**US BioTek** LABORATORIES • **PATIENT REPORT**
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Clinical Laboratory Improvement Amendments

26066-0004

*** US BioTek** US BioTek. 16020 Linden Av N, Shoreline WA 98133

**Lab ID**
**Patient ID** P029035
**Ext ID** 26066-0004

## Test Patient

Sex: Female • 2yrs • 01-Jan-24

RECEIVED
07-Mar-26

# BABY-Biome (0 - 3y)

Specimen type - Stool

Collected
20-Feb-26

## MACROSCOPIC DESCRIPTION

| TEST | RESULT |
|---|---|
| Stool Colour | Brown |
| Stool Form | Semiformed |
| 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 | 5.8 | | (5.5-7.5) | |
| Secretory IgA | 800 | | (200-1500) | ng/mL |
| Steatocrit | 0.4 | | (<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 | 66.0 | | (>8.0) | umol/g |
| Acetate | 68.30 | | (40.00-80.00) | % |
| Butyrate | 10.80 | | (4.00-27.00) | % |
| Propionate | 18.90 | | (0.00-20.00) | % |
| Valerate | 2.00 | | (0.00-3.00) | % |

## 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 | 0.4050 | | (<3.0000) | % |

### 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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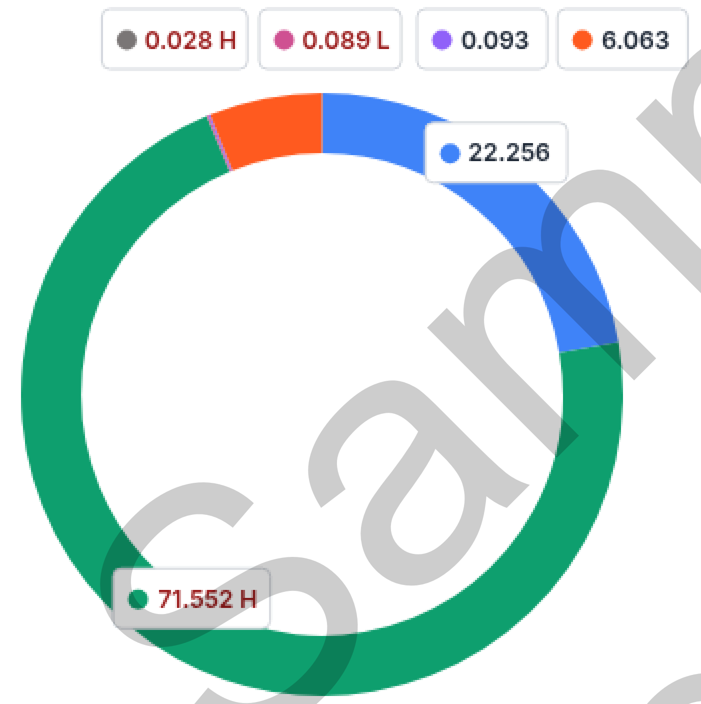
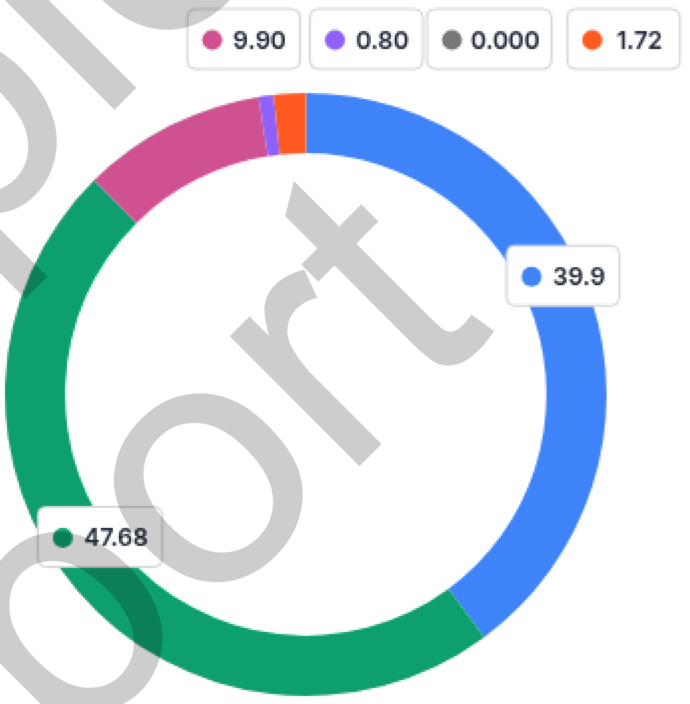
## MICROBIOTA PHYLA

| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| ● Actinobacteria Phylum | 0.089 | L | (0.100-20.000) | % |
| ● Bacteroidetes Phylum | 22.256 | | (20.000-55.000) | % |
| ● 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 | | (0.040-3.500) | % |

