

VIOME

V' I O M E

DEMO TWO'S RESULTS

V I O M E

Dear demo two,

The information on this report is for educational and informational use only. The information is not intended to be used by the customer for any diagnostic purpose and is not a substitute for professional medical advice. You should always seek the advice of your physician or other healthcare providers with any questions you may have regarding diagnosis, cure, treatment, mitigation, or prevention of any disease or other medical condition or impairment or the status of your health.



Test Name: Gut Intelligence Test
Authorized Order Person: demo two
Customer Name: demo two
DOB: 02/28/1998
Gender: Female
Customer Id: 183d8abe-94c0-4872-85fa-8763251ad504
Sample Source: Fecal
Date Collected: 03/15/2019
Date Received: Not Available
Date Issued: 03/28/2019
Sample ID: 153668298766

All My Scores

Let's improve these.

Inflammatory Activity

 Needs Improvement

This score measures all the activities of your microbes that can contribute to or reflect inflammation in your gut environment. Inflammation in your gut can be caused by harmful things your microbes produce when you are either inefficiently digesting your proteins, have excessive microbial gas production, or simply have a gut environment that your microbes perceive as threatening.

A score that needs improvement means that there are relatively more pro-inflammatory activities, as opposed to anti-inflammatory or protective ones. Everyone's pattern is unique, so if your score needs



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improvement, some of your recommendations may focus on boosting more of the protective and healing anti-inflammatory functions, while others may focus more on controlling and balancing out the more harmful pro-inflammatory microbes and functions. Follow your recommendations to maintain or improve this score.

Inflammatory Activity Key

Reference Ranges:

-  **Needs Improvement** represents 19% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 63% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 18% of Viome customers, including both healthy and unhealthy individuals.

**Scores are based on Viome's proprietary algorithm that incorporates relevant functional categories each consisting of multiple manually curated taxonomic and pathway scoring components.*

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Digestive Efficiency




 Needs Improvement

This score is a comprehensive microbial reflection of your Gastrointestinal (GI) tract functions. The score consists of multiple activity patterns related to digestion, such as the movement of food, specific macronutrient breakdown ability, and your gut lining health from your first bite of food to the time it leaves your body. When this score needs improvement or is suboptimal, it means that some of your digestive functions need support.



Digestive Efficiency Key

Reference Ranges:

-  **Needs Improvement** represents 34% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 32% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 34% of Viome customers, including both healthy and unhealthy individuals.

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Intestinal Barrier Health




 **Needs Improvement**

This score focuses on your gut lining (or intestinal barrier) and the health of the mucosal layer that protects it. When your gut lining is compromised, things from the outside environment, like toxins, medications, and harmful bacteria, can make their way into your bloodstream from your gut and negatively affect your immune system and overall wellbeing. A good score means more optimal microbial functions that support your intestinal barrier and fewer disruptive or harmful functions are active in your gut. Follow your recommendations to address your specific pattern of microbial functions, and to prevent any intestinal permeability known as 'leaky gut'.



Intestinal Barrier Health Key

Reference Ranges:

-  **Needs Improvement** represents 34% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 32% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 34% of Viome customers, including both healthy and unhealthy individuals.

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Overall Gas Production




 Needs Improvement

This score is an assessment of your overall gas production activity by the microbes in your gut. Overall high microbial gas production has been associated with digestive difficulties, discomfort, and gut inflammation. A good score means that your microbes are not actively engaged in gas production functions.



Overall Gas Production Key

Reference Ranges:

-  **Needs Improvement** represents 31% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 27% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 42% of Viome customers, including both healthy and unhealthy individuals.

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Butyrate Production Pathways




 Needs Improvement

This score assesses the levels of activity of all microbial pathways that lead to the production of a beneficial nutrient - butyrate. Butyrate is a short-chain fatty acid known to beneficially affect many wellness areas from gut lining to insulin sensitivity and satiety (feeling full). A score that needs improvement means that your microbial butyrate production could really use a good boost! Individuals with low butyrate production activity would benefit from supplements or foods that either feed or add butyrate producing microbes into your gut ecosystem.



