



Report Date August 02, 2019
Report Type Final

Patient

- Name: John Doe
- DOB: 11/19/1989
- Sex: Male

Results

- Type: Swab
- Source: Fecal
- Completed date: 08/02/2019
- Received date: 07/28/2019
- Sampled date: 07/24/2019

Methodology / Protocol

- Extraction: Magnetic Bead Based DNA method
- Library Prep: [Earth Microbiome Protocol](#)
- Sequencing: 16s rRNA on v4 region
- Machine: MiSeq PE150 (Illumina)
- Bioinformatics: Kraken

Summary & Interpretation

Please Note: Detecting a microorganism by this test does not imply having a disease. Similarly, not detecting a microorganism by this test does not exclude the presence of a disease-causing microorganism. Further, other organisms may be present that are not detected by this test. This test is not a substitute for established methods for identifying microorganisms or their antimicrobial susceptibility profile. Please consult your medical professional.

At-a-Glance

ABC Bacteria Akkermansia ❗ Bifidobacteria ✅ Clostridiales ❗	Inflammation Index Butyrate ❗ Polyamine ❗ Propionate ✅	Nutrient Absorption Carbohydrates ❗ Lipids ✅ Amino Acids ❗
Microbiome Diversity Diversity ❗ Richness ✅ Evenness ❗	Food Intolerance Panel Gluten ❗ Lactose ❗ Sweeteners ✅	Imbalance Panel Digestion ❗ Metabolic ✅ Wellness ❗

ABC BACTERIA [1]

The following keystone bacteria (Akkermansia, Bifidobacteria, Clostridiales) have been shown to be reside in the majority of the healthy population. Furthermore, tribal societies with limited exposure to modern and western living have shown to have an abundance of these bacteria.

Akkermansia

	RESULT	MIN	MID	MAX	RR
Akkermansia muciniphila	32%	5%	15%	35%	5-35%

Bifidobacteria

	RESULT	MIN	MID	MAX	RR
Bifidobacteria longum	26%	7%	21%	40%	15-30%
Bifidobacteria lactis	3.5%	2%	3%	6%	2%-4%
Bifidobacteria infantim	32%	12%	30%	70%	15-35%

Clostridiales

	RESULT	MIN	MID	MAX	RR
Faecalibacterium prausnitzii	1%	4%	5%	9%	4-9%
Roseburia spp.	9%	12%	30%	70%	15-35%
Eubacteria spp.	6%	12%	30%	70%	15-35%

INFLAMMATION INDEX [2]

The following inflammation index provides analysis on specific microbes that are known to produce short-chain fatty acids within the gut. Short-chain fatty acids such as Butyrate, Polyamine, and Propionate provide integrity and anti-inflammatory benefits to the epithelial cells within the gut.

Butyrate

A type of short-chain fatty acid — is a molecule produced by certain gut microbes. Butyrate has many jobs, including helping to control inflammation. We've analyzed your levels of several butyrate-producing gut microbes.

Bacteria Referenced: Anaerostipes, Coprococcus catus, Eubacterium rectale, Roseburia faecis, Roseburia hominis, Roseburia intestinalis, Roseburia inulinivorans, and Subdoligranulum variabile

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

Polyamine

Molecules that aid in the growth, survival, and renewal of your cells. These molecules may also help to control inflammation. We've analyzed your levels of several polyamine-producing gut microbes.

Bacteria Referenced: Bifidobacterium

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

Propionate

Type of short-chain fatty acid — is a molecule produced by certain gut microbes. Propionate has many jobs, including helping to control inflammation. We've analyzed your levels of several propionate-producing gut microbes.

Bacteria Referenced: Veillonella, Akkermansia muciniphila, Bacteroides uniformis, Bacteroides vulgatus, Coprococcus catus, Dialister invisus, Dialister succinatiphilus, Phascolarctobacterium succinatutens, Prevotella copri, Roseburia intestinalis, and Roseburia inulinivorans.

	RESULT	MIN	MID	MAX	RR
Overall Abundance	23%	12%	23%	50%	12-30%

NUTRIENT ABSORPTION [3]

The following nutrient absorption analysis is based on specific bacteria that help digest carbs, fats, and proteins. The better the balance of microbes the more likely your gut will be to absorption nutrients.

