



3901115

COMPLETE MICROBIOME MAPPING

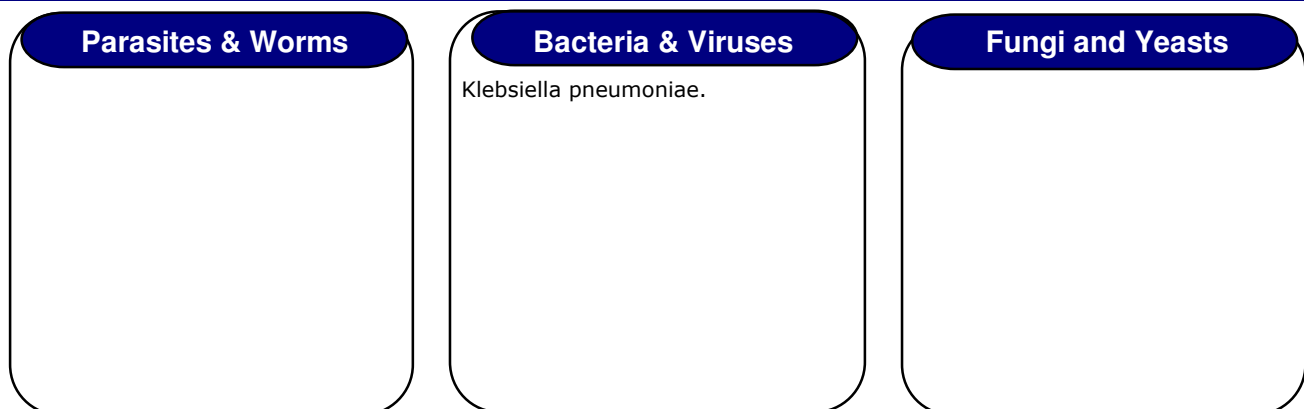
General Macroscopic Description

	Result	Markers
Stool Colour	Brown	Colour - Brown is the colour of normal stool. Other colours may indicate abnormal gut health.
Stool Form	Unformed	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	POSITIVE	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	Result	Range	Units	
Short Chain Fatty Acids, Beneficial	41.7	> 13.6	umol/g	
Butyrate	15.2	10.8 - 33.5	%	
Acetate	62.5	44.5 - 72.4	%	
Propionate	19.3	0.0 - 32.0	%	
Valerate	3.1	0.5 - 7.0	%	

GIT Functional Markers	Result	Range	Units	
Calprotectin.	5.0	0.0 - 50.0	ug/g	
Pancreatic Elastase	353.4	> 200.0	ug/g	
Secretory (slgA)	142.2 *L	510.0 - 2010.0	ug/g	
Zonulin	60.5	0.0 - 107.0	ng/g	
Beta glucuronidase	2734.2	337.0 - 4433.0	U/g	
Steatocrit	<1.0	0.0 - 15.0	%	
a-Transglutaminase IgA	<20	0.0 - 100.0	units/L	

Microbiome Mapping Summary



Key Phyla Microbiota

Firmicutes:Bacteroidetes Ratio

0.28

< 1.00

RATIO



Relative Commensal Abundance of the 6 Phyla groups can be found on page 4 of this report





3901115

Parasites and Worms.

Parasitic Organisms

Cryptosporidium species	<dl	< 1.0	x10 ⁶ org/g	
Entamoeba histolytica.	<dl	< 1.0	x10 ⁴ org/g	
Giardia intestinalis	<dl	< 1.0	x10 ³ org/g	
Blastocystis hominis.	<dl	< 1.0	x10 ³ org/g	
Dientamoeba fragilis.	<dl	< 1.0	x10 ⁵ org/g	
Endolimax nana	<dl	< 1.0	x10 ⁴ org/g	
Entamoeba coli.	<dl	< 5.0	x10 ⁶ org/g	
Pentatrichomonas hominis	<dl	< 1.0	x10 ² org/g	