Butyrate Production Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 22% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 51% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 27% of Viome customers, including both healthy and unhealthy individuals.

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Methane Gas Production Pathways




 Needs Improvement

This score assesses the levels of activity of all microbial pathways that result in giving off methane gas in your gut. This kind of activity, when high, has been linked with some motility issues in the gut (how your food moves along the digestive tract), as well as pro-inflammatory patterns that can negatively affect your intestinal lining. A good score means that the activity of methane production pathways is low.



Methane Gas Production Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 30% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 18% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 52% of Viome customers, including both healthy and unhealthy individuals.

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Sulfide Gas Production Pathways




 Needs Improvement

This score assesses the levels of activity of all microbial pathways that result in the production of hydrogen sulfide gas. It can be made from some proteins that contain sulfur amino acids or from ingested sulfate or sulfite molecules found in foods like dried fruit, preserved meats, and some alcoholic beverages. This kind of activity, when high, contributes to pro-inflammatory patterns potentially harmful to the gut lining, as well as slowing of your motility (moving the food down your digestive tract). A good score means that the activity of sulfide production pathways is low.



Sulfide Gas Production Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 33% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 37% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 30% of Viome customers, including both healthy and unhealthy individuals.

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Putrescine Production Pathways




 Needs Improvement

This score assesses the levels of activity of all microbial pathways that lead to putrescine production. Putrescine is a molecular byproduct of protein fermentation - a microbial breakdown of protein. If the activities of putrescine production pathways are too high, it can be harmful to the gut environment and the intestinal barrier lining. It is also one of the signs that you may be eating too much protein that may not be digested properly.



Putrescine Production Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 34% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 49% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 17% of Viome customers, including both healthy and unhealthy individuals.

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Uric Acid Production Pathways




 Needs Improvement

This score assesses the levels of activity of all microbial pathways that lead to the production of uric acid (or urate). Uric Acid is a normal byproduct that comes from the breakdown of compounds called purines, which can be found in beer, sugary sodas, seafood and shellfish, turkey, veal, bacon, and organ meats. Excessive amounts of uric acid can contribute to gout. A good score means that your uric acid production pathway levels are low.



Uric Acid Production Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 48% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 43% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 9% of Viome customers, including both healthy and unhealthy individuals.

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TMA Production Pathways




 **Needs Improvement**

This score assesses the levels of all activity of metabolic pathways that result in TMA production. TMA (trimethylamine) is a molecule that gets converted to TMAO (Trimethylamine N-oxide) in the liver. TMAO is associated with unfavorable metabolic and cardiovascular effects. Since one of the substances used for microbial TMA production is choline, reducing high-choline-containing foods in the diet may be one of the options for improving this pattern. A good score means these TMA production pathway activity levels are low.



TMA Production Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 28% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 29% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 43% of Viome customers, including both healthy and unhealthy individuals.

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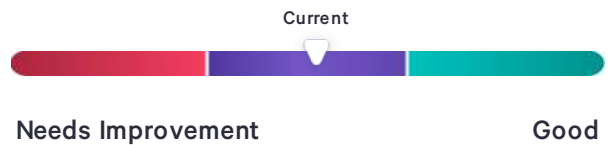
DOB: 02/28/1998

You're getting there.

Metabolic Fitness




 **Average**

This score represents active microbial organisms and functions that are associated with your blood sugar, insulin resistance, or weight control. A good score means high activity of microbes and their functions favorably associated with your metabolic fitness. A Metabolic Fitness score that indicates the need for improvement does not necessarily mean weight loss or gain. Follow your recommendations to support or improve healthy metabolic functions.



Metabolic Fitness Key

Reference Ranges:

-  **Needs Improvement** represents 18% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 65% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 17% of Viome customers, including both healthy and unhealthy individuals.

