VIOME



CHARLES WARDEN'S RESULTS

\'IOME

Dear Charles Warden,

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: Charles Warden

Customer Name: Charles Warden

DOB: 04/05/1985 **Gender**: Male

Customer Id: e16bdd01 **Sample Source:** Fecal

Date Collected: 06/27/2021 **Date Received:** 07/15/2021 **Date Issued:** 09/08/2021

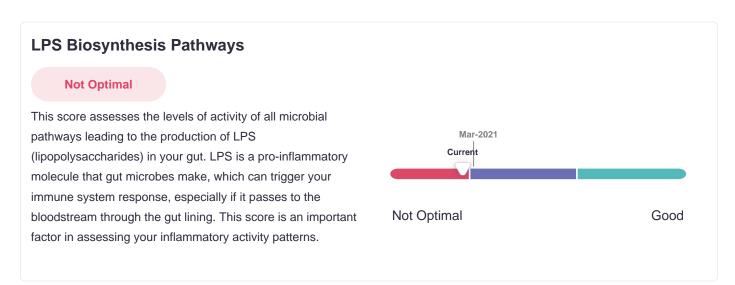
Sample ID: 14CA2CA696F1



DOB: 04/05/1985

All My Scores

Let's improve these.



LPS Biosynthesis Pathways Key

Reference Ranges:

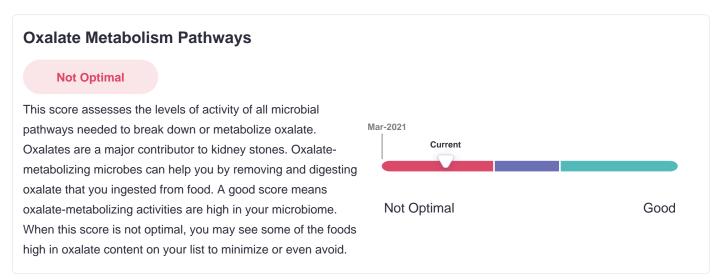
- Not Optimal Represents 37.0% of the Viome population
- Average Represents 53.0% of the Viome population
- Good Represents 10.0% of the Viome population

Learn more by reading our references: https://viome.com/referenceresults



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

DOB: 04/05/1985



Oxalate Metabolism Pathways Key

Reference Ranges:

- Not Optimal Represents 70.0% of the Viome population
- Average Represents 17.0% of the Viome population
- Good Represents 13.0% of the Viome population



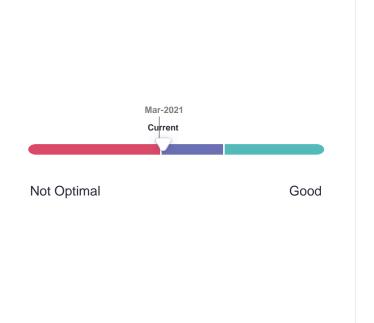
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Bile Acid Metabolism Pathways

Not Optimal

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 proinflammatory 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:

- Not Optimal Represents 38.0% of the Viome population
- Average Represents 50.0% of the Viome population
- Good Represents 12.0% of the Viome population



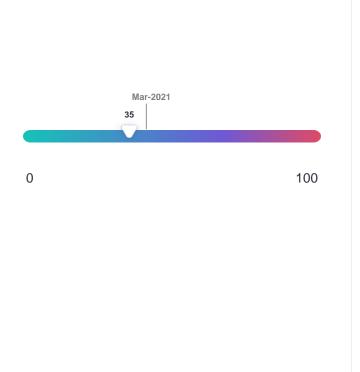
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DOB: 04/05/1985

Inflammatory Activity

Good

This score measures 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 in the red zone (not optimal) 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 is in the red, 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 a good range or improve this score.



Inflammatory Activity Key

Reference Ranges:

- Not Optimal 50 to 100 which represents 5.0% of the Viome population
- Average 36 to 49 which represents 83.0% of the Viome population
- Good 0 to 35 which represents 12.0% of the Viome population

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DOB: 04/05/1985

Good 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. 0 100

Gas Production Key

Reference Ranges:

Not Optimal 60 to 100 which represents 22.0% of the Viome population

Average 36 to 59 which represents 61.0% of the Viome population

Good 0 to 35 which represents 17.0% of the Viome population

*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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DOB: 04/05/1985

Sulfide Gas Production Pathways

Good

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 proinflammatory 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:

- Not Optimal Represents 35.0% of the Viome population
- Average Represents 58.0% of the Viome population
- Good Represents 7.0% of the Viome population

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DOB: 04/05/1985

Flagellar Assembly Pathways Good This score assesses the levels of activity of all microbial Mar-2021 pathways leading to the making of a structure called flagella. Current Flagellar structures serve as "fins" or "tails" for various microbes to help them move. A score that is not optimal suggests that these signaling pathway activities are high, Not Optimal Good 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

Flagellar Assembly Pathways Key

assessing your inflammatory activity patterns.