Worms

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

Bacillus species.	<dl	< 1.00	x10 ⁵ CFU/g	
Enterococcus faecalis	<dl	< 1.00	x10 ⁴ CFU/g	
Enterococcus faecium	<dl	< 1.00	x10 ⁴ CFU/g	
Morganella species	<dl	< 1.00	x10 ³ CFU/g	
Pseudomonas species	<dl	< 1.00	x10 ⁴ CFU/g	
Pseudomonas aeruginosa.	<dl	< 3.00	x10 ² CFU/g	
Staphylococcus species	<dl	< 1.00	x10 ⁴ CFU/g	
Staphylococcus aureus	<dl	< 5.00	x10 ² CFU/g	
Streptococcus species	2.59	< 3.00	x10 ³ CFU/g	
Methanobrevibacter smithii	<dl	< 3.50	x10 ⁹ CFU/g	
Desulfovibrio piger	<dl	< 18.00	x10 ⁷ CFU/g	
Enterobacter complex.	<dl	< 5.00	x10 ⁶ CFU/g	

Potential Autoimmune Triggers

Citrobacter species.	<dl	< 5.00	x10 ⁵ CFU/g	
Citrobacter freundii.	<dl	< 5.00	x10 ⁵ CFU/g	
Klebsiella species	<dl	< 5.00	x10 ³ CFU/g	
Klebsiella pneumoniae.	5.55 *H	< 5.00	x10 ⁴ CFU/g	
Prevotella copri	<dl	< 1.00	x10 ⁷ CFU/g	
Proteus species	<dl	< 5.00	x10 ⁴ CFU/g	
Proteus mirabilis.	<dl	< 1.00	x10 ³ CFU/g	
Fusobacterium species	2.02	< 10.00	x10 ⁷ CFU/g	

Fungi & Yeast

Candida species.	<dl	< 5.00	x10 ³ CFU/g	
Candida albicans.	<dl	< 5.00	x10 ² CFU/g	
Geotrichum species.	<dl	< 3.00	x10 ² CFU/g	
Saccharomyces cerevisiae.	<dl	< 3.00	x10 ³ CFU/g	
Rhodotorula species.	<dl	< 1.00	x10 ³ CFU/g	



3901115

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

Normal Bacterial GUT Flora	Result	Range	Units	
Bacteroides fragilis	1.1 *L	1.6 - 250.0	x10 ⁹ CFU/g	
Bifidobacterium species	3.0 *L	> 6.7	x10 ⁷ CFU/g	
Bifidobacterium longum	2.2 *L	> 5.2	x10 ⁶ CFU/g	
Enterococcus species	184.6	1.9 - 2000.0	x10 ⁵ CFU/g	
Escherichia species	1355.0	3.7 - 3800.0	x10 ⁶ CFU/g	
Lactobacillus species	1007.9	8.6 - 6200.0	x10 ⁵ CFU/g	
Lactobacillus Rhamnosus	825.9	8.3 - 885.0	x10 ⁴ CFU/g	
Clostridium species	20.2	5.0 - 50.0	x10 ⁶ CFU/g	
Oxalobacter formigenes	16.00	> 15.00	x10 ⁷ CFU/g	
Akkermansia muciniphila	43.20	1.00 - 50.00	x10 ³ CFU/g	
Faecalibacterium prausnitzii	240.8	200.0 - 3500.0	x10 ³ CFU/g	

Methodology:

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



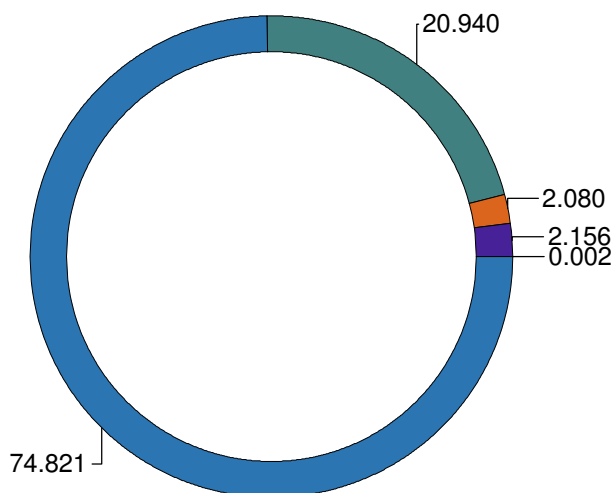
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Introduction:

