

YOUR PERSONALIZED REPORT

PATHOGENS

The testing includes pathogens (bacterial, parasitic and viral) commonly known to cause gastroenteritis. Note that not all individuals with positive findings will present with symptoms. Many factors, including the health of the individual (such as immune health, digestive function, and microbiome balance), the transient nature of most pathogens, and the presence and expression of virulence factors, all contribute to pathogen virulence and individual symptoms.

BACTERIAL PATHOGENS	Result	Reference
<i>Campylobacter</i>	<dl	< 1.00e3
<i>C. difficile</i> Toxin A	3.47e5 High ↑	< 1.00e3
<i>C. difficile</i> Toxin B	2.52e5 High ↑	< 1.00e3
<i>E. coli</i> - EPEC/EHEC	<dl	< 1.00e3
<i>E. coli</i> O157	<dl	< 1.00e3
Enteroinvasive <i>E. coli</i> /Shigella	<dl	< 1.00e3
Enterotoxigenic <i>E. coli</i> LT/ST	<dl	< 1.00e3
Shiga-like Toxin <i>E. coli</i> stx1	<dl	< 1.00e3
Shiga-like Toxin <i>E. coli</i> stx2	5.93e2	< 1.00e3
<i>Salmonella</i>	<dl	< 1.00e4
<i>Vibrio cholerae</i>	<dl	< 1.00e5
<i>Yersinia enterocolitica</i>	<dl	< 1.00e5
PARASITIC PATHOGENS		
<i>Cryptosporidium</i>	<dl	< 1.00e6
<i>Entamoeba histolytica</i>	<dl	< 1.00e4
<i>Giardia</i>	<dl	< 5.00e3
VIRAL PATHOGENS		
Adenovirus 40/41	<dl	< 1.00e10
Norovirus GI/II	<dl	< 1.00e7

KEY: Results are reported as genome equivalents per gram of stool, which is a standard method for estimating the number of microbes measured per gram of stool, based on qPCR analysis of DNA samples.

Results are expressed in standard scientific notation. For example, a reported result of 3.5e7 is equivalent to 3.5×10^7 microbes per gram, which equals 35,000,000 (35 million) microbes per gram of stool.

< dl represents results below detectable limit.

The assays were developed and/or the performance characteristics determined by Diagnostic Solutions Laboratory.

Patient: Sample, Ima

Accession: 20250230-0001

HELICOBACTER PYLORI

H. PYLORI & VIRULENCE FACTORS

	Result	Reference
<i>Helicobacter pylori</i>	<dl	< 1.00e3
Virulence Factor, babA	N/A	Negative
Virulence Factor, cagA	N/A	Negative
Virulence Factor, dupA	N/A	Negative
Virulence Factor, iceA	N/A	Negative
Virulence Factor, oipA	N/A	Negative
Virulence Factor, vacA	N/A	Negative
Virulence Factor, virB	N/A	Negative
Virulence Factor, virD	N/A	Negative

COMMENSAL/KEYSTONE BACTERIA

COMMENSAL BACTERIA

	Result		Reference
<i>Bacteroides fragilis</i>	3.00e10		1.6e9 - 2.5e11
<i>Bifidobacterium</i> spp.	3.85e10		> 6.7e7
<i>Enterococcus</i> spp.	1.44e7		1.9e5 - 2.0e8
<i>Escherichia</i> spp.	3.79e9		3.7e6 - 3.8e9
<i>Lactobacillus</i> spp.	9.04e6		8.6e5 - 6.2e8
<i>Enterobacter</i> spp.	5.04e6		1.0e6 - 5.0e7
<i>Akkermansia muciniphila</i>	<dl L		1.0e1 - 8.2e6
<i>Faecalibacterium prausnitzii</i>	1.37e3		1.0e3 - 5.0e8
<i>Roseburia</i> spp.	8.60e8		5.0e7 - 2.0e10

BACTERIAL PHYLA

<i>Bacteroidetes</i>	1.75e12		8.6e11 - 3.3e12
<i>Firmicutes</i>	1.48e11		5.7e10 - 3.0e11
<i>Firmicutes:Bacteroidetes</i> Ratio	0.08		< 1.0

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OPPORTUNISTIC/OVERGROWTH MICROBES

