GutID™

Healthy Microbiome, Healthy You

GutID Complete Microbiome Assessment (CMA) test identifies all bacteria present in an individual's microbiome down to the strain level. Bacterial abundances are analyzed based on well-established indices like diversity and enterotypes, and according to their specific beneficial or detrimental effects. The presence of bacteria may negatively impact both intestinal and systemic health, such as multiple gut axes (brain, gastrointestinal, metabolism, heart, and immune health). Furthermore, a separate section examines the abundance of bacteria involved in certain nutrients metabolism.

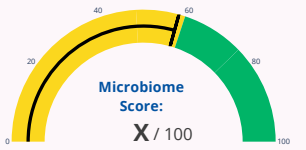
GutID™

How to Read This Report

GutID's CMA report, while comprehensive, is designed for easy navigation. Page 1 provides an "at-a-glance" summary, allowing quick identification of any microbiome issues that may warrant further investigation.

PAGE 1

EXAMPLE



Summary: Low Microbiome Score. Focus on flagged areas.

Resistome: Poor. High load of antibiotic resistant bacteria suggests recent or historic high antibiotic use.

Pathogens: X.XX% **Proteobacteria:** X.X% **Fusobacteria:** X.X%

Review: X/24 areas. **Worst:** Beta Diversity

Learn More: See "How To Use This Report" below.

Microbiome Score: A score below 60 means there are known issues with the bacterial composition of the microbiome. The score is calculated based on measures of fundamental microbiome metrics consistent across populations using our proprietary algorithm. Those include microbiome diversity, richness, evenness, Firmicutes/Bacteroidetes ratio, total percentages of pathogens, resistome and top 10 species.
Resistome: Indicates tendency to carry bacteria with antibiotic-resistant genes.
Pathogens, Proteobacteria, Fusobacteria: Percentages should be as low as possible. Some fusobacteria are associated with food poisoning and a wide range of cancers.
Review: Indicates the number of 24 areas that differ from those in 75% of the reference population.
Worst: Highlights the metric element that is the biggest negative contributor to the overall score.
Target Plot: A visualization of the entire bacterial content of the microbiome, down to strain level. A variety of colors in the plot represents a healthier microbiome. An overabundance of a single bacterium, or a few bacteria overall, indicates improvements can be made.

PAGE 2 & BEYOND

From more detailed sections, specific areas are flagged for your attention, along with some comments and advice.

Understanding the Flags in Your Report:

⚠ **Yellow Exclamation Marks (Left Side):** Indicate that your microbiome shows unusual patterns in that specific area. They help you focus on the most important parts of your report.

High **Flags in Species Tables ("High" or "Low"):** Point out specific species or groups in your microbiome that are outside the normal range. Even if the overall analysis of a section appears normal, individual species that fall out of range are flagged as a caution. These details may still be important and relevant for clinicians.

1. Microbiome Scoring Factors:

- **Resistome:** Indicates tendency to carry bacteria with antibiotic-resistant genes.
- **Enterotype:** Ranges from type 1 to type 4, based on the dominant bacteria in the sample.
- **Pathogens, Proteobacteria, Fusobacteria:** Percentages should be as low as possible. Some fusobacteria are associated with food poisoning and a wide range of cancers.

2. Beneficial Bacteria: Represents overall gut health.
3-7. Multiple Gut Axes: Information on the assessment of both the major markers of gut microbiome health and the abundance of bacteria influencing the Gut-Axes including Gut-Brain Axis, Gut-Gastrointestinal Axis, Gut-Metabolism Axis, Gut-Heart Axis, and Gut-Immune Axis.
8. Nutrient & Dietary Component Metabolism: This information can provide insight into food sensitivity and how diet can affect general health.

Additional Information Section: Included to help understand each test result and recommendation in more detail.

GutID™

Report
Accession Number: NA
Order Number: NA
Barcode: NA
Report Generated: 2025-03-11

Sample
NFN NLN
DOB: NA
Sample Collected: NA

CMA - Complete Microbiome Assessment

FOR MANAGING THE MICROBIOME TO ENHANCE HEALTH

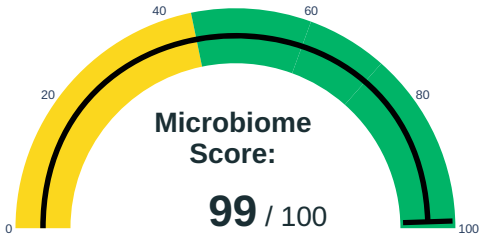
Summary: Score is in the top 25% of the reference population.

Resistome: Good. Low load of antibiotic resistant bacteria suggests limited recent antibiotic use.

Pathogens: 1.07% **Proteobacteria:** 3.35% **Fusobacteria:** 0.0%

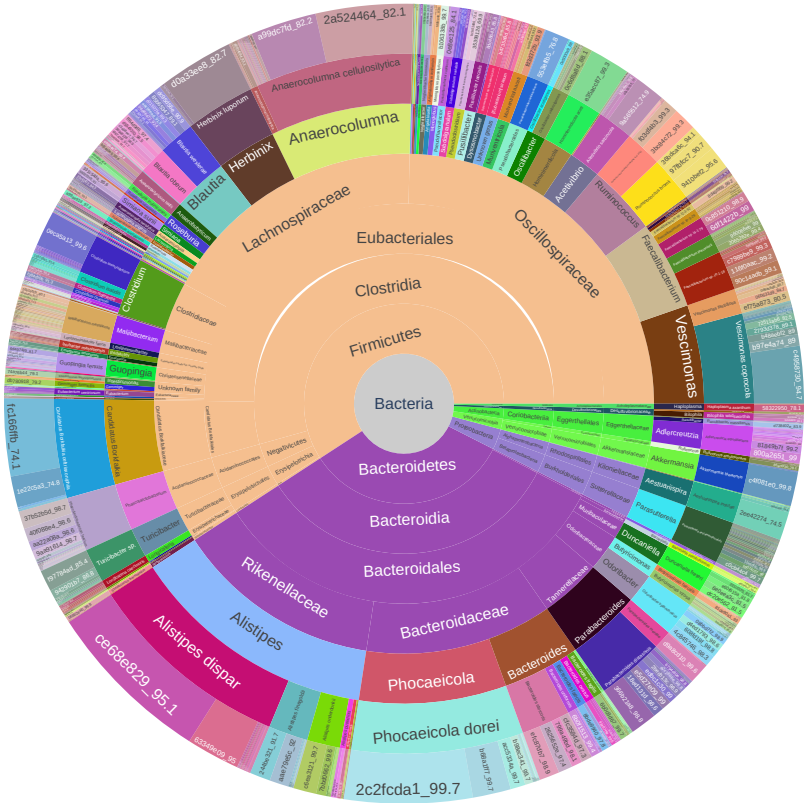
Review: 2 / 34 areas. **Worst: Beta Diversity**

Learn More: See "How To Use This Report" below.



Microbiome Composition

The target plot illustrates the individual microbiome composition at all levels, from phylum to strain. Each bacterial species has a specific number of genomic sequences. Therefore, the outermost part of the chart indicates the number assigned to each strain. It is also possible that the gut microbiome sample contains bacteria that have not yet been sequenced or are unknown. Microbiome profiles can be evaluated in terms of their richness, evenness, and peculiar composition immediately by looking at the graphic representation of the bacterial evolutionary tree.



Resilience & Biodiversity

- Alpha Diversity
- Richness
- Evenness
- **Beta Diversity**
- Firmicutes/Bacteroidetes (F/B) Ratio
- Fusobacteria
- Resistome Score
- Enterotype
- Proteobacteria
- Pathogens
- Top 10 Species

Summary:

Imbalance of bacterial distribution. Antibiotic Resistome score: good. Enterotype 1 - Bacteroides.

Suggestions:

- Biodiversity: Increase consumption of dietary fiber, fermented foods, polyphenols (powerful antioxidants found in fruits, vegetables, and whole grains), nuts, and seeds. Decrease sugars, animal-derived saturated fats, and artificial sweeteners. Maintain healthy weight (Body Mass Index).

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Beneficial Bacteria

- ☑ Probiotics
- ☑ Mucosa Protection
- ☑ Short-Chain Fatty Acids (SCFAs) Production

Summary:

Low Akkermansia muciniphila. Low Bifidobacterium spp. Low Lactobacillus spp.

Suggestions:

- Lactobacillus: Consider supplementing Lactobacillus with targeted probiotic.
- Bifidobacterium: Consider supplementing Bifidobacterium with targeted probiotic.
- Akkermansia: Increase intake of FOS and polyphenols. Decrease animal-derived saturated fat, alcohol. Consider Akkermansia supplementation in case of metabolic disorder(s).

Gut-Brain Axis

- ☑ Mood Disorders
- ☑ Alzheimer's Disease (AD) Risk
- ☑ Parkinson's Disease (PD) Risk
- ☑ Irritable Bowel Syndrome (IBS)

Summary:

Within typical range.

Gut-Gastrointestinal Axis

- ☑ Small Intestinal Bacterial Overgrowth (SIBO)
- ☑ Inflammatory Bowel Disease (IBD)
- ☑ Bile Acids (BAs) Metabolism

Summary:

Within typical range.

Gut-Metabolism Axis

- ☑ Obesity
- ⚠ Type 2 Diabetes (T2D)
- ☑ Non-Alcoholic Fatty Liver Disease (NAFLD)

Summary:

Imbalances detected in bacteria associated with: Type 2 Diabetes.

Suggestions:

- Type 2 Diabetes: Make sure diversity and distribution are well balanced and address overabundant species (see the list of the top ten bacteria and pathobionts). There may be a decrease in mucosa-protective bacteria, such as Akkermansia muciniphila and Faecalibacterium prausnitzii . It may be appropriate to consider Akkermansia supplements (if contraindications do not exist and if not already overabundant) or to focus solely on diet through fibers and anti-inflammatory foods. Lactobacillus spp. may be overabundant while Bifidobacterium species may be in low abundance (or vice versa). As a result, supplement carefully in accordance with the probiotics section. The supplementation of butyrate may help improve glycemic control.

Gut-Heart Axis

- ☑ Hypertension (HTN)
- ☑ Atherosclerosis
- ☑ Trimethylamine (TMA) Production

Summary:

Within typical range.

Gut-Immune Axis

- ☑ Lipopolysaccharide (LPS) Production
- ☑ Histamine Production
- ☑ Eczema & Atopic Dermatitis

Summary:

Within typical range.

Nutrient and Dietary Component Metabolism

- ☑ FODMAP Sensitivity Score
- ☑ FODMAP Fermentation
- ☑ Indole Production
- ☑ Vitamin B Production

Summary:

Within typical range.

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Resilience & Biodiversity

Alpha Diversity

Index of a microbiome's resilience and diverse composition, also known as Shannon Index. Higher values are generally associated with better resilience potential.

Value: **52.42**

Typical Range: **6.22 - 12.44**

Richness

Index referring to the number of unique species present within a sample.

Value: **140.00**

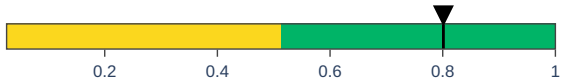
Typical Range: **32.00 - 64.00**

Evenness

Index referring to the distribution of species identified in a microbiome sample. Values closer to 1 indicate a more desirable, even distribution.

Value: **0.80**

Typical Range: **0.51 - 1.00**

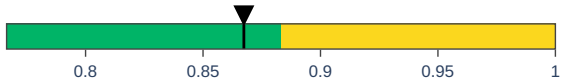


Beta Diversity

Index quantifying how different a microbial community is to the reference population, with values closer to 0 representing more similarity.

Value: **0.87**

Typical Range: **0.77 - 0.88**

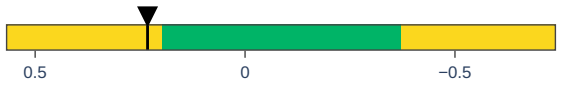


Firmicutes/Bacteroidetes (F/B) Ratio

Negative scores correspond to Bacteroidetes dominance, and positive scores correspond to Firmicutes dominance. A balanced F/B ratio is associated with intestinal homeostasis.

Value: **0.23**

Typical Range: **-0.37 - 0.20**



Fusobacteria

Bacterial species that may become opportunistic pathogens, most commonly found in the mouth. If detected in the gut, they may be associated with intestinal inflammation, IBS, IBD and chronic diseases.

