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# Your personal microbiome report

The aim of myBioma microbiome analysis is to examine all bacteria in your stool using next-generation gene analysis, determining the 16S gene of the bacteria. It is thus possible to classify these organisms in the intestine and draw conclusions about your health by utilizing the myBioma knowledge database.



Your microbial composition is varied and well balanced. You seem to be eating a balanced diet, but your intestinal bacteria could help you more efficiently in the utilization of the ingested food. There is some need for improvement in your health, especially regarding the following health conditions: Metabolic syndrome, Insulin balance, Intestinal mucosa, Irritable bowel syndrome, Gut-brain axis, Diarrhea, Gut-liver axis, Gut-heart axis, Gut-skin axis, Gallstones, Joint health.

You can find your personal suggestions for improvement on page 36.

Please note: The detection of a microorganism by this test does not mean that it is a disease. Similarly, failure to detect a microorganism by this test does not preclude the presence of a disease-causing microorganism. Other organisms may also be present which are not detected by this test. This test is not a substitute for established methods of identifying microorganisms or their antimicrobial sensitivity profile. The bacteria and results described in the health conditions only give an indication of possible problems. It is not a diagnosis and cannot be considered as such.

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# Summary

Your personal microbiome report is comprehensive and contains a lot of knowledge about the effect of bacteria on your health. Below is a summary of the most relevant results to give you a quick overview. Further information about the results can be found on the detail pages - please use the table of contents.

#### **Microbial composition**

Index	Value	Average	Interpretation
Species richness	259	231 - 346	Excellent!
Diversity	6.45	5.80 - 6.56	Excellent!
Species evenness	0.80	0.74 - 0.79	Excellent!

#### Nutrition and food utilisation

	Parameter	Result	Average	Interpretation
Ŷ	Enterotypes	Prevotella	-	Enterotype 2
	Caloric intake	1.1	1.0 - 1.8	Excellent!
$\bigcirc$	Sugar metabolism	83	100	Good!
$\bigcirc$	Lipid metabolism	75	100	Good!
$\bigcirc$	Vitamin metabolism	84	100	Good!
$\bigcirc$	Protein metabolism	84	100	Good!

#### Health

- Solution Intestinal mucosa
- Irritable bowel syndrome
- 🗠 🛛 Gut-brain axis
- 🔗 🛛 Gut-heart axis
- 😔 Gut-liver axis
- 🔄 🛛 Gut-skin axis

- Metabolic syndrome
- Solution Insulin balance
- Kidney stones
- 🗠 Gallstones
- 🔄 🛛 Joint health



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Find out what health conditions your bacteria can be associated with.

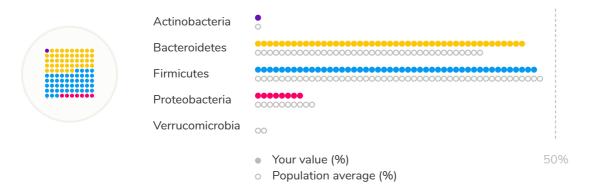
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# Microbial composition

# Overview of all bacteria



Your microbiome is unique. Therefore, the composition of the bacteria in your gut system may differ from that of the average population

#### Description

The human gut system is dominated by five bacterial strains - Actinobacteria, Bacteroidetes, Firmicutes, Proteobacteria and Verrucomicrobia.

These complicated names describe the taxonomy (= classification) of the bacterial strains. The further you read through your personal report, the better your understanding of these will be. In this chapter, we compare the composition of your intestinal bacteria with the average values of the population. Since your microbiome is unique, it is normal for your values to be different from the average.<sup>7,8</sup>

Туре	You (%)	Population (%)
Actinobacteria	0.11%	1.08%
<ul> <li>Bacteroidetes</li> </ul>	44.98%	37.72%
Firmicutes	47.34%	48.29%
Proteobacteria	7.52%	9.81%
Verrucomicrobia	0.00%	1.64%



# **Species richness**



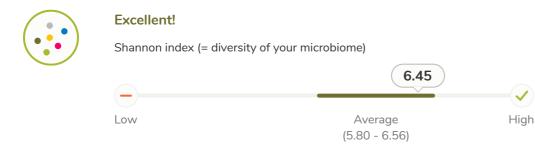
The number of different bacterial species in your intestine is **259**. Thus, the microbial diversity in your gut system is within normal levels. If your species richness was a bit higher, your microbiome could help you fight off diseases even better. You can find out how to support your microbiome in your personalized recommendations.

#### Description

Species richness describes the number of different species / types of bacteria in your gut system. In a more diverse microbiome, the large number of different bacterial species can contribute to many different functions being carried out by bacteria. As a consequence, your body can utilize food and nutrients better, as well as handle stress and malnutrition more easily.<sup>9,10</sup>



# Diversity



The diversity of your microbiome is outstanding. This means that your microbiome ideally supports you during your daily challenges.

