GutMapDx®

GI Axis Advanced

Complete Gut Microbial Test

For

Infants & Toddlers

Sample ID : Example-GI-Axis

Patient Name

Sample Date :

Test Report Index

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.

Page 04 - 05 Core Metrics & Functional Pathways

Page 06 Gut Health Axes Dashboard

Page 07 Gut Interaction Insights Dashboard

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 150 published studies have been referenced to unlock these comprehensive gut health insights.

Page 09 Significant Bacteria - abundance and mechanisms

Page 10 - 20 20 Gut Axes Deep Dive - pathways, mechanisms, and specific bacteria

Page 21 - 38 38 Gut Interaction Insights Dashboard - pathways, mechanisms, and specific bacteria

Page 39 - 41 Parasites, Fungi, Pathogenic Bacteria, Viruses, and Archaea

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.

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

Pages 43 - 46 Unique Gut Based Nutrition Plan

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Gut Interaction Insights

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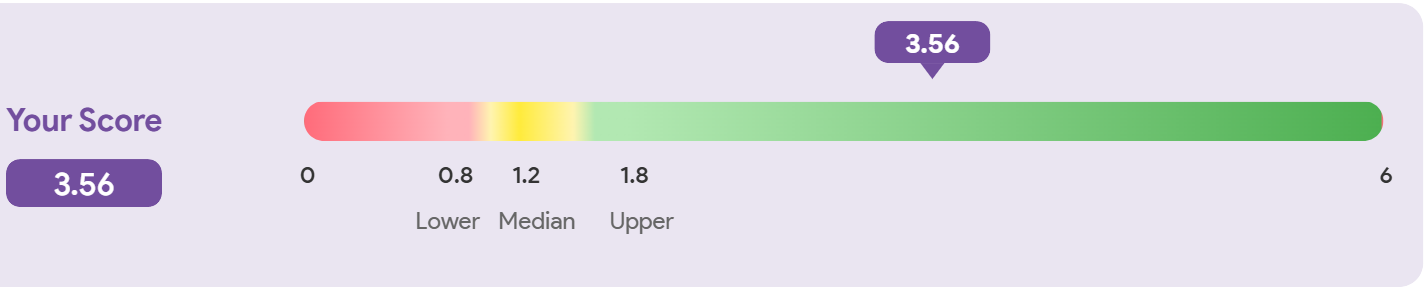
Microbiome Diversity - Shannon Index

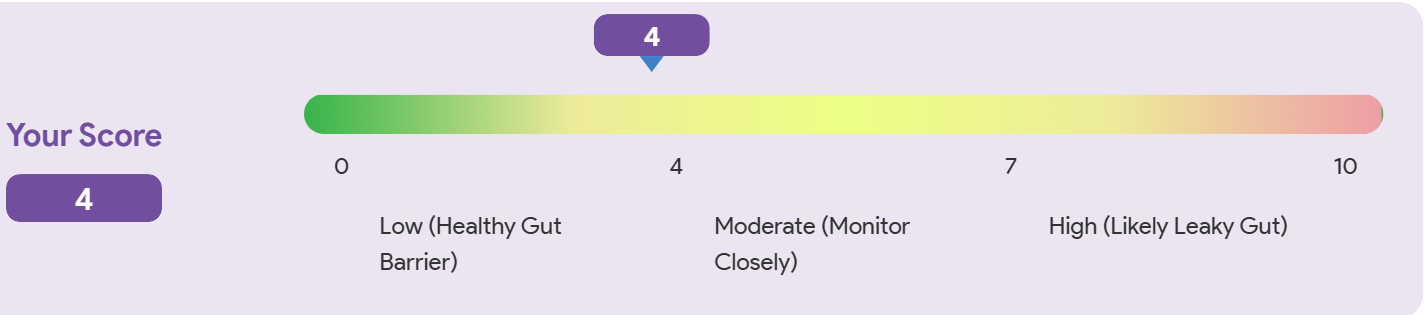
The Shannon Index quantifies gut microbial diversity by measuring both the number of species and their relative balance. Covering hundreds of bacterial taxa across major phyla (Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria), it provides a single metric of community richness and evenness.

Age Group	Lower Quartile	Median Quartile	Upper Quartile	Shannon Index Result
0-3m	0.8	1.2	1.8	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 is indicative of a "leaky gut" and risk of inflammation. A low index suggests a healthy barrier.

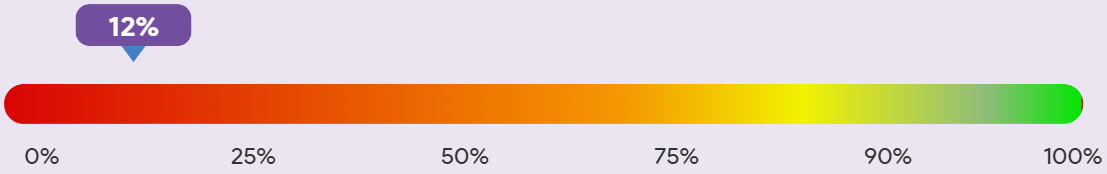


Microbiome Development Matrix

The Microbiome Development Matrix provides a quantitative "age-matching" score that evaluates whether a child's gut ecosystem is maturing in alignment with established clinical milestones. It tracks the critical transition from an infant-style microbiome,dominated by milk-fermenting Bifidobacterium spp., to a high-diversity adult-style landscape rich in Functional Keystone Species

Your Score

12%



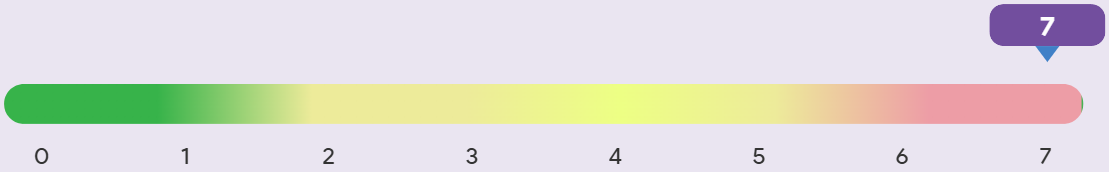
Antibiotic Degradation

Studies show these bacteria to be some of the most damaged by antibiotic use.

Bacteria considered : Bifidobacterium spp., Faecalibacterium prausnitzii, Akkermansia muciniphila, Bacteroides spp., Roseburia spp., Lactobacillus spp., Blautia spp.

Your Score

7



Hydrogen Producers (SIBO)

Elevated levels of these organisms may increase hydrogen gas production during carbohydrate fermentation. This mechanism is identified in research as a key driver of hydrogen-dominant SIBO and associated symptoms such as bloating and abdominal discomfort.

Bacteria considered : Bacteroides spp., Streptococcus spp., Enterococcus spp., Veillonella spp., Prevotella spp., Clostridium spp., Ruminococcus spp.