### Your Phyla



### Healthy Phyla



## 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 | N/A | | (<0.10) | ratio |
| Proteobacteria/Actinobacteria | 67.87 | H | (<14.00) | ratio |

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## PARASITES

| TEST | RESULT | H/L | | REFERENCE | UNITS |
|---|---|---|---|---|---|
| Blastocystis hominis | 54.10 | 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 | 2.48 | H | ─────● | (<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 | 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

| | 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 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 | | (<3.000) | % |
| 🔵 | Bacteroides fragilis | <DL | | (<8.000) | % |
| 🔵 | Phocaeicola vulgatus | 0.431 | | (<11.000) | % |
| 🟠 | Bilophila wadsworthia | 0.068 | | (<0.300) | % |
| 🟠 | 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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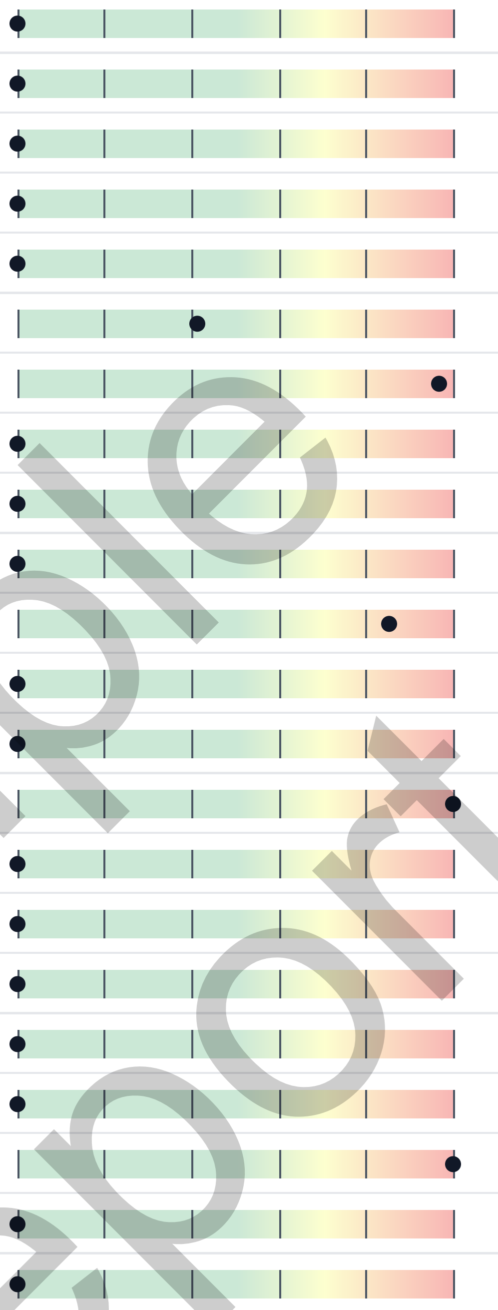
| TEST | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| ● Enterococcus gallinarum | <DL | | (<0.010) | % |
| ● Escherichia coli | 0.016 | | (<4.000) | % |
| ● Fusobacterium nucleatum | <DL | | (<0.010) | % |
| ● Fusobacterium ulcerans | <DL | | (<0.010) | % |
| ● Klebsiella oxytoca | <DL | | (<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 | 0.960 | H | (<0.100) | % |
| ● 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 | 0.960 | 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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## BENEFICIAL BACTERIA / PROBIOTICS

| SERVICE | RESULT | H/L | REFERENCE | UNITS |
|---|---|---|---|---|
| ● Akkermansia muciniphila | 0.012 | | (<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 | | (<0.150) | % |
| ● Lactococcus lactis. | 0.007 | | (<0.030) | % |
| ● Oxalobacter formigenes | 0.034 | | (<0.100) | % |
| ● Pediococcus acidilactici | <DL | | (<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 | 0.045 | | (<1.000) | % |

## 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.

MUCOUS PRESENT:

Marker Type: Visual stool inflammatory marker

Age group: 0–3 years

What this represents at this age:

Visible mucous reflects increased mucin secretion from goblet cells in response to irritation or immune activation. In infants and toddlers, mucous can be seen during viral infections, food protein sensitivity, teething-associated GI shifts, or transient dysbiosis.