DYSBIOTIC & OVERGROWTH BACTERIA

	Result	Reference
<i>Bacillus</i> spp.	1.22e6	< 1.76e6
<i>Enterococcus faecalis</i>	<dl	< 1.00e4
<i>Enterococcus faecium</i>	<dl	< 1.00e4
<i>Morganella</i> spp.	<dl	< 1.00e3
<i>Pseudomonas</i> spp.	6.08e5 High ↑	< 1.00e4
<i>Pseudomonas aeruginosa</i>	1.70e3 High ↑	< 5.00e2
<i>Staphylococcus</i> spp.	1.24e5 High ↑	< 1.00e4
<i>Staphylococcus aureus</i>	3.65e2	< 5.00e2
<i>Streptococcus</i> spp.	1.02e4 High ↑	< 1.00e3

COMMENSAL OVERGROWTH MICROBES

<i>Desulfovibrio</i> spp.	<dl	< 7.98e8
<i>Methanobacteriaceae</i> (family)	9.97e6	< 3.38e8

INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA

<i>Citrobacter</i> spp.	<dl	< 5.00e6
<i>Citrobacter freundii</i>	<dl	< 5.00e5
<i>Klebsiella</i> spp.	<dl	< 5.00e3
<i>Klebsiella pneumoniae</i>	<dl	< 5.00e4
<i>M. avium</i> subsp. <i>paratuberculosis</i>	<dl	< 5.00e3
<i>Proteus</i> spp.	<dl	< 5.00e4
<i>Proteus mirabilis</i>	<dl	< 1.00e3

COMMENSAL INFLAMMATORY & AUTOIMMUNE-RELATED BACTERIA

<i>Enterobacter</i> spp.	5.04e6	< 5.00e7
<i>Escherichia</i> spp.	3.79e9	< 3.80e9
<i>Fusobacterium</i> spp.	3.21e7	< 1.00e8
<i>Prevotella</i> spp.	1.74e7	< 1.00e8

FUNGI/YEAST

FUNGI/YEAST

	Result	Reference
<i>Candida</i> spp.	<dl	< 5.00e3
<i>Candida albicans</i>	<dl	< 5.00e2
<i>Geotrichum</i> spp.	<dl	< 3.00e2
<i>Microsporidium</i> spp.	<dl	< 5.00e3
<i>Rhodotorula</i> spp.	<dl	< 1.00e3

VIRUSES

VIRUSES

	Result	Reference
Cytomegalovirus	<dl	< 1.00e5
Epstein-Barr Virus	<dl	< 1.00e7

The assays were developed and/or the performance characteristics determined by Diagnostic Solutions Laboratory.

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PARASITES

PROTOZOA

	Result	Reference
<i>Blastocystis hominis</i>	<dl	< 2.00e3
<i>Chilomastix mesnili</i>	<dl	< 1.00e5
<i>Cyclospora</i> spp.	<dl	< 5.00e4
<i>Dientamoeba fragilis</i>	<dl	< 1.00e5
<i>Endolimax nana</i>	<dl	< 1.00e4
<i>Entamoeba coli</i>	<dl	< 5.00e6
<i>Pentatrichomonas hominis</i>	<dl	< 1.00e2

WORMS

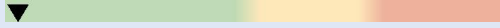
<i>Ancylostoma duodenale</i>	Not Detected	Not Detected
<i>Ascaris lumbricoides</i>	Not Detected	Not Detected
<i>Necator americanus</i>	Not Detected	Not Detected
<i>Trichuris trichiura</i>	Not Detected	Not Detected
<i>Taenia</i> spp.	Not Detected	Not Detected

INTESTINAL HEALTH MARKERS

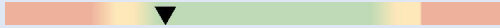
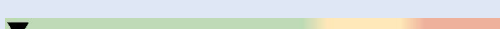
DIGESTION

	Result	Reference
Steatocrit	<dl 	< 15 %
Elastase-1	332 	> 200 ug/g

GI MARKERS

β-Glucuronidase	624 	< 2486 U/mL
Occult Blood - FIT	<dl 	< 10 ug/g

IMMUNE RESPONSE

Secretory IgA	685 	510 - 2010 ug/g
Anti-gliadin IgA	107 	< 175 U/L
Eosinophil Activation Protein (EDN, EPX)	0.32 	< 2.34 ug/g

INFLAMMATION

Calprotectin	0 	< 173 ug/g
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ADD-ON TESTS