#### Description

Diversity describes the variety of the microbiome. Species richness describes how many different types of bacteria are in your gut. Diversity also indicates whether the different types of bacteria occur evenly in the intestine or whether some types of bacteria dominate. The Shannon index is the most commonly used numerical indicator to represent this biological diversity. The more different bacterial types are evenly distributed in your gut, the greater the diversity in your gut and the more resilient your microbiome is. Furthermore, many studies have shown that a low degree of diversity is associated with disease. <sup>6,10,11,12,13</sup>

#### **Risk factors**

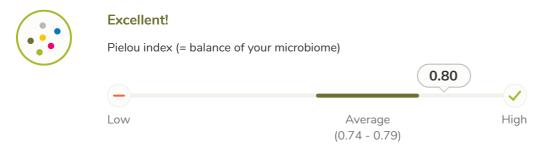
The personal microbiome is individually shaped by various environmental influences, such as antibiotic intake, infections, stays abroad, an unbalanced diet or smoking. Another factor influencing biodiversity and diversity is increasing age.

A varied diet with **lots of fiber** promotes bacterial diversity. Whole grain products, natural rice, fruit and vegetables contain a lot of fiber. Find out more in your personal suggestions for improvement.



Microbial composition

# **Species evenness**



Your microbiome is well balanced. This means that your bacteria are distributed evenly.

#### Description

Species evenness is a further measure to characterize the biodiversity of the intestinal bacteria. It expresses how often one type of bacteria occurs in your intestine compared to other bacteria. The higher the equitability, the more balanced the spread of different bacteria between species. For example, if there were only two species in your microbiome, Lactobacillus and Enterococcus, then 2% of Lactobacilli and 98% of Enterococci would have a low equivalence. However, if 50% Lactobacilli and 50% Enterococci are present, the species equivalence would be very high.

#### **Risk factors**

Just like diversity, species evenness is influenced by various environmental factors, in particular infections, antibiotic intake and an unbalanced diet.



Microbial composition

# **Probiotic bacteria**

•	Good, easy to improve!	
••	<ul> <li>very good</li> <li>improvable</li> </ul>	

You have many probiotic bacteria. However, a few bacteria are under-represented. Find out how you can improve the ratio of these bacteria in your personalized recommendations.

#### Description

The World Health Organization (WHO) defines probiotics as living microorganisms that are beneficial to your health when administered in sufficient quantities. The probiotic bacteria listed here are typically found in readily available foods or probiotic supplements. It is important to keep in mind that your microbiome is unique and that the amount of each bacterial species does not necessarily have a negative impact on your health. As diverse as nature is, there are certainly healthy people in whose gut few probiotic bacteria can be detected.

#### **Detailed information**

Bacterium	Your result	Food containing the probiotic bacterium
<ul> <li>Bifidobacterium</li> <li>14 15 16 17 18 19 20</li> </ul>	Low	Natural yoghourt, kefir
<ul> <li>Enterococcus</li> <li>25 26</li> </ul>	Normal	Mozzarella, camembert, goat cheese, green olives, millet products
<ul> <li>Lactobacillus</li> <li>21 22 23 24</li> </ul>	Low	Natural yoghourt, cheese, kefir, kombucha, sauerkraut, sourdough bread, pickles, olives
<ul> <li>Lactococcus</li> <li>26</li> </ul>	Normal	Buttermilk, kefir, cheese
Streptococcus 24 26	Low	Natural yoghourt, kefir, cheese

The scientific situation regarding probiotic bacteria has not been fully clarified, therefore a general recommendation for taking probiotic supplements is currently not possible. However, they can be supplied by diet or dietary supplements.



# Nutrition and food utilisation

# Enterotypes



**Enterotype 2** 

This enterotype is particularly common among vegetarians. Only every 10th vegetarian has an enterotype 1. Prevotella bacteria mainly degrade sugar protein complexes that are found in the mucous membranes of the intestinal mucosa. In addition, these bacteria mainly produce vitamin B1 (thiamine) and folic acid. Enterotype 2 is often a strong indicator for a healthy gut system. Your enterotype can also break down and store sugar quickly.

#### Description

Although your microbiome is as individual as your fingerprint, it can still be roughly subdivided into a basic microbiome, the socalled enterotype. The enterotype develops during the first years of life. It is independent of gender, age or geographical origin. Your enterotype is mainly related to your genetics and eating habits. Each enterotype is dominated by a different bacterial strain. The enterotype affects energy production from food as well as the production of vitamins. 49,50,51,52

A distinction is made between three enterotypes:

- Enterotype 1
- = Especially for people who often eat meat: Bacteroides <sup>49,50,51</sup>



#### Enterotype 2

- = Especially for people who eat vegan or vegetarian food: Prevotella <sup>49,50,53,96</sup>
- Enterotype 3
  - = Especially for people who prefer a balanced diet: Ruminococcus <sup>49,51</sup>

Bacteria type	Ratio
Bacteroides	0.4 ×
Prevotella	4.0 ×
Ruminococcus	0.2 x



#### Nutrition and food utilisation

# **Caloric intake**



The ratio between Bacteroidetes and Firmicutes in your gut is very good. Your bacteria can utilize enough calories from the ingested food. Because these bacteria are in a balanced ratio, the probability of being overweight is lower.