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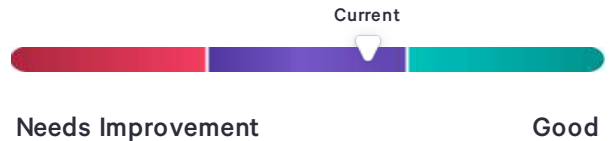
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Protein Fermentation




 **Average**

This score reflects whether or not you are digesting your proteins properly. Protein digestion begins when you first start chewing and continues down in your stomach. If the protein is not fully broken down through this process, your microbes will digest the excess protein available and may convert it into harmful byproducts. Overly high microbial protein fermentation translates into a score that needs improvement suggesting your protein digestion is suboptimal.



Protein Fermentation Key

Reference Ranges:

-  **Needs Improvement** represents 25% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 41% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 34% of Viome customers, including both healthy and unhealthy individuals.

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Microbial Richness

 Average

The score is your percentile for total count of active microbial species detected and sequenced from your sample. A good score means there is more richness, which in turn can provide more resilience to your microbial gut ecosystem and your body. This score needs improvement when the count of active microbes is relatively low and your gut flora could use additional microbes in its active composition. Your recommendations may include certain supplements or fermented foods that address this score.

43rd



Needs Improvement

Good




0th
Percentile

100th
Percentile

Microbial Richness Key

Reportable Range: 0 to 300 number of microbial species

Reference Ranges:

-  **Needs Improvement:** 0 to 83 microbial species represents 0 to 5th percentile of the Viome population
 -  **Average:** 84 to 189 microbial species represents the 5th percentile to 95th percentile of the Viome population
 -  **Good:** 190 to 300 microbial species represents the 95th to 100th percentile of the Viome population
- Mean:** 132

**Richness utilizes taxonomic data of known annotated microbial organisms and represents the total number of species.*

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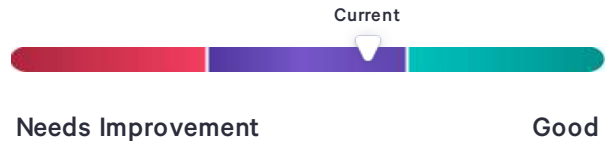
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LPS Biosynthesis Pathways




 Average

This score assesses the levels of activity of all microbial pathways leading to the production of LPS (lipopolysaccharides) in your gut. LPS is a pro-inflammatory molecule that gut microbes make, which can trigger your immune system response, especially if it passes to the bloodstream through the gut lining. This score is an important factor in assessing your inflammatory activity patterns.



LPS Biosynthesis Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 19% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 53% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 28% of Viome customers, including both healthy and unhealthy individuals.

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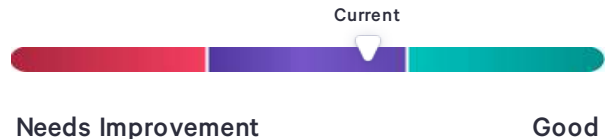
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Flagellar Assembly Pathways




 Average

This score assesses the levels of activity of all microbial pathways leading to the making of a structure called flagella. Flagellar structures serve as "fins" or "tails" for various microbes to help them move. A score that needs improvement suggests that these signaling pathway activities are high, indicating unrest in your microbiome as flagellar structures are helping beneficial organisms move away from a perceived threat. Higher than usual activity can also signal the presence of opportunistic organisms that are known to have these flagellar structures. This score is an important factor in assessing your inflammatory activity patterns.



Flagellar Assembly Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 14% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 44% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 42% of Viome customers, including both healthy and unhealthy individuals.

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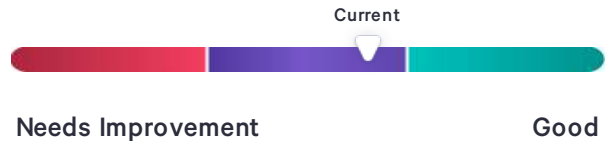
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Ammonia Production Pathways




 **Average**

This score assesses the levels of activity of all microbial pathways that result in the production of ammonia. Ammonia gas can be made from amino acids as a byproduct of the breaking down of protein or from ingested nitrate or nitrite molecules found in things like food preservatives or additives, preserved meats, and dried fruit. This kind of activity, when high, contributes to pro-inflammatory patterns potentially harmful to the gut lining, as well as slowing of your motility (moving the food down your digestive tract), and is also one of the signs that your proteins may not be digested properly. A good score means that the activity of ammonia production pathways is low.



