



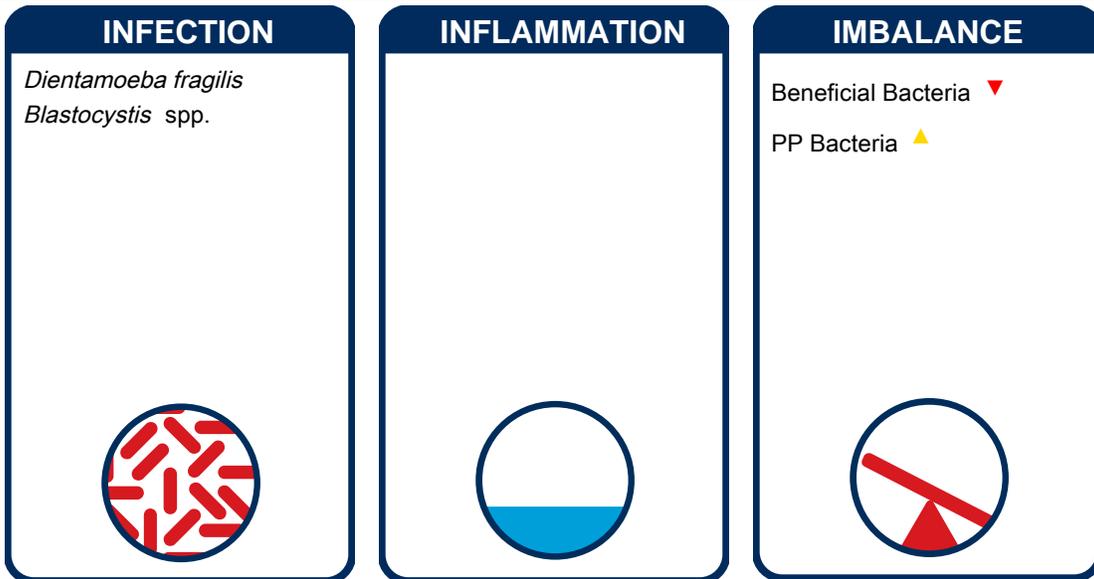
Patient: **MALE**
TEST
DOB: February 02, 1956
Sex: M
MRN: 0001558085

Order Number: M9300998
Completed: January 31, 2019
Received: January 30, 2019
Collected: January 30, 2019

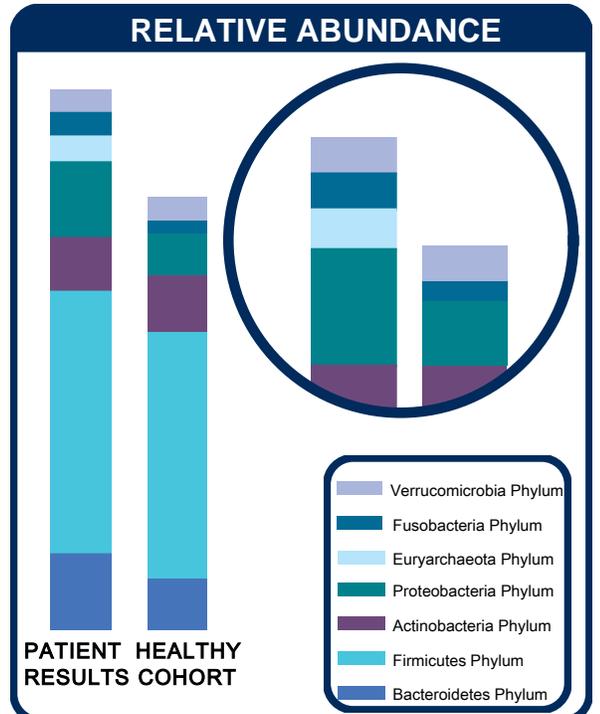
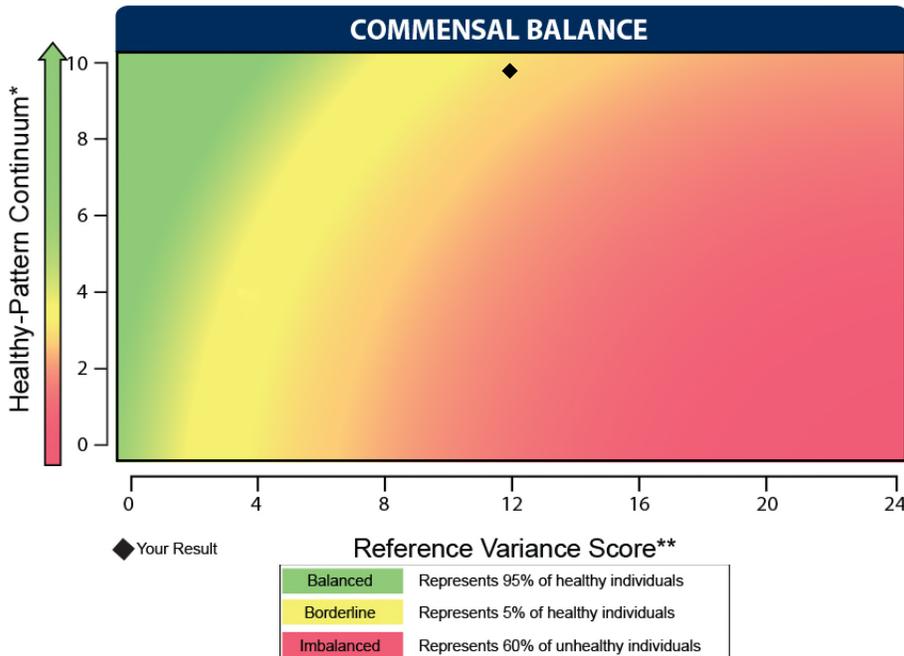
Test Doctor
84 Peachtree Rd
Asheville, NC 28803

