

**invivo<sup>®</sup>**

The Human Microbiome Company

TEST REPORTED: 02/11/2022

CLINICIAN NAME: CLINICIAN

Lab Director:  
Emma Beamish, PhD

TEST RECEIVED: 02/11/2022

PATIENT NAME: FIRST LAST

SAMPLE TYPE: STOOL

PATIENT DOB: 02/11/2022

SEX: FEMALE

**Helicobacter pylori****RESULTS:***Helicobacter pylori* Stool Antigen NEGATIVE**Immune****RESULTS:****RANGE:**

Beta Defensin 2	4.0ng/g	NORMAL		<68ng/g
Secretory IgA	9.0ug/g	NORMAL		<188ug/g

**Inflammation****RESULTS:****RANGE:**

Calprotectin	0.0ug/g	NORMAL		<100ug/g
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**Digestion****RESULTS:****RANGE:**

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

**Other****RESULTS:****RANGE:**

FIT (Occult Blood)	0.0ug/g	NORMAL		<10ug/g
Zonulin	0.0ng/g	NORMAL		<100ng/g

Scan for more information and  
resources on GI EcologiX

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## Commensal Bacteria

RESULTS:

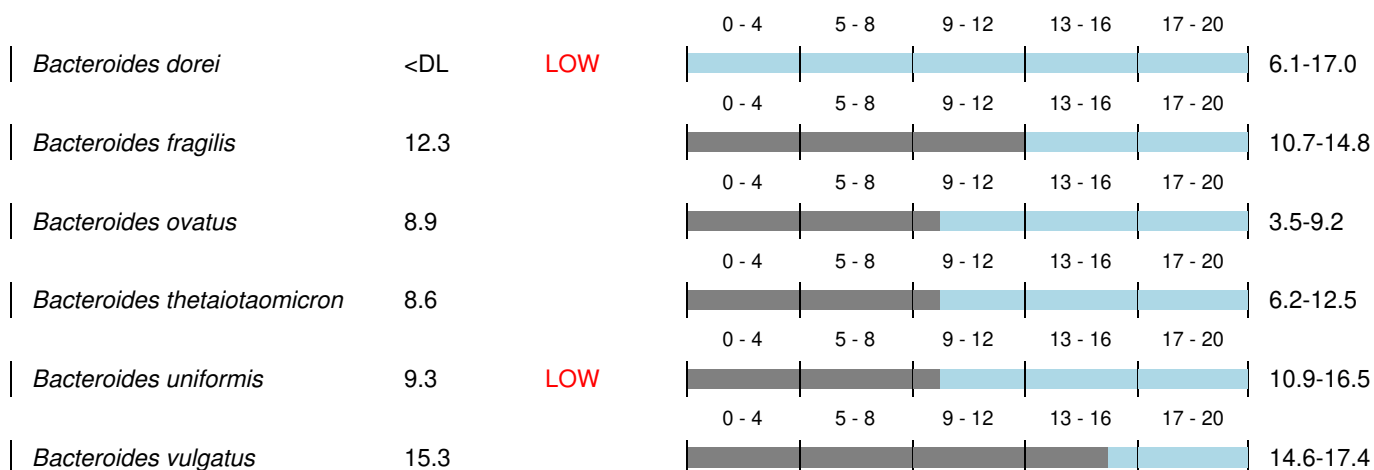
RANGE:



## Bacteroides Sub Group

RESULTS:

RANGE:



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## Gram Negative (-) Bacteria

RESULTS:

RANGE:

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








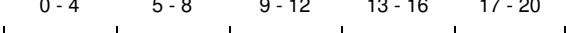
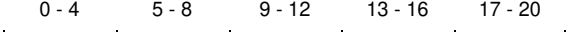
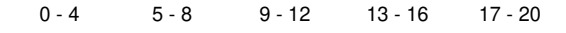
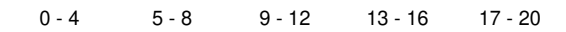
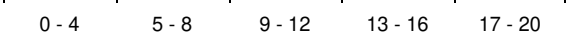
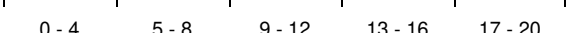
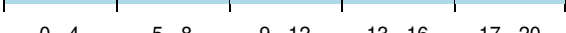

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## Gram Positive (+) Bacteria

RESULTS:

RANGE:

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




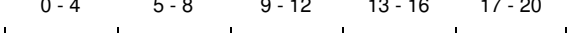


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## Mycology

RESULTS:


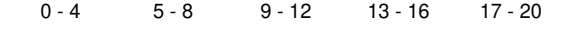


RANGE:

		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:


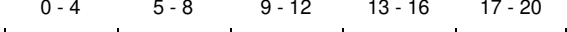
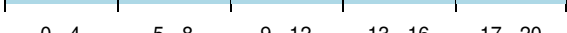

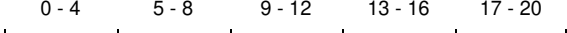
RANGE:

		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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