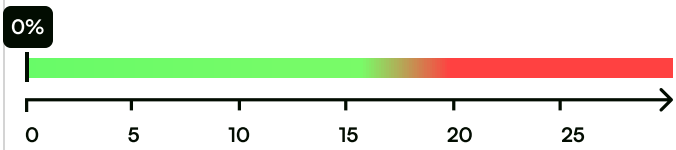
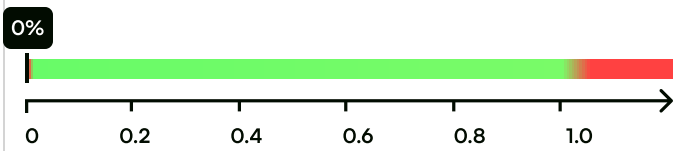
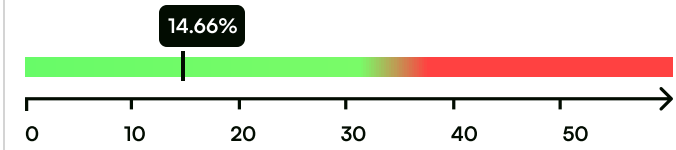
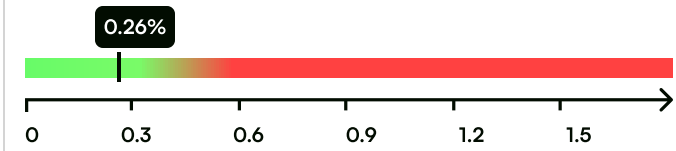
#	Commensals	Implication
5	*Clostridium butyricum* - 0% Optimal Optimal Range (0-3%) 	Optimal Levels seen are optimal.
6	*Dorea* - 0.26% Optimal Optimal Range (0-2.5%) 	Optimal Levels seen are optimal.
7	*Eubacterium* - 0% Optimal Optimal range (0-15%) 	Optimal Levels seen are optimal.
8	*Oxalobacter* - 0% Low Optimal range (0.01-1%) 	Low Low levels or the absence of *Oxalobacter*, particularly *Oxalobacter formigenes* in the gut microbiome have been linked to an increased risk of hyperoxaluria, a condition characterized by elevated levels of oxalate in the urine.
9	*Prevotella* - 14.66% Optimal Optimal range (0-30% for vegetarians) Optimal range (0-20% for non-vegetarians) 	Optimal Levels seen are optimal.
10	*Streptococcus* - 0.26% Optimal Optimal range (0-0.3%) 	Optimal Levels seen are optimal.

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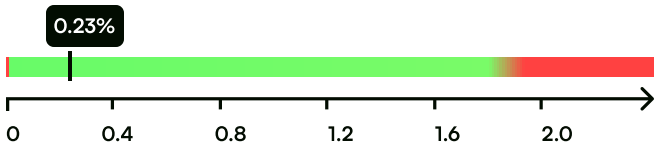
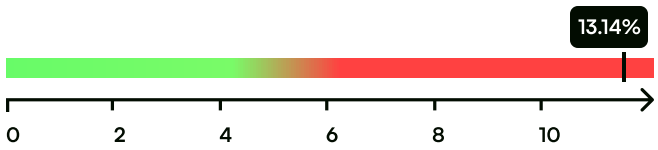
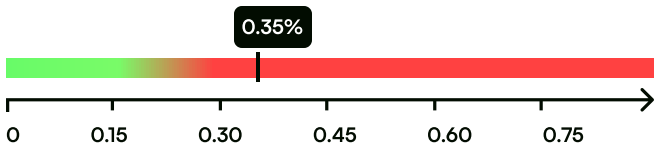
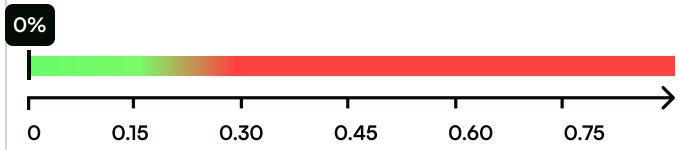
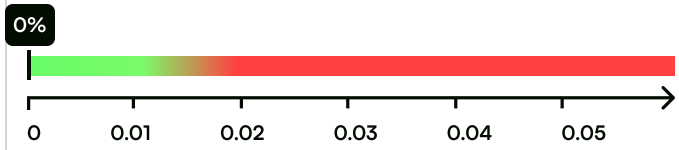
#	Commensals	Implication
12	*Veillonella* - 0.23% Optimal Optimal range (0.001-1.7%) 	Optimal Levels seen are optimal.

Pathobionts - 64

Pathobionts are microorganisms that typically reside harmlessly in the gut but have the potential to cause disease under certain conditions or when the host's immune system is compromised. Pathobionts in this test are shown in 4 sub-categories:

#	Inflammatory lipopolysaccharide producers	Implication
1	*Proteobacteria* - 13.14% High Optimal range (0-4%) 	High Overabundance of pathogenic *Proteobacteria* can indicate an imbalance in the gut microbiota, known as dysbiosis. Dysbiosis can lead to various health issues including inflammation and disruption in the gut barrier, allowing harmful substances to enter the bloodstream.