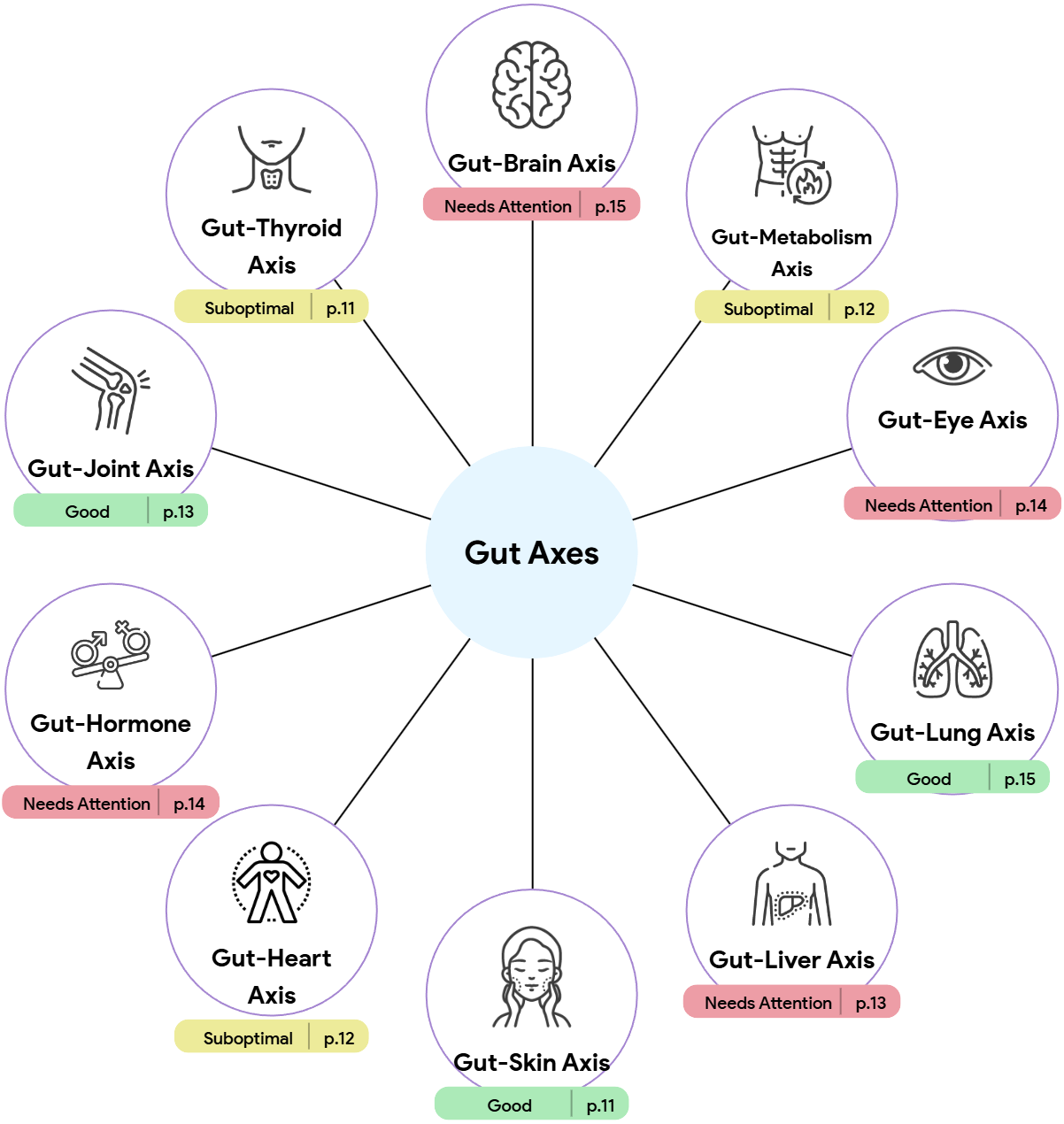
Your Score

4

Gut Axes Dashboards

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.

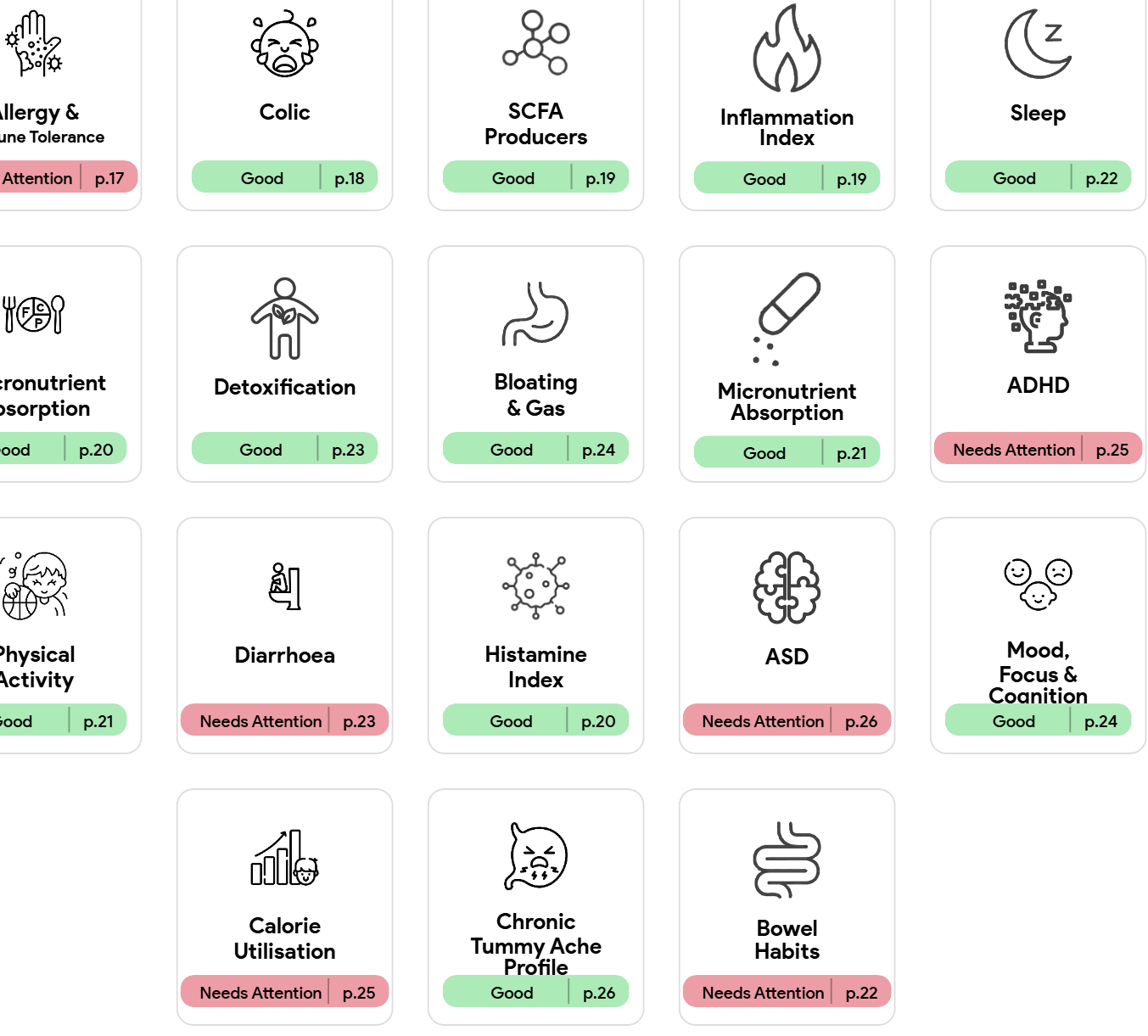
Good	The bacteria balance is at an optimal level for the specific gut axis
Suboptimal	Some of bacteria levels show signs of imbalances for the specific gut axis
Needs Attention	The bacteria levels identified are imbalanced for the specific gut axis



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



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GI Axis Advanced

Microbial Analysis

For

Infants & Toddlers

Significant Bacteria

This section of the report details some of the most well researched and abundant bacteria in the gut microbiome, comparing the relative abundance to optimal abundance ranges based on the latest clinical research.

