

**invivo<sup>®</sup>**

The Human Microbiome Company

TEST REPORTED: 02/11/2022  
 TEST RECEIVED: 02/11/2022  
 PATIENT NAME: FIRST LAST  
 PATIENT DOB: 02/11/2022

CLINICIAN NAME: CLINICIAN  
 SAMPLE TYPE: STOOL  
 SEX: FEMALE

Lab Director:  
 Emma Beamish, PhD



## Helicobacter pylori RESULTS:

Helicobacter pylori Stool Antigen NEGATIVE

## Immune RESULTS: RANGE:

Test	Result	Normal	Range
Beta Defensin 2	4.0ng/g	NORMAL	<68ng/g
Secretory IgA	9.0ug/g	NORMAL	<188ug/g

## Inflammation RESULTS: RANGE:

Test	Result	Normal	Range
Calprotectin	0.0ug/g	NORMAL	<100ug/g

## Digestion RESULTS: RANGE:

Test	Result	Normal	Range
Bile Acids	611.0umol/L	NORMAL	<3477umol/L
Pancreatic Elastase	521.0ug/g	NORMAL	>200ug/g

## Other RESULTS: RANGE:

Test	Result	Normal	Range
FIT (Occult Blood)	0.0ug/g	NORMAL	<10ug/g
Zonulin	0.0ng/g	NORMAL	<100ng/g



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## Commensal Bacteria

RESULTS:

RANGE:

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
<i>Akkermansia muciniphila</i>	3.9							1.7-7.1
<i>Anaerostipes caccae</i>	8.4	HIGH						3.0-7.3
<i>Bacteroides spp.</i>	15.6							14.8-17.5
<i>Bifidobacterium spp.</i>	8.7							7.3-16.3
<i>Blautia obeum</i>	17.4							15.5-17.9
<i>Coprococcus eutactus</i>	15.3							10.4-16.5
<i>Escherichia coli</i>	4.9							4.5-12.0
<i>Eubacterium rectale</i>	9.4							7.7-14.8
<i>Faecalibacterium prausnitzii</i>	16.8							14.2-18.3
<i>Lactobacillus spp.</i>	8.0							2.7-8.9
<i>Roseburia homini</i>	7.6							5.7-10.2
<i>Ruminococcus bromii</i>	16.5							14.2-17.7
<i>Subdoligranulum variabile</i>	11.9							6.3-12.5

## Bacteroides Sub Group

RESULTS:

RANGE:

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
<i>Bacteroides dorei</i>	<DL	LOW						6.1-17.0
<i>Bacteroides fragilis</i>	12.3							10.7-14.8
<i>Bacteroides ovatus</i>	8.9							3.5-9.2
<i>Bacteroides thetaiotaomicron</i>	8.6							6.2-12.5
<i>Bacteroides uniformis</i>	9.3	LOW						10.9-16.5
<i>Bacteroides vulgatus</i>	15.3							14.6-17.4



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## Gram Negative (-) Bacteria

	RESULTS:		RANGE:
<i>Bilophila wadsworthia</i>	5.0	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	2.4-9.5
<i>Citrobacter freundii</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<1.0
<i>Citrobacter koseri</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<DL
<i>Desulfovibrio spp.</i>	0.5	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<6.9
<i>Enterobacter cloacae</i>	0.0	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<2.8
<i>Fusobacterium nucleatum</i>	4.8	<b>HIGH</b>	<2.8
<i>Hafnia alvei</i>	3.7	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	0.8-9.0
<i>Klebsiella oxytoca</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<1.5
<i>Klebsiella pneumoniae</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<2.5
<i>Morganella morganii</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<0.5
<i>Oxalobacter formigenes</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<1.6
<i>Prevotella copri</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<11.4
<i>Proteus mirabilis</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<0.4
<i>Pseudomonas aeruginosa</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<0.7
<i>Serratia marcescens</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	<0.4
<i>Veillonella spp.</i>	8.3	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20	4.0-10.0



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## Gram Positive (+) Bacteria

	RESULTS:	RANGE:
<i>Clostridium perfringens</i>	4.8 HIGH	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <4.0
<i>Clostridium sporogenes</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <DL
<i>Enterococcus faecalis</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <3.0
<i>Enterococcus faecium</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <2.6
<i>Enterococcus gallinarum</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <0.9
<i>Methanobrevibacter smithii</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <8.3
<i>Mycobacterium avium</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <0.2
<i>Ruminococcus gnavus</i>	9.4	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   4.1-10.7
<i>Ruminococcus torques</i>	4.3 HIGH	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <2.3
<i>Staphylococcus aureus</i>	3.5 HIGH	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <3.5
<i>Streptococcus agalactiae</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <0.9
<i>Streptococcus pneumoniae</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <0.1
<i>Streptococcus pyogenes</i>	<DL	0 - 4   5 - 8   9 - 12   13 - 16   17 - 20   <DL



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## Mycology

RESULTS:

RANGE:

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
<i>Aspergillus fumigatus</i>	<DL							<0.1
<i>Candida albicans</i>	<DL							<0.6
<i>Candida tropicalis</i>	<DL							<0.3
<i>Malassezia restricta</i>	<DL							<0.5

## Parasitology

RESULTS:

RANGE:

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
<i>Blastocystis hominis</i>	9.5	<b>HIGH</b>						< 6.4
<i>Dientamoeba fragilis</i>	<DL							< 12.5
<i>Entamoeba histolytica</i>	<DL							< DL
<i>Giardia lamblia</i>	<DL							< DL

## Bacterial Pathogens

RESULTS:

RANGE:

			0 - 4	5 - 8	9 - 12	13 - 16	17 - 20	
<i>B. fragilis</i> Enterotoxigenic	<DL							< DL
<i>Clostridium difficile</i>	<DL							< DL
<i>Clostridium difficile</i> (tox A)	<DL							< DL
<i>Clostridium difficile</i> (tox B)	<DL							< DL
<i>Yersinia enterocolitica</i>	<DL							< DL

The GI EcologiX™ profile utilises the highly sensitive quantitative PCR (qPCR) TaqMan technology for analysis of the gastrointestinal microbiota. Microbial genes of interest are quantified within a sample and their abundances are normalised to an endogenous and highly conserved gene. The qPCR results are therefore reported as the relative abundance of a microorganism as proportional to the whole microbial community.



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