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MADI GILLESPIE'S RESULTS

VIOME

Dear Madi Gillespie,

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: Madi Gillespie

Customer Name: Madi Gillespie

DOB: 02/24/1996

Gender: Female

Customer Id: 43adb958

Sample Source: Fecal

Date Collected: 01/20/2021

Date Received: 02/01/2021

Date Issued: 03/08/2021

Sample ID: 1C2683ED9341

Test Name: Gut Intelligence Test

Customer Name: Madi Gillespie

DOB: 02/24/1996

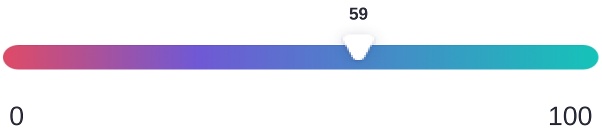
All My Scores

Let's improve these.

Gut Lining Health

Not Optimal

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 14% of the Viome population
- 🟪 **Average** 66 to 77 which represents 65% of the Viome population
- 🟩 **Good** 78 to 100 which represents 21% 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.*

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

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Protein Fermentation

Not Optimal

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 within the red zone, suggesting your protein digestion is suboptimal.

Protein Fermentation Key

Reference Ranges:

- 🟥 **Not Optimal** 65 to 100 which represents 26% of the Viome population
- 🟪 **Average** 36 to 64 which represents 56% of the Viome population
- 🟩 **Good** 0 to 35 which represents 18% of the Viome population

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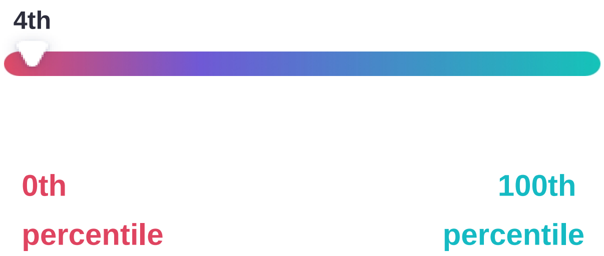
Active Microbial Diversity

Not Optimal

The score is your percentile for total count of active microbial species detected and sequenced from your sample. A good 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 additional microbes in its active composition. Your recommendations may include certain supplements or fermented foods that address this score.



Active Microbial Diversity Key

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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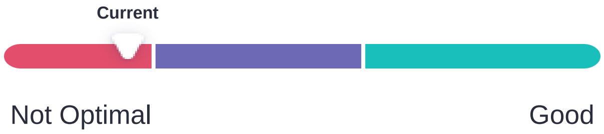
LPS Biosynthesis Pathways

Not Optimal

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:

- 🟥 **Not Optimal** Represents 25% of the Viome population
- 🟪 **Average** Represents 55% of the Viome population
- 🟩 **Good** Represents 20% of the Viome population

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Sulfide Gas Production Pathways

Not Optimal

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:

🟥 **Not Optimal** Represents 28% of the Viome population

🟪 **Average** Represents 60% of the Viome population

🟩 **Good** Represents 12% of the Viome population

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Ammonia Production Pathways

Not Optimal

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 24% of the Viome population
- 🟪 **Average** Represents 47% of the Viome population
- 🟩 **Good** Represents 29% of the Viome population

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Putrescine Production Pathways

Not Optimal

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:

- 🟥 **Not Optimal** Represents 25% of the Viome population
- 🟪 **Average** Represents 62% of the Viome population
- 🟩 **Good** Represents 13% of the Viome population

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Oxalate Metabolism Pathways

Not Optimal

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 is not optimal, 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:

- 🟥 **Not Optimal** Represents 79% of the Viome population
- 🟪 **Average** Represents 14% of the Viome population
- 🟩 **Good** Represents 7% of the Viome population

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Uric Acid Production Pathways

Not Optimal

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:

🟥 **Not Optimal** Represents 29% of the Viome population

🟪 **Average** Represents 52% of the Viome population

🟩 **Good** Represents 19% of the Viome population

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Biofilm, Chemotaxis, and Virulence Pathways

Not Optimal

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 25% of the Viome population
- 🟪 **Average** Represents 46% of the Viome population
- 🟩 **Good** Represents 29% of the Viome population

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TMA Production Pathways

Not Optimal

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:

- 🟥 **Not Optimal** Represents 27% of the Viome population
- 🟪 **Average** Represents 0% of the Viome population
- 🟩 **Good** Represents 73% of the Viome population

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Gut Microbiome Health

Not Optimal

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 43 which represents 17% of the Viome population
- 🟪 **Average** 44 to 54 which represents 71% of the Viome population
- 🟩 **Good** 55 to 100 which represents 12% of the Viome population

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Microbiome-Induced Stress

Not Optimal

Your Microbiome-Induced Stress score offers insights about those microbial activities that can lead to stress or inflammatory response not only in your gut, but also in your body. Toxins and other molecules produced by the gut microbiome may enter the bloodstream and contribute to cellular stress and pro-inflammatory pathways throughout your body. If this score is not optimal, it may suggest that these microbial activities need to be mitigated by either suppressing them, balancing them out with beneficial and protective microbial activities, or by strengthening your gut lining to prevent them from crossing the gut lining and affecting the rest of your body.

