MetaBiome™ Score

70

0   100
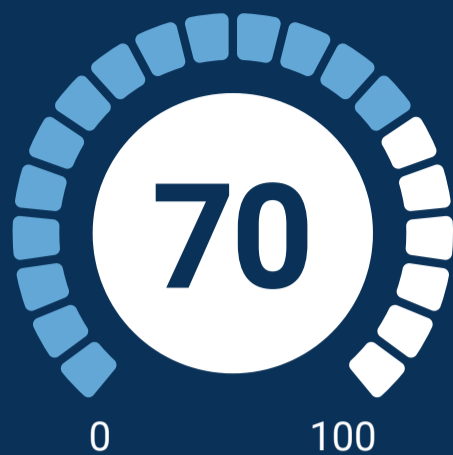
MetaBiome™ Report

Report issue date
29/07/2019

Sample ID
BBC9530

This score is an indication of your overall gut health, based on the eleven categories listed below. These are key indicators of gut health, and their contributions to the MetaBiome score are weighted based on the scientific evidence showing the level of influence each one has shown to have on our health. The healthy comparison range for the MetaBiome™ Score is 70-98

MetaBiome™ Score Contributors

Potential to **promote** health

Butyrate production

10.3   18.4   27.7

The typical range in healthy people is 10.32% to 27.71%
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, help control appetite, and stimulate the production of serotonin from our gut cells. Consuming foods high in resistant starch (e.g. lentils, peas, beans, rolled oats) has been shown to increase butyrate levels.

Propionate production

22.5   43.6 9.8

The typical range in healthy people is 22.46% to 49.77%
Propionate is a short-chain fatty acid that is important for gut health. It helps maintain blood glucose levels, can reduce inflammation, helps control appetite and can stimulate the production of serotonin. The consumption of fibre from foods such as fruits, vegetables, legumes and grains are associated with increased short-chain fatty acids including propionate.

Acetate production

48.4   65.7

The typical range in healthy people is 48.41% to 69.81%
Acetate is the most abundant short-chain fatty acid produced in the gut. It plays an important role in fat metabolism, glucose metabolism and the immune system. Several bacterial species can also convert acetate to butyrate. The consumption of fruits, vegetables, legumes and fibre are associated with increased short-chain fatty acids, including acetate.

Fibre degradation

55.2   68.6

The typical range in healthy people is 55.22% to 71.8%
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.

Microbial Diversity

3.1 3.5   4.2

The typical range in healthy people is 3.14% to 4.15%
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.

Potential to **reduce** health

Hexa-acylated Lipopolysaccharide

0   0.73   14.4

The typical range in healthy people is 0% to 0.73%
Lipopolysaccharides (LPS) are an important component of the cell wall of many bacteria, but when these bacteria die, the LPS is released into the gut where it can be pro-inflammatory, in particular hexa LPS. Diets high in fat, especially saturated fat, allow LPS to cross the intestinal barrier and enter the bloodstream. High levels of LPS in the blood have been observed in individuals with metabolic and inflammatory conditions. Avoiding excessive intake of saturated fat can help reduce the ability of LPS to enter the bloodstream.

Trimethylamine production

0   0.2   1.1

The typical range in healthy people is 0% to 0.2%
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 disorders. However, the role of TMAO in these disorders is still not clear. It is unknown if TMAO plays a causal role, is a marker of the disorder, or if it plays a protective role in repairing damage from the disorder. Levels of TMAO are influenced by many factors including our gut microbiome, diet, integrity of the gut barrier, liver function and kidney function. Although diet may only play a small role, diets high in animal protein containing choline and carnitine (e.g. eggs, red meat), as well as salt, have been associated with increased TMAO levels while diets high in soluble fibre have been shown to reduce trimethylamine and TMAO levels. If your potential to produce trimethylamine is high, you may wish to increase your consumption of fibre and avoid eating excessive amounts of red meat and eggs.

Hydrogen sulphide production

1   5.6   16.9

The typical range in healthy people is 1.03% to 5.55%
The gas hydrogen sulphide is produced by some species in the gut microbiome when sulphur-containing foods such as eggs, garlic, onion, cabbage, kale or Brussels sprouts are broken down. 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. This gas is also responsible for the rotton egg smell of flatulence. Laboratory based studies have suggested that fibre can reduce the production of hydrogen sulphide.

3-indolepropionic acid (IPA) production

0.12 **0.9** **1.7**

The typical range in healthy people is 0.12% to 1.74%

3-indolepropionic acid (IPA) is a strong anti-oxidant produced by some gut bacteria that can help protect the nervous system from damage. Research has shown 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 foods containing rye, can increase IPA production.

