



4025042

## COMPLETE MICROBIOME MAPPING


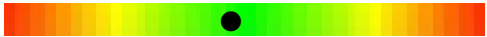



### General Macroscopic Description

	Result	Markers
Stool Colour	Brown	<b>Colour</b> - Brown is the colour of normal stool. Other colours may indicate abnormal gut health.
Stool Form	Semi-formed	<b>Form</b> -Sample form is categorised using the Bristol stool chart. A comment on stool appearance can be found in the comments section.
Mucous	Not Detected	<b>Mucous</b> - Mucous production may indicate the presence of an infection and/or inflammation.
Occult Blood	Negative	<b>Blood (Macro)</b> - The presence of blood in the stool may be the result of several causes besides colorectal bleeding, including hemorrhoids or gastrointestinal infection.

### Short Chain Fatty Acids

Result Range Units









Methodology: GC/MS

Short Chain Fatty Acids, Beneficial	61.5	> 13.6	umol/g	
Butyrate	21.3	10.8 - 33.5	%	
Acetate	47.6	44.5 - 72.4	%	
Propionate	28.4	0.0 - 32.0	%	
Valerate	2.7	0.5 - 7.0	%	

### GIT Functional Markers

Result Range Units

Methodology: FEIA, EIA, CLIA, pH electrode

Calprotectin.	<5.0	0.0 - 50.0	ug/g	
Pancreatic Elastase	537.0	> 200.0	ug/g	
Secretory (slgA)	516.5	510.0 - 2040.0	ng/mL	
Zonulin	25.3	0.0 - 107.0	ng/mL	
Beta glucuronidase	4887.4	368.0 - 6266.0	U/g	
Steatocrit	16.0 *H	0.0 - 10.0	%	
a-Transglutaminase IgA	<20	0.0 - 100.0	units/L	
pH	6.2 *L	6.3 - 7.7		

### Microbiome Mapping Summary

#### Parasites & Worms

#### Bacteria & Viruses

#### Fungi and Yeasts

#### Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio

0.10 < 1.00

RATIO



Relative Commensal Abundance of the 6 Phyla groups can be found on page 5 of this report



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THRIVE HEALTH  
SHOP 6/115 SHINGLEY DRIVE  
AIRLIE BEACH QLD 4802

**MARTYN LILLFORD**  
**02-Apr-1990** **Male**

240 FRONT STREET  
WHITSUNDAYS QLD 4802

LAB ID : 4025042  
UR NO. : 6297449  
Collection Date : 03-Sep-2024  
Received Date: 18-Sep-2024



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## Parasites and Worms.

### Parasitic Organisms

Result	Range	Units	
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●
<dl	< 5.0	x10 <sup>5</sup> org/g	●
<dl	< 1.0	x10 <sup>5</sup> org/g	●

### Worms

Ancylostoma duodenale, Roundworm	Not Detected		
Ascaris lumbricoides, Roundworm	Not Detected	Necator americanus, Hookworm	Not Detected
Trichuris trichiura, Whipworm	Not Detected	Enterobius vermicularis, Pinworm	Not Detected
Enterocytozoon spp	Not Detected	Hymenolepis spp, Tapeworm	Not Detected
Strongyloides spp, Roundworm	Not Detected	Taenia species, Tapeworm	Not Detected

Comment: Not Detected results indicate the absence of detectable DNA in the sample for the worms reported.  
NOTE: Reflex testing is performed on clinically indicated samples

## Opportunistic Bacteria/Overgrowth

Result	Range	Units	
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
<dl	< 3.00	x10 <sup>4</sup> CFU/g	●
<dl	< 1.00	x10 <sup>3</sup> CFU/g	●
<dl	< 5.00	x10 <sup>3</sup> CFU/g	●
<dl	< 3.00	x10 <sup>4</sup> CFU/g	●
<dl	< 1.00	x10 <sup>6</sup> CFU/g	●
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
0.12	< 1.00	x10 <sup>6</sup> CFU/g	●
0.29	< 5.00	x10 <sup>6</sup> CFU/g	●
<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
<dl	< 18.00	x10 <sup>6</sup> CFU/g	●
<dl	< 5.00	x10 <sup>5</sup> CFU/g	●