2205 GI Effects™ Microbial Ecology Profile - Stool

Interpretation At-a-Glance



See individual sections for detailed results



*A progressive ranking scale based on a Genova proprietary algorithm that differentiates healthy and unhealthy commensal patterns.

**The total number of Commensal Bacteria (PCR) that are out of reference ranges for this individual.



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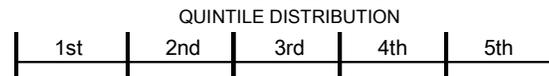
2205 GI Effects™ Microbial Ecology Profile - Stool

Methodology: DNA by PCR

Gastrointestinal Microbiome

Commensal Bacteria (PCR)

Result
CFU/g stool



Reference Range
CFU/g stool

Bacteroidetes Phylum

<i>Bacteroides-Prevotella</i> group	2.4E8		3.4E6-1.5E9
<i>Bacteroides vulgatus</i>	1.2E9		<=2.2E9
<i>Barnesiella</i> spp.	3.6E7		<=1.6E8
<i>Odoribacter</i> spp.	7.1E7		<=8.0E7
<i>Prevotella</i> spp.	1.4E8 H		1.4E5-1.6E7

Firmicutes Phylum

<i>Anaerotruncus colihominis</i>	3.4E7 H		<=3.2E7
<i>Butyrivibrio crossotus</i>	5.0E7 H		5.5E3-5.9E5
<i>Clostridium</i> spp.	2.1E8		1.7E8-1.5E10
<i>Coprococcus eutactus</i>	1.0E8		<=1.2E8
<i>Faecalibacterium prausnitzii</i>	7.5E8		5.8E7-4.7E9
<i>Lactobacillus</i> spp.	1.6E8		8.3E6-5.2E9
<i>Pseudoflavonifractor</i> spp.	3.0E8 H		4.2E5-1.3E8
<i>Roseburia</i> spp.	7.6E7 L		1.3E8-1.2E10
<i>Ruminococcus</i> spp.	1.9E9 H		9.5E7-1.6E9
<i>Veillonella</i> spp.	1.5E8 H		1.2E5-5.5E7

Actinobacteria Phylum

<i>Bifidobacterium</i> spp.	1.5E8		<=6.4E9
<i>Bifidobacterium longum</i>	1.4E8		<=7.2E8
<i>Collinsella aerofaciens</i>	5.1E8		1.4E7-1.9E9

The gray-shaded portion of a quintile reporting bar represents the proportion of the reference population with results below detection limit.

