VIOME

MOHAMMED BANAT'S RESULTS

VIOME

Dear Mohammed Banat,

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: Mohammed Banat
Customer Name: Mohammed Banat
DOB: 01/27/1978
Gender: Male
Customer Id: d69bfeb4-fe77-4132-ad77-c225b26d6d0a
Sample Source: Fecal
Date Collected: 11/07/2019
Date Received: Not Available
Date Issued: 12/15/2019
Sample ID: 1B9101503001

All My Scores

Let's improve these.

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.

Current

Needs Improvement   Good

Test Name: Gut Intelligence Test
Customer Name: Mohammed Banat
DOB: 01/27/1978

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.

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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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.

Current

Needs Improvement   Good

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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Los Alamos, NM 87544
CLIA License Number: 32D2156145

UPMC Genome Center
5560 Centre Avenue
Pittsburgh, PA 15232
CLIA License Number: 39D2144302

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(505) 672-5785

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Oxalate Metabolism Pathways

😞 **Needs Improvement**

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.

Current

Needs Improvement   Good

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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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, 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.

Current

Needs Improvement   Good

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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Keep it up!

Inflammatory Activity

😊 **Good**

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 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.

Current

Needs Improvement   Good

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.

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Digestive Efficiency

🙂 **Good**

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.

Current

Needs Improvement   Good

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

🙂 **Good**

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'.

Current

Needs Improvement   Good

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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Protein Fermentation

🙂 **Good**

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.

Current

Needs Improvement   Good

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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Overall Gas Production

🙂 **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.

Current

Needs Improvement   Good

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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DOB: 01/27/1978

Butyrate Production Pathways

😊 **Good**

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.

Current

Needs Improvement   Good

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.

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

🙂 **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.

Current

Needs Improvement   Good

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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Flagellar Assembly Pathways

😊 **Good**

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.

Current

Needs Improvement   Good

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.

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

😊 **Good**

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.

Current

Needs Improvement   Good

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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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 pathway levels that signal microbial salt stress are low.

Current

Needs Improvement   Good

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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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.

Current

Needs Improvement   Good

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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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.

Current

Needs Improvement   Good

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.

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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TMA Production Pathways

🙂 **Good**

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.

Current

Needs Improvement   Good

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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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.

Current

Needs Improvement   Good
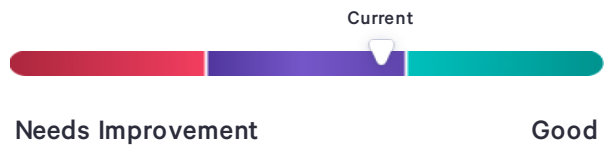
Metabolic Fitness Key

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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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.

Current

Needs Improvement   Good
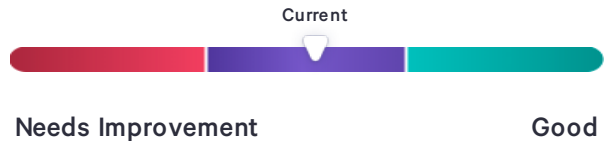
LPS Biosynthesis Pathways Key

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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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.

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My Active Microbes

Actinomyces graevenitzii
B   Bacterium

Agaricus bisporus
E   Eukaryote

Alistipes finegoldii DSM 17242
B   Bacterium

Alistipes finegoldii strain 2789STDY5608890
B   Bacterium

Alistipes finegoldii strain 2789STDY5834947
B   Bacterium

Alistipes indistinctus YIT 12060
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. Marseille-P2431 sp. Marseille-P2431
B   Bacterium

Alistipes timonensis JC136

B Bacterium

Anaerostipes hadrus

B Bacterium

Anaerotruncus colihominis DSM 17241

B Bacterium

Atopobium

B Bacterium

Bacteroides cellulosilyticus

B Bacterium

Bacteroides coprocola DSM 17136

B Bacterium

Bacteroides dorei CL03T12C01

B Bacterium

Bacteroides finegoldii DSM 17565

B Bacterium

Bacteroides fragilis

B Bacterium

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

B Bacterium

Bacteroides nordii WAL 11050 = JCM 12987

B Bacterium

Bacteroides ovatus

B Bacterium

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Bacteroides salanitronis DSM 18170

B Bacterium

Bacteroides sp. 14(A)

