MetaBiome™ Score

MetaBiome^{TM} Report

Report issue date

29/11/2021

Sample ID

BBF2826

The Metabiome^{TM} score provides a snapshot of overall microbiome health, based on eleven key indicators. Their contribution to the MetaBiome^{TM} score is weighted based on scientific evidence showing the level of influence each one has on health. When all indicators are within the healthy comparison range, the score will be 98-100.

Other markers in the Metabiome^{TM} report provide additional information to be used in conjunction with the Metabiome^{TM} score.

MetaBiome™ Score Contributors

Potential to promote health

Butyrate production

The typical range in healthy people is 12.31% to 23.09%

Butyrate is a short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.

[1] [2] [3] [4] [5] [6] [7] [8]

Propionate production

The typical range in healthy people is 1.66% to 8.66%

Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, and helps control appetite. The prebiotic fibre beta-glucan, found in oats and barley, has been shown to increase propionate production.

[1] [2] [3] [4] [5] [6]

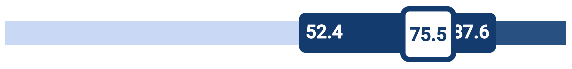
Acetate production

The typical range in healthy people is 62.94% to 76.66%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. Several bacterial species can also convert acetate to the beneficial short chain fatty acid, butyrate. The consumption of wholegrains, fruits, vegetables, legumes, nuts and seeds are associated with increased short chain fatty acids, including acetate.

[1] [2] [3]

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

Potential to reduce health

Hexa-acylated lipopolysaccharide production

The typical range in healthy people is 0% to 0.65%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.

[1] [2] [3] [4] [5] [6]

Trimethylamine production

The typical range in healthy people is 1.45% to 4.52%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.

[1] [2] [3] [4] [5] [6] [7]

Hydrogen sulphide production

The typical range in healthy people is 5.09% to 12.06%

The gas hydrogen sulphide is produced by bacteria when they break down sulphur-containing amino acids found in foods such as eggs, meat, and fish. This gas is responsible for the rotten egg smell of flatulence. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. Laboratory based studies have suggested that eating foods high in resistant starch (e.g. lentils, peas, beans, rolled oats and cooked and cooled potatoes) or fructooligosaccharides (FOS) (e.g. onions, garlic, leek, banana, peaches, wheat, barley) can reduce the production of hydrogen sulphide by the microbiome.

[1] [2]

Microbial Diversity

The typical range in healthy people is 3.37% to 4.56%

Microbial diversity is a measure of both the different types and the amount of bacterial species in your sample.
A varied diet rich in plant-based foods such as fruits, vegetables, whole grains and nuts is associated with increased microbial diversity. Low microbial diversity is often associated with poor health.

3-indolepropionic acid (IPA) production

The typical range in healthy people is 0.03% to 2.37%

3-indolepropionic acid (IPA) is a beneficial substance produced by some gut bacteria when they break down the amino acid tryptophan. It is a strong anti-oxidant that can help protect the nervous system from damage. Research has also shown that IPA may play a role in glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.
[1] [2] [3] [4]

Protein degradation

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Human DNA

The typical range in healthy people is 0.03% to 4%

A high amount (greater than 4%) of human DNA may indicate gut inflammation. If there is greater than 4% human DNA, and there was no contamination (e.g. accidentally touched the swab during sampling), further clinical investigation is needed.

Functional Insights

Going beyond which microbes are in the gut, what they are capable of doing is more important. Through comprehensive analysis of the genes in each and every microbe, we can understand the functional capacity of the microbiome to contribute to the health of different systems in the body.

General Gut Health 87%

These metabolites and microorganisms have been shown to influence your gut barrier function.

Metabolites

Potential to **promote** health

Butyrate production

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[1] [2] [3]

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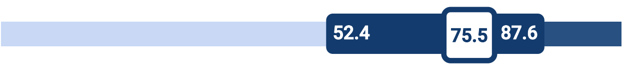

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Lactate production

The typical range in healthy people is 60.08% to 78.47%

Lactate or lactic-acid producing bacteria have a long tradition of beng used to produce fermented foods such as yoghurt, kefir, sauerkraut and kimchi. Lactate can reduce inflammation and help keep the gut cell barrier intact. Some bacterial species can also convert lactate to the short chain fatty acids acetate, propionate and butyrate.

[1] [2]

3-indolepropionic acid (IPA) production

The typical range in healthy people is 0.03% to 2.37%

3-indolepropionic acid (IPA) is a beneficial substance produced by some gut bacteria when they break down the amino acid tryptophan. It is a strong anti-oxidant that can help protect the nervous system from damage. Research has also shown that IPA may play a role in glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.

[1] [2] [3] [4]

Ammonia (urease) production

The typical range in healthy people is 3.3% to 9.95%

Ammonia production is a normal way that bacteria recycle protein in the gut. However, excess ammonia production has been observed in individuals with impaired gut barrier function and inflammation of the gut.

[1] [2]

Histamine production

The typical range in healthy people is 0.06% to 1.88%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.

[1] [2] [3]

B. fragilis toxin production

The typical range in healthy people is 0% to 0.02%

Most people's gut microbiome contain a species of bacteria called *Bacteroides fragilis*. A small proportion of *B. fragilis* strains have the ability to secrete a toxin. In some people this toxin can cause symptoms such as diarrhoea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If you are experiencing diarrhoea and have this toxin, consider seeing a healthcare practitioner.

[1] [2]

Protein degradation

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.

Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.

If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Species

Potential to promote health

Potential to reduce health

Agathobacter faecis

The typical range in healthy people is 0% to 3.05%

Previously named *Roseburia faecis*. This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in patients with liver cirrhosis.
[1] [2] [3]

Agathobacter rectale

The typical range in healthy people is 0% to 5.16%

Previously named *Eubacterium rectale*, this is a common member of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in inflammatory conditions.
[1] [2] [3]

Akkermansia muciniphila

The typical range in healthy people is 0% to 2.17%

This species is associated with a healthy metabolic status and it is being investigated as a probiotic to treat obesity, diabetes and other related metabolic disorders.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
By living in the mucus layer, *A. muciniphila* prevents potentially harmful bacteria from colonising this space through competition. Studies have associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients called PD-1 inhibitors.

Levels of this bacterium tend to decrease with age.

Although this bacterium appears to have mostly beneficial effects, studies have shown elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bilophila wadsworthia

The typical range in healthy people is 0% to 0.28%

This is a common inhabitant of the human gut, but can become problematic at high levels.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Clostridium_M bolteae

The typical range in healthy people is 0% to 0%

This is an inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging research:
Elevated levels of this species has been associated with metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Eggerthella lenta

The typical range in healthy people is 0% to 0.06%

This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, GABA, histamine, lactate, vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium adolescentis

The typical range in healthy people is 0% to 1.54%

This is a common and beneficial inhabitant of the gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), GABA, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Low levels of this species have been associated with inflammation.
[1] [2] [3] [4] [5]

Bifidobacterium animalis

The typical range in healthy people is 0% to 0.2%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis*.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5]

Bifidobacterium bifidum

The typical range in healthy people is 0% to 0%

This is a naturally occurring human gut bacterium and a probiotic. This is one of the first colonisers of the human gut, and is important in the development of the infant immune system.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5]

Fusobacterium nucleatum

The typical range in healthy people is 0% to 0%

Although a common member of the human oral microbiome, this pro-inflammatory bacterium can also be found in the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: 3-IPA, acetate, biotin (B7), butyrate, cobalamin (B12), lactate, propionate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species have been associated with inflammatory conditions and poor gut health. Laboratory-based studies suggest that black and green tea may reduce the growth of this species.
[1] [2] [3] [4] [5] [6] [7] [8]

Peptostreptococcus stomatis

The typical range in healthy people is 0% to 0%

This is an inhabitant of the oral microbiome that can also be found in the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, folate (B9), lactate, propionate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Elevated levels of this species has been associated with poor gut health.
[1] [2] [3] [4] [5] [6] [7]

Bifidobacterium longum

The typical range in healthy people is 0% to 0.82%

This is a beneficial inhabitant of the gut in adults and a popular probiotic.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Coprococcus eutactus

The typical range in healthy people is 0% to 0.33%

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

The typical range in healthy people is 0% to 0.95%

This is an important member of the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species can also use the short chain fatty acid acetate, as well as lactate produced by bacterial species such as *Bifidobacterium spp.* for energy.

One study observed lower levels of this species in patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_C

The typical range in healthy people is 0% to 1.79%

Faecalibacterium prausnitzii_C (aka strain A2-165) is an important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

The typical range in healthy people is 0% to 0.36%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

The typical range in healthy people is 0% to 0.96%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a good degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), beta-glucuronidase, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

The typical range in healthy people is 0% to 0.62%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

The typical range in healthy people is 0% to 0%

This is a common member of the human gut and is considered a keystone species of the gut microbiome for its ability to break down resistant starch.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Gut Mucosal Health

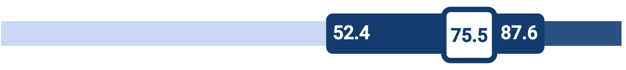
82%

These metabolites and microorganisms have been shown to influence your gut barrier function.

