Atlas Biomed

Microbiome Test

Sample Report

About your raw data

Kit barcode	000-000-000
Type of biomaterial	Feces
Sample reception date	-
Analysis method	16s rRNA sequence
Report preparation date	1.2.2019

Report content

Microbiome rating

The microbiome rating is a point-based system that evaluates how balanced your gut ecosystem is. Four different parameters are assessed: level of disease protection; ability to synthesise butyrate and vitamins; diversity. Use your rating and recommendations to improve your well-being.

7 of 10

Your microbiome is able to cope with its workload. Check out your food recommendations to balance your gut's ecosystem and improve your health.

Disease protection 7 of 10	Gut bacteria are involved in the body's metabolic and inflammatory processes. So far, research has identified microbiome traits and characteristics associated with various diseases. If your microbiome doesn't have these traits, it means your level of protection is high and vice versa. This is evaluated on a scale of 1 to 10.
Dietary fibre and butyrate 6 of 10	The body can't break down complex carbohydrates like fibre, but our bacteria can. They transform them into simpler compounds like short-chain fatty acids, especially butyrate, which has anti-inflammatory properties. When more bacteria are able to break down fibre, more butyrate is produced, thus increasing the level of protection from disease.
Vitamin synthesis 6 of 10	Vitamins constitute coenzymes that participate in many biochemical reactions. They are present in food and also synthesised by the microbiome. When certain bacteria are more represented in your gut, they improve the likelihood of producing sufficient vitamin concentrations.
Microbiome diversity 8 of 10	Microbiome diversity shows the approximate proportion of each species in your gut. They perform specific roles and are often able to take over the work of other species, should they disappear. When there’s a greater variety of bacteria, it increases your microbiome’s potential for regulation and compensation, making the system more stable as a whole.

Disease protection

Gut bacteria are involved in the body's metabolic and inflammatory processes. So far, research has identified microbiome traits and characteristics associated with various diseases. If your microbiome doesn't have these traits, it means your level of protection is high and vice versa. This is evaluated on a scale of 1 to 10.

Disease	Description
Diabetes type 2	Your bacteria composition reveals normal protection from disease
Ulcerative colitis	Your bacteria composition reveals normal protection from disease
Crohn's disease	Your bacteria composition reveals normal protection from disease
Atherosclerosis	Your bacteria composition reveals normal protection from disease
Obesity	Your bacteria composition reveals high protection from disease

Diabetes type 2

Protection level: 6 of 10

There are specific microbiome features linked to diabetes type II. Measured on a scale of 1 to 10, the fewer features shared with your microbiome, the greater your level of protection from this disease. Firmicute bacteria produce butyrate, a short-chain fatty acid that plays an anti-inflammatory role.

Patients with diabetes type II have fewer Firmicutes and are at higher risk of inflammation. There are also lower levels of Akkermansia, Haemophilus, Lactobacillus and Paraprevotella.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Faecalibacterium	4.62%	Increase
Eubacterium	2.88%	Increase
(Faecalibacterium-unclassified)	2%	Increase
Roseburia	1.14%	Increase
Akkermansia	0.86%	Increase
Lactobacillus	0.2%	Increase
Subdoligranulum	0.08%	Increase
Paraprevotella	0%	Increase
Haemophilus	0%	Increase
(Haemophilus-unclassified)	0%	Increase

Ulcerative colitis

Protection level: 7 of 10

There are specific microbiome features linked to ulcerative colitis. Measured on a scale of 1 to 10, the fewer features shared with your microbiome, the greater your level of protection from this disease. The microbiomes of patients with these diseases have lower levels of commensal bacteria like Faecalibacterium, Eubacterium, Ruminococcus, Akkermansia and Phascolarctobacterium. This is accompanied by the increased presence of the pathogenic bacteria called Escherichia coli.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Bacteroides	48.54%	Decrease
Faecalibacterium	4.62%	Increase
Rikenellaceae	3.22%	Decrease
Eubacterium	2.88%	Increase
(Faecalibacterium-unclassified)	2%	Increase
Clostridium	1.1%	Increase
Lachnospira	1.02%	Decrease
Akkermansia	0.86%	Increase
(Ruminococcus-unclassified)	0.68%	Increase
Ruminococcus	0.54%	Increase
Christensenellaceae	0.5%	Increase
Dorea	0.44%	Decrease
Lactobacillus	0.2%	Increase
[Mogibacteriaceae]	0.16%	Increase
(Shigella-unclassified)	0.08%	Decrease
Adlercreutzia	0.06%	Increase
Enterococcus	0.02%	Decrease
Dehalobacterium	0.02%	Increase
Methanobrevibacter	0%	Increase
unclassified Enterobacteriaceae	0%	Decrease

(Erwinia-unclassified)	0%	Decrease
Sutterella	0%	Decrease
Desulfovibrio	0%	Increase
Corynebacterium	0%	Increase
Phascolarctobacterium	0%	Increase
Catenibacterium	0%	Increase
Leuconostocaceae	0%	Increase

Crohn's disease

Protection level: 7 of 10

There are specific microbiome features linked to Crohn's disease. Measured on a scale of 1 to 10, the fewer features shared with your microbiome, the greater your level of protection from this disease. Crohn's disease is associated with increased levels of Escherichia coli.