Value: **0.00**

Typical Range: **0.00 - 0.02**

Resistome Score

This score includes the number and types of bacteria that are likely to contain antibiotic-resistant genes, which may play a role in spreading antibiotic resistance. It is important to note that this indicator compares the relative abundance of species associated with antibiotic-resistant genes and does not sequence these genes directly.

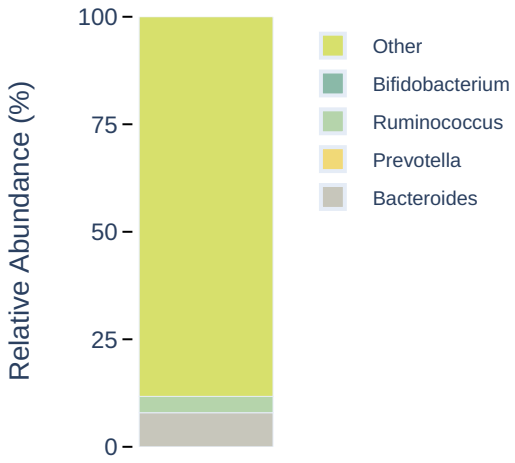
Value: **1.28**

Typical Range: **0.00 - 3.92**

Enterotype

In microbiome research, enterotypes serve as a classification method for identifying particular clusters of microbial species that tend to be more prevalent: Bacteroides (Type 1) is most likely to be observed in individuals consuming a diet high in protein and animal fat, Prevotella (Type 2) is usually associated with a plant based diet rich in carbohydrates and simple sugars, whereas Ruminococcus (Type 3) is found in individuals consuming a diet rich in complex carbohydrates, fruits, and vegetables. Bifidobacterium-dominant enterotypes (Type 4) have also been observed, though their significance is unclear.

Value:
Bacteroides



Proteobacteria

Bacterial species that may exhibit toxic and pathogenic mechanisms of action including lipopolysaccharide (LPS) and endotoxin synthesis and promote gastrointestinal and systemic inflammation. They are strongly associated with IBS, SIBO, IBD and immune dysregulation.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		3.35	0.26 - 15.74	
	Parasutterella excrementihominis	1.94	0 - 5.11	
	Aestuariispira insulae	1.37	0 - 0.32	high
	Bradyrhizobium tropiciagri	0.04	Not Established	high

Pathogens

Bacterial species that may cause severe gastrointestinal symptoms and be associated with intestinal or systemic chronic illnesses.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		1.07	0.0 - 9.92	
	Bacteroides fragilis	0.43	0 - 0.02	high
	Bilophila wadsworthia	0.32	0 - 0.5	
	Clostridium chauvoei	0.23	0 - 0.04	high
	Desulfovibrio desulfuricans	0.10	0	high

Top 10 Species

An indication of the overall composition of a microbiome can be obtained from a list of the ten most abundant species. The F/B ratio, enterotype, and alpha diversity index alone cannot determine which species are overabundant. A review of the top 10 can very quickly reveal the presence of potential pathobionts or an overabundance of certain species.

Species	Relative Abundance (%)	Reference Range (%)	Flag
Alistipes dispar	9.53	0.05 - 7.87	high
Phocaeicola dorei	7.93	0.08 - 42.48	
Anaerocolumna cellulosilytica	7.24	0.03 - 2.99	high
Candidatus Borkfalkia ceftriaxoniphila	4.57	0.02 - 6.51	
Vescimonas coprocola	4.16	0.06 - 1.46	high
Herbinix luporum	3.22	0.03 - 1.2	high
Parabacteroides distasonis	3.11	0.08 - 3.17	
Phascolarctobacterium faecium	2.53	0.54 - 8.91	
Bacteroides stercoris	2.26	0.05 - 2.35	
Ruminococcus bromii	2.07	0.1 - 4.71	

Beneficial Bacteria

Probiotics

Well-characterized bacterial species and strains that can either be ingested via supplements and/or foods or occur naturally in the human gut.

Probiotic	Species	Relative Abundance (%)	Reference Range (%)	Flag
Other	Overall	0.0	0.01 - 8.09	low
Akkermansia	Overall	0.0	0.11 - 25.68	low
Lactobacillus	Overall	0.0	0.02 - 2.6	low
Bifidobacterium	Overall	0.0	0.27 - 52.27	low
Akkermansia, Bifidobacterium, Lactobacillus, Other	None detected			

Mucosa Protection

Bacterial species that support normal gut barrier function. Abnormally low or high levels of these bacteria may lead to alterations in the intestinal mucosa and be associated with inflammation and immune dysregulation.

Protective Species	Species	Relative Abundance (%)	Reference Range (%)	Flag
Akkermansia	Overall	0.0	0.11 - 25.68	low
Faecalibacterium	Overall	0.89	0.21 - 6.49	
Faecalibacterium	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
Akkermansia	None detected			

Short-Chain Fatty Acids (SCFAs) Production

Anaerobic gut bacteria producing SCFAs such as acetate, propionate, and butyrate, which play a crucial role in maintaining gut and systemic health. A balanced presence of SCFA-producing bacteria is strongly associated with decreased inflammation, reduced risk of disease, and improved immune and metabolic function.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		4.44	1.56 - 50.15	
	Ruminococcus bromii	2.07	0.1 - 4.71	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Anaerobutyricum hallii	0.73	0.03 - 0.88	
	Roseburia inulinivorans	0.30	0.06 - 3.16	
	Roseburia intestinalis	0.23	0.05 - 1.42	
	Anaerostipes hadrus	0.15	0.04 - 1.25	
	Roseburia hominis	0.08	0.03 - 0.51	

Gut-Brain Axis

Mood Disorders

The neurotransmitters synthesized in the gut do not reach the brain directly (with the exception of GABA) but can affect the local nervous system or activate the vagus nerve, which relays these signals back to the brain. In addition, some intestinal bacteria produce precursors to neurotransmitters. Dopamine is a neurotransmitter promoting positive feelings of pleasure, reward, and motivation. Intestinal bacteria contribute to dopamine bioavailability in both enteric and central nervous systems by interfering with its metabolism. Imbalances in the abundance of these bacteria may impact dopaminergic pathways. Serotonin is a neurotransmitter modulating several neuropsychological and behavioral processes such as happiness, anger, appetite, memory, aggression, and sexuality. Several intestinal bacteria can produce or interfere with serotonin production. Therefore, imbalances in their abundance may alter the communication between the central and enteric nervous systems, contribute to emotional distress or cause local disturbances (e.g. abnormal GI motility). GABA is the main inhibitory neurotransmitter involved in controlling stress, fear, and anxiety. Intestinal bacteria are capable of producing and metabolizing GABA. As a result, imbalances in their abundance may alter the available level, thereby directly or indirectly affecting mental health issues such as anxiety or depression. Noradrenalin is both a neurotransmitter and a hormone involved in the so called “fight or flight response” as well as regulation of alertness, learning, energy, satiation and metabolism. In excess, it may cause anxiety and irritability. High levels in the gut may predispose to the colonization and infection of pathogens. Dysregulation in the production and metabolism from bacteria has been linked to depression and anxiety.

Neurotransmitter	Species	Relative Abundance (%)	Reference Range (%)	Flag
GABA	Overall	21.54	2.15 - 56.8	
Dopamine	Overall	0.14	0.09 - 11.34	
Serotonin	Overall	0.0	0.05 - 16.34	low
Noradrenaline	Overall	0.0	0.04 - 11.91	low
GABA	Alistipes dispar	9.53	0.05 - 7.87	high
	Parabacteroides distasonis	3.11	0.08 - 3.17	
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Alistipes finegoldii	1.82	0.06 - 3.68	
	Alistipes onderdonkii	1.53	0.08 - 4.54	
	Parabacteroides merdae	0.86	0.05 - 0.7	high
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Alistipes putredinis	0.26	0.14 - 1.6	
	Alistipes communis	0.16	0.03 - 0.23	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
	Alistipes shahii	0.08	0.09 - 1.69	low
	Alistipes indistinctus	0.02	0.03 - 0.54	low
Dopamine	Coprococcus catus	0.14	0.03 - 0.29	
Noradrenaline, Serotonin	None detected			

Alzheimer’s Disease (AD) Risk

Evidence suggests that changes in the composition and production of metabolites in the microbiome may be related to beta-amyloid and tau protein levels in the brain as well as neuroinflammation, all factors linked to AD risk. Bacteria-induced inflammation, both intestinal and systemic, has been hypothesized to be a significant contributor to AD pathogenesis.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		0.06	0.05 - 3.56	
	Thomasclavelia spiroformis	0.06	0.03 - 0.91	
Detrimental species		20.31	4.29 - 60.99	
	Alistipes dispar	9.53	0.05 - 7.87	high
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Alistipes finegoldii	1.82	0.06 - 3.68	
	Alistipes onderdonkii	1.53	0.08 - 4.54	
	Akkermansia biwaensis	1.43	0.08 - 17.93	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Eubacterium ventriosum	0.28	0.04 - 0.61	
	Alistipes putredinis	0.26	0.14 - 1.6	
	Alistipes communis	0.16	0.03 - 0.23	
	Coprococcus catus	0.14	0.03 - 0.29	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
	Alistipes shahii	0.08	0.09 - 1.69	
	Alistipes indistinctus	0.02	0.03 - 0.54	
Overall species balance		-20.25	-58.37 - -3.29	

Parkinson’s Disease (PD) Risk

Alteration in the microbiome diversity and distribution have been demonstrated to correlate with the risk of PD by affecting neuroinflammation and aggregation of alpha-synuclein. Furthermore, curli proteins synthesized in the gut may be a triggering factor. Bacteria-derived metabolites may also affect the risk.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		0.0	0.08 - 27.76	low
Detrimental species		0.0	0.24 - 50.83	
Overall species balance		0.0	-50.52 - -0.05	high

Irritable Bowel Syndrome (IBS)

Various types of bacteria and their metabolites may alter intestinal motility and affect the perception of visceral pain. It is possible that IBS symptoms are positively affected by adjusting the abundance and distribution of these bacteria. There is no doubt that the composition of the intestinal bacterial population is critically important in cases of post-infectious IBS. However, it should be noted that infections of the gastrointestinal tract (as well as a systemic infection) do not necessarily have to occur for this condition to be triggered.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		13.69	6.71 - 61.16	
	Ruminococcus bromii	2.07	0.1 - 4.71	
	Faecalibacterium sp. IP-1-18	1.82	0.06 - 2.69	
	Ruminococcus bicirculans [ex Wegman et al. 2014]	1.72	0.04 - 7.61	
	Blautia wexlerae	1.68	0.03 - 1.09	high
	Blautia obeum	1.29	0.02 - 0.57	high
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Faecalibacterium sp. I4-1-79	0.88	0.06 - 2.78	
	Anaerobutyricum hallii	0.73	0.03 - 0.88	
	Faecalibacterium sp. IP-3-29	0.48	0.09 - 2.32	
	Subdoligranulum variabile	0.47	0.08 - 2.46	
	Longicatena caecimuris	0.38	0.06 - 7.5	
	Faecalibacterium sp. I2-3-92	0.29	0.07 - 2.47	
	Fusicatenibacter saccharivorans	0.23	0.02 - 0.32	
	Anaerostipes hadrus	0.15	0.04 - 1.25	
	Faecalibacterium sp. HTF-F	0.13	0.04 - 1.32	
	Faecalibacterium sp. I3-3-33	0.13	0.07 - 3.07	
	Faecalibacterium sp. I4-3-84	0.10	0.1 - 3.95	low
	Dorea phocaeensis	0.09	0.03 - 1.53	
	Merdibacter massiliensis	0.07	0.05 - 2.16	
	Dorea formicigenerans	0.04	0.02 - 0.32	
	Blautia faecicola	0.02	0.01 - 0.09	
	Faecalibacterium sp. I3-3-89	0.02	0.06 - 2.12	low
Detrimental species		0.00	0.03 - 11.92	
Overall species balance		13.69	5.05 - 59.0	

Gut-Gastrointestinal Axis

Small Intestinal Bacterial Overgrowth (SIBO)

This test identifies specific bacteria that are typically observed in the aspirates obtained from the duodenum or jejunum of patients suffering from SIBO. An abnormal abundance of these bacteria in the colon and in the stool may suggest SIBO and warrant follow-up testing to confirm. Archaea causing Intestinal Methanogen Overgrowth (IMO) are not included.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		4.40	0.38 - 16.63	
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Streptococcus thermophilus	0.20	0.02 - 2.0	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
	Streptococcus sp. LPB0220	0.03	0.02 - 1.22	

Inflammatory Bowel Disease (IBD)