#### Description

Firmicutes and Bacteroidetes are the most common representatives of colon bacteria. Firmicutes can split nondigestible fiber and store it for "bad times". Thereby giving the body more energy when needed. The number of Bacteroidetes increases as soon as the bodyweight is reduced. Therefore, one can draw conclusions about how good the calorie utilization in your body is. When you lose weight through a calorie-restricted diet, this ratio usually decreases as well. <sup>50,54,67,137</sup>

You can change the number of Bacteroidetes by altering your diet. Bacteroidetes prefer e.g. high-fiber diets such as flaxseed, legumes and whole grains.



# Sugar metabolism



Your microbiome delivers support in the processing of sugar.

#### Description

The body obtains about half of the energy it needs from carbohydrates. Dietary carbohydrates can be divided into three main categories:

- 1. Sugars, such as granulated sugar and fruit juices
- 2. Starch, such as found in rice and cereals
- 3. Fibers, such as found in vegetables and nuts. In fact, we humans cannot digest dietary fiber, though they promote your microbial growth.

The first two categories - sugar and starch - are broken down and absorbed in the intestine. Amino sugars, pentose, sucrose and glucose belong to the first two categories. Your body obtains its energy by burning these sugar molecules. This energy can also be converted into fat and stored for later use. <sup>27,28,29,</sup>

#### Microbiome

Intestinal bacteria can partly utilize these carbohydrates and also influence how much sugar you absorb. This predictive functional analysis of intestinal bacteria tells you how your intestinal bacteria perform the task of recycling sugar. These values are compared to the average population (average = 100%).

Sugar	Your value (%)	
Amino sugar	88	$\downarrow$
Pentose	83	$\downarrow$
Sucrose	78	$\downarrow$
Glucose	83	$\downarrow$



Nutrition and food utilisation

# Lipid metabolism



Your microbiome delivers support in the processing of fatty acids.

#### Description

Lipid metabolism includes all processes involved in the breaking down of dietary fats and the building up of fatty acids in the intestine. Important components such as triglycerides, cholesterol and other fatty acids from your diet are absorbed by your digestive system.<sup>27,28,29</sup>

#### Microbiome

Steroids, fatty acids and sphingolipids are important representatives of fats and are processed and reused by the intestinal bacteria. These serve as energy sources and are important for your brain and nervous system as well as being cell building blocks and the basis for the production of hormones. This predictive functional analysis of intestinal bacteria tells you how your intestinal bacteria perform the task of recycling fats. These values are compared to the average population (average = 100%).

Fat	Your value (%)	
Steroid	67	$\downarrow$
Fatty acid	85	$\downarrow$
Sphingolipid	72	$\downarrow$



# Vitamin metabolism



Your microbiome delivers support in the production of vitamins.

#### Description

Vitamins are vital substances and necessary for energy production, immune function, blood clotting and other functions. Minerals, that along with vitamins belong to the group of micronutrients, play an important role in growth, bone health, fluid balance and various other processes. The body cannot produce most micronutrients itself. Therefore, these micronutrients must be ingested regularly with food. <sup>27,28,29</sup>

#### Microbiome

Some bacteria can produce vitamins themselves. Among other things, they produce vitamin B6, vitamin K, lipoic acid and folic acid in small amounts.

This predictive functional analysis of intestinal bacteria reveals how your intestinal bacteria divide tasks regarding the utilization and production of vitamins. These values are compared to the average population (average = 100%).

Vitamin	Your value (%)
Vitamin B6	90 🗸
Folate	93 🗸
Lipoic acid	62 🗸
Vitamin K	92 🗸



Nutrition and food utilisation

# Protein metabolism



Your microbiome delivers support in the processing of proteins.

#### Description

Proteins do most of the work in the cell and have many other tasks. Examples include growth and maintenance of tissue, production of enzymes and hormones, regulation of the concentration of acids and bases in your blood and other body fluids, and formation of antibodies in your immune system to fight infections. Likewise, proteins have a storage function (e.g. ferritin, which stores iron) and they can supply your body with energy. Important protein building blocks (= amino acids) are phenylalanine, arginine and glutamine. <sup>27,28,29</sup>

#### Microbiome

Your intestinal bacteria contribute to the proper metabolism of proteins and thus help keep the processes described above running smoothly.

This predictive functional analysis of intestinal bacteria reveals how your intestinal bacteria divide the tasks of utilizating and further processing of proteins and their building blocks. These values are compared to the average population (average = 100%).

Protein	Your value (%)	
Phenylalanine	81	$\checkmark$
Arginine	79	$\downarrow$
Glutamine	91	$\downarrow$



# Health

# Stomach pains

•		$\checkmark$	very good
		_	improvable

Stomach pain is a symptom. From a medical and scientific perspective, it is currently impossible to distinguish between short-term complaints and chronic symptoms using microbial analysis. Therefore, we cannot give an overall assessment here.