Ammonia Production Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 16% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 68% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 16% of Viome customers, including both healthy and unhealthy individuals.

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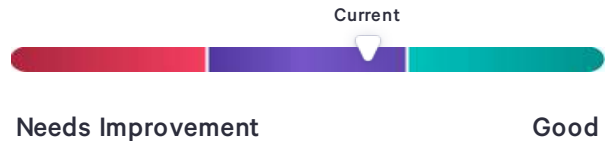
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Biofilm, Chemotaxis, and Virulence Pathways




 **Average**

This score assesses the levels of all activity of all metabolic pathways that suggest a pro-inflammatory or hostile environment in the gut. This includes virulence factors, biofilm formation, and chemotaxis signaling, which are all important parts of your overall inflammatory activity patterns. When this score is relatively high it means that there is some threat in the environment and your microbes are trying to either defend themselves, attack each other, or move. This type of a "microbial war zone" can negatively impact your gut environment, and some of the "bullets" secreted by the microbes may trigger an immune response. A good score means that these pathway activities are at low levels.



Biofilm, Chemotaxis, and Virulence Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 17% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 65% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 18% of Viome customers, including both healthy and unhealthy individuals.

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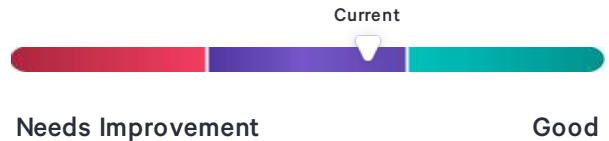
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Bile Acid Metabolism Pathways




 **Average**

This score assesses the levels of activity of all metabolic pathways that include bile acids. Normally bile acids are made by the liver to help with fat digestion. Bile acids enter the colon in the form of bile salts. Your gut microbiota can change them back into bile acids, after which they can even be recycled back to the liver. If this activity is relatively high or excessive, it may be an indicator of your inability to break down fat or absorb nutrients properly, which can contribute to a pro-inflammatory environment or negative liver-related effects, as microbiome's bile acid pathways have been implicated in fatty deposits in the liver. A good score means these pathway activity levels are low in your sample.



Bile Acid Metabolism Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 19% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 54% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 27% of Viome customers, including both healthy and unhealthy individuals.

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Keep it up!

Oxalate Metabolism Pathways




 Good

This score assesses the levels of activity of all microbial pathways needed to break down or metabolize oxalate. Oxalates are a major contributor to kidney stones. Oxalate-metabolizing microbes can help you by removing and digesting oxalate that you ingested from food. A good score means oxalate-metabolizing activities are high in your microbiome. When this score needs improvement, you may see some of the foods high in oxalate content on your list to minimize or even avoid.



Oxalate Metabolism Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 75% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 5% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 20% of Viome customers, including both healthy and unhealthy individuals.

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Salt Stress Pathways




 Good

This score assesses the levels of activity of all microbial pathways that signal excessive salt in the gut environment. This kind of signaling activity, when high, suggests that you may need to adjust your salt or sodium intake and/or your hydration levels. Too much salt for your gut microbiome makes your gut environment less favorable for some beneficial or probiotic organisms to thrive. A good score means that that pathway levels that signal microbial salt stress are low.



Salt Stress Pathways Key

Reference Ranges:

-  **Needs Improvement** represents 28% of Viome customers, including both healthy and unhealthy individuals.
-  **Average** represents 22% of Viome customers, including both healthy and unhealthy individuals.
-  **Good** represents 50% of Viome customers, including both healthy and unhealthy individuals.

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Meet your probiotic microbes

These are microbes that are found in commercially available probiotic products that are also active in your sample. If there are no organisms listed, no probiotics were identified in your sample.