Protein degradation

57.7 **69.3**

The typical range in healthy people is 57.74% to 72.84%

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

0.04 **4**

The typical range in healthy people is 0% 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   67%

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

Metabolites

Potential to promote health

Butyrate production

| 10.3 | 18.4 | 27.7 |

The typical range in healthy people is 10.32% to 27.71%

Propionate production

| 22.5 | 43.6 | 49.8 |

The typical range in healthy people is 22.46% to 49.77%

Acetate production

| 48.4 | 65.7 |

The typical range in healthy people is 48.41% to 69.81%

Fibre degradation

| 55.2 | 68.6 |

The typical range in healthy people is 55.22% to 71.8%

Microbial Diversity

| 3.1 | 3.5 | 4.2 |

The typical range in healthy people is 3.14% to 4.15%

Lactate production

| 25.8 | 41.3 | 56.1 |

The typical range in healthy people is 25.76% to 56.12%

3-indolepropionic acid (IPA) production

| 0.12 | 0.9 | 1.7 |

The typical range in healthy people is 0.12% to 1.74%

Potential to reduce health

Hexa-acylated Lipopolysaccharide

| 0 | 0.73 | 14.4 |

The typical range in healthy people is 0% to 0.73%

Hydrogen sulphide production

| 1 | 5.6 | 16.9 |

The typical range in healthy people is 1.03% to 5.55%

Trimethylamine production

| 0 | 0.2 | 1.1 |

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

Human DNA

| 0.04 | 4 |

The typical range in healthy people is 0% to 4%

Ammonia (urease) production

| 1.4 | 7.5 | 9.6 |

The typical range in healthy people is 1.4% to 7.5%

Histamine production

| 0 | 0.83 | 1.2 |

The typical range in healthy people is 0% to 0.83%

B. fragilis toxin production

| 0 | 0.12 | 6 |

The typical range in healthy people is 0% to 0.16%

Protein degradation

| 57.7 | 69.3 |

The typical range in healthy people is 57.74% to 72.84%

Species

Potential to promote health

Agathobacter faecis

| 0 | 1.5 |

The typical range in healthy people is 0% to 1.5%

Agathobacter rectalis

| 0 | 2.5 | 4.8 |

The typical range in healthy people is 0% to 4.77%

Akkermansia muciniphila

| 0 | 2.2 |

The typical range in healthy people is 0% to 2.15%

Bifidobacterium adolescentis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Potential to reduce health

Bilophila wadsworthia

| 0 | 0.2 |

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

Clostridium_M bolteae

| 0 |

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

Eggerthella lenta

| 0 |

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

Fusobacterium nucleatum

| 0 |

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

Bifidobacterium animalis

| 0 | 0.1 | 0.11 |

The typical range in healthy people is 0% to 0.1%

Bifidobacterium bifidum

| 0 |

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

Bifidobacterium longum

| 0 | 0.7 |

The typical range in healthy people is 0% to 0.7%

Coprococcus eutactus

| 0 |

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

Eubacterium_E hallii

| 0 | 0.63 |

The typical range in healthy people is 0% to 0.63%

Faecalibacterium prausnitzii_C

| 0 | 2.3 |

The typical range in healthy people is 0% to 2.31%

Roseburia hominis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Roseburia intestinalis

| 0 | 1.6 |

The typical range in healthy people is 0% to 1.63%

Roseburia inulinivorans

| 0 |

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

Ruminococcus_E bromii

| 0 | 0.97 | 2.5 |

The typical range in healthy people is 0% to 2.5%

Peptostreptococcus stomatis

| 0 |

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

Gut Mucosal Health   **64%**

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

Metabolites

Potential to promote health

Fibre degradation

| 55.2 | 68.6 |

The typical range in healthy people is 55.22% to 71.8%

Lactate production

| 25.8 | 41.3 | 56.1 |

The typical range in healthy people is 25.76% to 56.12%

3-indolepropionic acid (IPA) production

| 0.12 | 0.9 | 1.7 |

The typical range in healthy people is 0.12% to 1.74%

Butyrate production

| 10.3 | 18.4 | 27.7 |

The typical range in healthy people is 10.32% to 27.71%

Potential to reduce health

Hydrogen sulphide production

| 1 | 5.6 | 16.9 |

The typical range in healthy people is 1.03% to 5.55%

Ammonia (urease) production

| 1.4 | 7.5 | 9.6 |

The typical range in healthy people is 1.4% to 7.5%

Hexa-acylated Lipopolysaccharide

| 0 | 0.73 | 14.4 |

The typical range in healthy people is 0% to 0.73%

Protein degradation

| 57.7 | 69.3 |

The typical range in healthy people is 57.74% to 72.84%

Human DNA

| 0.04 | 4 |

The typical range in healthy people is 0% to 4%

B. fragilis **toxin production**

| 0 | 0.12 | 6 |

The typical range in healthy people is 0% to 0.16%

Histamine production

| 0 | 0.83 | 1.2 |

The typical range in healthy people is 0% to 0.83%

Species

Potential to promote health

Agathobacter faecis

| 0 | 1.5 |

The typical range in healthy people is 0% to 1.5%

Agathobacter rectalis

| 0 | 2.5 | 4.8 |

The typical range in healthy people is 0% to 4.77%

Akkermansia muciniphila

| 0 | 2.2 |

The typical range in healthy people is 0% to 2.15%

Bifidobacterium animalis

| 0 | 0.1 | 0.11 |

The typical range in healthy people is 0% to 0.1%

Bifidobacterium bifidum

| 0 |

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

Coprococcus eutactus

| 0 |

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

Eubacterium_E hallii

| 0 | 0.63 |

The typical range in healthy people is 0% to 0.63%

Potential to reduce health

Bilophila wadsworthia

| 0 | 0.2 |

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

Faecalibacterium prausnitzii_C

| 0 | 2.3 |

The typical range in healthy people is 0% to 2.31%

Roseburia hominis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Roseburia intestinalis