Reference Ranges:

- Not Optimal Represents 38.0% of the Viome population
- Average Represents 51.0% of the Viome population
- **Good** Represents 11.0% of the Viome population



^{*}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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Ammonia Production Pathways

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

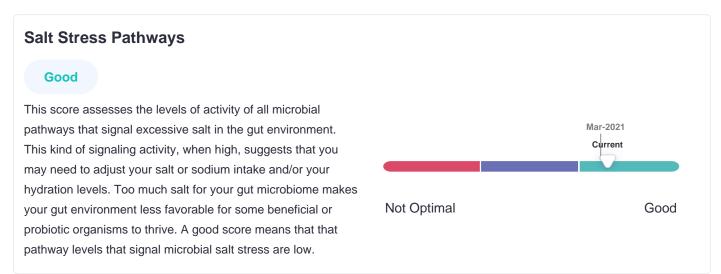
Reference Ranges:

- Not Optimal Represents 63.0% of the Viome population
- Average Represents 23.0% of the Viome population
- Good Represents 14.0% of the Viome population



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DOB: 04/05/1985



Salt Stress Pathways Key

Reference Ranges:

Not Optimal Represents 16.0% of the Viome population

Average Represents 70.0% of the Viome population

Good Represents 14.0% of the Viome population



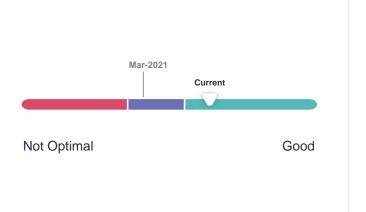
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DOB: 04/05/1985

Biofilm, Chemotaxis, and Virulence Pathways

Good

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

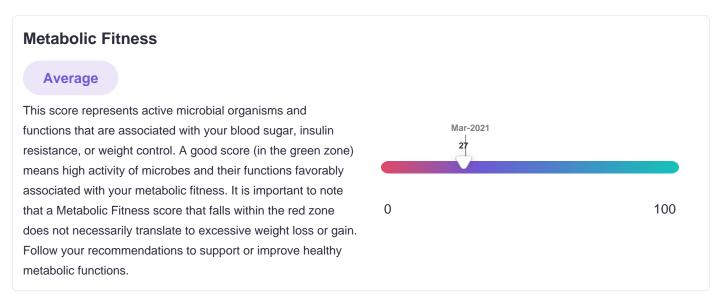
Reference Ranges:

- Not Optimal Represents 64.0% of the Viome population
- Average Represents 24.0% of the Viome population
- Good Represents 12.0% of the Viome population



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Metabolic Fitness Key

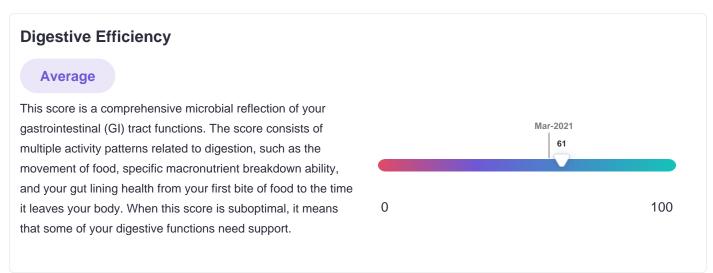
Reference Ranges:

- Not Optimal 0 to 22 which represents 10.0% of the Viome population
- Average 23 to 31 which represents 65.0% of the Viome population
- Good 32 to 100 which represents 25.0% of the Viome population



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

DOB: 04/05/1985



Digestive Efficiency Key

Reference Ranges:

Not Optimal 0 to 46 which represents 42.0% of the Viome population

Average 47 to 64 which represents 48.0% of the Viome population

Good 65 to 100 which represents 10.0% of the Viome population

Learn more by reading our references: https://viome.com/referenceresults

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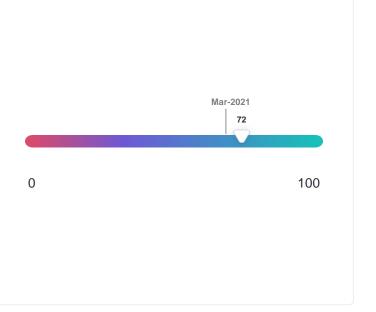
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Gut Lining Health

Average

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 (in the green zone) 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'.



Gut Lining Health Key

Reference Ranges:

- Not Optimal 0 to 65 which represents 11.0% of the Viome population
- Average 66 to 77 which represents 77.0% of the Viome population
- Good 78 to 100 which represents 12.0% of the Viome population



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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

Protein Fermentation Key

protein digestion is suboptimal.