Streptococcus thermophilus

P Probiotic



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My Active Microbes

Acidaminococcus fermentans

B Bacterium

Acinetobacter baumannii 24975_5

B Bacterium

Acinetobacter baumannii 855125

B Bacterium

Actinomyces graevenitzii

B Bacterium

Actinomyces sp. ICM47

B Bacterium

Adlercreutzia equolifaciens DSM 19450

B Bacterium

Akkermansia muciniphila strain YL44

B Bacterium

Alistipes finegoldii strain 2789STDY5608890

B Bacterium

Alistipes ihumii AP11

B Bacterium

Alistipes indistinctus YIT 12060

B Bacterium

Alistipes obesi

B Bacterium



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Alistipes senegalensis JC50

B Bacterium

Alistipes shahii WAL 8301

B Bacterium

Alistipes sp. Marseille-P2431 sp. Marseille-P2431

B Bacterium

Anaerofustis stercorihominis DSM 17244

B Bacterium

Anaerostipes hadrus

B Bacterium

Anaerotruncus colihominis DSM 17241

B Bacterium

Anaerotruncus rubiinfantis sp. MT15

B Bacterium

Bacteroides caccae

B Bacterium

Bacteroides cellulosilyticus

B Bacterium

Bacteroides clarus YIT 12056

B Bacterium

Bacteroides dorei CL03T12C01

B Bacterium

Bacteroides faecichinchillae

B Bacterium



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Bacteroides finegoldii DSM 17565

B Bacterium

Bacteroides finegoldii strain 2789STDY5608840

B Bacterium

Bacteroides intestinalis strain KLE1704

B Bacterium

Bacteroides massiliensis B84634 = Timone 84634 = DSM 17679 = JCM 13223

B Bacterium

Bacteroides massiliensis dnLKV3

B Bacterium

Bacteroides ovatus SD CMC 3f

B Bacterium

Bacteroides salyersiae

B Bacterium

Bacteroides stercoris CC31F

B Bacterium

Bacteroides stercoris strain CL09T03C01

B Bacterium

Bacteroides thetaiotaomicron

B Bacterium

Bacteroides uniformis dnLKV2

B Bacterium

Bacteroides uniformis strain 2789STDY5608791

B Bacterium



Test Name: Gut Intelligence Test

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Bacteroides vulgatus ATCC 8482

B Bacterium

Bacteroides vulgatus CL09T03C04

B Bacterium

Bacteroides vulgatus strain 2789STDY5834842

B Bacterium

Bacteroides vulgatus strain 2789STDY5834944

B Bacterium

Bacteroides xylanisolvens strain 2789STDY5608839

B Bacterium

Barnesiella intestinihominis YIT 11860

B Bacterium

Bifidobacterium mongoliense DSM 21395

B Bacterium

Bilophila wadsworthia ATCC 49260

B Bacterium

Blastocystis hominis isolate B

E Eukaryote

Blastocystis sp. subtype 3

E Eukaryote

Blastocystis sp. subtype 4 strain WR1

E Eukaryote

Blautia hydrogenotrophica

B Bacterium



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Blautia massiliensis sp. GD8