Microbiome-Induced Stress Key

Reference Ranges:

- 🟥 **Not Optimal** 61 to 100 which represents 20% of the Viome population
- 🟪 **Average** 36 to 60 which represents 65% of the Viome population
- 🟩 **Good** 0 to 35 which represents 15% of the Viome population

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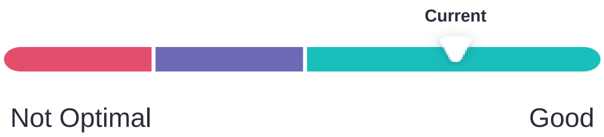
DOB: 02/24/1996

Methane Gas Production Pathways

Good

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:

- 🟥 **Not Optimal** Represents 26% of the Viome population
- 🟪 **Average** Represents 30% of the Viome population
- 🟩 **Good** Represents 44% of the Viome population

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Bile Acid Metabolism Pathways

Good

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:

- 🟥 **Not Optimal** Represents 31% of the Viome population
- 🟪 **Average** Represents 49% of the Viome population
- 🟩 **Good** Represents 20% of the Viome population

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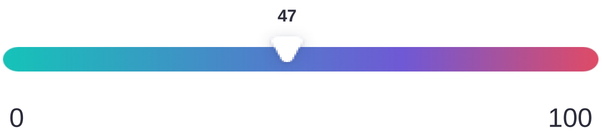
Inflammatory Activity

Average

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 9% of the Viome population
- 🟪 **Average** 36 to 49 which represents 69% of the Viome population
- 🟩 **Good** 0 to 35 which represents 22% of the Viome population

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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 (in the green zone) means high activity of microbes and their functions favorably associated with your metabolic fitness. It is important to note that a Metabolic Fitness score that falls within the red zone does not necessarily translate to excessive weight loss or gain. Follow your recommendations to support or improve healthy metabolic functions.

Metabolic Fitness Key

Reference Ranges:

- 🟥 **Not Optimal** 0 to 22 which represents 25% of the Viome population
- 🟪 **Average** 23 to 30 which represents 58% of the Viome population
- 🟩 **Good** 31 to 100 which represents 17% of the Viome population

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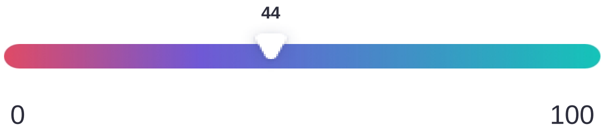
Digestive Efficiency

Average

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 is suboptimal, it means that some of your digestive functions need support.



Digestive Efficiency Key

Reference Ranges:

- 🟥 **Not Optimal** 0 to 43 which represents 19% of the Viome population
- 🟪 **Average** 44 to 64 which represents 63% of the Viome population
- 🟩 **Good** 65 to 100 which represents 18% of the Viome population

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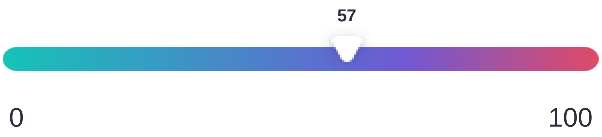
Gas Production

Average

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.



Gas Production Key

Reference Ranges:

- 🟥 **Not Optimal** 65 to 100 which represents 20% of the Viome population
- 🟪 **Average** 36 to 64 which represents 65% of the Viome population
- 🟩 **Good** 0 to 35 which represents 15% of the Viome population

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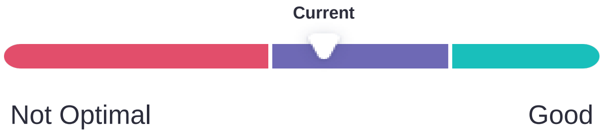
Butyrate Production Pathways

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 20% of the Viome population
- 🟪 **Average** Represents 65% of the Viome population
- 🟩 **Good** Represents 15% of the Viome population

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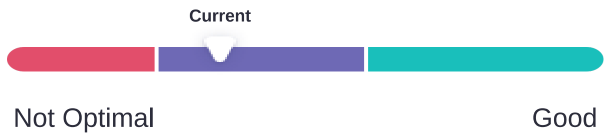
Flagellar Assembly Pathways

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 is not optimal 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:

- 🟥 **Not Optimal** Represents 24% of the Viome population
- 🟪 **Average** Represents 55% of the Viome population
- 🟩 **Good** Represents 21% of the Viome population

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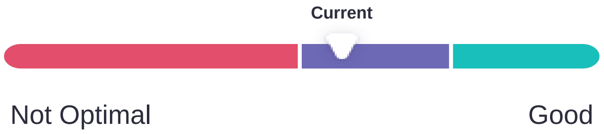
Salt Stress Pathways

Average

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:

- 🟥 **Not Optimal** Represents 11% of the Viome population
- 🟪 **Average** Represents 61% of the Viome population
- 🟩 **Good** Represents 28% 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 fermentum

P Probiotic

My Active Microbes

Acinetobacter
B Bacterium

Actinobaculum sp. oral taxon 183 str. F0552
B Bacterium

Actinomyces graevenitzii C83
B Bacterium

Actinomyces graevenitzii F0530
B Bacterium

Actinomyces odontolyticus
B Bacterium

Actinomyces oris strain T14V
B Bacterium

Actinomyces sp. HMSC035G02
B Bacterium

Actinomyces sp. HMSC08A09
B Bacterium

Actinomyces sp. HPA0247
B Bacterium

Actinomyces sp. ICM39
B Bacterium

Actinomyces sp. ICM47
B Bacterium

Actinomyces sp. ICM54
B Bacterium

Actinomyces sp. ICM58
B Bacterium

Actinomyces sp. Marseille-P2825 sp. Marseille-P2825
B Bacterium

Actinomyces sp. Marseille-P2985 strain Marseille-P2985T
B Bacterium

Actinomyces sp. S6-Spd3
B Bacterium

Actinomyces sp. oral taxon 171 str. F0337
B Bacterium

Actinomyces sp. oral taxon 172 str. F0311
B Bacterium

Actinomyces sp. oral taxon 175 str. F0384
B Bacterium

Actinomyces sp. oral taxon 180 str. F0310
B Bacterium

Actinomyces sp. oral taxon 848 str. F0332
B Bacterium

Actinomyces sp. ph3
B Bacterium

Adlercreutzia equolifaciens DSM 19450
B Bacterium

Agaricus bisporus var. bisporus H97
E Eukaryote

Agaricus bisporus var. burnettii JB137-S8
E Eukaryote

Test Name: Gut Intelligence Test

Customer Name: Madi Gillespie

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Alistipes finegoldii DSM 17242

B Bacterium

Alistipes indistinctus

B Bacterium

Alistipes onderdonkii WAL 8169 = DSM 19147

B Bacterium

Alistipes putredinis DSM 17216

B Bacterium

Alistipes shahii WAL 8301

B Bacterium

Alistipes sp. HGB5

B Bacterium

Anaerostipes caccae

B Bacterium

Anaerostipes hadrus strain BPB5

B Bacterium

Anaerostipes sp. 3_2_56FAA

B Bacterium

Anaerotruncus colihominis

B Bacterium

Angelakisella massiliensis strain Marseille-P3217

B Bacterium

Atopobium sp. BS2

B Bacterium

Atopobium sp. ICM42b

B Bacterium

Bacteroides acidifaciens
B Bacterium

Bacteroides acidifaciens JCM 10556
B Bacterium

Bacteroides barnesiae DSM 18169 = JCM 13652
B Bacterium

Bacteroides caccae
B Bacterium

Bacteroides caecimuris strain I48
B Bacterium

Bacteroides cellulosilyticus strain WH2
B Bacterium

Bacteroides dorei CL03T12C01
B Bacterium

Bacteroides eggerthii 1_2_48FAA
B Bacterium

Bacteroides eggerthii DSM 20697
B Bacterium

Bacteroides faecichinchillae strain DSM
B Bacterium

Bacteroides faecis
B Bacterium

Bacteroides finegoldii
B Bacterium

Bacteroides fluxus
B Bacterium

Bacteroides fragilis
B Bacterium

Bacteroides fragilis NCTC 9343
B Bacterium

Bacteroides fragilis YCH46
B Bacterium

Bacteroides fragilis str. 3-F-2 #6
B Bacterium

Bacteroides fragilis strain BOB25
B Bacterium

Bacteroides helcogenes P 36-108
B Bacterium

Bacteroides heparinolyticus
B Bacterium

Bacteroides intestinalis
B Bacterium

Bacteroides massiliensis dnLKV3
B Bacterium

Bacteroides nordii
B Bacterium

Bacteroides ovatus V975
B Bacterium

Bacteroides ovatus strain ATCC
B Bacterium

Bacteroides plebeius
B Bacterium

Bacteroides pyogenes

B Bacterium

Bacteroides salyersiae

B Bacterium

Bacteroides sp. 14(A)

