

Validation BCT4021

Patient

Date of Birth: 18 Sep, 1986
Sex: UNKNOWN
Phone number: 372-376-7628
Location: 1479 Mitchell Drives Davidbury
Vermont 3228 Australia

Practice

Practitioner: John Doe
Practice phone number: 1-832-696-8446
Practice: Microba Medical
Practice
3833 Adrienne Trail Tyreeton
Address: Connecticut 8706 Australia

Report

Report ID: R326090000021-1
Primary Sample ID: BCT4021
Report released: 18 Sep, 2026
Sample Type: Stool
Test Assay: PCR (Pathogens), Immunoassay
(GI), FIT (Faecal Occult Blood)

Overview

Pathologist Notes

Submitted sample was assayed at >48 hours after collection which may result in reduced reported Secretory IgA concentrations. In such cases, we recommend to also consider clinical symptoms and other diagnostic tests for the final diagnosis and/or to request another patient sample. Diagnostic assays (exclusive of expert summary): Approved by Prof. Paul Griffin, FRCPA Clinical Microbiologist.

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Targeted Pathogen Panel

Status	Name
Detected	Enteropathogenic <i>E. coli</i> (EPEC)
Not Detected	Hypervirulent <i>Clostridium difficile</i>
Not Detected	<i>Dientamoeba fragilis</i>
Not Detected	Enterotoxigenic <i>E. coli</i> (ETEC)
Not Detected	<i>Aeromonas</i> spp.
Not Detected	<i>Campylobacter</i> spp.
Not Detected	<i>Salmonella</i> spp.
Not Detected	<i>Clostridium difficile</i> toxin B
Not Detected	<i>Yersinia enterocolitica</i>
Not Detected	<i>Shigella</i> spp./Enteroinvasive <i>E. coli</i> (EIEC)
Not Detected	Shiga toxin-producing <i>E. coli</i>
Not Detected	<i>Giardia lamblia</i>
Not Detected	<i>Cryptosporidium</i> spp.
Not Detected	<i>Entamoeba histolytica</i>
Not Detected	<i>Vibrio</i> spp.

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Status	Name
Not Detected	<i>E. coli</i> O157
Not Detected	<i>Cyclospora cayetanensis</i>
Not Detected	Enteraggregative <i>E. coli</i> (EAEC)

Validation BCT4O21

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Report

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Primary Sample ID: BCT4O21
Report released: 18 Sep, 2026
Sample Type: Stool
Test Assay: PCR (Pathogens), Immunoassay (GI), FIT (Faecal Occult Blood)

Gastrointestinal (GI) Markers

	Marker	Result	Reference Range
Borderline High	Human DNA *	0.70 %	< 0.67 %
Not Detected	Faecal Occult Blood		
Optimal	Calprotectin *	49.40 µg/g	< 50.00 µg/g
Optimal	Secretory IgA *	1716.03 µg/g	500.00 µg/g - 2000.00 µg/g
Optimal	Pancreatic Elastase *	304.30 µg/mL	≥ 200.00 µg/mL
Optimal	Lactoferrin *	0.64 µg/g	< 7.20 µg/g
Optimal	Zonulin family peptides *	67.90 ng/mL	< 100.00 ng/mL

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Microbiome Health Report

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Expert Summary

- *Enteropathogenic E. coli* (EPEC) detected. *Escherichia coli* naturally colonises the gastrointestinal tract and encompasses a wide number of strains. Most *E. coli* strains are harmless but some are foodborne pathogens and can cause gastroenteritis. *Enteropathogenic E. coli* (EPEC) is a major cause of infantile diarrhoea in the developing world. Medical treatment is recommended for symptomatic patients.
- There are no Gastrointestinal Health Markers out of range.
- The microbiome demonstrated borderline low species count with only 152 species detected.
- IPA producing microbes are notably low compared to the healthy cohort. Low levels of IPA-producing microbes may limit the production of IPA, reducing its anti-inflammatory effects and its protection of the intestinal barrier. Low blood levels of IPA may be associated with elevated systemic inflammatory markers.
- There is a high level of branched-chain amino acid (BCAA) producing microbes in this microbiome. BCAAs produced by the microbiome can contribute to elevated levels of plasma BCAAs. High levels of plasma BCAAs may be associated with systemic inflammation.
- This microbiome contains borderline low levels of propionate producing microbes compared to the healthy cohort. Propionate will reduce inflammation when the immune system is in its normal state but will enhance the immune response when the immune system is activated.

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Microbiome Markers

	Marker	Relative Abundance	Compared to Healthy Cohort	
High	BCAA-producing microbes	71.97 %	+1.41	RESEARCH USE ONLY
Low	IPA-producing microbes	0.03 %	-2.14	RESEARCH USE ONLY
Borderline Low	Propionate-producing microbes	2.16 %	-0.75	RESEARCH USE ONLY
Optimal	Oral Species	0.25 %	-0.96	RESEARCH USE ONLY
Optimal	Beta-glucuronidase producing microbes	14.82 %	-0.46	RESEARCH USE ONLY
Optimal	Hydrogen sulphide-producing microbes	3.60 %	-1.28	RESEARCH USE ONLY
Optimal	Acetate-producing microbes	78.40 %	+1.26	RESEARCH USE ONLY
Optimal	Trimethylamine-producing microbes	3.42 %	+0.49	RESEARCH USE ONLY
Optimal	Histamine-producing microbes	0.20 %	-0.48	RESEARCH USE ONLY
Optimal	Methane-producing Archaea	0.11 %	-0.56	RESEARCH USE ONLY
Optimal	Butyrate-producing microbes	20.95 %	+0.58	RESEARCH USE ONLY
Not Detected	<i>B. fragilis</i> toxin-producing microbes	0.00 %	-	RESEARCH USE ONLY
Optimal	Oxalate-consuming microbes	0.92 %	-0.51	RESEARCH USE ONLY
Optimal	Hexa-LPS producing microbes	0.06 %	-0.48	RESEARCH USE ONLY

Measurement

	Marker	Result	Compared to Healthy Cohort	
Borderline Low	Microbial Richness	152 species	-0.79	RESEARCH USE ONLY

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	Marker	Result	Compared to Healthy Cohort	
Optimal	Mucin Degradation	652.71*	+0.08	RESEARCH USE ONLY
Optimal	Microbial Diversity	4.01^	-0.14	RESEARCH USE ONLY

* calculated using the Shannon Index
^ calculated using the number of pathways detected

Gastrointestinal (GI) Markers

	Marker	Result	Reference Range	
Optimal	Faecal pH	5.96	5.70 - 7.30	RESEARCH USE ONLY