Reference Ranges:

Not Optimal 65 to 100 which represents 59.0% of the Viome population

Average 36 to 64 which represents 32.0% of the Viome population

Good 0 to 35 which represents 9.0% of the Viome population

harmful byproducts. Overly high microbial protein fermentation translates into a score within the red zone, suggesting your

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100

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Active Microbial Diversity Average The score is your percentile for total count of active microbial Mar-2021 species detected and sequenced from your sample. A good 12nd score translates to more richness, which in turn can provide more resilience to your microbial gut ecosystem and your body. This score could use some improvement when the count of active microbes is relatively low and your gut flora could use 0th 100th additional microbes in its active composition. Your recommendations may include certain supplements or

percentile

Active Microbial Diversity Key

fermented foods that address this score.

Reportable Range -13.6 to 8.53

Reference Ranges:

- Not Optimal -13.6 to -2.77 combined metric represents 0 to 5th percentile of the Viome population
- Average -2.76 to 2.44 combined metric represents 6th to 94th percentile of the Viome population
- Good 2.45 to 8.53 combined metric represents 95th to 100th percentile of the Viome population

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percentile

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Butyrate Production Pathways

Average

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 is not optimal 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

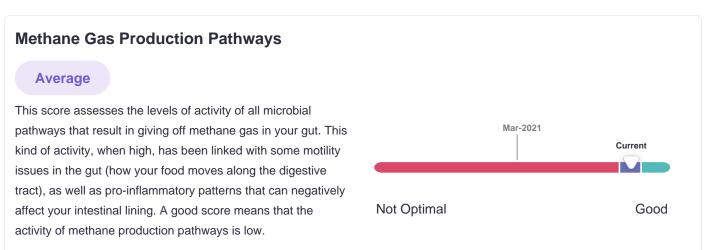
Reference Ranges:

- Not Optimal Represents 10.0% of the Viome population
- Average Represents 65.0% of the Viome population
- Good Represents 25.0% of the Viome population



^{*}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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Methane Gas Production Pathways Key

Reference Ranges:

Not Optimal Represents 30.0% of the Viome population

Average Represents 42.0% of the Viome population

Good Represents 28.0% of the Viome population



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Putrescine Production Pathways Average 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

Putrescine Production Pathways Key

Reference Ranges:

not be digested properly.

Not Optimal Represents 36.0% of the Viome population

Average Represents 56.0% of the Viome population

Good Represents 8.0% of the Viome population

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Uric Acid Production Pathways Average 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

Uric Acid Production Pathways Key

production pathway levels are low.

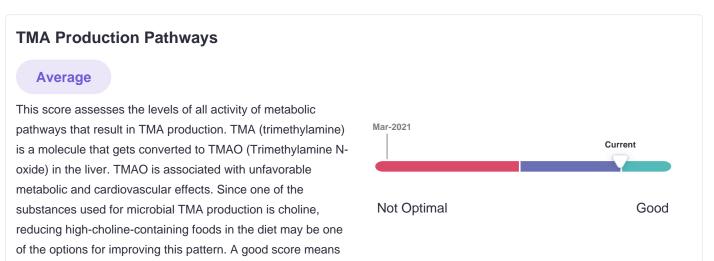
Reference Ranges:

- Not Optimal Represents 48.0% of the Viome population
- Average Represents 42.0% of the Viome population
- **Good** Represents 10.0% of the Viome population



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

DOB: 04/05/1985



TMA Production Pathways Key

Reference Ranges:

- Not Optimal Represents 10.0% of the Viome population
- Average Represents 69.0% of the Viome population
- Good Represents 21.0% of the Viome population

these TMA production pathway activity levels are low.

Learn more by reading our references: https://viome.com/referenceresults



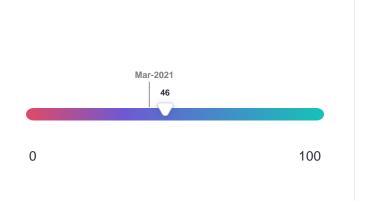
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Gut Microbiome Health

Average

Your Gut Microbiome Health score integrates over 20 microbial functional scores. When this score is low it means that your gut microbiome may be producing chemicals that are causing inflammation (such as LPS, sulfide, or ammonia) or not producing enough nutrients that your body needs (such as butyrate, serotonin, and other vitamins). Our food and supplement recommendations are designed specifically for you to optimize your microbial functions and bring your gut microbiome into balance. Scroll down below to the section titled "How We Calculate This Score" to learn more. Did you know? In many ways, your gut bacteria are as vast and mysterious as the Milky Way. About 100 trillion bacteria, both good and bad, live inside your digestive system. Optimizing your microbial functions can help you achieve a healthy weight, boost energy, reduce stress, improve sleep, and strengthen your immunity.



