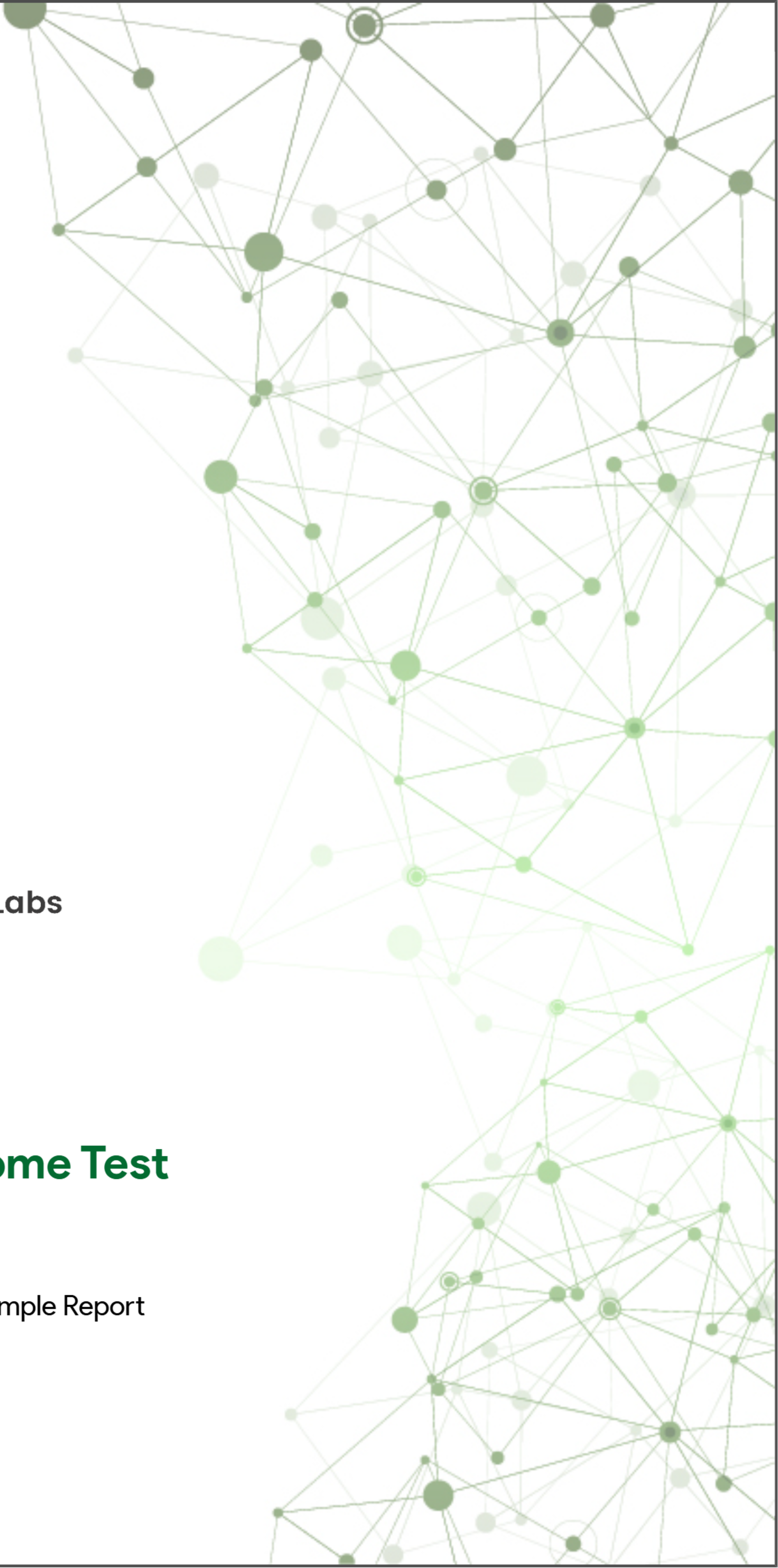

EverWell Labs

GI Axis

Gut Microbiome Test

Sample ID :

Patient Name : Example Report

Sample Date :

Test Report Index

After analysing thousands of microbes, YourGutMap's test report is broken down into three sections:

Module 1 = Gut Interaction Insights

A snapshot of how the current balance of the gut microbiome impacts health. This section contains colour coded dashboards and easy to understand graphs - to provide a detailed summary of the gut microbiome.

Module 2 = Microbial Analysis

Designed for health practitioners, this section explores the synergistic relationship between bacteria involved in 10 Gut Health Axes, and 20 Health Insights. With detailed explanations of roles and mechanisms of specific bacteria, more than 120 published studies to unlock these comprehensive gut health insights.

Module 3 = Unique Gut Based Nutrition Plan

Now that we have unlocked health insights based on the microbial balance, we can suggest tailored nutritional interventions to help naturally rebalance the gut microbiome.

Based on the concept of starving the bacteria that need to be reduced, and feeding that bacteria that need to be increased - we assess the nutritional breakdown of over 200 foods.

Considering fibres, polyphenols, micronutrients, and many other factors - we provide suggestions to change the diet to help take care of imbalances and overgrowths.

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Module 1

Gut Interaction Insights

Shannon Index

The Shannon Index is a widely used scientific measure that helps us understand the diversity of the gut microbiome.

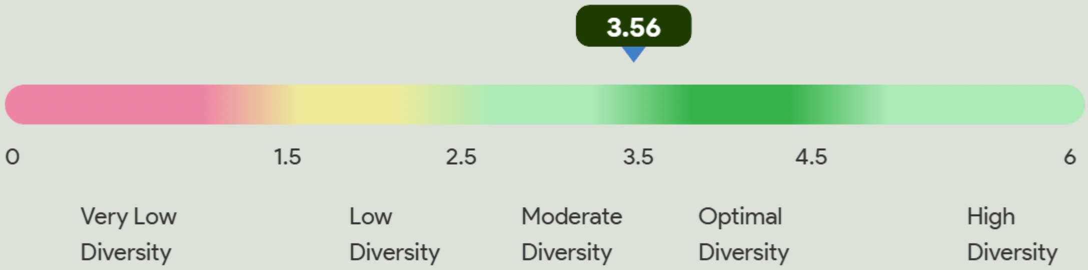
It takes into account not just how many different types of bacteria are present, but also how evenly they are distributed. A higher Shannon score generally means the gut has a richer and more balanced community of bacteria, which is often linked in published research to better resilience, digestion, and overall health

This section shows the specific diversity score. Subsequent sections of the report will breakdown what the bacteria balance means for specific health conditions and health goal

Microbiome Diversity - Shannon Index

Your Score

3.56



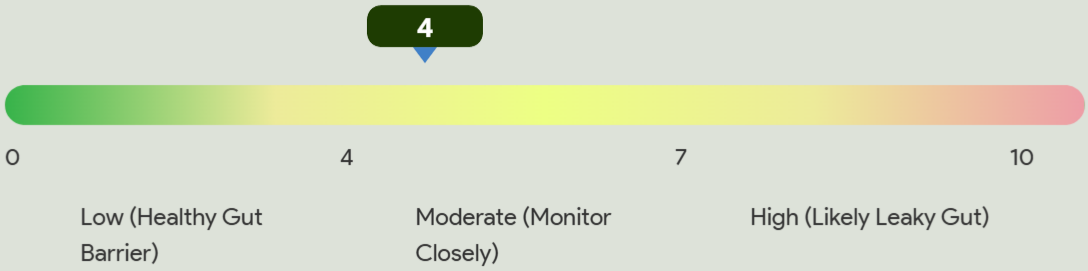
Intestinal Permeability index

The Intestinal Permeability Index measures how well the gut barrier prevents harmful substances from entering the bloodstream. A high index suggests a healthy barrier, while a low index may indicate a "leaky gut" and risk of inflammation.