#	Hydrogen sulfide producers	Implication
1	*Bilophila* - 0.35% High Optimal range (0-0.15%) 	High An excessive growth of *B. wadsworthia* can lead to intestinal barrier defect, systemic inflammation, bile acid dysmetabolism, and changes in microbiome functional profile. All these disorders can lead to pathophysiological conditions.
2	*Desulfovibrio* - 0% Optimal Optimal range (0-0.15%) 	Optimal Levels seen are optimal.

#	Methane-producing archaea	Implication
1	*Methanobrevibacter* - 0% Optimal Optimal range (0-0.01%) 	Optimal Levels seen are optimal.

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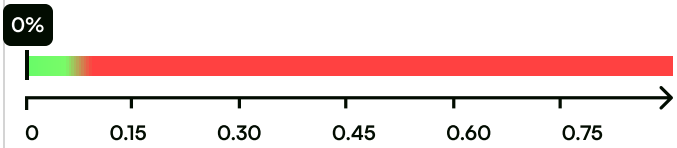
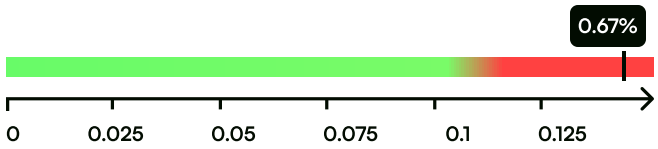
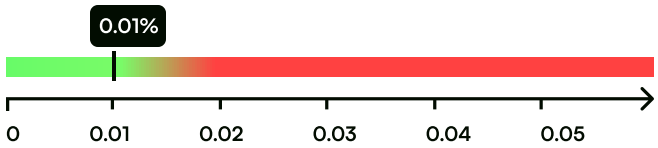
#	Enterotoxic & Inflammatory pathobionts	Implication
1	*Enterococcus faecalis* - 0% Optimal Optimal range (0-0.06%) 	Optimal Levels seen are optimal.
2	*Escherichia coli* - 0.67% High Optimal range (0-0.1%) 	High An overabundance of pathogenic or toxin-producing *E. coli* strains can lead to various health complications such as diarrheal, peritonitis, colitis, bacteremia, and urinary tract infections.
3	*Fusobacterium* - 0.01% Optimal Optimal range (0-0.01%) 	Optimal Levels seen are optimal.

Pathogens

Detected Not Detected represents bacteria detection.

#	Pathogens	Implication
1	*Campylobacter* - 0% Not Detected	Not Detected
2	*Shigella* - 0% Not Detected	Not Detected
3	*Salmonella* - 0% Not Detected	Not Detected
4	*Staphylococcus* - 0% Not Detected	Not Detected
5	*Vibrio* - 0% Not Detected	Not Detected
6	*Yersinia* - 0% Not Detected	Not Detected
7	*Helicobacter Pylori* - 0% Not Detected	Not Detected
8	*Clostridioides difficile* - 0% Not Detected	Not Detected

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SECTION 3: Insights into metabolites

Please note that the predicted metabolites and enzymes in this section are computed based on your gut bacterial composition, and not the direct measurement of the metabolite or enzyme

Satisfactory | Needs work | High represents rating.

SHORT CHAIN FATTY ACIDS PRODUCERS

The closer your score is to 100, the better.

• Above 50: Satisfactory • 0 to 50: Needs work

Metabolites	Percentile score	Impact
Butyrate Needs work	42 (0–100)	Energy source for colonocytes; Anti-inflammatory effects; Maintenance of gut barrier function
Acetate Needs work	9 (0–100)	Metabolic regulation; Anti-inflammatory effects; Neuroprotection and cognitive function
Propionate Needs work	30 (0–100)	Colonic pH regulation; Appetite regulation; Anti-inflammatory effects by promoting immune regulatory responses.

NEUROTRANSMITTER PRODUCERS

The closer you score is to 100, the better, except for histamine which should not be too low or too high

• Above 50: Satisfactory • 0 to 50: Needs work

• 26 to 75: Satisfactory • 0 to 25: Needs work • Above 75: High For Histamine

Metabolites	Percentile score	Impact
Acetylcholine Needs work	1 (0–100)	Key mediator of peristalsis; Stimulates the release of digestive enzymes from glands in the digestive system
Dopamine Needs work	16 (0–100)	Cognitive function; Regulates mood and sleep
GABA Needs work	19 (0–100)	Influences smooth muscle contraction and relaxation; Contributes to mood regulation and relaxation
Histamine Needs work	1 (0–100)	Metabolic regulation; Contributes to the body's defense mechanisms against pathogens; Involved in the regulation of wakefulness, arousal, and cognitive functions
Norepinephrine Satisfactory	95 (0–100)	Increases alertness; Involved in cognitive functions such as attention, learning, and memory
Serotonin Satisfactory	73 (0–100)	Mood regulation; Gastrointestinal motility; Involved in the regulation of appetite and satiety

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VITAMINS PRODUCERS

The closer your score is to 100, the better.