| 0 | 1.6 |

The typical range in healthy people is 0% to 1.63%

Roseburia inulinivorans

| 0 |

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

Ruminococcus_E bromii

| 0 | 0.97 | 2.5 |

The typical range in healthy people is 0% to 2.5%

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

| 10.3 | 18.4 | 27.7 |

The typical range in healthy people is 10.32% to 27.71%

Fibre degradation

| 55.2 | 68.6 |

The typical range in healthy people is 55.22% to 71.8%

Propionate production

| 22.5 | 43.6 | 49.8 |

The typical range in healthy people is 22.46% to 49.77%

Tyramine production

| 0 |

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

Potential to **reduce** health

Methane

| 0 | 0.15 |

The typical range in healthy people is 0% to 0.15%

Hydrogen sulphide production

| 1 | 5.6 | 16.9 |

The typical range in healthy people is 1.03% to 5.55%

Protein degradation

| 57.7 | 69.3 |

The typical range in healthy people is 57.74% to 72.84%

Species

Potential to **promote** health

Potential to **reduce** health

Methanobrevibacter_A smithii

| 0 | 0.19 |

The typical range in healthy people is 0% to 0.19%

Bilophila wadsworthia

| 0 | 0.2 |

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

Metabolic Health
80%

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

| 10.3 | 18.4 | 27.7 |

The typical range in healthy people is 10.32% to 27.71%

Propionate production

| 22.5 | 43.6 | 49.8 |

The typical range in healthy people is 22.46% to 49.77%

Acetate production

| 48.4 | 65.7 |

The typical range in healthy people is 48.41% to 69.81%

Fibre degradation

| 55.2 | 68.6 |

The typical range in healthy people is 55.22% to 71.8%

3-indolepropionic acid (IPA) production

| 0.12 | 0.9 | 1.7 |

The typical range in healthy people is 0.12% to 1.74%

Folate (B9) production

| 29.1 | 55.3 | 57 |

The typical range in healthy people is 29.11% to 55.25%

Potential to reduce health

Branched chain amino acids production

| 34.3 | 58.2 | 5.3 |

The typical range in healthy people is 34.26% to 65.26%

Hexa-acylated Lipopolysaccharide

| 0 | 0.73 | 14.4 |

The typical range in healthy people is 0% to 0.73%

Trimethylamine production

| 0 | 0.2 | 1.1 |

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

Succinate production

| 14.2 | 4 | 46.5 |

The typical range in healthy people is 14.23% to 47.2%

Species

Potential to promote health

Akkermansia muciniphila

| 0 | 2.2 |

The typical range in healthy people is 0% to 2.15%

Bifidobacterium adolescentis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Bifidobacterium animalis

| 0 | 0.1 | 0.11 |

The typical range in healthy people is 0% to 0.1%

Bifidobacterium bifidum

| 0 |

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

Bifidobacterium longum

| 0 | 0.7 |

The typical range in healthy people is 0% to 0.7%

Eubacterium_E hallii

| 0 | 0.63 |

The typical range in healthy people is 0% to 0.63%

Faecalibacterium prausnitzii_C

| 0 | 2.3 |

The typical range in healthy people is 0% to 2.31%

Roseburia hominis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Potential to reduce health