Microbiome Diversity - Intestinal Permeability index

Your Score

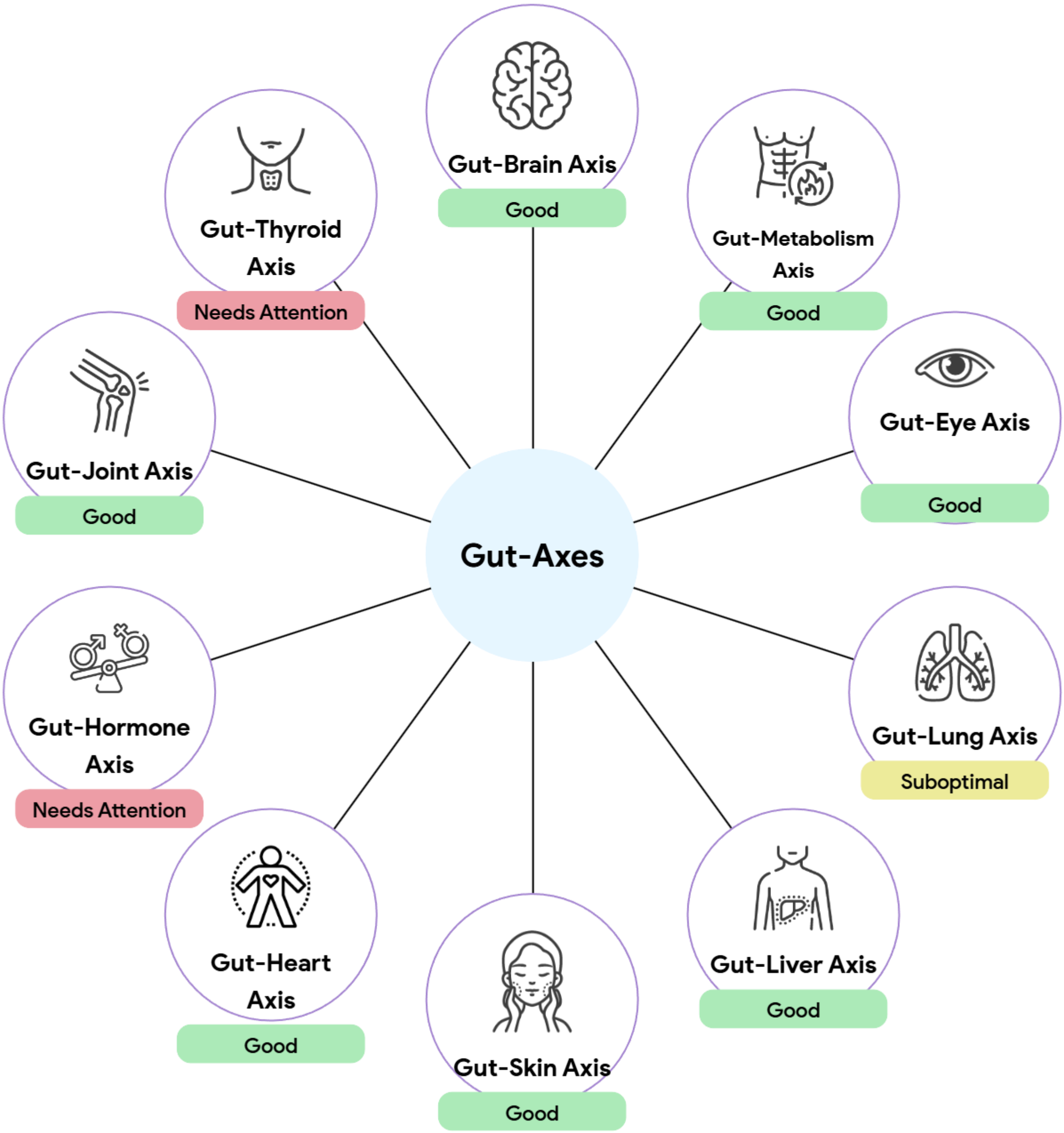
4



Gut-Axes Dashboard

The gut doesn't just digest food - it also communicates with key systems throughout the body. These communication pathways are known as gut axes. The gut axes dashboard considers all of the individual bacteria that are involved in the specific gut axis, both those bacteria that have a beneficial effect, and those that can have negative effects as well.

Good	The bacteria balance is at an optimal level for the specific gut axis
Suboptimal	Some of bacteria levels show signs of imbalances for the specific gut axis
Needs Attention	The bacteria levels identified are imbalanced for the specific gut axis



Gut Interaction Insights Dashboard

Based on the unique balance of bacteria in the gut, we've identified 20 key health insights that may be relevant to your overall well-being. These insights are drawn from the latest clinical research and reflect how specific bacteria in the microbiome are linked to various aspects of health.

Good	The bacteria balance is at an optimal level for the specific area of health
Suboptimal	Some of bacteria levels show signs of imbalances for the specific area of health
Needs Attention	The bacteria levels identified are imbalanced for the specific area of health

SCFA Producers
Suboptimal

Inflammation Index
Good

Immunity
Suboptimal

Histamine Index
Good

Protein Absorption
Needs Attention

Carbohydrate Absorption
Good

Fat Absorption
Good

Micronutrient Absorption
Needs Attention

Bowel Habits
Good

Fitness
Good

Mood & Mental Health
Suboptimal

Autoimmunity
Good

Detoxification
Suboptimal

Stress Resilience
Good

Longevity
Good

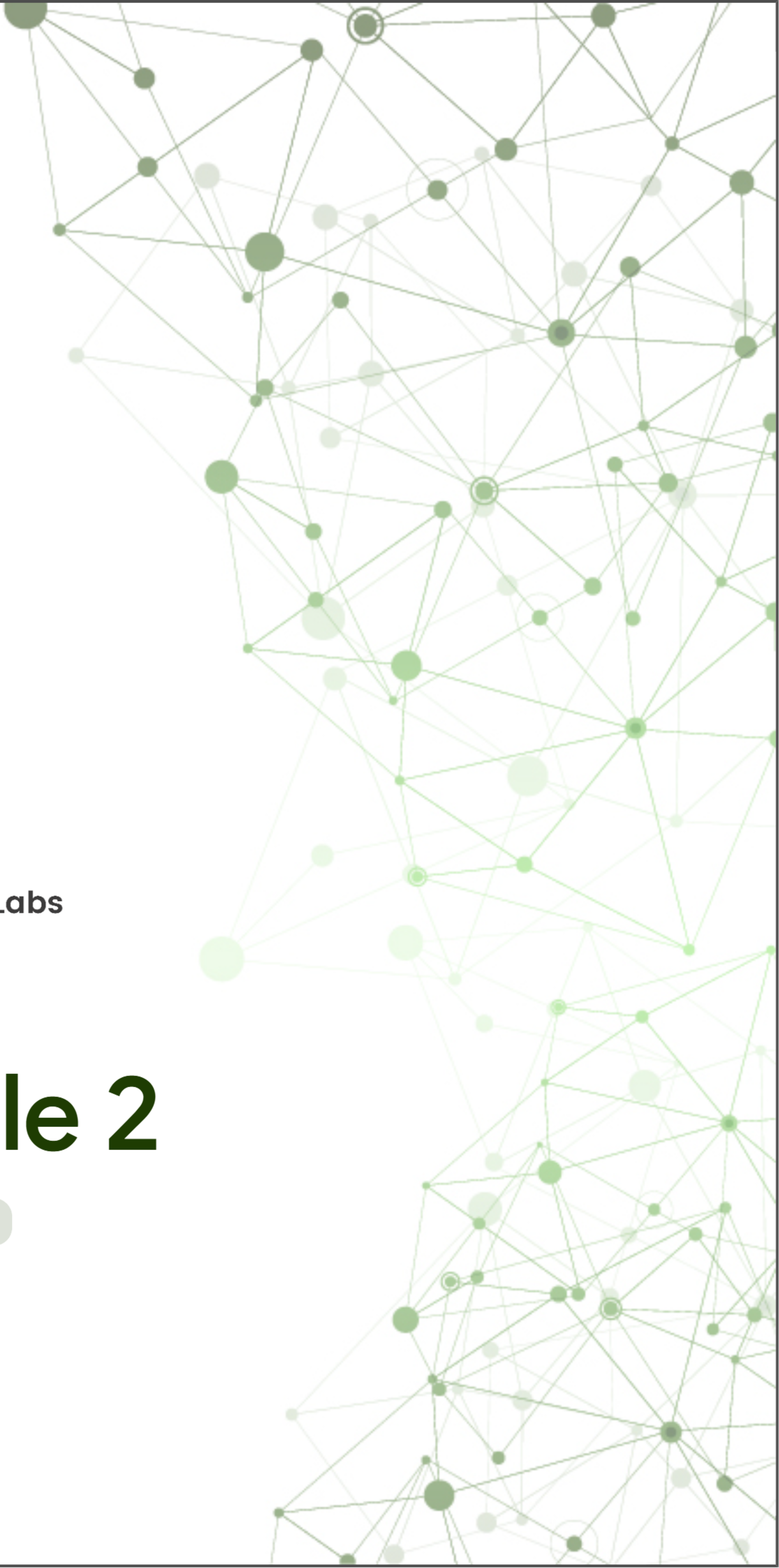
Insulin Balance
Needs Attention

Bloating & Gas
Good

ADHD
Good

ASD
Suboptimal

Sleep
Good



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Module 2

Microbial Analysis

Significant Bacteria

This section of the report details 9 of the most well researched and abundant bacteria in the gut microbiome.

Significant bacteria can give insights into the levels of bacteria in the gut compared to the average person, and optimal abundance ranges based on the latest clinical research.

It is important to note, that looking at these bacteria in isolation does not give the full picture, as bacteria in the gut have a synergistic relationship. The Gut-Axes and Health Insights sections will provide more detailed insight of bacteria levels for specific health concerns.

Bacteria	Role	Optimal Abundance %	Average Abundance %	Your Abundance %
Faecalibacterium prausnitzii	Butyrate-producing; supports anti-inflammatory signalling and gut lining repair.	0.188 - 2.62%	~1.084%	5.3671
Akkermansia muciniphila	Degrades mucin to strengthen the gut barrier and regulate immune responses.	0.0012 - 0.28%	~0.0084%	4.3232
Bifidobacterium spp.	Ferments fibres and supports immune maturation and gut wall integrity.	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium longum	Reduces gut inflammation and promotes barrier and cognitive health.	0.0134 - 0.76%	~0.137%	0.4700
Bifidobacterium adolescentis	Produces SCFAs and assists in fibre breakdown and immune balance.	0.0022 - 0.35%	~0.018%	0.0490
Lactobacillales spp.	Produces lactic acid; supports microbial balance and mucosal immunity.	0.076 - 0.85%	~0.246%	0.2040
Roseburia spp.	Butyrate-producing; promotes colonic health and energy regulation.	0.124 - 1.55%	~0.611%	1.8385
Coprococcus spp.	Butyrate-producing; involved in gut-brain signalling and mood.	0.039 - 0.25%	~0.1445%	0.8029
Adlercreutzia equolifaciens	Converts soy isoflavones into equol with hormonal activity.	0.0035 - 0.072%	~0.017%	Not Detected
Barnesiella spp.	Competes with pathogens and supports microbial diversity.	0.0022 - 0.013%	~0.005%	0.1855
Bacteroides thetaiotaomicron	Breaks down plant fibres and supports nutrient absorption.	0.104 - 1.33%	~0.47%	0.0495
Streptococcus thermophilus	Aids lactose digestion and supports gut microbial balance.	0.00075 - 0.023%	~0.002%	0.1274
Lactococcus lactis	Produces lactic acid and supports mucosal immunity.	0.00048 - 0.0058%	~0.0012%	Not Detected
Anaerostipes spp.	Converts lactate to butyrate for gut energy and repair.	0.056 - 0.96%	~0.313%	0.8668
Anaerobutyricum hallii	Produces butyrate from lactate and acetate for gut health.	0.03 - 0.74%	~0.172%	Not Detected

Antibiotic Degradation

These bacteria have been shown in studies to be some of the most damaged by antibiotic use. It’s important to consider these specific bacteria that these bacteria can also be substantially reduced through inadvertent antibiotic digestion, which can occur from the consumption of meat and dairy products.