#### Description

One of the most common and unspecific symptoms is abdominal pain. It can be quite diverse, such as dull, stinging or crampy, diffuse or focal, acute or chronic. Chronic abdominal pain can be an indicator of an irritated bowel (irritable bowel syndrome). Whereas acute abdominal pain is, in most cases, caused by infections. Some abdominal pain is associated with bacteria. <sup>154</sup>

#### Associations

	Associated bacteria	Your result	Protective bacteria	Your result
<b></b>	Bifidobacterium 120 154 168	Low	Akkermansia muciniphila 91	Low
<b>I</b>	Blautia 154	Normal 🥑	Prevotella 154	High
<b></b>	Streptococcus 154	Low		

Peppermint: menthol, a compound found in mint, helps reduce muscle cramps in your intestines, as well as pain.



Health

# Flatulence and bloating

very good
mprovable

Flatulence and bloating are symptoms. From a medical and scientific perspective, it is currently impossible to distinguish between short-term complaints and chronic symptoms using microbial analysis. Therefore, we cannot give an overall assessment here.

#### Description

Flatulence and bloating are symptoms. They occur when there is too much gas in the intestine, which is caused by the fermentation of food components and the metabolic processes of your intestinal bacteria. It is called flatulence as soon as the gases escape through the anus. These can sometimes have a strong smell. Bloating (= meteorism) occurs when the gases cannot escape via the anus as wind. Bloating describes an inflated abdomen and can cause severe abdominal pain. <sup>156,157,158</sup>

#### Causes

Both symptoms are often triggered by hasty eating habits, whereby a lot of air is swallowed. Further causes include poor diet, psychological factors, hormones (during menstruation & pregnancy), as well as irritable bowel syndrome. Very rich, greasy or sweet food and excessive coffee and alcohol consumption can significantly influence the development of bloating as well as alter your microbiome. Moreover, sugar substitutes such as sorbitol or xylitol, which are found in many diet, light and sugar-free products, can promote these symptoms. Some bacteria are associated with bloating or flatulence.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
Blautia 99 121	Normal	Oscillospira 121	High
Coprococcus	Normal		
Desulfovibrio 99 118	Low		
Phascolarctobacterium 121	Normal		

Ginger contains essential oil and bitter substances. These stimulate digestive activity in the stomach and intestine which can help let the accumulated air in the intestine escape.



Health

# Constipation

				$\checkmark$	very good
•				_	improvable

Constipation is a symptom. From a medical and scientific perspective, it is currently impossible to distinguish between short-term complaints and chronic symptoms using microbial analysis. Therefore, we cannot give an overall assessment here.

#### Description

Constipation is already accepted as a lifestyle disease and one of the most common complaints in industrialized countries. Constipation is characterized by having less than three bowel movements per week. A distinction is made between acute and chronic constipation. For the most part, constipation is considered harmless. However, it can also be a symptom of other diseases (e.g. irritable bowel syndrome, colonic inertia, changes or disorders of the rectum). <sup>124</sup>

#### Causes

Constipation is often caused by a lack of daily physical activity, one's diet or hydration level. Some bacteria can be associated with constipation.

#### Associations

	Associated bacteria	Your result	Protective bacteria	Your result
<b>I</b>	Butyricimonas 32	Normal	<ul> <li>Faecalibacterium prausnitzii</li> <li>32 102 122</li> </ul>	Normal
<b>I</b>	Coprococcus 32 122	Normal	<ul> <li>Lactococcus</li> <li>32</li> </ul>	Normal
<b>I</b>	Phascolarctobacterium 32	Normal	Roseburia 32 104 122	Low
<b>S</b>	Ruminococcus 101 104 123	Low		
<b></b>	Veillonella 18	Low		

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Figs contain laxatives, which help to relieve constipation and thus stimulate healthy digestion.



Health

### Diarrhea



Diarrhoea is a symptom. From a medical and scientific perspective, it is currently impossible to distinguish between short-term complaints and chronic symptoms using microbial analysis. Therefore, we cannot give an overall assessment here.

#### Description

Diarrhea is a common symptom and is determined by stool frequency and stool composition. In adults, diarrhea occurs when bowel movements occur more than three times a day. The consistency must be fluid and accompanied by a strong urge to pass a bowel movement. Diarrheal diseases are usually accompanied by vomiting, nausea and a loss of appetite. One differentiates between acute and chronic diarrhea. <sup>33</sup>

#### Causes

Acute diarrheal diseases are often caused by gastrointestinal infections, perishable foods or intolerances. Chronic diarrheal diseases can often be associated with irritable bowel syndrome, food intolerances or metabolic diseases. Stress can also be a cause of diarrhea. Some bacteria can be associated with diarrhea.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
<ul> <li>Bacteroides fragilis</li> <li>30 31 35 101</li> </ul>	Low	Collinsella 104 105	Low
Eggerthella	Low	Faecalibacterium prausnitzii 308	Normal
<ul> <li>Parabacteroides</li> <li>35 101</li> </ul>	Low	Lactobacillus 104 307	Low
<ul> <li>Prevotella</li> <li>35 101</li> </ul>	High		
Slackia	High		
Streptococcus	Low		

The mucilage in the shells of psyllium seeds can bind a lot of water and thus serve as a swelling agent. They increase the volume of stool, exerting more pressure on the intestinal wall, which in turn stimulates intestinal peristalsis.