ORA = Optimal Relative Abundance

Foundational Genus	Role	ORA %	Your Abundance %
Bifidobacterium spp.	Primary fermenters of milk sugars; they produce large amounts of lactic and acetic acid.	60-80%	1.9551
Lactobacillus species spp.	Specialists in the small intestine that break down lactose and produce antimicrobial "bacteriocins."	1-5%	3.94
Functional Keystone Species	**Role**	**ORA %**	**Your Abundance %**
Akkermansia muciniphila	Feeds on the mucus layer of the gut, stimulating the body to produce new, thicker mucus.	0-1%	2.18
Bacteroides fragilis	Produces Polysaccharide A (PSA), which communicates directly with the baby's immune cells.	5-15%	0.0872
Clostridium butyricum	Produces high concentrations of butyrate and facilitates the growth of other beneficial Firmicutes.	0.1-1%	5.33
Enterococcus faecium	A commensal that produces bacteriocins—natural antibiotics that target harmful bacteria.	0.1-1%	2.41
Faecalibacterium prausnitzii	A primary producer of butyrate, a short-chain fatty acid (SCFA) that fuels the cells of the colon.	0-0.5%	1.5483
Lactobacillus acidophilus	Ferments lactose into lactic acid and assists in the synthesis of Vitamin K and B12.	1-5%	0.82
Lactobacillus rhamnosus	Produces lactic acid and adheres strongly to the intestinal mucus, creating a protective barrier.	1-5%	0.91
Prevotella copri	A specialist in degrading complex plant carbohydrates and non-cellulosic polysaccharides.	0-1%	1.1482
Roseburia intestinalis	Ferments dietary fibres (hemicellulose) into butyrate as the child transitions to complex solids.	0%	4.60

Functional Keystone Species	Role	ORA %	Your Abundance %
Bacteroides vulgatus	A common Bacteroides species that competes for space with more beneficial strains.	< 5%	3.33
Clostridium difficile	An opportunistic coloniser that can release toxins (TcdA/TcdB) if the good bacteria are depleted.	< 1%	2.41
Enterococcus faecalis	A resilient bloomer that often takes up residence in the gut after C-section deliveries.	< 5%	5.64
Enterotoxigenic Bacteroides fragilis	A specific strain of B. fragilis that carries the BFT (Bacteroides fragilis toxin) gene.	0%	3.55
Escherichia coli (Pathogenic)	A facultative anaerobe that consumes oxygen, allowing beneficial anaerobes to eventually move in.	< 5%	3.77

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

Suboptimal

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	ORA%	Your Abundance%
Lactobacillus rhamnosus	Reduces risk of eczema and atopies.	1-5%	5.61
Bifidobacterium infantis	Suppresses Th2/Th17 allergic inflammation.	20-50%	0.93
Faecalibacterium prausnitzii	Produces butyrate to prevent skin flares.	0-0.5%	1.5483
Akkermansia muciniphila	Strengthens mucus barrier against allergens.	0-1%	3.97

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	ORA%	Your Abundance%
Staphylococcus aureus	Colonises gut before appearing as eczema.	<0.5%	3.26
Bacteroides vulgatus	Primary marker for egg and milk allergies.	<5%	2.86

Gut-Thyroid Axis

Good

Beneficial Bacteria for Thyroid Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Lactobacillus reuteri	Supports Iodine/Selenium absorption.	0.1-2%	6.76
Bifidobacterium longum	Dampens thyroid auto-antibodies.	10-30%	0.4519
Akkermansia muciniphila	Supports efficient thyroid signalling.	0-1%	3.08
Bacteroides fragilis	Prevents Hashimoto-like responses.	5-15%	0.0872

Disruptive Bacteria for Thyroid Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Prevotella copri	Risk of autoimmune thyroiditis.	<1%	1.1482
Enterococcus faecalis	Disrupts mineral absorption for thyroid.	<5%	3.42

Gut-Metabolism Axis

Suboptimal

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	ORA%	Your Abundance%
Akkermansia muciniphila	Regulates GLP-1 for blood sugar/insulin.	0-1%	4.50
Christensenella minuta	Linked to lean phenotype and healthy fat.	0%	1.02
Bifidobacterium animalis	Prevents fat accumulation from carbs.	1-5%	0.0511
Lactobacillus gasseri	Reduces visceral fat storage.	0.1-1%	Not Detected

Disruptive Bacteria for Metabolism Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Methanobrevibacter smithii	Increases calorie harvest from food.	<0.1%	3.94
Escherichia coli	Drives endotoxaemia and insulin resistance.	<10%	1.8683

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	ORA%	Your Abundance%
Roseburia intestinalis	Regulates pressure and vascular tone.	0-0.1%	5.42
Eubacterium rectale	Healthy lipid (cholesterol) metabolism.	0-1%	3.59
Lactobacillus plantarum	Lowers systemic CRP inflammation.	0.1-1%	1.19
Bifidobacterium bifidum	Prevents inflammatory TMAO production.	10-20%	4.12

Disruptive Bacteria for Heart Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Eggerthella lenta	Produces cardiotoxic metabolites.	<0.1%	1.82
Klebsiella aerogenes	Drives inflammation in the heart wall.	<0.5%	3.89

Gut-Liver Axis

Needs Attention

Beneficial Bacteria for Liver Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Lactobacillus paracasei	Supports bile and heavy metal clearance.	0.1-1%	1.57
Bifidobacterium infantis	Prevents toxins entering portal vein.	20-50%	0.77
Bacteroides thetaiotaomicron	Essential for deconjugating bile acids.	1-5%	0.0205
Lactobacillus helveticus	Supports glutathione production.	0.1-1%	5.04

Disruptive Bacteria for Liver Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Proteus mirabilis	Ammonia levels overwhelm liver detox.	<0.5%	3.09
Klebsiella pneumoniae	Linked to "Auto-Brewery" fatty liver.	<1%	4.74

Gut-Joint Axis

Good

Beneficial Bacteria for Joint Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Bifidobacterium adolescentis	Prevents juvenile joint inflammation.	0-1%	0.6972
Lactobacillus casei	Reduces stiffness/inflammatory markers.	0.1-1%	1.24
Akkermansia muciniphila	Keeps "joint-killing" LPS out of blood.	0-1%	2.24
Faecalibacterium prausnitzii	Protects bone density via SCFAs.	0-0.5%	1.5483

Disruptive Bacteria for Joint Axis

Bacteria with links to joint related problems

Bacteria	Mechanism	ORA%	Your Abundance%
Prevotella copri	Primary marker for Juvenile Arthritis.	<1%	1.1482
Bacteroides vulgatus	Molecular mimicry triggers joint attack.	<5%	3.91

Gut-Eye Axis

Needs Attention

Beneficial Bacteria for Eye Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Lactobacillus acidophilus	Supports Vitamin A/Lutein for retina.	1-5%	3.25
Bifidobacterium longum	Reduces risk of uveitis (inflammation).	10-30%	0.4519
Bacteroides fragilis	Prevents autoimmune eye conditions.	5-15%	0.0872
Roseburia hominis	SCFAs protect the optic nerves.	0-0.1%	Not Detected

Disruptive Bacteria for Eye Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Pseudomonas aeruginosa	High-risk for severe ocular infections.	<0.1%	3.26
Bacillus cereus	Toxins trigger rapid inflammatory damage.	<0.1%	1.49

Gut-Hormone Axis

Suboptimal

Beneficial Bacteria for Hormone Axis

Bacteria that have been shown in studies to support hormonal regulation

Bacteria	Mechanism	ORA%	Your Abundance%
Bacteroides thetaiotaomicron	Breaks down glycans for hormone precursors.	1-5%	0.0205
Lactobacillus gasseri	Modulates recycling of oestrogen.	0.1-1%	Not Detected
Bifidobacterium breve	Supports endocrine growth phases.	10-20%	Not Detected
Akkermansia muciniphila	Protects from hormone-disrupting signals.	0-1%	3.19

Disruptive Bacteria for Hormone Axis

Studies show this bacteria may negative effect hormonal circulation

Bacteria	Mechanism	ORA%	Your Abundance%
Escherichia coli	Leads to excessive hormone recirculation.	<10%	1.8683
Clostridioides difficile	Disrupts Estrobolome/nutrient uptake.	<1%	4.95

Gut-Brain Axis

Needs Attention

Beneficial Bacteria for Brain Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Bifidobacterium adolescentis	High producer of GABA (calmness).	0-1%	0.6972
Lactobacillus helveticus	Reduces cortisol and supports focus.	0.1-1%	1.09
Bifidobacterium longum	Supports serotonin and neuroplasticity.	10-30%	0.4519
Bacteroides fragilis	Helps seal the blood-brain barrier.	5-15%	0.0872

Disruptive Bacteria for Brain Axis

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

Bacteria	Mechanism	ORA%	Your Abundance%
Sutterella wadsworthensis	Linked to GI issues in neurodivergent kids.	<1%	2.6562
Clostridium bolteae	Linked to irritability and repetitive habits.	<0.1%	5.88

Gut-Lung Axis

Good

Beneficial Bacteria for Lung Health

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

Bacteria	Mechanism	ORA%	Your Abundance%
Lactobacillus rhamnosus	Protects against viral lung infections.	1-5%	1.22
Faecalibacterium prausnitzii	Butyrate dampens asthma inflammation.	0-0.5%	1.5483
Bifidobacterium breve	Reduces severity of childhood wheezing.	10-20%	Not Detected
Roseburia intestinalis	Regulates Th1/Th2 balance in lungs.	0-0.1%	2.57

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	ORA%	Your Abundance%
Veillonella parvula	Primary predictive marker for asthma risk.	<5%	3.74
Haemophilus influenzae	Can migrate and cause respiratory distress.	<0.5%	2.88

Gut Interaction Insights Dashboard

Based on the unique balance of bacteria in the gut, we have identified 18 key health insights that may be relevant to overall well-being. These insights are drawn from the latest clinical research, and reflect how specific microbes in the gut microbiome are linked to various aspects of health.