Bilophila wadsworthia

| 0 | 0.2 |

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

Eggerthella lenta

| 0 |

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

Prevotella copri

| 0 | 12.6 | 4 |

The typical range in healthy people is 0% to 23.37%

Roseburia intestinalis

0	1.6

The typical range in healthy people is 0% to 1.63%

Roseburia inulinivorans

0

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

Ruminococcus_E bromii

0	0.97	2.5

The typical range in healthy people is 0% to 2.5%

Roseburia intestinalis

0	1.6

The typical range in healthy people is 0% to 1.63%

Roseburia inulinivorans

0

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

Ruminococcus_E bromii

0	0.97	2.5

The typical range in healthy people is 0% to 2.5%

Nervous System Health   **64%**

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

| 0.12 | 0.9 | 1.7 |

The typical range in healthy people is 0.12% to 1.74%

Butyrate production

| 10.3 | 18.4 | 27.7 |

The typical range in healthy people is 10.32% to 27.71%

Fibre degradation

| 55.2 | 68.6 |

The typical range in healthy people is 55.22% to 71.8%

GABA production

| 5.5 | 24.3 | 26 |

The typical range in healthy people is 5.47% to 24.28%

Propionate production

| 22.5 | 43.6 | 49.8 |

The typical range in healthy people is 22.46% to 49.77%

Tyramine production

| 0 |

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

Folate (B9) production

| 29.1 | 55.3 | 57 |

The typical range in healthy people is 29.11% to 55.25%

Potential to reduce health

Histamine production

| 0 | 0.83 | 1.2 |

The typical range in healthy people is 0% to 0.83%

GABA consumption

| 0.74 | 5.3 | 15.5 |

The typical range in healthy people is 0.74% to 5.27%

Hexa-acylated Lipopolysaccharide

| 0 | 0.73 | 14.4 |

The typical range in healthy people is 0% to 0.73%

Trimethylamine production

| 0 | 0.2 | 1.1 |

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

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

| 10.3 | 18.4 | 27.7 |

The typical range in healthy people is 10.32% to 27.71%

Propionate production

| 22.5 | 43.6 | 49.8 |

The typical range in healthy people is 22.46% to 49.77%

Acetate production

| 48.4 | 65.7 |

The typical range in healthy people is 48.41% to 69.81%

Fibre degradation

| 55.2 | 68.6 |

The typical range in healthy people is 55.22% to 71.8%

Folate (B9) production

| 29.1 | 55.3 | 57 |

The typical range in healthy people is 29.11% to 55.25%

Potential to reduce health

Hexa-acylated Lipopolysaccharide

| 0 | 0.73 | 14.4 |

The typical range in healthy people is 0% to 0.73%

***B. fragilis* toxin production**

| 0 | 0.12 | 16 |

The typical range in healthy people is 0% to 0.16%

Histamine production

| 0 | 0.83 | 1.2 |

The typical range in healthy people is 0% to 0.83%

Protein degradation

| 57.7 | 69.3 |

The typical range in healthy people is 57.74% to 72.84%

Species

Potential to promote health

Bifidobacterium adolescentis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Bifidobacterium animalis

| 0 | 0.1 | 0.11 |

The typical range in healthy people is 0% to 0.1%

Bifidobacterium bifidum

| 0 |

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

Bifidobacterium longum

| 0 | 0.7 |

The typical range in healthy people is 0% to 0.7%

Coprococcus eutactus

| 0 |

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

Eubacterium_E hallii

| 0 | 0.63 |

The typical range in healthy people is 0% to 0.63%

Faecalibacterium prausnitzii

| 0 |

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

Roseburia hominis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Roseburia intestinalis

| 0 | 1.6 |

The typical range in healthy people is 0% to 1.63%

Potential to reduce health

Eggerthella lenta

| 0 |

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

Fusobacterium nucleatum

| 0 |

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

Roseburia inulinivorans

0

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

Roseburia inulinivorans

0

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

Inflammatory Balance   **64%**

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

Metabolites

Potential to **promote** health

Butyrate production

| 10.3 | 18.4 | 27.7 |

The typical range in healthy people is 10.32% to 27.71%

Propionate production

| 22.5 | 43.6 | 49.8 |

The typical range in healthy people is 22.46% to 49.77%

Acetate production

| 48.4 | 65.7 |

The typical range in healthy people is 48.41% to 69.81%

Fibre degradation

| 55.2 | 68.6 |

The typical range in healthy people is 55.22% to 71.8%

Lactate production

| 25.8 | 41.3 | 56.1 |

The typical range in healthy people is 25.76% to 56.12%

3-indolepropionic acid (IPA) production

| 0.12 | 0.9 | 1.7 |

The typical range in healthy people is 0.12% to 1.74%

Potential to reduce health

Hexa-acylated Lipopolysaccharide

| 0 | 0.73 | 14.4 |

The typical range in healthy people is 0% to 0.73%

Histamine production

| 0 | 0.83 | 1.2 |

The typical range in healthy people is 0% to 0.83%

Ammonia (urease) production

| 1.4 | 7.5 | 9.6 |

The typical range in healthy people is 1.4% to 7.5%

Trimethylamine production

| 0 | 0.2 | 1.1 |

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

Human DNA

| 0.04 | 4 |

The typical range in healthy people is 0% to 4%

Protein degradation

| 57.7 | 69.3 |

The typical range in healthy people is 57.74% to 72.84%

Hydrogen sulphide production

| 1 | 5.6 | 16.9 |

The typical range in healthy people is 1.03% to 5.55%

B. fragilis **toxin production**

| 0 | 0.12 | 16 |

The typical range in healthy people is 0% to 0.16%

Species

Potential to **promote** health

Agathobacter faecis

| 0 | 1.5 |

The typical range in healthy people is 0% to 1.5%

Agathobacter rectalis

| 0 | 2.5 | 4.8 |

The typical range in healthy people is 0% to 4.77%

Akkermansia muciniphila

| 0 | 2.2 |

The typical range in healthy people is 0% to 2.15%

Bifidobacterium adolescentis

| 0 | 0.4 |

The typical range in healthy people is 0% to 0.4%

Bifidobacterium longum

| 0 | 0.7 |

The typical range in healthy people is 0% to 0.7%

Coprococcus eutactus

| 0 |

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

Potential to reduce health

Bilophila wadsworthia

| 0 | 0.2 |

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

Clostridium_M bolteae

| 0 |

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

Eggerthella lenta

| 0 |

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

Fusobacterium nucleatum

| 0 |

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

Eubacterium_E hallii

0	0.63

The typical range in healthy people is 0% to 0.63%

Faecalibacterium prausnitzii_C

0	2.3

The typical range in healthy people is 0% to 2.31%

Roseburia hominis

0	0.4

The typical range in healthy people is 0% to 0.4%

Roseburia intestinalis

0	1.6

The typical range in healthy people is 0% to 1.63%

Roseburia inulinivorans

0

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

Ruminococcus_E bromii

0	0.97	2.5

The typical range in healthy people is 0% to 2.5%

Detoxification   **100%**

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

7.4   17

The typical range in healthy people is 7.39% to 17%

Fibre degradation

55.2   68.6

The typical range in healthy people is 55.22% to 71.8%

Potential to **reduce** health

Beta-glucuronidase production

6.5   14.1   20.5

The typical range in healthy people is 6.5% to 20.53%

Species

Potential to **promote** health

Oxalobacter formigenes

0

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

Potential to **reduce** health

Eggerthella lenta

0

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

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.