Bacteria	Average Relative Abundance (%)	Healthy Relative Abundance (%)	Abundance if Damaged by Antibiotics (%)	Your Abundance (%)
Bifidobacterium spp.	5	0.1239 - 4.497%	~1.006%	1.3900
Lactobacillales spp.	3	0.076 - 0.85%	~0.246%	0.2040
Faecalibacterium prausnitzii	6	0.188 - 2.62%	~1.084%	5.3671
Akkermansia muciniphila	1	0.0012 - 0.28%	~0.0084%	4.3232
Ruminococcus spp.	4	0.007 - 0.174%	~0.021%	0.4513
Bacteroides spp.	25	5.885 - 31.13%	~17.051%	4.4168
Clostridium spp.	10	≤0.085%	~0.035%	1.7748

Studies referenced: (76), (77) , (78) , (79) , (80)

Gut-Axes Deep Dive

This section of the report provides a specific bacteria analysis for each of the gut axes. If there are signs of imbalance, the Personal Nutrition Guide will help to remodulate the gut microbiome.

Beneficial Bacteria - are the bacteria that have been shown in clinical research to influence a positive mechanism for the specific gut axis.

Disruptive Bacteria - these bacteria have been shown in clinical research to have negative effects on the specific gut-axis.

The mechanism for each bacteria is explained for each pathway, specific to the relevant gut axis.

Good	The bacteria balance is at an optimal level for the specific gut axis
Suboptimal	Some of bacteria levels show signs of imbalances for the specific gut axis
Needs Attention	The bacteria levels identified are imbalanced for the specific gut axis

Gut-Skin Axis

Good

Beneficial Bacteria for Skin Health

These bacteria are associated with healthy, hydrated, low-inflammation skin and protection from acne, eczema, rosacea, and psoriasis.

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Faecalibacterium prausnitzii	Anti-inflammatory, gut barrier support	0.188 - 2.62%	5.3671
Lactobacillales spp.	Controls inflammation, helps eczema/acne	0.076 - 0.85%	0.2040
Bifidobacterium spp.	Enhances gut & skin barrier	0.1239 - 4.497%	1.3900
Roseburia spp.	Butyrate-producing; supports gut lining and reduces inflammation	0.124 - 1.55%	1.8385
Blautia spp.	SCFA-producing; supports gut barrier and balances immune response	0.297 - 3.89%	0.5694
Parabacteroides distasonis	Anti-inflammatory; helps regulate bile acids and metabolism	0.095 - 0.74%	1.0206
Bacteroides fragilis	Produces polysaccharide A; regulates immune system and gut barrier	0.0496 - 0.94%	0.0658

Disruptive Bacteria for Skin Health

Overgrowth of these may be linked to acne, rosacea, eczema, psoriasis, and general skin inflammation through increased gut permeability, endotoxin production, and systemic inflammation.

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Prevotella spp.	Can drive chronic inflammation	≤2.011%	Not Detected
Clostridioides difficile	Produces toxins; causes diarrhea and gut inflammation	≤0.047%	Not Detected
Klebsiella pneumoniae	Pathogenic; promotes gut inflammation and antibiotic resistance	≤0.011%	Not Detected
[Ruminococcus] gnavus	Produces inflammatory polysaccharides; linked to IBD and mood issues	≤0.34%	0.5128
Bilophila wadsworthia	Produces hydrogen sulfide; associated with inflammation and bile acid imbalance	≤0.457%	0.1385

Gut-Thyroid Axis

Needs Attention

Beneficial Bacteria for Thyroid Axis

Studies have shown the potential positive impact of these bacteria in thyroid health

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Bifidobacterium spp.	Supports barrier, reduces inflammation, and aids micronutrient absorption (e.g., zinc, selenium)	0.1239 - 4.497%	1.3900
Roseburia spp.	Butyrate-producing; enhances gut barrier and reduces inflammation linked to thyroid function	0.124 - 1.55%	1.8385
Faecalibacterium prausnitzii	Anti-inflammatory SCFA producer; protects against autoimmune thyroid inflammation	0.188 - 2.62%	5.3671
Bacteroides spp.	Overgrowth linked to endotoxins and gut barrier dysfunction; may impact thyroid autoimmunity	5.885 - 31.13%	4.4168

Disruptive Bacteria for Thyroid Axis

Research shows links to higher levels of these bacteria correlating to impaired thyroid function.

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Klebsiella spp.	Often elevated in AITD; involved in molecular mimicry and inflammation	≤0.168%	18.7765
Eggerthella lenta	Pro-inflammatory; stimulates Th17 pathways and systemic inflammation	≤0.017%	0.0761
Escherichia coli	Produces LPS; promotes inflammation and disrupts micronutrient absorption	≤0.12%	13.0332
Clostridium spp.	Toxin-producing; triggers inflammation and thyroid dysfunction	≤0.085%	1.7748

Studies referenced: (31), (32) , (33) , (34) , (35)

Gut-Metabolism Axis

Good

Beneficial Bacteria for Metabolism Axis

These bacteria are have a multifactorial impact on the metabolism, and have been linked to lower fat mass, and higher lean mass

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Blautia wexlerae	Regulates lipid metabolism; associated with improved glucose tolerance	0.1062 - 1.83%	0.0631
Roseburia spp.	Produces butyrate; supports insulin sensitivity and energy regulation.	0.124 - 1.55%	1.8385
Faecalibacterium prausnitzii	Produces butyrate; reduces inflammation and supports metabolic homeostasis.	0.188 - 2.62%	5.3671
Akkermansia muciniphila	Improves gut barrier; enhances insulin sensitivity and metabolic balance.	0.0012 - 0.28%	4.3232
Bacteroides thetaiotaomicron	Overgrowth may promote gut inflammation and impair metabolic signalling	0.104 - 1.33%	0.0495
Coprococcus	Overgrowth may disrupt SCFA balance, affecting metabolic regulation.	0.039 - 1.047%	0.8029

Disruptive Bacteria for Metabolism Axis

Studies show the link between these bacteria and weight gain and obesity

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Methanobrevibacter smithii	Excess activity may slow transit and promote energy harvest and weight gain	≤0.24%	0.3063
Bacteroidetes	Imbalance may impair bile acid metabolism and promote insulin resistance.	≤1.24%	Not Detected

Studies referenced: (06), (07) , (08) , (09) , (10)

Gut-Heart Axis

Good

Beneficial Bacteria for Heart Axis

Studies link optimal levels of these bacteria to cardiometabolic health, through a variety of pathways

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Bifidobacterium spp.	Reduces inflammation; supports lipid metabolism and cardiovascular health	0.1239 - 4.497%	1.3900
Bifidobacterium adolescentis	Produces SCFAs; helps regulate cholesterol and reduce vascular inflammation.	0.0022 - 0.35%	0.0490
Bifidobacterium longum	Lowers LDL cholesterol; supports endothelial function and heart health.	0.0134 - 0.76%	0.4700
Akkermansia muciniphila	Strengthens gut barrier; improves lipid profiles and vascular integrity.	0.0012 - 0.28%	4.3232
Faecalibacterium prausnitzii	Produces butyrate; reduces systemic inflammation and supports heart health.	0.188 - 2.62%	5.3671
Roseburia spp.	Butyrate-producing; reduces inflammation and improves lipid metabolism linked to heart health.	0.124 - 1.55%	1.8385

Disruptive Bacteria for Heart Axis

These bacteria cover some of the known pathways of cardiovascular health problems

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Clostridium spp.	Some species produce toxins; linked to inflammation and cardiovascular risk.	≤0.085%	1.7748
[Clostridium] hylemonae	Disrupts gut-heart axis via secondary bile acid metabolism, impacting cholesterol.	≤0.006%	Not Detected
[Clostridium] innocuum	Triggers inflammation and impairs endothelial function.	≤0.084%	0.0710
Bacteroidetes spp.	Overgrowth can lead to endotoxin release and chronic low-grade inflammation.	≤0.9%	Not Detected
Proteobacteria spp.	Includes endotoxin-producing species; linked to systemic inflammation and CVD.	≤4.6%	Not Detected

Gut-Liver Axis

Good

Beneficial Bacteria for Liver Axis

These bacteria have been shown in published research to postively influence pathways linked to liver health

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Akkermansia muciniphila	Improves gut barrier and reduces liver inflammation.	0.0012 - 0.28%	4.3232
Faecalibacterium prausnitzii	Produces anti-inflammatory SCFAs like butyrate.	0.188 - 2.62%	5.3671
Roseburia spp.	Enhances SCFA production, supporting liver metabolism.	0.124 - 1.55%	1.8385
Roseburia intestinalis	Butyrate producer; reduces hepatic inflammation and supports liver energy metabolism.	0.054 - 0.69%	0.2305
Roseburia hominis	Enhances gut barrier and reduces hepatic oxidative stress.	0.0314 - 0.13%	0.0102
Roseburia rectibacter	Supports SCFA production linked to liver health.	0.01114 - 0.061%	Not Detected
Bifidobacterium spp.	Improves gut integrity and lowers endotoxin load to the liver.	0.1239 - 4.497%	1.3900
Bifidobacterium adolescentis	Modulates immune response and reduces liver fat accumulation.	0.0022 - 0.35%	0.0490
Bifidobacterium longum	Reduces endotoxemia and liver inflammation.	0.0134 - 0.76%	0.4700

Disruptive Bacteria for Liver Axis

Bacteria that are linked to liver, and related problems in published studies

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Escherichia coli	Produces endotoxins and contributes to liver inflammation and gut barrier disruption.	≤0.12%	13.0332
Pseudomonas	Produces endotoxins that may worsen liver inflammation.	≤0.002%	Not Detected
Streptococcus spp.	Increases gut permeability and liver injury risk.	≤0.4%	0.1274
[Ruminococcus] gnavus	Produces inflammatory polysaccharides; contributes to metabolic inflammation and gut–liver axis disruption.	≤0.34%	0.5128
Methanobrevibacter	Alters bile acid metabolism and contributes to NAFLD.	≤0.316%	0.4565