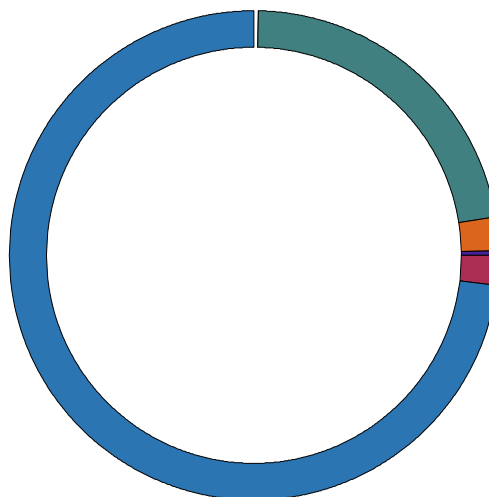
Your gut microbiome is a collective name for the 40 trillion cells and up to 1000 microbial species that include bacteria, viruses, fungi, parasites, and archaea and reside in our gut. The number of gut bacterial cells is approximately equal to the total number of human cells in our body, so if we consider 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	74.821	50.000 - 95.000	%
 Firmicutes Phylum	20.940	3.500 - 40.000	%
 Verrucomicrobia Phylum	2.156	0.000 - 2.400	%
 Proteobacteria Phylum	2.080	0.500 - 12.500	%
 Actinobacteria Phylum	0.002	0.001 - 4.818	%
 Euryarchaeota Phylum	0.000	0.000 - 0.017	%

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.



3901115

Pathogen Summary:

Macroscopy Comment

BROWN coloured stool is considered normal in appearance.

UNFORMED/LIQUID stools may indicate the presence of infection and/or inflammation.

Consider dysbiosis, food sensitivity, high dose vitamin C and magnesium, infection, intestinal permeability, laxative use, malabsorption, maldigestion, stress. Other causes: bacterial, fungal, viral and other parasitic infections.

Treatment:

- Investigate and treat possible underlying cause.
- Assess other gut markers (e.g pH, pancreatic elastase 1, etc).

FAECAL OCCULT BLOOD POSITIVE:

Faecal occult blood has been detected in this specimen. The presence of blood in the stool may be the result of several causes besides colorectal bleeding, including hemorrhoids or gastrointestinal infection. Results should be considered with other clinical information available to the physician.

Please note: A positive result indicates that the sample likely contains a human haemoglobin concentration >20ng/ml (Limit of detection).

Review this result with other inflammation markers such as calprotectin.

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.

SCFA PRODUCTION TABLE

BACTERIA	BUTYRATE	PROPIONATE	ACETATE
<i>Akkermansia muciniphila</i>		▲▲▲	▲▲
<i>Anaerostipes caccae</i>	▲▲▲		
<i>Bacteroides</i> spp.		▲▲▲	
<i>Bifidobacterium</i> spp.		▲	▲▲▲
<i>Blautia obeum</i>		▲▲	▲▲▲
<i>Coprococcus eutactus</i>	▲		
<i>Escherichia coli</i>			▲
<i>Eubacterium rectale</i>	▲▲		
<i>Faecalibacterium prausnitzii</i>	▲▲▲		
<i>Lactobacillus</i> spp.	▲	▲	▲
<i>Roseburia homini</i>	▲▲		
<i>Ruminococcus bromii</i>	▲		▲
<i>Subdoligranulum variabile</i>	▲		

KEY

▲ Low Producers

▲▲ Moderate Producers

▲▲▲ High Producers



P: 1300 688 522
E: info@nutripath.com.au

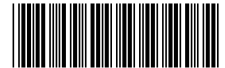
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COLIN BUTLER
02-Feb-1968

Male

15 KINTYRE CRESCENT
BANORA POINT NSW 2486

LAB ID : 3901115
UR NO. : 6199219
Collection Date : 26-Jun-2023
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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.

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.

BETA-GLUCURONIDASE NORMAL:

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

Opportunistic Bacteria Comment

METHANOBREVIBACTER SMITHII:

PHYLUM: Euryarchaeota

DESCRIPTION:

Methanobrevibacter smithii is a methane-producing microbe that plays an important role in the gut ecosystem by facilitating carbohydrate fermentation and production of short-chain fatty acids by commensal bacteria. Approximately 70% of the healthy cohort has below detectable levels of Methanobrevibacter smithii.