Carbohydrates (Carbs)

Numerous gut microbes can metabolize carbohydrates. We've looked at many of these, and compared your levels of these microbes with those of our selected samples. (Selected samples are from individuals who report no ailments and high levels of wellness.)

Bacteria Referenced: Anaerostipes, Bacteroides, Bifidobacterium, Blautia, Clostridium, Coprococcus, Dialister, Dorea, Eubacterium, Faecalibacterium, Lactobacillus, Lactococcus, Odoribacter, Oscillospira, Phascolarctobacterium, Roseburia, Ruminococcus, and Veillonella.

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

Lipids (Fat)

A diverse group of gut microbes can help your body metabolize lipids, also known as "fats". We've looked at many of these and compared your levels of these microbes with those of our selected samples. (Selected samples are from individuals who report no ailments and high levels of wellness.)

Bacteria Referenced: Bacteroides, Bifidobacterium, Bilophila, Blautia, Butyricimonas, Coprococcus, Dorea, Eggerthella, Holdemania, Lachnospira, Lactobacillus, Odoribacter, Oscillospira, and Ruminococcus.

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

Amino Acids (Protein)

Many gut microbes can metabolize proteins to produce amino acids. We've looked at a number of these and compared your levels of these microbes with those of our selected samples. (Selected samples are from individuals who report no ailments and high levels of wellness.)

Bacteria Referenced: Bacillus, Bacteroides, Bifidobacterium, Clostridium, Escherichia, Hafnia, Klebsiella, Lactococcus, Morganella, Odoribacter, Propionibacterium, Staphylococcus, and Streptococcus.

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

FOOD INTOLERANCE PANEL [4]

The following food intolerance panel provides details on specific microbes that help digest and filter out gluten, lactose, and artificial sweeteners. A healthy balance of these microbes provides your body with the resources to tolerate foods that contain these allergens.

Gluten

A variety of gut microbes may help your body digest gluten. Keep in mind: low levels of these microbes, alone, do not indicate a gluten intolerance or sensitivity. Many factors may influence how you respond to gluten.

Bacteria Referenced: Bacillus licheniformis, Lactobacillus mucosae, Lactobacillus rhamnosus

	RESULT	MIN	MID	MAX	RR
Overall Abundance	2%	6%	8%	12%	6-9%

Lactose

When gut bacteria digest lactose, this can cause gas, bloating, and other symptoms of lactose intolerance. Certain lactose-digesting bacteria, however, may help reduce these symptoms. Here, we look at your levels of several of these microbes. Keep in mind: these results do not indicate whether you are lactose intolerant or sensitive. Many factors may affect how you respond to lactose.

Bacteria Referenced: Bifidobacterium, Faecalibacterium, Lactobacillus, Roseburia.

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4.6%	3%	6%	15%	4-12%

Artificial Sweeteners

Artificial sweeteners may disrupt the balance of your gut microbiome by increasing your levels of certain microbes. We've looked at several of these microbes and compared your levels to those of people who regularly consume artificial sweeteners.

Bacteria Referenced: Actinomicrobes, Deltaproteomicrobes, Enteromicrobesceae

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

IMBALANCE PANEL [5]

The following imbalance panel provides details on specific microbes that may be associated on inversely associated with the pathology of different digestive, metabolic, and wellness outcomes.

Digestion

Diarrhea

Probability Ratio (4/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

Associated

Clostridium difficile [1-3], Campylobacter [4,5], Escherichia-Shigella [6-10], Salmonella enterica [11-15], Vibrio cholerae [16,17], Clostridium [18,19], Bacteroides fragilis [20,21]

Inversely associated

Lactobacillus [22], Microbial Diversity [23,24]

Irritable Bowel Syndrome

Probability Ratio (1.2/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4.6%	3%	6%	15%	4-12%

Associated

Salmonella enterica [25], Campylobacter [25], Escherichia-Shigella [25], Veillonella [26]

Inversely associated

Alistipes [27], Bifidobacterium [28], Collinsella aerofaciens [28-30], Lactobacillus [26,28]

Inflammatory Bowel Disease

Probability Ratio (5/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	12%	17%	25%	40%	15-32%

Associated

Desulfovibrio piger [31], Fusobacterium [32]

Inversely associated

Roseburia [33]

Crohn's Disease

Probability Ratio (4/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%
Associated Escherichia-Shigella [33-35], Ruminococcus [36,38]					
Inversely associated Akkermansia muciniphila [36], Bifidobacterium [37], Dialister invisus [37], Odoribacter [33], Roseburia [38,39], Microbial Diversity [40]					