	3.1	3.5	4.2

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	
➕	Bacteroidetes	*Prevotella copri*	12.65%	0.00% - 23.37%	Average	▾
➕	Proteobacteria	*Escherichia coli*	8.62%	0.00% - 0.33%	High	▾
➕	Proteobacteria	*Klebsiella pneumoniae*	6.30%	0.00% - 0.00%	High	▾
	Bacteroidetes	*Prevotella sp*	3.83%	0.00% - 0.85%	High	▾
	Firmicutes_A	*Ruminiclostridium_E siraeum*	3.04%	0.00% - 0.80%	High	▾
➕	Bacteroidetes	*Alistipes putredinis*	2.66%	0.00% - 3.22%	Average	▾
➕	Firmicutes_A	*Agathobacter rectalis*	2.47%	0.00% - 4.77%	Average	▾
➕	Bacteroidetes	*Bacteroides_B vulgatus*	2.37%	0.00% - 3.86%	Average	▾
	Bacteroidetes	*Muribaculum sp*	1.60%	0.00% - 0.00%	High	▾
	Bacteroidetes	*Bacteroides_B sp*	1.06%	0.00% - 0.00%	High	▾
	Firmicutes_A	*Fusicatenibacter saccharivorans*	0.99%	0.00% - 2.34%	Average	▾
➕	Firmicutes_A	*Ruminococcus_E bromii*	0.97%	0.00% - 2.50%	Average	▾
	Firmicutes_A	*Faecalibacterium prausnitzii_B*	0.93%	0.00% - 2.48%	Average	▾
	Firmicutes_A	*CAG-65 sp*	0.86%	0.00% - 1.52%	Average	▾
➕	Bacteroidetes	*Bacteroides uniformis*	0.76%	0.00% - 4.39%	Average	▾
	Firmicutes_A	*ER4 sp*	0.72%	0.00% - 0.54%	High	▾
➕	Bacteroidetes	*Bacteroides_B massiliensis*	0.62%	0.00% - 1.32%	Average	▾
	Proteobacteria	*Sutterella sp3*	0.60%	0.00% - 0.83%	Average	▾
➕	Firmicutes_A	*Coprococcus eutactus_A*	0.58%	0.00% - 1.52%	Average	▾
➕	Bacteroidetes	*Bacteroides_B dorei*	0.58%	0.00% - 2.32%	Average	▾
	Firmicutes_A	*CAG-24 sp1*	0.57%	0.00% - 0.42%	High	▾
➕	Bacteroidetes	*Bacteroides fragilis*	0.56%	0.00% - 0.66%	Average	▾
	Bacteroidetes	*Bacteroides stercoris*	0.54%	0.00% - 1.77%	Average	▾
➕	Bacteroidetes	*Parabacteroides distasonis*	0.51%	0.00% - 0.93%	Average	▾
	Firmicutes_A	*Lachnospira eligens*	0.49%	0.00% - 1.32%	Average	▾
	Bacteroidetes	*Bacteroides thetaiotaomicron*	0.48%	0.00% - 0.81%	Average	▾
	Firmicutes_A	*CAG-83 sp2*	0.48%	0.00% - 0.44%	High	▾