B Bacterium

Bacteroides sp. 1_1_30

B Bacterium

Bacteroides sp. 1_1_6

B Bacterium

Bacteroides sp. 2_1_16

B Bacterium

Bacteroides sp. 2_1_22

B Bacterium

Bacteroides sp. 2_1_33B

B Bacterium

Bacteroides sp. 2_1_56FAA

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

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. HMSC068A09

B Bacterium

Bacteroides sp. HMSC073E02

B Bacterium

Bacteroides sp. HPS0048

B Bacterium

Bacteroides sp. Marseille-P2653

B Bacterium

Bacteroides sp. Marseille-P3108 sp. Marseille-P3108

B Bacterium

Bacteroides sp. Marseille-P3132 sp. Marseille-P3132

B Bacterium

Bacteroides stercorirosoris

B Bacterium

Bacteroides stercoris ATCC 43183

B Bacterium

Bacteroides stercoris CC31F

B Bacterium

Bacteroides stercoris strain CL09T03C01

B Bacterium

Bacteroides thetaiotaomicron VPI-5482

B Bacterium

Bacteroides thetaiotaomicron strain 7330

B Bacterium

Bacteroides timonensis AP1

B Bacterium

Bacteroides uniformis

B Bacterium

Bacteroides vulgatus ATCC 8482

B Bacterium

Bacteroides xylanisolvens

B Bacterium

Bifidobacterium adolescentis ATCC 15703

B Bacterium

Bifidobacterium adolescentis strain 22L

B Bacterium

Bifidobacterium adolescentis strain BBMN23

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

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 Bl-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

Bifidobacterium bifidum strain LMG

B Bacterium

Bifidobacterium breve ACS-071-V-Sch8b

B Bacterium

Bifidobacterium breve HPH0326

B Bacterium

Bifidobacterium breve MCC 1114

B Bacterium

Bifidobacterium breve MCC 1605

B Bacterium

Bifidobacterium breve strain BR-14

B Bacterium

Bifidobacterium breve strain BR-15

B Bacterium

Bifidobacterium breve strain BR-19

B Bacterium

Bifidobacterium breve strain BR-21

B Bacterium

Bifidobacterium catenulatum DSM 16992 = JCM 1194 = LMG 11043

B Bacterium

Bifidobacterium longum isolate Bifido_04

B Bacterium

Bifidobacterium longum isolate Bifido_12

B Bacterium

Bifidobacterium longum subsp. longum strain LO-K29a

B Bacterium

Bifidobacterium longum subsp. suis strain BSM11-5

B Bacterium

Bifidobacterium moukalabense

B Bacterium

Bifidobacterium pseudocatenulatum DSM 20438 = JCM 1200 = LMG 10505

B Bacterium

Bifidobacterium pseudocatenulatum IPLA36007

B Bacterium

Bifidobacterium pseudocatenulatum strain 2789STDY5834840

B Bacterium

Bifidobacterium pseudocatenulatum strain CA-05

B Bacterium

Bifidobacterium pseudocatenulatum strain CA-B29

B Bacterium

Bifidobacterium pseudocatenulatum strain CA-C29

B Bacterium

Bifidobacterium pseudocatenulatum strain CA-D29

B Bacterium

Bifidobacterium pseudocatenulatum strain CA-K29a

B Bacterium

Bifidobacterium pseudocatenulatum strain CA-K29b
B Bacterium

Bifidobacterium pseudocatenulatum strain CECT
B Bacterium

Blautia hydrogenotrophica DSM 10507
B Bacterium

Blautia hydrogenotrophica strain 2789STDY5608857
B Bacterium

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 2789STDY5834921
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. Marseille-P3087 sp. Marseille-P3087
B Bacterium