Ulcerative Colitis

Probability Ratio (1.5/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%
Associated Ruminococcus [36]					
Inversely associated Akkermansia muciniphila [36], Odoribacter [33], Prevotella [38,39,41], Roseburia [42], Ruminococcus albus [43], Microbial Diversity [41]					

Constipation

Probability Ratio (4.5/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%
Associated Methanobrevibacter smithii [44]					
Inversely associated Bifidobacterium [45]					

Abdominal Tenderness ✓

Probability Ratio (2.2/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

Associated

Anaerotruncus colihominis [47]

Bloating ✓

Probability Ratio (.5/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

Associated

Anaerotruncus colihominis [47]

Flatulence ✓

Probability Ratio (1/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

Associated

Bacteroides fragilis [48]

Metabolic

Obesity ✓

Probability Ratio (2/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

Associated

Lactobacillus [49-51]

Inversely associated

Akkermansia muciniphila [52,53], Alistipes [27], Anaerotruncus colihominis [27,54], Barnesiella [27], Butyrivibrio crossotus [55,56], Lactobacillus [51], Methanobrevibacter smithii [50,57], Microbial Diversity [55,56,58]

Type II Diabetes

Probability Ratio (4/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

Associated

Akkermansia muciniphila [59]

Inversely associated

Lactobacillus [60,61], Roseburia [59,62,63]

Prediabetes

Probability Ratio (1.5/5)

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

Inversely associated

Microbial Diversity [55]

Wellness

Trimethylamine (TMA)

Your gut microbiome may be associated with your overall cardiovascular wellness.[6] After you eat red meat and eggs, some of your gut microbes convert compounds found in these foods into a chemical called trimethylamine (TMA). Your body then converts TMA to trimethylamine N-oxide (TMAO).

People with higher levels of TMAO in their blood tend to have lower levels of cardiovascular wellness, although it's not clear whether TMA and TMAO are the culprits or simply bystanders. Here, we explore your TMA-producing microbes.

Bacteria Referenced: Acinetobacter, Aeromonas, Alcaligenes, Alteromonas, Anaerococcus, Bacillus, Burkholderia, Campylobacter, Clostridium, Desulfitobacterium, Desulfovibrio, Desulfuromonas, Edwardsiella, Edwardsiella, Enterococcus, Eubacterium, Flavobacterium, Lactobacillus, Micrococcus,

Mobiluncus, Olsenella, Photobacterium, Proteus, Providencia, Pseudomonas, Rhodopseudomonas, Salmonella, Sarcina, Serratia, Shewanella, Sporomusa, Staphylococcus, Stigmatella, Streptococcus, and Vibrio

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

Sleep

GABA

GABA (short for gamma-aminobutyric acid) is a chemical messenger that helps turn down brain activity for a deeper, more restorative sleep. Much of your body’s GABA is produced in your brain, but your gut microbes also contribute. Here, we look at your levels of some of the main GABA-producing microbes. Keep in mind: these results don’t indicate whether you are low or high in GABA. They simply show your levels of certain microbes that may contribute to your supply.

Bacteria Referenced: Lactobacillus, Bifidobacterium

	RESULT	MIN	MID	MAX	RR
Overall Abundance	4%	12%	30%	70%	15-35%

Serotonin

Serotonin is a chemical messenger that helps promote healthy sleep patterns. While your body’s cells produce most of your serotonin, your gut microbes also pitch in. Here, we look at your levels of some of the key serotonin-producing microbes. Keep in mind: these results don’t indicate whether you are low or high in serotonin. They simply show your levels of certain microbes that may contribute to your supply.