### Potential Autoimmune Triggers

<dl	< 5.00	x10 <sup>4</sup> CFU/g	●
<dl	< 5.00	x10 <sup>4</sup> CFU/g	●
<dl	< 5.00	x10 <sup>3</sup> CFU/g	●
<dl	< 5.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>9</sup> CFU/g	●
<dl	< 5.00	x10 <sup>5</sup> CFU/g	●
<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
0.32	< 10.00	x10 <sup>4</sup> CFU/g	●



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Mycology	Result	Range	Units	
Candida dubliniensis.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida glabrata.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida intermedia.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida krusei.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida lambica.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida lusitanae.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida parapsilosis.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida albicans.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida famata.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida keyfr.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Candida lipolytica.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Geotrichum species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Rhodotorula species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Saccharomyces cerevisiae:	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●

Bacterial Pathogens	Result	Range	Units	
Aeromonas hydrophila.	<dl	< 1.00	x10 <sup>3</sup> CFU/g	●
Campylobacter species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
C. difficile, Toxin A	<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
C. difficile, Toxin B	<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
Enterohemorrhagic E. coli	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Enteroinvasive E. coli/Shigella	<dl	< 1.00	x10 <sup>3</sup> CFU/g	●
Enterotoxigenic E. coli LT/ST	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Shiga-like Toxin E. coli stx1	<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
Shiga-like Toxin E. coli stx2	<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
Salmonella species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Vibrio species.	<dl	< 1.00	x10 <sup>4</sup> CFU/g	●
Yersinia species.	<dl	< 1.00	x10 <sup>5</sup> CFU/g	●
Helicobacter pylori	<dl	< 1.0	x10 <sup>3</sup> CFU/g	●

**Comment: Helico Pylori virulence factors will be listed below if detected POSITIVE**

H.pylori Virulence Factor, babA	Not Detected	H.pylori Virulence Factor, cagA	Not Detected
H.pylori Virulence Factor, dupA	Not Detected	H.pylori Virulence Factor, iceA	Not Detected
H.pylori Virulence Factor, oipA	Not Detected	H.pylori Virulence Factor, vacA	Not Detected
H.pylori Virulence Factor, virB	Not Detected	H.pylori Virulence Factor, virD	Not Detected

Viral Pathogens	Result	Range	Units
Adenovirus 40/41	Not Detected		
Norovirus GI/II	Not Detected		
Rotavirus A	Not Detected		
Sapovirus (I,II,IV,V)	Not Detected		
Astrovirus (hAstro)	Not Detected		

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Normal Bacterial GUT Flora	Result	Range	Units	
<i>Bacteroides fragilis</i>	228.2	1.6 - 250.0	x10 <sup>5</sup> CFU/g	
<i>Bifidobacterium adolescentis</i>	6.6	4.6 - 1000.0	x10 <sup>5</sup> CFU/g	
<i>Bifidobacterium bifidum</i>	<dl*L	4.6 - 1000.0	x10 <sup>6</sup> CFU/g	
<i>Bifidobacterium breve</i>	<dl*L	4.6 - 1000.0	x10 <sup>3</sup> CFU/g	
<i>Bifidobacterium longum</i>	123.1	4.6 - 1000.0	x10 <sup>4</sup> CFU/g	
<i>Enterococcus species</i>	<dl*L	1.9 - 2000.0	x10 <sup>3</sup> CFU/g	
<i>Escherichia species</i>	592.8	3.7 - 3800.0	x10 <sup>4</sup> CFU/g	
<i>Lactobacillus acidophilus</i>	<dl*L	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus casei</i>	<dl*L	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus delbrueckii</i>	3.9	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus plantarum</i>	<dl*L	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus rhamnosus</i>	2.6	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Lactobacillus salivarius</i>	<dl*L	1.7 - 500.0	x10 <sup>3</sup> CFU/g	
<i>Clostridium species</i>	9.5	5.0 - 50.0	x10 <sup>7</sup> CFU/g	
<i>Oxalobacter formigenes</i>	0.67*L	> 5.00	x10 <sup>6</sup> CFU/g	
<i>Akkermansia muciniphila</i>	1.80	1.00 - 50.00	x10 <sup>7</sup> CFU/g	
<i>Faecalibacterium prausnitzii</i>	9.3*L	200.0 - 3500.0	x10 <sup>6</sup> CFU/g	