ORA % = Healthy Relative Abundance Percentage. 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.

Allergy & Immune Tolerance Pathway

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Bacteroides fragilis	Produces Polysaccharide A to "train" T-cells not to overreact.	5-15%	0.0872
Lactobacillus rhamnosus	Clinically linked to reduced risk of eczema and atopies.	1-5%	1.44
Faecalibacterium prausnitzii	Produces butyrate to maintain the "Tight Junctions" of the gut.	0-0.5%	1.5483
Akkermansia muciniphila	Strengthens the mucus barrier to prevent allergens leaking into blood.	0-1%	4.60
Bifidobacterium infantis	Suppresses Th2/Th17 (allergic) inflammation in early infancy.	20-50%	4.95
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Bacteroides vulgatus	Disruptor: High levels are a primary marker for egg/milk allergies.	< 5%	5.08
Escherichia coli (Path.)	Disruptor: Promotes a pro-inflammatory Th2 environment.	< 5%	5.88
Staphylococcus aureus	Disruptor: Often colonises the gut before appearing as skin eczema.	< 0.5%	6.65
Clostridium difficile	Disruptor: Its presence early on is linked to increased asthma risk.	< 1%	6.21
Enterococcus faecalis	Disruptor: Promotes inflammation that hinders immune education.	< 5%	2.07

Colic

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Bifidobacterium longum	Acidifies gut to block gas-producing pathogens.	40-80%	0.4519
Lactobacillus rhamnosus	Calms the enteric nervous system; reduces pain.	1-5%	3.92
Clostridium butyricum	Regulates motility; prevents "trapped gas" spasms.	0.1-1%	1.44
Lactobacillus acidophilus	Ensures complete lactose/sugar breakdown.	1-5%	4.77
Bifidobacterium animalis	Improves transit time and stool consistency.	5-10%	0.0511
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Escherichia coli (Path.)	Major gas producer; causes abdominal pressure.	< 5%	3.14
Enterococcus faecalis	Pro-inflammatory; inhibits beneficial acidifiers.	< 5%	5.44
Klebsiella pneumoniae	Linked to severe bloating and hydrogen gas.	< 1%	4.56
Bacteroides vulgatus	Associated with increased visceral pain sensitivity.	< 5%	5.21
Clostridium difficile	Toxins trigger gut irritability and cramping.	< 1%	4.48

SCFA Producers

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Faecalibacterium prausnitzii	Primary producer of anti-inflammatory butyrate.	0-0.5%	1.5483
Roseburia intestinalis	Specialist in converting complex plant fibres to butyrate.	0%	5.24
Clostridium butyricum	Early-life butyrate producer from milk sugars.	0.1-1%	4.71
Eubacterium rectale	Key acetate and butyrate contributor in toddlers.	0%	4.31
Bifidobacterium longum	Major acetate producer; supports brain development.	40-80%	0.4519

Inflammation Index

Good

Anti Inflammatory Bacteria	Mechanism	ORA %	Your Abundance %
Faecalibacterium prausnitzii	Suppresses pro-inflammatory cytokines (IL-12).	0-0.5%	1.5483
Akkermansia muciniphila	Strengthens barrier to stop "leaky gut" inflammation.	0-1%	5.12
Anti Inflammatory Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Escherichia coli	Disruptor: Triggers low-grade systemic inflammation.	< 5%	1.8683
Enterococcus faecalis	Disruptor: Promotes oxidative stress in the lining.	< 5%	2.13
Klebsiella pneumoniae	Disruptor: High inflammatory driver in infants.	< 1%	3.71

Macronutrient Absorbtion

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Lactobacillus acidophilus	Facilitates the proteolysis of casein and whey proteins.	1-5%	6.32
Bacteroides fragilis	Breaks down large peptides into absorbable amino acids.	5-15%	0.0872
Lactobacillus rhamnosus	Protects villi to maximise the surface area for absorption.	1-5%	3.32
Enterococcus faecium	Secretes peptidases that assist in terminal digestion.	0.1-1%	5.51
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Clostridioides difficile	Toxin production damages the absorptive lining.	< 1%	6.03

Histamine Index

Needs Attention

Histamine Degrading Bacteria	Mechanism	ORA%	Your Abundance %
Lactobacillus reuteri	Down-regulates histamine receptors and reduces itch/flare.	1-5%	6.30
Lactobacillus rhamnosus	Stabilises mast cells to prevent the release of histamine.	1-5%	4.03
Bifidobacterium infantis	Known histamine-degrading species in early life.	20-50%	1.25
Histamine Producing Bacteria	**Mechanism**	**ORA%**	**Your Abundance %**
Morganella morganii	High producer of histamine; triggers hives, fog, and congestion.	0%	3.21
Klebsiella pneumoniae	Produces biogenic amines that increase the total histamine load.	< 1%	5.27

Physical Activity  Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Veillonella atypica	Converts lactate (exercise byproduct) into energy-boosting SCFAs.	0%	0.74
Faecalibacterium prausnitzii	Reduces post-exercise inflammation; aids muscle recovery.	0-0.5%	1.5483
Akkermansia muciniphila	Improves metabolic flexibility and oxygen utilisation efficiency.	0-1%	6.88
Bacteroides fragilis	Facilitates energy harvest from complex carbohydrates for stamina.	5-15%	0.0872
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Escherichia coli	Pro-inflammatory levels increase fatigue and recovery time.	< 5%	1.8683

Micronutrient Absorption  Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Lactobacillus acidophilus	Facilitates absorption of Vitamin B12 and Calcium.	1-5%	3.81
Bifidobacterium adolescentis	Major synthesiser of natural Folate (Vitamin B9).	0.1-1%	0.6972
Faecalibacterium prausnitzii	Produces Vitamin K2, essential for bone density and growth.	0-0.5%	1.5483
Bifidobacterium longum	Synthesises Vitamin B6 and Biotin; aids mineral transport.	40-80%	0.4519
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Escherichia coli	Can compete for micronutrients like Iron, hindering uptake.	< 5%	1.8683

Bowel Habits

Needs Attention

Positive Bacteria for Bowel Habits	Mechanism	ORA %	Your Abundance %
Bifidobacterium animalis	Modulates gut transit and water secretion. Prevents hard stools and chronic constipation.	5-10%	0.0511
Bifidobacterium longum	Produces acetic acid to trigger peristalsis. Vital for establishing regular daily movements.	40-80%	0.4519
Akkermansia muciniphila	Maintains the mucus "glide" layer. Reduces friction and irritation during passage.	0-1%	0.67
Negative Bacteria for Bowel Habits	**Mechanism**	**ORA %**	**Your Abundance %**
Methanobrevibacter smithii	Disruptor: Slows motor activity via methane. High levels are the primary marker for bloat/stasis.	< 0.1%	4.61
Escherichia coli	Disruptor: Triggers osmotic water shifts. Overgrowth leads to urgency and loose stools.	< 5%	1.8683