Bacteria Referenced: Streptococcus, Enterococcus

	RESULT	MIN	MID	MAX	RR
Overall Abundance	17%	12%	30%	70%	15-35%

MICROBIOME RESULTS

Bacteroidetes Phylum

	RESULT	MIN	MID	MAX	RR
Bacteroides-Prevotella Group	1%	4%	5%	9%	4-9%
B. vulgatus	1%	4%	5%	9%	4-9%
Barnesiella spp.	1%	4%	5%	9%	4-9%
Odoribacter spp.	1%	4%	5%	9%	4-9%
Prevotella spp.	1%	4%	5%	9%	4-9%

Firmicutes Phylum

	RESULT	MIN	MID	MAX	RR
Anaerotruncus colihominis	1%	4%	5%	9%	4-9%
Butyrivibrio crossotus	1%	4%	5%	9%	4-9%
Clostridium spp.	1%	4%	5%	9%	4-9%
Coprococcus eutactus	1%	4%	5%	9%	4-9%
Faecalibacterium prausnitzii	1%	4%	5%	9%	4-9%
Lactobacillus spp.	1%	4%	5%	9%	4-9%
Pseudoflavonifractor spp.	1%	4%	5%	9%	4-9%
Roseburia spp.	1%	4%	5%	9%	4-9%
Ruminococcus spp.	1%	4%	5%	9%	4-9%
Veillonella spp.	1%	4%	5%	9%	4-9%

Actinobacteria Phylum

	RESULT	MIN	MID	MAX	RR
Bifidobacterium spp.	1%	4%	5%	9%	4-9%
B. longum	1%	4%	5%	9%	4-9%
Collinsella aerofaciens	1%	4%	5%	9%	4-9%

Proteobacteria Phylum

	RESULT	MIN	MID	MAX	RR
Desulfovibrio piger	1%	4%	5%	9%	4-9%
Escherichia coli	1%	4%	5%	9%	4-9%
Oxalobacter formigenes	1%	4%	5%	9%	4-9%

Euryarchaeota Phylum

	RESULT	MIN	MID	MAX	RR
Methanobrevibacter smithii	1%	4%	5%	9%	4-9%

Fusobacteria Phylum

	RESULT	MIN	MID	MAX	RR
Fusobacterium spp.	1%	4%	5%	9%	4-9%

Verrucomicrobia Phylum

	RESULT	MIN	MID	MAX	RR
Akkermansia muciniphila	32%	4%	5%	9%	4-9%

RECOMMENDATIONS [6]

The following recommendations are based on the imbalance of microbes that may be causing inflammation, poor nutrient absorption, food intolerances, digestive symptoms, metabolic symptoms, and wellness symptoms. All recommendations currently utilize food sources to replenish or decrease specific microbes for better health. Please consult your medical professional prior to starting any new regime.

ABC Bacteria [6A]

Bacteria	Take Action (Foods)	Take Action (Supplements)
Akkermansia muciniphila	Fast 24 hours, high polyphenols foods (Wine, Grapes, Green Tea, Dark Chocolate, Berries, Dark Greens)	high polyphenols supplements
Bifidobacteria longum	Artichokes, Garlic, Onions, Dandelion Roots, Almonds, Red Wine, Green Tea, Kefir	Probiotic, Magnesium, Inulin, Resveratrol
Bifidobacteria lactis	Artichokes, Garlic, Onions, Dandelion Roots, Almonds, Red Wine, Green Tea, Kefir	Probiotics, Magnesium, Inulin, Resveratrol
Bifidobacteria infantim	Artichokes, Garlic, Onions, Dandelion Roots, Almonds, Red Wine, Green Tea, Kefir	Probiotics, Magnesium, Inulin, Resveratrol
Faecalibacterium prausnitzii	Chicory, Apples, Artichokes, Whole Grains, Red Wine, Sweet Potatoes	N-Acetyl-D-Glucosamine, Probiotic Strains (Bacillus Coagulans), Epinephrine
Roseburia spp.	Sea Fish, Whole Grains, Extra Virgin Olive Oil, Dark Green Vegetables, Red Wine	n/a
Eubacteria spp.	Fish Protein, Garlic/Onions, Free-Range Eggs, Almonds, Dark Green Vegetables	n/a

Inflammation [6B]

Anti-inflammatory molecules	Take Action (Foods)	Take Action (Supplements)
Butyrate	Whole-grain foods, Whole-grain breakfast cereal, Mushrooms, Consume arabinoxylan oligosaccharides (AXOS), Consume dietary fiber	LC-AX supplements, Inulin supplements, Mushroom fiber supplements, Polyphenol supplements
Polyamine	Whole-grain foods, Whole-grain breakfast cereal,	LC-AX supplements, Inulin supplements, Mushroom