Gluten Peptide	129.6 	< 5.0 ng/g
Zonulin	188.9 H 	< 175 ng/g

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H. PYLORI ANTIBIOTIC RESISTANCE GENES

	Result	Reference
Amoxicillin	N/A	Negative
<i>Genes associated with amoxicillin resistance</i>		
PBP1A S414R	N/A	
PBP1A T556S	N/A	
PBP1A N562Y	N/A	

	Result	Reference
Clarithromycin	N/A	Negative
<i>Genes associated with clarithromycin resistance</i>		
A2142C	N/A	
A2142G	N/A	
A2143G	N/A	

	Result	Reference
Fluoroquinolones	N/A	Negative
<i>Genes associated with fluoroquinolone resistance</i>		
gyrA N87K	N/A	
gyrA D91N	N/A	
gyrA D91G	N/A	
gyrB S479N	N/A	
gyrB R484K	N/A	

	Result	Reference
Tetracycline	N/A	Negative
<i>Genes associated with tetracycline resistance</i>		
A926G	N/A	
AGA926-928TTC	N/A	

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UNIVERSAL ANTIBIOTIC RESISTANCE GENES

	Result	Reference		Result	Reference		Result	Reference
b-Lactams	Positive	Negative	Macrolides	Positive	Negative	Trimethoprim	Negative	Negative
blaNDM-1	Absent		acrA	Absent		dfrA1	Absent	
CTX-M 1	Present		acrB	Absent		dfrA12	Absent	
CTX-M 2	Absent		emrE	Present		dfrA14	Absent	
CTX-M 8/25	Absent		ermA	Absent		dfrA15	Absent	
CTX-M 9	Present		ermB	Present		dfrA17	Absent	
GES	Absent		ermC	Absent		dfrA5	Absent	
OXA-1	Absent		macA	Absent		dfrA7	Absent	
PER-1	Absent		macB	Absent		dfrB1	Absent	
PER-2	Absent		mefA	Present		dfrB2	Absent	
SHV	Absent		mphA	Absent		dfrB3	Absent	
TEM	Present		msrA	Absent				
VEB	Absent		tolC	Present				
Fluoroquinolones	Negative	Negative	Ciprofloxacin	Positive	Negative	Sulfonamides	Negative	Negative
qnrA	Absent		emea	Absent		sul1	Absent	
qnrB	Absent		pmrA	Present		sul2	Absent	
qnrS1	Absent					sul3	Absent	
qnrS2	Absent							
Vancomycin	Negative	Negative	Nitroimidazoles	Negative	Negative	Methacillin	Negative	Negative
vanA	Absent		nimA	Absent		mecA	Absent	
vanB	Absent		nimB	Absent		Chloramphenicol	Negative	Negative
vanC1	Absent		nimC	Absent				
vanC2-1	Absent		nimD	Absent		cata13	Absent	
vanC2-2	Absent		nimE	Absent				

Detection of resistance-associated genes may not confer phenotypic drug resistance. Detected genes cannot be associated with specific microbes.



BILE ACIDS - SUMMARY

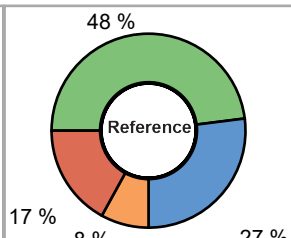
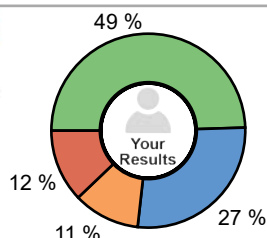
The **Bile Acids Panel** assesses fecal concentrations of primary and secondary bile acids and provides insights into microbiome diversity, digestive function, motility, and various gut-related conditions.

SUMMARY INFO

Total Bile Acids - ng/g	1.76e6		2.37e5 - 6.29e6
Secondary Bile Acids - %	98.7		> 90.5
Primary Bile Acids - %	1.3		< 7.8

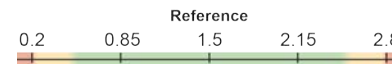
Bile Acid Percentages

- Deoxycholic Acid-DCA
- Lithocholic Acid-LCA*
- Iso-LCA
- Other



Reference set at 50th percentile.