Sleep

Good

Positive Bacteria for Bowel Habits	Mechanism	ORA %	Your Abundance %
Bifidobacterium adolescentis	Primary producer of GABA (inhibitory neurotransmitter for calm)	0.1-1%	0.6972
Lactobacillus helveticus	Clinically shown to reduce cortisol and improve sleep depth.	0.1-1%	1.62
Bifidobacterium longum	Supports the early development of the infant circadian rhythm.	40-80%	0.4519
Streptococcus thermophilus	Synthesises serotonin precursors from dietary proteins.	0.1-2%	3.52
Negative Bacteria for Bowel Habits	**Mechanism**	**ORA %**	**Your Abundance %**
Escherichia coli	High levels can cause irritability and disrupt sleep cycles.	< 5%	1.8683

Diarrhoea

Needs Attention

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Lactobacillus acidophilus	Competes with pathogens for space; prevents colonisation.	1-5%	6.93
Bifidobacterium animalis	Modulates transit time and improves stool consistency.	5-10%	0.0511
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Escherichia coli	Primary driver of watery diarrhoea via osmotic imbalance.	< 5%	1.8683
Clostridioides difficile	Secretes toxins that cause severe inflammation and fluid loss.	< 1%	4.27
Klebsiella pneumoniae	Associated with antibiotic-associated diarrhoea and gas.	< 1%	1.67

Detoxification

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Oxalobacter formigenes	Specifically degrades oxalates to prevent crystal and stone formation.	0%	1.50
Bifidobacterium longum	Binds and facilitates the excretion of heavy metals and mycotoxins.	40-80%	0.4519
Lactobacillus rhamnosus	Reduces the bioavailability of environmental toxins and pesticides.	1-5%	5.74
Faecalibacterium prausnitzii	Maintains the mucosal barrier to prevent toxin "leakage" into the blood.	0-0.5%	1.5483
Desulfovibrio piger	Disruptor: Produces hydrogen sulphide (H2S), which can be toxic to colonocytes.	< 0.1%	1.26

Bloating / Gas

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Bifidobacterium infantis	Efficiently ferments milk sugars without excess gas.	20-50%	4.16
Akkermansia muciniphila	Maintains mucus depth to prevent gas from irritating nerves.	0-1%	1.75
Methanobrevibacter smithii	Disruptor: Produces methane gas; causes "trapped" bloat.	< 0.1%	1.99
Desulfovibrio piger	Disruptor: Produces H2S gas; causes foul-smelling gas and pain.	< 0.1%	5.86
Klebsiella pneumoniae	Disruptor: Rapidly ferments sugars into hydrogen gas/bloat.	< 1%	4.27

Mood, Focus & Cognition

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Bifidobacterium adolescentis	GABA producer for emotional stability and anxiety reduction.	0.1-1%	0.6972
Lactobacillus helveticus	Regulates cortisol levels; helps maintain focus under stress.	0.1-1%	1.73
Clostridium butyricum	Produces butyrate, which crosses the BBB to support neurogenesis.	0.1-1%	0.96
Bifidobacterium longum	Known psychobiotic that reduces perception of emotional stress.	40-80%	0.4519
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Enterococcus faecalis	Overgrowth is linked to cognitive fatigue and irritability.	< 5%	4.12

ADHD

Needs Attention

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Bifidobacterium adolescentis	Primary producer of GABA; supports focus and emotional regulation.	0.1-1%	0.6972
Lactobacillus reuteri	Promotes oxytocin and modulates social focus/attention.	1-5%	1.46
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Sutterella wadsworthensis	Strongly associated with neuro-inflammation and ADHD.	< 0.5%	2.6562
Bacteroides vulgatus	High levels linked to altered neurotransmitter metabolism.	< 5%	6.10
Klebsiella pneumoniae	Produces metabolites that can contribute to "brain fog."	< 1%	4.01

Weight Status & Calorie Utilisation

Needs Attention

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Akkermansia muciniphila	Regulates the mucus layer to improve insulin sensitivity and weight control.	0-1%	3.88
Christensenella minuta	Strongly associated with a lean body type and healthy metabolic rate.	0%	1.52
Lactobacillus gasseri	Known to help reduce visceral fat and regulate energy storage.	0.1-1%	Not Detected
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Methanobrevibacter smithii	Increases calorie harvest from food, often linked to a higher BMI.	< 0.1%	3.13
Staphylococcus aureus	Overgrowth in early childhood is correlated with later-life obesity risk.	< 0.5%	6.18

ASD

Needs Attention

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Bifidobacterium longum	Supports the development of the vagus nerve and social signalling.	40-80%	0.4519
Akkermansia muciniphila	Strengthens the gut-blood barrier to prevent neuro-active metabolites from leaking.	0-1%	2.11
Clostridium bolteae	Highly correlated with gastrointestinal issues in children with ASD.	< 0.1%	1.63
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Sutterella wadsworthensis	Associated with mucosal inflammation and altered sensory processing.	< 0.5%	2.6562
Desulfovibrio piger	Produces hydrogen sulphide (H2S) which may affect mitochondrial function in neurons.	< 0.1%	3.15

Chronic Tummy Ache Profile

Good

Positive Bacteria	Mechanism	ORA %	Your Abundance %
Lactobacillus rhamnosus	Clinically proven to reduce visceral pain and gut sensitivity.	1-5%	0.72
Bifidobacterium longum	Strengthens the mucosal barrier to prevent irritation of nerve endings.	40-80%	0.4519
Negative Bacteria	**Mechanism**	**ORA %**	**Your Abundance %**
Bacteroides vulgatus	Associated with increased gut pain and inflammatory discomfort.	< 5%	3.39
Pseudomonas aeruginosa	Produces metabolites that can trigger sharp abdominal cramping.	0%	5.41
Escherichia coli	Triggers gas production and inflammation, leading to distention pain.	< 5%	1.8683

GutMapDx

Microbial Analysis

Patient Name :

Parasites, Fungi, Pathogenic Bacteria, Viruses & Archaea

Parasites	Potential Health Impact	Result
Blastocystis hominis	Often linked to hives (urticaria) and unexplained abdominal pain in children.	Not Detected
Giardia lamblia	Causes "greasy" stools and significant malabsorption of fats and vitamins.	Not Detected
Dientamoeba fragilis	Frequently co-exists with pinworms; causes "morning tummy ache" and irritability.	Not Detected
Entamoeba histolytica	A more aggressive parasite that can cause bloody stools and high inflammation.	Not Detected
Cryptosporidium parvum	Common in swimming pools; leads to watery diarrhoea and rapid dehydration risk.	Not Detected

Viruses	Potential Health Impact	Result
Norovirus	Causes rapid epithelial sloughing and temporary lactose intolerance.	Not Detected
Adenovirus (type 41)	Primarily causes long-lasting diarrhoea and respiratory symptoms in toddlers.	Not Detected
Enterovirus	Linked to Hand, Foot, and Mouth; can cause prolonged post-viral gut dysfunction.	Not Detected
Rotavirus	Severe vomiting/diarrhoea; can damage the "brush border" where nutrients are absorbed.	Not Detected
Cytomegalovirus (CMV)	In immune-stressed children, it can drive chronic fatigue and low-grade gut inflammation.	Not Detected
Epstein-Barr virus (EBV)	Can cause liver/spleen swelling and a feeling of gut "heaviness."	Not Detected

Fungi	Potential Health Impact	Result
Candida albicans	Drives "brain fog," sugar cravings, and persistent nappy rash or oral thrush.	Not Detected
Candida glabrata	Less common than C. albicans but linked to antifungal resistance and systemic infections.	Not Detected
Candida tropicalis	Associated with invasive candidiasis and gastrointestinal imbalance.	Not Detected
Candida parapsilosis	Opportunistic yeast; may be involved in bloodstream infections and gut dysbiosis.	Not Detected
Candida krusei	Known for resistance to fluconazole; emerging gut and bloodstream pathogen.	Not Detected
Candida auris	Highly drug-resistant species; associated with hospital outbreaks and severe systemic infections.	Not Detected

GutMapDx

Microbial Analysis

Patient Name :