Health

### Intestinal mucosa



Your intestinal bacteria support your intestinal mucosa. With small improvements your intestinal bacteria can help regenerate the intestinal mucosa even more efficiently. Learn more about this in your personalized recommendations.

#### Description

The mucus of the intestinal mucosa serves as a protective layer. The production and breakdown of the mucus is stimulated by your bacteria. The mucus ensures that your intestinal bacteria keep enough distance to the mucous membrane, so as not to permanently irritate the local immune cells thereby triggering an inflammatory process and disrupting the barrier function. When your bacteria are imbalanced, it can lead to increased degradation of the mucus, which results in a reduction of this important protective layer. One type of intestinal barrier disorder is the so-called "leaky gut". In this case, the increased intestinal permeability is due to loosened tight junctions between the mucosal cells in the small intestine. This creates unwanted gaps that allow small amounts of toxins to overcome your intestinal barrier and thus enter your bloodstream. <sup>89,90,167</sup>

#### **Risk factors**

Among the triggers of Leaky Gut are infections, medication, chronic inflammations, consumption of toxins, such as smoking, alcohol, sugar-rich food, as well as a changed composition of bile acids.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
Collinsella	Low	<ul> <li>Akkermansia muciniphila</li> <li>61 91 97</li> </ul>	Low
<ul> <li>Pseudomonas</li> <li>86 167</li> </ul>	Normal	<ul> <li>Bifidobacterium bifidum</li> <li>92 93 94</li> </ul>	Normal
<ul> <li>Salmonella enterica</li> <li>41 42</li> </ul>	Normal	Catenibacterium 50	Normal
Sutterella 87 177	Normal	<ul> <li>Faecalibacterium prausnitzii</li> <li>34 36 49</li> </ul>	Normal
		<ul> <li>Prevotella</li> <li>49 96</li> </ul>	High
		Roseburia	Low
		Ruminococcus gnavus 97 98	Low



Health



The most important measure for a healthy intestinal mucosa is a balanced diet. Your diet should be rich in healthy fatty acids, fiber, vitamins and minerals to help calm your bowels and stop inflammation.



Health

### Irritable bowel syndrome



Most intestinal bacteria associated with irritable bowel syndrome are within average levels.

#### Description

Irritable bowel syndrome is a functional disorder of the digestive system. Although this disorder is not life threatening, it often reduces the quality of life. This usually manifests itself in constipation, diarrhea and pain. Reasons for this might be problems in digestion and absorption (e.g. problems with bile acid), a disturbed protective barrier of the intestinal mucosa (intestinal permeability), the microbiome, immune modulations and inflammations, as well as the nervous system. There is a so-called "second brain" in your gut, the enteric nervous system, which is in constant communication with your head via the gut-brain axis. When you are stressed a number of different circuits, which are communicated across the gut-brain axis, get stressed. Thus, your microbiome significantly influences the development of inflammatory processes in your intestine via immune changes caused by intestinal mucosal damage and bacterial imbalances. <sup>101,171</sup>

#### **Risk factors**

There are many factors that can cause irritable bowel syndrome. Stress and emotions are often associated with this disorder. Other triggers that may aggravate the symptoms and also amplify the causes listed above include malnutrition and lack of nutrients, other diseases, toxins, lack of gastric acid, medication, infections and a bacterial imbalance.



Health

#### Associations

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Associated bacteria	Your result	Protective bacteria	Your result
Blautia 101 201	Normal	<ul> <li>Akkermansia muciniphila</li> <li>91 178</li> </ul>	Low
Coprococcus 100 310	Normal	<ul> <li>Bifidobacterium</li> <li>100 102 104 108 168 309</li> </ul>	Low
<ul> <li>Dialister</li> <li>37 101</li> </ul>	Low	<ul> <li>Collinsella</li> <li>18 35 104 105 311</li> </ul>	Low
Oorea 101 104	Normal	<ul> <li>Faecalibacterium prausnitzii</li> <li>109 152 178 201 308</li> </ul>	Normal
<ul> <li>Enterobacteriaceae</li> <li>101 103</li> </ul>	Low	Odoribacter 101 152	Normal
Roseburia 101 104	Low	<ul> <li>Prevotellaceae</li> <li>37 201</li> </ul>	High
<ul> <li>Ruminococcus</li> <li>100 101 104 105 106 107</li> </ul>	Low		
Salmonella 40 170	Normal		
Veillonella 177 309	Low		

Unfortunately, you can't relax at the touch of a button. Likewise, there is no "proper nutritional behavior" for irritable bowel syndrome because it needs to be individually adjusted. However, one can begin with small steps, such as being calm while eating and having 5 meals a day.