Gut Microbiome Health Key

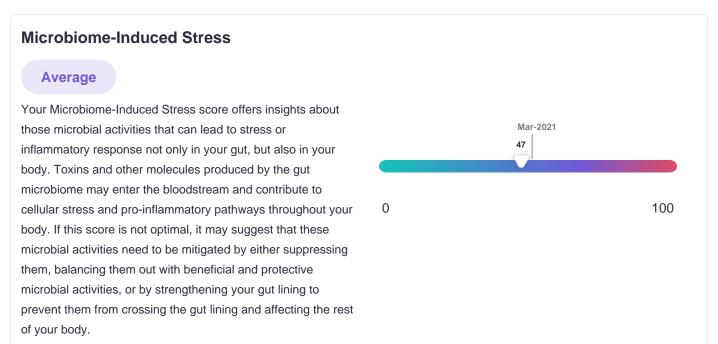
Reference Ranges:

- Not Optimal 0 to 44 which represents 31.0% of the Viome population
- Average 45 to 54 which represents 65.0% of the Viome population
- Good 55 to 100 which represents 4.0% of the Viome population

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Microbiome-Induced Stress Key

Reference Ranges:

- Not Optimal 60 to 100 which represents 46.0% of the Viome population
- Average 36 to 59 which represents 49.0% of the Viome population
- Good 0 to 35 which represents 5.0% of the Viome population



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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.

Bifidobacterium animalis subsp. lactis

P Probiotic

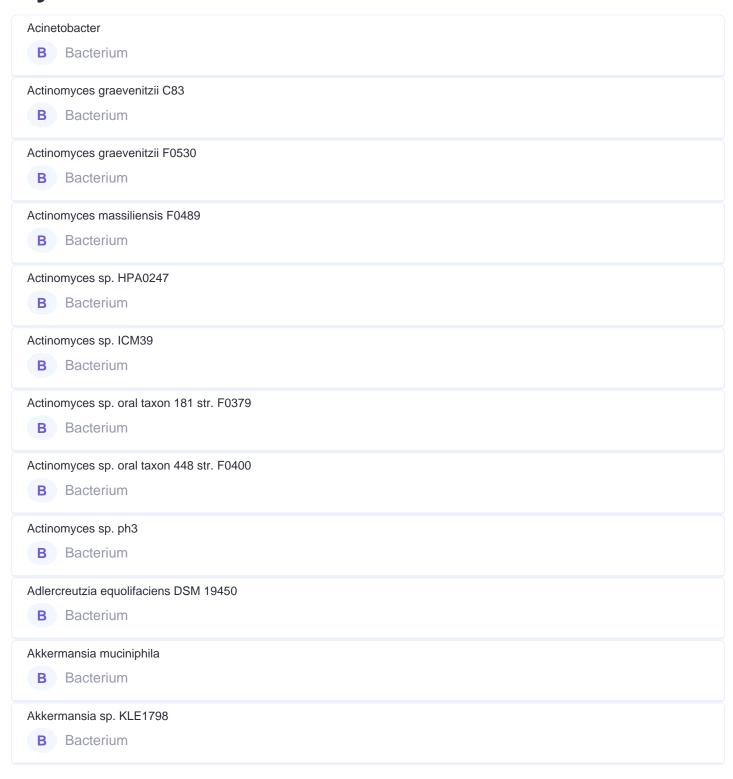
Lactobacillus delbrueckii subsp. bulgaricus

P Probiotic



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My Active Microbes





DOB: 04/05/1985 Alicycliphilus denitrificans K601 **B** Bacterium Alistipes finegoldii DSM 17242 **B** Bacterium Alistipes indistinctus YIT 12060 **B** Bacterium Alistipes obesi **B** Bacterium Alistipes onderdonkii WAL 8169 = DSM 19147 **B** Bacterium Alistipes putredinis DSM 17216 **B** Bacterium Alistipes senegalensis JC50 **B** Bacterium Alistipes shahii WAL 8301 **B** Bacterium Alistipes sp. AL-1 **B** Bacterium Alistipes sp. HGB5 **B** Bacterium Anaerococcus lactolyticus ATCC 51172 **B** Bacterium Anaerococcus sp. Marseille-P2143 strain Marseille-P2143, sp. FC4 **B** Bacterium Anaerostipes caccae



B Bacterium

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Anaerostipes hadrus strain BPB5

B Bacterium

Anaerostipes sp. 3_2_56FAA

B Bacterium

Anaerotruncus colihominis

B Bacterium

Anaerotruncus rubiinfantis

B Bacterium

Angelakisella massiliensis strain Marseille-P3217

B Bacterium

Atopobium rimae ATCC 49626

B Bacterium

Atopobium rimae strain DSM

B Bacterium

Atopobium sp. ICM42b

B Bacterium

Bacillus siamensis strain SRCM100169

B Bacterium

Bacteroides acidifaciens

B Bacterium

Bacteroides acidifaciens JCM 10556

B Bacterium

Bacteroides barnesiae DSM 18169 = JCM 13652

B Bacterium

Bacteroides caccae

B Bacterium



DOB: 04/05/1985 Bacteroides caecimuris strain I48 **B** Bacterium Bacteroides cellulosilyticus strain WH2 **B** Bacterium Bacteroides coprocola **B** Bacterium Bacteroides dorei CL03T12C01 **B** Bacterium Bacteroides eggerthii 1_2_48FAA **B** Bacterium Bacteroides faecis **B** Bacterium Bacteroides finegoldii **B** Bacterium Bacteroides fluxus **B** Bacterium Bacteroides fragilis **B** Bacterium Bacteroides fragilis str. 3-F-2 #6 **B** Bacterium Bacteroides helcogenes P 36-108 **B** Bacterium Bacteroides massiliensis **B** Bacterium Bacteroides nordii **B** Bacterium