These bacteria participate in inflammatory processes. On the other hand, there are less Faecalibacterium prausnitzii, bacteria that normally protect the gut from inflammation.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Bacteroides	48.54%	Decrease
Faecalibacterium	4.62%	Increase
(Faecalibacterium-unclassified)	2%	Increase
Coprococcus	1.38%	Increase
Blautia	1.34%	Decrease
(Blautia-unclassified)	1.2%	Decrease
Clostridium	1.1%	Increase
Akkermansia	0.86%	Increase
(Ruminococcus-unclassified)	0.68%	Increase
Ruminococcus	0.54%	Increase
Parabacteroides	0.54%	Decrease
Christensenellaceae	0.5%	Increase
Dorea	0.44%	Decrease
Anaerostipes	0.32%	Increase
Turicibacter	0.2%	Increase
[Mogibacteriaceae]	0.16%	Increase
(Shigella-unclassified)	0.08%	Decrease
Peptococcus	0.08%	Increase
Eggerthella	0.06%	Decrease
Adlercreutzia	0.06%	Increase

Enterococcus	0.02%	Decrease
Dehalobacterium	0.02%	Increase
Streptococcus	0%	Decrease
Aerococcaceae	0%	Decrease
Butyricimonas	0%	Increase
Slackia	0%	Increase
unclassified Enterobacteriaceae	0%	Decrease
Sutterella	0%	Decrease
Methanobrevibacter	0%	Increase
(Erwinia-unclassified)	0%	Decrease
Desulfovibrio	0%	Increase
Erysipelatoclostridium	0%	Decrease
Phascolarctobacterium	0%	Increase
Catenibacterium	0%	Increase
Collinsella	0%	Increase
Bifidobacterium	0%	Increase

Atherosclerosis

Protection level: 7 of 10

There are specific microbiome features linked to atherosclerosis (hardening of the arteries) and its associated illness, coronary heart disease. Measured on a scale of 1 to 10, the fewer features shared with your microbiome, the greater your level of protection from this disease. Akkermansia muciniphila bacteria support functions of the gut lining and lower the risk of atherosclerosis.

On the other hand, this disease reduces levels of beneficial bacteria like Roseburia, Eubacterium and Dorea, while increasing levels of Collinsella and Prevotella. Bacteria like Proteus, Lachnoclostridium and Providencia produce trimethylamine (TMA) from choline (found in egg yolks) and L-carnitine (found in red meat and fish). TMA is absorbed by the liver and oxidised into trimethylamine-N-oxide (TMAO). This compound is associated with higher risk of atherosclerosis and coronary heart disease.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Eubacterium	2.88%	Increase
Lachnoclostridium	1.28%	Decrease
Roseburia	1.14%	Increase
Akkermansia	0.86%	Increase
Dorea	0.44%	Increase
(Lachnoclostridium-unclassified)	0.16%	Decrease
Proteus	0%	Decrease
Edwardsiella	0%	Decrease
Collinsella	0%	Decrease
Escherichia	0%	Decrease
Providencia	0%	Decrease

Obesity

Protection level: 8 of 10

The ratio of different microbiome bacteria influences inflammation and the risk of developing obesity and other metabolic diseases. Measured on a scale of 1 to 10, the fewer features shared with your microbiome, the greater your level of protection from this disease. Akkermansia muciniphila and Christensenella minuta protect the microbiome from obesity.

In particular, the first is associated with lower body mass and protects against metabolic disorders and insulin resistance. The microbiome of people with a normal metabolism is characterised by higher levels of Faecalibacterium and Bifidobacterium. On the other hand, patients suffering from obesity have increased abundance of Bacteroides and Parabacteroides. Furthermore, the presence of metabolic disorders are associated with the presence of Enterobacteriaceae and Desulfovibrionaceae.

Raw data

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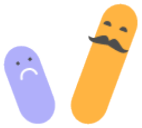
Faecalibacterium	4.62%	Increase
Alistipes	3.22%	Increase
(Faecalibacterium-unclassified)	2%	Increase
Enterobacteriaceae	1.68%	Decrease
Coprococcus	1.38%	Increase
Akkermansia	0.86%	Increase
Christensenellaceae	0.5%	Increase
Desulfovibrionaceae	0.2%	Decrease
Lactobacillus	0.2%	Increase
(Shigella-unclassified)	0.08%	Decrease
Butyrivibrio	0%	Increase
Enterobacter	0%	Decrease
(Erwinia-unclassified)	0%	Decrease
Methanobrevibacter	0%	Increase
unclassified Enterobacteriaceae	0%	Decrease

Bifidobacterium	0%	Increase

Microbiome type

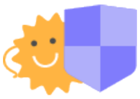
Your microbiome is organised into one of three types that have been established by analysing thousands of samples from around the world. Large-scale metagenomic studies have identified "enterotypes": stable combinations of bacteria co-existing in communities. Each person's microbiome falls into one of these three groups, which correspond with different styles of nutrition. Your microbiome type can change should you significantly modify your diet or be subjected to external factors.

> **Your microbiome type — Western gourmand**
>
> Bacteroides dominate this type of microbiome, where they represent 80% of the ecosystem on average, meaning that there is a lack of diversity. Other bile-resistant genera present in this cluster include Parabacteroides, Paraprevotella and Odoribacter. Some researchers associate the first type with the \"Western diet\" that is rich in simple sugars, animal fats and protein. This cluster is similar to the first enterotype described by M. Arumugam (Arumugam et al., 2011).

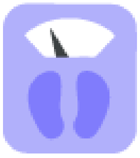


Bacteria of the Bacteroides genus have longer genomes than other microbes that allow them to metabolise more substances.

Bacteroides and Odoribacter produce vitamin K.



Odoribacter produce alpha oleic acid that protects the gut from inflammatory diseases.



A. muciniphila is considered a biomarker of normal metabolism and weight. Increased representation can be seen in lean people because of this bacterium's ability to metabolise glucose. Patients with inflammation or suffering from type 2 diabetes have less A. muciniphila than healthy people.

The presence of Akkermansia increases significantly in situations of prolonged starvation because it can feed on mucin present on the gut membrane in the absence of other nutrients.

Dietary fibre and butyrate

The body can't break down complex carbohydrates like fibre, but our bacteria can. They transform them into simpler compounds like short-chain fatty acids, especially butyrate, which has anti-inflammatory properties. When more bacteria are able to break down fibre, more butyrate is produced, thus increasing the level of protection from disease.

Trait	Result
Dietary fibre intake	Your microbiome's potential for fibre metabolism is average
Butyrate	Your microbiome's potential for butyrate synthesis is high

Dietary fibre intake

Your microbiome's potential for fibre metabolism is average

The human body can only process a few types of complex carbohydrates like vegetable starches and animal glycogen. Food contains several dozen types of such compounds, many of which are transformed by bacteria into important substances like butyrate.