## Actions

	<i>L. plantarum</i> HEAL9	<i>L. paracasei</i> 8700:2	<i>L. plantarum</i> 6595	<i>L. plantarum</i> 299V	<i>L. rhamnosus</i> GG	<i>L. acidophilus</i> LA02	<i>B. animalis</i> subsp. <i>lactis</i> B801	<i>L. casei</i> LC03	<i>B. breve</i> BR03	<i>L. fermentum</i> LF08	<i>L. crispatus</i> strains	<i>B. animalis</i> subsp. <i>lactis</i> BA05	<i>L. plantarum</i> LP01	<i>L. rhamnosus</i> LR06	<i>B. longum</i> 04	<i>L. fermentum</i> LF16	<i>L. salivarius</i> LS01	<i>B. breve</i> B632	<i>L. fermentum</i> LF10	<i>L. salivarius</i> LS03	<i>L. helveticus</i> Rosell-52	<i>L. rhamnosus</i> Rosell-11	<i>B. longum</i> Rosell-75	<i>S. boulardii</i> CNCM I-1079	<i>S. thermophilus</i> FP4
Intestinal epithelial barrier health																									
Mucous membrane health																									
Normalisation of bowel movements																									
Normalisation of bloating																									
Normalisation of peristalsis																									
Autoimmune immunomodulation																									
Inhibition of pathogenic overgrowth																									
Inactivate microbial toxins																									
Increase infection resistance																									
Th1/Th2 immune cell modulation																									
Staphylococci inhibition																									
Gut-brain axis support																									
GABA production																									
Bone resorption inhibition																									
E. coli inhibition																									
Oxalate degradation																									



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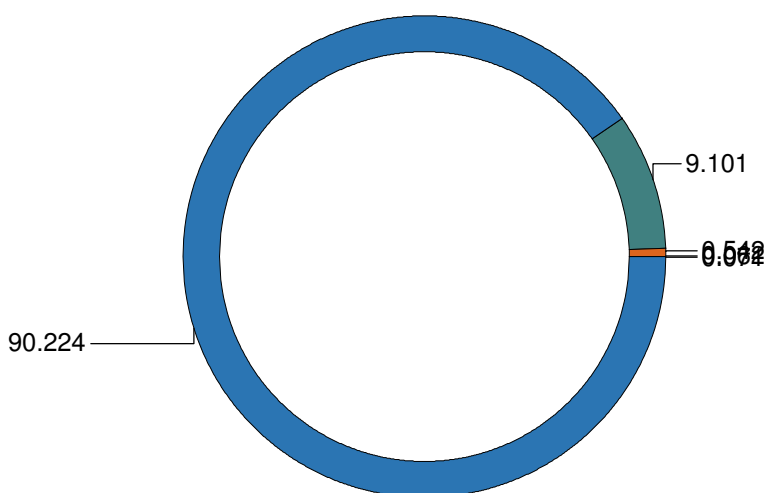
4025042

#### Introduction:

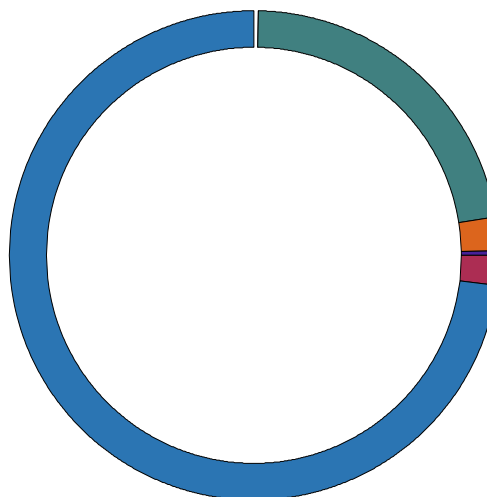
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider only cell counts, we are only about half human. In terms of gene counts, the microbiome contains about 200 times more genes than the human genome, making bacterial genes responsible for over 99% of our body's gene content! Of all the microbial communities in the human body, the gut microbiome is by far the most dense, diverse, and physiologically important ecosystem to our overall health.

Relative Commensal Abundance	Result	Range	Units
 Bacteroidetes Phylum	90.224	50.000 - 95.000	%
 Firmicutes Phylum	9.101	3.500 - 40.000	%
 Proteobacteria Phylum	0.542	0.050 - 12.500	%
 Actinobacteria Phylum	0.071	0.001 - 4.818	%
 Verrucomicrobia Phylum	0.062	0.000 - 2.400	%
 Euryarchaeota Phylum	0.000	0.000 - 0.010	%

**Your Phyla:**



**Healthy Phyla:**



#### References:

NOTE: Relative abundance reference ranges have been based on a healthy population study.