Studies referenced: (41), (42) , (43) , (44) , (45)

Gut-Joint Axis

Good

Beneficial Bacteria for Joint Axis

Bacteria that are involved in specific anti inflamatory pathways and joint health

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Faecalibacterium prausnitzii	Reduces joint inflammation via anti-inflammatory SCFAs.	0.188 - 2.62%	5.3671
Roseburia spp.	Produces butyrate, which protects against joint inflammation.	0.124 - 1.55%	1.8385
Roseburia intestinalis	Modulates immune response to prevent arthritis progression.	0.054 - 0.69%	0.2305
Roseburia hominis	Maintains gut barrier and reduces systemic inflammation.	0.0314 - 0.13%	0.0102
Roseburia rectibacter	Supports gut–joint homeostasis through SCFA production.	0.01114 - 0.061%	Not Detected
Akkermansia muciniphila	Supports gut barrier and reduces inflammation.	0.0012 - 0.28%	4.3232
Bifidobacterium spp.	Modulates gut–immune axis and helps alleviate systemic inflammation in joints.	0.1239 - 4.497%	1.3900
Bifidobacterium adolescentis	Regulates immune cells and reduces joint inflammation.	0.0022 - 0.35%	0.0490
Bifidobacterium longum	Decreases pro-inflammatory cytokines linked to arthritis.	0.0134 - 0.76%	0.4700

Disruptive Bacteria for Joint Axis

Bacteria with links to joint related problems

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Collinsella spp.	Increases gut permeability and joint inflammation.	≤0.779%	0.6197
Collinsella aerofaciens	Promotes pro-inflammatory cytokine release.	≤0.779%	0.6197
Collinsella aerofaciens ATCC 25986	Impairs gut barrier and triggers arthritis-related genes.	≤0.0152%	Not Detected
Eggerthella lenta	Modifies immune signaling and may worsen joint disease.	≤0.017%	0.0761
Escherichia coli	Produces endotoxins that promote systemic and joint inflammation.	≤0.12%	13.0332
Prevotella copri	Linked to rheumatoid arthritis onset and severity.	≤0.0043%	Not Detected
Klebsiella pneumoniae	Triggers immune responses in arthritis and spondylitis.	≤0.011%	Not Detected
Proteus mirabilis	Mimics host proteins; linked to rheumatoid arthritis.	≤0.012%	Not Detected

Gut-Eye Axis

Good

Beneficial Bacteria for Eye Axis

Published studies show the mechanisms involved in a variety of eye conditions

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Bifidobacterium spp.	Supports ocular immunity and tear film stability	0.1239 - 4.497%	1.3900
Faecalibacterium prausnitzii	Anti-inflammatory; protects retina & ocular barriers	0.188 - 2.62%	5.3671
Roseburia spp.	Supports gut-retina axis via SCFA metabolites	0.124 - 1.55%	1.8385
Roseburia intestinalis	Supports retinal barrier via butyrate	0.054 - 0.69%	0.2305
Roseburia hominis	Reduces ocular inflammation via SCFA production	0.0314 - 0.13%	0.0102
Bifidobacterium adolescentis	Regulates ocular immunity and barrier integrity.	0.0022 - 0.35%	0.0490
Bifidobacterium longum	Protects against eye inflammation and oxidative stress.	0.0134 - 0.76%	0.4700

Disruptive Bacteria for Eye Axis

Bacteria that have been shown to influence stressors and inflamation linked to eye health

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Escherichia coli	Promote uveitis, AMD, barrier breakdown	≤0.12%	13.0332
Betaproteobacteria Spp.	Found in glaucoma; promotes immune dysregulation	≤0.149%	0.1643
Prevotella spp.	Linked to autoimmune ocular inflammation	≤2.011%	Not Detected
Anaerotruncus spp.	Enriched in AMD—associated with degeneration	≤0.052%	Not Detected
Anaerotruncus colihominis	Worsens retinal health via immune activation.	≤0.052%	Not Detected

Studies referenced: (01), (02) , (03) , (04) , (05)

Gut-Hormone Axis

Needs Attention

Beneficial Bacteria for Hormone Axis

Bacteria that have been shown in studies to support hormonal regulation

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Faecalibacterium prausnitzii	Produces SCFAs; regulates gut–hormone axis via inflammation control.	0.188 - 2.62%	5.3671
Lactobacillus spp.	Supports estrogen metabolism and hormonal balance.	0.0004 - 0.0107%	Not Detected
Lactobacillus delbrueckii	Ferments lactose; may influence hormonal signalling pathways.	0.0004 - 0.0098%	Not Detected
Ligilactobacillus ruminis	Modulates gut immunity; may affect endocrine functions.	0.0012 - 0.0063%	Not Detected
Bacteroides spp.	Involved in bile acid metabolism and hormone signalling.	5.885 - 31.13%	4.4168

Disruptive Bacteria for Hormone Axis

Studies show this bacteria may negative effect hormonal circulation

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Clostridium spp.	Produces beta-glucuronidase, may re-circulate estrogens	≤0.085%	1.7748
Escherichia coli	Produces beta-glucuronidase; may re-circulate estrogens and promote inflammation	≤0.12%	13.0332
Betaproteobacteria Spp.	Linked to hormonal imbalance via gut inflammation and dysbiosis	≤0.149%	0.1643

Gut-Brain Axis

Good

Beneficial Bacteria for Brain Axis

These bacteria are associated with healthy mood regulation, reduced inflammation, and cognitive suppor.

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Faecalibacterium prausnitzii	Anti-inflammatory; promotes gut health.	0.188 - 2.62%	5.3671
Bifidobacterium spp.	Supports digestion; balances gut microbiota.	0.1239 - 4.497%	1.3900
Bifidobacterium adolescentis	Aids in fermentation of dietary fiber; supports immune health.	0.0022 - 0.35%	0.0490
Bifidobacterium longum	Reduces inflammation; supports brain and gut health.	0.0134 - 0.76%	0.4700
Roseburia spp.	Produces butyrate; promotes colon health.	0.124 - 1.55%	1.8385
Roseburia intestinalis	Butyrate producer; improves glucose metabolism & lowers inflammation.	0.054 - 0.69%	0.2305
Roseburia hominis	Butyrate producer; supports metabolic balance & reduces insulin resistance.	0.0314 - 0.13%	0.0102
Roseburia rectibacter	Butyrate producer; improves metabolism & glucose regulation.	0.01114 - 0.061%	Not Detected
Lactobacillus spp.	Produces lactic acid; maintains gut pH & immune function.	0.0004 - 0.0107%	Not Detected
Lactobacillus crispatus	Maintains vaginal & gut health; inhibits pathogens.	0.0004 - 0.0023%	Not Detected

Disruptive Bacteria for Brain Axis

These microbes are associated in research with neuroinflammation, anxiety, or impaired gut-brain signaling when overabundant.

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Gammaproteobacteria spp.	Includes endotoxin-producing species; linked to neuroinflammation.	≤4.6%	32.0398
Escherichia coli	Produces endotoxins; may affect gut-brain signaling and inflammation.	≤0.12%	13.0332
Clostridium spp.	Some species are harmful; linked to toxin production.	≤0.085%	1.7748
[Clostridium] hylemonae	May produce harmful secondary bile acids.	≤0.006%	Not Detected
[Clostridium] innocuum	Opportunistic; can contribute to infection.	≤0.084%	0.0710
[Clostridium] asparagiforme	Potentially linked to metabolic disruption.	≤0.036%	Not Detected
Enterobacter spp.	Opportunistic pathogens; linked to inflammation.	0.00000%	0.1679

Studies referenced: (11), (12) , (13) , (14) , (15)

Gut-Lung Axis

Suboptimal

Beneficial Bacteria for Lung Health

These bacteria are associated with reduced respiratory inflammation, immune modulation, and lung barrier support.

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Faecalibacterium prausnitzii	Anti-inflammatory; improves lung immunity via gut signaling	0.188 - 2.62%	5.3671
Rothia spp.	Helps maintain mucosal barrier; contributes to immune balance	0.0009 - 0.0093%	Not Detected
Rothia mucilaginosa	Involved in oral-lung microbial defense; modulates immune response	0.0007 - 0.0023%	Not Detected
Veillonella spp.	Converts lactate to SCFAs; supports lung immunity	0.0052 - 0.095%	Not Detected
Roseburia spp.	Produces butyrate; reduces inflammation in lungs and gut	0.124 - 1.55%	1.8385
Roseburia intestinalis	Butyrate production; supports lung-gut barrier and anti-inflammatory response	0.054 - 0.69%	0.2305
Roseburia hominis	Improves immune tolerance; reduces allergic inflammation	0.0314 - 0.13%	0.0102
Roseburia rectibacter	Butyrate producer; enhances respiratory mucosal defense	0.01114 - 0.061%	Not Detected
Lachnospira spp.	SCFA producer; reduces airway inflammation	0.022 - 0.92%	0.1110

Disruptive Bacteria for Lung Health

These microbes are associated with pro-inflammatory responses, increased susceptibility to respiratory conditions, or impaired gut-lung axis signaling.

Bacteria	Mechanism	Healthy Relative Abundance%	Your Abundance%
Escherichia coli	Can trigger lung inflammation via endotoxins	≤0.12%	13.0332
Haemophilus spp.	Respiratory pathogen; may worsen lung conditions like asthma	≤0.075%	0.0183
Aspergillus spp.	Fungal pathogen; linked to lung infections and allergy	≤0.01%	Not Detected
Penicillium spp.	Airborne mold; may cause respiratory irritation or allergic reactions	≤0.0007%	Not Detected
Prevotella spp.	Overgrowth linked to chronic lung inflammation and immune dysregulation	≤2.011%	Not Detected

Gut Interaction Insights Dashboard

Based on the unique balance of bacteria in your gut, we've identified 20 key health insights that may be relevant to your overall well-being. These insights are drawn from the latest clinical research, and reflect how specific microbes in your microbiome are linked to various aspects of health.