Dietary fibre is not only the main source of energy for commensal bacteria, it normalises intestinal motility and prevents constipation. It has also been shown to positively affect the cardiovascular system and reduce cholesterol levels and blood pressure. A diet rich in fibre can reduce your risk of developing several serious conditions.Your microbiome can cleave dietary fibre and convert it into sufficient levels of short-chain fatty acids that are good for your gut and overall well-being.

Your microbiome can cleave dietary fibre and convert it into sufficient levels of short-chain fatty acids that are good for your gut and overall well-being.

Dietary fibre

Sufficient amount

Amylopectin	9
Arabinan	9
Arabinoxylan	9
Lichenin	9
Pectin	9
-glucan	9
Isomaltose	8
Inulin	6

Insufficient amount

Resistant starch	3
GOS	3
Arabinogalactan	4
Cellulose	4
Dextrin	4
FOS	4
Oligofructose	4
XOS	4

Butyrate

> **Your microbiome's potential for butyrate synthesis is high**

Butyrate, also known as "butyric acid", is an essential short-chain fatty acid (SCFA) that is produced from dietary fibre by bacteria in the gut. With two other SCFAs called acetate and propionate, they provide 15% of the body's energy needs.

Butyrate maintains the gut lining by stimulating the growth of villi, which are tiny little extrusions on the intestinal wall that are responsible for absorbing nutrients. It also has anti-inflammatory and antioxidant properties. This SCFA plays a role in reducing the risk of cancer by preventing unfavourable bacteria from overgrowth, thus regulating the composition of the microbiome.

Bacteria make butyrate from dietary fibre that is found in complex carbohydrates (e.g.,fruit, vegetables, whole grains), which the body couldn't otherwise digest. Bacteria that produce this SCFA include members of Firmicutes, like Anaerostipes, Faecalibacterium, Roseburia, Eubacterium and Gemminger.

Here, we determine your average butyrate production potential based on the composition of your microbiome:Your microbiome has the potential to produce enough butyrate, a short-chain fatty acid that improves the immune system and prevents inflammation.

Your diet contains plenty of fibre. Keep it up and your gut bacteria will continue to supply you with butyrate.

Your microbiome has the potential to produce enough butyrate, a short-chain fatty acid that improves the immune system and prevents inflammation.

Your diet contains plenty of fibre. Keep it up and your gut bacteria will continue to supply you with butyrate.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Bacteroides	48.54%	9
unclassified Lachnospiraceae	10.44%	9
Faecalibacterium	4.62%	6
unclassified Ruminococcaceae	2.92%	7

unclassified Clostridiales	2.16%	6
(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
Lachnospira	1.02%	8
Akkermansia	0.86%	8
(Ruminococcus-unclassified)	0.68%	8
Parabacteroides	0.54%	6
Ruminococcus	0.54%	3
Dorea	0.44%	3
unclassified Peptostreptococcaceae	0.42%	8
Anaerostipes	0.32%	3
Bilophila	0.2%	8
unclassified Clostridiaceae	0.2%	8
Turicibacter	0.2%	8
Odoribacter	0.2%	8
Lactobacillus	0.2%	7
unclassified Christensenellaceae	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
Veillonella	0.04%	8
Enterococcus	0.02%	8
unclassified Erysipelotrichaceae	0.02%	3
Cloacibacillus	0.02%	8

Vitamin synthesis

Vitamins constitute coenzymes that participate in many biochemical reactions. They are present in food and also synthesised by the microbiome. When certain bacteria are more represented in your gut, they improve the likelihood of producing sufficient vitamin concentrations.

Vitamin	Description
Vitamin B9	Below-average microbiome ability to produce vitamin B9 in sufficient amounts
Vitamin B5	Below-average microbiome ability to produce vitamin B5 in sufficient amounts
Vitamin B3	Below-average microbiome ability to produce vitamin B3 in sufficient amounts
Vitamin B2	Average microbiome ability to produce vitamin B2 in sufficient amounts
Vitamin B1	Average microbiome ability to produce vitamin B1 in sufficient amounts
Vitamin K	Above-average microbiome ability to produce vitamin K
Vitamin B7	Above-average microbiome ability to produce vitamin B7
Vitamin B6	Above-average microbiome ability to produce vitamin B6

Vitamin B9

> **Microbiome potential for synthesis: 4 of 10**
>
> Your microbiome isn't able to synthesise enough B9, a deficiency of which can result in apathy, depression, chronic fatigue, poor memory and anaemia. This vitamin is also essential for your microbiome.

The body can't synthesise B vitamins, including thiamine. Instead, these nutrients must be obtained from your diet or produced by your gut bacteria. Until recently, it was believed that water-soluble vitamins were only absorbed by the small intestine.

Nowadays, we know that it is equally possible in the colon, the main habitat of your microbiome. Lactobacillus and Bifidobacteria are the main producers of B vitamins.

Raw data

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Bacteroides	48.54%	9
unclassified Lachnospiraceae	10.44%	9
Faecalibacterium	4.62%	6
unclassified Ruminococcaceae	2.92%	7
unclassified Clostridiales	2.16%	6
(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
Lachnospira	1.02%	8
Akkermansia	0.86%	8
(Ruminococcus-unclassified)	0.68%	8
Ruminococcus	0.54%	3
Parabacteroides	0.54%	6
Dorea	0.44%	3

unclassified Peptostreptococcaceae	0.42%	8
Anaerostipes	0.32%	3
Bilophila	0.2%	8
Odoribacter	0.2%	8
Turicibacter	0.2%	8
Lactobacillus	0.2%	7
unclassified Christensenellaceae	0.2%	8
unclassified Clostridiaceae	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Peptococcus	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
Veillonella	0.04%	8
unclassified Erysipelotrichaceae	0.02%	3
Enterococcus	0.02%	8
Cloacibacillus	0.02%	8

Vitamin B5

> **Microbiome potential for synthesis: 4 of 10**
>
> Your microbiome isn't able to synthesise enough B5, a deficiency of which can result in depression, poor sleep and a weaker immune system. This vitamin is also essential for your microbiome.