• Above 50: Satisfactory • 0 to 50: Needs work

Metabolites	Percentile score	Impact
Vitamin B1 (Thiamin) Satisfactory	85 (0–100)	Serves as a coenzyme in carbohydrate metabolism; Cellular growth and repair; Essential for the proper functioning of the enteric nervous system
Vitamin B2 (Riboflavin) Needs work	35 (0–100)	Aids in the breakdown of carbohydrates, proteins, and fats for energy; Antioxidant defense; Supports the growth and maintenance of gut epithelial cells
Vitamin B3 (Niacin) Satisfactory	87 (0–100)	Aids metabolism of fats, carbohydrates and proteins; Aids in neurotransmitter synthesis; Essential for maintaining skin health
Vitamin B5 (Pantothenic Acid) Satisfactory	87 (0–100)	Energy production through metabolism of carbohydrates, proteins, and fats; Contributes to the synthesis of acetylcholine; Fatty acid and hormone synthesis
Vitamin B6 (Pyridoxine) Satisfactory	87 (0–100)	Essential for the synthesis of neurotransmitters like serotonin, dopamine, and GABA; Supports the immune system
Vitamin B7 (Biotin) Satisfactory	87 (0–100)	Fatty acid synthesis; Carbohydrate metabolism; Cell growth and maintenance of gene expression
Vitamin B9 (Folate) Satisfactory	87 (0–100)	DNA synthesis and repair; Metabolism of amino acids; Involved in the synthesis of serotonin, dopamine, and norepinephrine
Vitamin B12 (Cobalamine) Satisfactory	82 (0–100)	Supports neurological function; Red blood cell formation; Energy production
Vitamin K2 Satisfactory	83 (0–100)	Essential for proper blood clotting and coagulation; Improves bone health; Prevents arterial calcification and reduces the risk of atherosclerosis

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TOXIN PRODUCERS

The closer your score is to 0, the better.

- 0 to 50: Satisfactory • 51 to 74: Needs work • Above 74: High
- 0 to 25: Satisfactory • 26 to 74: Needs work • Above 75: High — For Methane
- 0 to 50: Satisfactory • Above 50: Needs work — For Trimethylamine (TMA) and Trimethylamine-N-Oxide (TMAO)

Metabolites	Percentile score	Impact
Hydrogen sulfide Needs work	58 (0–100)	Increased risk of colorectal cancer; Impaired mucin production; Bloating and abdominal pain; Malodorous breath
Ammonia Satisfactory	40 (0–100)	Disruptions in the intestinal barrier function; Inflammation and abdominal pain; Neurotoxic effect; Gut microbiota disruption
Methane Satisfactory	1 (0–100)	Abdominal distension or bloating; Constipation, cramping and flatulence; Increased methane breath
Trimethylamine (TMA) and Trimethylamine-N-Oxide (TMAO) Satisfactory	40 (0–100)	Increased cardiovascular health risk; Cognitive function and neurological disorders; Inflammation and lipid accumulation in the blood vessels
Lipopolysaccharides (LPS) High	93 (0–100)	Increased inflammation; Metabolic dysfunction and insulin resistance; Neurological effect; Increased contribution to chronic diseases

DETOXIFICATION BIOMARKERS

Scores too close to 0 or 100 are not desirable.

- 26 to 75: Satisfactory • 0 to 25: Needs work • Above 75: High

Metabolites	Percentile score	Impact
Beta glucoronidase Satisfactory	67 (0–100)	Deconjugation of bile acids; Influence the pharmacokinetics of drugs; Regulation of physiological estrogen metabolism

LONGEVITY

The closer your score is to 100, the better.

- Above 50: Satisfactory • 0 to 50: Needs work

Metabolites	Percentile score	Impact
Indoles and Phenols Satisfactory	93 (0–100)	Indole is a precursor for neurotransmitter synthesis; Indoles regulates mood and sleep-wake cycles; Phenol reduces oxidative stress and inflammation

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LONGEVITY

The closer your score is to 100, the better.

• Above 50: Satisfactory • 0 to 50: Needs work

Metabolites	Percentile score	Impact
Myrosinase Needs work	28 (0–100)	Anti-cancer potential; Antioxidant and anti-inflammatory properties; Detoxification of harmful substances
Urolithin Needs work	23 (0–100)	Antioxidant activity; Mitochondrial health; Muscle health and exercise performance; Cellular senescence regulation

LACTOSE AND OXALATE DEGRADERS

The closer your score is to 100, the better.

