

VIOME

V' I O M E

BENNY SMALL'S RESULTS

V I O M E

Dear Benny Small,

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: Benny Small
Customer Name: Benny Small
DOB: 01/03/2019
Gender: Female
Customer Id: 52745e14

Sample Source: Fecal
Date Collected: Not Available
Date Received:
Date Issued: 10/09/2018
Sample ID: 131631830590176

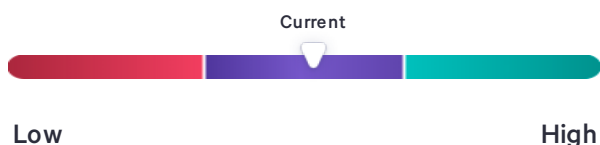
Microbiome Overview

Average

Metabolic Fitness




An analysis of some of the microorganisms and functions that have been shown to be associated with body weight and glycemic response.

This score includes several types of microbes and pathway activities that have been shown to be associated with satiety, macronutrient use, blood sugar control, and caloric intake.



Metabolic Fitness Key

Reference Ranges:

-  Low represents 24% of the Viome population.
-  Average represents 58% of the Viome population.
-  High represents 18% of the Viome population.

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

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



Viome, Inc.
81 Camino Entrada, ste 100
Los Alamos, NM 87544
CLIA Number: 32D2156145

The OMRF Clinical Genomics Center
825 NE 13th Street, RT2101
Oklahoma City, OK 73104
CLIA License Number: 37D2111727

Lab Contact: support@viome.com
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High

Inflammatory Activity

Your microbiome's activities and functions related to inflammation.

Several pro- and anti-inflammatory types of microbes and pathway activities are used integratively to calculate this score



Inflammatory Activity Key

Reference Ranges:

-  **Low** represents 27% of the Viome population.
-  **Average** represents 60% of the Viome population.
-  **High** represents 13% of the Viome population.

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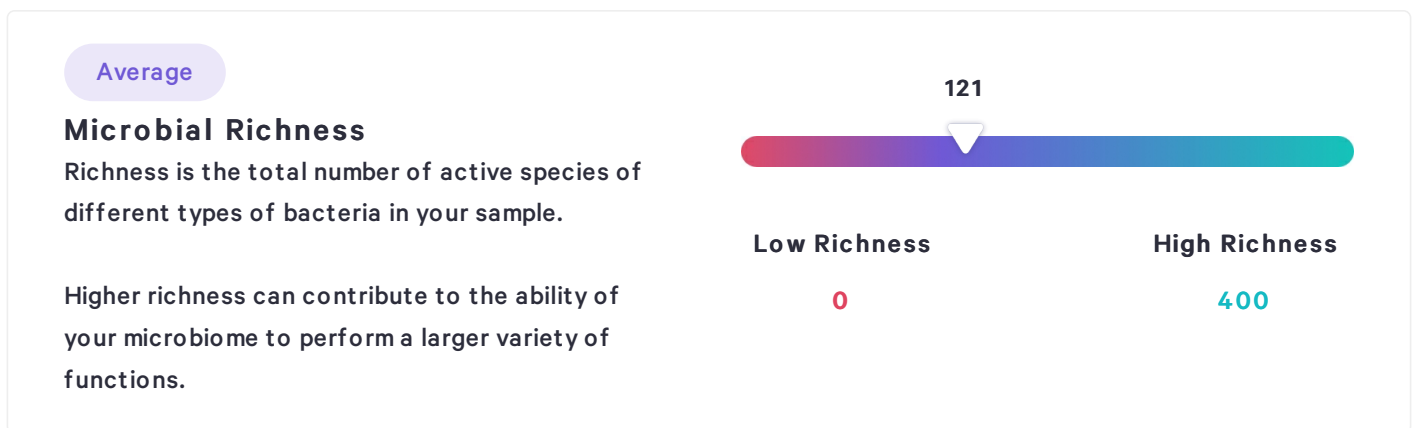
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My Gut Ecosystem

Your microbiome's richness

The types of bacteria that live inside your gut have been shown to affect your health and well-being. Richness of bacteria is associated with a resilient microbiome.