The 'Average Person' label on the graph reflects exactly that - the average person's result for the specific health insight. This data is derived from over 150,000 other gut microbiome samples.

Important - the Average Person isn't necessarily the health goal, but rather a point of reference. The colour coding of the graphs shows the optimal and suboptimal ranges.

As well as the graphical representation, this section of the reports also includes a detailed bacterial breakdown, explaining the mechanisms of specific bacteria for each health insight.

ARA % = Average Relevant Abundance. This is derived from our reference bioinformatics base of 150,000+ gut microbiome samples.

HRA % = Healthy Relative Abundance. This is derived by referencing the available published literature.

Your Abundance % = The abundance of specific bacteria found from analysis of the stool sample submitted for testing.

SCFA Producers

Suboptimal

Bacteria	Mechanism	HRA %	ARA %	Your Abundance %
Faecalibacterium prausnitzii	Major butyrate producer	0.188 - 2.62%	~1.084%	5.3671
Roseburia spp.	Produces butyrate; supports gut inflammation reduction	0.124 - 1.55%	~0.611%	1.8385
Anaerobutyricum hallii	Butyrate & propionate producer	0.03 - 0.74%	~0.172%	Not Detected
Eubacterium rectale	Major butyrate producer; supports colon health	0.0173 - 1.2%	~0.0894%	Not Detected
Butyricicoccus spp.	Produces butyrate; supports gut barrier	0.0006 - 0.0034%	~0.0013%	0.1551
Anaerostipes spp.	Ferments lactate to butyrate	0.056 - 0.96%	~0.313%	0.8668
Ruminococcus bromii	Starch degrader supporting butyrate	0.0089 - 0.59%	~0.0345%	Not Detected
Akkermansia muciniphila	Acetate producer, mucin specialist	0.0012 - 0.28%	~0.0084%	4.3232
Bifidobacterium spp.	Cross-feeder; supports butyrate synthesis from acetate/lactate	0.1239 - 4.497%	~1.006%	1.3900
Veillonella spp.	Converts lactate to propionate; helps butyrate-producers indirectly	0.0052 - 0.095%	~0.02%	Not Detected
Rothia spp.	Acetate producer; supports mucosal health & SCFA producers	0.0009 - 0.0093%	~0.0027%	Not Detected
Lactobacillales spp.	Lactate producer; supports butyrate-producing bacteria	0.076 - 0.85%	~0.246%	0.2040

Studies referenced: (106), (107) , (108) , (109) , (110) , (111) , (112) , (113)

Inflammation Index

Good

Anti Inflamatory Bacteria	Mechanism	HRA %	ARA %	Your Abundance %
Faecalibacterium prausnitzii	Major butyrate producer; reduces inflammation	0.188 - 2.62%	~1.084%	5.3671
Roseburia spp.	Produces butyrate; anti-inflammatory	0.124 - 1.55%	~0.611%	1.8385
Roseburia intestinalis	Butyrate-producing; supports anti-inflammatory pathways	0.054 - 0.69%	~0.23%	0.2305
Roseburia hominis	Improves immune balance; reduces gut inflammation	0.0314 - 0.13%	~0.364%	0.0102
Lachnospira eligens	SCFA producer; supports mucosal and immune health	0.0222 - 0.92%	~0.186%	0.1110
Bacteroides thetaiotaomicron	Maintains mucosal health; involved in SCFA production	0.104 - 1.33%	~0.47%	0.0495
Akkermansia muciniphila	Supports gut barrier & immune modulation	0.0012 - 0.28%	~0.0084%	4.3232
Bifidobacterium spp.	Immune-modulating acetate producers	0.1239 - 4.497%	~1.006%	1.3900
Lactobacillales spp.	Immune modulating and antimicrobial	0.076 - 0.85%	~0.246%	0.2040
Anaerobutyricum hallii	Cross-feeding, anti-inflammatory	0.03 - 0.74%	~0.172%	Not Detected
Pro Inflamatory Bacteria	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Escherichia coli	Produces endotoxins; promotes inflammation	≤0.12%	~0.019%	13.0332
Enterobacteriaceae spp.	Includes pro-inflammatory species; linked to gut dysbiosis	≤3.903%	~0.603%	32.0186
Klebsiella spp.	Triggers immune response; linked to inflammation and autoimmunity	≤0.168%	~0.019%	18.7765
Shigella spp.	Pathogenic; causes intestinal inflammation and damage	≤0.0021%	~0.0008%	Not Detected
Clostridioides difficile	Toxin-producing and inflammatory	≤0.047%	~0.023%	Not Detected
Desulfovibrio spp.	Sulfate reducer, pro-inflammatory	≤0.581%	~0.225%	Not Detected
Proteus spp.	Urease activity and inflammatory role	≤0.01%	~0.0009%	Not Detected

Studies referenced: (61), (62) , (63) , (64) , (65) , (114) , (115) , (116) , (117) , (118)

Immunity

Suboptimal

Positive Bacteria for Immunity	Mechanism	HRA %	ARA %	Your Abundance %
Faecalibacterium prausnitzii	Anti-inflammatory; modulates immune signaling	0.188 - 2.62%	~1.084%	5.3671
Akkermansia muciniphila	Strengthens mucosal barrier; modulates immune response	0.0012 - 0.28%	~0.0084%	4.3232
Lactobacillus spp.	Enhances mucosal immunity and antimicrobial peptide production	0.0004 - 0.0107%	~0.0017%	Not Detected
Lactobacillus delbrueckii	Supports epithelial integrity; involved in adaptive immunity	0.0004 - 0.0098%	~0.0017%	Not Detected
Bifidobacterium spp.	Modulates dendritic cells and T-reg cells; enhances immune tolerance	0.1239 - 4.497%	~1.006%	1.3900
Lachnospira eligens	SCFA production supports anti-inflammatory pathways	0.0222 - 0.92%	~0.186%	0.1110
Bacteroides fragilis	Produces polysaccharide A (PSA); modulates T-cell balance	0.0496 - 0.94%	~0.183%	0.0658
Negative Bacteria for Immunity	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Escherichia coli	Can impair mucosal immunity and promote inflammation via endotoxins (LPS)	≤0.12%	~0.019%	13.0332
Enterobacteriaceae spp.	Associated with gut dysbiosis and immune activation	≤3.903%	~0.603%	32.0186
Prevotella spp.	Overgrowth linked to Th17-mediated inflammation and immune imbalance	≤2.011%	~0.162%	Not Detected
Clostridium spp.	Some species produce toxins that impair immune signaling	≤0.085%	~0.035%	1.7748
Clostridioides difficile	Produces toxins A & B; disrupts gut barrier and immune tolerance	≤0.047%	~0.023%	Not Detected

Histamine Index

Good

Histamine Degrading Bacteria	Mechanism	HRA %	ARA %	Your Abundance %
Bifidobacterium spp.	May support histamine degradation and reduce gut inflammation	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium longum	Supports mucosal integrity; linked to histamine degradation pathways	0.0134 - 0.76%	~0.137%	0.4700
Bifidobacterium bifidum	May degrade histamine and modulate immune responses	0.0006 - 0.053%	~0.0032%	0.3612
Lactobacillus spp.	Some strains degrade histamine; others produce it (strain-specific)	0.0004 - 0.0107%	~0.0017%	Not Detected
Lactobacillus plantarum	Known to degrade histamine and regulate DAO (diamine oxidase)	0.000335 - 0.0029%	~0.0016%	Not Detected
Faecalibacterium spp.	Anti-inflammatory; indirectly supports histamine balance	0.675-9.12%	~4.363%	8.6092
Faecalibacterium prausnitzii	Reduces inflammation and strengthens gut barrier; supports histamine regulation	0.188 - 2.62%	~1.084%	5.3671
Akkermansia spp.	Improves gut barrier function; may help reduce histamine response indirectly	0.0012- 0.35%	~0.01%	4.3232
Roseburia spp.	Butyrate producer; supports gut lining integrity, helping with histamine modulation	0.124 - 1.55%	~0.611%	1.8385

Histamine Producing Bacteria	Mechanism	HRA %	ARA %	Your Abundance %
Morganella morganii	Converts histidine to histamine via histidine decarboxylase	≤0.0018%	~0.0006%	Not Detected
Klebsiella pneumoniae	Produces histamine through decarboxylation of histidine	≤0.011%	~0.0019%	Not Detected
Proteus mirabilis	Histidine decarboxylase activity; contributes to histamine buildup	≤0.012%	~0.001%	Not Detected
Enterobacter cloacae	Capable of histamine production via histidine decarboxylase	≤0.0036%	~0.0009%	Not Detected
Citrobacter freundii	Known to decarboxylate histidine to histamine	≤0.0037%	~0.0009%	0.0102

Studies referenced: (119), (120) , (121) , (122)