	Firmicutes_A	CAG-352 sp	0.47%	0.00% - 0.58%	Average	▼
	Firmicutes_A	UBA3626 sp	0.47%	0.00% - 0.00%	High	▼
	Firmicutes_A	UBA11524 sp1	0.46%	0.00% - 3.45%	Average	▼
	Firmicutes_A	Eubacterium_R sp	0.45%	0.00% - 0.00%	High	▼
	Firmicutes_A	COE1 sp	0.39%	0.00% - 0.00%	High	▼
	Firmicutes_A	Negativibacillus sp	0.38%	0.00% - 0.00%	High	▼
	Firmicutes_A	Lachnospira sp	0.37%	0.00% - 0.15%	High	▼
➕	Bacteroidetes	Alistipes finegoldii	0.36%	0.00% - 0.58%	Average	▼
	Bacteroidetes	Bacteroides salyersiae	0.34%	0.00% - 0.08%	High	▼
➕	Bacteroidetes	Paraprevotella clara	0.33%	0.00% - 0.55%	Average	▼
	Firmicutes_A	UBA1394 sp	0.33%	0.00% - 0.09%	High	▼
➕	Bacteroidetes	Odoribacter splanchnicus	0.32%	0.00% - 0.34%	Average	▼
➕	Firmicutes_A	Dorea longicatena	0.32%	0.00% - 0.60%	Average	▼
	Firmicutes_A	Lachnospira sp	0.31%	0.00% - 0.09%	High	▼
➕	Bacteroidetes	Parabacteroides merdae	0.31%	0.00% - 0.66%	Average	▼
	Firmicutes_A	CAG-56 sp	0.30%	0.00% - 0.65%	Average	▼
➕	Bacteroidetes	Alistipes shahii	0.30%	0.00% - 1.47%	Average	▼
➕	Desulfobacterota	Desulfovibrio piger	0.29%	0.00% - 0.39%	Average	▼
	Bacteroidetes	UBA6382 sp	0.29%	0.00% - 0.00%	High	▼
	Proteobacteria	CAG-267 sp	0.29%	0.00% - 0.39%	Average	▼
	Firmicutes_A	Ruminococcus_B faecis	0.29%	0.00% - 0.49%	Average	▼
	Bacteroidetes	Prevotella corporis	0.28%	0.00% - 0.00%	High	▼
	Firmicutes_A	CAG-110 sp	0.25%	0.00% - 0.00%	High	▼
	Firmicutes_A	CAG-632 sp	0.23%	0.00% - 0.00%	High	▼
	Firmicutes_A	KLE1615 sp1	0.23%	0.00% - 0.77%	Average	▼
	Firmicutes_A	CAG-180 sp	0.21%	0.00% - 0.00%	High	▼
	Firmicutes_A	Oscillibacter sp	0.20%	0.00% - 0.43%	Average	▼
	Firmicutes_A	CAG-882 sp	0.20%	0.00% - 0.00%	High	▼
	Proteobacteria	51-20 sp	0.20%	0.00% - 1.05%	Average	▼
➕	Firmicutes_A	Ruminococcus_B lactaris	0.20%	0.00% - 0.34%	Average	▼
	Firmicutes_A	CAG-303 sp	0.19%	0.00% - 0.76%	Average	▼
	Firmicutes_A	UBA4263 sp	0.18%	0.00% - 0.25%	Average	▼
	Actinobacteria	Collinsella aerofaciens	0.18%	0.00% - 0.31%	Average	▼
	Firmicutes_A	Faecalibacterium sp	0.18%	0.12% - 1.14%	Average	▼
	Firmicutes_A	F23-B02 sp	0.17%	0.00% - 0.00%	High	▼
	Firmicutes_A	Butyricicoccus sp1	0.16%	0.00% - 0.78%	Average	▼
	Firmicutes_A	Faecalibacterium sp	0.15%	0.00% - 0.54%	Average	▼

	Phylum	Species	Abundance	Range	Level	
	Firmicutes_A	*CAG-110 sp*	0.15%	0.00% - 0.00%	High	▼
	Bacteroidetes	*Butyricimonas virosa*	0.14%	0.00% - 0.00%	High	▼
	Bacteroidetes	*Parabacteroides goldsteinii*	0.14%	0.00% - 0.00%	High	▼
	Firmicutes_A	*CAG-83 sp*	0.14%	0.00% - 0.12%	High	▼
	Firmicutes_A	*CAG-110 sp*	0.14%	0.00% - 0.00%	High	▼
	Firmicutes_A	*CAG-81 sp*	0.14%	0.00% - 0.11%	High	▼
	Firmicutes_A	*ER4 sp*	0.14%	0.00% - 0.27%	Average	▼
	Firmicutes_A	*Subdoligranulum sp*	0.14%	0.00% - 0.35%	Average	▼
	Proteobacteria	*CAG-495 sp*	0.14%	0.00% - 1.21%	Average	▼
	Firmicutes_A	*CAG-226 sp*	0.13%	0.00% - 0.33%	Average	▼
	Firmicutes_A	*Oscillibacter sp*	0.13%	0.00% - 0.41%	Average	▼
	Firmicutes_A	*TF01-11 sp*	0.12%	0.00% - 0.07%	High	▼
➕	Actinobacteria	*Bifidobacterium animalis*	0.11%	0.00% - 0.10%	High	▼
	Firmicutes_A	*COE1 sp*	0.11%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Anaerotignum sp1*	0.11%	0.00% - 0.14%	Average	▼
	Firmicutes_A	*ER4 sp*	0.11%	0.00% - 0.00%	High	▼
	Bacteroidetes	*Porphyromonas sp*	0.10%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Negativibacillus massiliensis*	0.10%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Ruminiclostridium_C sp*	0.10%	0.00% - 0.20%	Average	▼
	Firmicutes_A	*UBA1206 sp*	0.10%	0.00% - 0.00%	High	▼
	Firmicutes_A	*CAG-170 sp*	0.10%	0.00% - 0.48%	Average	▼
	Firmicutes_A	*CAG-170 sp*	0.09%	0.00% - 0.15%	Average	▼
	Proteobacteria	*CAG-495 sp*	0.08%	0.00% - 0.00%	High	▼
	Firmicutes_A	*Coprococcus_A catus*	0.07%	0.00% - 0.22%	Average	▼
	Firmicutes_A	*Blautia_A obeum_A*	0.07%	0.00% - 0.17%	Average	▼
	Proteobacteria	*Duodenibacillus sp*	0.06%	0.00% - 0.00%	High	▼
	Firmicutes_A	*UBA10281 sp*	0.06%	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	
➕	Bacteroidetes	*Prevotella copri*	12.65%	0.00% - 23.37%	Average	▼

This is a common inhabitant of the human gut and includes a large number of strains.