B Bacterium

Blautia obeum ATCC 29174

B Bacterium

Blautia sp. Marseille-P3087 sp. Marseille-P3087

B Bacterium

Butyricoccus pullicaecorum

B Bacterium

Butyricimonas synergistica DSM 23225

B Bacterium

Butyricimonas virosa DSM 23226

B Bacterium

Christensenella timonensis strain Marseille-P2437

B Bacterium

Clostridia bacterium UC5.1-1D1

B Bacterium

Clostridiales bacterium KLE1615

B Bacterium

Clostridiales bacterium VE202-13

B Bacterium

Clostridioides difficile

B Bacterium

Clostridium phoceensis strain GD3

B Bacterium



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Clostridium sp. L2-50

B Bacterium

Clostridium sp. Marseille-P3244 sp. Marseille-P3244

B Bacterium

Collinsella aerofaciens ATCC 25986

B Bacterium

Collinsella sp. 4_8_47FAA

B Bacterium

Coprococcus comes strain 2789STDY5834962

B Bacterium

Dorea formicigenerans ATCC 27755

B Bacterium

Dorea longicatena DSM 13814

B Bacterium

Dorea longicatena strain 2789STDY5834914

B Bacterium

Eisenbergiella tayi strain NML150140-1

B Bacterium

Emergencia timonensis strain SN18

B Bacterium

Enterococcus faecium isolate Hp_23-14

B Bacterium

Enterococcus faecium isolate Hp_6-9

B Bacterium



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DOB: 02/28/1998

Enterococcus faecium isolate Hp_7-6

B Bacterium

Enterococcus faecium isolate Hp_74-d6

B Bacterium

Escherichia

B Bacterium

Eubacterium ramulus strain 2789STDY5608891

B Bacterium

Eubacterium ventriosum ATCC 27560

B Bacterium

Faecalibacterium cf. prausnitzii KLE1255

B Bacterium

Faecalibacterium prausnitzii A2-165

B Bacterium

Faecalibacterium prausnitzii M21/2

B Bacterium

Faecalibacterium prausnitzii strain 2789STDY5608869

B Bacterium

Faecalibacterium prausnitzii strain 2789STDY5834930

B Bacterium

Faecalibacterium prausnitzii strain 2789STDY5834970

B Bacterium

Fusicatenibacter saccharivorans

B Bacterium



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Gemella sanguinis M325

B Bacterium

Gordonibacter pamelaee 7-10-1-b

B Bacterium

Haemophilus

B Bacterium

Holdemania filiformis DSM 12042

B Bacterium

Intestinimonas butyriciproducens strain AF211

B Bacterium

Intestinimonas massiliensis sp. GD2

B Bacterium

Lachnospira pectinoschiza strain 2789STDY5834836

B Bacterium

Lachnospiraceae bacterium 1_4_56FAA

B Bacterium

Lachnospiraceae bacterium 7_1_58FAA

B Bacterium

Lachnospiraceae bacterium TF01-11

B Bacterium

Lactobacillus rossiae DSM 15814

B Bacterium

Lactobacillus siliginis strain DSM

B Bacterium



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Lactococcus

B Bacterium

Leuconostoc citreum

B Bacterium

Methanobrevibacter smithii TS94 C

A Archaeon

Mogibacterium

B Bacterium

Neglecta timonensis strain SN17

B Bacterium

Odoribacter splanchnicus DSM 20712

B Bacterium

Oryza sativa endornavirus

V Virus

Oscillibacter sp. ER4

B Bacterium

Oscillospiraceae bacterium VE202-24

B Bacterium

Parabacteroides distasonis

B Bacterium

Parabacteroides distasonis str. 3999B T(B) 6

B Bacterium

Parabacteroides distasonis strain 2789STDY5608822

B Bacterium



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Parabacteroides goldsteinii CL02T12C30

B Bacterium

Parabacteroides goldsteinii strain 910340

B Bacterium

Parabacteroides merdae ATCC 43184

B Bacterium

Parabacteroides merdae CL03T12C32

B Bacterium

Parasutterella

B Bacterium

Pea streak virus isolate VRS-541

V Virus

Pediococcus argentinicus strain DSM

B Bacterium

Phascolarctobacterium succinatutens YIT 12067

B Bacterium

Porphyromonas bennonis DSM 23058 = JCM 16335

B Bacterium

Prevotella copri DSM 18205

B Bacterium

Romboutsia

B Bacterium

Roseburia faecis

B Bacterium



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Roseburia faecis strain 2789STDY5608863