There is evidence that changes to the gut microbiome can occur before the onset of an IBD flare-up, and may be correlated with the severity and duration of symptoms during all phases of the disease. Intestinal bacteria and their metabolites may affect the intestinal epithelial barrier and mucosa health, inducing immune activation and inflammation. The subsequent increased intestinal permeability (IP) sustains the inflammatory responses and favors pathogens invasion.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		42.43	6.67 - 58.11	
	Anaerocolumna cellulosilytica	7.24	0.03 - 2.99	high
	Vescimonas coprocola	4.16	0.06 - 1.46	high
	Herbinix luporum	3.22	0.03 - 1.2	high
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Faecalibacterium sp. IP-1-18	1.82	0.06 - 2.69	
	Blautia wexlerae	1.68	0.03 - 1.09	high
	Acetivibrio saccincola	1.65	0.04 - 2.88	
	Hominimerdicola aceti	1.63	0.06 - 9.02	
	Blautia obeum	1.29	0.02 - 0.57	high
	Vescimonas fastidiosa	1.16	0.04 - 1.81	
	Pseudobacteroides cellulosolvens	1.02	0.06 - 3.09	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Faecalibacterium sp. I4-1-79	0.88	0.06 - 2.78	
	Oscillibacter valericigenes	0.77	0.05 - 1.08	
	Anaerobutyricum hallii	0.73	0.03 - 0.88	
	Muriventricola aceti	0.67	0.02 - 0.18	high
	[Eubacterium] siraeum	0.64	0.04 - 2.23	
	Pusillibacter faecalis	0.59	0.02 - 0.65	
	Pseudoclostridium thermosuccinogenes	0.56	0.05 - 3.4	
	Dysosmobacter sp. Marseille-Q4140	0.52	0.03 - 0.56	
	Faecalibacterium sp. IP-3-29	0.48	0.09 - 2.32	
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Subdoligranulum variabile	0.47	0.08 - 2.46	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Simiaoa sunii	0.42	0.02 - 0.32	high
	Pseudoflavonifractor capillosus	0.41	0.02 - 0.4	high
	Anaerocolumna chitinilytica	0.35	0.03 - 0.23	high
	Monoglobus pectinilyticus	0.31	0.03 - 0.58	
	Anaeromicropila herbilytica	0.30	0.02 - 0.27	high
	Roseburia inulinivorans	0.30	0.06 - 3.16	
	Angelakisella massiliensis	0.30	0.02 - 0.39	
	Faecalibacterium sp. I2-3-92	0.29	0.07 - 2.47	
	Neglectibacter timonensis	0.28	0.03 - 0.72	
	Lachnospira eligens	0.26	0.04 - 0.88	
	Oscillibacter acetigenes	0.26	0.03 - 0.66	
	Fusicatenibacter saccharivorans	0.23	0.02 - 0.32	
	Roseburia intestinalis	0.23	0.05 - 1.42	
	Brotolimicola acetigignens	0.21	0.03 - 0.23	
	Massiliimalia timonensis	0.16	0.02 - 0.37	
	Anaerostipes hadrus	0.15	0.04 - 1.25	
	Coprococcus catus	0.14	0.03 - 0.29	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
	Faecalibacterium sp. HTF-F	0.13	0.04 - 1.32	
	Faecalibacterium sp. I3-3-33	0.13	0.07 - 3.07	
	Agathobaculum butyriciproducens	0.12	0.02 - 0.57	
	Faecalibacterium sp. I4-3-84	0.10	0.1 - 3.95	low
	Dorea phocaeensis	0.09	0.03 - 1.53	
	Roseburia hominis	0.08	0.03 - 0.51	
	Dysosmobacter welbionis	0.08	0.02 - 0.57	
	Acetivibrio ethanolgignens	0.07	0.01 - 0.12	
	Anaerotignum faecicola	0.06	0.02 - 0.14	
	Anthropogastromicrobium aceti	0.06	0.03 - 0.66	
	[Eubacterium] rectale	0.06	0.03 - 0.56	
	Lacrimispora saccharolytica	0.05	0.03 - 0.23	
	Laedolimicola ammoniilytica	0.05	0.01 - 0.06	
	[Ruminococcus] lactaris	0.05	0.02 - 0.65	
	Caproiciproducens galactitolivorans	0.05	0.01 - 0.12	
	Fumia xinanensis	0.05	0.03 - 0.1	
	Solibaculum mannosilyticum	0.05	0.05 - 1.61	
	Dorea formicigenerans	0.04	0.02 - 0.32	
	Lachnoclostridium sp. YL32	0.03	0.01 - 0.08	
	[Ruminococcus] gnavus	0.03	0.02 - 1.4	
	Flavonifractor plautii	0.03	0.02 - 0.41	

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
	Merdimmobilis hominis	0.03	0.01 - 0.1	
	Porcipelethomonas ammoniilytica	0.03	0.04 - 0.6	low
	Blautia faecicola	0.02	0.01 - 0.09	
	Enterocloster bolteae	0.02	0.02 - 0.45	low
	Gallintestinimicrobium propionicum	0.02	0.02 - 0.36	low
	Roseburia rectibacter	0.02	0.02 - 0.21	
	Faecalibacterium sp. I3-3-89	0.02	0.06 - 2.12	low
	Qingrenia yutianensis	0.02	0.03 - 0.59	low
	Ruthenibacterium lactatiformans	0.02	0.02 - 0.44	
Detrimental species		7.14	0.89 - 26.73	
	Ruminococcus bromii	2.07	0.1 - 4.71	
	Parasutterella excrementihominis	1.94	0.08 - 10.01	
	Ruminococcus bicirculans [ex Wegman et al. 2014]	1.72	0.04 - 7.61	
	Aestuariispira insulae	1.37	0.06 - 4.56	
	Bradyrhizobium tropiciagri	0.04	Not Established	high
Overall species balance		35.29	-11.85 - 49.18	

Bile Acids (BAs) Metabolism

The abundance of BAs-metabolizing bacteria can negatively affect symptoms in IBS and IBD, particularly when increasing intestinal motility in patients with IBS-D. Clostridium spp and their metabolites can upregulate BAs secretion. Secondary BAs, however, usually exert an anti-inflammatory effect. Therefore, balancing the abundance and type of BAs-metabolizing bacteria may help address motility, mucosal, and inflammatory issues. Note: the abundance of BAs-metabolizing bacteria should also be considered in several other conditions such as obesity, metabolic syndrome and neurodegenerative disorders.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Overall		17.30	6.33 - 66.16	
	Phocaeicola dorei	7.93	0.08 - 42.48	
	Parabacteroides distasonis	3.11	0.08 - 3.17	
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Parabacteroides merdae	0.86	0.05 - 0.7	high
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Subdoligranulum variabile	0.47	0.08 - 2.46	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Lachnospira eligens	0.26	0.04 - 0.88	
	Roseburia intestinalis	0.23	0.05 - 1.42	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
	Hungatella hathewayi	0.07	0.01 - 0.12	
	[Ruminococcus] lactaris	0.05	0.02 - 0.65	
	Dorea formicigenerans	0.04	0.02 - 0.32	
	[Ruminococcus] gnavus	0.03	0.02 - 1.4	
	Eggerthella lenta	0.02	0.02 - 0.94	
	Enterocloster bolteae	0.02	0.02 - 0.45	low
	Alistipes indistinctus	0.02	0.03 - 0.54	low

Gut-Metabolism Axis

Obesity

Individuals affected by obesity have a different microbiome composition than those with a normal weight. There may be an increase in F/B ratio (but not necessarily) while specific species may contribute to hypertension, metabolic syndrome, impaired insulin response, and low HDL-cholesterol levels. Further, pathobionts may induce pro-inflammatory cytokines, increase intestinal permeability, and cause endotoxemia, which all contribute to obesity's vicious cycle.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		13.00	5.99 - 65.05	
	Phocaeicola dorei	7.93	0.08 - 42.48	
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
Detrimental species		1.25	0.84 - 33.52	
	Roseburia inulinivorans	0.30	0.06 - 3.16	
	Eubacterium ventriosum	0.28	0.04 - 0.61	
	Roseburia intestinalis	0.23	0.05 - 1.42	
	Streptococcus thermophilus	0.20	0.02 - 2.0	
	Dorea phocaeensis	0.09	0.03 - 1.53	
	Roseburia hominis	0.08	0.03 - 0.51	
	Dorea formicigenerans	0.04	0.02 - 0.32	
	Streptococcus sp. LPB0220	0.03	0.02 - 1.22	
	Roseburia rectibacter	0.02	0.02 - 0.21	
Overall species balance		11.74	-19.75 - 59.96	

Type 2 Diabetes (T2D)

By participating in the breakdown of complex carbohydrates and regulating inflammatory responses, specific bacteria and their metabolites may affect insulin signaling and glucose homeostasis. Some bacterial-mediated mechanisms are detrimental (e.g. low levels of secondary BAs that mediate insulin sensitivity), while others are beneficial (e.g. butyrate modulates GLP-1 ,GLP-2 and PYY secretion).

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		18.91	17.59 - 84.16	
	Phocaeicola dorei	7.93	0.08 - 42.48	
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Faecalibacterium sp. IP-1-18	1.82	0.06 - 2.69	
	Akkermansia biwaensis	1.43	0.08 - 17.93	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Faecalibacterium sp. I4-1-79	0.88	0.06 - 2.78	
	Faecalibacterium sp. IP-3-29	0.48	0.09 - 2.32	
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Roseburia inulinivorans	0.30	0.06 - 3.16	
	Faecalibacterium sp. I2-3-92	0.29	0.07 - 2.47	
	Roseburia intestinalis	0.23	0.05 - 1.42	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
	Faecalibacterium sp. HTF-F	0.13	0.04 - 1.32	
	Faecalibacterium sp. I3-3-33	0.13	0.07 - 3.07	
	Faecalibacterium sp. I4-3-84	0.10	0.1 - 3.95	low
	Roseburia hominis	0.08	0.03 - 0.51	
	Roseburia rectibacter	0.02	0.02 - 0.21	
	Faecalibacterium sp. I3-3-89	0.02	0.06 - 2.12	low
Detrimental species		9.88	0.3 - 26.79	
	Ruminococcus bromii	2.07	0.1 - 4.71	
	Clostridium ammoniilyticum	1.78	0.08 - 8.99	
	Ruminococcus bicirculans [ex Wegman et al. 2014]	1.72	0.04 - 7.61	
	Blautia wexlerae	1.68	0.03 - 1.09	high
	Blautia obeum	1.29	0.02 - 0.57	high
	Clostridium isatidis	0.52	0.02 - 0.64	
	Clostridium nigeriense	0.25	0.03 - 1.22	
	Clostridium chauvoei	0.23	0.02 - 0.69	
	Clostridium sp. C1	0.13	0.03 - 1.88	
	Clostridium sp. M62/1	0.12	0.01 - 0.17	
	Clostridium phoceensis	0.03	0.02 - 0.16	
	Clostridium sp. BNL1100	0.03	0.03 - 1.45	
	Blautia faecicola	0.02	0.01 - 0.09	
Overall species balance		9.02	-1.52 - 82.37	

Non-Alcoholic Fatty Liver Disease (NAFLD)

Animal studies have already found significative causative links between NAFLD and gut microbiome. Although human studies are more recent, they indicate that specific bacteria, especially potential pathogens like Proteobacteria, Clostridium, and Escherichia spp., are involved in the pathogenesis of the disease. The most significant bacterial-related factors are altered levels of TMAO, BAs, and SCFAs.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		6.60	4.0 - 58.01	
	Faecalibacterium sp. IP-1-18	1.82	0.06 - 2.69	
	Akkermansia biwaensis	1.43	0.08 - 17.93	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Faecalibacterium sp. I4-1-79	0.88	0.06 - 2.78	
	Faecalibacterium sp. IP-3-29	0.48	0.09 - 2.32	
	Faecalibacterium sp. I2-3-92	0.29	0.07 - 2.47	
	Eubacterium ventriosum	0.28	0.04 - 0.61	
	Coprococcus catus	0.14	0.03 - 0.29	
	Faecalibacterium sp. HTF-F	0.13	0.04 - 1.32	
	Faecalibacterium sp. I3-3-33	0.13	0.07 - 3.07	
	Faecalibacterium sp. I4-3-84	0.10	0.1 - 3.95	low
	Faecalibacterium sp. I3-3-89	0.02	0.06 - 2.12	low
Detrimental species		8.32	0.76 - 22.2	
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Ruminococcus bromii	2.07	0.1 - 4.71	
	Ruminococcus bicirculans [ex Wegman et al. 2014]	1.72	0.04 - 7.61	
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Streptococcus thermophilus	0.20	0.02 - 2.0	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
	Dorea phocaeensis	0.09	0.03 - 1.53	
	Dorea formicigenerans	0.04	0.02 - 0.32	
	Streptococcus sp. LPB0220	0.03	0.02 - 1.22	
Overall species balance		-1.71	-9.69 - 49.02	