Protein Absorption

Needs Attention

Positive Bacteria forProtein Metabolism	Mechanism	HRA %	ARA %	Your Abundance %
Bacteroides thetaiotaomicron	Breaks down proteins and complex carbohydrates; aids in amino acid utilization	0.104 - 1.33%	~0.47%	0.0495
Bacteroides spp.	Some strains degrade protein and generate ammonia and sulfides	5.885 - 31.13%	~17.051%	4.4168
Coprococcus spp.	Ferments protein-derived substrates into SCFAs	0.039 - 0.25%	~0.1445%	0.8029
Coprococcus eutactus	Involved in amino acid fermentation; SCFA producer	0.0035 - 0.027%	~0.01%	0.4963
Coprococcus catus	Ferments protein and carbohydrates; promotes gut health	0.0116 - 0.156%	~0.049%	0.0814
Coprococcus comes	Produces SCFAs from amino acids; may help regulate gut pH	0.0135 - 0.382%	~0.084%	0.1875
Anaerobutyricum hallii	Ferments amino acids to produce butyrate; protein metabolizer	0.03 - 0.74%	~0.172%	Not Detected
Bacteroides fragilis	Can degrade amino acids; some strains linked to inflammation	0.0496 - 0.94%	~0.183%	0.0658
Negative Bacteria for Protein Metabolism	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Klebsiella spp.	Produces putrefactive byproducts; associated with ammonia & toxic amines	≤0.168%	~0.019%	18.7765
Enterobacteriaceae spp.	Ferments proteins to harmful compounds; increases gut pH	≤3.903%	~0.603%	32.0186
Bacteroides caccae	Protein fermentation; may promote mucin degradation	≤1.012%	~0.21%	0.0267
Bacteroides ovatus	Involved in protein metabolism; may release harmful nitrogen byproducts	≤0.37%	~0.143%	0.6966
Clostridium spp.	Putrefaction of protein; produces toxins	≤0.085%	~0.035%	1.7748
Escherichia coli	Produces ammonia and other toxic byproducts	≤0.12%	~0.019%	13.0332

Studies referenced: (133), (134) , (135) , (136) , (137), (138) , (139), (140) , (141) , (142)

Carbohydrate Absorption

Good

Positive Bacteria for Carbohydrate Metabolism	Mechanism	HRA %	ARA %	Your Abundance %
Ruminococcus bromii	Breaks down resistant starch	0.0089 - 0.59%	~0.0345%	Not Detected
Bacteroides thetaiotaomicron	Degrades complex polysaccharides; key in carb breakdown	0.104 - 1.33%	~0.47%	0.0495
Roseburia spp.	Ferments carbohydrates to produce SCFAs	0.124 - 1.55%	~0.611%	1.8385
Roseburia intestinalis	Converts carbohydrates into butyrate	0.054 - 0.69%	~0.23%	0.2305
Roseburia hominis	Butyrate producer; ferments dietary fiber	0.0314 - 0.13%	~0.364%	0.0102
Coprococcus spp.	Ferments carbs into SCFAs (especially acetate, butyrate)	0.039 - 0.25%	~0.1445%	0.8029
Coprococcus eutactus	Ferments carbohydrates; SCFA-producing	0.0035 - 0.027%	~0.01%	0.4963
Coprococcus catus	Known to ferment lactate to propionate	0.0116 - 0.156%	~0.049%	0.0814
Coprococcus comes	SCFA producer via carbohydrate metabolism	0.0135 - 0.382%	~0.084%	0.1875
Faecalibacterium prausnitzii	Converts carbs to butyrate; anti-inflammatory	0.188 - 2.62%	~1.084%	5.3671
Anaerobutyricum hallii	Ferments carbs and lactate to butyrate	0.03 - 0.74%	~0.172%	Not Detected
Akkermansia muciniphila	Degrades mucin; involved in mucosal carb metabolism	0.0012 - 0.28%	~0.0084%	4.3232
Negative Bacteria for Carbohydrate Metabolism	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Enterobacteriaceae spp.	Ferments simple sugars; linked to dysbiosis when overgrown	≤3.903%	~0.603%	32.0186
Clostridium perfringens	Produces gas and toxins from carb fermentation; associated with gut disruption	≤0.0046%	~0.0015%	Not Detected

Studies referenced: (133), (134) , (135) , (136) , (137), (138) , (139), (140) , (141) , (142)

Fat Absorption

Good

Positive Bacteria for Fat Metabolism	Mechanism	HRA %	ARA %	Your Abundance %
Bacteroides spp.	Contributes to bile acid metabolism and lipid breakdown	5.885 - 31.13%	~17.051%	4.4168
Bacteroides thetaiotaomicron	Aids digestion of polysaccharides; influences lipid metabolism indirectly	0.104 - 1.33%	~0.47%	0.0495
Akkermansia spp.	Enhances gut barrier; modulates fat absorption and lipid metabolism	0.0012-0.35%	~0.01%	4.3232
Akkermansia muciniphila	Supports mucin layer; improves metabolic health including fat processing	0.0012 - 0.28%	~0.0084%	4.3232
Roseburia spp.	Produces SCFAs that may influence lipid metabolism	0.124 - 1.55%	~0.611%	1.8385
Roseburia intestinalis	Butyrate producer; modulates fat absorption and gut barrier	0.054 - 0.69%	~0.23%	0.2305
Bifidobacterium spp.	Enhances bile salt hydrolase activity; may improve fat digestion	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium longum	Promotes bile metabolism; may support healthy fat absorption	0.0134 - 0.76%	~0.137%	0.4700
Negative Bacteria for Fat Metabolism	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Bilophila wadsworthia	Promotes bile acid imbalance, associated with high-fat diet	≤0.457%	~0.166%	0.1385
Escherichia coli	Can disrupt gut barrier, influence fat metabolism negatively	≤0.12%	~0.019%	13.0332
Klebsiella pneumoniae	May impair lipid digestion; linked to metabolic inflammation	≤0.011%	~0.0019%	Not Detected
Enterococcus faecalis	Associated with gut inflammation; may disrupt bile metabolism	≤0.0049%	~0.001%	Not Detected
Pseudomonas aeruginosa	Linked to gut dysbiosis; may interfere with fat absorption mechanisms	≤0.0007%	~0.0007%	Not Detected

Studies referenced: (133), (134) , (135) , (136) , (137), (138) , (139), (140) , (141) , (142)

Micronutrient Absorption

Needs Attention

	Bacteria	Mechanism	HRA %	ARA %	Your Abundance %
Vitamin B1 (Thiamine)	Bacteroides fragilis	Synthesises thiamine; supports host absorption in colon.	0.0496 - 0.94%	~0.183%	0.0658
Vitamin B2 (Riboflavin)	Lactobacillus spp.	Produces riboflavin; enhances mucosal absorption efficiency.	0.0004 - 0.0107%	~0.0017%	Not Detected
Vitamin B3 (Niacin)	Bacteroides spp.	Converts precursors into niacin for host use.	5.885 - 31.13%	~17.051%	4.4168
Vitamin B5 (Pantothenic acid)	Enterococcus spp.	Synthesises pantothenate in gut lumen.	0.0036 - 0.0347%	~0.009%	0.0427
Vitamin B6 (Pyridoxine)	Bifidobacterium spp.	Contributes to pyridoxine pool for host metabolism.	0.1239 - 4.497%	~1.006%	1.3900
Folic acid	Lactobacillus plantarum	Synthesises folate; promotes enterocyte uptake.	0.000335 - 0.0029%	~0.0016%	Not Detected
Biotin	Bacteroides thetaiotaomicron	Produces biotin; aids epithelial absorption and balance.	0.104 - 1.33%	~0.47%	0.0495
Vitamin K	Bacteroides spp.	Produces menaquinones (K2) for host absorption.	5.885 - 31.13%	~17.051%	4.4168
Vitamin B12 (Cobalamin)	Propionibacterium spp.	Synthesises B12 analogues aiding microbiota balance.	0.0004 - 0.002%	~0.0009%	Not Detected
Magnesium	Lactobacillus spp.	May support magnesium solubility via pH modulation and gut health.	0.0004 - 0.0107%	~0.0017%	Not Detected
Calcium	Bifidobacterium spp.	Improves calcium uptake via SCFA production.	0.1239 - 4.497%	~1.006%	1.3900
Iron	Bacteroides thetaiotaomicron	Influences iron metabolism through microbial metabolites.	0.104 - 1.33%	~0.47%	0.0495
Zinc	Lactobacillus plantarum	Binds zinc; improves mucosal uptake and stability.	0.000335 - 0.0029%	~0.0016%	Not Detected

Studies referenced: (123), (124) , (125) , (126) , (127), (128) , (129) , (130) , (131) , (132)

Bowel Habits

Good

Positive Bacteria for Bowel Habits	Mechanism	HRA %	ARA %	Your Abundance %
Faecalibacterium prausnitzii	SCFA (especially butyrate) producer; supports gut motility and anti-inflammatory effect	0.188 - 2.62%	~1.084%	5.3671
Roseburia spp.	SCFA producer, especially butyrate; improves bowel movement	0.124 - 1.55%	~0.611%	1.8385
Roseburia intestinalis	SCFA producer, especially butyrate; improves bowel movement	0.054 - 0.69%	~0.23%	0.2305
Roseburia hominis	SCFA producer, especially butyrate; improves bowel movement	0.0314 - 0.13%	~0.364%	0.0102
Bifidobacterium spp.	Enhances gut transit and stool formation	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium adolescentis	Involved in carbohydrate fermentation; mild support for motility	0.0022 - 0.35%	~0.018%	0.0490
Bifidobacterium longum	Documented to support regularity and improve stool quality	0.0134 - 0.76%	~0.137%	0.4700

Negative Bacteria for Bowel Habits	Mechanism	HRA %	ARA %	Your Abundance %
Methanobrevibacter smithii	Slows gut transit via methane production, leading to constipation	≤0.24%	~0.017%	0.3063
Enterobacteriaceae spp.	May increase gas, bloating, and gut dysbiosis	≤3.903%	~0.603%	32.0186
Methanobrevibacter spp.	Methane production linked to sluggish bowel motility	≤0.316%	~0.009%	0.4565
Clostridioides difficile	Toxin-producing; causes diarrhea and gut inflammation	≤0.047%	~0.023%	Not Detected
Escherichia coli	Pathogenic strains may cause diarrhea or constipation via inflammation	≤0.12%	~0.019%	13.0332

Studies referenced: (66), (67) , (68) , (69) , (70) , (71) , (72) , (73) , (74) , (75)