Commensal results and reference range values are displayed in a computer version of scientific notation, where the capital letter "E" indicates the exponent value (e.g., 7.3E6 equates to 7.3 x 10⁶ or 7,300,000).

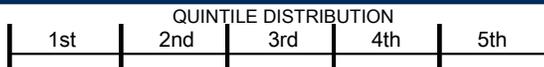
Methodology: DNA by PCR



Gastrointestinal Microbiome

Commensal Bacteria (PCR)

Result
CFU/g stool



Reference Range
CFU/g stool

Proteobacteria Phylum

Desulfovibrio piger

8.7E7 H



<=1.8E7

Escherichia coli

1.3E8 H



9.0E4 -4.6E7

Oxalobacter formigenes

5.0E7 H



<=1.5E7

Euryarchaeota Phylum

Methanobrevibacter smithii

1.4E8 H



<=8.6E7

Fusobacteria Phylum

Fusobacterium spp.

2.3E7 H



<=2.4E5

Verrucomicrobia Phylum

Akkermansia muciniphila

3.1E7



>=1.2E6

Firmicutes/Bacteroidetes Ratio

Firmicutes/Bacteroidetes (F/B Ratio)

11 L



12-620

The gray-shaded portion of a quintile reporting bar represents the proportion of the reference population with results below detection limit.

Commensal results and reference range values are displayed in a computer version of scientific notation, where the capital letter "E" indicates the exponent value (e.g., 7.3E6 equates to 7.3 x 10⁶ or 7,300,000).

The Firmicutes/Bacteroidetes ratio (F/B Ratio) is estimated by utilizing the lowest and highest values of the reference range for individual organisms when patient results are reported as <DL or >UL.



Gastrointestinal Microbiome**

Human microflora is influenced by environmental factors and the competitive ecosystem of the organisms in the GI tract. Pathogenic significance should be based upon clinical symptoms.

Additional Bacteria

Non-Pathogen: Organisms that fall under this category are those that constitute normal, commensal flora, or have not been recognized as etiological agents of disease.

Potential Pathogen: Organisms that fall under this category are considered potential or opportunistic pathogens when present in heavy growth.

Pathogen: The organisms that fall under this category have a well-recognized mechanism of pathogenicity in clinical literature and are considered significant regardless of the quantity that appears in the culture.

Microbiology Legend			
NG	NP	PP	P
No Growth	Non-Pathogen	Potential Pathogen	Pathogen

Bacteriology (Culture)

Lactobacillus spp.

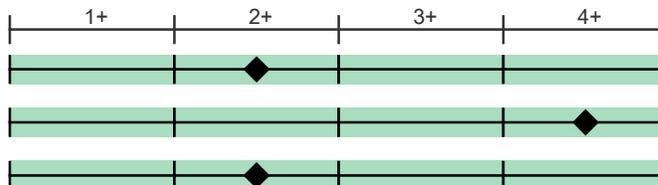
2+ NP

Escherichia coli

4+ NP

Bifidobacterium

2+ NP



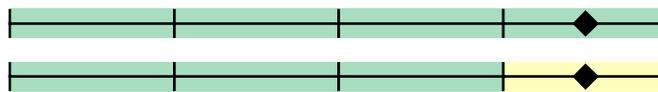
Additional Bacteria

alpha haemolytic Streptococcus

4+ NP

Proteus mirabilis

4+ PP



Mycology (Culture)

NG



KOH Preparation for Yeast

Methodology: Potassium Hydroxide (KOH) Preparation for Yeast

Potassium Hydroxide (KOH) Preparation for Yeast

These yeast usually represent the organisms isolated by culture. In the presence of a negative yeast culture, microscopic yeast may reflect organisms not viable enough to grow in culture. The presence of yeast on KOH prep should be correlated with the patient's symptoms. However, moderate to many yeast suggests yeast overgrowth.

