NUTRI**PATH** · **PATIENT REPORT**
16 Harker St, Burwood VIC, 3125 • info@nutripath.com.au • 1300 688 522

NATA Accreditation: #20770

25203-0057

*** NutriPATH Pathology** NutriPath. 16 Harker Street, Burwood VIC 3125

Order ID	6386012
Lab ID	4119036
Patient ID	P002344
Ext ID	25203-0057

SHAE AITKEN

Sex: Female • 42yrs • 24-Jun-83
5/10-12 ALEXANDRIA PARADE, MAROOCHYDORE QLD 4558

RECEIVED
22-Jul-25

MICROBIOMIX

Specimen type - Stool, Spot

Collected
07-Jul-25 08.25am

MACROSCOPIC EXAMINATION AND OCCULT BLOOD

SERVICE	RESULT
Stool Colour	**Brown**
Stool Form	**Semiformed**

MACROSCOPIC EXAMINATION AND OCCULT BLOOD

SERVICE	INTERPRETATION
Mucous	Absent
Occult Blood	Negative

GIT FUNCTIONAL MARKERS

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Pancreatic Elastase 1	**721**		(>200)	ug/g
b-Glucuronidase	**2002**		(368-6266)	U/g
Calprotectin	**< 5.0**		(<50.0)	ug/g
Secretory IgA	**1540**		(510-2040)	ng/mL
Transglutaminase IgA	**14.0**		(0.0-100.0)	ug/g
Zonulin	**80**		(0-107)	ng/mL
Steatocrit	**19.0**	**H**	(0.0-10.0)	%
pH	**6.9**		(6.3-7.7)	

SHORT CHAIN FATTY ACIDS, BENEFICIAL

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Short Chain Fatty Acids, Beneficial	**26.0**		(>13.6)	umol/g
Butyrate	**12.70**		(10.80-33.50)	%
Acetate	**60.80**		(44.50-72.40)	%
Propionate	**22.50**		(0.00-32.00)	%
Valerate	**3.90**		(0.50-7.00)	%

Parasites & Worms

Blastocystis hominis

Bacteria and Viruses

Bacteroides vulgatus
Pseudoflavonifractor capillosus

Mycology

Candida tropicalis

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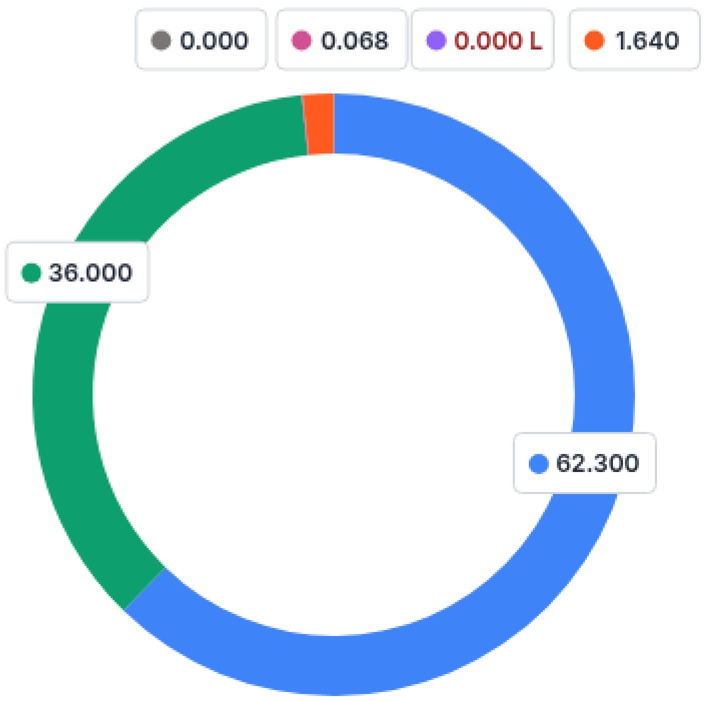
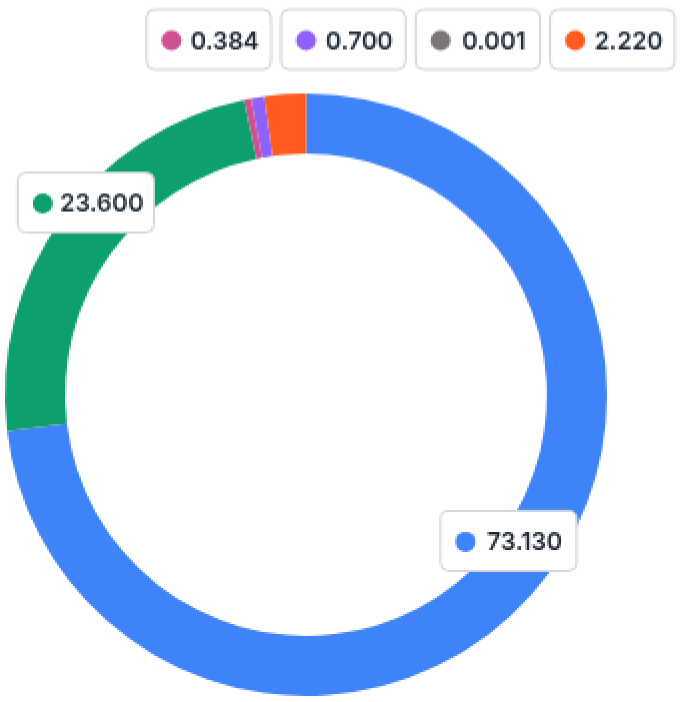
MICROBIOTA PHYLA