Clinical significance:

Mild mucous may be transient and benign. Persistent or heavy mucous, especially with diarrhoea or blood, suggests mucosal irritation or inflammation.

Clinical interpretation note:

Interpret alongside calprotectin, occult blood, infection markers, and recent dietary changes.

Suggestions:

-Correlate with stool frequency and consistency

-Review recent infections or dietary transitions

-Monitor if persistent

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: 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:

Interpret cautiously in 0–3 years. Consider relevance primarily if constipation, bloating, or slow transit features are present, and if methane-associated organisms are elevated consistently.

Suggestions:

-Correlate with stool frequency, stool form, and constipation patterns

-Interpret alongside hydrogen-producing fermenters and overall diversity

-Consider longitudinal tracking before drawing conclusions

FIRMICUTES ELEVATED:

Phylum: Firmicutes (Bacillota)

Age group: 0–3 years

What this represents at this age:

Elevated Firmicutes in toddlers may reflect increasing anaerobic fermentation capacity and maturation of the microbiome as solid foods diversify. This phylum includes both beneficial butyrate producers and opportunistic organisms, so interpretation depends heavily on species-level composition and inflammatory context.

Clinical interpretation note:

Not inherently adverse. Interpret with species composition and symptom context. Concern increases only if elevated Firmicutes is driven by pathobiont patterns or accompanied by inflammatory markers.

Suggestions:

-Interpret with species-level breakdown (butyrate producers vs opportunists)

-Correlate with diet changes and stool pattern

-Track longitudinally during weaning

## Microbial Diversity Comment

SHANNON DIVERSITY INDEX ELEVATED:

Marker type: Alpha diversity

Age group: 0–3 years

What this represents at this age:

Higher diversity may reflect broader colonisation and dietary/environmental complexity. In early life, “higher” is not always “better” and can occur with increased facultatives in disturbed states.

Clinical significance:

Non-diagnostic; quality of taxa matters more than the number of taxa.

Clinical interpretation note:

Interpret alongside whether diversity is driven by healthy anaerobes vs expansion of opportunistic taxa.

Suggestions:

Interpret composition-first; do not treat diversity as a standalone target

## Mycology Comment

CANDIDA TROPICALIS ELEVATED:

Kingdom: Fungi

Age group: 0–3 years

What this represents at this age:

C. tropicalis is less common and may reflect environmental exposure or altered gut ecology following antibiotics or infection.

Clinical interpretation note:

Elevation alone does not imply pathology; consider persistence and symptoms.

Suggestions:

Review infection history and antibiotic exposure

Track longitudinally

## Opportunistic Pathogens Comment

METHANOBREVIBACTER SMITHII ELEVATED:

Phylum: Methanobacteriota (Archaea)

Age group: 0–3 years

What this represents at this age:

M. smithii is the dominant human gut methanogen. Colonisation is often low/absent in infancy and may increase with age, dietary complexity, and a more established anaerobic ecosystem.

Clinical significance:

Higher relative abundance can indicate increased methanogenic activity and is sometimes associated with slower transit/constipation phenotypes. However, methanogen presence is variable in early life and not inherently abnormal.

Clinical interpretation note:

In 0–3 years, interpret with the clinical bowel pattern. Relevance increases if constipation, bloating, or delayed transit is a dominant clinical feature.

Suggestions:

-Correlate with stool frequency/consistency and clinical constipation phenotype

-Interpret alongside fibre-fermenting and butyrate-network taxa (which influence substrate availability)

PSEUDOFLAVONIFRACTOR CAPILLOSUS ELEVATED:

Phylum: Bacillota (Firmicutes)

Age group: 0–3 years

What this represents at this age:

Pseudoflavonifractor capillosus is an obligate anaerobe involved in polyphenol and flavonoid metabolism and is part of the adult-type anaerobic microbiome. In early life, it is typically low or absent and increases with dietary complexity and fibre/polyphenol exposure.