Blautia sp. Marseille-P3201T strain Marseille-P3201
B Bacterium

Blautia sp. N6H1-15
B Bacterium

Blautia wexlerae
B Bacterium

Blueberry shoestring virus
V Virus

Burkholderiales bacterium 1_1_47
B Bacterium

Burkholderiales bacterium YL45
B Bacterium

Butyricimonas
B Bacterium

Butyrivibrio crossotus DSM 2876
B Bacterium

Butyrivibrio fibrisolvens FE2007
B Bacterium

Candidatus Stoquefichus sp. KLE1796
B Bacterium

Capnocytophaga sp. oral taxon 329 str. F0087
B Bacterium

Clavispora lusitaniae ATCC 42720
E Eukaryote

Clostridia bacterium UC5.1-1D1
B Bacterium

Clostridia bacterium UC5.1-1E11
B Bacterium

Clostridia bacterium UC5.1-2H11
B Bacterium

Clostridiales bacterium
B Bacterium

Clostridiales bacterium 1_7_47FAA
B Bacterium

Clostridiales bacterium VE202-03
B Bacterium

Clostridiales bacterium VE202-06
B Bacterium

Clostridiales bacterium VE202-07
B Bacterium

Clostridiales bacterium VE202-15
B Bacterium

Clostridiales bacterium VE202-18
B Bacterium

Clostridiales bacterium VE202-26
B Bacterium

Clostridiales bacterium VE202-27
B Bacterium

Clostridiales bacterium VE202-28
B Bacterium

Clostridioides difficile 630
B Bacterium

Clostridium disporicum strain 2789STDY5608827
B Bacterium

Clostridium disporicum strain 2789STDY5834855
B Bacterium

Clostridium neonatale
B Bacterium

Clostridium paraputrificum
B Bacterium

Clostridium perfringens strain JP55
B Bacterium

Clostridium saudiense strain JCC
B Bacterium

Clostridium sp. 1_1_41A1FAA
B Bacterium

Clostridium sp. AT4
B Bacterium

Clostridium sp. ATCC BAA-442
B Bacterium

Clostridium sp. L2-50
B Bacterium

Clostridium sp. M62/1
B Bacterium

Collinsella intestinalis DSM 13280
B Bacterium

Coprobacillus sp. 3_3_56FAA
B Bacterium

Coprobacillus sp. 8_1_38FAA
B Bacterium

Coprobacillus sp. 8_2_54BFAA
B Bacterium

Coprobacter fastidiosus NSB1
B Bacterium

Coprobacter secundus strain 177
B Bacterium

Coprococcus comes
B Bacterium

Coprococcus eutactus ATCC 27759
B Bacterium

Coprococcus eutactus strain 2789STDY5608829
B Bacterium

Coprococcus eutactus strain 2789STDY5608843
B Bacterium

Coprococcus eutactus strain 2789STDY5834963
B Bacterium

Corynebacterium durum F0235
B Bacterium

Corynebacterium matruchotii
B Bacterium

Dialister invisus DSM 15470

B Bacterium

Dorea formicigenerans 4_6_53AFAA

B Bacterium

Dorea longicatena AGR2136

B Bacterium

Dorea longicatena strain 2789STDY5834914

B Bacterium

Dorea longicatena strain 2789STDY5834961

B Bacterium

Drancourtella massiliensis strain GD1

B Bacterium

Eggerthella lenta

B Bacterium

Enterococcus faecalis

B Bacterium

Enterococcus faecium Aus0004

B Bacterium

Enterococcus faecium Aus0085

B Bacterium

Enterococcus faecium isolate Hp_21-11

B Bacterium

Enterococcus faecium isolate Hp_23-14

B Bacterium

Enterococcus faecium isolate Hp_76-7

B Bacterium

Test Name: Gut Intelligence Test

Customer Name: Madi Gillespie

DOB: 02/24/1996

Enterococcus sp. HMSC072F02

B Bacterium

Erysipelatoclostridium ramosum DSM 1402

B Bacterium

Erysipelotrichaceae bacterium 21_3

B Bacterium

Erysipelotrichaceae bacterium 2_2_44A

B Bacterium

Erysipelotrichaceae bacterium 6_1_45

B Bacterium

Escherichia coli 042

B Bacterium

Escherichia coli JJ1886

B Bacterium

Escherichia coli JJ1887

B Bacterium

Escherichia coli O139:H28 str. E24377A

B Bacterium

Escherichia coli O157 strain 180-PT54

B Bacterium

Escherichia coli O157 strain 644-PT8

B Bacterium

Escherichia coli O157:H7

B Bacterium

Escherichia coli O25b:H4-ST131

B Bacterium

Escherichia coli O6:H16
B Bacterium

Escherichia coli O7:K1 str. CE10
B Bacterium

Escherichia coli O83:H1 str. NRG 857C
B Bacterium

Escherichia coli SE15
B Bacterium

Escherichia coli VR50
B Bacterium

Escherichia coli strain 2012C-4227
B Bacterium

Escherichia coli strain 7784
B Bacterium

Escherichia coli strain C1
B Bacterium

Escherichia coli strain C4
B Bacterium

Escherichia coli strain C8
B Bacterium

Escherichia coli strain CD306
B Bacterium

Escherichia coli strain Eco889
B Bacterium

Escherichia coli strain Ecol_316
B Bacterium

Escherichia coli strain Ecol_448

B Bacterium

Escherichia coli strain Ecol_656

B Bacterium

Escherichia coli strain Ecol_743

B Bacterium

Escherichia coli strain Ecol_AZ146

B Bacterium

Escherichia coli strain JJ2434

B Bacterium

Escherichia coli strain M8

B Bacterium

Escherichia coli strain MRSN346647

B Bacterium

Escherichia coli strain MVAST0167

B Bacterium

Escherichia coli strain SF-166

B Bacterium

Escherichia coli strain ST2747

B Bacterium

Escherichia coli strain ST648

B Bacterium

Eubacterium ramulus ATCC 29099

B Bacterium

Eubacterium ramulus strain 2789STDY5608891

B Bacterium

Eubacterium sp. 3_1_31
B Bacterium

Eubacterium sp. ER2
B Bacterium

Eubacterium ventriosum
B Bacterium

Faecalibacterium prausnitzii
B Bacterium

Flavonifractor plautii strain YL31
B Bacterium

Fusicatenibacter saccharivorans
B Bacterium

Gemella sanguinis ATCC 700632
B Bacterium

Gemella sanguinis strain 1094_BTHU
B Bacterium

Haemophilus sp. HMSC61B11
B Bacterium

Holdemania sp. Marseille-P2844 sp. Marseille-P2844
B Bacterium

Intestinibacter bartlettii DSM 16795
B Bacterium

Intestinimonas butyriciproducens strain AF211
B Bacterium

Kocuria kristinae strain SA12
B Bacterium

Lachnoclostridium phocaeense strain Marseille-P3177T sp. Marseille-P3177
B Bacterium