SERVICE	RESULT	H/L	REF - RANGE	UNITS
● Actinobacteria Phylum	0.068		(0.052-1.820)	%
● Bacteroidetes Phylum	62.300		(55.200-91.130)	%
● Euryarchaeota Phylum	0.000		(<0.003)	%
● Firmicutes Phylum	36.000		(6.630-42.300)	%
● Proteobacteria Phylum	1.640		(0.357-4.000)	%
● Verrucomicrobia Phylum	0.000	L	(0.010-5.000)	%

Your Phyla



Healthy Phyla



GUT MICROBIAL DIVERSITY

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Shannon Diversity Index	2.53		(2.15-3.50)	
Simpson Diversity Index	0.88		(0.80-1.00)	

MICROBIOTA RATIOS

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Firmicutes/Bacteroidetes ratio	0.58		(<1.00)	ratio
Fus. nucleatum/Faec. prausnitzii ratio	0.00		(<1.00)	ratio
Gram-Positive/Gram-Negative ratio	0.56		(0.40-1.50)	ratio
Prevotella/Bacteroides ratio	0.00		(0.00-0.15)	ratio
Proteobacteria/Actinobacteria	24.22	H	(0.00-8.00)	ratio

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IMPORTANT BIOCHEMICAL FUNCTIONS

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Ageing Factors (Oxidative Stress)	0.4920		(<1.0000)	%
Ammonia/Urease Production	0.1320		(<0.5000)	%
Branched Chain AA Production	2.6100		(<5.0000)	%
Carbohydrate Metabolism	5.5000		(3.0000-7.0000)	%
Histamine Production	0.0000		(<1.0000)	%
Iron/Other Ion Metabolism	1.7100		(<3.0000)	%
Indolepropionic Acid (IPA) Production	6.8600		(>1.0000)	%
Lipid Metabolism	6.6500		(4.0000-8.0000)	%
Lipopolysaccharides (LPS) Production	2.9400		(<4.0000)	%
Protein/Other Energy Metabolism	12.7000		(9.0000-18.0000)	%
Sulphate Production	1.9200		(<3.0000)	%
Trimethylamine (TMA) Production	0.0001		(<0.3000)	%

DISEASE RISKS

SERVICE	RESULT
Colon Cancer Risk	Low Risk
Crohns Disease Risk	Low Risk
Fatty Liver Risk	Low Risk
Type 2 Diabetes Risk	Low Risk
Ulcerative Colitis Risk	Low Risk

Disease Risk Disclaimer:

The results from this shotgun microbiome sequencing analysis are for informational and research purposes only. They do not diagnose, treat, or predict any disease or health condition. While certain bacterial compositions may be associated with an increased or decreased risk of specific health outcomes, having a higher risk does not mean you will develop the disease, nor does a lower risk guarantee protection.