Gut-Heart Axis

Hypertension (HTN)

Intestinal bacteria and their metabolites contribute to blood pressure (BP) regulation through several mechanisms, including SCFAs production that influences circadian cycles and host internal clocks and gaseous signaling molecules such as nitric oxide and hydrogen sulfide, which have vasodilator effects. Bioactive peptides derived from bacteria may also have anti-inflammatory and blood pressure lowering effects. Specific bacteria confer both positive and negative effects on BP.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		8.98	0.8 - 18.07	
	Ruminococcus bromii	2.07	0.1 - 4.71	
	Ruminococcus bicirculans [ex Wegman et al. 2014]	1.72	0.04 - 7.61	
	Adlercreutzia equolifaciens	1.37	0.08 - 1.85	
	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
	Oscillibacter valericigenes	0.77	0.05 - 1.08	
	Subdoligranulum variabile	0.47	0.08 - 2.46	
	Roseburia inulinivorans	0.30	0.06 - 3.16	
	Eubacterium ventriosum	0.28	0.04 - 0.61	
	Oscillibacter acetigenes	0.26	0.03 - 0.66	
	Roseburia intestinalis	0.23	0.05 - 1.42	
	Intestinimonas butyriciproducens	0.23	0.02 - 0.32	
	Coprococcus catus	0.14	0.03 - 0.29	
	Intestinimonas timonensis	0.12	0.04 - 1.31	
	Roseburia hominis	0.08	0.03 - 0.51	
	Flavonifractor plautii	0.03	0.02 - 0.41	
	Roseburia rectibacter	0.02	0.02 - 0.21	
Detrimental species		24.94	3.73 - 43.77	
	Alistipes dispar	9.53	0.05 - 7.87	high
	Parabacteroides distasonis	3.11	0.08 - 3.17	
	Phascolarctobacterium faecium	2.53	0.54 - 8.91	
	Alistipes finegoldii	1.82	0.06 - 3.68	
	Blautia wexlerae	1.68	0.03 - 1.09	high
	Alistipes onderdonkii	1.53	0.08 - 4.54	
	Akkermansia biwaensis	1.43	0.08 - 17.93	
	Blautia obeum	1.29	0.02 - 0.57	high
	Parabacteroides merdae	0.86	0.05 - 0.7	high
	Barnesiella intestinihominis	0.26	0.04 - 0.76	
	Alistipes putredinis	0.26	0.14 - 1.6	
	Streptococcus thermophilus	0.20	0.02 - 2.0	
	Alistipes communis	0.16	0.03 - 0.23	
	Desulfovibrio desulfuricans	0.10	0.08 - 0.78	
	Alistipes shahii	0.08	0.09 - 1.69	
	Streptococcus sp. LPB0220	0.03	0.02 - 1.22	
	Christensenella timonensis	0.03	0.03 - 1.78	
	Blautia faecicola	0.02	0.01 - 0.09	
	Ruthenibacterium lactatiformans	0.02	0.02 - 0.44	
	Alistipes indistinctus	0.02	0.03 - 0.54	
Overall species balance		-15.95	-36.95 - 6.81	

Atherosclerosis

SCFAs-producing bacteria may be reduced in atherosclerosis, which negatively affect intestinal mucosa. Consequently, bacteria may translocate and produce toxins that trigger systemic and vascular inflammatory responses. It has been found that atherosclerotic plaques contain bacterial DNA. TMAO and LPS contribute significantly to vascular inflammation and oxidative stress at the site of atherosclerotic plaques.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		7.93	3.02 - 55.51	
	Phocaeicola dorei	7.93	0.08 - 42.48	
Detrimental species		0.23	0.08 - 19.28	
	Streptococcus thermophilus	0.20	0.02 - 2.0	
	Streptococcus sp. LPB0220	0.03	0.02 - 1.22	
Overall species balance		7.71	-7.87 - 50.62	

Trimethylamine (TMA) Production

Trimethylamine (TMA) is synthesized by gut bacteria such as Desulfovibrio, Proteobacteria, Clostridium etc. This molecule is produced by the intestinal bacterial transformation of dietary choline, L-carnitine and betaine. When formed in the gut, TMA is transported to the liver through the portal vein and oxidized into TMAO. The level of TMAO is considered an independent risk factor and predictor of cardiovascular diseases. TMAO can alter cholesterol metabolism and induce inflammation, platelet activation and endothelial dysfunction.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		3.17	0.08 - 9.76	
	Clostridium ammoniilyticum	1.78	0.08 - 8.99	
	Clostridium isatidis	0.52	0.02 - 0.64	
	Clostridium nigeriense	0.25	0.03 - 1.22	
	Clostridium chauvoei	0.23	0.02 - 0.69	
	Clostridium sp. C1	0.13	0.03 - 1.88	
	Clostridium sp. M62/1	0.12	0.01 - 0.17	
	Hungatella hathewayi	0.07	0.01 - 0.12	
	Clostridium phoceensis	0.03	0.02 - 0.16	
	Clostridium sp. BNL1100	0.03	0.03 - 1.45	

Gut-Immune Axis

Lipopolysaccharide (LPS) Production

The cell surface of most Gram-negative bacteria, such as Proteobacteria, contains LPS. In some cases, this glycolipid can even lead to a toxic reaction from the host due to its strong ability to elicit an immune response. Therefore, LPS is also referred to as an "endotoxin". Although the immune system must recognize LPS and mount a prompt response, a chronic or excessive immune activation is detrimental to the host. LPS-induced inflammation may increase intestinal and blood-brain-barrier permeability and trigger significant inflammatory and pro-oxidative reactions.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Detrimental species		0.0	0.11 - 15.33	

Histamine Production

Specific gut bacteria metabolize histidine contained in foods. Itchy skin, increased vasodilation (resulting in facial flashing, for example), runny nose, and headache are just a few of the unpleasant symptoms caused by high levels of histamine. It has also been suggested that histamine increases pain perception and may be associated with visceral hypersensitivity in IBS. The release of histamine by intestinal bacteria can affect immune responses at a variety of mucosal surfaces, even at distant sites such as the lungs.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		0.77	0.27 - 49.31	
	Butyricimonas virosa	0.47	0.07 - 1.16	
	Butyricimonas faecalis	0.31	0.03 - 0.44	
Detrimental species		0.82	0.19 - 10.72	
	Roseburia inulinivorans	0.30	0.06 - 3.16	
	Roseburia intestinalis	0.23	0.05 - 1.42	
	Streptococcus thermophilus	0.20	0.02 - 2.0	
	Roseburia hominis	0.08	0.03 - 0.51	
	Roseburia rectibacter	0.02	0.02 - 0.21	
Overall species balance		-0.05	-5.2 - 38.05	

Eczema & Atopic Dermatitis

Skin disorders are clearly linked to the intestinal microbiome, as demonstrated by the prevalence of certain dermatoses in GI conditions (e.g. psoriasis in IBD and rosacea in SIBO or H. Pylori). Damaged gut mucosa, low levels of SCFAs and high abundance of pathobionts such as Clostridium and Escherichia are some of mechanisms behind this connection.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		12.10	8.79 - 76.31	
	Phocaeicola dorei	7.93	0.08 - 42.48	
	Bacteroides stercoris	2.26	0.05 - 2.35	
	Bacteroides uniformis	0.48	0.07 - 2.19	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
Detrimental species		0.00	0.04 - 11.91	
Overall species balance		12.10	7.47 - 75.16	

Nutrient and Dietary Component Metabolism

FODMAP Sensitivity Score

This score assesses the potential response to foods high in FODMAP (fermentable oligosaccharides, disaccharides, monosaccharides, and polyols). An excessive representation of certain bacterial taxa and altered population dynamics may cause an increased sensitivity to foods high in FODMAPs as compared to the general population.

Value: **1.12**

Typical Range: **0.00 - 1.93**

FODMAP Fermentation

This list includes bacteria fermenting FODMAPs that create common undesirable symptoms. It is possible for the same species to ferment more than one type of FODMAP. Use this list to identify foods that are more likely to be problematic, but don't exclude entire categories of foods based on it.

Type of FODMAP	Species	Relative Abundance (%)	Reference Range (%)	Flag
FOS	Overall	5.29	1.81 - 50.61	
GOS	Overall	0.0	0.21 - 49.61	
Inulin	Overall	2.15	1.58 - 47.51	
Isomalt	Overall	0.23	0.22 - 49.88	
Lactose	Overall	0.0	0.25 - 50.59	
Xylitol	Overall	0.0	0.02 - 0.1	
Fructose	Overall	0.89	0.69 - 47.38	
Maltitol	Overall	0.0	0.25 - 50.59	
Mannitol	Overall	0.23	0.04 - 5.47	
Sorbitol	Overall	0.0	0.04 - 11.91	
FOS	Bacteroides stercoris	2.26	0.05 - 2.35	
	Bacteroides faecis	0.44	0.04 - 1.31	
	Bacteroides ovatus	0.43	0.03 - 1.15	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Bacteroides xylanisolvens	0.14	0.03 - 0.87	
Inulin	Roseburia inulinivorans	0.3	0.06 - 3.16	
	Anaerostipes hadrus	0.15	0.04 - 1.25	
	Roseburia hominis	0.08	0.03 - 0.51	
	Roseburia rectibacter	0.02	0.02 - 0.21	
FOS, Inulin	Bacteroides uniformis	0.48	0.07 - 2.19	
	Roseburia intestinalis	0.23	0.05 - 1.42	
Isomalt, Mannitol	Streptococcus thermophilus	0.2	0.02 - 2.0	
	Streptococcus sp. LPB0220	0.03	0.02 - 1.22	
FOS, Fructose, Inulin	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
GOS, Lactose, Maltitol, Sorbitol, Xylitol	None detected			

Indole Production

Indole produced by the bacterial metabolism of dietary tryptophan may have beneficial effects on intestinal mucosa and barrier functions. However, an excess of some indole-derived compounds (especially indoxyl sulfate) may have detrimental effects on kidney and intestinal cells. Additionally, indole and its metabolites may negatively affect behavior and brain function.

Category	Species	Relative Abundance (%)	Reference Range (%)	Flag
Beneficial species		7.37	0.6 - 46.15	
	Parabacteroides distasonis	3.11	0.08 - 3.17	
	Clostridium ammoniilyticum	1.78	0.08 - 8.99	
	Anaerobutyricum hallii	0.73	0.03 - 0.88	
	Clostridium isatidis	0.52	0.02 - 0.64	
	Bacteroides fragilis	0.43	0.03 - 1.55	
	Clostridium nigeriense	0.25	0.03 - 1.22	
	Clostridium chauvoei	0.23	0.02 - 0.69	
	Clostridium sp. C1	0.13	0.03 - 1.88	
	Clostridium sp. M62/1	0.12	0.01 - 0.17	
	Clostridium phoceensis	0.03	0.02 - 0.16	
	Clostridium sp. BNL1100	0.03	0.03 - 1.45	low

Vitamin B Production

Although vitamins produced in the gut are not a significant contributor to the host's nutritional needs, they can affect colon health and immune function. This list is not intended to identify vitamin deficiencies or suboptimal intake, but to rebalance bacteria associated with their metabolism.

Type of Vitamin B	Species	Relative Abundance (%)	Reference Range (%)	Flag
1	Overall	0.47	0.04 - 26.9	
2	Overall	0.47	0.04 - 24.74	
3	Overall	0.47	0.04 - 28.1	
5	Overall	0.47	0.04 - 24.64	
6	Overall	0.43	0.21 - 57.14	
7	Overall	0.43	0.04 - 14.38	
9	Overall	0.62	0.07 - 24.42	
12	Overall	1.37	0.58 - 51.99	
9	Streptococcus thermophilus	0.2	0.02 - 2.0	
12	Faecalibacterium prausnitzii	0.89	0.21 - 6.49	
1, 2, 3, 5, 12	[Ruminococcus] lactaris	0.05	0.02 - 0.65	
1, 2, 3, 5, 6, 7, 9, 12	Bacteroides fragilis	0.43	0.03 - 1.55	

Quality Metrics

Sequencing Quality Control

This sample exceeds the minimum quality control standard of 10,000 sequencing reads per sample.