The body can't synthesise B vitamins, including thiamine. Instead, these nutrients must be obtained from your diet or produced by your gut bacteria. Until recently, it was believed that water-soluble vitamins were only absorbed by the small intestine.

Nowadays, we know that it is equally possible in the colon, the main habitat of your microbiome. Lactobacillus and Bifidobacteria are the main producers of B vitamins.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Bacteroides	48.54%	9
unclassified Lachnospiraceae	10.44%	9
Faecalibacterium	4.62%	6
unclassified Ruminococcaceae	2.92%	7
unclassified Clostridiales	2.16%	6
(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
Lachnospira	1.02%	8
Akkermansia	0.86%	8
(Ruminococcus-unclassified)	0.68%	8
Ruminococcus	0.54%	3
Parabacteroides	0.54%	6
Dorea	0.44%	3

unclassified	0.42%	8
Peptostreptococcaceae		
Anaerostipes	0.32%	3
Odoribacter	0.2%	8
Lactobacillus	0.2%	7
unclassified	0.2%	8
Christensenellaceae		
unclassified Clostridiaceae	0.2%	8
Bilophila	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Peptococcus	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
Veillonella	0.04%	8
unclassified	0.02%	3
Erysipelotrichaceae		
Enterococcus	0.02%	8
Cloacibacillus	0.02%	8

Vitamin B3

> **Microbiome potential for synthesis: 4 of 10**
>
> Your microbiome isn't able to synthesise enough B3, a deficiency of which can result in nicotinic acid deficiency, depression, sensitivity of skin to UV rays, fatigue and heartburn. This vitamin is also essential for bacteria.

The body can't synthesise B vitamins, including thiamine. Instead, these nutrients must be obtained from your diet or produced by your gut bacteria. Until recently, it was believed that water-soluble vitamins were only absorbed by the small intestine.

Nowadays, we know that it is equally possible in the colon, the main habitat of your microbiome. Lactobacillus and Bifidobacteria are the main producers of B vitamins.

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unclassified Lachnospiraceae	10.44%	9
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unclassified Ruminococcaceae	2.92%	7
unclassified Clostridiales	2.16%	6
(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
Lachnospira	1.02%	8
Akkermansia	0.86%	8
(Ruminococcus-unclassified)	0.68%	8
Ruminococcus	0.54%	3
Parabacteroides	0.54%	6
Dorea	0.44%	3

unclassified Peptostreptococcaceae	0.42%	8
Anaerostipes	0.32%	3
Bilophila	0.2%	8
Odoribacter	0.2%	8
Turicibacter	0.2%	8
Lactobacillus	0.2%	7
unclassified Christensenellaceae	0.2%	8
unclassified Clostridiaceae	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Peptococcus	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
Veillonella	0.04%	8
unclassified Erysipelotrichaceae	0.02%	3
Enterococcus	0.02%	8
Cloacibacillus	0.02%	8

Vitamin B2

> **Microbiome potential for synthesis: 6 of 10**
>
> Your microbiome is able to synthesise enough B2. This vitamin is essential for the immune system, hair and skin.

The body can't synthesise B vitamins, including thiamine. Instead, these nutrients must be obtained from your diet or produced by your gut bacteria. Until recently, it was believed that water-soluble vitamins were only absorbed by the small intestine.

Nowadays, we know that it is equally possible in the colon, the main habitat of your microbiome. Lactobacillus and Bifidobacteria are the main producers of B vitamins.

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(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
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Akkermansia	0.86%	8
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Ruminococcus	0.54%	3
Parabacteroides	0.54%	6
Dorea	0.44%	3
unclassified Peptostreptococcaceae	0.42%	8

Anaerostipes	0.32%	3
Turicibacter	0.2%	8
Bilophila	0.2%	8
unclassified Clostridiaceae	0.2%	8
unclassified Christensenellaceae	0.2%	8
Lactobacillus	0.2%	7
Odoribacter	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Peptococcus	0.08%	8
Veillonella	0.04%	8
Cloacibacillus	0.02%	8
Enterococcus	0.02%	8

Vitamin B1

> **Microbiome potential for synthesis: 6 of 10**
>
> Your microbiome is able to synthesise enough B1. This vitamin is essential for the nervous system, appetite and mood.

The body can't synthesise B vitamins, including thiamine. Instead, these nutrients must be obtained from your diet or produced by your gut bacteria. Until recently, it was believed that water-soluble vitamins were only absorbed by the small intestine.

Nowadays, we know that it is equally possible in the colon, the main habitat of your microbiome. Lactobacillus and Bifidobacteria are the main producers of B vitamins.

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(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
Lachnospira	1.02%	8
Akkermansia	0.86%	8
(Ruminococcus-unclassified)	0.68%	8
Ruminococcus	0.54%	3
Parabacteroides	0.54%	6
Dorea	0.44%	3
unclassified Peptostreptococcaceae	0.42%	8

Anaerostipes	0.32%	3
Bilophila	0.2%	8
Odoribacter	0.2%	8
Turicibacter	0.2%	8
Lactobacillus	0.2%	7
unclassified Christensenellaceae	0.2%	8
unclassified Clostridiaceae	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Peptococcus	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
Veillonella	0.04%	8
unclassified Erysipelotrichaceae	0.02%	3
Enterococcus	0.02%	8
Cloacibacillus	0.02%	8

Vitamin K

> **Microbiome potential for synthesis: 8 of 10**
>
> Your gut has enough bacteria to synthesise enough vitamin K. This nutrient is essential for bone and vascular health.