	Mushrooms, Consume arabinoxylan oligosaccharides (AXOS), Consume dietary fiber	fiber supplements, Polyphenol supplements
Propionate	Whole-grain foods, Whole-grain breakfast cereal, Mushrooms, Consume arabinoxylan oligosaccharides (AXOS), Consume dietary fiber	LC-AX supplements, Inulin supplements, Mushroom fiber supplements, Polyphenol supplements

Nutrient Absorption [6C]

Nutrients	Take Action (Foods)	Take Action (Supplements)
Carbs	Consume more dietary fiber, Fiber-rich foods, Eat Apples and Kiwi Fruit	Take Inulin, Take GOS Supplements, Wheat bran extract, Consume arabinoxylan oligosaccharides (AXOS), Take XOS Supplements, Fructan Supplements, Take Inulin-Oligofructose Supplements
Lipids	Consume more dietary fiber, Fiber-rich foods, Eat Apples and Kiwi Fruit	Take Inulin, Take GOS Supplements, Wheat bran extract, Consume arabinoxylan oligosaccharides (AXOS), Take XOS Supplements, Fructan Supplements, Take Inulin-Oligofructose Supplements
Amino Acids	Consume more dietary fiber, Fiber-rich foods, Eat Apples and Kiwi Fruit	Take Inulin, Take GOS Supplements, Wheat bran extract, Consume arabinoxylan oligosaccharides (AXOS), Take XOS Supplements, Fructan Supplements, Take Inulin-Oligofructose Supplements

Food Intolerance [6D]

Allergens	Take Action (Foods)	Take Action (Supplements)
Gluten	Kochujang	Supplements Containing Lactobacillus rhamnosus GG

Lactose	Fermented Milk, apples, fiber-rich foods (beans, brown rice, nuts, veggies, whole grains), Inulin foods (artichokes, asparagus, bananas, chicory root, endive, jerusalem artichokes, lettuce, onions, peaches, peas, pomegranates, root vegetables, watermelon, shallots, whole grain wheat, whole grain rye, and soft-necked garlic), high polyphenol foods (berries, tea, coffee, and red wine), Resistant starch foods (beans, bananas, potatoes, and some grains)	Galacto-oligosaccharides (GOS), Xylo-oligosaccharides (XOS), Fructan powder made from agave
Artificial Sweeteners	Apples, fiber-rich foods (beans, brown rice, nuts, veggies, whole grains), Inulin foods (artichokes, asparagus, bananas, chicory root, endive, jerusalem artichokes, lettuce, onions, peaches, peas, pomegranates, root vegetables, watermelon, shallots, whole grain wheat, whole grain rye, and soft-necked garlic)	Avoid saturated milk fat-derived diet.

DEFINITIONS

The reference range for each organism and the microbial diversity score was established using 1000+ samples from self-reported information provided by healthy individuals from the American Gut Project. The microbial diversity score is a measure of the microorganism richness, evenness and distinctness in the sample. Pathogenic microorganisms included in the Thryve Gut Health test are microorganisms that have been linked to disease and health risk. As noted above, a positive result in your sample is not a diagnosis, nor does it imply you have a disease. Similarly, a negative result does not preclude disease. Consult your medical professional regarding any positive test results.

Results

Results based on organisms count compared to total count of their microbiome and % of overall abundance found in patients gut microbiome sample.

Associated

These microorganisms have an observed association with the condition in the scientific literature

Inversely Associated

These microorganisms are found to be less abundant in people who have this condition in the scientific literature

Reference Range (RR)

Benchmark of the min and max of specific organism found in our 1000+ patient population

Overall Abundance (OA)

The percentage of a specific microbe found in the relative abundance of their microbiome.

Probability Ratio

Based on the makeup for the microbiome from the test result a patient would be categorized by the following on a 5 point scale:

- 1- Improbable
- 2- Mildly Probable
- 3- Moderately Probable
- 4- Probable
- 5- More Probabl

Require Opinion

Results outside of the healthy reference range are highlighted with an alert symbol

Optimal Levels

Results within the healthy reference range. Does not require opinion

References

References to scientific publications associating organisms with conditions are listed in brackets

METHODS & LIMITATIONS

Microbial DNA is extracted and marker genes are amplified by polymerase chain reaction (PCR) and then sequenced using the Illumina® MiSeq sequencer. The sequence data is processed using a proprietary phylogenetic analysis algorithm.