Microbial Richness Key

Reportable Range: 0 to 400 number of microbial species

Reference Ranges:



Low: 0 to 108 microbial species represents 0 to 5th percentile of the Viome population



Average: 109 to 217 microbial species represents the 5th percentile to 95th percentile of the Viome population



High: 218 to 400 microbial species represents the 95th to 100th percentile of the Viome population

Mean: 157

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

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Meet your probiotic microbes

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

Streptococcus thermophilus

P Probiotic



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My Active Microbes

Acinetobacter baumannii 24975_5 B Bacterium
Acinetobacter baumannii 25307_2 B Bacterium
Adlercreutzia equolifaciens DSM 19450 B Bacterium
Akkermansia muciniphila B Bacterium
Alistipes finegoldii DSM 17242 B Bacterium
Alistipes finegoldii strain 2789STDY5608890 B Bacterium
Alistipes finegoldii strain 2789STDY5834947 B Bacterium
Alistipes ihumii AP11 B Bacterium
Alistipes indistinctus YIT 12060 B Bacterium
Alistipes obesi B Bacterium
Alistipes onderdonkii WAL 8169 = DSM 19147 B Bacterium



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Alistipes putredinis DSM 17216 B Bacterium
Alistipes senegalensis JC50 B Bacterium
Alistipes shahii WAL 8301 B Bacterium
Alistipes sp. HGB5 B Bacterium
Alistipes sp. Marseille-P2431 sp. Marseille-P2431 B Bacterium
Anaerostipes B Bacterium
Arthrospira B Bacterium
Bacteroides caccae CL03T12C61 B Bacterium
Bacteroides caccae strain 2789STDY5834946 B Bacterium
Bacteroides cellulosilyticus DSM 14838 B Bacterium
Bacteroides coprocola DSM 17136 B Bacterium
Bacteroides dorei B Bacterium
Bacteroides faecichinchillae B Bacterium



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Bacteroides finegoldii CL09T03C10 B Bacterium
Bacteroides finegoldii DSM 17565 B Bacterium
Bacteroides finegoldii strain 2789STDY5608840 B Bacterium
Bacteroides fragilis 638R B Bacterium
Bacteroides fragilis strain DCMOUH0085B B Bacterium
Bacteroides intestinalis B Bacterium
Bacteroides intestinalis DSM 17393 B Bacterium
Bacteroides intestinalis strain KLE1704 B Bacterium
Bacteroides nordii CL02T12C05 B Bacterium
Bacteroides nordii WAL 11050 = JCM 12987 B Bacterium
Bacteroides sp. 3_1_13 B Bacterium
Bacteroides sp. 3_1_33FAA B Bacterium
Bacteroides sp. 4_3_47FAA B Bacterium



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Bacteroides sp. D2 B Bacterium
Bacteroides sp. HPS0048 B Bacterium
Bacteroides stercoris CC31F B Bacterium
Bacteroides stercoris strain CL09T03C01 B Bacterium
Bacteroides thetaiotaomicron strain 14-106904-2 B Bacterium
Bacteroides thetaiotaomicron strain 19_BTHE B Bacterium
Bacteroides thetaiotaomicron strain 7330 B Bacterium
Bacteroides uniformis dnLKV2 B Bacterium
Bacteroides uniformis strain 2789STDY5834847 B Bacterium
Bacteroides uniformis strain 2789STDY5834942 B Bacterium
Bacteroides vulgatus CL09T03C04 B Bacterium
Bacteroides vulgatus PC510 B Bacterium
Bacteroides vulgatus strain 2789STDY5834842 B Bacterium



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Bacteroides xylanisolvens CL03T12C04 B Bacterium
Barnesiella intestinihominis YIT 11860 B Bacterium
Bilophila wadsworthia ATCC 49260 B Bacterium
Blautia massiliensis sp. GD8 B Bacterium
Blautia obeum ATCC 29174 B Bacterium
Blautia obeum strain 2789STDY5834957 B Bacterium
Blautia sp. Marseille-P3087 sp. Marseille-P3087 B Bacterium
Butyricimonas virosa DSM 23226 B Bacterium
Cannabis cryptic virus isolate hemp09 V Virus
Capnocytophaga sp. oral taxon 329 str. F0087 B Bacterium
Cherry leaf roll virus isolate Olm1 V Virus
Clostridiales bacterium KLE1615 B Bacterium



