NUTRIPATH · PATIENT REPORT
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NATA Accreditation: #20770

26060-0001

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

**Lab ID**
**Patient ID** P029036
**Ext ID** 26060-0001

## Test Patient

Sex: Female • 16yrs • 01-Jan-10
123 Test Street, Burwood Victoria 3125

RECEIVED
01-Mar-26

## PAEDIATRIC-Biome (3 - 17y)

Specimen type - Stool

Collected
15-Feb-26

### MACROSCOPIC EXAMINATION

| TEST | RESULT |
|---|---|
| Stool Colour | Brown |
| Stool Form | Semiformed |
| Mucous | Absent |

### OCCULT BLOOD

| TEST | INTERPRETATION |
|---|---|
| Occult Blood | Negative |

### GIT FUNCTIONAL MARKERS

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Calprotectin | <5.0 | | (<50.0) | ug/g |
| b-Glucuronidase | 3033 | | (300-7000) | U/g |
| Pancreatic Elastase 1 | 370 | | (>200) | ug/g |
| pH | 7.1 | | (6.0-7.5) | |
| Secretory IgA | 1374 | | (350-2000) | ng/mL |
| Steatocrit | 2.0 | | (<10.0) | % |
| Transglutaminase IgA | 1.0 | | (<100.0) | ug/g |
| Zonulin | 54 | | (<130) | ng/mL |

### SHORT CHAIN FATTY ACIDS

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Short Chain Fatty Acids, Beneficial | 73.5 | | (>12.0) | umol/g |
| Acetate | 68.30 | | (45.00-75.00) | % |
| Butyrate | 10.80 | | (6.00-30.00) | % |
| Propionate | 18.90 | | (0.00-30.00) | % |
| Valerate | 2.00 | | (0.50-6.00) | % |

### 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 | | (<5.0000) | % |
| Sulphate Production | 0.4050 | | (<3.0000) | % |

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## Practitioner Summary

### 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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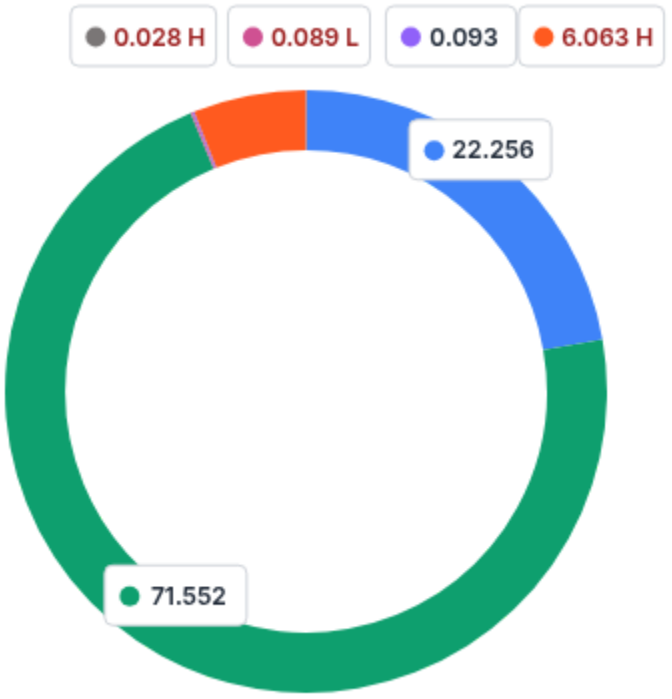
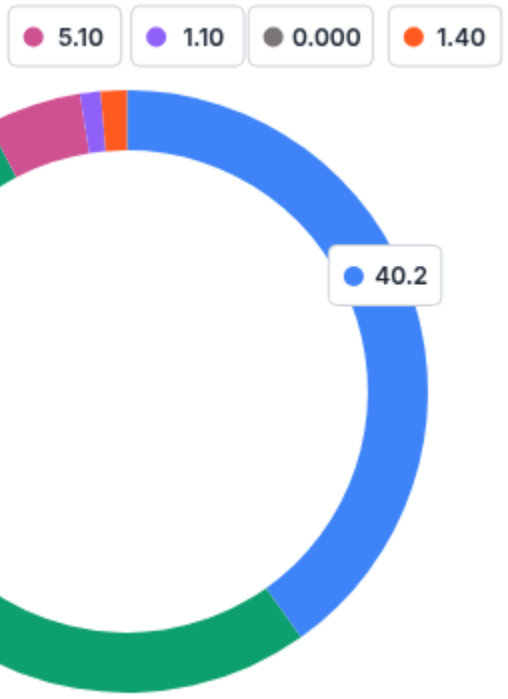
## MICROBIOTA PHYLA