This test detects the presence of the following microorganisms with 99% sensitivity and specificity: Akkermansia muciniphila, Alistipes, Anaerotruncus colihominis, Bacteroides fragilis, Barnesiella, Bifidobacterium, Butyrivibrio crossotus, Campylobacter, Clostridium, Clostridium difficile, Collinsella aerofaciens, Desulfovibrio piger, Dialister invisus, Escherichia-Shigella, Fusobacterium, Lactobacillus, Methanobrevibacter smithii, Odoribacter, Oxalobacter formigenes, Prevotella, Roseburia, Ruminococcus, Ruminococcus albus, Salmonella enterica, Veillonella, and Vibrio cholerae.

Some of these microorganisms may not be considered pathogenic, but are included as they reflect the state of the patients microbiome. The microbiome and its clinical relevance is an area of active investigation. This sample has 85.2 Mb of sequenced DNA, in 283,855 reads, exceeding our 10,000 read quality control threshold.

ABOUT THIS TEST

This test was developed and its performance characteristics were determined by Quantbiome, Inc. (dba Thryve) This test has not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary. This test may be used for clinical purposes and should not be regarded as investigational or for research only.

This test is a next-generation sequencing-based assay that can identify 13 species and 13 genera of gastrointestinal microbiome related microorganisms from a stool swab sample, including 5 pathogenic organisms. The detection (or lack thereof) of microorganisms, as the case may be, is reported to a patients treating medical professional in this report. The report should be considered in context with other clinical criteria (e.g. patient history, physical exam), as well as other studies (such as laboratory, pathology, and imaging) by a qualified medical professional prior to initiating or changing a patients diagnostic work-up or treatment plan.

This test is not a substitute for established methods for identifying microorganisms or their antimicrobial susceptibility profile. Patient management decisions must be based on the independent medical judgment of the treating medical professional. The test and accompanying report are not intended to be used as the sole means for clinical diagnosis or patient management decisions.

The report may include information on the relevance of reported microorganisms. This information is derived from peer-reviewed studies and other publicly available databases and may include associations between the microorganism and a health condition. Careful consideration must be made by the medical professional when using this information, as it may or may not be relevant to this patient. Organisms not included in this test may also have an effect on the mentioned health conditions. The organisms on this test may affect additional health conditions not mentioned on this report.

REFERENCES

[1] ABC BACTERIA

Genomic encyclopedia of type strains of the genus *Bifidobacterium*, 2014
Introduction to pre- and probiotics, 2002
Fusobacterium prausnitzii and Related Species Represent a Dominant Group Within the Human Fecal Flora, 2001
Growth requirements and fermentation products of *Fusobacterium prausnitzii*, and a proposal to reclassify it as *Faecalibacterium prausnitzii* gen. nov., comb. nov., 2002
A decrease of the butyrate-producing species *Roseburia hominis* and *Faecalibacterium prausnitzii* defines dysbiosis in patients with ulcerative colitis., 2013
FXR is a molecular target for the effects of vertical sleeve gastrectomy, 2014
The Human Vaginal Bacterial Biota and Bacterial Vaginosis, 2008
Eubacterium lentum (Eggerth) Prévot 1938: Emendation of Description and Designation of the Neotype Strain, 1971
Molecular details of a starch utilization pathway in the human gut symbiont *Eubacterium rectale*., 2014

[2] INFLAMMATION INDEX

Low-grade inflammation, diet composition and health: current research evidence and its translation.
Role of the microbiota in immunity and inflammation.
Chapter three: The role of short-chain fatty acids in health and disease.
Linking the human gut microbiome to inflammatory cytokine production capacity.
Links between diet, gut microbiota composition and gut metabolism.
Formation of propionate and butyrate by the human colonic microbiota.
Regulation of inflammation by microbiota interactions with the host.
A double-blind, placebo-controlled, cross-over study to establish the bifidogenic effect of a very-long-chain inulin extracted from globe artichoke (*Cynara scolymus*) in healthy human subjects.
Arabinoxylans and inulin differentially modulate the mucosal and luminal gut microbiota and mucin - degradation in humanized rats.
Arabinoxylans and human health.
Prebiotic and other health-related effects of cereal-derived arabinoxylans, arabinoxylan-oligosaccharides, and xylooligosaccharides.
Whole-grain wheat breakfast cereal has a prebiotic effect on the human gut microbiota: a double-blind, placebo-controlled, crossover study.
Dietary modulation of clostridial cluster XIVa gut bacteria (*Roseburia* spp.) by chitin-glucan fiber improves host metabolic alterations induced by high-fat diet in mice.
Scientific opinion on the safety of 'Chitin-glucan' as a novel food ingredient.
Pilot dietary intervention with heat-stabilized rice bran modulates stool microbiota and metabolites in healthy adults.
A polyphenol-rich cranberry extract protects from diet-induced obesity, insulin resistance and intestinal inflammation.
Lupin kernel fiber consumption modifies fecal microbiota in healthy men as determined by rRNA gene fluorescent in situ hybridization.
Digestive and physiologic effects of a wheat bran extract, arabinoxylan-oligosaccharide, in breakfast cereal.