Health

### **Gut-brain** axis

$\bigcirc$	G	00	d,	ea	sy	to	im	pr	ove	e!						
$(\sim)$					•	•	•	•	•	•	•	•	•	•	$\checkmark$	very good
	•	•	•	•											_	improvable

You seem to have everything under control! Your intestinal bacteria are trying to support you in the best possible way. Try to reward them a little more by following your personalized recommendations.

#### Description

Gut over head! Your gut is home to over 100 million nerve cells that lead directly to the brain. That's even more nerve cells than those that lead from the brain to the entire body. This means that your gut is constantly exchanging information with your brain. The nervous system of your gut uses the same neurotransmitters (information carriers between cells) as your brain. Neurotransmitters play an important part in mental illness, such as depression. Your microbiome is also an indispensable player, because the metabolism of your bacteria in the digestive tract can disturb the balance of brain messengers such as norepinephrine, dopamine or serotonin and thus influence your frame of mind. <sup>146,153,172</sup>

#### **Risk factors**

There are usually many factors that can contribute to listlessness or depression. Often, they are physical or circumstantial causes such as chronic illness, hormonal imbalance, permanent stress and conflicts, loneliness or other misfortunes.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
<ul> <li>Actinomycetaceae</li> <li>38 99</li> </ul>	Normal	<ul> <li>Bifidobacterium</li> <li>114 117 182 183</li> </ul>	Low
Anaerostipes 41 153 180	Normal	Coprococcus	Normal
<ul> <li>Anaerotruncus</li> <li>100 181</li> </ul>	Low	<ul> <li>Dialister</li> <li>112 153</li> </ul>	Low
Bacteroides 39 41 100	Low	Dorea 41 113	Normal
Blautia	Normal	<ul> <li>Faecalibacterium</li> <li>110 111 153</li> </ul>	Normal
<ul> <li>Lachnospiraceae</li> <li>100 153 180</li> </ul>	Normal	<ul> <li>Lactobacillus</li> <li>112 114 115 116 117</li> </ul>	Low
<ul> <li>Verrucomicrobia</li> <li>180 181</li> </ul>	Low	Ruminococcus 41 111 153	Low



Health

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Our gut communicates closely with our brains, so we can actually influence our disposition a little bit through food. Omega-3 fatty acids, folic acid and vitamin B enhance our mental performance.



Health

### **Gut-heart** axis

$\bigcirc$	Good, easy to improve!
$\bigcirc$	<ul> <li>very good</li> <li>mprovable</li> </ul>

Most gut bacteria that are associated with a healthy gutheart axis are doing alright. That's good. To strengthen your intestinal-heart-axis further we have a few suggestions. These can be found in your personalized recommendations.

#### Description

Diseases of the vascular system and/or the heart (cardiovascular diseases) affect approximately one third of the population. Recently, it has been shown that the microbiome is involved in the development of such diseases.

#### **Risk factors**

Bacteria metabolize certain substances such as choline and L-carnitine (contained in eggs and milk) to trimethylamine. These are then converted into trimethylamine N-oxides (TMAO) in the liver . TMAO promotes the absorption of cholesterol and can thus contribute to the development of cardiovascular diseases. In addition, a disturbed barrier function of the intestinal mucosa (see Leaky Gut) can trigger an inflammatory cascade. Metabolic products of bacteria can penetrate the blood circulation system and contribute to the development of atherosclerosis (deposition of fat, blood clots, connective tissue and calcium in the blood vessels) and heart failure (weakness of the heart muscle). <sup>42,43,44</sup>

#### Associations

Associated bacter	ia Your result	Protective bacteria	Your result
Collinsella 202	Low	Bacteroides	Low
<ul> <li>Enterobacter</li> <li>203 205</li> </ul>	Normal	Blautia 45 203	Normal
Megamonas 205	Normal	Faecalibacterium 202 203	Normal
Streptococcus 203	Low	<ul> <li>Roseburia</li> <li>83 202 203 204</li> </ul>	Low

j

A low-fat diet helps to improve your bowelheart axis.



Health

### **Gut-liver** axis



Your gut bacteria support the functions of your liver. Help your gut bacteria continue in doing their job well by following your personalized recommendations.