The microbiome is a complex and dynamic ecosystem influenced by various factors, including diet, lifestyle, genetics, and environment. These results should be interpreted in conjunction with other clinical assessments and professional medical advice.

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BACTERIAL PATHOGENS

	SERVICE	RESULT	H/L	REF - 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)	x10^3 CFU/g
🟢	**C. difficile, Toxin B**	**<dL**		(<1.00)	x10^3 CFU/g
🟢	**Clostridium difficile, Hypervirulent**	**<dL**		(<1.00)	x10^3 CFU/g
🟠	**Enteroaggregative E. coli**	**<dL**		(<1.00)	x10^3 CFU/g
🟠	**Enteropathogenic E. coli**	**0.17**		(<1.00)	x10^3 CFU/g
🟠	**E. coli O157**	**<dL**		(<1.00)	x10^2 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
🟠	**Salmonella species**	**<dL**		(<1.00)	x10^5 CFU/g
🟠	**Shiga toxigenic E. coli**	**<dL**		(<1.00)	x10^3 CFU/g
🟠	**Vibrio species**	**<dL**		(<1.00)	x10^4 CFU/g
🟠	**Yersinia species**	**<dL**		(<1.00)	x10^5 CFU/g
🟠	**Helicobacter pylori**	**<dL**		(<1.00)	x10^3 CFU/g

H.Pylori Virulence Factors

SERVICE	RESULT
Virulence Factor, babA	Not Detected
Virulence Factor, cagA	Not Detected
Virulence Factor, dupA	Not Detected
Virulence Factor, iceA	Not Detected
Virulence Factor,oipA	Not Detected
Virulence Factor, vacA	Not Detected
Virulence Factor, virB	Not Detected
Virulence Factor, virD	Not Detected

H.Pylori Resistance Genes

SERVICE	RESULT
Resistance gene A2142C	Not Detected
Resistance gene A2142G	Not Detected
Resistance gene A2143G	Not Detected

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MYCOLOGY

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Candida albicans	<dL		(<1.00)	x10^5 CFU/g
Candida dubliniensis	<dL		(<1.00)	x10^5 CFU/g
Candida famata	<dL		(<1.00)	x10^5 CFU/g
Candida glabrata	<dL		(<1.00)	x10^5 CFU/g
Candida guilliermondii	<dL		(<1.00)	x10^5 CFU/g
Candida intermedia	<dL		(<1.00)	x10^5 CFU/g
Candida kefyr	<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 lipolytica	<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 tropicalis	12.00	H	(<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

PATHOGENS / OPPORTUNISTIC PATHOGENS

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Abiotrophia defectiva	<dL		(<0.010)	%
Acinetobacter baumannii	<dL		(<0.010)	%
Acinetobacter haemolyticus	<dL		(<0.010)	%
Acinetobacter junii	<dL		(<0.010)	%
Bacteroides caccae	<dL		(<3.000)	%
Bacteroides fragilis	1.330		(<2.000)	%
Bacteroides vulgatus	8.220	H	(<7.500)	%
Bilophila wadsworthia	<dL		(<0.120)	%
Citrobacter freundii	<dL		(<0.010)	%
Citrobacter koseri	<dL		(<0.010)	%
Citrobacter youngae	<dL		(<0.010)	%
Corynebacterium urealyticum	<dL		(<0.010)	%
Desulfovibrio piger	<dL		(<0.120)	%
Enterobacter cloacae	<dL		(<0.010)	%
Enterococcus casseliflavus	<dL		(<0.010)	%