*LCA value is the summation of LCA + Allo-LCA



LCA*/DCA Ratio

Lithocholic Acid / Deoxycholic Acid Ratio based on absolute values.



SHORT CHAIN FATTY ACIDS - SUMMARY

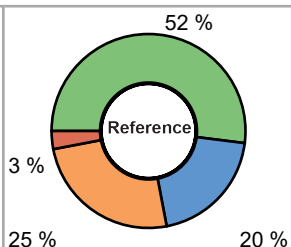
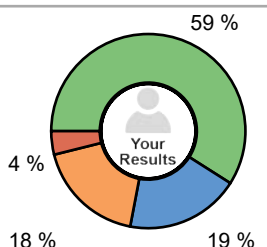
The **Postbiotic Fatty Acid Metabolite Panel** assesses fecal concentrations of straight chain and branched chain fatty acids. These metabolites provide a variety of beneficial effects for intestinal health, anti-inflammation, metabolism and immunity, and give dietary insight.

SUMMARY INFO

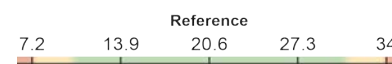
Major Straight Chain Fatty Acids - µg/g	1.98e4 H		3.63e3 - 1.95e4
Acetate - %	59.0		38.3 - 68.0
Butyrate - %	19.0		7.7 - 32.6
Propionate - %	18.1		14.1 - 33.6
Valerate - %	3.9		0.5 - 6.2

Major SCFA Percent

- Acetate
- Butyrate
- Propionate
- Valerate



Reference set at 50th percentile.



SCFA/BCFA Ratio

Ratio of total straight chain fatty acids (SCFA) to total branched chain fatty acids (BCFA).



BILE ACIDS - RESULTS

PRIMARY BILE ACIDS	Abbreviation	Conjugation**	Result ng/g	Reference ng/g
Total Primary Bile Acids			2.31e4	3.50e3 - 7.90e4
Cholic Acid	CA	U	3.50e2	< 5.92e4
Chenodeoxycholic Acid	CDCA	U	2.07e4	2.16e3 - 6.87e4
Taurochenodeoxycholic Acid	TCDCA	C	6.93e2 H	< 4.14e2
Taurocholic Acid	TCA	C	8.01e2 H	< 5.19e2
Glycochenodeoxycholic Acid	GCDCA	C	2.06e2	1.18e1 - 8.11e2
Glycocholic Acid	GCA	C	2.65e2	< 7.55e2
Hyocholeic Acid	HCA	U	<dl	< 5.50e3
SECONDARY BILE ACIDS	Abbreviation	Conjugation**	Result ng/g	Reference ng/g
Total Secondary Bile Acids			1.73e6	1.97e5 - 6.23e6
Deoxycholic Acid	DCA	U	8.66e5	2.24e3 - 2.33e6
Lithocholic Acid*	LCA	U	4.80e5	6.12e3 - 1.37e6
Isolithocholic Acid	ISO-LCA	U	1.94e5	2.21e3 - 5.36e5
12-Ketolithocholic Acid	12-KLCA	U	1.01e5	1.87e3 - 5.30e5
3-oxoDeoxycholic Acid	3-oxoDCA	U	2.10e4	3.53e2 - 1.12e5
Ursodeoxycholic Acid	UDCA	U	<dl	< 5.77e4
7-Ketolithocholic Acid	7-KLCA	U	1.01e2	< 8.94e3
7-Ketodeoxycholic Acid	7-KDCA	U	1.55e2	< 1.01e4
Dehydrolithocholic Acid	DHLCA	U	2.09e4	< 4.52e4
Hyodeoxycholic Acid	HDCA	U	2.13e4	< 5.27e4
Alloisolithocholic Acid	AlloIso-LCA	U	2.90e4	< 7.53e4
3-Dehydrocholic Acid	3-DHCA	U	1.68e1	< 5.85e2
Glycolithocholic Acid	GLCA	C	<dl	< 2.20e2
Glycoursodeoxycholic Acid	GUDCA	C	1.14e2	< 3.08e2
Glycodeoxycholic Acid	GDCA	C	1.08e2	< 5.40e2
Tauroolithocholic Acid	TLCA	C	<dl	< 2.68e2
Tauroursodeoxycholic Acid	TUDCA	C	<dl	< 1.28e2
Taurodeoxycholic Acid	TDCA	C	2.70e2	< 8.56e2

