

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

Lab ID
Patient ID P029035
Ext ID 26059-0001

Test Patient

Sex: Female • 2yrs • 01-Jan-24
123, Test Street, Burwood Victoria 3125

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28-Feb-26

BabyBiome GutIQ, Ages 0-3

Specimen type - Stool

Collected

20-Feb-26

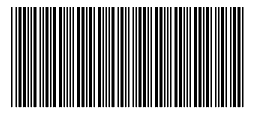
MACROSCOPIC DESCRIPTION	
TEST	RESULT
Stool Colour	Brown
Stool Form	Formed
Mucous	PRESENT

OCCULT BLOOD	
TEST	INTERPRETATION
Occult Blood	Negative

GIT FUNCTIONAL MARKERS					
TEST	RESULT	H/L		REFERENCE	UNITS
Calprotectin	60.0			(<100.0)	ug/g
b-Glucuronidase	3922			(100-8000)	U/g
Pancreatic Elastase 1	355			(>200)	ug/g
pH	5.4	L			
Secretory IgA	800			(200-1500)	ng/mL
Steatocrit	0.5			(<15.0)	%
Transglutaminase IgA	25.0			(<100.0)	ug/g
Zonulin	32			(<180)	ng/mL

Short Chain Fatty Acids, Beneficial					
Test	Result	H/L		Reference	Units
Short Chain Fatty Acids, Beneficial	73.5			(>14.0)	umol/g
Acetate	68.30			(46.00-73.00)	%
Butyrate	10.80			(8.00-33.00)	%
Propionate	18.90			(0.00-30.00)	%
Valerate	2.00				%

Important Biochemical Functions										
Test	Result	H/L						Reference	Units	
Ammonia/Urease Production	0.2110								(<0.5000)	%
Histamine Production	0.0990								(<1.0000)	%
Lipopolysaccharides (LPS) Production	1.0157								(<7.0000)	%
Sulphate Production	0.0405								(<3.0000)	%



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Practitioner Summary – Early Life Gut Microbiome Development

The early-life gut microbiome is a critical determinant of immune education, metabolic programming, gut barrier integrity, and neuroendocrine signalling. Microbial colonisation begins at birth and is strongly influenced by mode of delivery, early feeding practices, antibiotic exposure, and environmental contact. These factors shape microbial composition and functional capacity during a sensitive developmental window spanning infancy and early childhood.

This report interprets results using a developmentally informed framework, recognising that there is no single “normal” infant microbiome. Instead, findings are contextualised against expected microbial trajectories associated with different delivery and feeding types, with emphasis on functional capacity and maturation trends rather than isolated taxonomic findings.

Expected Microbiome Trends

Vaginal Delivery

Early acquisition of maternal vaginal and intestinal microbiota

Typical dominance of Bifidobacterium (particularly in breastfed infants)

Earlier establishment of obligate anaerobes (e.g. Bacteroides)

Progressive reduction in Proteobacteria over time

Caesarean Delivery

Delayed microbial transfer and altered early colonisation

Reduced early Bifidobacterium and Bacteroides

Increased skin- and environment-associated taxa

Slower transition from facultative to obligate anaerobes

These patterns are considered developmental variants rather than pathological, particularly within the first year of life. Interpretation focuses on trajectory and functional development.

Breastfeeding

Selective enrichment of HMO-utilising *Bifidobacterium* species

Lower early microbial diversity (physiologically appropriate)

Reduced inflammatory signalling and enhanced gut barrier support

Formula Feeding

Earlier increase in microbial diversity

Reduced Bifidobacterium dominance

Greater representation of Firmicutes and Proteobacteria

Earlier establishment of adult-like microbial functions

Disclaimer: Baby/Paediatric Microbiome Tests

This report provides an analysis of the stool microbiome using shotgun metagenomic sequencing. The results reflect the microbial DNA detected in the sample at the time of collection.

The gut microbiome in infants, children, and adolescents is continuously developing and may vary considerably due to factors such as age, mode of delivery, diet, antibiotic exposure, illness, and environmental influences. Results are therefore interpreted using age-specific reference ranges developed for infant or paediatric patients aged 0–3 years or 0–17 years respectively.