Metabolites

Potential to promote health

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

Lactate production

The typical range in healthy people is 60.08% to 78.47%

Lactate or lactic-acid producing bacteria have a long tradition of beng used to produce fermented foods such as yoghurt, kefir, sauerkraut and kimchi. Lactate can reduce inflammation and help keep the gut cell barrier intact. Some bacterial species can also convert lactate to the short chain fatty acids acetate, propionate and butyrate.
[1] [2]

3-indolepropionic acid (IPA) production

The typical range in healthy people is 0.03% to 2.37%

3-indolepropionic acid (IPA) is a beneficial substance produced by some gut bacteria when they break down the amino acid tryptophan. It is a strong anti-oxidant that can help protect the nervous system from damage. Research has also shown that IPA may play a role in glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.
[1] [2] [3] [4]

Butyrate production

The typical range in healthy people is 12.31% to 23.09%

Butyrate is a short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.
[1] [2] [3] [4] [5] [6] [7] [8]

Potential to reduce health

Hydrogen sulphide production

The typical range in healthy people is 5.09% to 12.06%

The gas hydrogen sulphide is produced by bacteria when they break down sulphur-containing amino acids found in foods such as eggs, meat, and fish. This gas is responsible for the rotten egg smell of flatulence. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. Laboratory based studies have suggested that eating foods high in resistant starch (e.g. lentils, peas, beans, rolled oats and cooked and cooled potatoes) or fructooligosaccharides (FOS) (e.g. onions, garlic, leek, banana, peaches, wheat, barley) can reduce the production of hydrogen sulphide by the microbiome.
[1] [2]

Ammonia (urease) production

The typical range in healthy people is 3.3% to 9.95%

Ammonia production is a normal way that bacteria recycle protein in the gut. However, excess ammonia production has been observed in individuals with impaired gut barrier function and inflammation of the gut.
[1] [2]

Hexa-acylated lipopolysaccharide production

The typical range in healthy people is 0% to 0.65%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.
[1] [2] [3] [4] [5] [6]

Protein degradation

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Human DNA

The typical range in healthy people is 0.03% to 4%

A high amount (greater than 4%) of human DNA may indicate gut inflammation. If there is greater than 4% human DNA, and there was no contamination (e.g. accidentally touched the swab during sampling), further clinical investigation is needed.

B. fragilis toxin production

The typical range in healthy people is 0% to 0.02%

Most people's gut microbiome contain a species of bacteria called *Bacteroides fragilis*. A small proportion of *B. fragilis* strains have the ability to secrete a toxin. In some people this toxin can cause symptoms such as diarrhoea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If you are experiencing diarrhoea and have this toxin, consider seeing a healthcare practitioner.

[1] [2]

Histamine production

The typical range in healthy people is 0.06% to 1.88%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.

[1] [2] [3]

Species

Potential to promote health

Agathobacter faecis

The typical range in healthy people is 0% to 3.05%

Previously named *Roseburia faecis*. This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in patients with liver cirrhosis.

[1] [2] [3]

Agathobacter rectale

The typical range in healthy people is 0% to 5.16%

Previously named *Eubacterium rectale*, this is a common member of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in inflammatory conditions.

[1] [2] [3]

Potential to reduce health

Bilophila wadsworthia

The typical range in healthy people is 0% to 0.28%

This is a common inhabitant of the human gut, but can become problematic at high levels.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.

[1] [2] [3] [4] [5] [6]

Akkermansia muciniphila

The typical range in healthy people is 0% to 2.17%

This species is associated with a healthy metabolic status and it is being investigated as a probiotic to treat obesity, diabetes and other related metabolic disorders.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
By living in the mucus layer, *A. muciniphila* prevents potentially harmful bacteria from colonising this space through competition. Studies have associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients called PD-1 inhibitors.

Levels of this bacterium tend to decrease with age.

Although this bacterium appears to have mostly beneficial effects, studies have shown elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium animalis

The typical range in healthy people is 0% to 0.2%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis*.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5]

Bifidobacterium bifidum

The typical range in healthy people is 0% to 0%

This is a naturally occurring human gut bacterium and a probiotic. This is one of the first colonisers of the human gut, and is important in the development of the infant immune system.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5]

Coprococcus eutactus

The typical range in healthy people is 0% to 0.33%

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

The typical range in healthy people is 0% to 0.95%

This is an important member of the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species can also use the short chain fatty acid acetate, as well as lactate produced by bacterial species such as *Bifidobacterium spp.* for energy.

One study observed lower levels of this species in patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_C

The typical range in healthy people is 0% to 1.79%

Faecalibacterium prausnitzii_C (aka strain A2-165) is an important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

The typical range in healthy people is 0% to 0.36%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

The typical range in healthy people is 0% to 0.96%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a good degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), beta-glucuronidase, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

The typical range in healthy people is 0% to 0.62%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

The typical range in healthy people is 0% to 0%

This is a common member of the human gut and is considered a keystone species of the gut microbiome for its ability to break down resistant starch.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Gut Motility

86%

These metabolites and microorganisms have been shown to influence the rate at which food is moved through the digestive tract, which can impact bowel movement frequency.

Metabolites

Potential to **promote** health

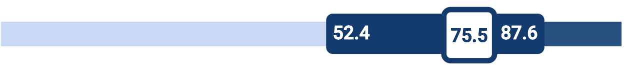
Butyrate production

The typical range in healthy people is 12.31% to 23.09%

Butyrate is a short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.

[1] [2] [3] [4] [5] [6] [7] [8]

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

Propionate production

The typical range in healthy people is 1.66% to 8.66%

Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, and helps control appetite. The prebiotic fibre beta-glucan, found in oats and barley, has been shown to increase propionate production.

[1] [2] [3] [4] [5] [6]

Tyramine production

The typical range in healthy people is 0.04% to 1.25%

Tyramine is a chemical that is produced from the breakdown of the amino acid tyrosine. It occurs naturally in foods such as smoked or aged meats, cheese, and chocolate and is also produced by gut bacteria. Tyramine that you consume in food is absorbed in the small intestine, and foods high in tyramine are thought to trigger migraines in sensitive individuals. In contrast, tyramine produced by your gut microbiota in the large intestine can stimulate serotonin production in the gut. Tyramine is only one of several compounds that can stimulate serotonin production in the gut. Other compounds include butyrate, propionate and vitamin E.

More than 90% of the body's serotonin is produced by cells in the gut, where it plays an important role in many bodily functions such as the immune response, gut motility, bone development, and cardiac function. Only about 10% of the body's serotonin is produced in the brain, where it is used to regulate mood, appetite and sleep. Consuming a sufficient amount of fibre, including fruits and vegetables, can help support serotonin production in your gut.

[1] [2]

Potential to reduce health

Methane production

The typical range in healthy people is 0% to 0.64%

The gas methane can be produced by some species of the gut microbiome, primarily through the reduction of carbon dioxide and hydrogen. Although methane production is often detected in healthy adult populations, elevated levels of methane production has been associated with slower intestinal transit times and constipation.

[1] [2] [3] [4]

Hydrogen sulphide production

The typical range in healthy people is 5.09% to 12.06%

The gas hydrogen sulphide is produced by bacteria when they break down sulphur-containing amino acids found in foods such as eggs, meat, and fish. This gas is responsible for the rotten egg smell of flatulence. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. Laboratory based studies have suggested that eating foods high in resistant starch (e.g. lentils, peas, beans, rolled oats and cooked and cooled potatoes) or fructooligosaccharides (FOS) (e.g. onions, garlic, leek, banana, peaches, wheat, barley) can reduce the production of hydrogen sulphide by the microbiome.

[1] [2]

Protein degradation

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.

Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.

If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Species

Potential to **promote** health

Potential to reduce health

Methanobrevibacter_A smithii

The typical range in healthy people is 0% to 0.54%

This is a single celled organism belonging to the Archaea domain and is the most common archaeal species found in the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, histamine, methane.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
M. smithii plays an important role in the gut because it is one of the few species that can remove excess hydrogen. However, large amounts of this species are not good either, as high levels of methane can promote constipation.
[1] [2] [3] [4] [5]

Bilophila wadsworthia

The typical range in healthy people is 0% to 0.28%

This is a common inhabitant of the human gut, but can become problematic at high levels.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Metabolic Health

90%

These metabolites and microorganisms have been shown to influence how the body metabolises nutrients such as glucose and fats, as well as the health of the circulatory system.

Metabolites

Potential to promote health

Butyrate production

The typical range in healthy people is 12.31% to 23.09%

Butyrate is a short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.

[1] [2] [3] [4] [5] [6] [7] [8]

Propionate production

The typical range in healthy people is 1.66% to 8.66%

Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, and helps control appetite. The prebiotic fibre beta-glucan, found in oats and barley, has been shown to increase propionate production.

[1] [2] [3] [4] [5] [6]

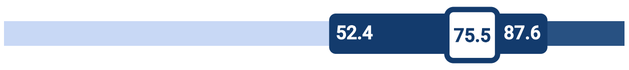
Acetate production

The typical range in healthy people is 62.94% to 76.66%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. Several bacterial species can also convert acetate to the beneficial short chain fatty acid, butyrate. The consumption of wholegrains, fruits, vegetables, legumes, nuts and seeds are associated with increased short chain fatty acids, including acetate.

[1] [2] [3]

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

3-indolepropionic acid (IPA) production

The typical range in healthy people is 0.03% to 2.37%

3-indolepropionic acid (IPA) is a beneficial substance produced by some gut bacteria when they break down the amino acid tryptophan. It is a strong anti-oxidant that can help protect the nervous system from damage. Research has also shown that IPA may play a role in glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.