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SERVICE	RESULT	H/L	REF - RANGE	UNITS
● Enterococcus faecalis	<dL		(<0.010)	%
● Enterococcus faecium	<dL		(<0.010)	%
● Enterococcus gallinarum	<dL		(<0.010)	%
● Escherichia coli	0.011		(<3.000)	%
● Fusobacterium nucleatum	<dL		(<0.010)	%
● Fusobacterium ulcerans	<dL		(<0.010)	%
● Klebsiella oxytoca	<dL		(<0.010)	%
● Klebsiella pneumoniae	<dL		(<0.010)	%
● Methanobrevibacter smithii	<dL		(<0.010)	%
● Morganella morganii	<dL		(<0.010)	%
● Mycoplasma hominis	<dL		(<0.010)	%
● Prevotella amnii	<dL		(<0.010)	%
● Prevotella bivia	<dL		(<0.010)	%
● Prevotella melaninogenica	<dL		(<0.010)	%
● Proteus mirabilis	<dL		(<0.010)	%
● Providencia rettgeri	<dL		(<0.010)	%
● Pseudoflavonifractor capillosus	0.113	H	(<0.010)	%
● Pseudomonas aeruginosa	<dL		(<0.010)	%
● Staphylococcus aureus	<dL		(<0.010)	%
STREPTOCOCCUS TOTAL	0.003		(<0.030)	%
● Streptococcus agalactiae	<dL		(<0.010)	%
● Streptococcus anginosus	<dL		(<0.010)	%
● Streptococcus dysgalactiae	<dL		(<0.010)	%
● Streptococcus mutans	<dL		(<0.010)	%
● Streptococcus pyogenes	<dL		(<0.010)	%
● Streptococcus salivarius	0.003		(<0.030)	%
● Streptococcus suis	<dL		(<0.010)	%
● Veillonella parvula	0.004		(<0.030)	%

● Actinobacteria Phylum ● Bacteroidetes Phylum ● Euryarchaeota Phylum ● Firmicutes Phylum ● Proteobacteria Phylum ● Verrucomicrobia Phylum

PROBIOTICS / BENEFICIAL BACTERIA

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Akkermansia muciniphila	<dL	L	(0.010-5.000)	%
Bacteroides thetaiotaomicron	1.050		(0.080-3.400)	%
Bacteroides uniformis	23.700	H	(0.500-16.000)	%
BIFIDOBACTERIUM TOTAL	0.000	L	(0.001-5.000)	%
Bifidobacterium adolescentis	<dL		(<10.000)	%
Bifidobacterium animalis	<dL		(<2.000)	%
Bifidobacterium bifidum	<dL		(<5.000)	%
Bifidobacterium breve	<dL		(<1.000)	%
Bifidobacterium longum	<dL		(<15.000)	%
Bifidobacterium pseudolongum	<dL		(<0.500)	%
Clostridium butyricum	<dL		(<0.001)	%
Faecalibacterium prausnitzii	8.120		(0.860-14.350)	%
LACTOBACILLUS TOTAL	0.010		(0.001-1.000)	%
Lactobacillus acidophilus	<dL		(<0.100)	%
Lactobacillus casei paracasei	<dL		(<0.200)	%
Lactobacillus crispatus	<dL		(<0.050)	%
Lactobacillus delbrueckii	<dL		(<0.050)	%
Lactobacillus fermentum	<dL		(<0.100)	%
Lactobacillus gasseri	<dL		(<0.100)	%
Lactobacillus helveticus	<dL		(<0.050)	%
Lactobacillus johnsonii	<dL		(<0.050)	%
Lactobacillus plantarum	0.000		(<0.200)	%
Lactobacillus reuteri	<dL		(<0.200)	%
Lactobacillus rhamnosus	0.010		(<0.100)	%
Lactobacillus salivarius	<dL		(<0.050)	%
Lactococcus lactis.	<dL		(<0.010)	%
Oxalobacter formigenes	<dL	L	(>0.001)	%
Pediococcus acidilactici	<dL		(<0.030)	%
Pediococcus pentosaceus	<dL		(<0.020)	%
Roseburia hominis	2.750	H	(0.010-0.900)	%
Roseburia intestinalis	<dL		(<3.730)	%
Roseburia inulinivorans	1.230		(0.010-3.560)	%
Streptococcus thermophilus	<dL		(<0.300)	%