Vitamin K is synthesised by Bacteroides in the microboime. This genus is common in people belonging to the first cluster. The latter tend to actively consume meat and sugary treats.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Bacteroides	48.54%	9
unclassified Lachnospiraceae	10.44%	9
unclassified Ruminococcaceae	2.92%	7
unclassified Clostridiales	2.16%	6
Coprococcus	1.38%	4
Akkermansia	0.86%	8
Parabacteroides	0.54%	6
Dorea	0.44%	3
Turicibacter	0.2%	8
Bilophila	0.2%	8
unclassified Clostridiaceae	0.2%	8
unclassified Christensenellaceae	0.2%	8
Lactobacillus	0.2%	7
Odoribacter	0.2%	8
unclassified Coriobacteriaceae	0.14%	6
Pseudomonas	0.1%	10
Peptococcus	0.08%	8
(Shigella-unclassified)	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
Veillonella	0.04%	8

Cloacibacillus	0.02%	8
Enterococcus	0.02%	8

Vitamin B7

> **Microbiome potential for synthesis: 8 of 10**
>
> Your gut has enough bacteria to synthesise enough B7. This vitamin is essential for the immune system, hair and skin.

The body can't synthesise B vitamins, including thiamine. Instead, these nutrients must be obtained from your diet or produced by your gut bacteria. Until recently, it was believed that water-soluble vitamins were only absorbed by the small intestine.

Nowadays, we know that it is equally possible in the colon, the main habitat of your microbiome. Lactobacillus and Bifidobacteria are the main producers of B vitamins.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Bacteroides	48.54%	9
unclassified Lachnospiraceae	10.44%	9
Faecalibacterium	4.62%	6
unclassified Ruminococcaceae	2.92%	7
unclassified Clostridiales	2.16%	6
(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
Lachnospira	1.02%	8
Akkermansia	0.86%	8
(Ruminococcus-unclassified)	0.68%	8
Ruminococcus	0.54%	3
Parabacteroides	0.54%	6
Dorea	0.44%	3
unclassified Peptostreptococcaceae	0.42%	8

Anaerostipes	0.32%	3
Bilophila	0.2%	8
Odoribacter	0.2%	8
Turicibacter	0.2%	8
Lactobacillus	0.2%	7
unclassified Christensenellaceae	0.2%	8
unclassified Clostridiaceae	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Peptococcus	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
Veillonella	0.04%	8
unclassified Erysipelotrichaceae	0.02%	3
Enterococcus	0.02%	8
Cloacibacillus	0.02%	8

Vitamin B6

> **Microbiome potential for synthesis: 8 of 10**
>
> Your gut has enough bacteria to synthesise enough B6. This vitamin is essential for the immune system and mood.

The body can't synthesise B vitamins, including thiamine. Instead, these nutrients must be obtained from your diet or produced by your gut bacteria. Until recently, it was believed that water-soluble vitamins were only absorbed by the small intestine.

Nowadays, we know that it is equally possible in the colon, the main habitat of your microbiome. Lactobacillus and Bifidobacteria are the main producers of B vitamins.

Raw data

Bacteria that participates in synthesis	Representation in the microbiome	Microbiome potential for synthesis
Bacteroides	48.54%	9
unclassified Lachnospiraceae	10.44%	9
Faecalibacterium	4.62%	6
unclassified Ruminococcaceae	2.92%	7
unclassified Clostridiales	2.16%	6
(Faecalibacterium-unclassified)	2%	4
Coprococcus	1.38%	4
Blautia	1.34%	3
(Blautia-unclassified)	1.2%	8
Roseburia	1.14%	4
Clostridium	1.1%	5
Lachnospira	1.02%	8
Akkermansia	0.86%	8
(Ruminococcus-unclassified)	0.68%	8
Ruminococcus	0.54%	3
Parabacteroides	0.54%	6
Dorea	0.44%	3
Anaerostipes	0.32%	3
Odoribacter	0.2%	8

Lactobacillus	0.2%	7
unclassified Christensenellaceae	0.2%	8
Bilophila	0.2%	8
unclassified Clostridiaceae	0.2%	8
Turicibacter	0.2%	8
Oscillospira	0.18%	4
unclassified Coriobacteriaceae	0.14%	6
Dialister	0.12%	6
Pseudomonas	0.1%	10
(Shigella-unclassified)	0.08%	8
Peptococcus	0.08%	8
Eggerthella	0.06%	9
Adlercreutzia	0.06%	8
unclassified Erysipelotrichaceae	0.02%	3
Enterococcus	0.02%	8
Cloacibacillus	0.02%	8

Microbiome diversity

> **You have a diverse microbiome that can help it resist the negative impact of external factors.**

Diversity indicates the approximate number of bacterial species that live in a person's gut. Each type has its own functions that are often complementary. A diverse microbiome can perform a broader range of tasks that regulate and compensate, making the whole system more stable. External factors like a poor diet or antibiotics can cause one or several key species to disappear from the community.

When there is a wide range of bacteria, other species take over these missing functions, but if the community lacks richness, this compensation mechanism may be compromised and cause dysbiosis, a condition known to precede illness. For example, patients with inflammatory bowel diseases and metabolic disorders have less bacterial diversity than healthy people – a pattern that is also observed in people who have taken antibiotics or have a poor diet.

Nationality of your microbiome: Asia

> The average Chinese diet contains lots of rice and little meat. Nevertheless, the eating habits of Chinese people in big cities is similar to that of Europeans and Americans.

People living together as a community throughout the centuries become similar not only genetically, but also in a way of sharing the common nutrition habits. As a result their microbiome profiles become similar too.

Asia	35.4%
North America	25%
Western Europe	25%
Eastern Europe	6.8%
South America	4%
Africa	3.8%

List of all bacteria

List of every bacterial genus detected in your sample. A colour has been assigned to each genus depending on its role in the microbiome. This classification has been established using the results of scientific research and is organised into "commensal", "beneficial" and "potentially pathogenic" bacteria. Remember that the presence of potential pathogens is not necessarily a cause for concern. Rather, it's important to consider the proportion it occupies in the microbiome compared to other bacteria. The overall assessment of your gut bacteria can be found in the section "microbiome rating".