Results

KOH Preparation, stool

No Yeast Present

The result is reported as the amount of yeast seen microscopically:

Rare: 1-2 per slide

Few: 2-5 per high power field (HPF)

Moderate: 5-10 per HPF

Many: >10 per HPF

** Indicates testing performed by Genova Diagnostics, Inc. 63 Zillicoa St., Asheville, NC 28801-0174

A. L. Peace-Brewer, PhD, D(ABMLI), Lab Director - CLIA Lic. #34D0655571 - Medicare Lic. #34-8475



Parasitology**

Microscopic O&P Results

Microscopic O&P is capable of detecting all described gastrointestinal parasites. The organisms listed in the box represent those commonly found in microscopic stool analysis. Should an organism be detected that is not included in the list below, it will be reported in the Additional Results section. For an extensive reference of all potentially detectable organisms, please visit www.gdx.net/product/gi-effects-comprehensive-stool-test

Genus/species	Result
Nematodes - roundworms	
<i>Ancylostoma/Necator</i> (Hookworm)	Not Detected
<i>Ascaris lumbricoides</i>	Not Detected
<i>Capillaria philippinensis</i>	Not Detected
<i>Enterobius vermicularis</i>	Not Detected
<i>Strongyloides stercoralis</i>	Not Detected
<i>Trichuris trichiura</i>	Not Detected
Cestodes - tapeworms	
<i>Diphyllobothrium latum</i>	Not Detected
<i>Dipylidium caninum</i>	Not Detected
<i>Hymenolepis diminuta</i>	Not Detected
<i>Hymenolepis nana</i>	Not Detected
<i>Taenia</i> spp.	Not Detected
Trematodes - flukes	
<i>Clonorchis/Opisthorchis</i> spp.	Not Detected
<i>Fasciola</i> spp./ <i>Fasciolopsis buski</i>	Not Detected
<i>Heterophyes/Metagonimus</i>	Not Detected
<i>Paragonimus</i> spp.	Not Detected
<i>Schistosoma</i> spp.	Not Detected
Protozoa	
<i>Balantidium coli</i>	Not Detected
<i>Blastocystis</i> spp.	Moderate Detected
<i>Chilomastix mesnili</i>	Not Detected
<i>Cryptosporidium</i> spp.	Not Detected
<i>Cyclospora cayetanensis</i>	Not Detected
<i>Dientamoeba fragilis</i>	Few Detected
<i>Entamoeba coli</i>	Not Detected
<i>Entamoeba histolytica/dispar</i>	Not Detected
<i>Entamoeba hartmanii</i>	Not Detected
<i>Entamoeba polecki</i>	Not Detected
<i>Endolimax nana</i>	Not Detected
<i>Giardia</i>	Not Detected
<i>Iodamoeba buetschlii</i>	Not Detected
<i>Cystoisospora</i> spp.	Not Detected
<i>Trichomonads</i> (e.g. <i>Pentatrichomonas</i>)	Not Detected
Additional Findings	
White Blood Cells	Not Detected
Charcot-Leyden Crystals	Not Detected
Other Infectious Findings	

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Parasitology

PCR Parasitology - Protozoa**

Methodologies: DNA by PCR, Next Generation Sequencing

Organism	Result	Units	Status	Expected Result
<i>Blastocystis</i> spp.	2.00e3	femtograms/microliter C&S stool	Detected	Not Detected
<i>Cryptosporidium</i> spp.	<4.87e2	genome copies/microliter C&S stool	Not Detected	Not Detected
<i>Cyclospora cayetanensis</i>	<2.65e2	genome copies/microliter C&S stool	Not Detected	Not Detected
<i>Dientamoeba fragilis</i>	2.96e3	genome copies/microliter C&S stool	Detected	Not Detected
<i>Entamoeba histolytica</i>	<1.14e3	genome copies/microliter C&S stool	Not Detected	Not Detected
<i>Giardia</i>	<1.57e2	genome copies/microliter C&S stool	Not Detected	Not Detected

Blastocystis spp. Reflex Subtyping

Type 1: Not Detected	Type 4: Not Detected	Type 7: Not Detected
Type 2: Detected	Type 5: Not Detected	Type 8: Not Detected
Type 3: Not Detected	Type 6: Not Detected	Type 9: Not Detected

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Additional Results

Color††	Result Brown
Consistency††	Formed/Normal

††Results provided from patient input.