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PARASITES

SERVICE	RESULT	H/L	REF - RANGE	UNITS
Blastocystis hominis	1.4	H	(<1.0)	x10^5 org/g
Cryptosporidium species	<dL		(<1.0)	x10^5 org/g
Dientamoeba fragilis	<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 Subtypes

SERVICE	RESULT
Subtype 1	Negative
Subtype 2	Negative
Subtype 3	Negative
Subtype 4	Negative
Subtype 5	Negative
Subtype 6	Negative
Subtype 7	Negative
Subtype 8	Negative
Subtype 9	Negative

HELMINTHS

SERVICE	RESULT
Ascaris lumbricoides, Roundworm	Not Detected
Enterobius vermicularis, Pinworm	Not Detected
Enterocytozoon spp	Not Detected
Hymenolepis spp, Tapeworm	Not Detected

HELMINTHS

SERVICE	RESULT
Necator americanus, Hookworm	Not Detected
Strongyloides spp, Roundworm	Not Detected
Taenia species, Tapeworm	Not Detected
Trichuris trichiura, Whipworm	Not Detected

VIRUSES

SERVICE	RESULT
Adenovirus 40/41	Not Detected
Astrovirus (hAstro)	Not Detected
Norovirus GI/II	Not Detected

VIRUSES

SERVICE	RESULT
Rotavirus A	Not Detected
Sapovirus (I,II,IV,V)	Not Detected

Macroscopy Comment

SEMI-FORMED STOOL:

A SEMI-FORMED stool specimen classified as Type 4 on the Bristol Stool Chart is generally considered optimal, indicating balanced gut motility, adequate hydration, and sufficient dietary fibre intake. This stool consistency is often associated with efficient digestion, proper colonic function, and microbial stability. However, while Type 4 stools typically suggest gastrointestinal homeostasis, they do not always correlate with a healthy gut microbiome. Pathogenic bacteria, viral infections, parasitic infestations, or gut dysbiosis may still be present, even in well-formed stools. Clinical recommendations include maintaining a fiber-rich diet with prebiotic and probiotic sources, ensuring consistent hydration, and promoting gut microbial diversity through fermented foods or supplementation.

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.

GIT Markers Comment

PANCREATIC ELASTASE NORMAL (>200 ug/g):

A faecal pancreatic elastase level >200 ug/g indicates normal exocrine pancreatic function.

beta-GLUCORONIDASE NORMAL:

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

ACCREDITATION SCOPE: Please note that the above test is currently not under the laboratory's scope of accreditation.

CALPROTECTIN NORMAL (<50 ug/g):

A normal faecal calprotectin level (<50 ug/g) is not suggestive of active gastrointestinal inflammation.

Calprotectin <50 ug/g is typically seen in healthy individuals or those with functional gastrointestinal disorders such as irritable bowel syndrome (IBS). No further invasive testing is usually required unless clinical symptoms persist or escalate. In patients with strong clinical indications of intestinal inflammation, repeat testing may be useful.

FAECAL TRANSGLUTAMINASE IgA: Negative

Tissue Transglutaminase is the most specific test for Coeliac Disease. Levels less than 100 are considered NEGATIVE.

Treatment:

No treatment required. However, If there is clinical suspicion of Coeliac disease consider testing serum Coeliac markers. Also assess IgG/IgA Food sensitivity tests to identify specific food intolerances.

ACCREDITATION SCOPE: Please note that the above test is currently not under the laboratory's scope of accreditation.

ZONULIN HIGH NORMAL:

Zonulin is a protein that modulates intestinal barrier function and can also be considered as a potential inflammatory marker. Although this result is within range, the result should be interpreted with patient clinical symptoms as well as reviewing the presence of other proteobacteria that may be the result of increased Zonulin.

ACCREDITATION SCOPE: Please note that the above test is currently not under the laboratory's scope of accreditation.