[1] [2] [3] [4]

Potential to reduce health

Branched chain amino acids production

The typical range in healthy people is 44.8% to 69.94%

Branched chain amino acids (BCAAs) are building blocks for muscles, are involved in the regulation of glucose and fat metabolism, and are involved in the regulation of the immune system. They can be obtained from your diet as well as from your gut microbiome. However, the right amount of BCAAs is important. High levels of BCAAs have been associated with metabolic conditions. Maintaining muscle mass plays an important role in regulating BCAA levels. A study has shown that increased microbial gene abundance for BCAA production correlated with increased BCAA levels in the blood. A high potential to produce BCAAs has also been associated with people who have a diet that is low in fibre. Maximising muscle mass through regular physical activity can help maintain metabolic balance.

[1] [2]

Hexa-acylated lipopolysaccharide production

The typical range in healthy people is 0% to 0.65%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.

[1] [2] [3] [4] [5] [6]

Trimethylamine production

The typical range in healthy people is 1.45% to 4.52%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.

[1] [2] [3] [4] [5] [6] [7]

Succinate production

The typical range in healthy people is 16.98% to 37.45%

Succinate is an important compound involved in glucose and protein metabolism and it is also involved in the production of the short chain fatty acid, propionate. It can be produced by both human cells and the gut microbiome. Although succinate plays many beneficial roles in our body, as with many compounds, too much may not be a good thing. High levels of succinate in the blood have been observed in individuals with obesity, heart disease and type 2 diabetes.

[1] [2]

Folate (B9) production

The typical range in healthy people is 47.1% to 66.6%

Folate or folic acid plays an important role in cell replication and repair and deficiencies can result in an increased risk of of heart disease, anemia, stroke, and neural tube defects in newborn infants. Folate cannot be produced by human cells and must be obtained through diet or from the microbiome. The large intestine has the ability to absorb folate produced by the gut microbiome and it is estimated that the human gut microbiome can provide up to 37% of the daily folate requirement. All non-organic bread in Australia must be fortified with folate while rich dietary sources include dark green leafy vegetables, fruit, legumes, and nuts.
[1] [2] [3]

Species

Potential to promote health

Akkermansia muciniphila

The typical range in healthy people is 0% to 2.17%

This species is associated with a healthy metabolic status and it is being investigated as a probiotic to treat obesity, diabetes and other related metabolic disorders.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
By living in the mucus layer, *A. muciniphila* prevents potentially harmful bacteria from colonising this space through competition. Studies have associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients called PD-1 inhibitors.

Levels of this bacterium tend to decrease with age.

Although this bacterium appears to have mostly beneficial effects, studies have shown elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium adolescentis

The typical range in healthy people is 0% to 1.54%

This is a common and beneficial inhabitant of the gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), GABA, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Low levels of this species have been associated with inflammation.
[1] [2] [3] [4] [5]

Potential to reduce health

Bilophila wadsworthia

The typical range in healthy people is 0% to 0.28%

This is a common inhabitant of the human gut, but can become problematic at high levels.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Eggerthella lenta

The typical range in healthy people is 0% to 0.06%

This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, GABA, histamine, lactate, vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium animalis

The typical range in healthy people is 0% to 0.2%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis*.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5]

Bifidobacterium bifidum

The typical range in healthy people is 0% to 0%

This is a naturally occurring human gut bacterium and a probiotic. This is one of the first colonisers of the human gut, and is important in the development of the infant immune system.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5]

Bifidobacterium longum

The typical range in healthy people is 0% to 0.82%

This is a beneficial inhabitant of the gut in adults and a popular probiotic.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Prevotella copri

The typical range in healthy people is 0% to 14.28%

This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a good degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of some strains within this species have been associated with metabolic and inflammatory conditions.
[1] [2] [3] [4] [5] [6]

Eubacterium_E hallii

The typical range in healthy people is 0% to 0.95%

This is an important member of the gut microbiome.

Fuel Sources Used:

This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:

In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:

This species can also use the short chain fatty acid acetate, as well as lactate produced by bacterial species such as *Bifidobacterium spp.* for energy.

One study observed lower levels of this species in patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_C

The typical range in healthy people is 0% to 1.79%

Faecalibacterium prausnitzii_C (aka strain A2-165) is an important member of the human gut microbiome.

Fuel Sources Used:

This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids.

Metabolites consumed:

In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:

Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

The typical range in healthy people is 0% to 0.36%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:

This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:

Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:

In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:

This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

The typical range in healthy people is 0% to 0.96%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a good degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), beta-glucuronidase, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

The typical range in healthy people is 0% to 0.62%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

The typical range in healthy people is 0% to 0%

This is a common member of the human gut and is considered a keystone species of the gut microbiome for its ability to break down resistant starch.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Nervous System Health

82%

These metabolites and microorganisms have been shown to have a role in regulating the function of the brain and nervous system.

Metabolites

Potential to promote health

3-indolepropionic acid (IPA) production

The typical range in healthy people is 0.03% to 2.37%

3-indolepropionic acid (IPA) is a beneficial substance produced by some gut bacteria when they break down the amino acid tryptophan. It is a strong anti-oxidant that can help protect the nervous system from damage. Research has also shown that IPA may play a role in glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.

[1] [2] [3] [4]

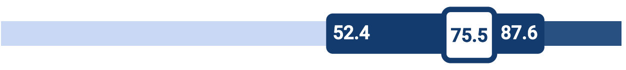
Butyrate production

The typical range in healthy people is 12.31% to 23.09%

Butyrate is a short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.

[1] [2] [3] [4] [5] [6] [7] [8]

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

GABA production

The typical range in healthy people is 8.09% to 32.98%

GABA is short for gamma-butyric acid and is an important signaling molecule for the brain (called a neurotransmitter). GABA's role is to reduce the activity of nerve cells and it is thought to reduce anxiety. GABA is primarily produced by your body, but some bacterial species can also produce (and consume) GABA. It is unknown if bacterially produced GABA can influence nerve cells in humans and this is currently an active area of research. If you are concerned about your mental health, it is important to seek professional help.

[1] [2] [3]

Propionate production

The typical range in healthy people is 1.66% to 8.66%

Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, and helps control appetite. The prebiotic fibre beta-glucan, found in oats and barley, has been shown to increase propionate production.

[1] [2] [3] [4] [5] [6]

Potential to reduce health

Histamine production

The typical range in healthy people is 0.06% to 1.88%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.

[1] [2] [3]

GABA consumption

The typical range in healthy people is 3.57% to 13.71%

GABA is short for gamma-butyric acid and is an important signaling molecule for the brain (called a neurotransmitter). GABA's role is to reduce the activity of nerve cells and it is thought to reduce anxiety. GABA is primarily produced by your body, but some bacterial species can also produce (and consume) GABA. It is unknown if bacterially produced GABA can influence nerve cells in humans and this is currently an active area of research. If you are concerned about your mental health, it is important to seek professional help.

[1] [2] [3]

Hexa-acylated lipopolysaccharide production

The typical range in healthy people is 0% to 0.65%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.

[1] [2] [3] [4] [5] [6]

Trimethylamine production

The typical range in healthy people is 1.45% to 4.52%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.

[1] [2] [3] [4] [5] [6] [7]

Tyramine production

The typical range in healthy people is 0.04% to 1.25%

Tyramine is a chemical that is produced from the breakdown of the amino acid tyrosine. It occurs naturally in foods such as smoked or aged meats, cheese, and chocolate and is also produced by gut bacteria. Tyramine that you consume in food is absorbed in the small intestine, and foods high in tyramine are thought to trigger migraines in sensitive individuals. In contrast, tyramine produced by your gut microbiota in the large intestine can stimulate serotonin production in the gut. Tyramine is only one of several compounds that can stimulate serotonin production in the gut. Other compounds include butyrate, propionate and vitamin E.

More than 90% of the body's serotonin is produced by cells in the gut, where it plays an important role in many bodily functions such as the immune response, gut motility, bone development, and cardiac function. Only about 10% of the body's serotonin is produced in the brain, where it is used to regulate mood, appetite and sleep. Consuming a sufficient amount of fibre, including fruits and vegetables, can help support serotonin production in your gut.
[1] [2]

Folate (B9) production

The typical range in healthy people is 47.1% to 66.6%

Folate or folic acid plays an important role in cell replication and repair and deficiencies can result in an increased risk of of heart disease, anemia, stroke, and neural tube defects in newborn infants. Folate cannot be produced by human cells and must be obtained through diet or from the microbiome. The large intestine has the ability to absorb folate produced by the gut microbiome and it is estimated that the human gut microbiome can provide up to 37% of the daily folate requirement. All non-organic bread in Australia must be fortified with folate while rich dietary sources include dark green leafy vegetables, fruit, legumes, and nuts.
[1] [2] [3]

Immune Health

78%

These metabolites and microorganisms have been shown to be involved in regulating the immune system.

Metabolites

Potential to promote health

Butyrate production

The typical range in healthy people is 12.31% to 23.09%

Butyrate is a short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.

[1] [2] [3] [4] [5] [6] [7] [8]

Propionate production

The typical range in healthy people is 1.66% to 8.66%

Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, and helps control appetite. The prebiotic fibre beta-glucan, found in oats and barley, has been shown to increase propionate production.

[1] [2] [3] [4] [5] [6]

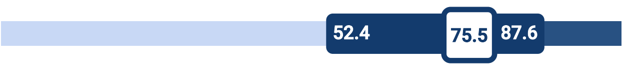
Acetate production

The typical range in healthy people is 62.94% to 76.66%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. Several bacterial species can also convert acetate to the beneficial short chain fatty acid, butyrate. The consumption of wholegrains, fruits, vegetables, legumes, nuts and seeds are associated with increased short chain fatty acids, including acetate.