Parasites, Fungi, Pathogenic Bacteria, Viruses & Archaea

Pathogenic Bacteria	Potential Health Impact	Result
Helicobacter pylori	Burrows into the stomach; causes reflux, burping, and poor protein digestion.	Not Detected
Clostridioides difficile	Usually follows antibiotic use; releases toxins that cause severe colonic inflammation.	Detected
Klebsiella pneumoniae	Can ferment sugar into alcohol (endogenous ethanol), causing foggy behaviour.	Not Detected
Campylobacter jejuni	Common from undercooked poultry; can trigger post-viral joint pain or nerve issues.	Not Detected
Salmonella enterica	Causes high fever and "food poisoning"; significantly depletes the healthy landscape.	Not Detected
Shigella spp.	Highly contagious; causes very frequent, painful, and often bloody bowel movements.	Not Detected
Yersinia enterocolitica	Can mimic appendicitis pain in the lower right abdomen; often linked to pork products.	Not Detected
Enterococcus faecalis	An opportunistic grower that can drive oxidative stress and gut "heat."	Not Detected
Pseudomonas aeruginosa	Highly resistant; often found in children with low stomach acid.	Not Detected

Archaea Species	Clinical Significance if Elevated	ARA	CAT	Your Abundance
Methanobrevibacter smithii	The primary methanogen in the human gut. It consumes hydrogen produced by other bacteria to create methane gas (CH_4). In children, this acts as a local anaesthetic to the gut wall, slowing transit time and causing chronic constipation, bloating, and increased calorie extraction.	0.1	0.5	Not Detected
Methanosphaera stadtmanae	A more "inflammatory" methanogen compared to M. smithii. It is specifically associated with triggering the host's innate immune response and has been linked to increased mucosal inflammation and inflammatory bowel conditions. It can contribute to both gas distension and visceral sensitivity.	0.01	0.1	Not Detected

Detected	Functional Medicine Suggestions
Clostridioides difficile	Focus on neutralising toxins. Transition to a high-fibre diet once the child is stable.

GutMapDx®

GI Axis Advanced

Unique Gut Based Nutrition Plan

For

Infants & Toddlers

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.

Important

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

- Ricotta cheese
- Cultured cottage cheese
- Navy beans
- Almond butter (thinly spread)
- Ground walnuts
- Buckwheat porridge
- Jerusalem artichoke (steamedmashed)
- Parsnips (mashed)
- Nectarines

Beneficial

- Asparagus tips (soft-boiled)
- Goat's milk
- Garlic (cooked into puree)
- Skyr
- Kimchi (mildwashed)
- Apricots
- Green peas
- Flaxseeds (ground)
- Tempeh (crumbledcooked)
- Wholemeal sourdough
- Sauerkraut juice
- Blueberries
- Pomegranate juice (diluted)
- Chicory root fibre (in cereal)
- Quinoa
- Pearl barley
- Carrots (mashed)
- Banana puree
- Raspberries
- Broccoli florets
- Rolled oats

Precision Prebiotics

We advocate for a food-first approach to remodulating the paediatric gut microbiome, prioritising dietary diversity to establish a resilient microbial foundation. High-potency prebiotics and concentrated prebiotic compounds should only be introduced to a child's protocol under the direct supervision of a qualified health practitioner to ensure appropriate titration and tolerance. Following a comprehensive metagenomic analysis of the stool sample, the following ingredients have been identified as the most effective targeted substrates for this specific microbial profile, based on the latest peer-reviewed clinical research.

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

Most Suitable Prebiotics
Galacto-oligosaccharides
2'-Fucosyllactose
Inulin
Acacia Fibre

References

1 Arck, P. et al. (2010) 'Is there a "gut-brain-skin axis"?', Experimental Dermatology, 19(5), pp. 401–405.
2 Berni Canani, R. et al. (2017) 'The role of DNA methylation and epigenetic regulation in adipocyte differentiation', World Journal of Gastroenterology, 23(11), pp. 1919–1930.
3 Kalliomäki, M. et al. (2001) 'Probiotics in primary prevention of atopic disease: a randomised placebo-controlled trial', The Lancet, 357(9262), pp. 1076–1079.
4 Paller, A. S. et al. (2019) 'The microbiome in patients with atopic dermatitis', Journal of Allergy and Clinical Immunology, 143(1), pp. 26–35.
5 Salem, I. et al. (2018) 'The Gut Microbiome as a Major Regulator of the Gut-Skin Axis', Frontiers in Microbiology, 9, p. 1459.
6 Vaughn, A. R. et al. (2017) 'Effects of Oral Supplementation with Probiotics on Skin Wellness: A Systematic Review', Dermatology Online Journal, 23(5).
7 Feldman, M. T. et al. (2020) 'The Gut-Thyroid Axis and the Role of the Microbiome in Thyroid Diseases', Thyroid, 30(11), pp. 1685–1698.
8 Fröhlich, E. and Wahl, R. (2019) 'Microbiota and Thyroid Interaction in Health and Disease', Molecular BioSystems, 15(1), pp. 31–45.
9 Ishaq, H. M. et al. (2017) 'Molecular estimation of Altered Gastrointestinal Microbiota in Thyroid Dysfunctions', Microbial Pathogenesis, 110, pp. 31–39.
10 Knezevic, J. et al. (2020) 'Thyroid-Gut-Axis: How Does the Microbiota Affect Thyroid Function?', Nutrients, 12(6), p. 1769.
11 Virili, C. et al. (2018) 'Gut microbiota and Hashimoto's thyroiditis', Reviews in Endocrine and Metabolic Disorders, 19(4), pp. 293–300.
12 Bäckhed, F. et al. (2004) 'The gut microbiota as an environmental factor that regulates fat storage', PNAS, 101(44), pp. 15718–15723.
13 Gomes, A. C. et al. (2018) 'Gut microbiota, probiotics and diabetes', Nutrition Journal, 17(1), p. 35.
14 Ley, R. E. et al. (2006) 'Microbial ecology: Human gut microbes associated with obesity', Nature, 444(7122), pp. 1022–1023.
15 Turnbaugh, P. J. et al. (2006) 'An obesity-associated gut microbiome with increased capacity for energy harvest', Nature, 444(7122), pp. 1027–1031.
16 Vrieze, A. et al. (2012) 'Transfer of intestinal microbiota from lean donors increases insulin sensitivity in individuals with metabolic syndrome', Gastroenterology, 143(4), pp. 913–916.
17 Brial, F. et al. (2018) 'Metabolic syndrome and cardiovascular disease: the role of the gut microbiome', Disease Models & Mechanisms, 11(2).
18 Karlsson, F. H. et al. (2012) 'Symptomatic atherosclerosis is associated with an altered gut metagenome', Nature Communications, 3, p. 1245.
19 Tang, W. W. et al. (2013) 'Intestinal Microbial Metabolism of Phosphatidylcholine and Cardiovascular Risk', New England Journal of Medicine, 368(17), pp. 1575–1584.
20 Zhu, W. et al. (2016) 'Gut Microbial Metabolite TMAO Enhances Platelet Hyperreactivity and Thrombosis Risk', Cell, 165(1), pp. 111–124.
21 Abu-Shanab, A. and Quigley, E. M. (2010) 'The role of the gut microbiota in nonalcoholic fatty liver disease', Nature Reviews Gastroenterology & Hepatology, 7(12), pp. 691–701.
22 Miele, L. et al. (2009) 'Increased intestinal permeability and tight junction alterations in nonalcoholic fatty liver disease', Hepatology, 49(6), pp. 1877–1887.
23 Schwabe, R. F. and Jobin, C. (2013) 'The microbiome and cancer', Nature Reviews Cancer, 13(11), pp. 800–812.