King CH, et., al. (2019) Baseline human gut microbiota profile in healthy people and standard reporting template. PLoS One. 2019 Sep 11;14(9):e0206484.



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## Pathogen Summary:

### Macroscopy Comment

BROWN coloured stool is considered normal in appearance.

Faecal Occult Blood Negative:

Faecal occult blood has not been detected in this specimen. If the test result is negative and clinical symptoms persist, additional follow-up testing using other clinical methods is recommended.

### Metabolism Comment

In a healthy gut Short Chain Fatty Acids (SCFAs) exhibited in the following proportions; Butyrate, Acetate, Propionate (16%:60%:24%).

The primary SCFAs butyrate, propionate and acetate are produced by predominant commensal bacteria via fermentation of soluble dietary fibre and intestinal mucus glycans.

Key producers of SCFAs include *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Bacteroides fragilis*, *Bifidobacterium*, *Clostridium* and *Lactobacillus* Spp.

The SCFAs provide energy for intestinal cells and regulate the actions of specialised mucosal cells that produce anti-inflammatory and antimicrobial factors, mucins that constitute the mucus barriers, and gut active peptides that facilitate appetite regulation and euglycemia. Abnormal SCFAs may be associated with dysbiosis, intestinal barrier dysfunction and inflammatory conditions.

LOW pH PRESENT: High Acidity stool.

Consider bacterial overgrowth, lipid or carbohydrate malabsorption, rapid transit time, pancreatic insufficiency.

Treatment:

- Supplement digestive enzymes or other digestive aids
- Assess other CDSA markers such as fat globules, food remnants, transglutaminase IgA & microbiology markers.
- Investigate causes of malabsorption or diarrhoea.



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## GIT Markers Comment

**PANCREATIC ELASTASE:** Normal exocrine pancreatic function.

Pancreatic Elastase reflects trypsin, chymotrypsin, amylase and lipase activity.

This test is not affected by supplements of pancreatic enzymes.

Healthy individuals should be producing >500 ug/g of PE-1 under normal/healthy conditions.

PE-1 levels between 200 - 500 ug/g may indicate suboptimal production.

PE-1 levels <200 ug/g indicate clear inadequate production.

The clinician should therefore consider digestive enzyme supplementation if one or more of the following conditions is present:

Loose watery stools, Undigested food in the stools, Post-prandial abdominal pain, Nausea or colicky abdominal pain, Gastroesophageal reflux symptoms, Bloating or food intolerance.

Testing performed by chemiluminescence immunoassay (CLIA).

**CALPROTECTIN Normal:**

Faecal calprotectin values <50 ug/g are not indicative of inflammation in the gastrointestinal tract. Subjects with low faecal calprotectin levels normally do not need to be further investigated by invasive procedures. In patients with strong clinical indications of intestinal inflammation, repeat testing may be useful.

Test performed by Phadia ELiA Fluorescence enzyme immunoassay (FEIA).

**SECRETORY IGA NORMAL:**

Secretory IgA is within range.

Secretory IgA represents the first line of defence of the gastrointestinal mucosa and is central to the normal function of the gastrointestinal tract as an immune barrier. Review this level with other pathogenic bacteria and normal commensal flora. Lower levels within reference range should be interpreted clinically.

**ZONULIN NORMAL:**

Zonulin is a protein that modulates intestinal barrier function. This results is considered normal.

**BETA-GLUCURONIDASE NORMAL:**

B-Glucuronidase is considered normal and is within reference range.

**ELEVATED STEATOCRIT:**

The presence of steatorrhea is an indirect indicator of incomplete fat digestion. Consider high dietary fat intake, cholestasis, malabsorption and digestion (diarrhoea, pancreatic or bile salt insufficiency), intestinal dysbiosis, parasites, NSAIDs use, short bowel syndrome, whipple disease, crohn's disease, food allergies & sensitivities.