This test provides supportive information about gut microbial composition and should be interpreted alongside clinical history, symptoms, diet, and other relevant investigations. The presence or absence of specific organisms does not necessarily indicate disease.

This report is not intended to diagnose medical conditions or replace medical advice. Results should be reviewed and interpreted by a qualified healthcare practitioner within the context of the patient's clinical presentation.

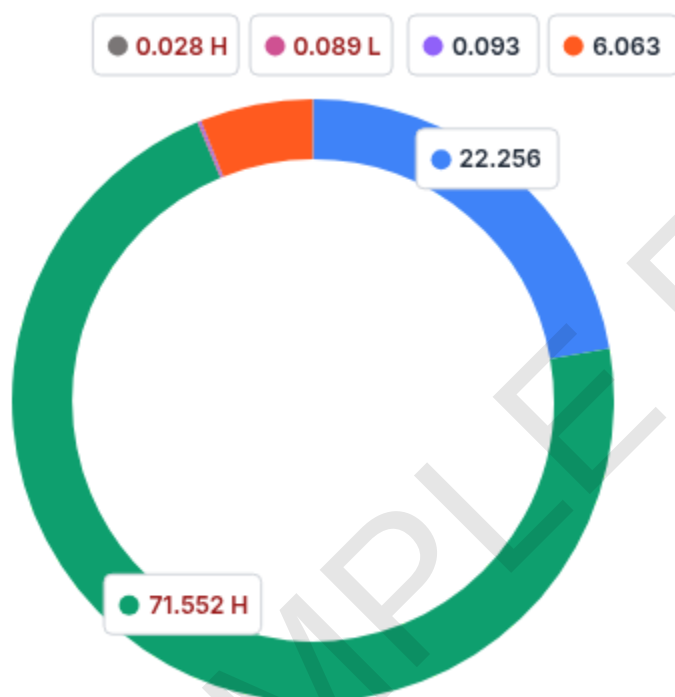
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MICROBIOTA PHYLA

TEST	RESULT	H/L		REFERENCE	UNITS
Actinobacteria Phylum	0.089	L		(0.100-20.000)	%
Bacteroidetes Phylum	22.256			(20.000-56.000)	%
Euryarchaeota Phylum	0.028	H		(<0.020)	%
Firmicutes Phylum	71.552	H		(35.000-70.000)	%
Proteobacteria Phylum	6.063			(0.300-9.000)	%
Verrucomicrobia Phylum	0.093			(0.030-3.500)	%

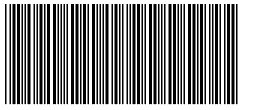


GUT MICROBIAL DIVERSITY

TEST	RESULT	H/L	REFERENCE	UNITS
Shannon Diversity Index	4.51	H		(1.80-4.10)
Simpson Diversity Index	0.97			(0.70-0.98)

MICROBIOTA RATIOS

TEST	RESULT	H/L		REFERENCE	UNITS
Firmicutes/Bacteroidetes ratio	3.21			(<4.00)	ratio
Fus. nucleatum/Faec. prausnitzii ratio	N/A			(<3.00)	ratio
Gram-Positive/Gram-Negative ratio	0.16			(<2.50)	ratio
Prevotella/Bacteroides ratio	0.52	H		(<0.10)	ratio
Proteobacteria/Actinobacteria	67.87	H		(<14.00)	ratio



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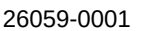
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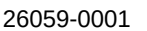
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PARASITES						Blastocystis Subtypes			
TEST	RESULT	H/L		REFERENCE	UNITS	TEST	RESULT		
Blastocystis hominis	95.00	H		(<1.00)	x10^5 org/g	Subtype 1	Negative		
Cryptosporidium species	<DL			(<1.00)	x10^5 org/g	Subtype 2	POSITIVE		
Cyclospora cayetanensis	<DL			(<1.00)	x10^5 org/g	Subtype 3	Negative		
Dientamoeba fragilis	2.48	H		(<1.00)	x10^5 org/g	Subtype 4	Negative		
Entamoeba histolytica	<DL			(<1.00)	x10^5 org/g	Subtype 5	Negative		
Enterocytozoon species	<DL			(<1.00)	x10^5 org/g	Subtype 6	Negative		
Giardia intestinalis	<DL			(<1.00)	x10^5 org/g	Subtype 7	Negative		
						Subtype 8	Negative		
						Subtype 9	Negative		
HELMINTHS						VIRUSES			
TEST		RESULT				TEST		RESULT	
Ancylostoma species Hookworm		Not Detected				Adenovirus 40/41		Not Detected	
Ascaris species, Roundworm		Not Detected				Astrovirus (hAstro)		Not Detected	
Enterobius vermicularis, Pinworm		Not Detected				Norovirus GI/II		Not Detected	
Hymenolepis spp, Tapeworm		Not Detected				Rotavirus A		DETECTED	
Necator americanus, Hookworm		Not Detected				Sapovirus (I,II,IV,V)		Not Detected	
Strongyloides spp, Roundworm		Not Detected							
Taenia species, Tapeworm		Not Detected							
Trichuris trichiura, Whipworm		Not Detected							