B Bacterium

Roseburia hominis A2-183

B Bacterium

Roseburia intestinalis L1-82

B Bacterium

Roseburia intestinalis strain 2789STDY5834960

B Bacterium

Roseburia inulinivorans DSM 16841

B Bacterium

Roseburia inulinivorans strain 2789STDY5608835

B Bacterium

Roseburia inulinivorans strain 2789STDY5608887

B Bacterium

Ruminococcaceae bacterium Marseille-P2963

B Bacterium

Ruminococcus bicirculans

B Bacterium

Ruminococcus champanellensis 18P13 = JCM 17042

B Bacterium

Ruminococcus gnavus ATCC 29149

B Bacterium

Ruminococcus lactaris ATCC 29176

B Bacterium



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Ruminococcus sp. AT10

B Bacterium

Ruminococcus sp. JC304

B Bacterium

Ruminococcus sp. Marseille-P3213 sp. Marseille-P3213

B Bacterium

Ruthenibacterium lactatiformans

B Bacterium

Saccharomyces cerevisiae

E Eukaryote

Serratia

B Bacterium

Slackia piriformis YIT 12062

B Bacterium

Streptococcus thermophilus

B Bacterium **P** Probiotic

Subdoligranulum sp. 4_3_54A2FAA

B Bacterium

Subdoligranulum variabile DSM 15176

B Bacterium

Sutterella sp. KLE1602

B Bacterium

Sutterella wadsworthensis 3_1_45B

B Bacterium



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Sutterella wadsworthensis HGA0223

B Bacterium

Tannerella sp. 6_1_58FAA_CT1

B Bacterium

Tidjanibacter massiliensis strain Marseille-P3084

B Bacterium

Turicibacter

B Bacterium

Veillonella dispar ATCC 17748

B Bacterium

[Bacteroides] pectinophilus ATCC 43243

B Bacterium

[Clostridium] hylemonae DSM 15053

B Bacterium

[Clostridium] leptum DSM 753

B Bacterium

[Clostridium] spiroforme DSM 1552

B Bacterium

[Eubacterium rectale] ATCC 33656

B Bacterium

[Eubacterium] eligens ATCC 27750

B Bacterium

[Eubacterium] eligens strain 2789STDY5834875

B Bacterium



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[Eubacterium] eligens strain 2789STDY5834878

B Bacterium

[Eubacterium] hallii DSM 3353

B Bacterium

[Eubacterium] hallii strain 2789STDY5834835

B Bacterium

[Eubacterium] rectale strain 2789STDY5834968

B Bacterium

[Eubacterium] rectale strain T1-815

B Bacterium

[Eubacterium] siraeum strain 2789STDY5834928

B Bacterium

bacterium LF-3

B Bacterium

<https://www.viome.com/reportablerange>



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DOB: 02/28/1998

Viome Methodology

Microbial total RNA is extracted, ribosomal RNA molecules are removed from total RNA, and the remaining RNA molecules are sequenced on Illumina NextSeq or NovaSeq. Proprietary bioinformatics algorithms are used to perform taxonomic classification and functional analysis of the sequencing data.

The Food Sensitivity Intelligence Test measures all four classes of IgG antibodies reactive to specific foods using an ELISA method.

Method Limitation

Viome's results and recommendations are based on our ability to identify and quantify thousands of microbial taxa . Such vast diversity has not been captured in the genomic databases, so it is impossible to assess it comprehensively. There are microorganisms that thrive in the gut whose genomes have not been sequenced. Viome is unable to identify those specific organisms, but can identify their near neighbors, which have similar homology. There are also taxa that we cannot discriminate because of their sequence similarity, for example at the strain level. There are some RNA transcripts that may not always align and match to specific known organisms, which may be due to the fact that these sequences are poorly characterized, reliable consensus sequence may not be available for reference. Viome monitors the growth of public genomic databases and will update its own databases when there is sufficient new information to be worthy of incorporation.

Detection of 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. Results are qualitative and identify the presence or absence of identified annotated organisms. The Food Sensitivity Intelligence Test measures relative IgG antibodies reactive to 40 specific foods using an ELISA method. It cannot distinguish between different classes of IgG nor can it detect other classes of Antibodies which may be associated with food allergies. This test is not appropriate for making a diagnosis of food allergy.



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The Gut Intelligence Test was developed by, and its performance characteristics determined by Viome Inc. It has not been cleared or approved by the US Food and Drug Administration. The FDA has determined that such clearance or approval is not necessary. This laboratory is registered under CLIA (32D2156145) to perform high complexity testing. Sequencing was performed at a lab that is not certified by CLIA conduct testing. The quality of sequencing is monitored and approved by Viome Inc. Contact Viome for any further questions.

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V I O M E

DEMO TWO'S RESULTS

VERSION: 1.13.0