Treatment:

- o Prebiotic and probiotic supplementation
- o Supplement hydrochloride, digestive enzymes or other digestive aids
- o Investigate underlying causes
- o Investigate food sensitivities and allergies
- o Remove potential irritants
- o Review markers such as pancreatic elastase 1 and calprotectin





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## Normal Bacterial Flora Comment

BIFIDOBACTERIUM BIFIDUM LOW:

PHYLUM: Actinobacteria

### DESCRIPTION:

Bifidobacterium bifidum is a Gram-positive, anaerobic bacterium integral to the human gut microbiota, especially in infants. It ferments a variety of carbohydrates, including human milk oligosaccharides, aiding in digestion, and promoting a healthy gut flora. B. bifidum produces short-chain fatty acids that lower gut pH and inhibit pathogenic bacteria while supporting intestinal cells. It also modulates the immune system, enhancing immune responses and reducing inflammation, and strengthens the intestinal barrier. Clinically, B. bifidum has shown promise in alleviating gastrointestinal disorders.

BIFIDOBACTERIUM BREVE LOW:

PHYLUM: Actinobacteria

### DESCRIPTION:

Bifidobacterium breve is a Gram-positive, anaerobic bacterium that is commonly found in the human gastrointestinal tract, particularly in the intestines of infants. B. breve is known for its ability to metabolise various carbohydrates, including human milk oligosaccharides, which is essential for the development of a healthy gut flora in newborns. Studies demonstrate that B. breve exhibits several beneficial properties, including the production of short-chain fatty acids (SCFAs) such as acetate, which contribute to gut health by lowering pH and inhibiting the growth of pathogenic bacteria. Additionally, B. breve may alleviate symptoms of irritable bowel syndrome (IBS) and improve symptoms of atopic dermatitis.

ENTEROCOCCUS SPECIES LOW:

PHYLUM: Firmicutes

### DESCRIPTION:

Enterococci are Gram-positive facultative anaerobic cocci commonly found in the environment, water, food, human skin, oral cavity and intestine. Strains belonging to the genus Enterococcus produce a wide variety of bacteriocins which are active against Gram-positive foodborne pathogens. Certain Enterococcus species have also been found to produce butyrate, a metabolic product that induces significant anti-inflammatory effects and contributes to intestine epithelial integrity. Low levels of enterococcus species may be associated with increased inflammation and susceptibility to foodborne pathogens. Review this with other beneficial flora.

TREATMENT SUGGESTIONS: Commensal probiotic cocktails are suggested to elevate colonization.

LACTOBACILLUS ACIDOPHILUS LOW:

PHYLUM: Firmicutes

### DESCRIPTION:

Lactobacillus acidophilus is a Gram-positive, rod-shaped, non-spore-forming bacterium commonly found in the human gut and fermented foods. It plays a key role in oxalate degradation, bowel normalisation and may assist patients with bloating.

### TREATMENT SUGGESTIONS:

Consider probiotic supplementation containing L. acidophilus.

LACTOBACILLUS CASEI LOW:

PHYLUM: Firmicutes

### DESCRIPTION:

Lactobacillus casei is a Gram-positive, rod-shaped, non-spore-forming, anaerobic probiotic bacterium involved in the fermentation of foods like cheese and yogurt. It produces antimicrobial substances, enhances gut barrier function, reduces pathogenic bacteria, and modulates the immune system. This bacterium is used to prevent and may assist various forms of diarrhea, including infectious diarrhea, traveller's diarrhea, and antibiotic-associated diarrhea.

### TREATMENT SUGGESTIONS:

Consider probiotic supplementation containing L. casei and consuming fermented foods such as cheese and yogurt.

LACTOBACILLUS PLANTARUM LOW:

PHYLUM: Firmicutes





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**DESCRIPTION:**

*Lactobacillus plantarum* is a Gram-positive, non-spore-forming, rod-shaped bacterium. *L. plantarum* plays a crucial role in gut health by enhancing intestinal barrier function, modulating the immune system, and inhibiting pathogenic bacteria. Additionally, it is beneficial for conditions such as irritable bowel syndrome, ulcerative colitis, and high cholesterol.

**TREATMENT SUGGESTIONS:**

Consider probiotic supplementation containing *L. plantarum*.