References

24 Vajro, P. et al. (2011) 'Probiotics in obese children with nonalcoholic fatty liver disease', Journal of Pediatric Gastroenterology and Nutrition, 52(6), pp. 740–743.
25 Brusca, S. B. et al. (2014) 'The mucosal origins of rheumatoid arthritis', Current Opinion in Rheumatology, 26(3), pp. 320–328.
26 Scher, J. U. et al. (2013) 'Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis', eLife, 2, p. e01202.
27 Zhang, X. et al. (2015) 'The oral and gut microbiomes are perturbed in rheumatoid arthritis and partly normalized after treatment', Nature Medicine, 21(8), pp. 895–905.
28 Arvonen, M. et al. (2016) 'Gut microbiota and juvenile idiopathic arthritis', Current Rheumatology Reports, 18(11), p. 64.
29 Floyd, J. L. and Grant, M. B. (2020) 'The Gut-Eye Axis: Is There a Role for Gut Microbiota in Diabetic Retinopathy?', Clinical Science, 134(11), pp. 1215–1229.
30 Huang, Y. et al. (2021) 'The Gut Microbiome and Ocular Health', Frontiers in Cellular and Infection Microbiology, 11, p. 654.
31 Lin, P. (2019) 'The role of the intestinal microbiome in ocular inflammatory disease', Current Opinion in Ophthalmology, 30(6), pp. 446–452.
32 Napolitano, P. et al. (2021) 'The Gut Microbiome and Eye Diseases: A New Frontier', Journal of Personalized Medicine, 11(10), p. 1043.
33 Baker, J. M. et al. (2017) 'Estrogen–gut microbiome axis: Physiological and clinical implications', Maturitas, 103, pp. 45–53.
34 Chen, K. L. and Madak-Erdogan, Z. (2016) 'Estrogen and Microbiota Crosstalk: Should We Pay Attention?', Trends in Endocrinology & Metabolism, 27(11), pp. 752–755.
35 Kwa, M. et al. (2016) 'The Intestinal Microbiome and Estrogen Receptor–Positive Female Breast Cancer', JNCI: Journal of the National Cancer Institute, 108(8).
36 Plottel, C. S. and Blaser, M. J. (2011) 'Microbiome and Malignancy', Cell Host & Microbe, 10(4), pp. 324–335.
37 Borre, Y. E. et al. (2014) 'The impact of microbiota on brain and behavior: mechanisms & therapeutic potential', Advances in Experimental Medicine and Biology, 817, pp. 373–403.
38 Cryan, J. F. and Dinan, T. G. (2012) 'Mind-altering microorganisms: the impact of the gut microbiota on brain and behaviour', Nature Reviews Neuroscience, 13(10), pp. 701–712.
39 Hsiao, E. Y. et al. (2013) 'Microbiota modulate behavioral and physiological abnormalities associated with neurodevelopmental disorders', Cell, 155(7), pp. 1451–1463.
40 Mayer, E. A. et al. (2014) 'Gut/brain axis and the microbiota', Journal of Clinical Investigation, 124(10), pp. 4220–4225.
41 Budden, K. J. et al. (2017) 'Emerging roles of the gut-lung axis in infectious and chronic respiratory diseases', Nature Reviews Microbiology, 15(1), pp. 55–63.
42 Marsland, B. J. et al. (2015) 'The Gut-Lung Axis in Health and Disease', Annals of the American Thoracic Society, 12(Supplement 2), pp. S150–S156.
43 Samuelson, D. R. et al. (2015) 'The gut-lung axis: the microbial contribution to pulmonary health and disease', Respiratory Research, 16(1), p. 145.
44 Trompette, A. et al. (2014) 'Gut microbiota metabolism of dietary fiber influences allergic airway disease and hematopoiesis', Nature Medicine, 20(2), pp. 159–166.
45 Kalliomäki, M. et al. (2001) 'Probiotics in primary prevention of atopic disease: a randomised placebo-controlled trial', The Lancet, 357(9262), pp. 1076–1079.

References

46 Lyons, A. et al. (2010) 'Bacterial strain-specific induction of Foxp3+ T regulatory cells is protective in murine allergy models', Clinical & Experimental Allergy, 40(10), pp. 1561–1570.
47 Marsland, B. J. et al. (2015) 'The Gut-Lung Axis in Health and Disease', Annals of the American Thoracic Society, 12(Supplement 2), pp. S150–S156.
48 Round, J. L. and Mazmanian, S. K. (2009) 'The gut microbiota shapes intestinal immune responses during health and disease', Nature Reviews Immunology, 9(5), pp. 313–323.
49 Indrio, F. et al. (2014) 'Prophylactic use of Lactobacillus reuteri DSM 17938 and gastrointestinal functional outcomes in infants', JAMA Pediatrics, 168(3), pp. 228–233.
50 Savino, F. et al. (2009) 'Bacterial flora of breast-fed infants with infantile colic', Microbes and Environments, 24(3), pp. 201–205.
51 Savino, F. et al. (2010) 'Lactobacillus reuteri DSM 17938 in infantile colic: a randomized, double-blind, placebo-controlled trial', Pediatrics, 126(3), pp. e526–e533.
52 Sung, V. et al. (2018) 'Lactobacillus reuteri to Treat Infant Colic: A Meta-analysis', Pediatrics, 141(1), pp. e20171811.
53 Holscher, H. D. (2017) 'Metabolism of nutrients by the gut microbiota', Nutrition Reviews, 75(12), pp. 1011–1022.
54 Koh, A. et al. (2016) 'From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites', Cell, 165(6), pp. 1332–1345.
55 Rios-Covian, D. et al. (2016) 'Intestinal Short Chain Fatty Acids and their Link with Diet and Human Health', Frontiers in Microbiology, 7, p. 185.
56 Valdes, A. M. et al. (2018) 'Role of the gut microbiota in nutrition and health', BMJ, 361, p. k2179.
57 Cani, P. D. et al. (2008) 'Changes in gut microbiota control metabolic endotoxemia-induced inflammation', Diabetes, 57(6), pp. 1470–1481.
58 Sokol, H. et al. (2008) 'Faecalibacterium prausnitzii is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients', PNAS, 105(43), pp. 16731–16736.
59 Turner, J. R. (2009) 'Intestinal mucosal barrier function in health and disease', Nature Reviews Immunology, 9(11), pp. 799–809.
60 Zhang, M. et al. (2017) 'Akkermansia muciniphila: Can it be the Holy Grail of microbiota-oriented immune therapy?', Critical Reviews in Microbiology, 43(1), pp. 79–93.
61 Li, Y. et al. (2018) 'The Role of Microbiome in Insomnia, Circadian Disturbance and Depression', Frontiers in Psychiatry, 9, p. 669.
62 Smith, R. P. et al. (2019) 'Gut microbiome diversity is associated with sleep physiology in humans', PLoS ONE, 14(10), p. e0222394.
63 Thaiss, C. A. et al. (2014) 'Transkingdom Control of Microbiota Diurnal Oscillations Promotes Host Metabolic Homeostasis', Cell, 159(3), pp. 514–529.
64 Takada, M. et al. (2016) 'Probiotic Lactobacillus helveticus GMNL-42 attenuates stress-induced sleep disturbance', Journal of Sleep Research, 25, pp. 105–106.
65 David, L. A. et al. (2014) 'Diet rapidly and reproducibly alters the human gut microbiome', Nature, 505(7484), pp. 559–563.
66 Guerstein, M. et al. (2016) 'Intestinal Microbiota and Nutrient Absorption', Journal of Clinical Gastroenterology, 50, pp. S151–S153.
67 Hehemann, J. H. et al. (2010) 'Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota', Nature, 464(7290), pp. 908–912.