[3] NUTRIENT ABSORPTION

Effects of Gut Microbes on Nutrient Absorption and Energy Regulation
Microbiota in Inflammatory Bowel Disease Pathogenesis and Therapy: Is It All About Diet?
The role of short chain fatty acids in appetite regulation and energy homeostasis
New-found link between microbiota and obesity
Microbial degradation of complex carbohydrates in the gut
Disease Control Priorities in Developing Countries
Essentials of Healthy Eating: A Guide
The Essentials of Essential Fatty Acids
Lipid Metabolism, Apoptosis and Cancer Therapy
Chapter Three - The Role of Short-Chain Fatty Acids in Health and Disease
The Gut Microbiome Contributes to a Substantial Proportion of the Variation in Blood Lipids
Utilization of protein by human gut bacteria
How serotonin shapes moral judgment and behavior
Indigenous Bacteria from the Gut Microbiota Regulate Host Serotonin Biosynthesis
Prebiotic inulin-type fructans induce specific changes in the human gut microbiota
Habitual dietary fibre intake influences gut microbiota response to an inulin-type fructan prebiotic: a randomised, double-blind, placebo-controlled, cross-over, human intervention study
A double-blind, placebo-controlled, cross-over study to establish the bifidogenic effect of a very-long-chain inulin extracted from globe artichoke (*Cynara scolymus*) in healthy human subjects
Hypocholesterolemic and Prebiotic Effects of a Whole-Grain Oat-Based Granola Breakfast Cereal in a Cardio-Metabolic "At Risk" Population
Whole-grain wheat breakfast cereal has a prebiotic effect on the human gut microbiota: a double-blind, placebo-controlled, crossover study
Impact of short-chain galactooligosaccharides on the gut microbiome of lactose-intolerant individuals
Galactooligosaccharide and Sialyllactose Content in Commercial Lactose Powders from Goat and Cow Milk

Lentil (*Lens culinaris* L.): A prebiotic-rich whole food legume
Prebiotic Effects of Xylooligosaccharides on the Improvement of Microbiota Balance in Human Subjects
Xylooligosaccharides (XOS) as an Emerging Prebiotic: Microbial Synthesis, Utilization, Structural Characterization, Bioactive Properties, and Applications
A randomised, double- blind, cross-over study investigating the prebiotic effect of agave fructans in healthy human subjects
Dietary Guidelines for Americans: 2015-2020
Effect of apple intake on fecal microbiota and metabolites in humans
Kiwifruit (*Actinidia deliciosa*) changes intestinal microbial profile
Lupin kernel fiber consumption modifies fecal microbiota in healthy men as determined by rRNA gene fluorescent in situ hybridization
Xylooligosaccharide increases bifidobacteria but not lactobacilli in human gut microbiota
Inulin modifies the bifidobacteria population, fecal lactate concentration, and fecal pH but does not influence iron absorption in women with low iron status
Inulin-type fructans modulate intestinal *Bifidobacterium* species populations and decrease fecal short-chain fatty acids in obese women
Hypocholesterolemic and Prebiotic Effects of a Whole-Grain Oat-Based Granola Breakfast Cereal in a Cardio-Metabolic "At Risk" Population
Wheat bran extract alters colonic fermentation and microbial composition, but does not affect faecal water toxicity: a randomised controlled trial in healthy subjects
Digestive and physiologic effects of a wheat bran extract, arabino-xylan-oligosaccharide, in breakfast cereal
Effects of Probiotics, Prebiotics, and Synbiotics on Human Health
Tolerance to low-digestible carbohydrates: symptomatology and methods
Tolerance of probiotics and prebiotics
Gastrointestinal effects of prebiotics
World Gastroenterology Organization Global Guidelines