• Above 50: Satisfactory • 0 to 50: Needs work

Metabolites	Percentile score	Impact
Oxalate Needs work	43 (0–100)	Prevention of kidney stone formation; Maintain gut microbial balance
Lactose Degraders Satisfactory	76 (0–100)	Digestive efficiency and nutrient absorption; Production of beneficial metabolites; Immune system modulation

Reference bacteria can be found on supplementary pages.

SECTION 4: Food and supplement recommendation

Bacteria out of range

Akkermansia Low , *Bifidobacterium* Low , *Bilophila* High , *Blautia* Low , *Clostridium* High , *Coprococcus* Optimal , *Escherichia coli* High , *Oxalobacter*

Modifiers	Bacteria shifted	Scientific evidence
FOOD To include: extra virgin olive oil [1], sea weed [2], chaga (mushroom) [3], Pulses [5], Konjaku flour [7], white button mushrooms [8], rye [9], buckwheat [10], Pistachio [11], grapes [12], Garlic [13], pomegranate [15], high amylose cornstarch [16], broccoli [17], almonds/ almond skins [19], green tea [20], potatoes [22], gallic acid (food additive) [23], basil [24], pomegranate blossom tea [25], walnuts [28], Okra [29], rhubarb [30], mulberry fruit polysaccharide [31], Kiwifruit [33] To avoid: oats [4], red wine polyphenols [14], wheat [18], lemon [27], glucose (sugar) [34]	Increase Akkermansia [1, 2, 3] Increase Bifidobacterium [5, 7, 8] Reduce Bilophila [9, 10, 11, 12, 13] Increase Blautia [2, 15, 16, 17] Reduce Clostridium [19, 20, 21] Reduce Coprococcus [22] Reduce Escherichia coli [23, 24, 25, 26] Reduce Proteobacteria [3, 28, 29, 30, 31] Increase Roseburia [32, 15, 33] Reduces Akkermansia [4] Increase Bilophila [14] Reduces Blautia [18] Increase Escherichia coli [27] Reduces Roseburia [34]	1. Fish Oil, but Not Olive Oil, Ameliorates Depressive-Like Behavior and ... 2. Ascophyllum nodosum polysaccharide regulates gut microbiota meta... 3. Methanol extract of Inonotus obliquus improves type 2 diabetes melli... 4. Concentrated Raw Fibers Enhance the Fiber-Degrading Capacity of ... 5. In vitro fermentation of lupin seeds (Lupinus albus) and broad beans (... 6. Dietary supplementation with olive oil co-products rich in polyphenol... 7. Amelioration of gut dysbiosis and gastrointestinal motility by konjac ol... 8. Effect of Agaricus bisporus Polysaccharides on Human Gut Microbiot... 9. The effects of fermented rye products on gut microbiota and their as... 10. Tartary Buckwheat (Fagopyrum tataricum) Ameliorates Lipid Metabol... 11. Pistachio Consumption Alleviates Inflammation and Improves Gut Mi... 12. Table grape consumption reduces adiposity and markers of hepatic l... 13. Black garlic melanoidins prevent obesity, reduce serum LPS levels a... 14. Resveratrol modulates the gut microbiota of cholestasis in pregnant ... 15. Effects of Pomegranate Peel Polyphenols Combined with Inulin on ... ***full references for recommendations can be found on supplementary pages***
PROBIOTICS To include: Lactobacillus Johnsonii [1], Bifidobacterium longum [2], Bifidobacterium adolescentis [3], Bifidobacterium bifidum [5], Lactobacillus plantarum [6], Lactobacillus rhamnosus [8], Lactobacillus fermentum [10], Lactobacillus casei shirota [11], Saccharomyces boulardii [14], Lactobacillus rhamnosus gg [17], Bacillus amyloliquefaciens [19] To avoid: Koji aspergillus oryzae [4], Pediococcus pentosaceus [9], bacillus subtilis,Lactobacillus acidophilus [12], Bifidobacterium breve [15], Bacillus subtilis [18], Lactobacillus paracasei [21], LentiLactobacillus buchneri [23]	Increase Akkermansia [1, 2] Increase Bifidobacterium [3] Reduce Bilophila [5, 6] Increase Blautia [7, 8] Reduce Clostridium [10, 11] Reduce Coprococcus [14] Reduce Escherichia coli [16, 17] Reduce Proteobacteria [19] Increase Roseburia [22] Reduces Bifidobacterium [4] Reduces Blautia [9] Increase Clostridium [12] Increase Coprococcus [15] Increase Escherichia coli [18] Increase Proteobacteria [21] Reduces Roseburia [23]	1. Probiotic Lactobacilli Administration Induces Changes in the Fecal Mi... 2. Bifidobacterium longum subsp. longum BL21 ameliorates alcoholic liv... 3. Mouse intestinal microbiome modulation by oral administration of a ... 4. Administration of Aspergillus oryzae suppresses DSS-induced colitis. 5. Bifidobacterium bifidum TMC3115 ameliorates milk protein allergy in ... 6. Effects of microencapsulated Lactobacillus plantarum LIP-1 on the gu... 7. Exopolysaccharides from Lactobacillus plantarum YW11 improve imm... 8. Effect of Lactobacillus rhamnosus HN001 and Bifidobacterium longu... 9. Protective effect of Pediococcus pentosaceus Li05 on diarrhea-pred... 10. The Impact in Intestines and Microbiota in BALB/c Mice Through Co... 11. Intestinal Microbiota Profiles of Healthy Pre-School and School-Age ... 12. Gaseous CO2 signal initiates growth of butyric-acid-producing Clost... 13. Lactobacillus plantarum-Derived Extracellular Vesicles Modulate Ma... 14. Saccharomyces cerevisiae boulardii CNCM I-1079 supplementation i... 15. Evaluation of the therapeutic effect and dose-effect of Bifidobacteri... ***full references for recommendations can be found on supplementary pages***