Fuel sources used: It can use resistant starch, fibre, simple sugars, and protein as energy sources.

Key metabolites produced: It can produce succinate, the short-chain fatty acids, acetate and propionate and ethanol. It can also produce branched chain amino acids (BCAA); high levels of BCAAs have been linked to metabolic conditions.

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

➕	Proteobacteria	*Escherichia coli*	8.62%	0.00% - 0.33%	High	▼

This species is a common inhabitant of the gut, although it is usually present at a low abundance compared to other normal gut species. This species encompasses a large number of strains with diverse properties; the most well-known are the pathogenic strains that are a common cause of gastrointestinal disease. However, most strains are not harmful.

Fuel sources used: This species can use fibre, simple sugars (including lactose), protein and fats. Some strains can also break down a compound called oxalate, which can form kidney stones.

Key metabolites produced: It can produce lactate, succinate, the short-chain fatty acid acetate, and essential B and K vitamins. Some strains can also produce histamine and a compound called trimethylamine, which has been associated with cardiovascular conditions.

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

➕	Proteobacteria	*Klebsiella pneumoniae*	6.30%	0.00% - 0.00%	High	▼

This species can be found in several body sites, such as the mouth, nose, lungs and gut and can cause infection.

Fuel sources used: It uses simple sugars (including lactose) and protein for energy.

Key metabolites produced: It can produce lactate, ethanol, and the short-chain fatty acid acetate.

Emerging research: An overgrowth of this species in the gut has been associated with diarrhea, inflammation and cardiovascular conditions. If you have high levels of this species and intestinal symptoms, please see a healthcare practitioner.
[1] [2] [3] [4] [5] [6]

➕	Bacteroidetes	*Alistipes putredinis*	2.66%	0.00% - 3.22%	Average	▼

This is a common inhabitant of the gut microbiome.

Fuel sources used: It can use limited types of simple sugars (including lactose) and protein for energy.

Key metabolites produced: It primarily produces succinate but can also produce low amounts of the short-chain fatty acids acetate, propionate and butyrate, and the neurotransmitter GABA.

Emerging research: High levels of this species have been associated with both poor gut health and improved markers of cardiac health.
[1] [2] [3] [4] [5] [6] [7] [8]

➕	Firmicutes_A	*Agathobacter rectalis*	2.47%	0.00% - 4.77%	Average	▼

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

Fuel sources used: It can use resistant plant resistant starches after initial degradation by Ruminococcus bromii.

Key metabolites produced: It produces the short-chain fatty acid butyrate. Butyrate is important for a healthy gut as it is the primary fuel of cells lining the intestinal tract and is an important mediator of inflammation.

Emerging research: Low levels of this species have been observed in inflammatory conditions.
[1] [2] [3]

➕	Bacteroidetes	*Bacteroides_B vulgatus*	2.37%	0.00% - 3.86%	Average	▼

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

Fuel sources used: It can use dietary fibre, simple sugars, protein and mucus for energy.

Key metabolites produced: It primarily produces succinate and the short-chain fatty acid propionate. It can also produce branched chain amino acids, which have been linked to metabolic conditions.

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]

➕	Firmicutes_A	*Ruminococcus_E bromii*	0.97%	0.00% - 2.50%	Average	▼

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: Ruminococcus bromii uses resistant starch for energy.

Key metabolites produced: It can produce the short-chain fatty acid acetate and simple sugars that other bacteria, such as Agathobacter rectalis can use to produce short-chain fatty acids such as butyrate.

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]

➕	Bacteroidetes	*Bacteroides uniformis*	0.76%	0.00% - 4.39%	Average	▼

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

Fuel sources used: It can use fibre, resistant starch, simple sugars (including lactose), protein and mucus for energy.

Key metabolites produced: It primarily produces succinate, although it can also produce lactate and the short-chain fatty acids, acetate and propionate. This species can also produce the neurotransmitter GABA, which is important for mental health.

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. Further research needs to be conducted to determine if these benefits translate to humans.
[1] [2] [3] [4]

➕	Bacteroidetes	*Bacteroides_B massiliensis*	0.62%	0.00% - 1.32%	Average	▼

This is a normal inhabitant of the human gut microbiome.

Fuel sources used: This species can use resistant starch, simple sugars (including lactose), protein and mucus for energy. It can also break down a compound called oxalate, which can form kidney stones.

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

| ✚ | Firmicutes_A | *Coprococcus eutactus_A* | 0.58% | 0.00% - 1.52% | Average | ▼ |

This is a common inhabitant of the human gut.

Fuel sources used: It can use fibre, simple sugars (including lactose) and limited types of protein for energy.

Key metabolites produced: It primarily produces formate and the short-chain fatty acid butyrate, but can also produce lactate and the short-chain fatty acids acetate and propionate in smaller amounts.

Emerging research: This species has been observed at decreased levels in children with inflammatory conditions.
[1] [2] [3] [4] [5] [6]

| ✚ | Bacteroidetes | *Bacteroides_B dorei* | 0.58% | 0.00% - 2.32% | Average | ▼ |

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

Fuel sources used: It can use fibre, resistant starch, simple sugars (including lactose), a wide range of proteins and mucus as energy sources.