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Actinobacteria Phylum | 0.089 | L | (0.100-11.000) | % |
| Bacteroidetes Phylum | 22.256 | | (21.000-60.000) | % |
| Euryarchaeota Phylum | 0.028 | H | (<0.020) | % |
| Firmicutes Phylum | 71.552 | | (38.000-75.000) | % |
| Proteobacteria Phylum | 6.063 | H | (0.200-6.000) | % |
| Verrucomicrobia Phylum | 0.093 | | (0.010-4.000) | % |

## Your Phyla




## Healthy Phyla




## GUT MICROBIAL DIVERSITY

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Shannon Diversity Index | 4.51 | H | (2.60-4.35) | |
| Simpson Diversity Index | 0.97 | | (0.85-0.98) | |

## MICROBIOTA RATIOS

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Firmicutes/Bacteroidetes ratio | 3.21 | | (<3.50) | ratio |
| Fus. nucleatum/Faec. prausnitzii ratio | N/A | | (<1.50) | ratio |
| Gram-Positive/Gram-Negative ratio | 0.16 | | (<2.00) | ratio |
| Prevotella/Bacteroides ratio | N/A | | (<0.70) | ratio |
| Proteobacteria/Actinobacteria | 67.87 | H | (<14.00) | ratio |

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## PARASITES

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Blastocystis hominis | 941.00 | H | (<1.00) | x10^5 org/g |
| Cryptosporidium species | <DL | | (<1.00) | x10^5 org/g |
| Cyclospora cayetanensis | <DL | | (<1.00) | x10^5 org/g |
| Dientamoeba fragilis | <DL | | (<1.00) | x10^5 org/g |
| Entamoeba histolytica | <DL | | (<1.00) | x10^5 org/g |
| Enterocytozoon species | <DL | | (<1.00) | x10^5 org/g |
| Giardia intestinalis | <DL | | (<1.00) | x10^5 org/g |

## Blastocystis Subtypes

| TEST | RESULT |
|---|---|
| Subtype 1 | Negative |
| Subtype 2 | POSITIVE |
| Subtype 3 | Negative |
| Subtype 4 | Negative |
| Subtype 5 | Negative |
| Subtype 6 | Negative |
| Subtype 7 | Negative |
| Subtype 8 | Negative |
| Subtype 9 | Negative |

## HELMINTHS

| TEST | RESULT |
|---|---|
| Ancylostoma species Hookworm | Not Detected |
| Ascaris species, Roundworm | Not Detected |
| Enterobius vermicularis, Pinworm | Not Detected |
| Hymenolepis spp, Tapeworm | Not Detected |
| Necator americanus, Hookworm | Not Detected |
| Strongyloides spp, Roundworm | Not Detected |
| Taenia species, Tapeworm | Not Detected |
| Trichuris trichiura, Whipworm | Not Detected |

## VIRUSES

| TEST | RESULT |
|---|---|
| Adenovirus 40/41 | Not Detected |
| Astrovirus (hAstro) | Not Detected |
| Norovirus GI/II | Not Detected |
| Rotavirus A | Not Detected |
| Sapovirus (I,II,IV,V) | Not Detected |

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## BACTERIAL PATHOGENS

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Aeromonas species | <DL | | (<1.00) | x10^3 CFU/g |
| Campylobacter species | <DL | | (<1.00) | x10^5 CFU/g |
| C. difficile, Toxin A | <DL | | (<1.00) | x10^4 CFU/g |
| C. difficile, Toxin B | <DL | | (<1.00) | x10^4 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 | 0.78 | | (<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 (stx1/2) | <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 |

## HELICOBACTER PYLORI PROFILE

| TEST | RESULT |
|---|---|
| H. pylori Antigen | Negative |

## H. pylori Virulence Factors

| TEST | 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

| TEST | RESULT |
|---|---|
| Resistance gene A2142C | Not Detected |
| Resistance gene A2142G | Not Detected |
| Resistance gene A2143G | Not Detected |

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

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## MYCOLOGY

| TEST | 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 lusitaniae | <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 | | (<3.200) | % |
| Bacteroides fragilis | <DL | | (<3.600) | % |
| Phocaeicola vulgatus | 0.431 | | (<14.000) | % |
| Bilophila wadsworthia | 0.068 | | (<0.300) | % |
| Citrobacter freundii | <DL | | (<0.100) | % |
| 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 | | (<0.500) | % |
| Enterococcus faecium | <DL | | (<0.010) | % |