#### Description

Your liver is the most important metabolic organ and its health is crucial for your quality of life. As the detoxification center of the body, it frees you from alcohol, nicotine, sugar and medication. In addition, it performs important metabolic tasks such as the production of coagulation factors and bile. How much the liver is used on a daily basis depends, among other things, on a healthy intestinal function. Your intestine and liver are in constant contact and are connected via the blood circulation (portal vein). Nutrients and bacterial components are released into the liver via this large blood vessel. In this analysis, we focus on the association between non-alcoholic fatty liver and intestinal bacteria. <sup>84,161,221</sup>

#### **Risk factors**

Risk factors for an imbalance of the gut-liver axis are often an unhealthy lifestyle and medication. Often an imbalance of the gut-liver axis occurs as a side effect of chronic disease.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
<ul> <li>Alcaligenaceae</li> <li>125 126</li> </ul>	Normal	Coprococcus 66 142 144	Normal
Orea 66 145	Normal	<ul> <li>Lachnospiraceae</li> <li>66 125 126</li> </ul>	Normal
<ul> <li>Enterobacteriaceae</li> <li>125 126</li> </ul>	Low	Odoribacter	Normal
<ul> <li>Fusobacteriaceae</li> <li>125 126</li> </ul>	Normal	Oscillospira 85	High
<ul> <li>Lactobacillus</li> <li>66 85 185</li> </ul>	Low	Prevotella 128 129	High
<ul> <li>Megasphaera</li> <li>85 125 126 176</li> </ul>	Normal	<ul> <li>Roseburia</li> <li>66 144</li> </ul>	Low
<ul> <li>Peptoniphilus</li> <li>144 145</li> </ul>	Normal	Ruminococcaceae 65 66 125 126 128 130	Normal
<ul> <li>Porphyromonas</li> <li>125 126 127 144</li> </ul>	High		
Streptococcus 85 128 179	Low		



Health

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A healthy liver increases your quality of life and performance. Liver damage develops slowly and over many years, so support your liver. Avocados contain many antioxidants and glutathione that support liver function.



Health

### **Gut-skin axis**

$\frown$	Good, easy to improve!
$(\sim)$	<ul> <li>very good</li> <li>mprovable</li> </ul>

Most gut bacteria associated with a functioning gut-skin axis, are doing their job well. That's good! You can strengthen your bacteria a little more by following your personalized recommendations.

#### Description

Your skin and your gut are both organs with dense vascular structures and rich in nerve fibers. Overall, your gutskin axis is composed of a complex communication network that includes the immune system, the hormonal system (endocrine system), the metabolic system and the nervous system. An imbalance in gut bacteria has recently been associated with psoriasis, rosacea (copper rose), atopic dermatitis and acne. In this analysis, we focus on associations between psoriasis and gut bacteria. <sup>119,160,162</sup>

#### **Risk factors**

When stressed, certain gut bacteria produce neurotransmitters that can have a negative effect on skin function. Diet and medications can affect your skin through nutrient signaling and long-chain fatty acids. In doing so, a specific protein (SREBP-1) as well as the buildup of fatty acids are activated, which in turn influences the condition of the skin.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
<ul> <li>Akkermansia</li> <li>184</li> </ul>	Low	Actinobacteria 198	Low
<ul> <li>Faecalibacterium prausnitzii</li> <li>184 197 200</li> </ul>	Normal	Bacteroides 184	Low
<ul> <li>Ruminococcus</li> <li>184</li> </ul>	Low	Coprobacillus	Normal
		Lactobacillus 159	Low



Health

### Metabolic syndrome

$\bigcirc$	Good, easy to improve!	
(	<ul> <li>very good</li> <li>e</li> <li>e<th></th></li></ul>	

Most gut bacteria that are scientifically associated with obesity are within normal levels. That's good! You can strengthen your bacteria a little more by following your personalized recommendations.

#### Description

Our body is subject to the laws of thermodynamics. Therefore, an "excess" of unneeded calories leads to weight gain. This in turn can lead to obesity (nutritional and metabolic disease with severe overweight - BMI > 30kg/m2). As a result, diseases such as insulin resistance, atherosclerosis (fat deposits in the artery walls) and hormonal problems can develop. Above all, however, your microbiome also suffers from this imbalance. Your intestinal bacteria are essentially involved in the utilization of your food and influence how many calories are gained from the food. In this analysis we have focused on the association of your intestinal bacteria with obesity. <sup>76,77,78,138,140,172</sup>

#### **Risk factors**

Unhealthy living and eating habits are the main cause of metabolic syndrome. Often there is also a genetic predisposition that can be promoted by an unhealthy lifestyle. In addition to a high-fat and high cholesterol diet, other risk factors include increased alcohol consumption, smoking and lack of physical activity.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
<ul> <li>Actinomyces</li> <li>20 138</li> </ul>	Normal	<ul> <li>Akkermansia muciniphila</li> <li>60 61 62 63 137</li> </ul>	Low
<ul> <li>Adlercreutzia</li> <li>138</li> </ul>	Low	Anaerotruncus 56 64	Low
<ul> <li>Lactobacillus</li> <li>22 23 47</li> </ul>	Low	<ul> <li>Bacteroides fragilis</li> <li>47 199</li> </ul>	Low
Prevotella 65 159	High	Dialister 214	Low
<ul> <li>Ruminococcus</li> <li>60 137</li> </ul>	Low	<ul> <li>Lachnospira</li> <li>20 137</li> </ul>	Normal
		Oscillospira 66 138	High



Health

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Saturated fatty acids increase blood lipids, which has a negative effect on cardiovascular health and increases the risk of metabolic syndrome. Try to reduce these. Saturated fatty acids are found mainly in milk chocolate, fatty meats and sausages, coconut oil and readymade meals.