Key metabolites produced: It can produce succinate, lactate, and the short-chain fatty acid acetate. It can also produce GABA, an important neurotransmitter.

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] [7]

| ✚ | Bacteroidetes | *Bacteroides fragilis* | 0.56% | 0.00% - 0.66% | Average | ▼ |

This is a normal inhabitant of the human gut.

Fuel sources used: It can use protein, mucus, resistant starch, and simple sugars (including lactose) for energy.

Key metabolites produced: It primarily produces succinate and the short-chain fatty acid, acetate.

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. 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]

| ✚ | Bacteroidetes | *Parabacteroides distasonis* | 0.51% | 0.00% - 0.93% | Average | ▼ |

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

Fuel sources used: It can use fibre, resistant starch, simple sugars (including lactose), protein and mucus for energy.

Key metabolites produced: It primarily produces succinate and the short-chain fatty acid, acetate. It can also produce GABA, an important neurotransmitter.

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]

| ✚ | Bacteroidetes | *Alistipes finegoldii* | 0.36% | 0.00% - 0.58% | Average | ▼ |

This is a common inhabitant of the gut microbiome.

Fuel sources used: It can use simple sugars and protein for energy.

Key metabolites produced: It primarily produces succinate and can also produce low amounts of the neurotransmitter GABA.

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]

| ✚ | Bacteroidetes | *Paraprevotella clara* | 0.33% | 0.00% - 0.55% | Average | ▼ |

This is a recently discovered bacterial species and a common inhabitant of the human gut microbiome.

Fuel sources used: It can use fibre, simple sugars (including lactose) and protein as energy sources.

Key metabolites produced: It can produce succinate and the short-chain fatty acid acetate.

Emerging research: Elevated levels of this species have been associated with poor gut health.
[1] [2]

| ✚ | Bacteroidetes | *Odoribacter splanchnicus* | 0.32% | 0.00% - 0.34% | Average | ▼ |

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

Fuel sources used: It can use fibre, resistant starch, simple sugars (including lactose), protein and mucus as energy sources.

Key metabolites produced: It can produce succinate, lactate and the short fatty acids, acetate, propionate and butyrate.

Emerging research: This species has been negatively correlated with metabolic conditions in postmenopausal obese women, suggesting it may have a beneficial role in metabolism. Another study observed this species was reduced in women with bladder pain.
[1] [2] [3]

| ✚ | Firmicutes_A | *Dorea longicatena* | 0.32% | 0.00% - 0.60% | Average | ▼ |

This is a common inhabitant of the human gut.

Fuel sources used: It can use fibre, simple sugars (including lactose) and protein for energy.

Key metabolites produced: It can produce formate, ethanol, and the short-chain fatty acids acetate and propionate.

Emerging research: There are conflicting results about the association of this species with metabolic conditions and more study is needed.
[1] [2] [3] [4] [5] [6] [7]

| | Bacteroidetes | *Parabacteroides merdae* | 0.31% | 0.00% - 0.66% | Average | |

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

Fuel sources used: It can use simple sugars (including lactose), protein and mucus as energy sources.

Key metabolites produced: It can produce succinate and the short fatty acid acetate and lactate.

Emerging research: High levels of this species have been associated with poor gut and cardiovascular health. This species has also been associated with a diet low in fruits and vegetables.
[1] [2] [3] [4] [5]

| | Bacteroidetes | *Alistipes shahii* | 0.30% | 0.00% - 1.47% | Average | |

This is a common inhabitant of the human gut.

Fuel sources used: It can use fibre, simple sugars (including lactose) and protein for energy.

Key metabolites produced: It primarily produces succinate, but can also produce the short-chain fatty acid acetate.

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 neurodegenerative conditions.
[1] [2] [3] [4] [5] [6]

| | Desulfobacterota | *Desulfovibrio piger* | 0.29% | 0.00% - 0.39% | Average | |

This is an inhabitant of the human gut.

Fuel sources used: It can use limited types of simple sugars as well as lactate and protein for energy. It can produce the short-chain fatty acid acetate. It can also reduce sulfate and nitrate to produce hydrogen sulphide and ammonia.

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

| | Firmicutes_A | *Ruminococcus_B lactaris* | 0.20% | 0.00% - 0.34% | Average | |

This is a common inhabitant of the human gut.

Fuel sources used: It can use simple sugars (including lactose) and protein for energy.

Key metabolites produced: It can produce lactate and the short-chain fatty acids acetate and propionate.

Emerging research: Elevated levels of this species have been observed with inflammatory conditions, but reduced levels have been observed with metabolic conditions.
[1] [2] [3]

| | Actinobacteria | *Bifidobacterium animalis* | 0.11% | 0.00% - 0.10% | High | |

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

Fuel sources used: It can use fibre, resistant starch, simple sugars (including lactose) and protein for energy.

Key metabolites produced: It produces lactate and the short-chain fatty acid, acetate. Acetate from Bifidobacteria promotes the growth of butyrate-producing bacteria and the production of butyrate.

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]