Processing Lab Director

Report Authorized By: **Kelly Lloyd, Lab Director, AveroDX**
CLIA# 50D2158817

Additional Information

Drug and Supplement Impact Table

Drug/Supplement	Main effects
Metformin hydrochloride	**Gut microbiota modulation:** increased abundance of Akkermansia, Bacteroides (especially *B. intestinalis*, *B. vulgatus*, and *B. acidifaciens),* Parabacteroides, Escherichia coli, *Bifidobacterium adolescentis*, Subdoligranulum.
PPIs	**Altered microbiota:** increased abundance of *Bifidobacterium dentium*, Streptococcus (especially *S.mutans*, *S. salivaris*, *S. parasanguinis*, *S. vestibularis*), *Veillonella parvula*. Increased risk of SIBO (increased abundance of Streptococcus, Clostridium, Escherichia, Klebsiella in small intestine). Increased risk of *C.difficile*, Salmonella, Shigella and Campylobacter infection. Increased abundance of oral bacteria in stool (i.e., *Fusobacterium nucleatum*).
Rifaximin	**Gut microbiota modulation:** overall eubiotic effect, increased abundance of Bifidobacterium, *Faecalibacterium prausnitzii and Lactobacillus,* decreased *C. difficile*
Statins	**Altered microbiota:** likely decreased diversity. They may cause increased abundance of Akkermansia and *F. prausnitzii*. Possible disturbances in SCFAs producing and BAs metabolizing bacteria. More human studies are needed.
L-thyroxine	**Altered microbiota:** likely contributor to SIBO. Possible alterations in abundance of Odoribacter and Enterococcus species (dose-dependent effect: higher abundance with medium dose, lower abundance with high dose of medication). Alistipes, Ruminococcus and Anaerotruncus species may result out of typical ranges.
Metronidazole	**Altered microbiota:** likely increased abundance of Bifidobacterium (especially *B. pseudolongum*) and Enterobacteria.
SSRI	**Altered microbiota:** increased abundance of *Eubacterium ramulus*. SSRIs in general have an antimicrobial effect. Long-term use may cause dysbiosis.
FOS (Fructooligosaccharides)	**Gut microbiota modulation:** increased abundance of Bifidobacterium and *F. prausnitzii*, decreased Proteobacteria.
Resveratrol	**Gut microbiota modulation:** inhibition of *E. coli* growth, *Enterococcus faecalis*. Increased abundance of Bifidobacterium and Lactobacillus.
Berberine chloride	**Gut microbiota modulation:** possible increased abundance of Akkermansia and SCFAs-producing bacteria in general. Decreased *Clostridium spp,* inhibition of *E. coli* growth. Microbiota conversion into dihydroberberine.

Food and Nutrient Impact Table

Foods, nutrients, diets	Main effects
Fibers	**Gut microbiota modulation:** in general, microbiota accessible carbohydrates (MAC) may increase microbial diversity and distribution as well as improve short chain fatty acid (SCFA) production by bacterial fermentation. Low abundance of beneficial species such as Akkermansia and/or Bifidobacterium may indicate an inadequate fiber intake. However, excess fiber intake, especially those high in FODMAPs may cause microbiota imbalances and exacerbate gastrointestinal symptoms such as gas, bloating, and abdominal pain. Extremely high fiber intake may decrease the absorption of key nutrients. Additionally, different types of fiber may promote specific modifications to intestinal bacterial composition: **-Inulin** (ex: dandelion greens, asparagus, onions, leeks, bananas, whole wheat) may increase Bifidobacterium spp, especially B. bifidum and F. prausnitzii **-Beta-glucans** (ex: oats, barley) may increase Bifidobacterium, Ruminococcus, Prevotella, Roseburia hominis, and other butyrate-producing bacteria as well as decrease Fusobacteria and Clostridium spp **-Resistant Starch** (ex: green banana, legumes, and potatoes, rice, and pasta that has been cooked and then cooled) may increase Bifidobacterium spp, Ruminococcus bromii, and F. prausnitzii
Polyphenols	**Gut microbiota modulation:** Polyphenols are metabolized by gut bacteria to positively affect microbiota composition, diversity, and distribution. Sources of polyphenols include berries, dark chocolate and pure cocoa powder, olives, extra virgin olive oil, green tea, black coffee, nuts, peanuts, seeds, and red wine. Adequate polyphenol intake may decrease the abundance of potential pathogens such as Clostridium spp and E. coli, promote LPS-induced inflammation, restore Lactobacillus and Bifidobacterium population, rebalance the F/B ratio, and increase mucosa protective bacteria such as Akkermansia and F. prausnitzii.
Nuts and seeds	**Gut microbiota modulation**: Nuts contain fiber, polyphenols, and healthy monounsaturated fatty acids (MUFAs) and act as a prebiotic that may promote a beneficial bacterial population. Adequate nut and seed intake is associated with improved bacterial diversity, reduced inflammation, and increased butyrate production. Almonds specifically have been shown to increase alpha diversity.
Fermented foods	**Gut microbiota modulation:** Consumption of fermented foods may lead to increased microbiome diversity and have a stronger effect than fiber alone. Additionally, adequate intake of fermented foods is associated with increased probiotic abundance, reduced inflammation, and improved microbiota-related immune function. Examples of fermented foods and specific modifications to bacterial composition and gastrointestinal function include: **-Kefir** may increase Lactobacillus spp and improve constipation **-Kombucha** may decrease abundance of pathogens such as E.coli and H.pylori **-Sauerkraut** may improve symptoms in all IBS subtypes **-Kimchi** my increase Lactobacillus **-Natto and Miso** may increase Bifidobacterium and decrease Enterobacteriaceae
Omega 3 and MUFAs	**Gut microbiota modulation:** Omega-3 fatty acids, found in fatty fish and nuts and seeds, may increase the abundance of butyrate-producing bacteria and probiotics such as Lactobacillus and Bifidobacterium spp. Furthermore, omega-3 may decrease LPS-induced inflammation. MUFAs, found in olive oil, avocado, nuts, and seeds may increase Bifidobacterium spp and favour Bacteroidetes over Firmicutes.
Supplements containing vitamins and minerals	**Gut microbiota modulation:** Effect of different supplement types depends on dosage, length of intervention, combination of nutrients, and genetic and epigenetic factors and may include: **-Vitamin D** may increase diversity, promote Akkermansia and Bifidobacterium spp, and decrease Proteobacteria abundance **-Iron** may increase Lactobacillus spp, which are dependent on iron availability. However, as excess iron intake may promote

Foods, nutrients, diets	Main effects
	inflammation, oxidative stress, and increased abundance of pathogenic bacteria, it is recommended to supplement only when a deficiency is identified.
Mediterranean Diet	**Gut microbiota modulation:** The MD is high in fiber, polyphenols, nuts and seeds, omega-3 fatty acids, and MUFAs. The MD may decrease the F/B ratio and abundance of Proteobacteria and increase abundance of beneficial bacteria such as probiotics, SCFA-producing bacteria, and mucosa-protective bacteria (as demonstrated in the PREDIMED study).
Ketogenic diet (KD)	**Gut microbiota modulation/ altered microbiota**: Effects of the KD depend on the health status of the host. KD may increase abundance of Akkermansia and decrease the F/B ratio. Given the very low intake of carbohydrates and fiber, a KD may also decrease probiotics species, particularly Bifidobacterium. KD may increase the abundance of pro-inflammatory Proteobacteria like Bilophila wadsworthia. While specific beneficial effects of a KD on refractory epilepsy and obesity may be mediated by positive changes in the microbiome composition, regular testing may be necessary to avoid negative intestinal bacterial imbalances.
Vegetarian and vegan diets	**Gut microbiota modulation/ possible alterations in microbiota**: High consumption of plant-based foods and fiber, a characteristic of vegetarian and vegan diets, may increase abundance of SCFA-producing bacteria, improve bacterial diversity, and decrease abundance of potential pathogens. However, sub-optimal intake of essential nutrients such as iron, omega-3, vitamin B12, and protein, associated with unbalanced and strict vegetarian and vegan diets, may negatively affect bacterial distribution and cause an overabundance of some species and should be monitored.
Artificial sweeteners	**Altered microbiota**: In general, artificial sweeteners may affect microbiome diversity. Acesulfame K, saccharine and sucralose consumption has been linked to decreased abundance of Akkermansia, though these results are controversial. Because research in this area is still early, it is not yet possible to draw conclusions about individual effects of artificial sweeteners on microbiome composition, which are likely dose-dependent and linked to duration of consumption.
Excess of sugars, saturated fats, salt and ultra-processed foods	**Altered microbiota**: The typical Western Diet (WD) is characterized by high intake of saturated fat, salt, and sugar and inadequate in fiber. The WD can negatively affect microbiome composition and may decrease microbial diversity, increase abundance of Proteobacteria and pathogens, and promote LPS biosynthesis. Specifically, excess saturated fat intake may decrease abundance of F.prausnitzii and increase abundance of species expressing bile acid hydrolases such as Clostridium, Alistipes, Bifidobacterium, and Lactobacillus spp. Furthermore, excessive salt intake may decrease Lactobacillus spp.
Alcohol	**Altered microbiota**: Chronic excessive alcohol intake may negatively affect bacterial diversity and distribution, increase abundance of Proteobacteria, and promote intestinal inflammation and IBS-related symptoms. However, moderate beer consumption, particularly if unpasteurized, has been demonstrated to exert some prebiotic effects due to polyphenolic compounds and melanoidins, which may increase Bifidobacterium spp and Akkermansia. Moderate consumption of red wine, which is also rich in polyphenols, may increase microbiota diversity. However, as alcohol has several known detrimental effects, non-alcoholic versions of beer and red wines should be consumed, if consumed at all.

Foods High In Specific FODMAPs

Type of FODMAP	Main food sources
Fructose	Monosaccharide found in high quantity in honey, dried fruits (for example raisins, dates, and figs), high fructose corn syrup, mango, watermelon, apple, pear, prunes, grapes, lychee, agave syrup, applesauce, and fruit juices.
Lactose	Disaccharide made of galactose and glucose found in high quantity in animal milk, cream, and some cheeses. Lactose reactions are individual, and some people may not have any problems eating moderate quantities of yogurt. Kefir is naturally very low in lactose. As a result of their processing, some hard cheeses may be better tolerated because their lactose content decreases (i.e. parmesan, gouda, provolone, brie, camembert). Fresh cheeses like ricotta, feta, mascarpone and spreadable cheeses, tend to be high in lactose.
FOS	Fructo-oligosaccharides found in high quantity in artichoke and Jerusalem artichoke, chicory, green bananas, leeks, onion, garlic, shallots, asparagus, yacon.
GOS	Galacto-oligosaccharides found in high quantity in legumes such as beans, lentils, soya and chickpeas, pistachios and cashew. Dairy products may contain some GOS.
Inulin	Mixture of oligo and polysaccharides, similar to FOS but with a longer and more polymerized structure (meaning with cross-links) found in high quantity in Jerusalem artichoke, dandelion, chicory, barley, burdock, stevia, garlic, agave.
Xylitol	Sugar alcohol that is normally used as a sweetener in chewing gum and sugar-free products. It is also naturally occurring in mushrooms, cauliflower, berries, corncob and husk and plant stalks. However, it tends to become problematic when used on its own as a sweetener.
Sorbitol	Sugar alcohol used as a sweetener in sugar-free products. It is naturally occurring in apple, dates, pear, apricots, prunes, raisins, peaches, nectarines, broccoli, fennel, red cabbage and aubergine.
Mannitol	Sugar alcohol used as a sweetener in sugar-free products. It also naturally occurring in mushrooms, pineapple, sweet potatoes, carrot, olives, asparagus, celery, snow peas, butternut squash.
Maltitol	Sugar alcohol used as a sweetener in sugar-free products. It is also naturally occurring in chicory leaves and roasted malt.
Isomalt	Sugar alcohol used as a sweetener derived from sugar beet. It does not naturally occur in foods.

Complete Microbiome Assessment FAQs

What is the Complete Microbiome Assessment (CMA)?

The CMA identifies all bacteria present in an individual microbiome down to the strain level. It is divided into sections that examine how specific bacteria and their abundance may influence a person's symptoms and predisposition to diseases. To facilitate interpretation and clinical actionability, the bacterial abundances are analyzed based on well-established indices like diversity and enterotypes, and also according to gut-axes. The presence of bacteria that may negatively impact both the intestinal and systemic health, such as Fusobacteria and Proteobacteria, is highlighted. Furthermore, two additional sections examine the abundance of beneficial bacteria and bacteria involved in the metabolism of certain nutrients.