Lachnoclostridium sp. YL32 sp. YL32
B Bacterium

Lachnospira pectinoschiza strain 2789STDY5834836
B Bacterium

Lachnospira pectinoschiza strain 2789STDY5834886
B Bacterium

Lachnospiraceae bacterium
B Bacterium

Lachnospiraceae bacterium 1_4_56FAA
B Bacterium

Lachnospiraceae bacterium 2_1_46FAA
B Bacterium

Lachnospiraceae bacterium 2_1_58FAA
B Bacterium

Lachnospiraceae bacterium 3_1_46FAA
B Bacterium

Lachnospiraceae bacterium 5_1_63FAA
B Bacterium

Lachnospiraceae bacterium 6_1_63FAA
B Bacterium

Lachnospiraceae bacterium 7_1_58FAA
B Bacterium

Lachnospiraceae bacterium A2
B Bacterium

Lachnospiraceae bacterium oral taxon 082 str. F0431

B Bacterium

Lactobacillus agilis DSM 20509

B Bacterium

Lactobacillus casei M36

B Bacterium

Lactobacillus delbrueckii subsp. bulgaricus 2038

B Bacterium

Lactobacillus delbrueckii subsp. delbrueckii

B Bacterium

Lactobacillus fermentum

B Bacterium P Probiotic

Lactobacillus harbinensis strain BM-LH14723

B Bacterium

Lactobacillus paracasei subsp. paracasei Lpp125

B Bacterium

Lactobacillus rhamnosus DSM 14870

B Bacterium

Lactobacillus rhamnosus strain BPL5

B Bacterium

Lactobacillus sakei strain RI-409

B Bacterium

Lactobacillus sakei strain wikim

B Bacterium

Lactococcus

B Bacterium

Lactonifactor longoviformis
B Bacterium

Leuconostoc lactis
B Bacterium

Massilioclostridium coli strain Marseille-P2976
B Bacterium

Massiliomicrobiota timonensis
B Bacterium

Mediterranea massiliensis strain Marseille-P2645
B Bacterium

Megasphaera micronuciformis F0359
B Bacterium

Mogibacterium diversum
B Bacterium

Odoribacter splanchnicus DSM 20712
B Bacterium

Olsenella sp. DNF00959
B Bacterium

Olsenella sp. oral taxon 807 strain F0089
B Bacterium

Ornithobacterium rhinotracheale
B Bacterium

Oscillibacter sp. ER4
B Bacterium

Oscillospiraceae bacterium VE202-24
B Bacterium

Parabacteroides distasonis ATCC 8503
B Bacterium

Parabacteroides goldsteinii CL02T12C30
B Bacterium

Parabacteroides goldsteinii DSM 19448 = WAL 12034
B Bacterium

Parabacteroides goldsteinii dnLKV18
B Bacterium

Parabacteroides goldsteinii strain 910340
B Bacterium

Parabacteroides johnsonii CL02T12C29
B Bacterium

Parabacteroides johnsonii DSM 18315
B Bacterium

Parabacteroides merdae ATCC 43184
B Bacterium

Parabacteroides merdae CL03T12C32
B Bacterium

Parabacteroides merdae strain 2789STDY5834848
B Bacterium

Parabacteroides sp. 20_3
B Bacterium

Parabacteroides sp. 2_1_7
B Bacterium

Parabacteroides sp. D13
B Bacterium

Parabacteroides sp. D26
B Bacterium

Parabacteroides sp. SN4 strain SN4, sp. SB4
B Bacterium

Paraprevotella clara YIT 11840
B Bacterium

Paraprevotella xylaniphila YIT 11841
B Bacterium