Family

Bacteria are divided into families of microbes that are similar in structure and diet but their "lifestyle" may differ, meaning that one family can host both healthy and potentially pathogenic bacteria.

Bacteroidaceae	48.54%
Lachnospiraceae	18.84%
Ruminococcaceae	11.22%
Rikenellaceae	3.22%
Oscillospiraceae	3.02%
Eubacteriaceae	2.88%
unclassified Clostridiales	2.16%
Sutterellaceae	1.96%
Enterobacteriaceae	1.68%
Clostridiaceae	1.3%
Verrucomicrobiaceae	0.86%
Porphyromonadaceae	0.82%
Peptostreptococcaceae	0.7%
Christensenellaceae	0.5%
unclassified (Bacilli-Clostridia)	0.28%
Coriobacteriaceae	0.26%

(Eubacteriaceae-Lachnospiraceae)	0.26%
(Lachnospiraceae-unclassified)	0.26%
Erysipelotrichaceae	0.22%
Desulfovibrionaceae	0.2%
Lactobacillaceae	0.2%
[Mogibacteriaceae]	0.16%
Veillonellaceae	0.16%
Pseudomonadaceae	0.1%
Peptococcaceae	0.08%
(Oscillospiraceae-Ruminococcaceae)	0.04%
Clostridiales_Family_XI._Incertae_Sedis	0.02%
Enterococcaceae	0.02%
Dehalobacteriaceae	0.02%
Synergistaceae	0.02%
Gordoniaceae	0%
Aeromonadaceae	0%
Desulfobulbaceae	0%
Micrococcaceae	0%
Mycoplasmataceae	0%
Vibrionaceae	0%
unclassified RF32	0%
Sinobacteraceae	0%
Staphylococcaceae	0%
Neisseriaceae	0%
[Melainabacteriaceae]	0%
Methanobacteriaceae	0%
Phyllobacteriaceae	0%
Helicobacteraceae	0%
Cytophagaceae	0%

Xanthobacteraceae	0%
Planctomycetaceae	0%
Brucellaceae	0%
(Clostridiaceae-unclassified)	0%
Victivallaceae	0%
Comamonadaceae	0%
Planococcaceae	0%
Xanthomonadaceae	0%
Halobacteriaceae	0%
unclassified Lactobacillales	0%
Dermabacteraceae	0%
[Exiguobacteraceae]	0%
(Clostridiaceae-Eubacteriaceae)	0%
Clostridiales_Family_XIII._Incertae_Sedis	0%
Bradyrhizobiaceae	0%
Rhodospirillaceae	0%
Streptococcaceae	0%
Bifidobacteriaceae	0%
Mycobacteriaceae	0%
Paenibacillaceae	0%
Spirochaetaceae	0%
Micromonosporaceae	0%
Succinivibrionaceae	0%
Cardiobacteriaceae	0%
Sphingobacteriaceae	0%
Corynebacteriaceae	0%
Streptomycetaceae	0%
Dietziaceae	0%
Actinomycetaceae	0%

(Ruminococcaceae-unclassified)	0%
Rhodobacteraceae	0%
Caulobacteraceae	0%
Bogoriellaceae	0%
Unclassified_Clostridiales	0%
Chitinophagaceae	0%
Prevotellaceae	0%
Aerococcaceae	0%
Flavobacteriaceae	0%
(Clostridiaceae-Ruminococcaceae)	0%
Hyphomicrobiaceae	0%
unclassified Unclassified	0%
Burkholderiaceae	0%
Gemellaceae	0%
Geodermatophilaceae	0%
unclassified Firmicutes	0%
[Paraprevotellaceae]	0%
Halobacteroidaceae	0%
Bacillaceae	0%
[Acidaminobacteraceae]	0%
Sanguibacteraceae	0%
Rhizobiaceae	0%
Sphingomonadaceae	0%
Halomonadaceae	0%
Sulfolobaceae	0%
Leptotrichiaceae	0%
Promicromonosporaceae	0%
Catabacteriaceae	0%
Listeriaceae	0%

Dermacoccaceae	0%
Leuconostocaceae	0%
Oxalobacteraceae	0%
Moraxellaceae	0%
unclassified Bacteroidales	0%
Methylobacteriaceae	0%
Nocardioidaceae	0%
unclassified Actinomycetales	0%
Deinococcaceae	0%
unclassified Alphaproteobacteria	0%
Rhodocyclaceae	0%
Cellulomonadaceae	0%
Unclassified_Actinomycetales	0%
Methanosaetaceae	0%
Campylobacteraceae	0%
Alcaligenaceae	0%
Brevibacteriaceae	0%
Brachyspiraceae	0%
Acetobacteraceae	0%
Intrasporangiaceae	0%
Microbacteriaceae	0%
Nocardiaceae	0%
[Methanomassiliicoccaceae]	0%
p-2534-18B5	0%
Aurantimonadaceae	0%
Fusobacteriaceae	0%
unclassified Selenomonadales	0%
Alicyclobacillaceae	0%
Nitrososphaeraceae	0%

unclassified Proteobacteria	0%
Rs-045	0%
Chromobacteriaceae	0%
[Weeksellaceae]	0%
Carnobacteriaceae	0%
Acidaminococcaceae	0%
unclassified Pseudomonadales	0%
Pasteurellaceae	0%
Propionibacteriaceae	0%

Genus

A single family of bacteria may include several genera. Microbes of the same genus are close relatives and often perform similar functions in the gut.