Who should use the test?

The CMA is intended to assist clinicians in determining whether intestinal microbiome imbalances are underlying patients' complaints or predispose them to chronic conditions. The reference to diseases inside the gut-axes is not meant to diagnose but rather to illustrate a link between specific conditions or risk of developing them and a particular group of bacteria that are out of range.

How is the CMA score calculated?

The overall CMA score is calculated by applying proprietary algorithms that consider both the general features of the microbial population, including bacterial diversity, evenness of distribution, and phyla present in the sample, while also focusing on abundance of potentially pathogenic as well as beneficial bacteria. All measurements in an individual sample are compared to the reference population to generate a quantitative comparison. As a

result, scores are designed to indicate where an individual sample differs from the general population, providing guidance for following up with specific actions, rather than providing a diagnosis of disease.

What is the reference population?

The reference population is made up of a significant and expanding number of individuals who have been screened using the test. The reference population includes all samples tested by Intus Biosciences. The rationale for including all individuals in the reference population, regardless of self-reported health status and symptoms, is to better observe trends associated with health status. Furthermore, as samples are self-collected and health status information is self-reported, inclusion of all data accounts for errors and eliminates scientific assumption bias. As more sample data is compiled, reference population norms will be adjusted to reflect the most updated information, which may result in a slight change to the ranges included in the report. The highest and lowest percentiles are flagged as abnormal values.

What is the meaning of the detrimental, beneficial, and overall species balance?

Specific bacteria likely to be associated with a condition may positively or negatively contribute to it. Therefore, most of the bacteria under the gut axes are listed in terms of beneficial, detrimental, and overall species balance. Bacteria that are beneficial may have a positive effect on a given condition if they are present in a balanced abundance and in the correct amount. As a result, we do not want their total to be low. Conversely, other bacteria may negatively affect a disorder or risk of developing it, so we aim to keep them within a normal and not elevated range.

There are, however, some bacterial lists that do not include this distinction. If, for example, certain bacteria are known to be potentially problematic, such as pathogens, or if they can only have a negative impact on a condition, only the detrimental category will be displayed. In contrast, if a group of bacteria is known to generally contribute to the host's health, such as probiotics, only the beneficial category will be displayed.

If a list of bacteria can contribute to both directions, a total of detrimental, beneficial, and their balance is displayed. The sections are flagged in accordance with this balance or the overall abundance of "good" and "bad" species. It is important to note that in order to facilitate clinicians' interpretation and actionability of bacterial lists, even when a section has a "green tick" and is considered overall within a normal range, if any species has an abnormal abundance (too low or too high), it will be flagged.

What is more important: The score, or individual sections of the report?

The score represents the overall microbiome balance. You should, however, focus on the sections that have been flagged rather than just the individual score, if you are concerned about one or more specific conditions (or just as a preventative measure).

What does ‘Typical Range’ mean and may the range change?

Typical ranges represent the findings in the majority of the reference population. As the reference population expands, the typical ranges will change to become more refined and precise.

Who provides the test?

The test is provided by AveroDX, using technology under license from Intus Biosciences, LLC.

What technology generates the results?

The test is powered by the patented, high resolution and high throughput Intus Bio Titan-1™ platform. Titan-1™ uses the latest Next Generation Sequencing (NGS) Technology, with a ‘long’ target sequence of 16S-ITS and partial 23S. Visit intusbio.com for more information.

What makes the test unique?

Side by side analysis of different approaches has demonstrated that the Intus Bio technology is the most effective and accurate method for strain level identification of bacteria - see https://doi.org/10.1099/mgen.0.000794. This is the only test of its type benefiting from the power of the technology.

Are there any drugs, supplements or foods that drastically interfere with the test’s results?

Antibiotics and probiotics can significantly change the microbiota composition, although not necessarily in the long-term. We suggest waiting for a couple of weeks after completing a course of antibiotics before taking this test. If you are interested in monitoring the effects of a probiotic intervention, the patient may take the test while on the supplement or after completing treatment. We also recommend that patients follow their typical diet in the weeks preceding the test so that the results reflect average and normal food intake (no drastic changes in the diet or new foods should be introduced prior to the test).

How many times should a patient take this test?

It is strongly recommended to take a test before and after any intervention. Regular testing can help monitor the development of chronic diseases and evaluate the effectiveness of treatments over time.

Test Category Definitions

Resilience & Biodiversity

Alpha Diversity

Calculated using the Shannon Index, the alpha diversity score incorporates measures of richness and evenness and is an indicator of microbiome resilience. Resilience can be defined as how resistant the bacterial community is to changes that may push it out of its current state, such as after an infection, course of antibiotics, a long period of ill-health, or another stressor. In general, a healthy and well-balanced gut bacterial community should have many different species that are well-distributed, such that no one species is dominant. Therefore, highest resilience is achieved when richness and evenness are in balance.

Richness

The number of total bacterial species detected in the sample, higher richness values generally are generally associated with a healthier microbiome. In rare cases, however, the presence of several pathogenic species may result in a higher richness score, making it important to evaluate the types and abundance of bacterial species present, including potentially harmful pathogenic species.

Evenness

A measure of how well different bacterial species are distributed throughout the microbiome. Scores closer to 1 indicate a more desirable, even distribution while scores closer to 0 suggest one or more species may be dominant.

Beta diversity

Calculated using the Bray-Curtis dissimilarity, beta diversity compares how similar or different the sample is from the reference population. In general, it is better to have a bacterial composition closer to that of the reference population. A high beta diversity score may be an indicator of an unusual microbial profile, typically dominated by a single species. Although a sample may be different due to a high abundance of beneficial bacteria, gut-related symptoms are frequently associated with higher beta diversity scores.

Firmicutes/Bacteroidetes (F/B) ratio
These two bacterial phyla are the dominant types of bacteria present in the healthy adult human gut. The phyla are usually present at about equal amounts, and together they typically represent more than 90% of the entire bacterial community. The F/B ratio is a well-recognized marker of microbiome health and balance, and an unusual ratio can indicate a predisposition to certain diseases. For example, higher abundance of Firmicutes tends to be associated with obesity, while higher abundance of Bacteroidetes is more common in individuals suffering from Inflammatory Bowel Disease (IBD). However, this result should be considered within the context of overall health rather than used as a primary indicator.

Fusobacteria Percentage
Typically absent or in very low abundance in the lower digestive system, Fusobacteria are naturally occurring bacteria that colonize mucosal surfaces, especially in the oral cavity. Fusobacteria are mostly associated with periodontal disease and formation of biofilm. When found in the gut, however, it may indicate that an insufficient immune surveillance and/or low gastric acidity have allowed these bacteria to translocate from the mouth to the intestine, or that disrupted conditions in the gut are allowing Fusobacteria to thrive. High abundance of Fusobacteria in the gut may be an indicator of chronic inflammation and an increased risk of disease and some cancers, such as is the case with Fusobacterium nucleatum.

Resistome
The concept of resistome has been introduced quite recently and refers to the presence of antibiotic resistant genes (ARGs) in bacteria present in a specific environment that play a significant role in the spread of antibiotic resistance, a significant threat to health. Antibiotic resistance reduces the effectiveness of antibiotics, and as bacteria develop resistance to multiple antibiotics, it limits the available treatment options, making infections more severe, prolonged, and difficult to treat and may lead to complications, morbidity and mortality, as well as an increased burden on healthcare systems. Antibiotic resistant bacteria can be transferred between individuals, and antibiotic resistant genes can be transferred between bacteria, even across different species. This horizontal gene transfer allows the rapid spread of resistance within bacterial populations. This means that resistance can emerge in one location and quickly become a global problem. The "Resistome Score" measures the number and types of bacteria likely to harbor ARGs in this gut microbiome sample as compared to the samples in the reference database. Problematic species are common in the genera Escherichia, Klebsiella, and Enterococcus. These species have been found to harbor a large number of ARGs. Additionally, species belonging to the genera Bacteroides, Prevotella, and Streptococcus also contribute to the gut microbiome resistome.

Enterotype
The identification of intestinal enterotypes that may reflect an individual's typical diet was first proposed by Arumugam et al. in 2011. Even though this concept has evolved, many still recognize and stratify the human microbiome based on enterotypes, most notably Bacteroides and Prevotella. The Intus Bio research team has also identified a fourth possible enterotype dominated by Bifidobacterium spp. We are continuously gathering data to determine whether this enterotype is linked to a specific diet, medication and supplement use or predisposition to a particular condition.

Proteobacteria Percentage
Proteobacteria are gram-negative bacteria characterized by the presence of lipopolysaccharide (LPS) on the outer membrane, that may activate the immune system response and cause systemic inflammation. Common examples of Proteobacteria include Shigella, E. coli, Salmonella, Enterobacter, and Klebsiella. As emerging research suggests that not all Proteobacteria negatively affect health, this score takes into consideration both the overall abundance of Proteobacteria as well as the presence of highly-pathogenic species.

Pathogens
Although many common human pathogenic bacteria belong to the Proteobacteria phylum, there are species belonging to other phyla, such as Streptococcus, Staphylococcus and Clostridium from the Firmicutes phylum. While Firmicutes do not have LPS, they are often associated with GI and systemic conditions. It is important to note that a microbiome test is not intended to diagnose a bacterial infection. While detection of small amounts of pathogenic bacteria in the absence of symptoms may not be a cause for concern, chronic presence of a high pathogen abundance may indicate that the microbiome is providing a favorable environment for pathogens to thrive. Abundance of pathogenic bacteria may increase after a course of antibiotics, surgery, serious illness, and/or elevated stress levels. Additionally, unhealthy dietary patterns, such as diets high in saturated fats and sugars, may favor increased levels of pathogenic bacteria in the gut. The term pathobionts is sometimes used instead of pathogens. Pathogens are bacteria known to cause infections while pathobionts are bacteria that are potentially pathogenic under specific circumstances such as during immune system dysfunction.

Top 10 Species
No scientific study has demonstrated the utility of indicating the top 10 most abundant species within an individual microbiome. From a clinical standpoint, however, knowing the species that are more abundant and often over dominant may offer an effective starting point when deciding whether or not to intervene. Overabundant bacteria, regardless of whether they are commensal or probiotics, should prompt further investigation into how diet, pharmaceuticals, and/or supplements may be altering microbial balance. Furthermore, tracking the changes in the top 10 species over time may help determine the effectiveness of interventions.

Beneficial bacteria
Several intestinal bacterial species and strains confer protection and health benefits to the host by supporting gut mucosa permeability and barrier function, producing anti-microbial molecules such as bacteriocins, regulating GI motility, optimizing metabolic health, metabolizing xenobiotics, and modulating the local and systemic immune system. Contrary to common perception, probiotic bacteria are not the only beneficial gut micro-organisms, as other common commensal bacteria can protect the host from opportunistic pathogens and sustain overall health. However, all bacteria, even those deemed as beneficial, may become pathobionts by negatively affecting diversity if present in excessive abundance. This report analyses the presence and abundance of three distinct categories of beneficial bacteria: probiotics, mucosa protective bacteria, and short chain fatty acid (SCFA) producing bacteria.

Probiotics
According to the definition provided by the International Scientific Association for Probiotics and Prebiotics (ISAPP), the term probiotic should be applied only to “live microorganisms that, when administered in adequate amounts, confer a health benefit on the host”. Although certain gut commensals can be considered probiotic strains, these must be well-characterized and clearly demonstrated to be beneficial. If well-recognized probiotic species such as Lactobacillus and Bifidobacterium are detected in the sample, relative abundance is reported in the probiotic table. Akkermansia muciniphila is a fairly newly recognized probiotic that may confer metabolic health benefits and be imbalanced in individuals with type 2 diabetes, obesity and/or metabolic syndrome. However, as abnormally high levels of Akkermansia muciniphilia have been observed in those with autoimmune and neurodegenerative disorders, careful evaluation of probiotic abundance is important.

Probiotic Supplementation
Supplements containing specific strains of probiotics are increasingly being used by patients and providers. As probiotic strain(s), dose, and duration are individualized, supplementation should be overseen by a trained practitioner. If abnormally high levels of Lactobacilli, Bifidobacterium, and/or Akkermansia are detected, current pre- and probiotic supplements may need to be reevaluated. Probiotic abundance may also be affected by pharmaceutical drugs, as is seen with metformin, which may promote intestinal barrier function and the production of beneficial short chain fatty acid (SCFA) producing bacteria.