Parasutterella excrementihominis YIT 11859
B Bacterium

Phocea massiliensis strain Marseille-P2769
B Bacterium

Prevotella buccalis DNF00985
B Bacterium

Prevotella copri DSM 18205
B Bacterium

Prevotella corporis strain MJR7716
B Bacterium

Prevotella disiens
B Bacterium

Prevotella sp. 109
B Bacterium

Prevotella sp. KHD1 sp. KHD1
B Bacterium

Prevotella stercorea DSM 18206
B Bacterium

Pseudopropionibacterium propionicum F0230a
B Bacterium

Ralstonia pickettii 12D
B Bacterium

Ralstonia pickettii 12J
B Bacterium

Ralstonia sp. MD27
B Bacterium

Romboutsia
B Bacterium

Roseburia faecis
B Bacterium

Roseburia hominis A2-183
B Bacterium

Roseburia intestinalis L1-82
B Bacterium

Roseburia inulinivorans
B Bacterium

Roseburia sp. 499
B Bacterium

Rothia mucilaginosa DY-18
B Bacterium

Rothia sp. HMSC062H08
B Bacterium

Rothia sp. HMSC065D02
B Bacterium

Test Name: Gut Intelligence Test

Customer Name: Madi Gillespie

DOB: 02/24/1996

Rothia sp. HMSC065G12

B Bacterium

Ruminococcus faecis JCM 15917

B Bacterium

Ruminococcus gnavus ATCC 29149

B Bacterium

Ruminococcus lactaris ATCC 29176

B Bacterium

Ruminococcus lactaris CC59_002D

B Bacterium

Ruminococcus sp. 5_1_39BFAA

B Bacterium

Ruminococcus sp. DSM 100440

B Bacterium

Ruminococcus sp. JC304

B Bacterium

Ruthenibacterium lactatiformans

B Bacterium

Saccharomyces cerevisiae S288C

E Eukaryote

Saccharomyces sp. 'boulardii' strain unique28

E Eukaryote

Salmonella enterica subsp. enterica

B Bacterium

Salmonella enterica subsp. enterica serovar California

B Bacterium

Test Name: Gut Intelligence Test

Customer Name: Madi Gillespie

DOB: 02/24/1996

Salmonella enterica subsp. enterica serovar Concord

B Bacterium

Salmonella enterica subsp. enterica serovar Derby

B Bacterium

Salmonella enterica subsp. enterica serovar Djakarta str. S-1087

B Bacterium

Salmonella enterica subsp. enterica serovar Goldcoast

B Bacterium

Salmonella enterica subsp. enterica serovar Hvittingfoss str. SA20014981

B Bacterium

Salmonella enterica subsp. enterica serovar Indiana

B Bacterium

Salmonella enterica subsp. enterica serovar Infantis

B Bacterium

Salmonella enterica subsp. enterica serovar Infantis strain CVM44454

B Bacterium

Salmonella enterica subsp. enterica serovar Infantis strain FSIS1502169

B Bacterium

Salmonella enterica subsp. enterica serovar Kentucky

B Bacterium

Salmonella enterica subsp. enterica serovar Mbandaka

B Bacterium

Salmonella enterica subsp. enterica serovar Mikawasima

B Bacterium

Salmonella enterica subsp. enterica serovar Milwaukee str. SA19950795

B Bacterium

Salmonella enterica subsp. enterica serovar Montevideo str. USDA-ARS-USMARC-1913
B Bacterium