Reference bacteria can be found on supplementary pages.

SECTION 4: Food and supplement recommendation

Bacteria out of range

Akkermansia Low , *Bifidobacterium* Low , *Bilophila* High , *Blautia* Low , *Clostridium* High , *Coprococcus* Optimal , *Escherichia coli* High , *Oxalobacter*

Modifiers	Bacteria shifted	Scientific evidence
SUPPLEMENTS To include: Rutin [1], quercetin [5], bentonite [7], Curcumin [9], whey protein supplement [10], Glucomannan [12], Baicalin [14]	Increase Akkermansia [1] Reduce Bilophila [5] Increase Blautia [7] Reduce Clostridium [9] Reduce Coprococcus [10] Reduce Escherichia coli [12] Reduce Proteobacteria [14]	1. Rutin alleviates colon lesions and regulates gut microbiota in diabetic ... 2. Increasing breast milk betaine modulates Akkermansia abundance in ... 3. Structural Insights into Amelioration Effects of Quercetin and Its Glyc... 4. Shen-Ling-Bai-Zhu-San (SL) and SL Derived-Polysaccharide (PL) Am... 5. A combination of quercetin and resveratrol reduces obesity in high-fa... 6. Propionate-Producing Consortium Restores Antibiotic-Induced Dysbi... 7. Microbiome Remodeling via the Montmorillonite Adsorption-Excretio... 8. Glucosamine Ameliorates Symptoms of High-Fat Diet-Fed Mice by R... 9. Prebiotic Potential and Chemical Composition of Seven Culinary Spi... 10. Effect of a Co-Feed Liquid Whey-Integrated Diet on Crossbred Pigs'... 11. Taxifolin increased semen quality of Duroc boars by improving gut m... 12. Antibacterial activity of konjac glucomannan/chitosan blend films an... 13. Preparation of selenium/zinc-enriched probiotics and their effect on ... 14. Protective effect of baicalin on the regulation of Treg/Th17 balance, ... 15. Helicobacter pylori eradication with bismuth quadruple therapy lead... ***full references for recommendations can be found on supplementary pages***
To avoid: betaine [2], Shen Ling Bai Zhu San [4], propionate [6], Glucosamine [8], Taxifolin [11], selenium [13], Bismuth Salts [15], cannabinoids [16]	Reduces Akkermansia [2] Reduces Bifidobacterium [4] Increase Bilophila [6] Reduces Blautia [8] Increase Coprococcus [11] Increase Escherichia coli [13] Increase Proteobacteria [15] Reduces Roseburia [16]	
PREBIOTICS To include: chitooligosaccharides [1], arabinogalactan [2], inulin [4], lactulose [5], gum arabic [7], galacto-oligosaccharides [8], fructo-oligosaccharides [9], mastic gum [10]	Increase Akkermansia [1] Increase Bifidobacterium [2] Reduce Bilophila [4, 5] Reduce Clostridium [7, 8] Reduce Escherichia coli [9, 10]	1. Pretreatment with chitosan oligosaccharides attenuate experimental s... 2. Relative abundance of the Prevotella genus within the human gut mi... 3. Characterization of fecal fat composition and gut derived fecal micro... 4. Prebiotic inulin-type fructans induce specific changes in the human ... 5. Effect of lactulose intervention on gut microbiota and short chain fatt... 6. Diets high in resistant starch and arabinoxylan modulate digestion pr... 7. Pharmacological benefits of Acacia against metabolic diseases: intest... 8. Prebiotic effect of an infant formula supplemented with galacto-oligo... 9. Dietary cellulose, fructooligosaccharides, and pectin modify fecal pro... 10. Spices as Sustainable Food Preservatives: A Comprehensive Review ... 11. In vitro fermentation of raffinose by the human gut bacteria. 12. Chitooligosaccahrides: Digestion characterization and effect of the ... 13. Effect of Prebiotic on Microbiota, Intestinal Permeability, and Glycem... ***full references for recommendations can be found on supplementary pages***
To avoid: raffinose(sugar beet) [11], oligofructose-enriched inulin [13]	Increase Escherichia coli [11] Reduces Roseburia [13]	

Reference bacteria can be found on supplementary pages.