Zonulin Family Peptide

Methodology: EIA	Result	Reference Range	Zonulin Family Peptide
Zonulin Family Peptide, Stool	100.0	22.3-161.1 ng/mL	<p>This test is for research use only. Genova will not provide support on interpreting the test results. This test does not detect zonulin.¹ The Scheffler paper suggests that the IDK kit may detect a zonulin family peptide, such as properdin. Genova's unpublished data demonstrated that the current IDK kit results were associated with stool inflammation biomarkers and an inflammation-associated dysbiosis profile.</p> <p>The performance characteristics of Zonulin Family Peptide have been verified by Genova Diagnostics, Inc. The assay has not been cleared by the U.S. Food and Drug Administration.</p>

Reference:

- Scheffler L, et al. Widely Used Commercial ELISA Does Not Detect Precursor of Haptoglobin2, but Recognizes Properdin as a Potential Second Member of the Zonulin Family. *Front Endocrinol.* 2018;9:22.



Macroscopic Exam for Worms **

Methodology: Macroscopic Evaluation

No larvae seen macroscopically.

Add-on Testing

Methodology: EIA

	Result	Expected Value	
HpSA - <i>H. pylori</i>	Negative	Negative	<p>HpSA (<i>Helicobacter pylori</i> stool antigen)</p> <p><i>Helicobacter pylori</i> is a bacterium which causes peptic ulcer disease and plays a role in the development of gastric cancer. Direct stool testing of the antigen (HpSA) is highly accurate and is appropriate for diagnosis and follow-up of infection.</p>
<i>Campylobacter</i> spp. ♦**	Negative	Negative	<p><i>Campylobacter</i> spp.</p> <p><i>Campylobacter jejuni</i> is the most frequent cause of bacterial-induced diarrhea. While transmission can occur via the fecal-oral route, infection is primarily associated with the ingestion of contaminated and poorly cooked foods of animal origin, notably, red meat and milk.</p>
<i>Clostridium difficile</i> ♦**	Negative	Negative	<p><i>Clostridium difficile</i></p> <p><i>Clostridium difficile</i> is an anaerobic, spore-forming gram-positive bacterium. After a disturbance of the gut flora (usually with antibiotics), colonization with <i>Clostridium difficile</i> can take place. <i>Clostridium difficile</i> infection is much more common than once thought.</p>
Shiga toxin <i>E. coli</i> ♦**	Negative	Negative	<p>Shiga toxin <i>E. coli</i></p> <p>Shiga toxin-producing <i>Escherichia coli</i> (STEC) is a group of bacterial strains that have been identified as worldwide causes of serious human gastrointestinal disease. The subgroup enterohemorrhagic <i>E. coli</i> includes over 100 different serotypes, with 0157:H7 being the most significant, as it occurs in over 80% of all cases. Contaminated food continues to be the principal vehicle for transmission; foods associated with outbreaks include alfalfa sprouts, fresh produce, beef, and unpasteurized juices.</p>
Fecal Lactoferrin ♦**	Negative	Negative	

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Tests were developed and their performance characteristics determined by Genova Diagnostics. Unless otherwise noted with ♦, the assays have not been cleared by the U.S. Food and Drug Administration.



Bacteria Sensitivity

Prescriptive Agents

<i>Proteus mirabilis</i>	R	I	S-DD	S	NI
Ampicillin	R				
Amox./Clavulanic Acid				S	
Cephalothin				S	
Ciprofloxacin				S	
Tetracycline	R				
Trimethoprim/Sulfa				S	

Natural Agents

<i>Proteus mirabilis</i>	LOW INHIBITION	HIGH INHIBITION
Berberine		
Oregano		
Plant Tannins		
Uva-Ursi		

Prescriptive Agents:

The R (Resistant) category implies isolate is not inhibited by obtainable levels of pharmaceutical agent.

The I (Intermediate) category includes isolates for which the minimum inhibition concentration (MIC) values usually approach obtainable pharmaceutical agent levels and for which response rates may be lower than for susceptible isolates.