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Clostridiales bacterium VE202-03 B Bacterium
Clostridiales bacterium VE202-27 B Bacterium
Clostridioides difficile strain CD105KSE11 B Bacterium
Clostridium baratii strain XCM B Bacterium
Clostridium celatum DSM 1785 B Bacterium
Clostridium disporicum strain 2789STDY5834-856 B Bacterium
Clostridium phoceensis strain GD3 B Bacterium
Clostridium sp. CL-2 B Bacterium
Collinsella B Bacterium
Coprobacillus sp. 8_1_38FAA B Bacterium
Coprococcus comes B Bacterium
Dorea longicatena B Bacterium
Eubacterium ramulus strain 2789STDY5608891 B Bacterium



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Eubacterium ventriosum ATCC 27560 B Bacterium
Faecalibacterium cf. prausnitzii KLE1255 B Bacterium
Faecalibacterium prausnitzii A2-165 B Bacterium
Faecalibacterium prausnitzii M21/2 B Bacterium
Faecalibacterium prausnitzii strain 2789STDY5608869 B Bacterium
Faecalibacterium prausnitzii strain 2789STDY5834930 B Bacterium
Faecalibacterium prausnitzii strain 2789STDY5834970 B Bacterium
Fusicatenibacter saccharivorans strain 2789STDY5834885 B Bacterium
Fusobacterium B Bacterium
Gemella sanguinis B Bacterium
Gordonibacter pamelaeeae 7-10-1-b B Bacterium
Haemophilus B Bacterium
Holdemanella biformis DSM 3989 B Bacterium



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Lachnospira pectinoschiza strain 2789STDY5834836 B Bacterium
Lachnospiraceae bacterium 7_1_58FAA B Bacterium
Lactococcus B Bacterium
Leptotrichia B Bacterium
Methanocorpusculum A Archaeon
Morococcus B Bacterium
Mycobacterium gordonae B Bacterium
Odoribacter splanchnicus DSM 20712 B Bacterium
Oscillibacter sp. ER4 B Bacterium
Parabacteroides distasonis B Bacterium
Parabacteroides distasonis CL03T12C09 B Bacterium
Parabacteroides distasonis str. 3999B T(B) 6 B Bacterium
Parabacteroides merdae ATCC 43184 B Bacterium



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Parabacteroides merdae CL03T12C32 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
Pepper mild mottle virus V Virus
Phascolarctobacterium succinatutens YIT 12067 B Bacterium
Phoceia massiliensis strain Marseille-P2769 B Bacterium
Prevotella sp. 109 B Bacterium
Pseudomonas fluorescens strain ATCC B Bacterium
Ralstonia pickettii B Bacterium
Ralstonia sp. MD27 B Bacterium



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Romboutsia B Bacterium
Roseburia hominis A2-183 B Bacterium
Roseburia inulinivorans B Bacterium
Ruminococcaceae bacterium D16 B Bacterium
Ruminococcus lactaris ATCC 29176 B Bacterium
Ruminococcus lactaris CC59_002D B Bacterium
Ruminococcus sp. Marseille-P3213 sp. Marseille-P3213 B Bacterium
Ruminococcus torques ATCC 27756 B Bacterium
Saccharomyces cerevisiae E Eukaryote
Serratia B Bacterium
Sphingomonas sp. Ant H11 B Bacterium
Streptococcus thermophilus B Bacterium P Probiotic



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Sutterella sp. KLE1602 B Bacterium
Sutterella wadsworthensis 2_1_59BFAA B Bacterium
Sutterella wadsworthensis 3_1_45B B Bacterium
Tannerella B Bacterium
Turicibacter sanguinis PC909 B Bacterium
Veillonella dispar ATCC 17748 B Bacterium
[Clostridium] spiroforme DSM 1552 B Bacterium
[Eubacterium] eligens strain 2789STDY5834-875 B Bacterium
[Eubacterium] eligens strain 2789STDY5834-878 B Bacterium
[Eubacterium] hallii DSM 3353 B Bacterium
[Eubacterium] rectale strain T1-815 B Bacterium
[Eubacterium] siraeum DSM 15702 B Bacterium
[Eubacterium] siraeum strain 2789STDY5834-928 B Bacterium



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[Ruminococcus] torques strain 2789STDY5608867

B Bacterium

To assess the overall activity of the microbial contributors for a single type the following are used 1) the relative quantity and activity levels compared to the mean of the Viome population 2) the relative contribution of the type of microbe to the entire sample's active composition.

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



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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 The OMRF Clinical Genomics Center (CLIA 37D2111727). Contact Viome for any further questions.



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VERSION: 1.10.1