SECTION 4: Food and supplement recommendation

Bacteria out of range

Akkermansia Low , *Bifidobacterium* Low , *Bilophila* High , *Blautia* Low , *Clostridium* High , *Coprococcus* Optimal , *Escherichia coli* High , *Oxalobacter*

Modifiers	Bacteria shifted	Scientific evidence
LIFESTYLE CHANGES To include: mediterranean diet [2], nuts [3], Fiber [6], Exercise [9]	Increase Bifidobacterium [2] Reduce Bilophila [3] Reduce Clostridium [6] Reduce Proteobacteria [9]	1. Fucoidan Improves D-Galactose-Induced Cognitive Dysfunction by P... 2. The gut microbial community in metabolic syndrome patients is modi... 3. Pistachio Consumption Alleviates Inflammation and Improves Gut Mi... 4. Interactions between Diet, Bile Acid Metabolism, Gut Microbiota, and... 5. Smoking cessation alters intestinal microbiota: insights from quantitat... 6. [Clinical benefits after soluble dietary fiber supplementation: a rando... 7. Gut Microbiome Composition in Non-human Primates Consuming a ... 8. Effects of the dietary protein level on the microbial composition and ... 9. Effect of an 8-week Exercise Training on Gut Microbiota in Physically ... 10. Metagenomic analyses of alcohol induced pathogenic alterations in ... 11. Nuts and their Effect on Gut Microbiota, Gut Function and Symptom... 12. Gut microbiome and metabolome in a non-human primate model of... ***full references for recommendations can be found on supplementary pages***
To avoid: high-saturated fat diet [1], smoking [5], low protein diet [8], alcoholic beverages [10]	Reduces Akkermansia [1] Reduces Blautia [5] Increase Coprococcus [8] Increase Proteobacteria [10]	

Reference bacteria can be found on supplementary pages.

SUPPLEMENTARY TABLE 1: References for dietary recommendations.

Food references

1. Fish Oil, but Not Olive Oil, Ameliorates Depressive-Like Behavior and Gut Microbiota Dysbiosis in Rats under Chronic Mild Stress.

2. Ascophyllum nodosum polysaccharide regulates gut microbiota metabolites to protect against colonic inflammation in mice.

3. Methanol extract of Inonotus obliquus improves type 2 diabetes mellitus through modifying intestinal flora.

4. Concentrated Raw Fibers Enhance the Fiber-Degrading Capacity of a Synthetic Human Gut Microbiome.

5. In vitro fermentation of lupin seeds (Lupinus albus) and broad beans (Vicia faba): dynamic modulation of the intestinal microbiota and metabolomic output.

6. Dietary supplementation with olive oil co-products rich in polyphenols: a novel nutraceutical approach in monogastric animal nutrition.

7. Amelioration of gut dysbiosis and gastrointestinal motility by konjac oligo-glucomannan on loperamide-induced constipation in mice.

8. Effect of Agaricus bisporus Polysaccharides on Human Gut Microbiota during In Vitro Fermentation: An Integrative Analysis of Microbiome and Metabolome.

9. The effects of fermented rye products on gut microbiota and their association with metabolic factors in Chinese adults - an explorative study.

10. Tartary Buckwheat (Fagopyrum tataricum) Ameliorates Lipid Metabolism Disorders and Gut Microbiota Dysbiosis in High-Fat Diet-Fed Mice.

11. Pistachio Consumption Alleviates Inflammation and Improves Gut Microbiota Composition in Mice Fed a High-Fat Diet.

12. Table grape consumption reduces adiposity and markers of hepatic lipogenesis and alters gut microbiota in butter fat-fed mice.

13. Black garlic melanoidins prevent obesity, reduce serum LPS levels and modulate the gut microbiota composition in high-fat diet-induced obese C57BL/6J mice.

14. Resveratrol modulates the gut microbiota of cholestasis in pregnant rats.

15. Effects of Pomegranate Peel Polyphenols Combined with Inulin on Gut Microbiota and Serum Metabolites of High-Fat-Induced Obesity Rats.

16. Starch acylation of different short-chain fatty acids and its corresponding influence on gut microbiome and diabetic indexes.

17. Sulforaphane and Sulforaphane-Nitrile Metabolism in Humans Following Broccoli Sprout Consumption: Inter-individual Variation, Association with Gut Microbiome Compos...

18. Diet Mediate the Impact of Host Habitat on Gut Microbiome and Influence Clinical Indexes by Modulating Gut Microbes and Serum Metabolites.

19. Benefits of Nut Consumption on Insulin Resistance and Cardiovascular Risk Factors: Multiple Potential Mechanisms of Actions.