[1] [2] [3]

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

Folate (B9) production

The typical range in healthy people is 47.1% to 66.6%

Folate or folic acid plays an important role in cell replication and repair and deficiencies can result in an increased risk of of heart disease, anemia, stroke, and neural tube defects in newborn infants. Folate cannot be produced by human cells and must be obtained through diet or from the microbiome. The large intestine has the ability to absorb folate produced by the gut microbiome and it is estimated that the human gut microbiome can provide up to 37% of the daily folate requirement. All non-organic bread in Australia must be fortified with folate while rich dietary sources include dark green leafy vegetables, fruit, legumes, and nuts.

[1] [2] [3]

Potential to reduce health

Hexa-acylated lipopolysaccharide production

The typical range in healthy people is 0% to 0.65%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.

[1] [2] [3] [4] [5] [6]

B. fragilis toxin production

The typical range in healthy people is 0% to 0.02%

Most people's gut microbiome contain a species of bacteria called *Bacteroides fragilis*. A small proportion of *B. fragilis* strains have the ability to secrete a toxin. In some people this toxin can cause symptoms such as diarrhoea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If you are experiencing diarrhoea and have this toxin, consider seeing a healthcare practitioner.

[1] [2]

Histamine production

The typical range in healthy people is 0.06% to 1.88%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.

[1] [2] [3]

Protein degradation

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.

Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.

If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Species

Potential to promote health

Potential to reduce health

Bifidobacterium adolescentis

The typical range in healthy people is 0% to 1.54%

This is a common and beneficial inhabitant of the gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), GABA, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Low levels of this species have been associated with inflammation.
[1] [2] [3] [4] [5]

Bifidobacterium animalis

The typical range in healthy people is 0% to 0.2%

This is a naturally occurring human gut bacterium and probiotic; it is sometimes also called *Bifidobacterium lactis.*

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

Emerging research:
B. animalis is associated with a low BMI and has been used to improve metabolic disorders such as obesity and diabetes. It can also produce antimicrobial substances effective against pathogenic bacteria and studies in mouse models suggest it can improve "leaky gut."
[1] [2] [3] [4] [5]

Bifidobacterium bifidum

The typical range in healthy people is 0% to 0%

This is a naturally occurring human gut bacterium and a probiotic. This is one of the first colonisers of the human gut, and is important in the development of the infant immune system.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5]

Eggerthella lenta

The typical range in healthy people is 0% to 0.06%

This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, GABA, histamine, lactate, vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Fusobacterium nucleatum

The typical range in healthy people is 0% to 0%

Although a common member of the human oral microbiome, this pro-inflammatory bacterium can also be found in the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: 3-IPA, acetate, biotin (B7), butyrate, cobalamin (B12), lactate, propionate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species have been associated with inflammatory conditions and poor gut health. Laboratory-based studies suggest that black and green tea may reduce the growth of this species.
[1] [2] [3] [4] [5] [6] [7] [8]

Bifidobacterium longum

The typical range in healthy people is 0% to 0.82%

This is a beneficial inhabitant of the gut in adults and a popular probiotic.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Coprococcus eutactus

The typical range in healthy people is 0% to 0.33%

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

The typical range in healthy people is 0% to 0.95%

This is an important member of the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species can also use the short chain fatty acid acetate, as well as lactate produced by bacterial species such as *Bifidobacterium spp.* for energy.

One study observed lower levels of this species in patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_H

The typical range in healthy people is 0% to 0%

This is an important member of the gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species can also use branched chain amino acids and the short chain fatty acid acetate for energy.

This species has recently been split into several different species, and low levels of some of these species have been observed in individuals with inflammatory conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia hominis

The typical range in healthy people is 0% to 0.36%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

The typical range in healthy people is 0% to 0.96%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a good degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), beta-glucuronidase, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

The typical range in healthy people is 0% to 0.62%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Inflammatory Balance

86%

These metabolites and microorganisms have been associated with the levels of inflammation in the body.

Metabolites

Potential to promote health

Butyrate production

The typical range in healthy people is 12.31% to 23.09%

Butyrate is a short chain fatty acid that is very important for gut health. It is the main fuel source for gut cells, helps keep the gut cell barrier intact, can reduce inflammation, and helps control appetite. Consuming foods high in resistant starch (e.g. lentils, peas, beans, cooked and cooled potatoes, rolled oats) or pectin (e.g. avocado, kiwifruit, berries, citrus fruits, pumpkin, zucchini) have been shown to increase butyrate levels.
[1] [2] [3] [4] [5] [6] [7] [8]

Propionate production

The typical range in healthy people is 1.66% to 8.66%

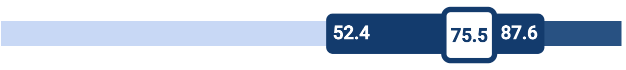
Propionate is a beneficial short chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, and helps control appetite. The prebiotic fibre beta-glucan, found in oats and barley, has been shown to increase propionate production.
[1] [2] [3] [4] [5] [6]

Acetate production

The typical range in healthy people is 62.94% to 76.66%

Acetate is the most abundant short chain fatty acid produced by our gut microbiome. It plays an important role in fat metabolism, glucose metabolism and the immune system. Several bacterial species can also convert acetate to the beneficial short chain fatty acid, butyrate. The consumption of wholegrains, fruits, vegetables, legumes, nuts and seeds are associated with increased short chain fatty acids, including acetate.
[1] [2] [3]

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

Lactate production

The typical range in healthy people is 60.08% to 78.47%

Lactate or lactic-acid producing bacteria have a long tradition of beng used to produce fermented foods such as yoghurt, kefir, sauerkraut and kimchi. Lactate can reduce inflammation and help keep the gut cell barrier intact. Some bacterial species can also convert lactate to the short chain fatty acids acetate, propionate and butyrate.
[1] [2]

3-indolepropionic acid (IPA) production

The typical range in healthy people is 0.03% to 2.37%

3-indolepropionic acid (IPA) is a beneficial substance produced by some gut bacteria when they break down the amino acid tryptophan. It is a strong anti-oxidant that can help protect the nervous system from damage. Research has also shown that IPA may play a role in glucose metabolism and research in animal models suggests that IPA may also play a role in maintaining the gut barrier. IPA is formed by breaking down the amino acid tryptophan. Studies have indicated that consuming foods high in dietary fibre, and in particular rye, can help increase IPA production.
[1] [2] [3] [4]

Potential to reduce health

Hexa-acylated lipopolysaccharide production

The typical range in healthy people is 0% to 0.65%

Hexa-lipopolysaccharide (hexa-LPS) is a pro-inflammatory compound produced by some species of bacteria within the Proteobacteria phylum. High levels of hexa-LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Diets high in fat, especially saturated fat, allow hexa LPS to cross the intestinal barrier and enter the bloodstream. Avoiding excessive intake of saturated fat can help reduce the ability of hexa-LPS to enter the bloodstream.Common dietary sources of saturated fats include butter, coconut products, palm oil, cheese, fatty meats, biscuit, cakes, chocolate and icecream.
[1] [2] [3] [4] [5] [6]

Histamine production

The typical range in healthy people is 0.06% to 1.88%

Histamine is a chemical produced by the breakdown of the amino acid histidine. It is produced by both human cells and some bacterial species and plays an important role in immune regulation, gut function and the nervous system. Individuals with food allergies and irrritable bowel syndrome have been observed to have high levels of specific histamine receptors in the gut, making them more sensitive to histamine in the gut.
[1] [2] [3]

Ammonia (urease) production

The typical range in healthy people is 3.3% to 9.95%

Ammonia production is a normal way that bacteria recycle protein in the gut. However, excess ammonia production has been observed in individuals with impaired gut barrier function and inflammation of the gut.
[1] [2]

Trimethylamine production

The typical range in healthy people is 1.45% to 4.52%

Trimethylamine is a compound produced by some gut microbes that is converted to another compound called trimethylamine-n-oxide (TMAO) in the liver. Increased TMAO levels have been observed in individuals with cardiometabolic and inflammatory disorders. However, the role of TMAO in these disorders is still not clear. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. The indoles diindolylmethane (DIM) and indole-3-carbinol (I3C) found in cruciferous vegetables (e.g. broccoli, cauliflower, cabbage, kale) may reduce the amount of trimethylamine that is converted to TMAO in the liver. In addition, excessive red meat consumption is associated with increased levels of TMAO in the blood. If your potential to produce trimethylamine is high, you may wish to increase your consumption of cruciferous vegetables and avoid eating excessive amounts of red meat.
[1] [2] [3] [4] [5] [6] [7]

Human DNA

The typical range in healthy people is 0.03% to 4%

A high amount (greater than 4%) of human DNA may indicate gut inflammation. If there is greater than 4% human DNA, and there was no contamination (e.g. accidentally touched the swab during sampling), further clinical investigation is needed.

Protein degradation

The typical range in healthy people is 86.24% to 95.05%

A similar or low proportion of species that can break down protein compared to the healthy group is generally considered beneficial. Everyone's microbiome contains species that can break down protein. However, a high proportion of these species may reflect an insufficient amount of fibre in the diet or an excessive intake of protein.
Most protein is absorbed by your body, however excess protein will get passed to the large intestine where it is available to the gut microbiome. Microorganisms that break down protein produce a variety of compounds, including some compounds that promote inflammation.
If there are a high proportion of species that can break down protein in the microbiome, make sure there is sufficient fibre in the diet and consider avoiding excessive consumption of protein.

