NutriPATH
INTEGRATIVE PATHOLOGY SERVICES
P: 1300 688 522
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VICKY TIECHE
25-Nov-1986 Female

27A SEYMOUR AVENUE
MASLIN BEACH SA 5170

-.KATHRYN MOLONEY
KATHRYN MOLONEY NATUROPATHY
22 YACCA WAY
ALDINGA SA 5173

LAB ID :	**4013814**
UR NO. :	**6296787**
Collection Date :	**12-Aug-2024**
Received Date:	**14-Aug-2024**

4013814

COMPLETE MICROBIOME MAPPING

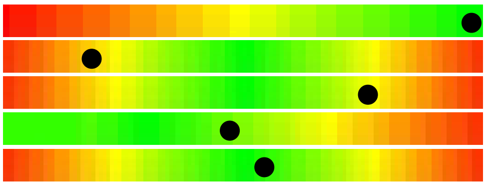
General Macroscopic Description

	Result	Markers
Stool Colour	**Brown**	**Colour** - Brown is the colour of normal stool. Other colours may indicate abnormal gut health.
Stool Form	**Semi-formed**	**Form** -Sample form is categorised using the Bristol stool chart. A comment on stool appearance can be found in the comments section.
Mucous	**Not Detected**	**Mucous** - Mucous production may indicate the presence of an infection and/or inflammation.
Occult Blood	**Negative**	**Blood (Macro)**- 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

Methodology: GC/MS

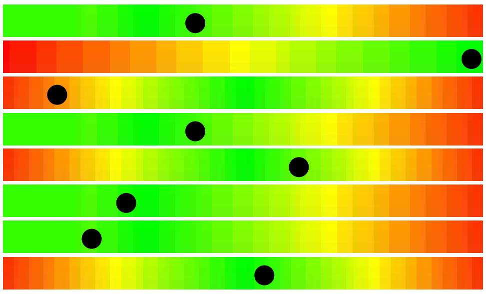
Short Chain Fatty Acids	Result	Range	Units
Short Chain Fatty Acids, Beneficial	**24.0**	> 13.6	umol/g
Butyrate	***8.2* *L**	10.8 - 33.5	%
Acetate	**72.3**	44.5 - 72.4	%
Propionate	**15.1**	0.0 - 32.0	%
Valerate	**4.4**	0.5 - 7.0	%



GIT Functional Markers

Methodology: FEIA, EIA, CLIA, pH electrode

GIT Functional Markers	Result	Range	Units
Calprotectin.	**19.0**	0.0 - 50.0	ug/g
Pancreatic Elastase	**>800.0**	> 200.0	ug/g
Secretory (sIgA)	***179.9* *L**	510.0 - 2040.0	ng/mL
Zonulin	**42.4**	0.0 - 107.0	ng/mL
Beta glucuronidase	**4964.0**	368.0 - 6266.0	U/g
Steatocrit	**<1.0**	0.0 - 10.0	%
a-Transglutaminase IgA	**<20**	0.0 - 100.0	units/L
pH	**7.1**	6.3 - 7.7	



Microbiome Mapping Summary

Parasites & Worms	Bacteria & Viruses	Fungi and Yeasts
Dientamoeba fragilis.	Pseudomonas aeruginosa. Desulfovibrio piger	Candida albicans.

Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio	**0.95**	< 1.00	RATIO

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

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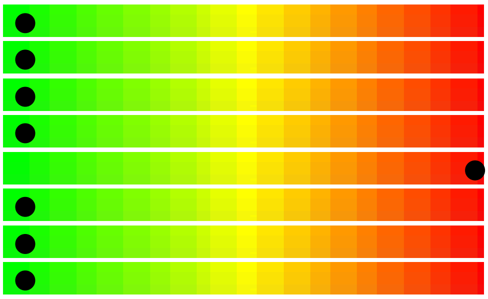
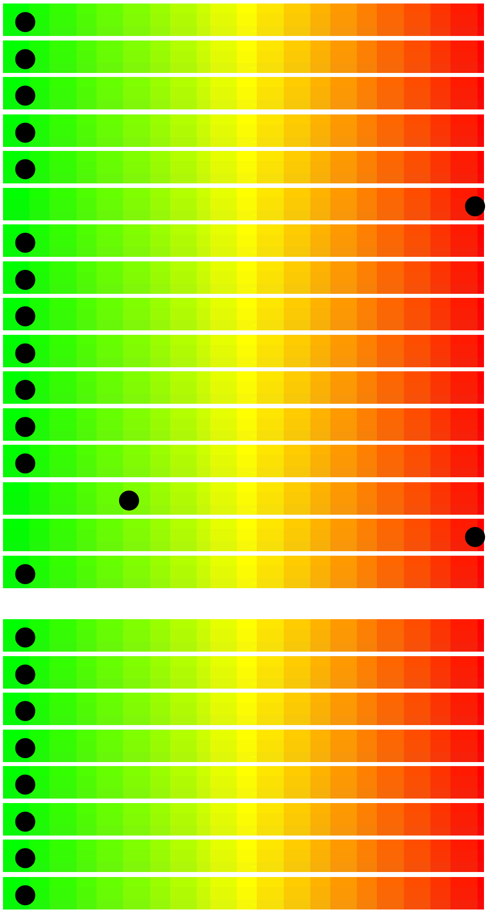
Parasites and Worms.	Result	Range	Units
Parasitic Organisms			
Cryptosporidium species	**<dl**	< 1.0	x10^5 org/g
Entamoeba histolytica.	**<dl**	< 1.0	x10^5 org/g
Giardia intestinalis	**<dl**	< 1.0	x10^5 org/g
Blastocystis hominis.	**<dl**	< 1.0	x10^5 org/g
Dientamoeba fragilis.	***14.6* *H**	< 1.0	x10^5 org/g
Endolimax nana	**<dl**	< 1.0	x10^5 org/g
Entamoeba coli.	**<dl**	< 5.0	x10^5 org/g
Pentatrichomonas hominis	**<dl**	< 1.0	x10^5 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
Bacillus species.	**<dl**	< 1.00	x10^4 CFU/g
Enterococcus faecalis	**<dl**	< 1.00	x10^5 CFU/g
Enterococcus faecium	**<dl**	< 1.00	x10^5 CFU/g
Morganella species	**<dl**	< 1.00	x10^5 CFU/g
Pseudomonas species	**<dl**	< 1.00	x10^4 CFU/g
Pseudomonas aeruginosa.	***9.58* *H**	< 3.00	x10^4 CFU/g
Staphylococcus species	**<dl**	< 1.00	x10^3 CFU/g
Staphylococcus aureus	**<dl**	< 5.00	x10^3 CFU/g
Streptococcus agalactiae.	**<dl**	< 3.00	x10^4 CFU/g
Streptococcus anginosus.	**<dl**	< 1.00	x10^6 CFU/g
Streptococcus mutans.	**<dl**	< 1.00	x10^4 CFU/g
Streptococcus oralis.	**0.28**	< 1.00	x10^6 CFU/g
Streptococcus salivarius.	**0.58**	< 5.00	x10^6 CFU/g
Methanobrevibacter smithii	**0.66**	< 1.00	x10^5 CFU/g
Desulfovibrio piger	***123.67* *H**	< 18.00	x10^6 CFU/g
Enterobacter cloacae complex.	**<dl**	< 5.00	x10^5 CFU/g
Potential Autoimmune Triggers			
Citrobacter species.	**<dl**	< 5.00	x10^4 CFU/g
Citrobacter freundii.	**<dl**	< 5.00	x10^4 CFU/g
Klebsiella species	**<dl**	< 5.00	x10^3 CFU/g
Klebsiella pneumoniae.	**<dl**	< 5.00	x10^5 CFU/g
Prevotella copri	**<dl**	< 1.00	x10^9 CFU/g
Proteus species	**<dl**	< 5.00	x10^5 CFU/g
Proteus mirabilis.	**<dl**	< 1.00	x10^4 CFU/g
Fusobacterium species	**3.08**	< 10.00	x10^4 CFU/g