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Bacteroides ovatus V975

B Bacterium

Bacteroides ovatus strain ATCC

B Bacterium

Bacteroides plebeius

B Bacterium

Bacteroides sp. 1_1_30

B Bacterium

Bacteroides sp. 1_1_6

B Bacterium

Bacteroides sp. 2_1_22

B Bacterium

Bacteroides sp. 2_1_33B

B Bacterium

Bacteroides sp. 2_2_4

B Bacterium

Bacteroides sp. 3_1_13

B Bacterium

Bacteroides sp. 3_1_19

B Bacterium

Bacteroides sp. 3_1_23

B Bacterium

Bacteroides sp. 3_1_33FAA

B Bacterium

Bacteroides sp. 3_1_40A

B Bacterium



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Bacteroides sp. 4_1_36

B Bacterium

Bacteroides sp. 4_3_47FAA

B Bacterium

Bacteroides sp. 9_1_42FAA

B Bacterium

Bacteroides sp. D2

B Bacterium

Bacteroides sp. D20

B Bacterium

Bacteroides sp. D22

B Bacterium

Bacteroides sp. HMSC067B03

B Bacterium

Bacteroides sp. HMSC073E02

B Bacterium

Bacteroides sp. HPS0048

B Bacterium

Bacteroides sp. Marseille-P3108 sp. Marseille-P3108

B Bacterium

Bacteroides sp. Marseille-P3208T strain Marseille-P3208

B Bacterium

Bacteroides stercoris ATCC 43183

B Bacterium

Bacteroides stercoris CC31F

B Bacterium



DOB: 04/05/1985 Bacteroides stercoris strain CL09T03C01 **B** Bacterium Bacteroides stercoris strain DSM **B** Bacterium Bacteroides thetaiotaomicron VPI-5482 **B** Bacterium Bacteroides thetaiotaomicron strain 7330 **B** Bacterium Bacteroides uniformis **B** Bacterium Bacteroides vulgatus ATCC 8482 **B** Bacterium Bacteroides xylanisolvens **B** Bacterium Bariatricus massiliensis strain AT12 **B** Bacterium Bifidobacterium animalis strain A6 **B** Bacterium Bifidobacterium animalis strain RH **B** Bacterium Bifidobacterium animalis subsp. lactis B Bacterium P Probiotic Bifidobacterium animalis subsp. lactis AD011 **B** Bacterium Bifidobacterium animalis subsp. lactis B420 **B** Bacterium



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Bifidobacterium animalis subsp. lactis BB-12

B Bacterium

Bifidobacterium animalis subsp. lactis BLC1

B Bacterium

Bifidobacterium animalis subsp. lactis Bi-07

B Bacterium

Bifidobacterium animalis subsp. lactis BI-04

B Bacterium

Bifidobacterium animalis subsp. lactis Bl12

B Bacterium

Bifidobacterium animalis subsp. lactis CNCM I-2494

B Bacterium

Bifidobacterium animalis subsp. lactis KLDS2.0603

B Bacterium

Bifidobacterium animalis subsp. lactis V9

B Bacterium

Bifidobacterium animalis subsp. lactis strain BF052

B Bacterium

Bilophila wadsworthia 3_1_6

B Bacterium

Bilophila wadsworthia ATCC 49260

B Bacterium

Bittarella massiliensis strain GD6

B Bacterium

Blautia hansenii DSM 20583

B Bacterium



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Blautia massiliensis sp. GD8 **B** Bacterium Blautia obeum ATCC 29174 **B** Bacterium Blautia obeum strain 2789STDY5608837 **B** Bacterium Blautia obeum strain 2789STDY5608838 **B** Bacterium Blautia obeum strain 2789STDY5834861 **B** Bacterium Blautia obeum strain 2789STDY5834957 **B** Bacterium Blautia producta **B** Bacterium Blautia sp. KLE 1732 **B** Bacterium Blautia sp. Marseille-P2398 **B** Bacterium Blautia sp. N6H1-15 **B** Bacterium Blautia wexlerae **B** Bacterium Bordetella trematum