Mucosa Protective Bacteria
Mucosa protective bacteria, including Akkermansia muciniphila and Faecalibacterium prausnitzii, have been demonstrated to support a normal intestinal barrier function, regulate mucosal inflammation and act as “sentinels of the gut”. While several chronic diseases may be associated with a low abundance of these species, abnormally high levels may also be harmful. High abundance of Akkermansia muciniphila, for example, has been observed in some neurodegenerative and autoimmune disorders. It is possible that inflammatory conditions may increase mucosal protective bacteria abundance as a defensive response.

Short chain Fatty Acid (SCFA) Producing Bacteria

Dietary fiber is metabolized by SCFA-producing bacteria to generate acetate, propionate, and butyrate, which play an important role in metabolic health and regulation of the immune system. For example butyrate is the main energy supply for colonocytes and has been extensively studied for its antiproliferative effects due to epigenetic regulation via histone deacetylase activity. Moreover, SCFAs can influence bacterial gene expression and reduce virulence of intestinal pathogens. A very high level of a single species, although not necessarily cause for concern, should be evaluated as dietary patterns, pharmaceuticals and supplements may cause alterations in bacterial distribution.

The Gut-Axes

The gut axes sections are designed to assist clinicians and patients in identifying potential areas of concern more quickly. There is, however, some overlap between the interactions of specific bacteria and their metabolites with different body systems. The gut-axis ought to be considered as well as the individual metabolic pathway or bacterial-derived metabolites since they may affect multiple systems simultaneously. This test identifies the bacteria that can produce certain metabolites (e.g. SCFAs, secondary bile acids, TMA, neurotransmitters) or interfere with their function but does not quantify them.

Bile Acid (BA) Metabolizing Bacteria

BAs are synthesized from cholesterol in the liver and enter the intestine as conjugated BAs where they are converted into secondary BAs by intestinal bacteria. Several types of bacteria express BA-metabolizing enzymes, including Clostridium, Bacteroides and Listeria species as well as some Lactobacilli and Bifidobacterium. Secondary BAs affect enterochromaffin cells (EC) and levels of 5-hydroxytryptamine (5-HT, serotonin) causing increased visceral sensitivity and intestinal motility. Upregulation of intestinal serotonin availability leads to increased bowel peristalsis and may cause diarrhea in individuals predisposed to IBS-D. Moreover, Clostridium species can promote a higher liver biosynthesis of BAs and increase their secretion. There is evidence that almost 70% of patients with IBS-D have high fecal BAs or some form of BA malabsorption. The association between certain bacterial species metabolizing BAs and IBS symptoms is stronger for the diarrhea subtype, with increased BA production and secretion and corresponding increased intestinal serotonin. However, a decreased abundance or impaired distribution of BA metabolizing bacteria may cause constipation. Detection of an abnormal abundance in the main bacteria involved in BA metabolism may help personalize treatment by addressing underling dysbiosis with possible use of antibiotics and/or herbal supplements as well as evaluate other factors affecting BA production and absorption. Neurodegenerative disorders, metabolic disturbances, and colorectal cancer can also be affected by secondary BAs. It is therefore essential to monitor any abnormal abundance of BA-metabolizing bacteria.

Small Intestinal Bacterial Overgrowth (SIBO)

SIBO is a specific form of dysbiosis caused by high levels of specific bacteria in the small intestine. A variety of symptoms have been attributed to SIBO which may depend on the specific bacteria involved and may include excessive bloating, diarrhea, macronutrient malabsorption, and less commonly, constipation. Bacteria categories associated with SIBO include Proteobacteria, hydrogen-producing bacteria, and hydrogen-sulfite producing bacteria. Proteobacteria and hydrogen-producing bacteria may cause or exacerbate diarrhea in both IBS and SIBO, while hydrogen sulfide-producing bacteria may be associated with constipation and/or diarrhea, foul smelling stools, excessive gas and bloating, and may negatively affect gut barrier function and inflammation. This test measures the abundance of species that are commonly present in duodenal and/or jejunal aspirates of patients with SIBO (as demonstrated by the REIMAGINE study, 2019) and indicates if relative abundance of these species is higher than in the reference population. This test does not diagnose SIBO and detection of SIBO-associated bacteria may need to be followed-up with additional diagnostic testing.

FODMAP Sensitivity

FODMAPs are short-chain carbohydrates that are poorly absorbed in the small intestine and fermented in the colon by bacteria. Overabundance of FODMAP-fermenting bacteria may cause GI symptoms such as gas, bloating, abdominal pain, diarrhea and/or constipation. IBS and/or SIBO sufferers may be particularly sensitive to FODMAP-containing foods. Being aware of a potential FODMAP sensitivity can assist the practitioner in recommending and personalizing a low-FODMAP diet trial. However, as a low-FODMAP diet is highly restrictive, it should only be followed for a short period of time and overseen by a knowledgeable practitioner who can determine specific intolerances and liberalize the diet as much as tolerated.

References

Drug and Supplement Impact Table References

1. Bruno et al. (2019) **Proton pump inhibitors and dysbiosis: Current knowledge and aspects to be clarified**. *World Journal of Gastroenterology, 25*(22), 2706-2719.
2. Caparrós-Martín et al. (2017) **Statin therapy causes gut dysbiosis in mice through a PXR-dependent mechanism**. *Microbiome, 5*(1), 1-15.
3. Cheng et al. (2022) **Interactions between gut microbiota and berberine, a necessary procedure to understand the mechanisms of berberine**. *Journal of Pharmaceutical Analysis, 12*(4), 541-555.
4. Dias et al. (2020) **Gut bacterial microbiome composition and statin intake—A systematic review**. *Pharmacology Research & Perspectives, 8*(3), e00601.
5. Dou et al. (2022) **Effect of Fructooligosaccharides Supplementation on the Gut Microbiota in Humans: A Systematic Review and Meta-Analysis**. *Nutrients, 14*(16), 3298.
6. Ermolenko et al. (2022) **Metformin Influence on the Intestinal Microbiota and Organism of Rats with Metabolic Syndrome**. *International Journal of Molecular Sciences, 23*(12), 6837.
7. Li et al. (2020) **RapidAIM: A culture-and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs**. *Microbiome, 8*(1), 1-16.
8. Mahalak et al. (2023) **Fructooligosaccharides (FOS) differentially modify the in vitro gut microbiota in an age-dependent manner**. *Frontiers in Nutrition, 9*, 3212.
9. Nathwani et al. (2021) **Review of Rifaximin: A Summary of the Current Evidence and Benefits Beyond Licensed Use**. *EMJ, 6*(3), 94-99.
10. Ng et al. (2019) **A systematic review of the use of rifaximin for Clostridium difficile infections**. *Anaerobe, 55*, 35-39.
11. Pélissier et al. (2010) **Metronidazole effects on microbiota and mucus layer thickness in the rat gut**. *FEMS Microbiology Ecology, 73*(3), 601-610.
12. Ponziani et al. (2017) **Eubiotic properties of rifaximin: Disruption of the traditional concepts in gut microbiota modulation**. *World Journal of Gastroenterology, 23*(25), 4491–4499.
13. Silamiķele et al. (2021) **Metformin strongly affects gut microbiome composition in high-fat diet-induced type 2 diabetes mouse model of both sexes**. *Frontiers in Endocrinology, 12*, 626359.
14. Sjöstedt et al. (2021) **Serotonin Reuptake Inhibitors and the Gut Microbiome: Significance of the Gut Microbiome in Relation to Mechanism of Action, Treatment Response, Side Effects, and Tachyphylaxis**. *Frontiers in Psychiatry, 12*, 682868.
15. Vich Vila et al. (2020) **Impact of commonly used drugs on the composition and metabolic function of the gut microbiota**. *Nature Communications, 11*(1), 362.
16. Wang et al. (2022) **Resveratrol in Intestinal Health and Disease: Focusing on Intestinal Barrier**. *Frontiers in Nutrition, 9*, 848400.
17. Zhang et al. (2021) **Effects of Berberine on the Gastrointestinal Microbiota**. *Frontiers in Cellular and Infection Microbiology, 10*, 588517.
18. Zhang & Hu (2020) **Effects of Metformin on the Gut Microbiota in Obesity and Type 2 Diabetes Mellitus**. *Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 13*, 5003–5014.

Food, Nutrient, and Diet Impact Table References

19. Attaye et al. (2021) **The Role of the Gut Microbiota on the Beneficial Effects of Ketogenic Diets**. *Nutrients, 14*(1), 191.
20. Beane et al. (2021) **Effects of dietary fibers, micronutrients, and phytonutrients on gut microbiome: a review**. *Applied Biological Chemistry, 64*(1), 36.
21. Carlson et al. (2018) **Health Effects and Sources of Prebiotic Dietary Fiber**. *Current Developments in Nutrition, 2*(3).
22. Conz et al. (2023) **Effect of Non-Nutritive Sweeteners on the Gut Microbiota**. *Nutrients, 15*(8), 1869.
23. Creedon et al. (2020) **Nuts and their Effect on Gut Microbiota, Gut Function and Symptoms in Adults: A Systematic Review and Meta-Analysis of Randomised Controlled Trials**. *Nutrients, 12*(8), 2347.
24. Cronin et al. (2021) **Dietary Fiber Modulates the Gut Microbiota**. *Nutrients, 13*(5), 1655.
25. Dimidi et al. (2019) **Fermented Foods: Definitions and Characteristics, Impact on the Gut Microbiota and Effects on Gastrointestinal Health and Disease**. *Nutrients, 11*(8), 1806.
26. Dobranowski & Stintzi (2021) **Resistant starch, microbiome, and precision modulation**. *Gut Microbes, 13*(1), 1926842.
27. García-Montero et al. (2021) **Nutritional Components in Western Diet Versus Mediterranean Diet at the Gut Microbiota–Immune System Interplay. Implications for Health and Disease**. *Nutrients, 13*(2), 699.
28. Hanes et al. (2022) **The gastrointestinal and microbiome impact of a resistant starch blend from potato, banana, and apple fibers: A randomized clinical trial using smart caps**. *Frontiers in Nutrition, 9*.
29. Kok et al. (2022) **Predicting Personalized Responses to Dietary Fiber Interventions: Opportunities for Modulation of the Gut Microbiome to Improve Health**. *Annual Review of Food Science and Technology, 14*, 157-182.
30. Kumar Singh et al. (2019) **Beneficial Effects of Dietary Polyphenols on Gut Microbiota and Strategies to Improve Delivery Efficiency**. *Nutrients, 11*(9), 2216.
31. Leeuwendaal et al. (2022) **Fermented Foods, Health and the Gut Microbiome**. *Nutrients, 14*(7), 1527.
32. Machate et al. (2020) **Fatty Acid Diets: Regulation of Gut Microbiota Composition and Obesity and Its Related Metabolic Dysbiosis**. *International Journal of Molecular Sciences, 21*(11), 4093.
33. Muralidharan et al. (2021) **Effect on gut microbiota of a 1-y lifestyle intervention with Mediterranean diet compared with energy-reduced Mediterranean diet and physical activity promotion: PREDIMED-Plus Study**. *The American Journal of Clinical Nutrition, 114*(3), 1148-1158.
34. Newsome et al. (2023) **Western diet influences on microbiome and carcinogenesis**. *Seminars in Immunology, 67*, 101756.
35. Pham et al. (2021) **Vitamins, the gut microbiome and gastrointestinal health in humans**. *Nutrition Research, 95*, 35-53.
36. Ravindra Pal Singh & Bhardwaj (2023) **β-glucans: a potential source for maintaining gut microbiota and the immune system**. *Frontiers in Nutrition, 10*, 1143682.
37. Richardson & Frese (2022) **Non-nutritive sweeteners and their impacts on the gut microbiome and host physiology**. *Frontiers in Nutrition, 9*, 988144.
38. Rusu et al. (2020) **Iron Supplementation Influence on the Gut Microbiota and Probiotic Intake Effect in Iron Deficiency—A Literature-Based Review**. *Nutrients, 12*(7), 1993.
39. Singh et al. (2020) **The potential role of vitamin D supplementation as a gut microbiota modifier in healthy individuals**. *Scientific Reports, 10*, 21641.
40. Smiljanec & Lennon (2019) **Sodium, hypertension, and the gut: does the gut microbiota go salty?** *American Journal of Physiology. Heart and Circulatory Physiology, 317*(6), H1173–H1182.
41. Sugizaki & Naves (2018) **Potential Prebiotic Properties of Nuts and Edible Seeds and Their Relationship to Obesity**. *Nutrients, 10*(11), 1645.
42. Tomova et al. (2019) **The Effects of Vegetarian and Vegan Diets on Gut Microbiota**. *Frontiers in Nutrition, 6*(47).
43. Wang et al. (2022) **Dietary Polyphenol, Gut Microbiota, and Health Benefits**. *Antioxidants, 11*(6), 1212.
44. Wastyk et al. (2021) **Gut-microbiota-targeted diets modulate human immune status**. *Cell, 184*(16), 4137–4153.
45. Zugravu et al. (2023) **Beer and Microbiota: Pathways for a Positive and Healthy Interaction**. *Nutrients, 15*(4), 844.