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

Dominant Phyla Comment

VERRUCOMICROBIA PHYLUM LOW:

Verrucomicrobiota is a phylum of Gram-negative bacteria that contains only a few described species, found in the environment and gastrointestinal tract. Verrucomicrobia aid in glucose homeostasis of the human gut and have anti-inflammatory properties that further aid in intestinal health. Decreased colonisation of Verrucomicrobia phylum may be associate with inflammation.

Microbiota Ratios Comment

PROTEOBACTERIA/ACTINOBACTERIA RATIO:

In general, the P/A ratio could serve as a potential indicator of gut microbiota balance or dysbiosis. Actinobacteria, particularly members like Bifidobacterium, are known for their health-promoting properties, including the production of short-chain fatty acids (SCFAs) and modulation of the immune system. In contrast, an overrepresentation of Proteobacteria is often associated with a state of dysbiosis and has been linked to various inflammatory and metabolic diseases. A higher P/A ratio might indicate a shift towards a less favorable gut microbiota composition, potentially signifying an increased risk of inflammation or disease.

Mycology Comment

CANDIDA TROPICALIS ELEVATED:

Candida tropicalis is a common gut inhabitant that can become pathogenic under certain conditions. Overgrowth of C. tropicalis can cause symptoms such as abdominal pain, bloating, and changes in bowel habits. It is known for its potential to translocate across the gut barrier, leading to systemic infections, especially in immunocompromised patients.

Pathogens/Opportunistic Pathogens Comment

BACTEROIDES VULGATUS ELEVATED: PHYLUM: Bacteroidetes

DESCRIPTION: Bacteroides vulgatus is a Gram-negative anaerobic bacterium commonly found in the human gut. While generally considered commensal, elevated levels may contribute to dysbiosis and have been linked to chronic inflammation and autoimmune conditions such as Crohn's disease and ulcerative colitis. Its overgrowth may result from a diet high in saturated fats and low in dietary fiber. Elevated B. vulgatus can increase gut barrier permeability and may promote pro-inflammatory pathways.

Suggested Treatment:

Natural support: Focus on a fiber-rich diet including legumes, whole grains, and leafy vegetables to support beneficial microbes.

Probiotics: Use Bifidobacterium breve and Lactobacillus rhamnosus to restore balance.

Lifestyle recommendations: Reduce stress and engage in regular physical activity to modulate gut health.

PSEUDOFLAVONIFRACTOR CAPILLOSUS ELEVATED: PHYLUM: Firmicutes

DESCRIPTION: Pseudoflavonifractor capillosus is a Gram-positive, anaerobic bacterium that is part of the normal gut microbiota. However, elevated levels can be linked to dysbiosis and gastrointestinal disorders such as inflammatory bowel disease (IBD) or irritable bowel syndrome (IBS). Dysbiosis, often induced by stress, poor diet, or antibiotic overuse, can cause an imbalance in the microbiome, contributing to gut inflammation and discomfort.

Suggested Treatment:

Natural support: Use antimicrobial herbs like turmeric, berberine, and oregano oil to help reduce overgrowth.

Probiotics: Supplement with Bifidobacterium longum and Lactobacillus acidophilus to support gut microbial balance.

Dietary changes: Focus on high-fiber, anti-inflammatory foods, and incorporate fermented foods like kefir and sauerkraut to promote healthy gut flora.

Lifestyle: Engage in regular exercise, stay hydrated, and manage stress to improve gut health and immune function.

Probiotics/Beneficial Bacteria Comment

AKKERMANSIA MUCINIPHILA LOW: PHYLUM: Verrucomicrobiota

DESCRIPTION: Akkermansia muciniphila is a Gram-negative anaerobic bacterium that resides predominantly in the intestinal mucus layer. It plays a vital role in maintaining gut barrier integrity, modulating immune responses, and promoting metabolic health through its ability to degrade mucin. Low levels of A. muciniphila have been associated with various metabolic and inflammatory disorders, including obesity, type 2 diabetes, and inflammatory bowel disease (IBD). Reduced abundance may reflect a compromised gut barrier or dysbiosis, often resulting from low dietary fiber intake, chronic stress, or antibiotic use. Additionally, decreased levels are commonly observed in individuals consuming high-fat or Western-style diets, which negatively impact microbial diversity and mucosal health. Optimizing A. muciniphila levels supports the maintenance of gut homeostasis and reduces the risk of systemic inflammation.