Bubaline alphaherpesvirus 1

V Virus



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Burkholderiales bacterium 1_1_47 **B** Bacterium Butyricicoccus pullicaecorum **B** Bacterium Butyricimonas virosa **B** Bacterium Candidatus Stoquefichus sp. KLE1796 **B** Bacterium Catabacter hongkongensis strain ABBA15k **B** Bacterium Christensenella timonensis **B** Bacterium Citrobacter **B** Bacterium Clostridia bacterium UC5.1-1D1 **B** Bacterium Clostridia bacterium UC5.1-1D10 **B** Bacterium Clostridia bacterium UC5.1-1E11 **B** Bacterium

Clostridia bacterium UC5.1-2F7

B Bacterium

Clostridiaceae bacterium MS3

B Bacterium

Clostridiales bacterium

B Bacterium



DOB: 04/05/1985

Clostridiales bacterium 1_7_47FAA **B** Bacterium Clostridiales bacterium KLE1615 **B** Bacterium Clostridiales bacterium VE202-01 **B** Bacterium Clostridiales bacterium VE202-03 **B** Bacterium Clostridiales bacterium VE202-06 **B** Bacterium Clostridiales bacterium VE202-07 **B** Bacterium Clostridiales bacterium VE202-13 **B** Bacterium Clostridiales bacterium VE202-15 **B** Bacterium Clostridiales bacterium VE202-16 **B** Bacterium Clostridiales bacterium VE202-21 **B** Bacterium Clostridiales bacterium VE202-26 **B** Bacterium Clostridiales bacterium VE202-27 **B** Bacterium



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Clostridiales bacterium VE202-28

DOB: 04/05/1985

Clostridioides difficile

B Bacterium

Clostridium phoceensis strain GD3

B Bacterium

Clostridium sp. 7_3_54FAA

B Bacterium

Clostridium sp. ASF502

B Bacterium

Clostridium sp. AT4

B Bacterium

Clostridium sp. ATCC BAA-442

B Bacterium

Clostridium sp. DSM 4029

B Bacterium

Clostridium sp. FS41

B Bacterium

Clostridium sp. KLE 1755

B Bacterium

Clostridium sp. L2-50

B Bacterium

Clostridium sp. M62/1

B Bacterium

Clostridium sp. Marseille-P3244 sp. Marseille-P3244

B Bacterium

Coprobacillus sp. 3_3_56FAA



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Coprobacillus sp. 8_2_54BFAA

B Bacterium

Coprococcus

B Bacterium

Corynebacterium pseudodiphtheriticum

B Bacterium

Desulfovibrio carbinolicus

B Bacterium

Dialister invisus DSM 15470

B Bacterium

Dielma fastidiosa

B Bacterium

Dorea formicigenerans

B Bacterium

Dorea longicatena strain 2789STDY5608851

B Bacterium

Dorea longicatena strain 2789STDY5834961

B Bacterium

Eggerthella lenta 1_1_60AFAA

B Bacterium

Eggerthella lenta DSM 2243

B Bacterium

Eggerthella sp. 1_3_56FAA

B Bacterium

Eggerthella sp. HGA1



DOB: 04/05/1985 Eisenbergiella tayi **B** Bacterium Enterobacter cloacae complex 'Hoffmann cluster IV' **B** Bacterium Enterococcus faecium Aus0085 **B** Bacterium Enterococcus faecium isolate Hp_21-11 **B** Bacterium Enterococcus faecium isolate Hp_6-9 **B** Bacterium Enterococcus faecium isolate Hp_74-d6 **B** Bacterium Erysipelotrichaceae bacterium 3_1_53 **B** Bacterium Erysipelotrichaceae bacterium 5_2_54FAA **B** Bacterium Escherichia coli **B** Bacterium Eubacterium ramulus **B** Bacterium Eubacterium sp. 3_1_31 **B** Bacterium Eubacterium sp. SB2 **B** Bacterium



Eubacterium ventriosum

B Bacterium

DOB: 04/05/1985

Faecalibacterium prausnitzii **B** Bacterium Fenollaria timonensis **B** Bacterium Fibrobacter sp. UWB12 sp. UWB12 **B** Bacterium Filifactor alocis ATCC 35896 **B** Bacterium Finegoldia magna ATCC 29328 **B** Bacterium Flavonifractor plautii strain YL31 **B** Bacterium Flintibacter **B** Bacterium Fournierella massiliensis **B** Bacterium Fusicatenibacter saccharivorans **B** Bacterium Gemella sanguinis ATCC 700632 **B** Bacterium Gemella sanguinis strain 1094_BTHU **B** Bacterium Gordonibacter pamelaeae 7-10-1-b **B** Bacterium Helicobacter bizzozeronii **B** Bacterium