Hydrogen sulphide production

The typical range in healthy people is 5.09% to 12.06%

The gas hydrogen sulphide is produced by bacteria when they break down sulphur-containing amino acids found in foods such as eggs, meat, and fish. This gas is responsible for the rotten egg smell of flatulence. Hydrogen sulphide plays an important role in gut health by acting as an energy source for gut cells and protecting the gut barrier function. However, some studies have suggested that high levels of hydrogen sulphide can also disrupt the gut mucus barrier. Laboratory based studies have suggested that eating foods high in resistant starch (e.g. lentils, peas, beans, rolled oats and cooked and cooled potatoes) or fructooligosaccharides (FOS) (e.g. onions, garlic, leek, banana, peaches, wheat, barley) can reduce the production of hydrogen sulphide by the microbiome.
[1] [2]

B. fragilis toxin production

The typical range in healthy people is 0% to 0.02%

Most people's gut microbiome contain a species of bacteria called *Bacteroides fragilis*. A small proportion of *B. fragilis* strains have the ability to secrete a toxin. In some people this toxin can cause symptoms such as diarrhoea while other people can remain symptom free. There are concerns that this toxin can cause intestinal inflammation. If you are experiencing diarrhoea and have this toxin, consider seeing a healthcare practitioner.
[1] [2]

Species

Potential to promote health

Agathobacter faecis

The typical range in healthy people is 0% to 3.05%

Previously named *Roseburia faecis*. This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in patients with liver cirrhosis.
[1] [2] [3]

Potential to reduce health

Bilophila wadsworthia

The typical range in healthy people is 0% to 0.28%

This is a common inhabitant of the human gut, but can become problematic at high levels.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), branched chain amino acids, hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species can promote inflammation in the gut and is associated with a diet high in saturated fats.
[1] [2] [3] [4] [5] [6]

Agathobacter rectale

The typical range in healthy people is 0% to 5.16%

Previously named *Eubacterium rectale*, this is a common member of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species is commonly associated with healthy controls in research studies. Low levels of this bacterium have been observed in inflammatory conditions.
[1] [2] [3]

Akkermansia muciniphila

The typical range in healthy people is 0% to 2.17%

This species is associated with a healthy metabolic status and it is being investigated as a probiotic to treat obesity, diabetes and other related metabolic disorders.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
By living in the mucus layer, *A. muciniphila* prevents potentially harmful bacteria from colonising this space through competition. Studies have associated low levels of *A. muciniphila* with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients called PD-1 inhibitors.

Levels of this bacterium tend to decrease with age.

Although this bacterium appears to have mostly beneficial effects, studies have shown elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Bifidobacterium adolescentis

The typical range in healthy people is 0% to 1.54%

This is a common and beneficial inhabitant of the gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), GABA, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Low levels of this species have been associated with inflammation.
[1] [2] [3] [4] [5]

Clostridium_M bolteae

The typical range in healthy people is 0% to 0%

This is an inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging research:
Elevated levels of this species has been associated with metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Eggerthella lenta

The typical range in healthy people is 0% to 0.06%

This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, GABA, histamine, lactate, vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Fusobacterium nucleatum

The typical range in healthy people is 0% to 0%

Although a common member of the human oral microbiome, this pro-inflammatory bacterium can also be found in the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: 3-IPA, acetate, biotin (B7), butyrate, cobalamin (B12), lactate, propionate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species have been associated with inflammatory conditions and poor gut health. Laboratory-based studies suggest that black and green tea may reduce the growth of this species.
[1] [2] [3] [4] [5] [6] [7] [8]

Bifidobacterium longum

The typical range in healthy people is 0% to 0.82%

This is a beneficial inhabitant of the gut in adults and a popular probiotic.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
B.longum has been associated with reductions in harmful bacteria, anti-allergy effects, and anti-obesity effects in mouse models, but further research still needs to be done in humans.
[1] [2] [3] [4] [5] [6] [7]

Coprococcus eutactus

The typical range in healthy people is 0% to 0.33%

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at decreased levels in children with inflammatory conditions.

Eubacterium_E hallii

The typical range in healthy people is 0% to 0.95%

This is an important member of the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species can also use the short chain fatty acid acetate, as well as lactate produced by bacterial species such as *Bifidobacterium spp.* for energy.

One study observed lower levels of this species in patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

Faecalibacterium prausnitzii_C

The typical range in healthy people is 0% to 1.79%

Faecalibacterium prausnitzii_C (aka strain A2-165) is an important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Low levels of *F. prausnitzii* have been associated with inflammatory and metabolic conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10]

Roseburia hominis

The typical range in healthy people is 0% to 0.36%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Roseburia intestinalis

The typical range in healthy people is 0% to 0.96%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a good degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), beta-glucuronidase, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at reduced levels in individuals with metabolic and inflammatory conditions.
[1] [2] [3]

Roseburia inulinivorans

The typical range in healthy people is 0% to 0.62%

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. This species has been observed at reduced levels in individuals with type 2 diabetes.
[1] [2] [3]

Ruminococcus_E bromii

The typical range in healthy people is 0% to 0%

This is a common member of the human gut and is considered a keystone species of the gut microbiome for its ability to break down resistant starch.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Studies suggest the role of *R. bromii* as a primary starch degrader helps stimulate the growth of butyrate-producing bacterial species.
[1] [2] [3]

Detoxification

67%

These markers and microorganism have been shown to influence the rates of inactivation and elimination of drugs and toxins from the body.

Metabolites

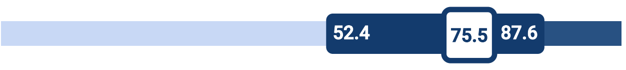
Potential to promote health

Oxalate consumption

The typical range in healthy people is 0.53% to 5.07%

Calcium oxalate is a common component of kidney stones. People who suffer from repeated unexplained kidney stones have been observed to have a reduced level of genes for oxalate degradation in their microbiome compared to healthy people.
[1] [2]

Fibre degradation



The typical range in healthy people is 52.4% to 87.58%

A similar or high proportion of species that can break down fibre compared to the healthy group is considered beneficial. Fibre-consuming bacteria are responsible for producing important by-products such as short chain fatty acids which play a critical role in keeping the gut healthy. Specific prebiotic fibres (detailed in the Microbiome Fuel section below) will promote the growth of beneficial bacteria.

Potential to reduce health

Beta-glucuronidase production

The typical range in healthy people is 8.83% to 27.2%

The human body will process and inactivate drugs and other compounds (hormones, neurotransmitters and environmental toxins) by adding a type of sugar to them called glucuronic acid. However, some bacteria can use this sugar as a fuel source, and they remove the sugar using beta-glucoronidase, thus re-activating the compound. These re-activated compounds can then be re-absorbed into the blood stream, increasing their potency. How increased levels of beta-glucoronidase in the gut influences drug metabolism is an active area of research. One human study has suggested that consuming glucomannan can reduce faecal beta-glucuronidase activity. Glucomannan is a type of prebiotic fibre found in konjac root which is commonly used to make low calorie pasta and noodles.
[1] [2]

Species

Potential to promote health

Oxalobacter formigenes_B

The typical range in healthy people is 0% to 0%

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, folate (B9), GABA, histamine, hydrogen sulphide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA, oxalate.

Potential to reduce health

Eggerthella lenta

The typical range in healthy people is 0% to 0.06%

This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, GABA, histamine, lactate, vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits *E. lenta* from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Microbiome Diversity

Microbial diversity is a measure of the number of different microorganisms and the amount of each of these microorganisms in the sample.

Average to high microbial diversity is associated with good health. A varied diet rich in plant-based foods such as fruits, vegetables, whole grains and nuts can help increase microbiome diversity. The Shannon Index is a measure of diversity which is used by members of the scientific community to compare results through time.

Shannon Diversity Index

Microbiome Composition

Complete Microbiome Profile

Below is a list of each species detected in your microbiome, listed in order of abundance. Click on any species name to learn more about that species. Some microbes have been associated with health outcomes in scientific studies, while for others, little is known about them.

Everybody's microbiome composition is different, and science is telling us that the functional capacity of the microbiome is more important than which species inhabit it.