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| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Enterococcus gallinarum | <DL | | (<0.010) | % |
| Escherichia coli | 0.016 | | (<3.000) | % |
| Fusobacterium nucleatum | <DL | | (<0.010) | % |
| Fusobacterium ulcerans | <DL | | (<0.010) | % |
| Klebsiella oxytoca | <DL | | (<0.020) | % |
| Klebsiella pneumoniae | <DL | | (<0.100) | % |
| 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 | | (<0.100) | % |
| Staphylococcus aureus | <DL | | (<0.300) | % |
| STREPTOCOCCUS TOTAL | 0.095 | H | (<0.050) | % |
| 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 | | (<0.100) | % |

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

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## BENEFICIAL BACTERIA / PROBIOTICS

| SERVICE | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| Akkermansia muciniphila | 0.012 | | (0.010-4.000) | % |
| Bacteroides thetaiotaomicron | 0.092 | | (<4.000) | % |
| Bacteroides uniformis | 0.437 | | (<8.500) | % |
| BIFIDOBACTERIUM TOTAL | 0.011 | | (0.010-11.000) | % |
| Bifidobacterium adolescentis | <DL | | (<5.000) | % |
| Bifidobacterium animalis | 0.011 | | (<0.500) | % |
| Bifidobacterium bifidum | <DL | | (<5.000) | % |
| Bifidobacterium breve | <DL | | (<5.000) | % |
| Bifidobacterium longum | <DL | | (<7.000) | % |
| Bifidobacterium pseudolongum | <DL | | (<0.500) | % |
| Clostridium butyricum | <DL | | (<0.005) | % |
| Faecalibacterium prausnitzii | 5.130 | | (2.000-16.000) | % |
| LACTOBACILLUS TOTAL | 0.0020 | | (<1.5000) | % |
| Lactobacillus acidophilus | 0.001 | | (<0.100) | % |
| Lactobacillus casei paracasei | 0.001 | | (<0.100) | % |
| Lactobacillus crispatus | <DL | | (<0.040) | % |
| Lactobacillus delbrueckii | <DL | | (<0.040) | % |
| Lactobacillus fermentum | <DL | | (<0.500) | % |
| Lactobacillus gasseri | <DL | | (<0.200) | % |
| Lactobacillus helveticus | <DL | | (<0.100) | % |
| Lactobacillus johnsonii | <DL | | (<0.100) | % |
| Lactobacillus plantarum | <DL | | (<0.100) | % |
| Lactobacillus reuteri | <DL | | (<0.100) | % |
| Lactobacillus rhamnosus | <DL | | (<0.100) | % |
| Lactobacillus salivarius | <DL | | (<0.100) | % |
| Lactococcus lactis. | 0.007 | | (<0.020) | % |
| Oxalobacter formigenes | 0.034 | | (<0.100) | % |
| Pediococcus acidilactici | <DL | | (<0.060) | % |
| Pediococcus pentosaceus | <DL | | (<0.040) | % |
| Roseburia hominis | 0.024 | | (0.010-0.500) | % |
| Roseburia intestinalis | <DL | | (<1.200) | % |
| Roseburia inulinivorans | 0.065 | | (0.010-1.400) | % |
| Streptococcus thermophilus | 0.045 | | (<0.500) | % |

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

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### 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.

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.*

### Dominant Phyla Comment

ACTINOBACTERIA LOW:

Phylum: Actinomycetota (Actinobacteria)

Age group: 3–17 years

What this represents at this age:

In older children, Actinobacteria still commonly reflect bifidobacteria, but they are typically less dominant than in infancy as Firmicutes and Bacteroidetes expand with diet diversity. Low Actinobacteria may indicate reduced fibre/prebiotic intake, higher ultra-processed dietary pattern, recent antibiotics, or reduced saccharolytic fermentation capacity.

Clinical interpretation note:

More relevant when paired with symptoms (bloating, constipation, IBS-like features) and broader patterns such as low diversity, low butyrate producers, or elevated Proteobacteria/inflammatory markers. In isolation, low is not diagnostic.

Suggestions:

-Review dietary fibre diversity and quality

-Correlate with antibiotics and GI symptom timeline

-Interpret alongside diversity indices and butyrate-producer status

EURYARCHAEOTA ELEVATED:

Phylum: Euryarchaeota (Archaea)

Age group: 3–17 years

What this represents at this age:

Elevated methanogenic archaea can reflect increased methane production potential. Methane is often associated with slower gut motility and constipation-predominant patterns in some individuals, although association strength varies and is not diagnostic.

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Clinical interpretation note:

More clinically relevant if constipation, hard stools, or slow transit features are present. Interpret in context and alongside other microbiome and inflammatory markers.