DOB: 04/05/1985 Holdemanella biformis **B** Bacterium Holdemania filiformis DSM 12042 **B** Bacterium Holdemania massiliensis AP2 **B** Bacterium Holdemania sp. Marseille-P2844 sp. Marseille-P2844 **B** Bacterium Intestinimonas butyriciproducens strain AF211 **B** Bacterium Intestinimonas massiliensis sp. GD2 **B** Bacterium Klebsiella **B** Bacterium Kocuria kristinae strain SA12 **B** Bacterium Lachnoclostridium sp. YL32 sp. YL32 **B** Bacterium Lachnospira pectinoschiza strain 2789STDY5834836 **B** Bacterium Lachnospiraceae bacterium **B** Bacterium

Lachnospiraceae bacterium 1_1_57FAA

B Bacterium

Lachnospiraceae bacterium 2_1_58FAA



DOB: 04/05/1985

Lachnospiraceae bacterium 3_1_46FAA **B** Bacterium Lachnospiraceae bacterium 3_1_57FAA_CT1 **B** Bacterium Lachnospiraceae bacterium 5_1_57FAA **B** Bacterium Lachnospiraceae bacterium 5_1_63FAA **B** Bacterium Lachnospiraceae bacterium 7_1_58FAA **B** Bacterium Lactobacillus delbrueckii subsp. bulgaricus B Bacterium P Probiotic Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842 = JCM 1002 **B** Bacterium Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365 **B** Bacterium Lactobacillus delbrueckii subsp. bulgaricus strain DSM **B** Bacterium Lactobacillus delbrueckii subsp. bulgaricus strain ND04 **B** Bacterium Lactococcus **B** Bacterium Lactonifactor longoviformis DSM 17459 **B** Bacterium Longibaculum **B** Bacterium



DOB: 04/05/1985

Marvinbryantia formatexigens DSM 14469

B Bacterium

Marvinbryantia formatexigens strain I-52

B Bacterium

Massilioclostridium coli strain Marseille-P2976

B Bacterium

Megasphaera sp. MJR8396C

B Bacterium

Mogibacterium diversum

B Bacterium

Neglecta timonensis

B Bacterium

Odoribacter laneus YIT 12061

B Bacterium

Odoribacter splanchnicus DSM 20712

B Bacterium

Olsenella

B Bacterium

Oscillibacter sp. ER4

B Bacterium

Oscillibacter sp. KLE 1745

B Bacterium

Oscillospiraceae bacterium VE202-24

B Bacterium

Parabacteroides distasonis ATCC 8503

B Bacterium



DOB: 04/05/1985

Parabacteroides goldsteinii CL02T12C30

B Bacterium

Parabacteroides goldsteinii DSM 19448 = WAL 12034

B Bacterium

Parabacteroides goldsteinii strain 910340

B Bacterium

Parabacteroides gordonii DSM 23371

B Bacterium

Parabacteroides gordonii MS-1

B Bacterium

Parabacteroides johnsonii

B Bacterium

Parabacteroides merdae CL03T12C32

B Bacterium

Parabacteroides sp. 2_1_7

B Bacterium

Parabacteroides sp. D26

B Bacterium

Parabacteroides sp. HGS0025

B Bacterium

Parabacteroides sp. Marseille-P3236 strain Marseille-P3236, sp. Marseille-P3136

B Bacterium

Parabacteroides sp. SN4 strain SN4, sp. SB4

B Bacterium

Paraprevotella xylaniphila YIT 11841



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Parasutterella excrementihominis YIT 11859

Bacterium

Pediococcus ethanolidurans strain CGMCC

B Bacterium

Pediococcus ethanolidurans strain DSM

B Bacterium

Pepper mild mottle virus

V Virus

Peptoniphilus senegalensis JC140

B Bacterium

Persea americana chrysovirus

V Virus

Porphyromonas bennonis DSM 23058 = JCM 16335

B Bacterium

Porphyromonas uenonis DSM 23387 = JCM 13868

B Bacterium

Prevotella buccalis ATCC 35310

B Bacterium

Prevotella sp. KHD1 sp. KHD1

B Bacterium

Prevotella sp. P5-60

B Bacterium

Prevotella stercorea DSM 18206

B Bacterium

Pseudoflavonifractor capillosus ATCC 29799



DOB: 04/05/1985

Pseudomonas aeruginosa **B** Bacterium Ralstonia pickettii 12D **B** Bacterium Ralstonia pickettii 12J **B** Bacterium Romboutsia **B** Bacterium Roseburia faecis **B** Bacterium Roseburia intestinalis L1-82 **B** Bacterium Roseburia inulinivorans **B** Bacterium Rothia mucilaginosa DY-18 **B** Bacterium Ruminococcaceae bacterium D16 **B** Bacterium Ruminococcaceae bacterium Marseille-P2963 **B** Bacterium Ruminococcaceae bacterium cv2 **B** Bacterium Ruminococcus bicirculans **B** Bacterium Ruminococcus champanellensis **B** Bacterium



