



* 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

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07-Mar-26

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

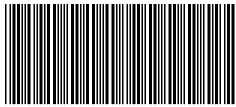
Disclaimer: Baby/Paediatric Microbiome Tests

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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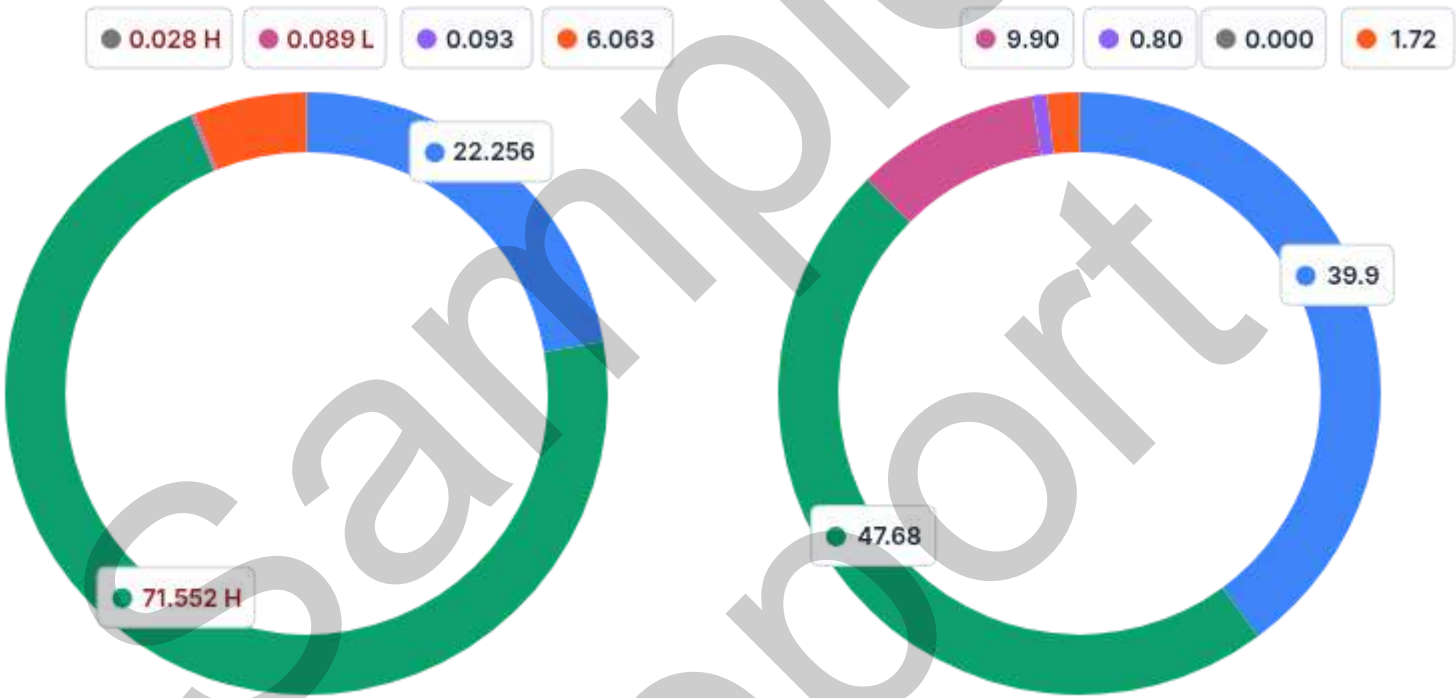
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MICROBIOTA PHYLA

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

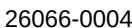


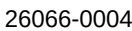
GUT MICROBIAL DIVERSITY

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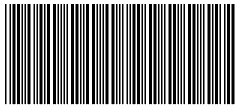
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TEST	RESULT	H/L	REFERENCE	UNITS
Aeromonas species	<DL		(<1.00)	x10^3 CFU/g
Campylobacter species	<DL		(<1.00)	x10^5 CFU/g
C. difficile, Toxin A	<DL		(<1.00)	x10^4 CFU/g
C. difficile, Toxin B	<DL		(<1.00)	x10^4 CFU/g
Clostridium difficile, Hypervirulent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

TEST	RESULT
H. pylori Antigen	Negative

TEST	RESULT	TEST	RESULT
Virulence Factor, babA	Not Detected	Resistance gene A2142C	Not Detected
Virulence Factor, cagA	Not Detected	Resistance gene A2142G	Not Detected
Virulence Factor, dupA	Not Detected	Resistance gene A2143G	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		

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



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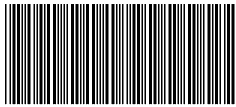
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MYCOLOGY

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		(<0.300)	%
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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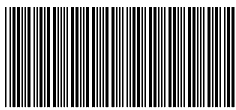
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TEST	RESULT	H/L		REFERENCE	UNITS
Enterococcus gallinarum	<DL			(<0.010)	%
Escherichia coli	0.016			(<4.000)	%
Fusobacterium nucleatum	<DL			(<0.010)	%
Fusobacterium ulcerans	<DL			(<0.010)	%
Klebsiella oxytoca	<DL			(<0.050)	%
Klebsiella pneumoniae	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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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

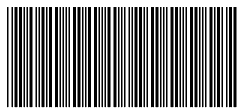
ACTINOBACTERIA LOW:

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



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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:

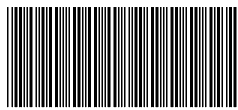
Not inherently adverse. Interpret with species composition and symptom context. Concern increases only if elevated Firmicutes is driven by pathobiont patterns or accompanied by inflammatory markers.

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:



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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.

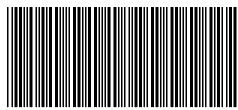
Suggestions:

-Correlate with stool frequency/consistency and clinical constipation phenotype

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

PSEUDOFILONIFRATOR CAPILLOSUS ELEVATED:

Phylum: Bacillota (Firmicutes)



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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:

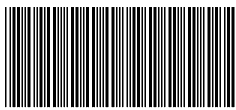
Elevated Streptococcus total is most commonly a pattern marker: either increased oral microbial contribution and/or relative expansion of facultative organisms due to suppression of obligate anaerobes (post-antibiotics, diarrhoea, inflammation). It is not a direct marker of streptococcal infection.

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



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Parasites/Worms Comment

DIENTAMOEBIA 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

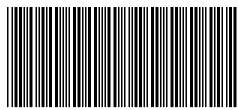
What this represents at this age:

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:



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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)

Sample Report