✚ *Species with this symbol beside the table have been implicated in influencing health.*

	Phylum	Species	Abundance ▲	Range	Level	
✚	Bacteroidota	*Bacteroides_B dorei*	11.64%	0.00% - 4.65%	High	▼
✚	Verrucomicrobiota	*Akkermansia muciniphila*	5.76%	0.00% - 2.17%	High	▼
✚	Bacteroidota	*Bacteroides uniformis*	4.66%	0.23% - 8.23%	Average	▼
✚	Bacteroidota	*Alistipes finegoldii*	4.01%	0.00% - 0.80%	High	▼
	Firmicutes_A	*Lachnospira eligens_B*	3.96%	0.00% - 1.80%	High	▼
	Firmicutes_A	*Gemmiger formicilis*	3.32%	0.00% - 1.66%	High	▼
	Bacteroidota	*Bacteroides clarus*	2.87%	0.00% - 0.36%	High	▼
	Firmicutes_A	*Lachnospira sp900316325*	2.36%	0.00% - 0.66%	High	▼
	Firmicutes_A	*KLE1615 sp900066985*	1.73%	0.08% - 0.99%	High	▼
	Bacteroidota	*Bacteroidaceae MIC8659*	1.63%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Faecalibacterium MIC7145*	1.60%	0.00% - 1.31%	High	▼
	Bacteroidota	*Bacteroides thetaiotaomicron*	1.59%	0.00% - 0.78%	High	▼
✚	Firmicutes_A	*Anaerostipes hadrus*	1.59%	0.15% - 2.67%	Average	▼
	Firmicutes_A	*Faecalibacterium prausnitzii_D*	1.58%	0.00% - 1.44%	High	▼
	Firmicutes_A	*CAG-269 sp001916005*	1.55%	0.00% - 0.08%	High	▼
✚	Bacteroidota	*Alistipes shahii*	1.52%	0.00% - 1.00%	High	▼
	Proteobacteria	*Sutterella wadsworthensis_B*	1.47%	0.00% - 0.90%	High	▼
✚	Bacteroidota	*Bacteroides_B vulgatus*	1.30%	0.00% - 10.36%	Average	▼
	Firmicutes_A	*Blautia_A massiliensis*	1.17%	0.00% - 0.75%	High	▼
✚	Bacteroidota	*Odoribacter splanchnicus*	1.13%	0.03% - 0.38%	High	▼
	Bacteroidota	*Bacteroides xylanisolvens*	1.12%	0.00% - 0.73%	High	▼
	Firmicutes_A	*UBA1691 MIC9536*	1.10%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Faecalibacterium prausnitzii_I*	1.10%	0.00% - 0.44%	High	▼
	Firmicutes	*CAG-302 sp000431795*	1.09%	0.00% - 0.20%	High	▼
	Firmicutes_A	*Blautia_A sp900066165*	1.04%	0.08% - 1.00%	High	▼
	Firmicutes_A	*Blautia_A sp000436615*	1.00%	0.00% - 0.75%	High	▼
	Firmicutes_A	*CAG-269 sp003525075*	0.98%	0.00% - 0.33%	High	▼

	Firmicutes_A	*Acutalibacteraceae MIC7363*	0.97%	0.00% - 0.00%	High	▼
	Firmicutes_A	*CAG-274 MIC9410*	0.82%	0.00% - 0.00%	High	▼
✚	Bacteroidota	*Bacteroides fragilis*	0.74%	0.00% - 0.55%	High	▼
	Firmicutes_A	*CAG-303 sp000437755*	0.74%	0.00% - 0.51%	High	▼
	Firmicutes	*CAG-1000 MIC8243*	0.71%	0.00% - 0.03%	High	▼
✚	Bacteroidota	*Parabacteroides distasonis*	0.56%	0.00% - 0.88%	Average	▼
	Firmicutes_C	*Phascolarctobacterium faecium*	0.56%	0.00% - 0.55%	High	▼
	Firmicutes_A	*UBA9502 MIC9781*	0.51%	0.00% - 0.02%	High	▼
	Firmicutes_A	*Agathobaculum butyriciproducens*	0.49%	0.00% - 0.49%	High	▼
	Firmicutes_A	*CAG-83 MIC8731*	0.43%	0.00% - 0.26%	High	▼
	Firmicutes	*UBA3631 MIC8443*	0.41%	0.00% - 0.00%	High	▼
✚	Bacteroidota	*Bacteroides cellulosilyticus*	0.41%	0.00% - 1.60%	Average	▼
	Bacteroidota	*Parabacteroides MIC7664*	0.39%	0.00% - 0.00%	High	▼
	Firmicutes_A	*ER4 sp900317525*	0.39%	0.00% - 0.56%	Average	▼
	Firmicutes	*Erysipelatoclostridium sp000752095*	0.36%	0.00% - 0.54%	Average	▼
✚	Firmicutes_A	*Ruminiclostridium_E siraeum*	0.35%	0.00% - 1.72%	Average	▼
	Proteobacteria	*CAG-267 sp001917135*	0.33%	0.00% - 0.77%	Average	▼
	Firmicutes_A	*Blautia sp000436935*	0.32%	0.00% - 0.37%	Average	▼
	Firmicutes_A	*Fournierella massiliensis*	0.31%	0.00% - 0.00%	High	▼
	Bacteroidota	*Bacteroides intestinalis*	0.28%	0.00% - 0.12%	High	▼
	Firmicutes_A	*Faecalibacterium prausnitzii_G*	0.28%	0.00% - 2.21%	Average	▼
	Firmicutes_A	*Lachnospiraceae MIC9280*	0.28%	0.00% - 0.08%	High	▼
✚	Firmicutes_A	*Fusicatenibacter saccharivorans*	0.25%	0.26% - 3.69%	Low	▼
	Firmicutes_A	*Oscillibacter sp900066435*	0.24%	0.00% - 0.17%	High	▼
	Bacteroidota	*Butyricimonas sp002161485*	0.24%	0.00% - 0.14%	High	▼
✚	Firmicutes_A	*Eubacterium_E hallii*	0.23%	0.00% - 0.95%	Average	▼
	Firmicutes_A	*CAG-74 MIC7103*	0.22%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Oscillibacter sp001916835*	0.22%	0.00% - 0.55%	Average	▼
	Firmicutes_A	*Ruminococcus_A sp000437095*	0.22%	0.00% - 0.14%	High	▼
	Firmicutes_A	*Acetatifactor sp003447295*	0.22%	0.00% - 0.05%	High	▼
	Firmicutes_A	*Hungatella_A MIC8772*	0.21%	0.00% - 0.08%	High	▼
✚	Bacteroidota	*Alistipes senegalensis*	0.21%	0.00% - 0.19%	High	▼
	Firmicutes_A	*TF01-11 sp003529475*	0.20%	0.00% - 0.35%	Average	▼
✚	Actinobacteriota	*Eggerthella lenta*	0.20%	0.00% - 0.06%	High	▼
✚	Firmicutes_A	*Ruminococcus_B gnavus*	0.19%	0.00% - 0.05%	High	▼
	Bacteroidota	*Bacteroides MIC8726*	0.18%	0.00% - 0.03%	High	▼
	Firmicutes	*CAG-313 sp000433035*	0.17%	0.00% - 0.26%	Average	▼

	Firmicutes_A	*CAG-110 sp000435995*	0.17%	0.00% - 0.22%	Average	▼
	Firmicutes_A	*CAG-917 MIC9678*	0.16%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UBA1685 sp002320595*	0.16%	0.00% - 0.02%	High	▼
	Firmicutes_A	*UBA7096 MIC8091*	0.15%	0.00% - 0.00%	High	▼
✚	Proteobacteria	*Escherichia coli*	0.15%	0.00% - 0.04%	High	▼
	Firmicutes_A	*Ruminiclostridium_C sp000435295*	0.15%	0.00% - 0.23%	Average	▼
	Firmicutes_A	*Ruminococcaceae MIC8509*	0.15%	0.00% - 0.06%	High	▼
✚	Firmicutes_A	*Intestinimonas butyriciproducens*	0.15%	0.00% - 0.01%	High	▼
	Firmicutes	*CAG-877 MIC8866*	0.15%	0.00% - 0.00%	High	▼
	Bacteroidota	*Bacteroides nordii*	0.14%	0.00% - 0.08%	High	▼
	Firmicutes_A	*Acutalibacteraceae MIC7526*	0.14%	0.00% - 0.03%	High	▼
	Firmicutes_A	*Ruthenibacterium lactatiformans*	0.14%	0.00% - 0.10%	High	▼
	Firmicutes_A	*GCA-900066575 MIC7948*	0.13%	0.00% - 0.10%	High	▼
	Firmicutes	*Erysipelatoclostridium sp000508865*	0.13%	0.00% - 0.01%	High	▼
✚	Firmicutes_A	*Dorea longicatena_B*	0.13%	0.00% - 0.37%	Average	▼
	Firmicutes_A	*Fournierella MIC7311*	0.13%	0.00% - 0.00%	High	▼
	Bacteroidota	*Butyricimonas sp900184685*	0.12%	0.00% - 0.00%	High	▼
✚	Firmicutes_A	*Faecalicatena lactaris*	0.12%	0.00% - 0.55%	Average	▼
✚	Firmicutes_A	*Roseburia hominis*	0.12%	0.00% - 0.36%	Average	▼
	Firmicutes_A	*Lawsonibacter asaccharolyticus*	0.11%	0.00% - 0.15%	Average	▼
	Firmicutes_A	*Clostridium_M sp000431375*	0.11%	0.00% - 0.16%	Average	▼
	Firmicutes_A	*CAG-110 sp003525905*	0.11%	0.00% - 0.28%	Average	▼
	Firmicutes_A	*Blautia_A sp900066145*	0.11%	0.00% - 0.20%	Average	▼
	Firmicutes_A	*Faecalicatena faecis*	0.10%	0.00% - 0.69%	Average	▼
	Firmicutes	*CAG-631 MIC9494*	0.10%	0.00% - 0.00%	High	▼
	Bacteroidota	*Parabacteroides gordonii*	0.10%	0.00% - 0.00%	High	▼
	Firmicutes	*CAG-776 sp000438195*	0.10%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Blautia_A wexlerae*	0.09%	0.15% - 2.79%	Low	▼
✚	Firmicutes_A	*Dorea formicigenerans*	0.09%	0.05% - 0.21%	Average	▼
	Firmicutes_A	*Dorea sp900066765*	0.08%	0.00% - 0.03%	High	▼
✚	Firmicutes_A	*Coprococcus_B comes*	0.08%	0.05% - 0.44%	Average	▼
	Firmicutes_A	*Acutalibacteraceae MIC6974*	0.08%	0.00% - 0.06%	High	▼
	Firmicutes_A	*CAG-81 sp900066785*	0.08%	0.00% - 0.14%	Average	▼
	Firmicutes_A	*UBA7160 MIC9207*	0.08%	0.00% - 0.09%	Average	▼
	Firmicutes_A	*CAG-273 sp000438355*	0.08%	0.00% - 0.04%	High	▼
	Firmicutes_A	*Anaerotignum sp000436415*	0.07%	0.00% - 0.15%	Average	▼
	Firmicutes_A	*Lawsonibacter sp900066825*	0.07%	0.00% - 0.03%	High	▼