References

68 Jandhyala, S. M. et al. (2015) 'Role of the normal gut microbiota', World Journal of Gastroenterology, 21(29), pp. 8787–8803.
69 Bisanz, J. E. et al. (2014) 'Influence of probiotics and the gut microbiome on toxic metal levels in children', mBio, 5(5), pp. e01580-14.
70 Hatch, M. and Freel, R. W. (2013) 'The role of the gastrointestinal tract in oxalate homeostasis', Comprehensive Physiology, 3(4), pp. 1433–1456.
71 Monachese, M. et al. (2012) 'Bioremediation and Tolerance of Toxic Metals by Probiotic Bacteria', Applied and Environmental Microbiology, 78(18), pp. 6397–6404.
72 Siva, S. et al. (2009) 'A prevalence study of Oxalobacter formigenes in the flora of human faeces', BJU International, 103(10), pp. 1388–1391.
73 Pimentel, M. et al. (2003) 'Methane slows intestinal transit and augments small intestinal contractile activity', Am J Physiol Gastrointest Liver Physiol, 290(6), pp. G1089–G1095.
74 Ringel-Kulka, T. et al. (2011) 'Probiotic Bacteria Lactobacillus acidophilus NCFM and Bifidobacterium lactis Bi-07 Versus Placebo for the Symptoms of Bloating', Journal of Clinical Gastroenterology, 45(6), pp. 518–524.
75 Schmulson, M. J. and Chang, L. (2014) 'Review article: the management of functional abdominal bloating and distension', Alimentary Pharmacology & Therapeutics, 33(10), pp. 1071–1086.
76 Yoon, S. L. et al. (2014) 'Effect of multispecies probiotics on irritable bowel syndrome: a randomized, double-blind, placebo-controlled trial', Journal of Gastroenterology and Hepatology, 29(1), pp. 52–59.
77 Ianiro, G. et al. (2016) 'Digestive Enzyme Supplementation in Gastrointestinal Diseases', Current Drug Metabolism, 17(2), pp. 187–193.
78 Lynch, S. V. and Pedersen, O. (2016) 'The Human Intestinal Microbiome in Health and Disease', New England Journal of Medicine, 375(24), pp. 2369–2379.
79 Rodes, L. et al. (2013) 'Production of water-soluble vitamins by different species of Bifidobacterium and Lactobacillus', International Journal of Food Sciences and Nutrition, 64(4), pp. 476–485.
80 Santos, F. et al. (2008) 'The Role of the Gut Microbiota in Vitamin B12 and Folate Metabolism', Journal of Nutrition, 138(1), pp. 1–5.
81 Aarts, E. et al. (2017) 'Gut microbiome in ADHD and its relation to neural reward anticipation', PLoS ONE, 12(9), p. e0183509.
82 Bundgaard-Nielsen, C. et al. (2020) 'Gut microbiota profiles of children and adolescents with ADHD', Nutrients, 12(11), p. 3540.
83 Pärtty, A. et al. (2015) 'A possible link between early probiotic intervention and the risk of neuropsychiatric disorders', Pediatric Research, 77(6), pp. 823–828.
84 Wang, L. J. et al. (2020) 'Gut microbial dysbiosis associated with attention-deficit/hyperactivity disorder', Journal of Clinical Medicine, 9(1), p. 201.
85 Barton, W. et al. (2018) 'The microbiome of professional athletes differs from that of sedentary controls', Gut, 67(11), pp. 1944–1954.
86 Clarke, S. F. et al. (2014) 'Exercise and associated dietary extremes impact on gut microbial diversity', Gut, 63(12), pp. 1913–1920.
87 Scheiman, J. et al. (2019) 'Meta-omics analysis of elite athletes identifies a performance-enhancing bacterium that functions via lactate metabolism', Nature Medicine, 25(7), pp. 1104–1109.
88 Ticinesi, A. et al. (2019) 'Exercise and the gut microbiota: A review of the evidence', Nutrients, 11(12), p. 2997.
89 Allen, S. J. et al. (2010) 'Probiotics for treating acute infectious diarrhoea', Cochrane Database of Systematic Reviews, (11).

References

90 Guarino, A. et al. (2015) 'Probiotics for the prevention of pediatric antibiotic-associated diarrhea', Expert Opinion on Drug Safety, 14(11), pp. 1709–1717.
91 Hempel, S. et al. (2012) 'Probiotics for the prevention and treatment of antibiotic-associated diarrhea: a systematic review and meta-analysis', JAMA, 307(18), pp. 1959–1969.
92 Szakajlo, P. and Akst, L. M. (2012) 'Probiotics in the prevention of antibiotic-associated diarrhea in children', Journal of Pediatric Health Care, 26(2), pp. 105–113.
93 Comas-Basté, O. et al. (2020) 'Histamine Intolerance: The Current State of the Art', Biomolecules, 10(8), p. 1181.
94 Hrubisko, M. et al. (2021) 'Histamine Intolerance—The More We Know the Less We Know. A Review', Nutrients, 13(7), p. 2228.
95 Schink, M. et al. (2018) 'Microbial patterns in patients with histamine intolerance', Journal of Physiology and Pharmacology, 69(4), pp. 579–593.
96 Thomas, C. M. et al. (2012) 'Histamine-derived from intestinal Lactobacillus reuteri suppresses TNF via PKA and ERK activation', PLoS ONE, 7(2), p. e31951.
97 Finegold, S. M. et al. (2010) 'Analysis of the fecal bacterial flora in children with autism', Anaerobe, 16(4), pp. 444–453.
98 Hsiao, E. Y. et al. (2013) 'Microbiota modulate behavioral and physiological abnormalities associated with neurodevelopmental disorders', Cell, 155(7), pp. 1451–1463.
99 Kang, D. W. et al. (2017) 'Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms', Scientific Reports, 7(1), p. 451.
100 Vuong, H. E. and Hsiao, E. Y. (2017) 'Emerging Roles for the Gut Microbiome in Autism Spectrum Disorder', Biological Psychiatry, 81(5), pp. 411–423.
101 Borre, Y. E. et al. (2014) 'The impact of microbiota on brain and behavior: mechanisms & therapeutic potential', Adv Exp Med Biol, 817, pp. 373–403.
102 Bravo, J. A. et al. (2011) 'Ingestion of Lactobacillus strain regulates emotional behavior and central GABA receptor expression', PNAS, 108(38), pp. 16050–16055.
103 Cryan, J. F. and Dinan, T. G. (2012) 'Mind-altering microorganisms: the impact of the gut microbiota on brain and behaviour', Nature Reviews Neuroscience, 13(10), pp. 701–712.
104 Steenbergen, L. et al. (2015) 'A randomized controlled trial to test the effect of multispecies probiotics on cognitive reactivity to sad mood', Brain, Behavior, and Immunity, 48, pp. 258–264.
105 Bäckhed, F. et al. (2004) 'The gut microbiota as an environmental factor that regulates fat storage', PNAS, 101(44), pp. 15718–15723.
106 Everard, A. et al. (2013) 'Cross-talk between Akkermansia muciniphila and intestinal epithelium controls diet-induced obesity', PNAS, 110(22), pp. 9066–9071.
107 Ley, R. E. et al. (2006) 'Microbial ecology: Human gut microbes associated with obesity', Nature, 444(7122), pp. 1022–1023.
108 Turnbaugh, P. J. et al. (2006) 'An obesity-associated gut microbiome with increased capacity for energy harvest', Nature, 444(7122), pp. 1027–1031.
109 Kannampalli, P. et al. (2014) 'Microbiotic flora and visceral pain: the joint ventures', Current Opinion in Pharmacology, 19, pp. 88–94.
110 McVey Neufeld, K. A. et al. (2013) 'Effects of intestinal microbiota on the development of visceral pain in mice', Frontiers in Neuroscience, 7, p. 156.
111 Pärtty, A. et al. (2017) 'Probiotic intervention influence on infant gut microbiota and subsequent risk of functional abdominal pain', Pediatrics, 139(2).

References

112 Rousseaux, C. et al. (2007) 'Lactobacillus acidophilus modulates intestinal pain and induces opioid and cannabinoid receptors', Nature Medicine, 13(1), pp. 35–37.

113 Dimidi, E. et al. (2017) 'The effect of probiotics on functional constipation in adults: a systematic review', The American Journal of Clinical Nutrition, 100(4), pp. 1075–1084.

114 Müller, M. et al. (2018) 'Gastrointestinal Transit Time and Microbiota-Derived Metabolites', Gut Microbes, 9(2), pp. 183–191.

115 Tabbers, M. M. et al. (2011) 'Is Bifidobacterium breve effective in the treatment of childhood constipation?', Nutrition Journal, 10(1), p. 19.

116 Zhao, Y. and Yu, Y. B. (2016) 'Intestinal microbiota and sigmoid colon motility in patients with functional constipation', World Journal of Gastroenterology, 22(32), pp. 7305–7315.