Bacteroides	48.54%
unclassified Lachnospiraceae	10.44%
Faecalibacterium	4.62%
Alistipes	3.22%
Oscillibacter	3.02%
unclassified Ruminococcaceae	2.92%
Eubacterium	2.88%
unclassified Clostridiales	2.16%
(Faecalibacterium-unclassified)	2%
Parasutterella	1.96%
Citrobacter	1.5%
Coprococcus	1.38%
Blautia	1.34%
Lachnoclostridium	1.28%
(Blautia-unclassified)	1.2%
Roseburia	1.14%
Clostridium	1.1%
Lachnospira	1.02%
Akkermansia	0.86%
(Ruminococcus-unclassified)	0.68%
Parabacteroides	0.54%
Ruminococcus	0.54%
Dorea	0.44%
unclassified Peptostreptococcaceae	0.42%
Anaerostipes	0.32%

Christensenella	0.3%
Intestinibacter	0.28%
unclassified (Bacilli-Clostridia)	0.28%
unclassified (Lachnospiraceae-unclassified)	0.26%
unclassified (Eubacteriaceae-Lachnospiraceae)	0.26%
Bilophila	0.2%
Turicibacter	0.2%
Odoribacter	0.2%
Lactobacillus	0.2%
unclassified Clostridiaceae	0.2%
unclassified Christensenellaceae	0.2%
Oscillospira	0.18%
unclassified [Mogibacteriaceae]	0.16%
(Lachnoclostridium-unclassified)	0.16%
unclassified Coriobacteriaceae	0.14%
(Faecalibacterium-Gemmiger)	0.14%
Dialister	0.12%
Pseudomonas	0.1%
(Citrobacter-Raoultella)	0.1%
Peptococcus	0.08%
Tyzzerella	0.08%
Subdoligranulum	0.08%
(Shigella-unclassified)	0.08%
Barnesiella	0.06%
Eggerthella	0.06%
Adlercreutzia	0.06%
unclassified (Oscillospiraceae-Ruminococcaceae)	0.04%
Intestinimonas	0.04%
Veillonella	0.04%

Cloacibacillus	0.02%
unclassified Erysipelotrichaceae	0.02%
Gemmiger	0.02%
[Ruminococcus]	0.02%
Cellulosilyticum	0.02%
Dehalobacterium	0.02%
Parvimonas	0.02%
Enterococcus	0.02%
unclassified Porphyromonadaceae	0.02%
Actinomyces	0%
unclassified Enterobacteriaceae	0%
Pseudoclavibacter	0%
Alloprevotella	0%
Erwinia	0%
(Cupriavidus-unclassified)	0%
Haloarcula	0%
Aureimonas	0%
Methanosaeta	0%
Kallipyga	0%
Bacillus	0%
Catabacter	0%
Plesiomonas	0%
Gordonia	0%
Geobacillus	0%
Ochrobactrum	0%
Dysgonomonas	0%
Abiotrophia	0%
Kurthia	0%
Mycoplasma	0%

Arthrobacter	0%
Morganella	0%
Massilia	0%
vadinCA11	0%
unclassified Unclassified	0%
Methylobacterium	0%
Oxalobacter	0%
Olsenella	0%
Treponema	0%
Halanaerobaculum	0%
Pseudoxanthomonas	0%
Novosphingobium	0%
Streptomyces	0%
Pseudoramibacter	0%
Eikenella	0%
Sphingomonas	0%
(Erwinia-unclassified)	0%
Raoultella	0%
Escherichia	0%
(Citrobacter-Escherichia)	0%
Anaerotruncus	0%
(Barnesiella-unclassified)	0%
Methanobrevibacter	0%
Pseudobutyrivibrio	0%
Paraprevotella	0%
Kingella	0%
Leptotrichia	0%
Brochothrix	0%
Agrobacterium	0%

Tumebacillus	0%
unclassified Desulfovibrionaceae	0%
Mesorhizobium	0%
Peptostreptococcus	0%
Bradyrhizobium	0%
RFN20	0%
Arcobacter	0%
Butyricimonas	0%
Bulleidia	0%
Porphyromonas	0%
Providencia	0%
Aquabacterium	0%
(Escherichia-Hafnia)	0%
Microvirga	0%
Candidatus_Soleaferrea	0%
Rhodanobacter	0%
unclassified Bacteroidales	0%
Sphingobacterium	0%
Comamonas	0%
unclassified Neisseriaceae	0%
Arcanobacterium	0%
Micrococcus	0%
Papillibacter	0%
Succinatimonas	0%
Nevskia	0%
Leuconostoc	0%
XKL75	0%
Moraxella	0%
unclassified [Weeksellaceae]	0%

(Blautia-Roseburia)	0%
unclassified (Ruminococcaceae-unclassified)	0%
Paenibacillus	0%
Allisonella	0%
Propionibacterium	0%
Helicobacter	0%
Methanomassiliicoccus	0%
Haloplanus	0%
Salmonella	0%
Victivallis	0%
(Gemmiger-unclassified)	0%
Streptococcus	0%
Peptoniphilus	0%
Eggerthia	0%
Sneathia	0%
Agrococcus	0%
Halonotius	0%
Cryptobacterium	0%
Mitsuokella	0%
(Haemophilus-unclassified)	0%
Afipia	0%
Aerococcus	0%
Cardiobacterium	0%
Timonella	0%
Acetanaerobacterium	0%
Campylobacter	0%
Anaerorhabdus	0%
Terrisporobacter	0%
Hylemonella	0%

Lactococcus	0%
Dermacoccus	0%
Tetragenococcus	0%
Brachyspira	0%
Yokenella	0%
Enorma	0%
Tropheryma	0%
Slackia	0%
Kerstersia	0%
Desulfobulbus	0%
Gluconacetobacter	0%
Halobacterium	0%
Sarcina	0%
Flavobacterium	0%
Pediococcus	0%
Leminorella	0%
unclassified Listeriaceae	0%
Haemophilus	0%
Schlesneria	0%
Anaerococcus	0%
unclassified (Clostridiaceae-unclassified)	0%
Parasporobacterium	0%
Marvinbryantia	0%
Lachnobacterium	0%
Desulfitobacterium	0%
Kocuria	0%
Cellulomonas	0%
Micromonospora	0%
Oribacterium	0%

unclassified Actinomycetales	0%
Methanobacterium	0%
Anaerovibrio	0%
Sulfolobus	0%
cc_115	0%
[Melainabacter]	0%
Gemella	0%
Butyricicoccus	0%
Paraeggerthella	0%
p-75-a5	0%
Aneurinibacillus	0%
Variovorax	0%
Moryella	0%
unclassified Selenomonadales	0%
Brevibacillus	0%
[Saccharibacteria]	0%
Staphylococcus	0%
Laribacter	0%
Enterobacter	0%
Halorubrum	0%
Sutterella	0%
Lactonifactor	0%
Lysobacter	0%
Romboutsia	0%
(Candidatus_Soleaferrea-unclassified)	0%
Herbaspirillum	0%
Robinsoniella	0%
[Clostridium]	0%
Asaccharobacter	0%

