

25283-0009

Dr Test Doctor (Test Doctor) Test Clinic. 123 Test Street, Test Suburb Victoria 3125

Lab ID
Patient ID PAT-100009
Ext ID 25283-0009

Test Patient

Sex: Male • 45yrs • 01-Jan-80
123 Home Street, Test Suburb Vic 3125

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10-Oct-25

COMPREHENSIVE DIGESTIVE STOOL ANALYSIS (CDSA) Level 3+

Specimen type - Stool

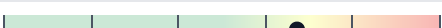
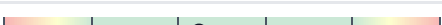
Collected

05-Oct-25

MACROSCOPIC EXAMINATION	
TEST	RESULT
Stool Colour	Brown
Stool Form	Formed
Mucous	Absent

OCCULT BLOOD	
TEST	INTERPRETATION
Occult Blood	Negative

SHORT CHAIN FATTY ACIDS						
TEST	RESULT	H/L		REFERENCE	UNITS	
Short Chain Fatty Acids, Beneficial	17.0			(>13.6)	umol/g	
Acetate	70.00			(44.00-72.00)	%	
Butyrate	16.00			(10.00-33.00)	%	
Propionate	10.00			(0.00-32.00)	%	
Valerate	4.00			(0.50-7.00)	%	

GIT FUNCTIONAL MARKERS						
TEST	RESULT	H/L		REFERENCE	UNITS	
Pancreatic Elastase 1	172	L		(>200)	ug/g	
b-Glucuronidase	5033			(368-6266)	U/g	
Calprotectin	66.0	H		(<100.0)	ug/g	
Secretory IgA	480	L		(200-1300)	ng/mL	
Transglutaminase IgA	22.0			(<100.0)	ug/g	
Steatocrit	9.0			(<10.0)	%	
pH	6.9			(6.3-7.7)		
M2-Pyruvate Kinase	2.80			(<4.00)	U/mL	
H. pylori Antigen	POSITIVE					

PATHOGENIC BACTERIA (PCR)		PARASITES (PCR)	
TEST	RESULT	TEST	RESULT
Aeromonas species	DETECTED	Blastocystis hominis	Not Detected
Campylobacter species	Not Detected	Cryptosporidium species	DETECTED
Salmonella species	Not Detected	Dientamoeba fragilis	DETECTED
Shigella species	Not Detected	Entamoeba histolytica	Not Detected
Yersinia species	Not Detected	Giardia intestinalis	Not Detected

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BENEFICIAL BACTERIA

TEST	RESULT	H/L	REFERENCE	UNITS
Bifidobacterium animalis	1+		(<4+)	
Bifidobacterium bifidum	2+		(<4+)	
Bifidobacterium breve	NEG		(<4+)	
Bifidobacterium longum	NEG		(<4+)	
Bifid. pseudocatenulatum	NEG		(<4+)	
Escherichia coli	3+		(NEG-4+)	
Lactobacillus acidophilus	2+		(<4+)	
Lactobacillus casei	2+		(<4+)	
Lactobacillus paracasei	1+		(<4+)	
Lactobacillus plantarum	NEG		(<4+)	
Lactobacillus rhamnosus	2+		(<4+)	

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

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

Antimicrobials	<i>Aeromonas hydrophila</i> Susceptible	<i>Citrobacter freundii</i> Susceptible	<i>Klebsiella oxytoca</i> Susceptible	<i>Pseudomonas aeruginosa</i> Susceptible
Ampicillin	R	S	S	NT
Augmentin	S	R	S	NT
Ciprofloxacin	S	S	S	R
Gentamicin	S	S	S	NT
Meropenem	S	S	S	S
Norfloxacin	S	S	S	NT
Trimethoprim/Sulpha	S	S	S	NT

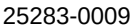
Disclaimer: The antibiotics listed have been reported as requested by the treating healthcare practitioner. Clinical necessity for antibiotic use may vary, and prescription should be based on the professional judgment of the healthcare practitioner and patient case. Information regarding natural inhibitors is provided for reference purposes only and is not intended to replace medical advice or treatment.