Clinical significance:

Elevation in a toddler may reflect advanced anaerobic maturation or relative abundance shifts as the microbiome transitions toward a more adult-like configuration.

Clinical interpretation note:

In younger infants, elevation is uncommon and should be interpreted cautiously as a relative effect. In older toddlers (≥2 years), presence may be developmentally appropriate.

Suggestions:

-Interpret with age and diet (plant foods, polyphenol exposure)

-Correlate with other adult-type anaerobes and SCFA-associated taxa

STREPTOCOCCUS SALIVARIUS ELEVATED:

Phylum: Bacillota (Firmicutes)

Age group: 0–3 years

What this represents at this age:

A dominant oral commensal; stool detection reflects oral-source transfer.

Clinical significance:

Usually benign and exposure-related.

Clinical interpretation note:

Not a gut-pathology marker; can rise with increased oral microbial contribution.

Suggestions:

Correlate with oral health; no gut-directed action required

STREPTOCOCCUS TOTAL ELEVATED:

Phylum: Bacillota (Firmicutes)

Age group: 0–3 years

What this represents at this age:

“STREP TOTAL” represents the combined relative abundance of Streptococcus species detected. In paediatric stool, streptococci commonly reflect oral-source organisms, dietary influences (e.g., fermented dairy exposure for certain species), and early-life microbiome immaturity (facultative organisms appear more prominent before obligate anaerobes fully establish).

Clinical significance:

Elevated Streptococcus total is most commonly a pattern marker: either increased oral microbial contribution and/or relative expansion of facultative organisms due to suppression of obligate anaerobes (post-antibiotics, diarrhoea, inflammation). It is not a direct marker of streptococcal infection.

Clinical interpretation note:

In 0–3 years, mild elevation can be age-expected. Clinical relevance increases when STREP TOTAL is markedly elevated together with other facultatives (Enterococcus/Enterobacteriaceae), low diversity, and persistent GI symptoms.

Suggestions:

-Review recent antibiotics, acute illness, oral health factors, and feeding pattern

-Interpret with anaerobe maturity (Bifidobacterium, butyrate-network taxa) and total Proteobacteria

-Avoid organism-specific treatment decisions based on STREP TOTAL alone

## Parasites/Worms Comment

DIENTAMOEBA FRAGILIS ELEVATED:

Organism Type: Colonic protozoan

Age group: 0–3 years

What this represents at this age:

Transmitted via the faecal–oral route and sometimes associated with helminth ova (notably Enterobius). It colonises the large intestine and may influence gut motility and local immune signalling.

Clinical significance:

Pathogenicity is variable in toddlers. It may contribute to intermittent loose stools, abdominal discomfort, irritability, or disturbed sleep. Often detected in daycare settings.

Clinical interpretation note:

Interpret in conjunction with symptoms, inflammatory markers, and possible pinworm co-infection.

Suggestions:

-Treat if symptomatic

-Screen for Enterobius co-infection

-Support microbiome diversity post-treatment

BLASTOCYSTIS HOMINIS ELEVATED:

Organism Type: Anaerobic colonic protozoan

Age group: 0–3 years

What this represents at this age:

Blastocystis is transmitted via faecal–oral exposure and is common in shared childcare environments. It inhabits the large intestine and interacts with the existing microbiome. Strain-dependent pathogenicity is recognised.

Clinical significance:

In toddlers, it may represent microbial immaturity or environmental exposure rather than overt infection. However, in the context of elevated calprotectin, altered stool form, or eczema/allergic tendency, it may contribute to immune activation and gut barrier permeability.

Clinical interpretation note:

Interpret alongside inflammatory markers, stool form, and overall microbial diversity.

Suggestions:

-Observe if asymptomatic

-Consider treatment if persistent GI symptoms

-Address gut barrier integrity if clinically indicated

## Viral Pathogens Comment

ROTAVIRUS ELEVATED:

Organism Type: Double-stranded RNA virus (severe paediatric gastroenteritis virus)

Age group: 0–3 years

What this represents at this age:

Rotavirus infects small intestinal enterocytes and leads to villous atrophy, enzyme disruption, and secretory diarrhoea. Vaccination has significantly reduced severe disease, but infection may still occur.

Clinical significance:

Historically a major cause of severe diarrhoea and dehydration in infants. Can cause high stool output, vomiting, fever, and risk of electrolyte imbalance. Temporary lactose intolerance is common post-infection.

Clinical interpretation note:

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)