Suggestions:

-Correlate with stool frequency/form and constipation history

-Interpret longitudinally to confirm persistence

-Consider broader dietary and motility assessment in symptomatic children

PROTEOBACTERIA ELEVATED:

Phylum: Proteobacteria (Pseudomonadota)

Age group: 3–17 years

What this represents at this age:

Elevated Proteobacteria in older children is commonly interpreted as a dysbiosis/inflammation-associated signal. It may reflect recent antibiotics, GI infection, dietary stressors, reduced colonisation resistance (low bifidobacteria/butyrate producers), or inflammatory gut conditions. It is often more clinically meaningful when persistent and accompanied by symptoms.

Clinical interpretation note:

Consider as a key imbalance marker, especially if paired with low butyrate producers (e.g., Faecalibacterium) and/or elevated inflammatory markers.

Suggestions:

-Correlate with symptoms, antibiotic/infection history, and inflammatory markers

-Interpret with butyrate-producer profile and diversity

-Consider longitudinal follow-up to confirm persistence

### Microbial Diversity Comment

SHANNON DIVERSITY INDEX ELEVATED:

Marker type: Alpha diversity

Age group: 3–17 years

What this represents at this age:

Broad and evenly distributed microbial community.

Clinical significance:

Often favourable, but still non-diagnostic.

Clinical interpretation note:

Interpret with overall balance of commensals vs opportunists.

Suggestions:

No action required in isolation

### Microbiota Ratios Comment

PROTEOBACTERIA / ACTINOBACTERIA RATIO ELEVATED (Proteobacteria-predominant):

Marker type: Phylum balance ratio

Age group: 3–17 years

What this represents at this age:

More consistent with Proteobacteria expansion and reduced anaerobic resilience.

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Clinical significance:

Supportive marker of dysbiosis patterning.

Clinical interpretation note:

Interpret with diversity indices, LPS potential, and symptoms.

Suggestions:

Consider follow-up if persistent and symptomatic

### Mycology Comment

CANDIDA TROPICALIS ELEVATED:

Kingdom: Fungi

Age group: 3–17 years

What this represents at this age:

In older children, C. tropicalis may be associated with dysbiosis and immune stress and is more often detected alongside other yeast elevations.

Clinical interpretation note:

Interpret in context of multi-species fungal overgrowth patterns.

Suggestions:

Interpret alongside C. albicans and bacterial balance

Correlate with symptoms and immune stressors

### Opportunistic Pathogens Comment

METHANOBREVIBACTER SMITHII ELEVATED:

Phylum: Methanobacteriota (Archaea)

Age group: 3–17 years

What this represents at this age:

Methanogenic activity within a mature anaerobic gut ecosystem.

Clinical significance:

May align with constipation-predominant patterns in some children; not diagnostic on its own.

Clinical interpretation note:

Interpret as a functional clue (transit) rather than “dysbiosis”.

Suggestions:

Correlate with constipation phenotype; consider follow-up if clinically useful

PSEUDOFLAVONIFRACTOR CAPILLOSUS ELEVATED:

Phylum: Bacillota (Firmicutes)

Age group: 3–17 years

What this represents at this age:

Reflects participation in polyphenol metabolism and mature anaerobic fermentation networks.

Clinical significance:

Generally benign and often favourable. Relative dominance may reflect dietary patterning.

Clinical interpretation note:

Normal within variation. Interpret in the context of overall diversity and symptoms.

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

**Lab ID**
**Patient ID** P029036
**Ext ID** 26060-0001

## Test Patient

Sex: Female • 16yrs • 01-Jan-10
123 Test Street, Burwood Victoria 3125

**RECEIVED**
01-Mar-26

Suggestions:

Review diet only if markedly dominant or symptoms are present

STREPTOCOCCUS TOTAL ELEVATED:

Phylum: Bacillota (Firmicutes)

Age group: 3–17 years

What this represents at this age:

Higher total streptococcal signal in stool typically reflects oral-source contribution, dietary exposures, or reduced anaerobic resilience.

Clinical significance:

Supportive marker of a facultative-dominant pattern when paired with reduced diversity and symptoms.

Clinical interpretation note:

Not diagnostic in isolation; interpret in context.

Suggestions:

-Review oral health, antibiotics, and symptoms

-Consider follow-up if persistent and clinically relevant

### Parasites/Worms Comment

BLASTOCYSTIS HOMINIS ELEVATED:

Organism Type: Anaerobic protozoan

Age group: 3–17 years

What this represents at this age:

Often acquired through travel, contaminated food/water, or environmental exposure. May coexist with altered microbial diversity.

Clinical significance:

In adolescents, certain strains have been associated with bloating, altered bowel habits, and low-grade inflammatory responses. Clinical impact is strain and host-dependent.

Clinical interpretation note:

Assess symptom burden, inflammatory markers, and overall microbiome balance before initiating treatment.

Suggestions:

-Treat if persistent GI symptoms present

-Optimise microbiome diversity

-Support gut barrier function if required

### 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)