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NATURAL INHIBITORS - BACTERIA		
Citrobacter freundii complex	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed (GSE)		
Coptis		
Garlic		
Golden Seal		
Oregano		
Klebsiella oxytoca	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed (GSE)		
Coptis		
Garlic		
Golden Seal		
Oregano		
Streptococcus agalactiae	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed (GSE)		
Coptis		
Garlic		
Golden Seal		
Oregano		

NATURAL INHIBITORS - BACTERIA		
Pseudomonas aeruginosa	Low Inhibition	High Inhibition
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed (GSE)		
Coptis		
Garlic		
Golden Seal		
Oregano		



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MYCOLOGY CULTURE

Organism	Growth	H/L	Ref Range	Classification
Candida albicans	3+	H	(<2+)	Possible Pathogen
Candida krusei	2+	H	(<2+)	Possible Pathogen
Candida parapsilosis	1+		(<2+)	Non-Pathogen
Geotrichum species	NEG		(<4+)	No Growth

SUSCEPTIBILITY - MYCOLOGY

Antimicrobials	<i>Candida albicans</i>	<i>Candida krusei</i>
Fluconazole	R	NT
Voriconazole	S	NT

R Resistant
 S Susceptible
 I Intermediate
 NT Not Tested

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NATURAL INHIBITORS - MYCOLOGY	
Candida albicans	
	Low InhibitionHigh Inhibition
Nystatin	
Berberine	
Black Walnut	
Caprylic Acid	
Citrus Seed (GSE)	
Coptis	
Garlic	
Golden Seal	
Oregano	

NATURAL INHIBITORS - MYCOLOGY		
Candida krusei	Low Inhibition	High Inhibition
Nystatin		
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed (GSE)		
Coptis		
Garlic		
Golden Seal		
Oregano		
Candida parapsilosis	Low Inhibition	High Inhibition
Nystatin		
Berberine		
Black Walnut		
Caprylic Acid		
Citrus Seed (GSE)		
Coptis		
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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 lactose, lactobacillus acidophilus, lactobacillus plantarum, lactobacillus casei, bifidobacterium breve, bifidobacterium bifidum, bifidobacterium longum, lactobacillus salivarius sup 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



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FAECAL OCCULT BLOOD NEGATIVE:

FORMED STOOL:

GIT Markers Comment

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.

A faecal pancreatic elastase level between 100–200 $\mu\text{g/g}$ is suggestive of moderate pancreatic insufficiency.

Repeat testing and correlation with clinical symptoms is recommended.

A borderline faecal calprotectin level (51–100 ug/g) may reflect mild inflammation or a non-specific increase and is not diagnostic of IBD.

This result may warrant further monitoring.

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

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.



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SECRETORY IGA LOW:

Secretory IgA is the predominant immunoglobulin in mucosal secretions, including the gastrointestinal tract, where it plays a critical role in maintaining mucosal immunity by neutralising pathogens and preventing microbial adhesion to the intestinal epithelium. Low levels of secretory IgA in stool may indicate impaired mucosal immune function or compromised gut barrier integrity. This reduction can result from chronic stress, malnutrition, immunodeficiency, certain infections, or prolonged use of immunosuppressive medications.

Clinically, low sIgA may predispose individuals to increased susceptibility to gastrointestinal infections, dysbiosis, and inflammation. It can also reflect a weakened first line of defense in the gut-associated lymphoid tissue, potentially contributing to increased antigen exposure and systemic immune activation.

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

M2-PYRUVATE KINASE NEGATIVE:

Negative M2-PK values should be correlated with carcinoembryonic antigen (CEA) markers. M2-PK has a lower sensitivity and specificity in diagnosing pancreatic cancer compared to CA 19-9. However, in patients with adenocarcinoma there is a simultaneous increase of M2-PK and CA 19-9.

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

HELICOBACTER PYLORI ANTIGEN: POSITIVE

A POSITIVE result, indicates a current infection and is not affected by the presence of other organisms, antacids, barium sulphate, blood or fat. Please correlate infection clinically with signs and symptoms.

Treatment:

Triple therapy: PPI, clarithromycin and amoxicillin or metronidazole, 7-14 days.

If penicillin allergic: PPI, clarithromycin and clindamycin or metronidazole, 7-14 days.

A suggested follow up test is recommended within 4 weeks post therapy.

If treatment is unsuccessful, further investigation of *H. pylori* may be warranted using metagenomic sequencing to evaluate virulence factors and potential resistance gene markers.

Microorganism Summary

AEROMONAS SPECIES DETECTED by PCR

DNA consistent with the presence of *Aeromonas* species has been detected using PCR techniques.

Aeromonas have been implicated as a cause of both acute and persistent diarrhoeal illness (usually watery) and may be accompanied by fever and/or abdominal pain. Aeromonas is widely distributed in the freshwater, estuarine and marine environments and infection usually occurs in the summer months.

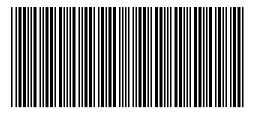
TREATMENT SUGGESTIONS:

Most cases of *Aeromonas*-associated diarrhoea are self-limited and can be managed with supportive therapy. If treatment is considered necessary, *Aeromonas* spp. are usually sensitive to Trimethoprim-Sulphamethoxazole and Fluoroquinolones. Sensitivity to tetracycline is variable.