[4] FOOD INTOLERANCE PANEL

Lactose intolerance: diagnosis, genetic, and clinical factors.
Lactase Non-persistence and Lactose Intolerance.
Lactose Intolerance in Adults: Biological Mechanism and Dietary Management.
Perception of lactose intolerance impairs health-related quality of life.
Impact of short-chain galactooligosaccharides on the gut microbiome of lactose-intolerant individuals.
The Relationship Between the Human Genome and Microbiome Comes into View.
Strains and species of lactic acid bacteria in fermented milks (yogurts): effect on in vivo lactose digestion.
Dietary Guidelines for Americans: 2015-2020.
Effect of apple intake on fecal microbiota and metabolites in humans.
Hypocholesterolemic and Prebiotic Effects of a Whole-Grain Oat-Based Granola Breakfast Cereal in a Cardio-Metabolic "At Risk" Population.
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Prebiotic Effects of Xylooligosaccharides on the Improvement of Microbiota Balance in Human Subjects.
A randomised, double- blind, cross-over study investigating the prebiotic effect of agave fructans in healthy human subjects.
Kiwifruit (*Actinidia deliciosa*) changes intestinal microbial profile.
Lupin kernel fiber consumption modifies fecal microbiota in healthy men as determined by rRNA gene fluorescent in situ hybridization.
Effects of yogurt and bifidobacteria supplementation on the colonic microbiota in lactose-intolerant subjects.
Inulin modifies the bifidobacteria population, fecal lactate concentration, and fecal pH but does not influence iron absorption in women with low iron status.
Digestive and physiologic effects of a wheat bran extract, arabino-xylan-oligosaccharide, in breakfast cereal.
Galactooligosaccharide and Sialyllactose Content in Commercial Lactose Powders from Goat and Cow Milk.
Lentil (*Lens culinaris* L.): A prebiotic-rich whole food legume.
Red wine polyphenols modulate fecal microbiota and reduce markers of the metabolic syndrome in obese patients.
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[6] RECOMMENDATIONS

[6A] ABC BACTERIA

[6B] INFLAMMATION

- Arabinoxylans and inulin differentially modulate the mucosal and luminal gut microbiota and mucin - degradation in humanized rats.
- Arabinoxylans and human health.
- Prebiotic and other health-related effects of cereal-derived arabinoxylans, arabinoxylan-oligosaccharides, and xylooligosaccharides.
- Whole-grain wheat breakfast cereal has a prebiotic effect on the human gut microbiota: a double-blind, placebo-controlled, crossover study.
- Dietary modulation of clostridial cluster XIVa gut bacteria (*Roseburia* spp.) by chitin-glucan fiber improves host metabolic alterations induced by high-fat diet in mice.
- Scientific opinion on the safety of 'Chitin-glucan' as a novel food ingredient.
- Pilot dietary intervention with heat-stabilized rice bran modulates stool microbiota and metabolites in healthy adults.
- A polyphenol-rich cranberry extract protects from diet-induced obesity, insulin resistance and intestinal inflammation.
- Lupin kernel fiber consumption modifies fecal microbiota in healthy men as determined by rRNA gene fluorescent in situ hybridization.

[6C] NUTRIENT ABSORPTION

- Prebiotic inulin-type fructans induce specific changes in the human gut microbiota
- Habitual dietary fibre intake influences gut microbiota response to an inulin-type fructan prebiotic: a randomised, double-blind, placebo-controlled, cross-over, human intervention study
- A double-blind, placebo-controlled, cross-over study to establish the bifidogenic effect of a very-long-chain inulin extracted from globe artichoke (*Cynara scolymus*) in healthy human subjects
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- Inulin modifies the bifidobacteria population, fecal lactate concentration, and fecal pH but does not influence iron absorption in women with low iron status

[6D] FOOD INTOLERANCE

- Microbial Composition of the Korean Traditional Food "kochujang" Analyzed by a Massive Sequencing Technique. *Journal of Food Science*.
- Meta-analysis of probiotics for the treatment of irritable bowel syndrome. *World Journal of Gastroenterol.*
- Lactobacillus GG restoration of the gliadin induced epithelial barrier disruption. *BMC Microbiology*.
- Diversity of the cultivable human gut microbiome involved in gluten metabolism. *FEMS Microbiology Ecology*.