Salmonella enterica subsp. enterica serovar Ohio
B Bacterium

Salmonella enterica subsp. enterica serovar Panama str. ATCC 7378
B Bacterium

Salmonella enterica subsp. houtenae
B Bacterium

Salmonella enterica subsp. houtenae serovar Houten
B Bacterium

Salmonella enterica subsp. salamae
B Bacterium

Salmonella enterica subsp. salamae serovar Greenside
B Bacterium

Sellimonas intestinalis strain BR72
B Bacterium

Shewanella colwelliana strain CSB03KR
B Bacterium

Shigella boydii
B Bacterium

Shigella dysenteriae
B Bacterium

Shigella flexneri 2a str. 2457T
B Bacterium

Shigella flexneri 2a str. 301
B Bacterium

Streptococcus anginosus C238

B Bacterium

Streptococcus cristatus AS 1.3089

B Bacterium

Streptococcus cristatus ATCC 51100

B Bacterium

Streptococcus infantarius subsp. infantarius CJ18

B Bacterium

Streptococcus infantis ATCC 700779

B Bacterium

Streptococcus infantis SK1076

B Bacterium

Streptococcus milleri

B Bacterium

Streptococcus mutans UA159

B Bacterium

Streptococcus mutans UA159-FR

B Bacterium

Streptococcus parasanguinis ATCC 15912

B Bacterium

Streptococcus parasanguinis FW213

B Bacterium

Streptococcus salivarius JIM8777

B Bacterium

Streptococcus salivarius strain HSISS4

B Bacterium

Streptococcus sanguinis SK36
B Bacterium

Streptococcus sp. AS20
B Bacterium

Streptococcus sp. CCH5-D3
B Bacterium

Streptococcus sp. F0442
B Bacterium

Streptococcus sp. HMSC057G03
B Bacterium

Streptococcus sp. HMSC061E03
B Bacterium

Streptococcus sp. HMSC065C01
B Bacterium

Streptococcus sp. HMSC065E03
B Bacterium

Streptococcus sp. HMSC065H07
B Bacterium

Streptococcus sp. HMSC072C09
B Bacterium

Streptococcus sp. HMSC072G04
B Bacterium

Streptococcus sp. HMSC074F05
B Bacterium

Streptococcus sp. HMSC076C09
B Bacterium

Test Name: Gut Intelligence Test

Customer Name: Madi Gillespie

DOB: 02/24/1996

Streptococcus sp. HMSC078D09

B Bacterium

Streptococcus sp. HMSC078H03

B Bacterium

Streptococcus sp. HMSC10E12

B Bacterium

Streptococcus sp. SR1

B Bacterium

Streptococcus thermophilus

B Bacterium

Streptococcus thermophilus LMD-9

B Bacterium

Streptococcus thermophilus strain MN-BM-A01

B Bacterium

Streptococcus thermophilus strain ND07

B Bacterium

Streptococcus thermophilus strain S9

B Bacterium

Subdoligranulum sp. 4_3_54A2FAA

B Bacterium

Sutterella sp. KLE1602

B Bacterium

Sutterella wadsworthensis 2_1_59BFAA

B Bacterium

Turicibacter sanguinis

B Bacterium

Tyzzerella nexilis
B Bacterium

Tyzzerella sp. Marseille-P3062 sp. Marseille-P3062
B Bacterium

Veillonella atypica ACS-049-V-Sch6
B Bacterium

Veillonella atypica ACS-134-V-Col7a
B Bacterium

Veillonella atypica KON
B Bacterium

Veillonella atypica strain CMW7756B
B Bacterium

Veillonella dispar
B Bacterium

Veillonella parvula DSM 2008
B Bacterium

Veillonella parvula strain UTDB1-3
B Bacterium

Veillonella sp. 3_1_44
B Bacterium

Veillonella sp. 6_1_27
B Bacterium

Veillonella sp. ACP1
B Bacterium

Veillonella sp. AS16
B Bacterium

Veillonella sp. HPA0037

B Bacterium

Veillonella sp. ICM51a

B Bacterium

Veillonella tobetsuensis strain ATCC

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 90A1

B Bacterium

[Clostridium] clostridioforme 90A3

B Bacterium

[Clostridium] clostridioforme 90A6

B Bacterium

[Clostridium] clostridioforme 90A7

B Bacterium

[Clostridium] clostridioforme 90A8

B Bacterium

[Clostridium] clostridioforme 90B1
B Bacterium

[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 ATCC
B Bacterium

[Clostridium] clostridioforme strain NLAE-zl-C196
B Bacterium

[Clostridium] clostridioforme strain NLAE-zl-G208
B Bacterium

[Clostridium] glycyrrhizinilyticum JCM 13369
B Bacterium

[Clostridium] innocuum strain 2789STDY5834853
B Bacterium

[Clostridium] leptum DSM 753
B Bacterium

[Clostridium] saccharolyticum WM1
B Bacterium

[Clostridium] spiroforme
B Bacterium

[Clostridium] symbiosum WAL-14163

B Bacterium

[Eubacterium rectale] ATCC 33656

B Bacterium

[Eubacterium] eligens ATCC 27750

B Bacterium

[Eubacterium] hallii DSM 3353

B Bacterium

[Eubacterium] rectale strain T1-815

B Bacterium

[Ruminococcus] torques strain 2789STDY5608833

B Bacterium

[Ruminococcus] torques strain 2789STDY5608867

B Bacterium

[Ruminococcus] torques strain 2789STDY5834889

B Bacterium

https://www.viome.com/reportablerange

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 (32D2156145) to perform high complexity testing. Sequencing was performed at CLIA (). Contact Viome for any further questions.

VIOME

MADI GILLESPIE'S RESULTS

VERSION: 1.14.2