Other References

46. Ahmad Al Samarraie et al. (2023) **Role of the Gut Microbiome in the Development of Atherosclerotic Cardiovascular Disease**. *International Journal of Molecular Sciences, 24*(6), 5420-5420.
47. Avery et al. (2021) **The Gut Microbiome in Hypertension**. *Circulation Research, 128*(7), 934-950.
48. Bardacke et al. (2023) **The Long-Term Effects of a Low–Fermentable Oligosaccharides, Disaccharides, Monosaccharides, and Polyols Diet for Irritable Bowel Syndrome Management**. *Current Developments in Nutrition, 7*(10), 101997.
49. Barlow & Mathur (2022) **Type 2 Diabetes and the Microbiome**. *Journal of the Endocrine Society, 7*(2), bvac184.
50. Bartolomaeus et al. (2019) **Short-Chain Fatty Acid Propionate Protects From Hypertensive Cardiovascular Damage**. *Circulation, 139*(11), 1407-1421.
51. Bleibel et al. (2023) **Deciphering psychobiotics' mechanism of action: bacterial extracellular vesicles in the spotlight**. *Frontiers in Microbiology, 14*.
52. Cantero et al. (2022) **Trimethylamine N-oxide reduction is related to probiotic strain specificity: A systematic review**. *Nutrition Research, 104*, 29-35.
53. Dior et al. (2016) **Interplay between bile acid metabolism and microbiota in irritable bowel syndrome**. *Neurogastroenterology and Motility: The Official Journal of the European Gastrointestinal Motility Society, 28*(9), 1330-1340.
54. Duranti et al. (2020) **Bifidobacterium adolescentis as a key member of the human gut microbiota in the production of GABA**. *Scientific Reports, 10*.
55. Evans et al. (2023) **The dietary source of trimethylamine N-oxide and clinical outcomes: an unexpected liaison**. *Ndt Plus, 16*(11), 1804-1812.
56. Gehrig et al. (2022) **Finding the right fit: evaluation of short-read and long-read sequencing approaches to maximize the utility of clinical microbiome data**. *Microbial Genomics, 8*(3).
57. Grabrucker et al. (2023) **Microbiota from Alzheimer's patients induce deficits in cognition and hippocampal neurogenesis**. *Brain, 146*(12).
58. Hamamah et al. (2022) **Role of Microbiota-Gut-Brain Axis in Regulating Dopaminergic Signaling**. *Biomedicines, 10*(2), 436.
59. Hill et al. (2014) **Expert consensus document. The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic**. *Nature Reviews. Gastroenterology & Hepatology, 11*(8), 506-514.
60. Hossain et al. (2022) **B Vitamins and Their Roles in Gut Health**. *Microorganisms, 10*(6), 1168.
61. Koponen et al. (2021) **Associations of healthy food choices with gut microbiota profiles**. *The American Journal of Clinical Nutrition, 114*(2), 605-616.
62. Leite et al. (2019) **Optimizing microbiome sequencing for small intestinal aspirates: validation of novel techniques through the REIMAGINE study**. *BMC Microbiology, 19*(1).
63. Li et al. (2019) **Effects of regulating gut microbiota on the serotonin metabolism in the chronic unpredictable mild stress rat model**. *Neurogastroenterology and Motility: The Official Journal of the European Gastrointestinal Motility Society, 31*(10), e13677.

64. Li et al. (2023) **Gut Barrier Dysfunction and Bacterial Lipopolysaccharides in Colorectal Cancer**. *Journal of Gastrointestinal Surgery, 27*(7), 1466-1472.

65. Li et al. (2021) **New Insights Into Gut-Bacteria-Derived Indole and Its Derivatives in Intestinal and Liver Diseases**. *Frontiers in Pharmacology, 12*.

66. Li et al. (2022) **Gut bacterial profiles in Parkinson's disease: A systematic review**. *World Journal of Psychiatry, 29*(1), 140-157.

67. Liccardo et al. (2020) **Potential Bidirectional Relationship Between Periodontitis and Alzheimer's Disease**. *Frontiers in Physiology, 11*(11).

68. Liu & Dai (2020) **Trimethylamine N-Oxide Generated by the Gut Microbiota Is Associated with Vascular Inflammation: New Insights into Atherosclerosis**. *Mediators of Inflammation, 2020*, 1-15.

69. Magne et al. (2020) **The Firmicutes/Bacteroidetes Ratio: A Relevant Marker of Gut Dysbiosis in Obese Patients?** *Nutrients, 12*(5), 1474.

70. Maini Rekdal et al. (2019) **Discovery and inhibition of an interspecies gut bacterial pathway for Levodopa metabolism**. *Science, 364*(6445), eaau6323.

71. Martín et al. (2013) **Role of commensal and probiotic bacteria in human health: a focus on inflammatory bowel disease**. *Microbial Cell Factories, 12*(1), 71.

72. Mazur et al. (2023) **The Intestinal and Skin Microbiome in Patients with Atopic Dermatitis and Their Influence on the Course of the Disease: A Literature Review**. *Healthcare, 11*(5), 766.

73. Mittal et al. (2017) **Neurotransmitters: The Critical Modulators Regulating Gut-Brain Axis**. *Journal of Cellular Physiology, 232*(9), 2359-2372.

74. Monteagudo-Mera et al. (2022) **Gamma aminobutyric acid production by commercially available probiotic strains**. *Journal of Applied Microbiology, 134*(2).

75. Naomi et al. (2021) **Probiotics for Alzheimer's Disease: A Systematic Review**. *Nutrients, 14*(1), 20.

76. Nikolaki et al. (2023) **The Low-FODMAP Diet, IBS, and BCFAs: Exploring the Positive, Negative, and Less Desirable Aspects—A Literature Review**. *Microorganisms, 11*(10), 2387-2387.

77. O'Donnell et al. (2023) **The gut microbiome and hypertension**. *Nature Reviews Nephrology, 19*.

78. Obrenovich et al. (2023) **Natural Product Co-Metabolism and the Microbiota–Gut–Brain Axis in Age-Related Diseases**. *Life, 13*(1), 41.

79. Onaolapo & Onaolapo (2021) **Glutamate and depression: Reflecting a deepening knowledge of the gut and brain effects of a ubiquitous molecule**. *World Journal of Psychiatry, 11*(7), 297-315.

80. Pferschy-Wenzig et al. (2022) **Medicinal Plants and Their Impact on the Gut Microbiome in Mental Health: A Systematic Review**. *Nutrients, 14*(10), 2111.

81. Pimentel et al. (2020) **ACG Clinical Guideline**. *The American Journal of Gastroenterology, 115*(2), 165-178.

82. Qiu et al. (2022) **The Gut Microbiota in Inflammatory Bowel Disease**. *Frontiers in Pharmacology*.

83. Romano et al. (2021) **Meta-analysis of the Parkinson's disease gut microbiome suggests alterations linked to intestinal inflammation**. *npj Parkinson's Disease, 7*(1).

84. Sánchez-Pérez et al. (2022) **The dietary treatment of histamine intolerance reduces the abundance of some histamine-secreting bacteria of the gut microbiota in histamine intolerant women: A pilot study**. *Frontiers in Nutrition, 9*.

85. Sarmiento-Andrade et al. (2022) **Gut microbiota and obesity: New insights**. *Frontiers in Nutrition, 9*.

86. Satish Kumar et al. (2022) **Probiotics in Irritable Bowel Syndrome: a Review of Their Therapeutic Role**. *Cureus, 14*(4).

87. Singh et al. (2023) **Desulfovibrio in the Gut: The Enemy within?** *Microorganisms, 11*(7), 1772.

88. Strandwitz (2018) **Neurotransmitter modulation by the gut microbiota**. *Brain Research, 1693*(Pt B), 128-133.

89. Varesi et al. (2022) **The Potential Role of Gut Microbiota in Alzheimer's Disease: From Diagnosis to Treatment**. *Nutrients, 14*(3), 668.

90. Vijayvargiya et al. (2018) **Bile Acid Deficiency in a Subgroup of Patients With Irritable Bowel Syndrome With Constipation Based on Biomarkers in Serum and Fecal Samples**. *Clinical Gastroenterology and Hepatology, 16*(4), 522-527.

91. Wallen et al. (2022) **Metagenomics of Parkinson's disease implicates the gut microbiome in multiple disease mechanisms**. *Nature Communications, 13*(1).

92. Yu et al. (2021) **Lactobacillus lactis and Pediococcus pentosaceus-driven reprogramming of gut microbiome and metabolome ameliorates the progression of non-alcoholic fatty liver disease**. *Clinical and Translational Medicine, 11*(12).

93. Zhai et al. (2022) **Probiotics Bring New Hope for Atherosclerosis Prevention and Treatment**. *Oxidative Medicine and Cellular Longevity, 2022*, 1-13.

94. Zhang et al. (2023) **Vitamin D alleviates non-alcoholic fatty liver disease via restoring gut microbiota and metabolism**. *Frontiers in Microbiology, 14*.

Disclaimers

This test is not intended to diagnose, treat, or cure any medical condition, and is offered for information and guidance only. The results and associated information should be interpreted exclusively by certified practitioners such as physicians, nutritionists, dietitians, clinicians, or similar professional figures who are, therefore, able to evaluate the report and implement changes in patients' diet, drugs, or supplements regime, if considered necessary by said practitioner. The companies and organizations providing this test and its affiliates shall not be held responsible for any misinterpretation or misapplication

This report is not derived from a culture-based microbiological test. Therefore, it is not intended to diagnose any bacterial infection. The presence of pathogens included in the report is calculated based on sequencing methods and expressed as percents of relative abundance. Beneficial commensal or probiotics are characterized and expressed in the same way.

This report only characterizes and analyses the bacterial species/strains that have been reported in the scientific literature to be strongly associated with functional gastrointestinal disorders. Consequently, if a patient suffers from disorders/diseases that are not influenced by these groups of bacteria, the score and the summary of results may not show any abnormalities. Conversely, patients affected by functional GI disorders may still have a normal or almost normal bacterial gut composition. In fact, the impact of bacterial dysbiosis may present with different degrees of severity in individuals. If no abnormalities are detected, the etiology of the patient's symptoms may not be linked to gut dysbiosis but some other causes (i.e., psychological distress).

The gut bacterial microbiome composition is highly dynamic and tends to be significantly affected by changes in diet, drugs, and supplements. Patients may have a normal intestinal score if they are already taking medication or supplementations that alter the gut microbiota. We strongly recommend taking this test before and after any significant intervention such as dietary changes and drugs/supplements introduction or discontinuation. The companies and organizations providing this test and its affiliates shall not be held responsible for any adverse reactions or consequences resulting from any changes made to the patient's diet, drugs, or supplements regime based on the results of this test.

This test is subject to regular revision and updates based on the most recently published scientific literature. It may, therefore, be possible that the scoring methodology, guidance and/or selection of bacterial species and strains that have been included in this report are not included in future reports. This is because bacteria relevant for Functional GI disorders change in accordance with the most recent evidence-based research and/or improvements in microbiome sequencing methods, resolution, and interpretation of results.

By using this test, the patient consents to the collection, use, and analysis of their anonymized data for scientific research and development purposes by the company providing the test and its affiliates. The company guarantees that any such data will be anonymized and will not be used for any other commercial purposes, nor will it be shared with any third parties without the explicit consent of the patient. The patient agrees to indemnify and hold harmless the company providing the test and its affiliates from any and all claims, liabilities, damages, expenses, and costs, including reasonable attorneys' fees, arising from the collection, storage, use, and analysis of their anonymized data for scientific research and development purposes.

The patient acknowledges that they have been provided with a disclaimer and the patient fully understands and accepts the risks associated with a misinterpretation and/or any limitations of this test. The patient agrees to release all the companies and organizations providing the test from any and all claims, liabilities, damages, expenses, and other losses arising out of or in connection with the use of this test or the results of this test or the storage and use of their data.