Fitness

Good

Positive Bacteria for Athletic Performance & Fitness	Mechanism	HRA %	ARA %	Your Abundance %
Coprococcus eutactus	SCFA producer; supports mood, endurance, and recovery	0.0035 - 0.027%	~0.01%	0.4963
Bifidobacterium longum	Reduces gut inflammation and supports immune recovery post-exercise	0.0134 - 0.76%	~0.137%	0.4700
Roseburia spp.	Butyrate producer; supports gut health and muscle recovery	0.124 - 1.55%	~0.611%	1.8385
Roseburia intestinalis	Produces butyrate; linked to anti-inflammatory benefits post-workout	0.054 - 0.69%	~0.23%	0.2305
Roseburia hominis	Enhances energy metabolism via SCFA production	0.0314 - 0.13%	~0.364%	0.0102
Faecalibacterium prausnitzii	Anti-inflammatory SCFA producer; promotes post-exercise recovery	0.188 - 2.62%	~1.084%	5.3671
Coprococcus spp.	Some strains may shift to pro-inflammatory behavior in dysbiosis	0.039 - 0.25%	~0.1445%	0.8029
Lachnospiraceae spp.	Certain strains may promote inflammation when dominant	3.641 - 17.77%	~9.25%	8.7359
Veillonella spp.	While helpful in some exercise contexts, overgrowth may contribute to inflammation	0.0052 - 0.095%	~0.02%	Not Detected
Negative Bacteria for Athletic Performance & Fitness	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Clostridium spp.	Can produce endotoxins and contribute to post-exercise inflammation	≤0.085%	~0.035%	1.7748
Escherichia spp.	Linked to gut permeability and inflammation under stress	≤0.161%	~0.025%	13.0332
Shigella spp.	Pathogenic; triggers inflammation and impairs gut function	≤0.0021%	~0.0008%	Not Detected

Studies referenced: (101), (102) , (103) , (104) , (105)

Mood & Mental Health

Suboptimal

Positive Bacteria for Mood / Mental Health	Mechanism	HRA %	ARA %	Your Abundance %
Bifidobacterium adolescentis	Produces GABA and supports serotonin pathways	0.0022 - 0.35%	~0.018%	0.0490
Lactobacillus rhamnosus	Modulates GABA receptors; reduces anxiety-like behavior	0.0052 - 0.14%	~0.024%	Not Detected
Faecalibacterium prausnitzii	Anti-inflammatory; linked to improved emotional well-being	0.188 - 2.62%	~1.084%	5.3671
Bifidobacterium longum	Reduces stress hormones; supports gut-brain axis balance	0.0134 - 0.76%	~0.137%	0.4700

Negative Bacteria for Mood / Mental Health	Mechanism	HRA %	ARA %	Your Abundance %
Escherichia coli	Produces lipopolysaccharides (LPS); associated with anxiety and stress	≤0.12%	~0.019%	13.0332
Enterobacteriaceae spp.	Triggers neuroinflammation and gut-brain axis disruption	≤3.903%	~0.603%	32.0186
Clostridium spp.	Produces neurotoxins; may impair mood and cognition	≤0.085%	~0.035%	1.7748
Streptococcus spp.	Linked to brain fog and anxiety in excess	≤0.4%	~0.1323%	0.1274

Autoimmunity

Good

Positive Bacteria for Autoimmunity	Mechanism	HRA %	ARA %	Your Abundance %
Faecalibacterium prausnitzii	Produces anti-inflammatory butyrate and reduces cytokine levels	0.188 - 2.62%	~1.084%	5.3671
Akkermansia muciniphila	Supports mucosal immunity and reduces gut inflammation	0.0012 - 0.28%	~0.0084%	4.3232
Bacteroides fragilis	Modulates immune response; balances T-reg cells	0.0496 - 0.94%	~0.183%	0.0658

Negative Bacteria for Autoimmunity	Mechanism	HRA %	ARA %	Your Abundance %
Betaproteobacteria spp.	Associated with immune activation and gut inflammation	0.00000%	0.00000%	0.1643
Prevotella spp.	Linked to pro-inflammatory responses and autoimmunity	≤2.011%	~0.162%	Not Detected
Bilophila wadsworthia	Produces sulfides, linked to IBD	≤0.457%	~0.166%	0.1385
Klebsiella pneumoniae	Associated with inflammatory autoimmune conditions	≤0.011%	~0.0019%	Not Detected

Detoxification

Suboptimal

Positive Bacteria for Detoxification	Mechanism	HRA %	ARA %	Your Abundance %
Akkermansia muciniphila	Strengthens gut barrier and supports mucosal detoxification	0.0012 - 0.28%	~0.0084%	4.3232
Faecalibacterium prausnitzii	Reduces inflammation and assists in butyrate-supported detoxification	0.188 - 2.62%	~1.084%	5.3671
Bacteroides thetaiotaomicron	Breaks down dietary toxins and metabolizes xenobiotics	0.104 - 1.33%	~0.47%	0.0495
Negative Bacteria for Detoxification	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Alphaproteobacteria spp.	Can interfere with drug metabolism and modulate host liver enzymes	≤0.003%	~0.001%	0.3542
Staphylococcus spp.	Associated with bioactivation of toxins and xenobiotics	≤0.0017%	~0.0011%	Not Detected
Escherichia coli	Can produce β-glucuronidase that reactivates detoxified compounds	≤0.12%	~0.019%	13.0332

Stress Resilience

Good

Positive Bacteria for Stress Resilience	Mechanism	HRA %	ARA %	Your Abundance %
Lactobacillus spp.	Produces GABA and modulates stress-induced cortisol levels	0.0004 - 0.0107%	~0.0017%	Not Detected
Lactobacillus delbrueckii	Supports gut-brain axis via anti-inflammatory signaling	0.0004 - 0.0098%	~0.0017%	Not Detected
Lactobacillus crispatus	Helps regulate mood and dampen stress-related inflammation	0.0004 - 0.0023%	~0.0009%	Not Detected
Bifidobacterium spp.	Supports HPA axis balance and reduces stress hormone responses	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium adolescentis	Reduces anxiety-like behavior and modulates neuroinflammation	0.0022 - 0.35%	~0.018%	0.0490
Bifidobacterium longum	Modulates stress-induced cortisol and supports emotional regulation	0.0134 - 0.76%	~0.137%	0.4700
Roseburia spp.	Produces butyrate, promoting calmness via vagus nerve signaling	0.124 - 1.55%	~0.611%	1.8385
Roseburia intestinalis	Helps reduce systemic stress markers and supports resilience	0.054 - 0.69%	~0.23%	0.2305
Roseburia hominis	Linked to reduced stress reactivity and mood stability	0.0314 - 0.13%	~0.364%	0.0102

Studies referenced: (148) , (149) , (150) , (151) , (152),
Studies referenced: (81) , (82) , (83) , (84) , (85)

Longevity

Good

Positive Bacteria for Longevity	Mechanism	HRA %	ARA %	Your Abundance %
Akkermansia spp.	Promotes metabolic health and gut barrier integrity, supporting longevity	0.0012-0.35%	~0.01%	4.3232
Akkermansia muciniphila	Improves gut lining, reduces inflammation, and supports healthy aging	0.0012 - 0.28%	~0.0084%	4.3232
Faecalibacterium spp.	Produces anti-inflammatory butyrate, linked to reduced age-related diseases	0.675-9.12%	~4.363%	8.6092
Faecalibacterium prausnitzii	Anti-inflammatory species associated with longevity and healthy aging	0.188 - 2.62%	~1.084%	5.3671
Bifidobacterium spp.	Maintains gut microbiota diversity and immune regulation with age	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium longum	Linked to healthy aging through immune modulation and SCFA production	0.0134 - 0.76%	~0.137%	0.4700
Bifidobacterium adolescentis	Supports intestinal health and anti-aging immune response	0.0022 - 0.35%	~0.018%	0.0490
Roseburia spp.	Produces butyrate, reduces inflammation, supports metabolic aging	0.124 - 1.55%	~0.611%	1.8385
Roseburia hominis	Associated with gut homeostasis and metabolic resilience in aging	0.0314 - 0.13%	~0.364%	0.0102
Roseburia intestinalis	Linked to anti-inflammatory functions and improved aging markers	0.054 - 0.69%	~0.23%	0.2305
Roseburia rectibacter	Contributes to butyrate production, maintaining healthy gut with age	0.01114 - 0.061%	~0.03%	Not Detected

Studies referenced: (153) , (154) , (155) , (156) , (157)

Insulin Balance

Needs Attention

Positive Bacteria Insulin Balance	Mechanism	HRA %	ARA %	Your Abundance %
Akkermansia muciniphila	Improves insulin sensitivity and reduces systemic inflammation	0.0012 - 0.28%	~0.0084%	4.3232
Eubacterium rectale	Produces butyrate, supports glucose metabolism and insulin signaling	0.0173 - 1.2%	~0.0894%	Not Detected
Coprococcus spp.	Associated with improved glycemic control and SCFA production	0.039 - 0.25%	~0.1445%	0.8029
Lactobacillus spp.	Modulates gut barrier and improves glucose homeostasis	0.0004 - 0.0107%	~0.0017%	Not Detected
Lactobacillus delbrueckii	Supports insulin sensitivity via anti-inflammatory action	0.0004 - 0.0098%	~0.0017%	Not Detected
Lactobacillus crispatus	Linked to metabolic benefits including improved insulin response	0.0004 - 0.0023%	~0.0009%	Not Detected
Negative Bacteria for Insulin Balance	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
[Ruminococcus] gnavus	Associated with increased inflammation and insulin resistance	≤0.34%	~0.088%	0.5128
Flavonifractor	Linked to higher insulin levels and disrupted glucose metabolism	≤0.301%	~0.12%	Not Detected
Escherichia coli	Contributes to endotoxin production and impaired insulin signaling	≤0.12%	~0.019%	13.0332