The S-DD (Susceptible-Dose Dependent) category implies clinical efficacy when higher than normal dosage of a drug can be used and maximal concentration achieved.

The S (Susceptible) column implies that isolates are inhibited by the usually achievable concentrations of the pharmaceutical agent.

NI (No Interpretive guidelines established) category is used for organisms that currently do not have established guidelines for MIC interpretation.

Refer to published pharmaceutical guidelines for appropriate dosage therapy.

Natural Agents:

In this assay, inhibition is defined as the reduction level on organism growth as a direct result of inhibition by a substance. The level of inhibition is an indicator of how effective the substance was at limiting the growth of an organism in an in vitro environment. High inhibition indicates a greater ability by the substance to limit growth, while Low Inhibition a lesser ability to limit growth. The designated natural products should be considered investigational in nature and not be viewed as standard clinical treatment substances.



2205 GI Effects™ Microbial Ecology Profile - Stool

Interpretation At-a-Glance

Commensal Bacteria	Patient Results Out of Reference Range	Genova Diagnostics Commensal Bacteria Clinical Associations*							
		IBS	IBD	Metabolic Syndrome	Chronic Fatigue	Auto-immune	Type 2 Diabetes	High Blood Pressure	Mood Disorders
Bacteroidetes Phylum									
<i>Bacteroides-Prevotella</i> group		↑	↑	↑	↑	↑	↑	↑	↑
<i>Bacteroides vulgatus</i>		↑			↑	↑		↑	↑
<i>Barnesiella</i> spp.									
<i>Odoribacter</i> spp.									
<i>Prevotella</i> spp.	H	↑		↑	↑	↑		↑	↑
Firmicutes Phylum									
<i>Anaerotruncus colihominis</i>	H	↑	↑	↑	↑	↑	↑	↑	↑
<i>Butyrivibrio crossotus</i>	H								
<i>Clostridium</i> spp.									
<i>Coprococcus eutactus</i>		↑			↑	↑		↑	↑
<i>Faecalibacterium prausnitzii</i>		↑				↑			↑
<i>Lactobacillus</i> spp.									
<i>Pseudoflavonifractor</i> spp.	H	↑	↑	↑	↑	↑	↑	↑	↑
<i>Roseburia</i> spp.	L		↓						
<i>Ruminococcus</i> spp.	H	↕	↓	↓	↓	↕	↕	↕	↕
<i>Veillonella</i> spp.	H	↑	↑	↑	↑	↑	↑		↑
Actinobacteria Phylum									
<i>Bifidobacterium</i> spp.									
<i>Bifidobacterium longum</i>									
<i>Collinsella aerofaciens</i>		↕	↕	↓	↕	↕	↕	↕	↕
Proteobacteria Phylum									
<i>Desulfovibrio piger</i>	H								↑
<i>Escherichia coli</i>	H	↑	↑	↑	↑	↑	↑	↑	↑
<i>Oxalobacter formigenes</i>	H	↑		↑	↑				↑
Euryarchaeota Phylum									
<i>Methanobrevibacter smithii</i>	H	↑				↑			↑
Fusobacteria Phylum									
<i>Fusobacterium</i> spp.	H	↑	↑	↑	↑	↑	↑	↑	↑
Verrucomicrobia Phylum									
<i>Akkermansia muciniphila</i>		↓	↓	↓	↓	↓	↓	↓	↓

*Information derived from GDx results data comparing a healthy cohort to various clinical condition cohorts. The chart above showing a comparison of patient results to clinical conditions is meant for informational purposes only; it is not diagnostic, nor does it imply that the patient has a specific clinical diagnosis or condition.

The arrows indicate Genova's clinical condition cohort test results falling below ↓ or above ↑ the reference range that is greater than that of Genova's healthy cohort.

↕ Indicates Genova's clinical condition cohort test results falling below and above the reference range that are greater than that of Genova's healthy cohort.

Cells with bolded arrows indicate Genova's clinical condition cohort had more test results falling above versus below ↕ or more below versus above ↕ the reference range compared to that of Genova's healthy cohort.