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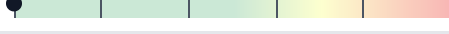
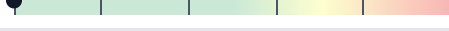
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MYCOLOGY

SERVICE	RESULT	H/L	REFERENCE	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 lusitanae	<DL		(<1.00)	x10^5 CFU/g
 Candida parapsilosis	<DL		(<1.00)	x10^5 CFU/g
 Candida tropicalis	1.10	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

TEST	RESULT	H/L	REFERENCE	UNITS
Abiotrophia defectiva	<DL		(<0.010)	%
Acinetobacter baumannii	<DL		(<0.010)	%
Acinetobacter haemolyticus	<DL		(<0.010)	%
Acinetobacter junii	<DL		(<0.010)	%
Bacteroides caccae	0.470		(<3.000)	%
Bacteroides fragilis	<DL		(<8.000)	%
Phocaeicola vulgatus	0.431		(<11.000)	%
Bilophila wadsworthia	0.068		(<0.400)	%
Citrobacter freundii	<DL		(<0.500)	%
Citrobacter koseri	<DL		(<0.010)	%
Citrobacter youngae	<DL		(<0.010)	%
Corynebacterium urealyticum	<DL		(<0.010)	%
Desulfovibrio piger	<DL		(<0.120)	%
Enterobacter cloacae	<DL		(<0.100)	%
Enterococcus casseliflavus	0.002		(<0.010)	%
Enterococcus faecalis	<DL		(<1.000)	%
Enterococcus faecium	<DL		(<0.010)	%

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TEST	RESULT	H/L	REFERENCE	UNITS
Enterococcus gallinarum	<DL		(<0.010)	%
Escherichia coli	0.016		(<4.000)	%
Fusobacterium nucleatum	<DL		(<0.010)	%
Fusobacterium ulcerans	<DL		(<0.010)	%
Klebsiella oxytoca	<DL		(<0.050)	%
Klebsiella pneumoniae	0.110		(<0.200)	%
Methanobrevibacter smithii	0.027	H	(<0.020)	%
Morganella morganii	<DL		(<0.010)	%
Proteus mirabilis	<DL		(<0.010)	%
Providencia rettgeri	<DL		(<0.010)	%
Pseudoflavonifractor capillosus	0.035	H	(<0.030)	%
Pseudomonas aeruginosa	<DL		(<0.200)	%
Staphylococcus aureus	<DL		(<0.500)	%
STREPTOCOCCUS TOTAL	0.095		(<1.200)	%
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	0.095	H	(<0.050)	%
Streptococcus suis	<DL		(<0.010)	%
Veillonella parvula	<DL		(<0.200)	%

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

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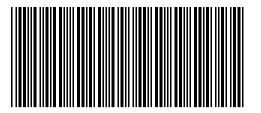
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BENEFICIAL BACTERIA / PROBIOTICS