20. In Vivo Effects of Tea Polyphenol Intake on Human Intestinal Microflora and Metabolism.

21. Effect of garlic powder on the growth of commensal bacteria from the gastrointestinal tract.

22. Potato resistant starch inhibits diet-induced obesity by modifying the composition of intestinal microbiota and their metabolites in obese mice.

23. Antiultraviolet, Antioxidant, and Antimicrobial Properties and Anticancer Potential of Novel Environmentally Friendly Amide-Modified Gallic Acid Derivatives.

24. In vitro antimicrobial activity of five essential oils on multidrug resistant Gram-negative clinical isolates.

25. Antimicrobial activities of widely consumed herbal teas, alone or in combination with antibiotics: an in vitro study.

26. Tartary buckwheat protein prevented dyslipidemia in high-fat diet-fed mice associated with gut microbiota changes.

27. Ascorbic acid-dependent gene expression in Streptococcus pneumoniae and the activator function of the transcriptional regulator UlaR2.

28. Effects of Walnut and Pumpkin on Selective Neurophenotypes of Autism Spectrum Disorders: A Case Study.

29. Supplementation of okra seed oil ameliorates ethanol-induced liver injury and modulates gut microbiota dysbiosis in mice.

30. What we already know about rhubarb: a comprehensive review.

31. Mulberry leaves ameliorate obesity through enhancing brown adipose tissue activity and modulating gut microbiota.

32. Effects of Konjaku Flour on the Gut Microbiota of Obese Patients.

33. Butyrogenic, bifidogenic and slight anti-inflammatory effects of a green kiwifruit powder (Kiwi FFG®) in a human gastrointestinal model simulating mild constipation.

34. A diet high in sugar and fat influences neurotransmitter metabolism and then affects brain function by altering the gut microbiota.

Continues on the next page

SUPPLEMENTARY TABLE 1: References for dietary recommendations.

Probiotics references

1. Probiotic Lactobacilli Administration Induces Changes in the Fecal Microbiota of Preweaned Dairy Calves.

2. Bifidobacterium longum subsp. longum BL21 ameliorates alcoholic liver disease in mice through enhancement of the hepatic antioxidant capacity and modulation of the gut...

3. Mouse intestinal microbiome modulation by oral administration of a GABA-producing Bifidobacterium adolescentis strain.

4. Administration of Aspergillus oryzae suppresses DSS-induced colitis.

5. Bifidobacterium bifidum TMC3115 ameliorates milk protein allergy in by affecting gut microbiota: A randomized double-blind control trial.

6. Effects of microencapsulated Lactobacillus plantarum LIP-1 on the gut microbiota of hyperlipidaemic rats.

7. Exopolysaccharides from Lactobacillus plantarum YW11 improve immune response and ameliorate inflammatory bowel disease symptoms.

8. Effect of Lactobacillus rhamnosus HN001 and Bifidobacterium longum BB536 on the healthy gut microbiota composition at phyla and species level: A preliminary study.

9. Protective effect of Pediococcus pentosaceus Li05 on diarrhea-predominant irritable bowel syndrome in rats.

10. The Impact in Intestines and Microbiota in BALB/c Mice Through Consumption of Milk Fermented by Potentially Probiotic Lacticaseibacillus casei SJRP38 and Limosilactob...

11. Intestinal Microbiota Profiles of Healthy Pre-School and School-Age Children and Effects of Probiotic Supplementation.

12. Gaseous CO2 signal initiates growth of butyric-acid-producing Clostridium butyricum in both pure culture and mixed cultures with Lactobacillus brevis.

13. Lactobacillus plantarum-Derived Extracellular Vesicles Modulate Macrophage Polarization and Gut Homeostasis for Alleviating Ulcerative Colitis.

14. Saccharomyces cerevisiae boulardii CNCM I-1079 supplementation in finishing male pigs helps to cope with heat stress through feeding behaviour and gut microbiota mo...

15. Evaluation of the therapeutic effect and dose-effect of Bifidobacterium breve on the primary Clostridioides difficile infected mice.

16. Antagonistic activity of probiotic lactobacilli and bifidobacteria against entero- and uropathogens.

17. Therapeutic potential of two probiotics in inflammatory bowel disease as observed in the trinitrobenzene sulfonic acid model of colitis.

18. Effect of Bacillus subtilis C-3102 spores as a probiotic feed supplement on growth performance, noxious gas emission, and intestinal microflora in broilers.

19. Probiotic Bacillus amyloliquefaciens C-1 Improves Growth Performance, Stimulates GH/IGF-1, and Regulates the Gut Microbiota of Growth-Retarded Beef Calves.

20. Bifidobacterium adolescentis IM38 ameliorates high-fat diet-induced colitis in mice by inhibiting NF-?B activation and lipopolysaccharide production by gut microbiota.

21. Modulation of fecal Clostridiales bacteria and butyrate by probiotic intervention with Lactobacillus paracasei DG varies among healthy adults.