Rule out allergy to above medication before prescribing/taking. Consult ID specialist if patient is showing severe symptoms or immunocompromised.

CRYPTOSPORIDIUM SPECIES DETECTED by PCR

DNA consistent with the presence of *Cryptosporidium* species has been detected using PCR techniques.



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TREATMENT SUGGESTIONS:

Nitoxanamide 500 mg (child 1 to 3 years: 100 mg; 4 to 11 years: 200 mg) orally, 12 hourly for 3 days

Rule out allergy to above medication before prescribing/taking. Consult ID specialist if patient is showing severe symptoms or immunocompromised.

PLEASE NOTE:

Cryptosporidium detection has been confirmed through a secondary PCR test.

This organism may be classified as a notifiable pathogen. Confirmation has been performed through repeat testing and/or verification on a secondary platform, where required. The result will be reported to the relevant Department of Health in accordance with statutory requirements. For specific state-based notification obligations, please refer to your local public health authority.

DIENTAMOEBIA FRAGILIS DETECTED by PCR.

DNA consistent with the presence of *Dientamoeba fragilis* has been detected using PCR techniques.

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.

AEROMONAS SPECIES: PHYLUM: Proteobacteria

Aeromonas species are Gram-negative bacteria belonging to the phylum Proteobacteria. While primarily found in aquatic environments, some Aeromonas species are transient or opportunistic members of the human gut microbiome. In healthy individuals, their presence is generally low, but in immunocompromised hosts or those with gut dysbiosis, species such as *A. hydrophila* and *A. caviae* can cause gastrointestinal infections, leading to symptoms like diarrhea and abdominal pain (Janda and Abbott, 2010). Aeromonas species are also notable for their ability to acquire and disseminate antimicrobial resistance genes, posing a risk in environments with frequent antibiotic use (Pablos et al., 2010). Although their exact role in the gut microbiome is not fully understood, monitoring these bacteria is crucial in assessing their impact on microbial diversity and potential for opportunistic infections.

CITROBACTER FREUNDII COMPLEX: PHYLUM: Proteobacteria

Citrobacter freundii complex consists of several species including *C. freundii*, *C. braakii*, *C. gillenii*, *C. murlinae*, *C. sedlakii*, *C. werkmanii* and *C. youngae* and are Gram-negative bacteria from the phylum Proteobacteria and is a common resident of the human gut microbiome. Typically found as a commensal organism, *C. freundii* plays a minor role in maintaining microbial diversity within the gut. However, it is also an opportunistic pathogen, particularly in immunocompromised individuals, and has been linked to infections such as urinary tract infections, pneumonia, and bacteremia (Whalen et al., 2007). In the context of gut health, *C. freundii* generally poses little risk, but during episodes of dysbiosis or antibiotic treatment, its population can increase, leading to potential infections. Its ability to acquire antibiotic resistance, especially through horizontal gene transfer, makes it a clinical concern when overgrowth occurs. Monitoring *C. freundii* in gut microbiome studies is essential for understanding its role in both health and disease.



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Enterococcus faecalis is a Gram-positive bacterium from the phylum Firmicutes and is a common inhabitant of the human gut microbiome. As a commensal organism, it plays a role in maintaining gut homeostasis and contributes to microbial diversity. However, E. faecalis is also an opportunistic pathogen, particularly in immunocompromised individuals or when gut dysbiosis occurs. It has been associated with serious infections such as bacteremia, endocarditis, urinary tract infections, and intra-abdominal infections (Arias and Murray, 2012). A major concern with E. faecalis is its ability to acquire antibiotic resistance, including resistance to vancomycin, making it a significant pathogen in healthcare settings. Although it is normally part of a healthy gut microbiome, monitoring its levels is important to prevent infection outbreaks, particularly in vulnerable populations.

Enterococcus faecium is a Gram-positive bacterium from the phylum Firmicutes and is commonly found in the human gut microbiome. While it generally functions as a commensal organism, contributing to microbial diversity and gut homeostasis, E. faecium is also a significant opportunistic pathogen. It is known for causing infections such as bacteremia, endocarditis, and urinary tract infections, particularly in immunocompromised individuals or during gut dysbiosis (Arias and Murray, 2012). A major concern with E. faecium is its high level of antibiotic resistance, especially to vancomycin, which has made it a major healthcare-associated pathogen. Its ability to acquire and transfer resistance genes elevates its clinical importance. While it plays a normal role in the gut microbiome, monitoring its levels is critical for preventing healthcare-related infections.