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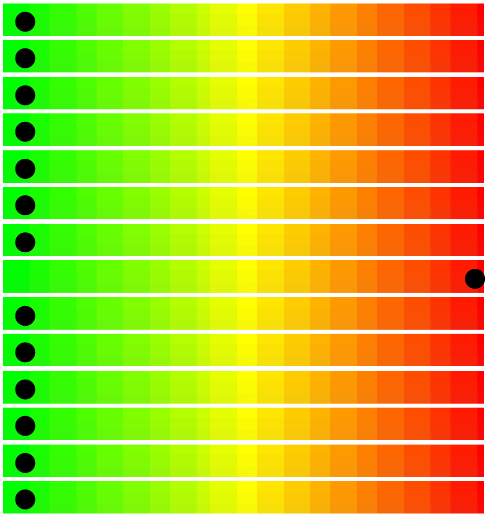
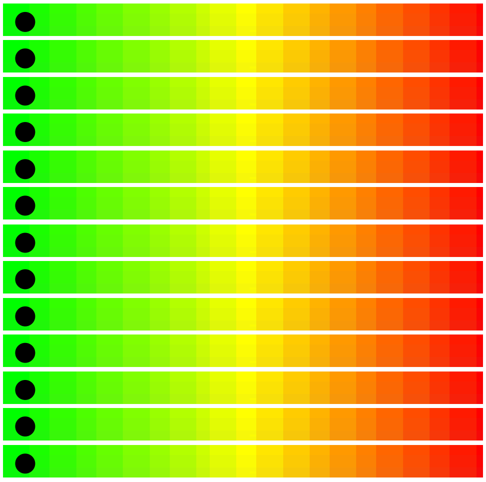
Mycology	Result	Range	Units
Candida dubliniensis.	<dl	< 1.00	x10^5 CFU/g
Candida glabrata.	<dl	< 1.00	x10^5 CFU/g
Candida intermedia.	<dl	< 1.00	x10^5 CFU/g
Candida krusei.	<dl	< 1.00	x10^5 CFU/g
Candida lambica.	<dl	< 1.00	x10^5 CFU/g
Candida lusitaniae.	<dl	< 1.00	x10^5 CFU/g
Candida parapsilosis.	<dl	< 1.00	x10^5 CFU/g
Candida albicans.	*1.60* *H	< 1.00	x10^5 CFU/g
Candida famata.	<dl	< 1.00	x10^5 CFU/g
Candida keyfr.	<dl	< 1.00	x10^5 CFU/g
Candida lipolytica.	<dl	< 1.00	x10^5 CFU/g
Geotrichum species.	<dl	< 1.00	x10^5 CFU/g
Rhodotorula species.	<dl	< 1.00	x10^5 CFU/g
Saccharomyces cerevisiae:	<dl	< 1.00	x10^5 CFU/g



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

GIT Functional markers performed by GCMS,EIA,FEIA.
Bacteriology,Virology,Fungi,Parasites & Worms performed by PCR,qPCR.
<dl = result below detectable limit. *H = Result greater than the reference range. *L = Result less than the reference range