B Bacterium

Bacteroides sp. 4_3_47FAA

B Bacterium

Bacteroides stercoris CC31F

B Bacterium

Bacteroides stercoris strain CL09T03C01

B Bacterium

Bacteroides thetaiotaomicron strain 2789STDY5834945

B Bacterium

Bacteroides uniformis

B Bacterium

Bacteroides uniformis dnLKV2

B Bacterium

Bacteroides uniformis strain 2789STDY5608864

B Bacterium

Bacteroides uniformis strain 2789STDY5834844

B Bacterium

Bacteroides uniformis strain 2789STDY5834847

B Bacterium

Bacteroides vulgatus CL09T03C04

B Bacterium

Barnesiella intestinihominis YIT 11860

B   Bacterium

Bifidobacterium

B   Bacterium

Bilophila wadsworthia ATCC 49260

B   Bacterium

Blautia massiliensis sp. GD8

B   Bacterium

Blautia obeum ATCC 29174

B   Bacterium

Blautia wexlerae

B   Bacterium

Burkholderiales bacterium YL45

B   Bacterium

Butyricimonas synergistica

B   Bacterium

Butyricimonas virosa DSM 23226

B   Bacterium

Christensenella minuta strain DSM

B   Bacterium

Clostridiales bacterium KLE1615

B   Bacterium

Clostridiales bacterium VE202-21

B   Bacterium

Clostridium phoceensis strain GD3

B Bacterium

Clostridium sp. AT4 sp. AT5

B Bacterium

Clostridium sp. ATCC BAA-442

B Bacterium

Collinsella aerofaciens ATCC 25986

B Bacterium

Collinsella aerofaciens strain 2789STDY5608823

B Bacterium

Collinsella sp. 4_8_47FAA

B Bacterium

Coprobacillus sp. 8_1_38FAA

B Bacterium

Coprobacter secundus strain 177

B Bacterium

Coprococcus comes ATCC 27758

B Bacterium

Cucumber green mottle mosaic virus

V Virus

Dorea formicigenerans ATCC 27755

B Bacterium

Dorea longicatena strain 2789STDY5834914

B Bacterium

Eggerthella lenta 1_1_60AFAA

B Bacterium

Eisenbergiella tayi strain NML

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 2789STDY5834970

B Bacterium

Fusicatenibacter saccharivorans strain 2789STDY5608849

B Bacterium

Fusicatenibacter saccharivorans strain 2789STDY5834885

B Bacterium

Fusicatenibacter saccharivorans strain 2789STDY5834923

B Bacterium

Gabonia massiliensis strain GM3

B   Bacterium

Gordonibacter pamelaeae 7-10-1-b

B   Bacterium

Holdemania filiformis DSM 12042

B   Bacterium

Hungatella hathewayi

B   Bacterium

Intestinimonas butyriciproducens

B   Bacterium

Lachnospira pectinoschiza strain 2789STDY5834836

B   Bacterium

Lachnospiraceae bacterium 5_1_57FAA

B   Bacterium

Lachnospiraceae bacterium 7_1_58FAA

B   Bacterium

Lachnospiraceae bacterium TF01-11

B   Bacterium

Lactococcus

B   Bacterium

Lactonifactor longoviformis DSM 17459

B   Bacterium

Leuconostoc gelidum

B   Bacterium

Megamonas rupellensis DSM 19944

B   Bacterium

Megasphaera cerevisiae

B   Bacterium

Odoribacter splanchnicus DSM 20712

B   Bacterium

Oscillibacter

B   Bacterium

Oscillospiraceae bacterium VE202-24

B   Bacterium

Parabacteroides distasonis str. 3999B T(B) 6

B   Bacterium

Parabacteroides merdae ATCC 43184

B   Bacterium

Parabacteroides merdae CL09T00C40

B   Bacterium

Paraprevotella clara YIT 11840

B   Bacterium

Paraprevotella xylaniphila YIT 11841

B   Bacterium

Parasutterella

B   Bacterium

Pseudoflavonifractor capillosus ATCC 29799

B   Bacterium

Romboutsia

B Bacterium

Roseburia faecis

B Bacterium

Roseburia hominis A2-183

B Bacterium

Roseburia intestinalis L1-82

B Bacterium

Roseburia intestinalis strain 2789STDY5834960

B Bacterium

Roseburia inulinivorans

B Bacterium

Ruminococcaceae bacterium D16

B Bacterium

Ruminococcus bicirculans

B Bacterium

Ruminococcus flavefaciens

B Bacterium

Ruminococcus lactaris ATCC 29176

B Bacterium

Ruminococcus lactaris CC59_002D

B Bacterium

Ruminococcus torques ATCC 27756

B Bacterium

Streptococcus

B   Bacterium

Subdoligranulum variabile DSM 15176

B   Bacterium

Tannerella sp. 6_1_58FAA_CT1

B   Bacterium

Tomato brown rugose fruit virus isolate Tom1-Jo

V   Virus

Veillonella dispar ATCC 17748

B   Bacterium

[Clostridium] innocuum 2959

B   Bacterium

[Clostridium] leptum DSM 753

B   Bacterium

[Clostridium] scindens ATCC 35704

B   Bacterium

[Clostridium] spiroforme DSM 1552

B   Bacterium

[Clostridium] viride DSM 6836

B   Bacterium

[Eubacterium] eligens strain 2789STDY5834875

B   Bacterium

[Eubacterium] eligens strain 2789STDY5834878

B   Bacterium

[Eubacterium] hallii DSM 3353

B Bacterium

[Eubacterium] hallii strain 2789STDY5834835

B Bacterium

[Eubacterium] rectale

B Bacterium

[Ruminococcus] torques strain 2789STDY5608833

B Bacterium

bacterium LF-3

B Bacterium

uncultured phage crAssphage

V Virus

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.
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.

Test Name: Gut Intelligence Test
Customer Name: Mohammed Banat
DOB: 01/27/1978

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 UPMC Genome Center (CLIA 39D2144302). Contact Viome for any further questions.

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MOHAMMED BANAT'S RESULTS

VERSION: 1.14.2