22. A metagenomic study of the preventive effect of Lactobacillus rhamnosus GG on intestinal polyp formation in Apc(Min/+) mice.

23. Exopolysaccharides from Lactobacillus buchneri TCP016 Attenuate LPS- and d-GalN-Induced Liver Injury by Modulating the Gut Microbiota.

Supplements references

1. Rutin alleviates colon lesions and regulates gut microbiota in diabetic mice.

2. Increasing breast milk betaine modulates Akkermansia abundance in mammalian neonates and improves long-term metabolic health.

3. Structural Insights into Amelioration Effects of Quercetin and Its Glycoside Derivatives on NAFLD in Mice by Modulating the Gut Microbiota and Host Metabolism.

4. Shen-Ling-Bai-Zhu-San (SL) and SL Derived-Polysaccharide (PL) Ameliorate the Severity of Diarrhea-Induced by High Lactose via Modification of Colonic Fermentation.

5. A combination of quercetin and resveratrol reduces obesity in high-fat diet-fed rats by modulation of gut microbiota.

6. Propionate-Producing Consortium Restores Antibiotic-Induced Dysbiosis in a Dynamic in vitro Model of the Human Intestinal Microbial Ecosystem.

7. Microbiome Remodeling via the Montmorillonite Adsorption-Excretion Axis Prevents Obesity-related Metabolic Disorders.

8. Glucosamine Ameliorates Symptoms of High-Fat Diet-Fed Mice by Reversing Imbalanced Gut Microbiota.

9. Prebiotic Potential and Chemical Composition of Seven Culinary Spice Extracts.

10. Effect of a Co-Feed Liquid Whey-Integrated Diet on Crossbred Pigs' Fecal Microbiota.

11. Taxifolin increased semen quality of Duroc boars by improving gut microbes and blood metabolites

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SUPPLEMENTARY TABLE 1: References for dietary recommendations.

Prebiotics references

1. Pretreatment with chitosan oligosaccharides attenuate experimental severe acute pancreatitis via inhibiting oxidative stress and modulating intestinal homeostasis.

2. Relative abundance of the Prevotella genus within the human gut microbiota of elderly volunteers determines the inter-individual responses to dietary supplementation with ...

3. Characterization of fecal fat composition and gut derived fecal microbiota in high-fat diet fed rats following intervention with chito-oligosaccharide and resistant starch com...

4. Prebiotic inulin-type fructans induce specific changes in the human gut microbiota.

5. Effect of lactulose intervention on gut microbiota and short chain fatty acid composition of C57BL/6J mice.

6. Diets high in resistant starch and arabinoxylan modulate digestion processes and SCFA pool size in the large intestine and faecal microbial composition in pigs.

7. Pharmacological benefits of Acacia against metabolic diseases: intestinal-level bioactivities and favorable modulation of gut microbiota.

8. Prebiotic effect of an infant formula supplemented with galacto-oligosaccharides: randomized multicenter trial.

9. Dietary cellulose, fructooligosaccharides, and pectin modify fecal protein catabolites and microbial populations in adult cats.

10. Spices as Sustainable Food Preservatives: A Comprehensive Review of Their Antimicrobial Potential.

11. In vitro fermentation of raffinose by the human gut bacteria.

12. Chitooligosaccahrides: Digestion characterization and effect of the degree of polymerization on gut microorganisms to manage the metabolome functional diversity in vitro.

13. Effect of Prebiotic on Microbiota, Intestinal Permeability, and Glycemic Control in Children With Type 1 Diabetes.

Lifestyle changes references

1. Fucoidan Improves D-Galactose-Induced Cognitive Dysfunction by Promoting Mitochondrial Biogenesis and Maintaining Gut Microbiome Homeostasis.

2. The gut microbial community in metabolic syndrome patients is modified by diet.

3. Pistachio Consumption Alleviates Inflammation and Improves Gut Microbiota Composition in Mice Fed a High-Fat Diet.

4. Interactions between Diet, Bile Acid Metabolism, Gut Microbiota, and Inflammatory Bowel Diseases.

5. Smoking cessation alters intestinal microbiota: insights from quantitative investigations on human fecal samples using FISH.

6. [Clinical benefits after soluble dietary fiber supplementation: a randomized clinical trial in adults with slow-transit constipation].

7. Gut Microbiome Composition in Non-human Primates Consuming a Western or Mediterranean Diet.

8. Effects of the dietary protein level on the microbial composition and metabolomic profile in the hindgut of the pig.

9. Effect of an 8-week Exercise Training on Gut Microbiota in Physically Inactive Older Women.

10. Metagenomic analyses of alcohol induced pathogenic alterations in the intestinal microbiome and the effect of Lactobacillus rhamnosus GG treatment.

11. Nuts and their Effect on Gut Microbiota, Gut Function and Symptoms in Adults: A Systematic Review and Meta-Analysis of Randomised Controlled Trials.

12. Gut microbiome and metabolome in a non-human primate model of chronic excessive alcohol drinking.