Potential Autoimmune Comments

KLEBSIELLA PNEUMONIAE ELEVATED:

PHYLUM: Proteobacteria

DESCRIPTION:

Klebsiella pneumoniae is a gram-negative, encapsulated, non-motile bacterium found in the environment and typically colonizes human mucosal surfaces of the oropharynx and gastrointestinal tract. Increased colonisation causes insult to the intestinal mucosa via the secretion of toxins and subsequent inflammatory response that may lead to inflammation-related gastrointestinal diseases. It is typically associated with diseases related to upper respiratory tract infection; however, elevated levels may be associated with gastrointestinal diseases such as Irritable bowel disease, Crohn's and ulcerative colitis.



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E: info@nutripath.com.au

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TREATMENT SUGGESTIONS:

Treating *K. pneumoniae* infections is difficult due to the increased emergence in resistant strains and if treatment is warranted, a combination of antibiotics may be used. *Klebsiella* appears to thrive in individuals on a high starch diet. Avoiding carbohydrates such as rice, potatoes, flour products and sugary foods may reduce the amount of *Klebsiella* in the gut. The use of herbal antimicrobials oregano (*Origanum vulgare*), sage (*Salvia officinalis*) or thyme (*Thymus vulgaris*) may also be effective.

Normal Bacterial Flora Comment

BACTEROIDES FRAGILIS LOW:

PHYLUM: Bacteroidetes

DESCRIPTION: *Bacteroides fragilis* is an anaerobic, Gram-negative bacterium. It is part of the normal microbiota of the human colon and is generally commensal. *Bacteroides fragilis* plays an intricate role in the human colon and usually has a beneficial relationship with the host. Low *Bacteroides fragilis* levels have been associated with inflammatory bowel disease and Crohn's.

TREATMENT SUGGESTIONS: Treatment may involve the use of probiotics and dietary modification.

BIFIDOBACTERIUM SPECIES LOW:

PHYLUM: Actinobacteria

DESCRIPTION:

Bifidobacterium is a genus of gram-positive, nonmotile anaerobic bacteria that are ubiquitous inhabitants of the gastrointestinal tract and considered a probiotic. *Bifidobacterium* species prevent diarrhea and intestinal infections, alleviate constipation, and stimulate the immune system. Low levels may be associated with irritable bowel syndrome, asthma, autism, depressive disorder and with pathogenic bacterial infection.

TREATMENT SUGGESTIONS: Treatment may involve the use of *Bifidobacterium* containing probiotics and treatment of any intestinal infection.

BIFIDOBACTERIUM LONGUM LOW:

PHYLUM: Actinobacteria

DESCRIPTION:

Bifidobacterium longum is a Gram-positive, catalase-negative, rod-shaped bacterium present in the human gastrointestinal tract and one of the *Bifidobacterium* species. It can induce and regulate immune responses, reduce the expression of inflammatory cytokines, and maintain the normal intestinal barrier function.

Bifidobacterium longum is a clinically effective, well-established, multifunctional probiotic that has a long history of human use in alleviating gastrointestinal, immunological, and infectious diseases such as constipation, antibiotic associated diarrhoea, irritable bowel syndrome and ulcerative colitis. Low levels may be associated with irritable bowel syndrome, asthma, autism, depressive disorder and with pathogenic bacteria infection.

TREATMENT SUGGESTIONS: Treatment may involve the use of *Bifidobacterium longum* containing probiotics and treatment of any intestinal infections.



3901115

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 subsp lactis, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius subsp salivarius, lactobacillus paracasei, lactobacillus rhamnosus, Saccharomyces 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	Saccharomyces boulardii, lauric acid
		INTESTINAL BARRIER REPAIR	L-Glutamine, aloe vera, liquorice, marshmallow root, okra, quercetin, slippery elm, zinc carnosine, Saccharomyces boulardii, omega 3 essential fatty acids, B vitamins
		SUPPORT CONSIDERATION	Sleep, diet, exercise, and stress management