*LCA value is the summation of LCA + Allo-LCA | ** C = Conjugated | U = Unconjugated



SHORT CHAIN FATTY ACIDS - RESULTS

Total Short Chain Fatty Acids - µg/g

2.12e4 H

4.23e3 - 2.10e4

SACCHAROLYTIC STRAIGHT CHAIN FATTY ACIDS (SCFA)

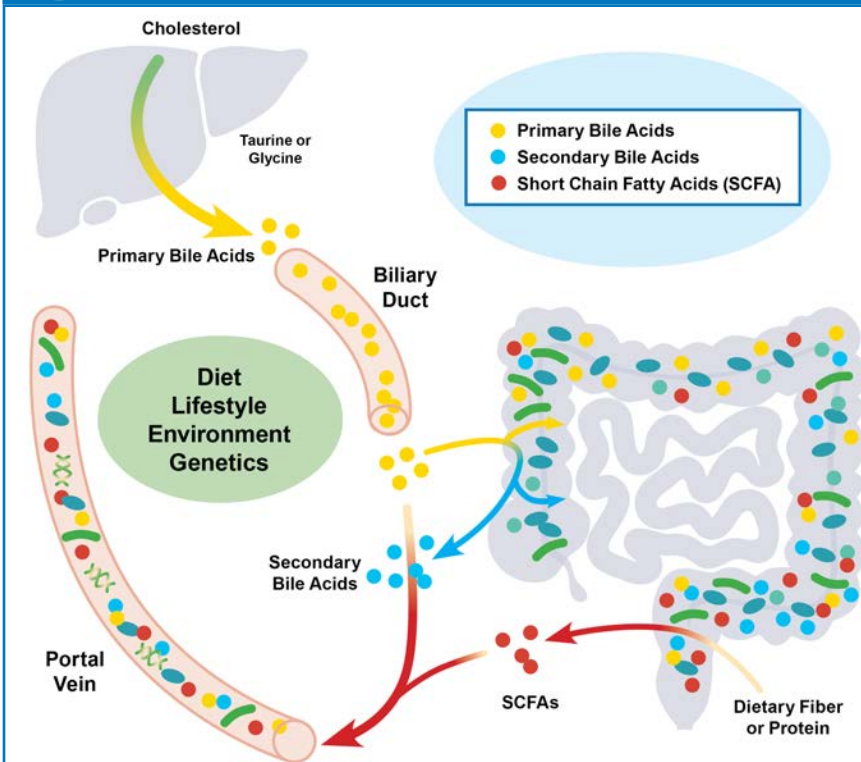
	Result µg/g	Reference µg/g
Total SCFA	2.04e4 H	3.65e3 - 1.95e4
Acetate	1.17e4 H	2.09e3 - 9.72e3
Butyrate	3.75e3	3.94e2 - 5.79e3
Propionate	3.59e3	5.91e2 - 5.45e3
Valerate	7.76e2 H	4.33e1 - 7.73e2
Caproate	5.92e2 H	7.15e-1 - 1.44e2

PROTEOLYTIC BRANCHED CHAIN FATTY ACIDS (BCFA)

	Result µg/g	Reference µg/g
Total BCFA	8.20e2	1.65e2 - 1.67e3
Iso-butyrate	3.17e2	5.65e1 - 5.64e2
Iso-valerate	2.21e2	4.45e1 - 6.58e2
2-Methylbutyrate	2.74e2	3.82e1 - 4.61e2
Iso-caproate	7.33e0	< 9.93e0



BILE ACIDS AND FATTY ACIDS OVERVIEW



Primary bile acids are synthesized from cholesterol in the liver and conjugated with either taurine or glycine. They are stored in the gallbladder and released during digestion to assist with the absorption of fat and fat-soluble vitamins.

95% of primary bile acids are reabsorbed via the portal vein, while 5% are metabolized by gut bacteria to produce secondary bile acids.

Saccharolytic short chain fatty acids (SCFAs) are primarily metabolites of dietary fiber fermentation in the gut while proteolytic branched chain fatty acids (BCFAs) are metabolites of protein fermentation.

Acetate, propionate, and butyrate are three major SCFAs, which account for 90% of the SCFAs produced by gut microbiota. SCFAs are known to have numerous health effects and can enhance fecal excretion of bile acids.