Bloating / Gas

Good

Positive Bacteria Bloating / Gas	Mechanism	HRA %	ARA %	Your Abundance %
Lactobacillus spp.	Ferments carbohydrates into lactic acid, limiting gas buildup	0.0004 - 0.0107%	~0.0017%	Not Detected
Enterococcus faecium	Assists in fermentation and limits pathogenic overgrowth	0.0013 - 0.0094%	~0.0035%	0.0427
Bifidobacterium spp.	Converts fibers to SCFAs; reduces gas and maintains gut balance	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium breve	Supports balanced fermentation and reduces bloating	≤0.013%	~0.0026%	0.0391
Negative Bacteria Bloating / Gas	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Bilophila wadsworthia	Produces sulfides, linked to bloating	≤0.457%	~0.166%	0.1385
Clostridium spp.	Produces gas and toxins from proteins	≤0.085%	~0.035%	1.7748
Clostridium perfringens	Gas-producing gut pathogen	≤0.0046%	~0.0015%	Not Detected
Methanobrevibacter smithii	Creates methane, slows gut motility	≤0.24%	~0.017%	0.3063
Desulfovibrio spp.	Releases hydrogen sulfide gas	≤0.581%	~0.225%	Not Detected

ADHD

Good

Positive Bacteria for ADHD	Mechanism	HRA %	ARA %	Your Abundance %
Faecalibacterium prausnitzii	Reduces gut inflammation; supports brain health	0.188 - 2.62%	~1.084%	5.3671
Veillonellaceae spp.	Linked to improved focus and energy metabolism	0.012 - 0.559%	~0.066%	0.1545
Veillonella	Converts lactate to propionate; may aid cognitive performance	0.0052 - 0.095%	~0.02%	Not Detected
Bifidobacterium spp.	Supports neurotransmitter balance and brain development	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium adolescentis	Involved in dopamine modulation; reduces ADHD symptoms	0.0022 - 0.35%	~0.018%	0.0490
Bifidobacterium longum	Promotes mental well-being and stress resilience	0.0134 - 0.76%	~0.137%	0.4700
Negative Bacteria for ADHD	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Enterobacteriaceae spp.	Linked to neuroinflammation and mood imbalance	≤3.903%	~0.603%	32.0186
Prevotella spp.	Associated with cognitive and behavioral issues	≤2.011%	~0.162%	Not Detected
Eggerthella spp.	Linked to neuroactive compound production	≤0.0825%	~0.02%	0.0761
Eggerthellaceae	Potential disruptor of gut-brain signaling	≤0.309%	~0.07%	0.1117
Eggerthella lenta	Associated with increased neurotoxin risk	≤0.017%	~0.011%	0.0761

ASD

Suboptimal

Positive Bacteria for ASD	Mechanism	HRA %	ARA %	Your Abundance %
Bifidobacterium spp.	Improves gut-brain signaling and reduces inflammation	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium adolescentis	Supports dopamine regulation and neurodevelopment	0.0022 - 0.35%	~0.018%	0.0490
Bifidobacterium longum	Enhances gut barrier and emotional balance	0.0134 - 0.76%	~0.137%	0.4700
Lactobacillus spp	Modulates GABA and serotonin; calms nervous system	0.0003 - 0.0008%	~0.0004%	Not Detected
Lactobacillus delbrueckii	Helps reduce oxidative stress in ASD	0.0004 - 0.0098%	~0.0017%	Not Detected
Lactobacillus crispatus	Supports microbiota balance and anti-inflammatory tone	0.0004 - 0.0023%	~0.0009%	Not Detected
Dorea spp.	Contributes to gut health and neuroactive compound production	0.0615 - 0.881%	~0.258%	0.1220
Dorea formicigenerans	Linked with better stool consistency in ASD	0.016 - 0.227%	~0.069%	Not Detected
Faecalibacterium prausnitzii	Anti-inflammatory; supports cognitive function	0.188 - 2.62%	~1.084%	5.3671

Negative Bacteria for ASD	Mechanism	HRA %	ARA %	Your Abundance %
Clostridium spp.	Produces neurotoxins and disrupts behavior	≤0.085%	~0.035%	1.7748
Peptostreptococcaceae spp.	Linked to gut inflammation in ASD	≤0.084%	~0.04%	0.0561
Clostridia spp.	Associated with higher neuroactive toxin load	≤34.08%	~19.97%	28.4569
Bacilli spp.	Imbalance may contribute to GI symptoms in ASD	≤0.27%	~0.17%	0.2040
Gammaproteobacteria	Linked to immune dysregulation and gut issues	≤4.604%	~0.814%	32.0398

Studies referenced: (56) , (57) , (58) , (59) , (60) , Studies referenced: (86) , (87) , (88) , (89) , (90)

Sleep

Good

Positive Bacteria for Sleep	Mechanism	HRA %	ARA %	Your Abundance %
Lachnospiraceae spp.	Supports SCFA production and circadian regulation	3.641 - 17.77%	~9.25%	8.7359
Faecalibacterium prausnitzii	Anti-inflammatory; helps regulate melatonin pathway	0.188 - 2.62%	~1.084%	5.3671
Bifidobacterium spp.	Modulates tryptophan metabolism for serotonin synthesis	0.1239 - 4.497%	~1.006%	1.3900
Bifidobacterium adolescentis	Enhances serotonin and GABA balance	0.0022 - 0.35%	~0.018%	0.0490
Bifidobacterium longum	Supports calm mood and healthy sleep cycles	0.0134 - 0.76%	~0.137%	0.4700
Lactiplantibacillus spp.	Contributes to GABA production and sleep onset	0.0004 - 0.0033%	~0.0008%	Not Detected
Negative Bacteria for Sleep	**Mechanism**	**HRA %**	**ARA %**	**Your Abundance %**
Desulfovibrio spp.	Produces hydrogen sulfide; linked to poor sleep quality	≤0.581%	~0.225%	Not Detected
Selenomonadales spp.	Associated with gut imbalance and circadian disruption	≤0.17%	~0.003%	0.4207
Negativicutes spp.	Linked to inflammation and neurotransmitter imbalance	≤2.24%	~0.921%	1.0528
Enterobacteriaceae spp.	May affect serotonin balance and sleep latency	≤3.903%	~0.603%	32.0186
[Ruminococcus] torques	Linked with gut permeability and disturbed sleep	≤0.38%	~0.099%	0.2291

EverWell Labs

Module 3

Unique Gut Based Nutrition Plan

Food & Nutrient Analysis

This module of the report details the food and nutrient suggestions that can be implemented to help naturally rebalance the gut microbiome. Nutrients within foods such as probiotics, prebiotics, polyphenols, and micronutrients - can be used to feed certain gut bacteria, and starve others.

The food recommendations are tailored and unique to each stool sample, based on the microbial analysis.

Top 30 Beneficial Foods

Based on the published scientific research, these foods contain the most appropriate nutritional elements to help rebalance the gut microbiome. These are the foods to focus on including in the diet.

Top 30 Detrimental Foods

These are the most prominent foods that have qualities that could further exacerbate microbial imbalances in the gut, based on the available published research. These should be reduced or removed from the diet.

Please bear in mind - this food recommendation module has no bias, other than rebalancing the gut microbiome. There may be foods in the lists that are not of preference, or cannot be consumed for medical reasons.

Foods appearing in the Detrimental Foods does not make them ‘bad’ foods - only they have qualities that could further imbalance the gut microbiota.

Important

When implemented under the supervision of a suitably qualified health practitioner, these recommended food choices are principles - other foods and drinks can, and should, still be consumed. It is important to consider other factors of health, especially when removing foods, to ensure the diet is still balanced from a macro and micro nutrient point of view.

Any dietary changes should only be made under the supervision of a suitably qualified health practitioner. This test does not diagnose allergies, intolerances, or food sensitivities. The food recommendations are purely principles of foods that feed, or starve, targeted bacteria based on the unique microbial balance in the gut.

Top 30 Beneficial Foods

Based on the published scientific research, these foods contain the most appropriate nutritional elements to help rebalance the gut microbiome. These are the foods to focus on including in the diet.

Priority to include in diet

- Lentils
- Asparagus
- Chicory root
- Bananas
- Black beans
- Leeks
- Barley
- Apples
- Oats

Beneficial

- Garlic
- Miso
- Jerusalem artichokes
- Fermented garlic
- Okra
- Fermented beets
- Sauerkraut
- Kale
- Quinoa
- Broccoli
- Blueberries
- Almonds
- Cottage cheese
- Pickles
- Flaxseeds
- Pomegranate
- Zucchini
- Tempeh
- Lettuce
- Cucumbers
- Pickled beets

Top 30 Detrimental Foods

These are the most prominent foods that have qualities that could further exacerbate microbial imbalances in the gut, based on the available published research. These should be reduced or removed from the diet.

Priority to remove, or reduce from diet

- Bacon
- Pastries
- Heavy cream

- Organ meats
- Sweetened tea
- Dates

- Peanuts
- White flour
- Fatty beef

Advisable to limit in diet

- Liver
- Cherries
- White pasta
- Energy drinks
- Sweetened cereal
- Processed cheese
- Sweet sauces

- Sweetcorn
- White rice
- Artificial creamers
- White sugar
- Fried fish
- Tomatoes
- Butter

- Milk chocolate
- Hard cheese
- Refined grains
- Biscuits
- Coconut Water
- Refined sugar
- Cola

Precision Prebiotics

Prebiotics are special types of dietary fibers that fuel bacteria in the gut, helping them grow and thrive. Unlike probiotics, which introduce new bacteria, prebiotics feed the bacteria that are already present in the gut.

In this section, we match the unique gut profile from the stool sample analysis, to the most suitable prebiotic supplements, selecting those that are most likely to support the growth of beneficial species based on your specific results.

We have no commercial affiliations with supplement companies, nor are we trying to promote our own prebiotics! Instead this section details the specific prebiotic ingredients that will be most effective based on the stool sample analysis. This allows an educated and targeted choice that can have the greatest positive impact on the gut health and overall well-being.

Based on the stool sample analysis, the most suitable prebiotics formulations will contain:

Most Suitable Prebiotics
Inulin
Resistant starch
Polydextrose
Lactulose

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