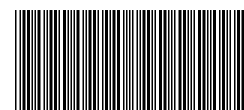
Klebsiella oxytoca is a Gram-negative bacterium from the phylum Proteobacteria and is part of the human gut microbiome, typically present in low abundance as a commensal organism. It contributes to the microbial diversity of the gut but can become an opportunistic pathogen, particularly in immunocompromised individuals or during gut dysbiosis. *K. oxytoca* has been associated with antibiotic-associated hemorrhagic colitis, a form of colitis characterized by mucosal damage and bleeding (Hofmann et al., 2020). Beyond the gut, *K. oxytoca* is linked to hospital-acquired infections, such as pneumonia, urinary tract infections, and septicemia. Its potential for antibiotic resistance, including resistance to beta-lactam antibiotics, raises concerns in clinical settings. Monitoring *K. oxytoca* in the gut is important for understanding its role in health, disease, and antibiotic resistance dynamics.

Pseudomonas aeruginosa is a Gram-negative bacterium commonly known for its opportunistic pathogenicity. While it is primarily associated with infections in immunocompromised patients and chronic infections such as cystic fibrosis, its presence in the gut microbiome is less well-characterized. In the gut, *P. aeruginosa* can be part of the microbial community, often as a transient or minor member. Its potential impact on gut health includes interactions with other gut microbiota, which could influence inflammation and microbial balance (Pang et al., 2019). Despite its role as a pathogen, understanding its dynamics within the gut microbiome could offer insights into its broader ecological roles and impact on gastrointestinal health (Kresse et al., 2018).

Streptococcus agalactiae is a Gram-positive bacterium commonly found in the human gut microbiome. It is part of the group known as beta-hemolytic streptococci. While *S. agalactiae* is predominantly recognized for its role as a pathogen causing infections in neonates, pregnant women, and immunocompromised individuals, it is also a normal component of the gut microbiota. Within the gut, *S. agalactiae* may influence microbial diversity and contribute to the overall balance of the gut flora. Its presence in the gut microbiome is linked to potential impacts on gut health and immune responses, though its pathogenic potential under certain conditions is well-documented (Schrag et al., 2002; Kline et al., 2011).

Candida krusei is a yeast belonging to the phylum Ascomycota and is found as part of the human gut microbiome. Unlike more common *Candida* species, *C. krusei* is intrinsically resistant to fluconazole, a widely used antifungal, which makes it a significant concern in clinical settings (Pfaller and Diekema, 2007). While generally present in low abundance in the gut, it can act as an opportunistic pathogen, particularly in immunocompromised individuals or those undergoing prolonged antibiotic or antifungal treatments. In the gut microbiome, *C.*

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Escherichia coli (E. coli) is a Gram-negative bacterium belonging to the phylum Proteobacteria and is a key component of the human gut microbiome. Most strains of E. coli are commensal, contributing to normal gut functions such as vitamin K production and preventing colonization by pathogenic bacteria. It plays a crucial role in maintaining gut homeostasis and microbial diversity (Tenaillon et al., 2010). However, certain strains of E. coli can become pathogenic, leading to gastrointestinal diseases such as diarrhea, urinary tract infections, and more severe conditions like hemolytic uremic syndrome. Pathogenic strains, such as enterohemorrhagic E. coli (EHEC), can produce toxins like Shiga toxin, which can cause serious infections (Kaper et al., 2004). While most E. coli strains are beneficial, monitoring its pathogenic variants is important for maintaining gut health.

Lactobacillus plantarum is a Gram-positive bacterium from the phylum Firmicutes, prominently present in the human gut microbiome. Known for its probiotic properties, *L. plantarum* contributes to gut health by fermenting dietary fibers into lactic acid, which lowers intestinal pH and inhibits the growth of harmful microorganisms (Hammes & Hertel, 2009). This species is also involved in maintaining the integrity of the gut barrier and modulating immune responses, which can help prevent or alleviate gastrointestinal disorders such as irritable bowel syndrome (IBS) and inflammatory bowel disease (IBD) (O'Callaghan & van Sinderen, 2016). Its ability to adhere to the gut lining and produce antimicrobial peptides makes *L. plantarum* a valuable component of a healthy gut microbiota.

Methodology

Automated Chemistry/Immunochemistry, Gas Chromatography-MS (GC/MS), Chemiluminescence Immunoassay (CLIA), Enzyme-Linked Immunosorbent Assay (ELISA), Microscopy, Fluorescence Enzyme Immunoassay (FEIA), pH Electrode, MALDI-TOF (Matrix-Assisted Laser Desorption/Ionization Time of Flight), Polymerase Chain Reaction (PCR), Quantitative PCR (qPCR)