**LACTOBACILLUS SALIVARIUS LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

*Lactobacillus salivarius* is a Gram-positive, rod-shaped, non-spore-forming bacterium predominantly found in the human oral cavity, gastrointestinal tract, and vagina. It plays a significant role in maintaining oral and gut health by producing lactic acid and bacteriocins, which inhibit the growth of pathogenic bacteria. *L. salivarius* enhances gut barrier function, modulates the immune system, and helps in the digestion of proteins and complex carbohydrates. It has been studied for its potential benefits in managing conditions such as irritable bowel syndrome (IBS), periodontal disease, and atopic dermatitis, highlighting its importance in promoting overall health and preventing infections.

**TREATMENT SUGGESTIONS:**

Consider *L. salivarius* as a probiotic strain which may improve intestinal permeability and immune response.

**OXOLOBACTER FORMIGENES LOW:**

**PHYLUM:** Proteobacterium

**DESCRIPTION:**

*Oxalobacter formigenes* is a Gram negative oxalate-degrading anaerobic bacterium. Oxalate is formed in the liver by amino acid catabolism as well as present in a wide range of foods including tea, coffee, chocolate and certain fruits and vegetables. High concentration of oxalate in the urine is related to the potential formation of calcium oxalate kidney stones. *Oxalobacter Formigenes* is the main known bacterial species involved in oxalate degradation in the gut and maintains oxalate homeostasis. Levels of *O. Formigenes* tends to decrease with age as well as with the use of antibiotics or other drugs. Low levels may be associated with calcium oxide stone formation, inflammatory bowel disease or Crohn's.

**TREATMENT SUGGESTIONS:**

Treatment options include probiotic treatment and low oxalate diet modification. Urinary oxalate levels may also need to be investigated.

**FAECALIBACTERIUM PRAUSNITZII LOW:**

**PHYLUM:** Firmicutes

**DESCRIPTION:**

*Faecalibacterium prausnitzii* is gram-positive, rod-shaped, anaerobic and is one of the most abundant and important commensal bacteria of the human gut microbiota. It is a key producer of Short Chain Fatty acids, has anti-inflammatory properties and may improve the imbalance in intestinal bacteria that leads to dysbiosis. Decreased colonisation of *F. prausnitzii* in the intestines have been associated with Crohn's disease, obesity, asthma, and major depressive disorders.

**TREATMENT SUGGESTIONS:** Treatment may involve the use of probiotics, treatment of any intestinal infections and dietary modification.



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# The Four “R” Treatment Protocol

<b>REMOVE</b>	Using a course of antimicrobial, antibacterial, antiviral or anti parasitic therapies in cases where organisms are present. It may also be necessary to remove offending foods, gluten, or medication that may be acting as antagonists.  Consider testing IgG96 foods as a tool for removing offending foods.	ANTIMICROBIAL	Oil of oregano, berberine, caprylic acid
		ANTIBACTERIAL	Liquorice, zinc carnosine, mastic gum, tribulus, berberine, black walnut, caprylic acid, oil of oregano
		ANTIFUNGAL	Oil of oregano, caprylic acid, berberine, black walnut
		ANTIPARASITIC	Artemesia, black walnut, berberine, oil of oregano
		ANTIVIRAL	Cat's claw, berberine, echinacea, vitamin C, vitamin D3, zinc, reishi mushrooms
		BIOFILM	Oil of oregano, protease
<b>REPLACE</b>	In cases of maldigestion or malabsorption, it may be necessary to restore proper digestion by supplementing with digestive enzymes.	DIGESTIVE SUPPORT	Betaine hydrochloride, tilactase, amylase, lipase, protease, apple cider vinegar, herbal bitters
<b>REINOCULATE</b>	Recolonisation with healthy, beneficial bacteria. Supplementation with probiotics, along with the use of prebiotics helps re-establish the proper microbial balance.	PREBIOTICS	Slippery elm, pectin, larch arabinogalactans
		PROBIOTICS	Bifidobacterium animalis subsp. lactis, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccaromyces boulardii
<b>REPAIR &amp; REBALANCE</b>	Restore the integrity of the gut mucosa by giving support to healthy mucosal cells, as well as immune support. Address whole body health and lifestyle factors so as to prevent future GI dysfunction.	INTESTINAL MUCOSA IMMUNE SUPPORT	Saccaromyces boulardii, lauric acid
		INTESTINAL BARRIER REPAIR	L-Glutamine, aloe vera, liquorice, marshmallow root, okra, quercetin, slippery elm, zinc carnosine, Saccaromyces boulardii, omega 3 essential fatty acids, B vitamins
		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management