	Firmicutes_A	*Oscillospiraceae MIC9482*	0.07%	0.00% - 0.03%	High	▼
	Firmicutes_A	*QALS01 MIC9566*	0.07%	0.00% - 0.05%	High	▼
	Firmicutes_A	*Acutalibacteraceae MIC7956*	0.07%	0.00% - 0.00%	High	▼
	Firmicutes_A	*GCA-900066135 MIC6659*	0.07%	0.00% - 0.13%	Average	▼
	Firmicutes_A	*Acetatifactor MIC6457*	0.07%	0.00% - 0.04%	High	▼
	Firmicutes_A	*Acetatifactor sp900066565*	0.07%	0.00% - 1.89%	Average	▼
	Firmicutes_A	*CAG-138 MIC9630*	0.07%	0.00% - 0.47%	Average	▼
➕	Firmicutes_A	*Coprococcus_A catus*	0.06%	0.00% - 0.22%	Average	▼
	Actinobacteriota	*Adlercreutzia equolifaciens*	0.06%	0.00% - 0.11%	Average	▼
➕	Firmicutes_A	*Pseudoflavonifractor capillosus*	0.06%	0.00% - 0.00%	High	▼
	Firmicutes_A	*CAG-170 sp002404795*	0.06%	0.00% - 0.31%	Average	▼
	Firmicutes_A	*CAG-74 MIC9837*	0.06%	0.00% - 0.05%	High	▼
	Firmicutes_A	*UBA1255 MIC8514*	0.06%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Lawsonibacter sp900066645*	0.06%	0.00% - 0.03%	High	▼
	Firmicutes_A	*Agathobacter MIC6372*	0.06%	0.00% - 0.19%	Average	▼
	Firmicutes_A	*CAG-727 MIC8506*	0.06%	0.00% - 0.05%	High	▼
	Firmicutes_A	*CAG-145 MIC8493*	0.06%	0.00% - 0.04%	High	▼
	Firmicutes_A	*CAG-552 MIC6484*	0.05%	0.00% - 0.00%	High	▼
	Firmicutes_A	*QALS01 sp003150575*	0.05%	0.00% - 0.11%	Average	▼
	Firmicutes_A	*UBA10677 MIC8686*	0.05%	0.00% - 0.00%	High	▼
	Firmicutes_A	*CAG-727 MIC7825*	0.05%	0.00% - 0.07%	Average	▼
	Firmicutes_A	*Acutalibacteraceae MIC7795*	0.05%	0.00% - 0.04%	High	▼
	Firmicutes_A	*Dorea sp900066555*	0.05%	0.00% - 0.06%	Average	▼
	Firmicutes_A	*Oscillospiraceae MIC9607*	0.04%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UBA7182 MIC8257*	0.04%	0.00% - 0.03%	High	▼
	Firmicutes_B	*UBA7185 sp002491065*	0.04%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Acutalibacteraceae MIC7081*	0.04%	0.00% - 0.00%	High	▼
➕	Bacteroidota	*Prevotella disiens*	0.04%	0.00% - 0.01%	High	▼
	Firmicutes_A	*Flavonifractor MIC8104*	0.04%	0.00% - 0.04%	High	▼
	Firmicutes_A	*Faecalicatena glycyrrhizinilyticum*	0.04%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UBA9502 MIC8595*	0.04%	0.00% - 0.00%	High	▼
	Firmicutes_A	*CAG-273 MIC8467*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Pseudoflavonifractor MIC6616*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes	*Holdemania massiliensis*	0.03%	0.00% - 0.00%	High	▼
	Bacteroidota	*Bacteroides MIC7427*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Flavonifractor sp000508885*	0.03%	0.00% - 0.02%	High	▼
	Firmicutes_A	*CAG-41 sp900066215*	0.03%	0.00% - 0.48%	Average	▼

	Firmicutes_A	*UBA1777 MIC7283*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes	*Dielma fastidiosa*	0.03%	0.00% - 0.00%	High	▼
⊕	Firmicutes_A	*Clostridium_Q symbiosum*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Marvinbryantia MIC7005*	0.03%	0.00% - 0.00%	High	▼
	Bacteroidota	*Bacteroides bouchesdurhonensis*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Oscillibacter MIC8850*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes	*Stoquefichus sp001244545*	0.03%	0.00% - 0.00%	High	▼
	Proteobacteria	*Comamonas kerstersii*	0.03%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UBA7182 MIC8422*	0.03%	0.00% - 0.07%	Average	▼
	Firmicutes_A	*CAG-269 sp001915995*	0.02%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Lachnobacterium MIC8093*	0.02%	0.00% - 0.00%	High	▼
	Proteobacteria	*Parasutterella excrementihominis*	0.02%	0.00% - 0.67%	Average	▼
	Firmicutes_A	*UBA1191 MIC6519*	0.02%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Anaerovoracaceae MIC7478*	0.02%	0.00% - 0.04%	Average	▼
	Firmicutes_A	*Oscillibacter MIC7169*	0.02%	0.00% - 0.02%	Average	▼
	Firmicutes_A	*CAG-145 MIC9484*	0.02%	0.00% - 0.00%	High	▼
	Firmicutes	*Holdemania filiformis*	0.02%	0.00% - 0.00%	High	▼
	Bacteroidota	*Prevotella bivia*	0.02%	0.00% - 0.00%	High	▼
	Actinobacteriota	*Gordonibacter pamelaeae*	0.02%	0.00% - 0.02%	Average	▼
⊕	Firmicutes_A	*Clostridium_M citroniae*	0.02%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Lachnospiraceae MIC8643*	0.02%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UBA1191 MIC6632*	0.02%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Lawsonibacter MIC8807*	0.02%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UCG-010 MIC9407*	0.02%	0.00% - 0.00%	High	▼
	Bacteroidota	*Prevotella colorans*	0.01%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UBA3818 MIC8425*	0.01%	0.00% - 0.05%	Average	▼
	Firmicutes_A	*UBA9502 MIC7609*	0.01%	0.00% - 0.00%	High	▼
	Firmicutes_A	*An200 sp003268275*	0.01%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Fournierella MIC7807*	0.01%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UC5-1-2E3 sp001304875*	0.01%	0.00% - 0.00%	High	▼

Health Associated Species

Below is a list of all species detected in the sample that have been implicated in influencing health.

	Phylum	Species	Abundance ^	Range	Level	

✚	Bacteroidota	*Bacteroides_B dorei*	11.64%	0.00% - 4.65%	High	▼

This is a common inhabitant of the gut and is closely related to Bacteroides vulgatus.

Fuel Sources Used:
This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging research:
High levels of this species have been associated with poor gut health and autoimmune conditions in children. This species has also been associated with diets high in red meat.
[1] [2] [3] [4] [5] [6]

✚	Verrucomicrobiota	*Akkermansia muciniphila*	5.76%	0.00% - 2.17%	High	▼

This species is associated with a healthy metabolic status and it is being investigated as a probiotic to treat obesity, diabetes and other related metabolic disorders.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
By living in the mucus layer, A. muciniphila prevents potentially harmful bacteria from colonising this space through competition. Studies have associated low levels of A. muciniphila with metabolic conditions. Research has also indicated this species can improve the efficacy of a common immunotherapy drug used in cancer patients called PD-1 inhibitors.

Levels of this bacterium tend to decrease with age.

Although this bacterium appears to have mostly beneficial effects, studies have shown elevated levels are associated with neurodegenerative conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

✚	Bacteroidota	*Bacteroides uniformis*	4.66%	0.23% - 8.23%	Average	▼

This is one of the most common inhabitants of the human gut.

Fuel Sources Used:
This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Certain strains have been observed to promote the production of anti-inflammatory compounds, improve immune function, and provide protection against diet induced obesity in mouse models, however this has not yet been validated in humans. One study observed higher levels of this species in patients with inflammatory conditions.
[1] [2] [3] [4] [5]

✚	Bacteroidota	*Alistipes finegoldii*	4.01%	0.00% - 0.80%	High	▼

This is a common inhabitant of the gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: ammonia (urease), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
High levels of this species have been associated with poor gut health and a diet high in red meat and/or low in fruits and vegetables.
[1] [2] [3] [4]

✚	Firmicutes_A	*Anaerostipes hadrus*	1.59%	0.15% - 2.67%	Average	▼

Formerly known as Eubacterium hadrum. This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.
[1] [2]

✚	Bacteroidota	*Alistipes shahii*	1.52%	0.00% - 1.00%	High	▼

This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: beta-glucuronidase, branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species appears to have mostly beneficial effects. It has been associated with beneficial markers of cardiac health, and a study in mice showed this species may improve the efficacy of immunotherapy. However, high levels of this species have also been observed in motorneuron conditions.
[1] [2] [3] [4] [5] [6] [7] [8]

✚	Bacteroidota	*Bacteroides_B vulgatus*	1.30%	0.00% - 10.36%	Average	▼

This is one of the most common inhabitants of the human gut.