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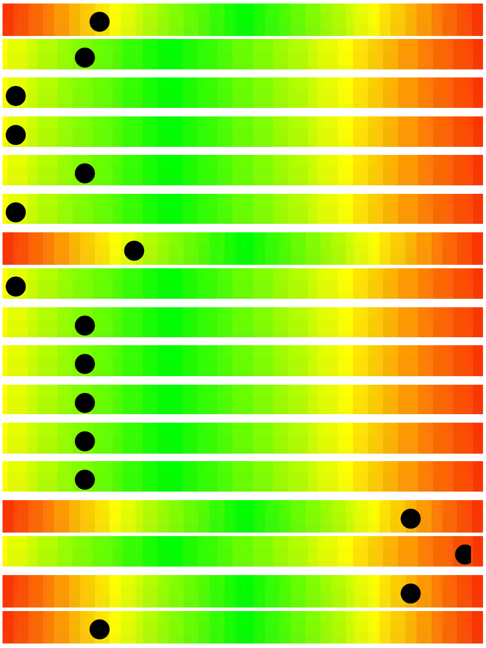
Normal Bacterial GUT Flora	Result	Range	Units
Bacteroides fragilis	4.9	1.6 - 250.0	x10^5 CFU/g
Bifidobacterium adolescentis	7.8	4.6 - 1000.0	x10^5 CFU/g
Bifidobacterium bifidum.	<dl *L	4.6 - 1000.0	x10^6 CFU/g
Bifidobacterium breve.	<dl *L	4.6 - 1000.0	x10^3 CFU/g
Bifidobacterium longum	7.0	4.6 - 1000.0	x10^4 CFU/g
Enterococcus species	<dl *L	1.9 - 2000.0	x10^3 CFU/g
Escherichia species	431.5	3.7 - 3800.0	x10^4 CFU/g
Lactobacillus acidophilus.	<dl *L	1.7 - 500.0	x10^3 CFU/g
Lactobacillus casei.	4.9	1.7 - 500.0	x10^3 CFU/g
Lactobacillus delbrueckii	17.6	1.7 - 500.0	x10^3 CFU/g
Lactobacillus plantarum.	11.7	1.7 - 500.0	x10^3 CFU/g
Lactobacillus rhamnosus	5.8	1.7 - 500.0	x10^3 CFU/g
Lactobacillus salivarius	2.0	1.7 - 500.0	x10^3 CFU/g
Clostridium species	*56.9* *H	5.0 - 50.0	x10^7 CFU/g
Oxalobacter formigenes	26.48	> 5.00	x10^6 CFU/g
Akkermansia muciniphila	*54.29* *H	1.00 - 50.00	x10^7 CFU/g
Faecalibacterium prausnitzii	312.7	200.0 - 3500.0	x10^6 CFU/g



Actions

	L. plantarum HEAL9	L. paracasei 8700:2	L. plantarum HEAL19	L. plantarum 6595	L. plantarum 299V	L. rhamnosus GG	L. acidophilus LA02	B. animalis subsp. lactis BS01	L. casei LC03	B. breve BR03	L. fermentum LF08	L. crispatus strains	B. animalis subsp. lactis BA05	L. plantarum LP01	L. rhamnosus LR06	B. longum 04	L. fermentum LF16	L. salivarius LS01	B. breve B632	L. fermentum LF10	L. salivarius LS03	L. helveticus Rosell-52	L. rhamnosus Rosell-11	B. longums Rosell-75	S. boulardii CNCM I-1079	S. thermophilus 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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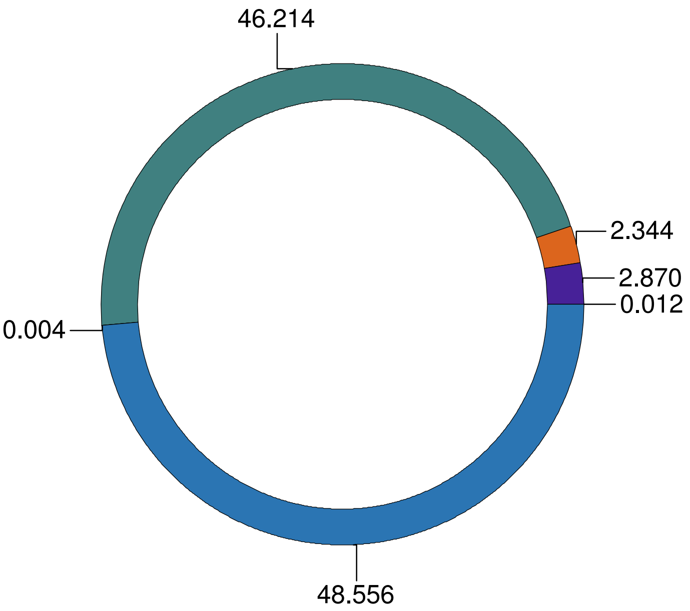
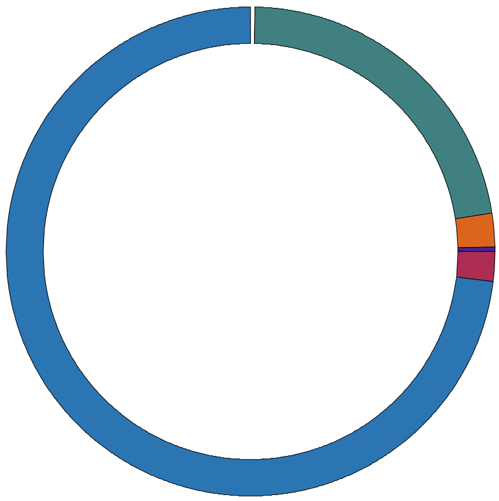
Introduction:
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, 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	*48.556* *L	50.000 - 95.000	%
🟩	Firmicutes Phylum	*46.214* *H	3.500 - 40.000	%
🟪	Verrucomicrobia Phylum	*2.870* *H	0.000 - 2.400	%
🟧	Proteobacteria Phylum	2.344	0.050 - 12.500	%
🟥	Actinobacteria Phylum	0.012	0.001 - 4.818	%
⬜	Euryarchaeota Phylum	0.004	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 mucinphila, 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 BUTYRATE LEVEL:
Butyrate is a short chain fatty acid that is extremely important for gut health. It is the main fuel source for gut cells, which helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Low levels of butyrate production have been observed in individuals with inflammatory bowel diseases, insufficient fibre intake, slow transit time, recent antibiotic therapy. Low butyrate may also be associated with an increased risk of colon cancer & constipation.