Suggested Treatment:

Natural support: Increase dietary intake of polyphenol-rich foods such as cranberries, pomegranates, and green tea, which have been shown to promote A. muciniphila growth.

Prebiotics: Incorporate prebiotic fibers such as inulin and fructooligosaccharides (FOS) to nourish mucin-degrading bacteria.

Dietary changes: Consume a fiber-rich diet with foods like asparagus, onions, and garlic to support overall microbial diversity and mucosal health.

Lifestyle: Engage in regular exercise and stress management techniques to promote a healthy gut environment.

BACTEROIDES UNIFORMIS ELEVATED: PHYLUM: Bacteroidetes

DESCRIPTION: Bacteroides uniformis is a Gram-negative, anaerobic bacterium commonly found in the human gut microbiome, where it plays a key role in the breakdown of complex carbohydrates, fiber fermentation, and production of short-chain fatty acids (SCFAs). It is beneficial in maintaining gut health, modulating the immune system, and supporting overall metabolic processes. Elevated levels of B. uniformis are generally associated with a healthy, fiber-rich diet, as it thrives on complex polysaccharides and is involved in their fermentation to produce beneficial SCFAs like butyrate and acetate. While elevated B. uniformis levels can be indicative of a positive microbial profile and a diet rich in plant-based foods, an overgrowth may indicate dysbiosis, especially when accompanied by other shifts in gut microbiota composition. Excessive levels could be linked to conditions such as irritable bowel syndrome (IBS), metabolic disorders, or an imbalance in the gut microbiota caused by prolonged antibiotic use or prebiotic supplementation. In some cases, an overabundance may also indicate an excess of SCFAs, which could lead to gut discomfort or inflammation, suggesting the need for a more balanced approach to diet and microbiome management.

TOTAL BIFIDOBACTERIUM LEVELS LOW: PHYLUM: Actinobacteria

DESCRIPTION: The total count of Bifidobacterium provides a comprehensive view of the collective abundance of species in this genus within the microbiome. These Gram-positive, anaerobic bacteria are key contributors to fermenting dietary fibers into short-chain fatty acids (SCFAs) like acetate and butyrate, which support gut health, immune function, and microbial diversity. They also inhibit pathogenic bacteria and modulate inflammation.

In Western populations, only 30–40% of individuals are estimated to have optimal levels of Bifidobacterium, reflecting common dietary patterns that are low in fiber and high in refined carbohydrates. Depleted levels have been linked to inflammatory conditions, metabolic disorders, and reduced gut barrier integrity.

A total count of Bifidobacterium has been included to offer a broad overview of the species present in the microbiome, which may assist in guiding clinical treatment decisions.

Parasites/Helminths Comment

ELEVATED BLASTOCYSTIS HOMINIS LEVEL:

Blastocystis hominis may be the cause of persistent, mild diarrhoea. Although considered endemic, it may also be associated with recent overseas travel. Detection suggests the ingestion of contaminated material or contact with farm animals. Continued symptoms may require further testing for the detection of bacterial, viral and/or parasitic co-pathogens.

TREATMENT SUGGESTIONS: Mild symptoms are self-limiting. If treatment is warranted, metronidazole 400 - 750mg (child 12-17mg/kg up to 750mg) three times daily for at least 10 days. Lower dosages are usually associated with treatment failure. Paromomycin has also shown to be effective as an alternative treatment option. Rule out allergy to above medication before prescribing/taking. Consult ID specialist if patient is showing severe symptoms or immunocompromised.

Methodology

Automated Chemistry/Immunochemistry, Chemiluminescence Immunoassay (CLIA), Enzyme-Linked Immunosorbent Assay (ELISA), Microscopy, Fluorescence Enzyme Immunoassay (FEIA), pH Electrode, Gas Chromatography-MS (GC/MS), Next Generation Sequencing (NGS), Quantitative PCR (qPCR), Polymerase Chain Reaction (PCR)