Fuel Sources Used:
This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging research:
High levels of this bacterium have been associated with metabolic and inflammatory conditions. This species has also been associated with a diet high in red meat.
[1] [2] [3] [4] [5] [6] [7] [8]

✚	Bacteroidota	*Odoribacter splanchnicus*	1.13%	0.03% - 0.38%	High	▼

Formerly known as Bacteroides splanchnicus. This a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), biotin (B7), branched chain amino acids, butyrate, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging research:
Lower levels of this species have been observed in postmenopausal obese women with insulin resistance, patients with irritable bowel syndrome and in women with bladder pain syndrome, indicating it likely plays a beneficial role in health.
[1] [2] [3] [4] [5]

✚	Bacteroidota	*Bacteroides fragilis*	0.74%	0.00% - 0.55%	High	▼

This is a normal inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, folate (B9), GABA, histamine, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has two different forms: a non-toxic form and a toxin-producing form. The majority of B. fragilis strains found in the gut microbiome are of the non-toxic form and have been shown to have a beneficial effect on the immune system by promoting the production of anticancer T cells. Additionally, some studies have shown it is depleted in children with autism. The toxin-producing form is much less common, but has been correlated with diarrhea and inflammation. This species can also become an opportunistic pathogen if it manages to infiltrate the gut wall and enter the body cavity (e.g. through surgery).
[1] [2] [3] [4] [5] [6]

✚	Bacteroidota	*Parabacteroides distasonis*	0.56%	0.00% - 0.88%	Average	▼

Formerly known as Bacteroides distasonis. This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.

Emerging research:
High levels of this species have been associated with poor gut health and metabolic conditions in pregnant women.
[1] [2] [3] [4] [5] [6]

✚	Bacteroidota	*Bacteroides cellulosilyticus*	0.41%	0.00% - 1.60%	Average	▼

This is a common gut inhabitant.

Fuel Sources Used:
This species is a good degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2] [3] [4] [5]

✚	Firmicutes_A	*Ruminiclostridium_E siraeum*	0.35%	0.00% - 1.72%	Average	▼

Formerly known as Eubacterium siraeum. This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, folate (B9).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species was observed at lower levels in individuals with type 2 diabetes, insulin resistance, and inflammatory conditions, suggesting it likely plays a beneficial role in health.
[1] [2] [3] [4]

✚	Firmicutes_A	*Fusicatenibacter saccharivorans*	0.25%	0.26% - 3.69%	Low	▼

This is a recently discovered species and an inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, ammonia (urease), beta-glucuronidase, branched chain amino acids, cobalamin (B12), folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.
[1] [2]

✚	Firmicutes_A	*Eubacterium_E hallii*	0.23%	0.00% - 0.95%	Average	▼

This is an important member of the gut microbiome.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species can also use the short chain fatty acid acetate, as well as lactate produced by bacterial species such as Bifidobacterium spp. for energy.

One study observed lower levels of this species in patients with intestinal disorders. Also, a study in mice suggested this species may be effective at improving insulin sensitivity.
[1] [2] [3] [4] [5]

✚	Bacteroidota	*Alistipes senegalensis*	0.21%	0.00% - 0.19%	High	▼

This is a newly discovered inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a good degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: ammonia (urease), beta-glucuronidase, branched chain amino acids, folate (B9), GABA, lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
A high BMI has been associated with a low abundance of this species. Lower levels of this species have also been observed in individuals with irritable bowel syndrome, suggesting it may play a beneficial role in health.
[1] [2] [3] [4]

⊕	Actinobacteriota	*Eggerthella lenta*	0.20%	0.00% - 0.06%	High	▼

This is an inhabitant of the gut microbiota, but has also been associated with gastrointestinal infections.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, GABA, histamine, lactate, vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Elevated levels of this species have been associated with cardiovascular and metabolic conditions. This species can also inactivate the cardiac drug digoxin by breaking it down. Interestingly, this species prefers the amino acid arginine for growth. When arginine is present, this inhibits E. lenta from breaking down digoxin.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

⊕	Firmicutes_A	*Ruminococcus_B gnavus*	0.19%	0.00% - 0.05%	High	▼

This species is one of the earliest colonisers of the infant human gut, and it persists in the adult human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, propionate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Higher levels of this species have been observed in individuals with inflammatory conditions.
[1] [2] [3] [4] [5] [6] [7] [8] [9] [10] [11] [12]

⊕	Proteobacteria	*Escherichia coli*	0.15%	0.00% - 0.04%	High	▼

This species is a common inhabitant of the gut, although it is usually present at a low abundance compared to other gut microbiome species.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, biotin (B7), branched chain amino acids, folate (B9), GABA, hexa-LPS, hydrogen sulphide, lactate, propionate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA, oxalate.

Emerging research:
The harmful strains can produce pro-inflammatory compounds, and toxins that cause infection and diarrhea.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

⊕	Firmicutes_A	*Intestinimonas butyriciproducens*	0.15%	0.00% - 0.01%	High	▼

This is a recently discovered species that can be found in the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), lactate, propionate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Reduced levels have been observed in individuals with inflammatory conditions, suggesting it likely plays a beneficial role in health.
[1] [2] [3]

⊕	Firmicutes_A	*Dorea longicatena_B*	0.13%	0.00% - 0.37%	Average	▼

This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Multiple studies have observed this species at higher levels in individuals with obesity comapred to lean controls. However in obese, postmenopausal women, this species was associated with improved insulin sensitivity. This species has also been observed at lower levels in individuals with inflammatory conditions.
[1] [2] [3] [4] [5] [6] [7] [8]

Firmicutes_A	*Faecalicatena lactaris*	0.12%	0.00% - 0.55%	Average

Previously called Ruminococcus lactaris, this is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a moderate degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at lower levels in individuals with inflammatory conditions. However, despite the likely beneficial role of this species, one study did observe this species at higher levels in patients with rheumatoid arthritis.
[1] [2] [3] [4]

Firmicutes_A	*Roseburia hominis*	0.12%	0.00% - 0.36%	Average

This is a common and important member of the human gut microbiome.

Fuel Sources Used:
This species is a moderate degrader of fibre, mucin, and protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, butyrate, folate (B9), hydrogen sulphide, lactate.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This is a primary producer of the beneficial short chain fatty acid butyrate. Lower levels of this species have been observed in patients with inflammatory conditions. Another study observed higher levels in active women compared to sedentary women. Laboratory studies suggest this species can help regulate the immune system and reduce inflammation.
[1] [2] [3] [4] [5] [6] [7] [8] [9]

Firmicutes_A	*Dorea formicigenerans*	0.09%	0.05% - 0.21%	Average

Formerly known as Eubacterium formicgenerans. This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species has been observed at decreased levels in individuals with inflammatory conditions, indicating it likely plays a beneficial role in health.
[1] [2] [3] [4] [5] [6]

Firmicutes_A	*Coprococcus_B comes*	0.08%	0.05% - 0.44%	Average

This is a common inhabitant of the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, butyrate, cobalamin (B12), folate (B9), lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
This species likely plays a beneficial role in health as it has been observed at decreased levels in individuals with inflammatory conditions.
[1] [2] [3] [4] [5] [6] [7]

Firmicutes_A	*Coprococcus_A catus*	0.06%	0.00% - 0.22%	Average

This is an inhabitant of the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), folate (B9), lactate, propionate, riboflavin (B2).

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
Its name catus comes from the Latin word for "clever," referring to its unusual property of some strains being able to produce large amounts of butyrate and propionate.
[1] [2]

✚	Firmicutes_A	*Pseudoflavonifractor capillosus*	0.06%	0.00% - 0.00%	High	▼

Formerly known as Bacteroides capillosus. This is an inhabitant of the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, branched chain amino acids, cobalamin (B12), lactate.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA.
[1] [2] [3]

✚	Bacteroidota	*Prevotella disiens*	0.04%	0.00% - 0.01%	High	▼

This is an inhabitant of the oral microbiome and can also be found in the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, folate (B9), lactate, riboflavin (B2), vitamin K.

Metabolites consumed:
In addition, the genomic analysis indicates that most members of this species do not consume any reported metabolites.

Emerging research:
One study observed higher levels of this species in patients with rheumatoid arthritis.
[1] [2] [3]

✚	Firmicutes_A	*Clostridium_Q symbiosum*	0.03%	0.00% - 0.00%	High	▼

This is an inhabitant of the human gut.

Fuel Sources Used:
This species is a poor degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, biotin (B7), branched chain amino acids, butyrate, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, propionate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: GABA, oxalate.

Emerging research:
This species has been observed at high levels in individuals with metabolic and poor gut health.
[1] [2] [3] [4] [5] [6] [7] [8]

✚	Firmicutes_A	*Clostridium_M citroniae*	0.02%	0.00% - 0.00%	High	▼

This species can be found in the human gut.

Fuel Sources Used:
This species is a moderate degrader of fibre, a poor degrader of mucin, and a moderate degrader of protein.

Metabolites produced:
Our genomic analysis indicates that most members of this species can produce the following metabolites: acetate, beta-glucuronidase, branched chain amino acids, cobalamin (B12), folate (B9), hydrogen sulphide, lactate, riboflavin (B2), trimethylamine.

Metabolites consumed:
In addition, the genomic analysis shows that most members of this species can consume: oxalate.

Emerging research:
This species has been observed at higher levels in individuals with inflammatory conditions.
[1] [2] [3] [4]