Consuming foods high in resistant starch has been shown to increase butyrate levels.

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 immunosassay (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).

LOW SECRETORY IGA:
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.

Secretory IgA binds to invading microorganisms and toxins and entrap them in the mucus layer or within the epithelial cells, so inhibiting microbial motility, agglutinating the organisms, and neutralising their exotoxins and then assist in their harmless elimination from the body in the faecal flow. sIgA also 'tags' food as acceptable, so low sIgA leads to increased sensitivity to foods.
Several studies link stress and emotionality with levels of sIgA. Production is adversely affected by stress, which is mediated by cortisol levels.
Often low levels of Secretory IgA correlates with low beneficial flora levels and an increase in pathogenic and parasitic organism being present.

Treatment: Investigate the root cause and rule out parasitic organisms or pathogenic bacteria. Consider the use of probiotics (saccharomyces boulardii), choline, essential fatty acids, glutathione, glycine, glutamine, phosphatidylcholine, Vitamin C and Zinc which are all required for efficient production of Secretory IgA.
PLEASE NOTE: A low Secretory IgA should be reviewed in conjunction with the stool formation. An artefactually low level may be due to fluid dilution effects in a watery or unformed/loose stool sample.

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

beta-GLUCORONIDASE NORMAL:
B-Glucuronidase is considered normal and is within reference range.

Parasites/Worms Comment

ELEVATED DIENTAMOEBA FRAGILIS LEVEL:
Dientamoeba fragilis appears to be extremely common and may have a cosmopolitan distribution, although there are large variations in prevalence. Dientamoeba fragilis has been linked to intestinal symptoms, especially in children. The most common symptoms associated with this organism are abdominal pain, intermittent diarrhoea, bloating and anorexia.

TREATMENT SUGGESTIONS:
Mild symptoms are self-limiting.
If treatment is warranted, metronidazole for 10 days or a single 2g dose of Tinidazole may be used. Tetracycline has also proven effective in adults.
Rule out allergy to above medication before prescribing/taking. Consult ID specialist if patient is showing severe symptoms or immunocompromised.

Opportunistic Bacteria Comment

PSEUDOMONAS AERUGINOSA ELEVATED:

PHYLUM: Proteobacteria

DESCRIPTION:
Pseudomonas aeruginosa is a gram-negative, aerobic, non-spore forming bacteria that can cause a variety of infections in both immunocompetent and immunocompromised hosts. It is commonly found in the environment, particularly in freshwater, hot tubs, and swimming pools. Chronic gastrointestinal colonization is acknowledged to be an important component of P. aeruginosa diarrheal disease and systemic infections. Since disruption of the normal flora by antibiotics can reduce colonization resistance and promote pathologic colonization with P. aeruginosa, enterocolitis due to P. aeruginosa may also be considered to be an antibiotic-associated gastroenteritis.

Pseudomonas aeruginosa in the gastrointestinal tract can cause inflammation, epithelial barrier dysfunction, tight cell junction interruption, and intestinal permeability.