SERVICE	RESULT	H/L	REFERENCE	UNITS
Akkermansia muciniphila	0.012		(0.030-3.500)	%
Bacteroides thetaiotaomicron	0.092		(<5.000)	%
Bacteroides uniformis	0.437		(<10.000)	%
BIFIDOBACTERIUM TOTAL	0.011		(0.010-20.000)	%
Bifidobacterium adolescentis	<DL		(<0.700)	%
Bifidobacterium animalis	0.011		(<0.100)	%
Bifidobacterium bifidum	<DL		(<12.000)	%
Bifidobacterium breve	<DL		(<10.000)	%
Bifidobacterium longum	<DL		(<15.000)	%
Bifidobacterium pseudolongum	<DL		(<0.500)	%
Clostridium butyricum	<DL		(<0.005)	%
Faecalibacterium prausnitzii	5.130		(1.000-14.000)	%
LACTOBACILLUS TOTAL	0.0020		(<3.0000)	%
Lactobacillus acidophilus	0.001		(<0.150)	%
Lactobacillus casei paracasei	0.001		(<0.150)	%
Lactobacillus crispatus	<DL		(<0.060)	%
Lactobacillus delbrueckii	<DL		(<0.060)	%
Lactobacillus fermentum	<DL		(<1.000)	%
Lactobacillus gasseri	<DL		(<0.300)	%
Lactobacillus helveticus	<DL		(<0.150)	%
Lactobacillus johnsonii	<DL		(<0.150)	%
Lactobacillus plantarum	<DL		(<0.150)	%
Lactobacillus reuteri	<DL		(<0.150)	%
Lactobacillus rhamnosus	<DL		(<0.150)	%
Lactobacillus salivarius	<DL		(<0.050)	%
Lactococcus lactis.	0.007		(<0.030)	%
Oxalobacter formigenes	<DL		(<0.100)	%
Pediococcus acidilactici	2.000	H	(<0.090)	%
Pediococcus pentosaceus	<DL		(<0.060)	%
Roseburia hominis	0.024		(0.010-0.300)	%
Roseburia intestinalis	<DL		(<0.500)	%
Roseburia inulinivorans	0.065		(0.000-0.500)	%
Streptococcus thermophilus	<DL		(<1.000)	%



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Clinical significance:

Clinical interpretation note:

Suggestions:

- Review recent illness history (post-infectious lactase deficiency common)
- Monitor stool consistency and growth trajectory
- Consider temporary lactose reduction if symptomatic
- Support microbiome maturation with age-appropriate fibre exposure (in solids phase)

Dominant Phyla Comment

ACTINOBACTERIA LOW:

Phylum: Actinomycetota (Actinobacteria)

Age group: 0–3 years

What this represents at this age:

In infancy and toddlerhood, Actinobacteria are largely represented by Bifidobacterium species, which are foundational early colonisers and key organisms for milk-carbohydrate utilisation (including HMOs) and early-life fermentation. Low Actinobacteria at this age typically reflects reduced bifidobacterial establishment and may indicate limited breastmilk exposure, early antibiotic disruption, caesarean-associated colonisation differences, early infection impacts, or a faster-than-expected shift toward a more adult-like microbiome where other phyla dominate fermentation.

Clinical interpretation note:

In 0–3 years, low Actinobacteria can be clinically meaningful, particularly if paired with low total bifidobacteria, elevated Proteobacteria, reduced diversity, or symptoms (colic, reflux, eczema/allergy tendencies, altered stooling). Interpret in context—this is often a developmental ecology signal rather than a disease marker.

Suggestions:

- Correlate with feeding history, antibiotic exposure, and recent GI infections
- Interpret alongside total bifidobacteria and Proteobacteria patterns
- Consider longitudinal tracking during weaning and after illness/antibiotics

EURYARCHAEOTA ELEVATED:

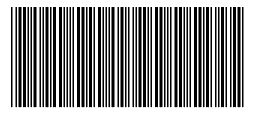
Phylum: Euryarchaeota (Archaea)

Age group: 0–3 years

What this represents at this age:

Elevated methanogenic archaea in early life may indicate earlier establishment of methanogenesis. Methanogens use hydrogen produced by bacterial fermentation, which can shift fermentation dynamics and is sometimes associated with slower transit in older individuals. In toddlers, significance is variable and strongly context-dependent.

Clinical interpretation note:



26059-0001

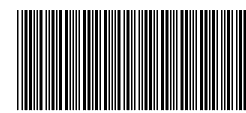
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Clinical interpretation note:



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Clinically significant in symptomatic toddlers. Severity depends on vaccination status and host factors.

Suggestions:

- Immediate hydration focus
- Monitor for signs of dehydration
- Temporary lactose reduction if ongoing diarrhoea
- Rebuild microbiome diversity post-recovery

Methodology

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