DOB: 04/05/1985 Ruminococcus gauvreauii **B** Bacterium Ruminococcus gnavus ATCC 29149 **B** Bacterium Ruminococcus lactaris CC59_002D **B** Bacterium Ruminococcus sp. 5_1_39BFAA **B** Bacterium Ruminococcus sp. JC304 **B** Bacterium Ruminococcus sp. Marseille-P3213 sp. Marseille-P3213 **B** Bacterium Ruminococcus torques ATCC 27756 **B** Bacterium Ruthenibacterium lactatiformans strain 585-1 **B** Bacterium Sellimonas intestinalis **B** Bacterium Shewanella colwelliana strain CSB03KR **B** Bacterium Staphylococcus gallinarum **B** Bacterium Staphylococcus vitulinus **B** Bacterium Streptococcus anginosus



B Bacterium

DOB: 04/05/1985

Streptococcus cristatus ATCC 51100 **B** Bacterium Streptococcus salivarius JIM8777 **B** Bacterium Streptococcus sanguinis **B** Bacterium Streptococcus sp. 1171_SSPC **B** Bacterium Streptococcus sp. 343_SSPC **B** Bacterium Streptococcus sp. A12 sp. A12 **B** Bacterium Streptococcus sp. CM7 **B** Bacterium Streptococcus sp. ChDC B345 **B** Bacterium Streptococcus sp. HMSC063B03 **B** Bacterium Streptococcus sp. HMSC065E03 **B** Bacterium Streptococcus sp. HMSC072C09 **B** Bacterium Streptococcus sp. HMSC072D03 **B** Bacterium Streptococcus sp. HMSC076C09 **B** Bacterium



DOB: 04/05/1985

Streptococcus sp. HMSC077D04

B Bacterium

Streptococcus sp. SR4

B Bacterium

Streptococcus thermophilus LMD-9

B Bacterium

Streptococcus thermophilus LMG 18311

B Bacterium

Streptococcus thermophilus ND03

B Bacterium

Streptococcus thermophilus strain CS8

B Bacterium

Streptococcus thermophilus strain ND07

B Bacterium

Streptococcus thermophilus strain S9

B Bacterium

Subdoligranulum sp. 4_3_54A2FAA

B Bacterium

Subdoligranulum variabile

B Bacterium

Tepidimonas fonticaldi strain PL17

B Bacterium

Tobacco mild green mosaic virus

V Virus

Tomato brown rugose fruit virus

V Virus



DOB: 04/05/1985

Traorella massiliensis strain Marseille-P3110 **B** Bacterium Tyzzerella nexilis **B** Bacterium Tyzzerella sp. Marseille-P3062 sp. Marseille-P3062 **B** Bacterium [Bacteroides] pectinophilus **B** Bacterium [Clostridium] asparagiforme **B** Bacterium [Clostridium] bolteae **B** Bacterium [Clostridium] citroniae **B** Bacterium [Clostridium] clostridioforme 2_1_49FAA **B** Bacterium [Clostridium] clostridioforme 90A3 **B** Bacterium [Clostridium] clostridioforme 90A4 **B** Bacterium [Clostridium] clostridioforme 90A7 **B** Bacterium [Clostridium] clostridioforme 90A8 **B** Bacterium [Clostridium] clostridioforme 90B1 **B** Bacterium



DOB: 04/05/1985

[Clostridium] clostridioforme AGR2157

B Bacterium

[Clostridium] clostridioforme CM201

B Bacterium

[Clostridium] clostridioforme WAL-7855

B Bacterium

[Clostridium] clostridioforme strain 2789STDY5834865

B Bacterium

[Clostridium] clostridioforme strain NLAE-zl-G208

B Bacterium

[Clostridium] innocuum strain AN88

B Bacterium

[Clostridium] lactatifermentans

B Bacterium

[Clostridium] leptum DSM 753

B Bacterium

[Clostridium] scindens ATCC 35704

B Bacterium

[Clostridium] spiroforme

B Bacterium

[Clostridium] symbiosum

B Bacterium

[Clostridium] symbiosum WAL-14163

B Bacterium

[Eubacterium rectale] ATCC 33656

B Bacterium



DOB: 04/05/1985

[Eubacterium] contortum strain 2789STDY5834876 **B** Bacterium [Eubacterium] eligens ATCC 27750 **B** Bacterium [Eubacterium] hallii DSM 3353 **B** Bacterium [Eubacterium] rectale strain T1-815 **B** Bacterium [Eubacterium] siraeum DSM 15702 **B** Bacterium [Eubacterium] siraeum strain 2789STDY5834928 **B** Bacterium [Ruminococcus] torques strain 2789STDY5834841 **B** Bacterium bacterium LF-3 **B** Bacterium

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DOB: 04/05/1985

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.

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 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 (50D2224932) to perform high complexity testing. Sequencing was performed at Viome Inc. CLIA (50D2224932). Contact Viome for any further questions.



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CHARLES WARDEN'S RESULTS

VERSION: 1.14.2