TREATMENT SUGGESTIONS:
If treatment is warranted, Pseudomonas is usually susceptible to antipseudomonal penicillins, aminoglycosides, carbapenems, 3rd generation cephalosporins and gentamycin. Plant-derived anti-biofilm products identified against P. aeruginosa include alkaloids, organosulfur compounds, flavonoids, phenolic compounds and terpenoids. Rule out allergy to above medication before prescribing/taking.

DESULFOVIBRIO PIGER ELEVATED:

PHYLUM: Proteobacterium

DESCRIPTION:
Desulfovibrio piger is part of a group called sulfate-reducing bacteria (SRB) and are normal inhabitants of the intestine. Sulfate is present in different concentrations in the intestine dependent on diet. Remnants not absorbed, alongside the presence of lactate, promote the growth of SRB. Desulfovibrio Piger has been implicated in gastrointestinal disorders such as ulcerative colitis via the reduction of sulfate to hydrogen sulfide in the gut. High Delsulfovibrio piger levels may be associated with diarrhea or inflammatory bowel disease.

TREATMENT SUGGESTIONS:
Treatment options include lowering the intake of sulfate rich foods such as some breads, dried fruits, beers, ciders and wines. It is also suggested to avoid foods high in fat.

Phyla Microbiota Comment

FIRMICUTES (PHYLUM) ELEVATED:

DESCRIPTION:
Firmicutes are a phylum of diverse bacteria which are primarily grouped into classes, Bacilli, Clostridia, Erysipelotrichia and Negativicutes. They are found in various environments, including the intestinal tract, and the group includes some notable pathogens. Firmicutes are involved in energy resorption in the gut microbiome and levels may be affected by diet. Elevated levels and disturbance of gastrointestinal microbiome balance, particularly Firmicutes/Bacteroidetes ratio, have been associated with inflammation, obesity, diabetes and with a high sugar/ fat diet.

TREATMENT SUGGESTIONS: Consider using Bifidobacterium or Saccharomyces containing probiotics. It may also be suggested to optimise the patient diet. A lower fat diet may help to normalize Firmicutes levels.

VERRUCOMICROBIA (PHYLUM) ELEVATED:

DESCRIPTION:
Verrucomicrobia is a phylum of Gram-negative bacteria that contains only a few described species, found in the environment and gastrointestinal tract.
Akkermansia spp. is involved in gut membrane integrity and may be increased with polyphenols and prebiotics.

Verrucomicrobia aid in glucose homeostasis of the human gut and have anti-inflammatory properties that further aid in intestinal health.

TREATMENT SUGGESTIONS: Probiotic use and dietary modification use may assist in the rebalancing of microbial flora.

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.

CLOSTRIDIUM SPECIES ELEVATED:

PHYLUM: Firmicutes

DESCRIPTION:
Clostridium is a genus of anaerobic, Gram-positive bacteria found in the environment and the intestinal tract. This genus includes several species and can utilize large amounts of nutrients that cannot be digested by host and produce short-chain fatty acids (SCFAs), which play a noticeable role in intestinal homeostasis. Colonisation of Clostridium species may be affected by diet (carbohydrate and protein in diet) and general health and may be protective against inflammation and infection. However, some species may act as potential pathogens. Elevated Clostridium species may indirectly damage the intestinal epithelial cells. Another symptom may include constipation.

TREATMENT SUGGESTIONS: Treatment may involve the use of probiotics, treatment of any intestinal infections and dietary modification (reduce consumption of different fibres, such as inulin, oligofructose, arabinoxylan, guar gum and starch).

AKKERMANSIA MUCINIPHILA ELEVATED:

PHYLUM: Verrucomicrobia

DESCRIPTION:
Akkermansia muciniphila is a Gram-negative, strictly anaerobic, non-motile bacterium, often considered a human intestinal symbiont. There is growing evidence to suggest that the prevalence of this bacteria is associated with intestinal homeostasis, immunity, and a healthy gut. However, elevated colonisation may be associated with intestinal inflammation.

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

The Four “R” Treatment Protocol

REMOVE	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
REPLACE	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
REINOCULATE	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 sup lactise, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius ssp salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccaromyces boulardii
REPAIR & REBALANCE	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