Acidaminococcus	0%
Halosimplex	0%
Vibrio	0%
unclassified Rhizobiaceae	0%
unclassified Halomonadaceae	0%
Acinetobacter	0%
(Diaphorobacter-Hylemonella)	0%
Trueperella	0%
Promicromonospora	0%
Tatumella	0%
Prevotella	0%
Phenylobacterium	0%
Planomicrobium	0%
Rhodococcus	0%
Spirosoma	0%
Catenibacterium	0%
unclassified Lactobacillales	0%
unclassified Pseudomonadales	0%
Solobacterium	0%
Yonghaparkia	0%
Zobellia	0%
Collinsella	0%
Senegalemassilia	0%
Lachnoanaerobaculum	0%
Fictibacillus	0%
Kytococcus	0%
Nitrososphaera	0%
Limnobacter	0%
Rothia	0%

Dielma	0%
Georgenia	0%
Edwardsiella	0%
Selenomonas	0%
Holdemanella	0%
[Bacteroides]	0%
Mycobacterium	0%
Microbispora	0%
Skermanella	0%
Blastomonas	0%
Methyloversatilis	0%
Weissella	0%
Filifactor	0%
Butyrivibrio	0%
unclassified Xanthomonadaceae	0%
unclassified Pasteurellaceae	0%
Actinobacillus	0%
Anoxystipes	0%
Hydrogenoanaerobacterium	0%
Capnocytophaga	0%
Aeromicrobium	0%
Ralstonia	0%
(Gluconacetobacter-Yersinia)	0%
Diaphorobacter	0%
Flexispira	0%
Psychrobacter	0%
unclassified Alcaligenaceae	0%
Coprobacillus	0%
Acidovorax	0%

Leucobacter	0%
Brevundimonas	0%
Facklamia	0%
Phyllobacterium	0%
Pyramidobacter	0%
unclassified Sutterellaceae	0%
(Finegoldia-Unclassified_Tissierellaceae)	0%
Dermabacter	0%
Kandleria	0%
Luteimonas	0%
Anoxynatronum	0%
Pelomonas	0%
Scardovia	0%
unclassified Prevotellaceae	0%
Candidatus_Stoquefichus	0%
Proteus	0%
Achromobacter	0%
Hymenobacter	0%
(Blastomonas-Novosphingobium)	0%
Grimontia	0%
Ancylobacter	0%
Dyadobacter	0%
Stenotrophomonas	0%
Dickeya	0%
Atopobium	0%
Wautersiella	0%
Trabulsiella	0%
Candidatus_Azobacteroides	0%
Fusobacterium	0%

Moellerella	0%
Paracoccus	0%
Asaccharospora	0%
Aggregatibacter	0%
Hespellia	0%
Megasphaera	0%
Corynebacterium	0%
Shigella	0%
unclassified Alphaproteobacteria	0%
Burkholderia	0%
Blastococcus	0%
Cellulosimicrobium	0%
unclassified Oxalobacteraceae	0%
Neisseria	0%
unclassified p-2534-18B5	0%
Halococcus	0%
Acetoanaerobium	0%
Anaerobiospirillum	0%
Paeniclostridium	0%
Mobiluncus	0%
Hydrogenophaga	0%
Peptoclostridium	0%
Serratia	0%
Roseomonas	0%
Peptostreptococcaceae	0%
(Averyella-Citrobacter-Enterobacter-Kluyvera)	0%
Delftia	0%
Lysinibacillus	0%
unclassified Sphingomonadaceae	0%

Succinivibrio	0%
Faecalicoccus	0%
Amaricoccus	0%
Howardella	0%
Janibacter	0%
Perlucidibaca	0%
Desulfovibrio	0%
Ureibacillus	0%
Virgibacillus	0%
Cronobacter	0%
Yersinia	0%
Curtobacterium	0%
Sporosarcina	0%
Fusibacter	0%
Bordetella	0%
Pedobacter	0%
unclassified (Clostridiaceae-Ruminococcaceae)	0%
Anaerofilum	0%
Granulicatella	0%
Phascolarctobacterium	0%
unclassified (Clostridiaceae-Eubacteriaceae)	0%
Oceanobacillus	0%
Tannerella	0%
Chryseobacterium	0%
Cedecea	0%
Rudanella	0%
Ureaplasma	0%
Deinococcus	0%
Halorhabdus	0%

Prosthecobacter	0%
Cloacibacterium	0%
Bifissio	0%
Brachybacterium	0%
Pedomicrobium	0%
Methanosphaera	0%
[Prevotella]	0%
Anaerofustis	0%
Aeromonas	0%
Alcaligenes	0%
Dietzia	0%
Klebsiella	0%
Brevibacterium	0%
Planococcus	0%
Haloferax	0%
Cupriavidus	0%
Absiella	0%
Aeribacillus	0%
Faecalitalea	0%
Cetobacterium	0%
unclassified RF32	0%
Varibaculum	0%
Holdemania	0%
Lautropia	0%
Megamonas	0%
unclassified Comamonadaceae	0%
Gordonibacter	0%
Erysipelatoclostridium	0%
Lampropedia	0%

Exiguobacterium	0%
Tissierella	0%
Microbacterium	0%
Pantoea	0%
Mogibacterium	0%
unclassified Proteobacteria	0%
Silanimonas	0%
unclassified Firmicutes	0%
Bifidobacterium	0%

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