Health

### Insulin balance

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	•	•	•											_	improvable

Your intestinal bacteria support you in the absorption and utilization of sugar! That's very good. You can further support your bacteria with a few tips in your personalized recommendations.

#### Description

A disorder of blood sugar metabolism means that your body can no longer properly transport the glucose it absorbs from a meal – such as sugar or certain carbohydrates – into your cells with the help of insulin, where it serves to supply energy. Insulin is a hormone produced by the pancreas that regulates blood sugar levels in the body. Normally, the glucose level in the blood drops again after eating. The speed at which this happens indicates how well your cells respond to insulin. However, if these values do not drop within a certain period of time, there may indicate a blood sugar disorder. This means that your cells no longer respond sufficiently to insulin. The sugar accumulates in the blood vessels, which can cause health problems. Your gut bacteria influence the absorption and utilization of sugar and thus your blood sugar levels. <sup>79,81,82,164</sup>

#### **Risk factors**

Lack of exercise, overweight and stress often lead to a disturbance of the insulin balance. However, lack of sleep, smoking and medication could also be involved in the development of such a disorder.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
Bacteroides 72 74	Low	<ul> <li>Bifidobacterium</li> <li>72 73 74</li> </ul>	Low
<ul> <li>Betaproteobacteria</li> <li>75</li> </ul>	Normal	<ul> <li>Blautia</li> <li>70 72 151 166</li> </ul>	Normal
Collinsella 69	Low	<ul> <li>Butyricimonas</li> <li>73</li> </ul>	Normal
<ul> <li>Eggerthella</li> <li>68 69 72</li> </ul>	Low	<ul> <li>Erysipelotrichaceae</li> <li>68 166</li> </ul>	Low
<ul> <li>Lactobacillaceae</li> <li>79</li> </ul>	Low	Firmicutes 70 75 79 190	Normal
<ul> <li>Ruminococcus</li> <li>70 166</li> </ul>	Low	<ul> <li>Lachnospiraceae</li> <li>68 70 166</li> </ul>	Normal
Veillonella 72 73 165	Low	Megamonas 70	Normal
		Roseburia 68 70	Low



Health

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A balanced diet with complex sugars, such as whole meal products, can help control and strengthen the insulin balance. Whole grain products also contain important fibers, vitamins and minerals.



Health

### **Kidney stones**



The gut bacteria associated with the formation of kidney stones are well within normal levels! That's optimal!

#### Description

Your kidneys produce your urine. Urine is used to excrete water-soluble substances such as harmful metabolites or drugs together with water. They also stabilize your blood pressure by monitoring the volume of fluid in your body. In addition, your kidneys also control the salt content in your body, because too much salt increases the amount of fluid, which in turn increases blood pressure.

Your gut bacteria help convert your food into metabolic products that can be further processed, so that your kidneys have less work to do. <sup>136</sup>

#### **Risk factors**

An example is oxalates. Oxalates are compounds of oxalic acid and potassium, calcium or magnesium found in your food. They are metabolized by certain bacteria in your gut. If the bacteria are unable to break down oxalates adequately, oxalates will be transported to your kidneys where they form unpleasant kidney stones. This analysis describes the association of intestinal bacteria with the utilization of oxalates.

#### Associations

	Associated bacteria	Your result		Protective bacteria	Your result
0	Bacteroides 131	Low	<	Oxalobacter formigenes 120 132 133 134 135	High
			<ul> <li>Image: A start of the start of</li></ul>	Prevotella 135 206	High

You can reduce the formation of oxalates in your body by drinking plenty of still water.



Health

### Gallstones

$\bigcirc$	Good, easy to improve!
$\bigcirc$	<ul> <li>very good</li> <li>mprovable</li> </ul>

Most gut bacteria that are associated with the formation of gallstones are within average levels. That's good! In order to continue supporting your bacteria, we have a few recommendations for you in your personalized recommendations.

#### Description

Gallstones often occur in people over 40 years old. Women in particular often suffer from gallstones. Almost 90% of diagnosed gallstones are cholesterol gallstones. These consist of crystallized components of the bile fluid with an increased bile cholesterol content. Whether symptoms occur is strongly related to the size and location of the gallstones. Possible symptoms include unpleasant, cramp-like upper abdominal pain that occurs in waves, or bloating, flatulence, nausea, and belching. Your intestinal bacteria are involved in regulating the bile acid recycling process and may even alter the properties of the bile acid. This is related to your diet and the metabolic activity of your bacteria. An imbalance of the bacteria can thus promote gallstone formation. <sup>209,217,218</sup>

#### **Risk factors**

Risk factors for gallstones include a cholesterol-rich diet, elevated blood fat levels and metabolic diseases.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
<ul> <li>Bilophila</li> <li>88 177</li> </ul>	Low	<ul> <li>Bacteroides uniformis</li> <li>208</li> </ul>	Normal
Oscillospira 208 209	High	<ul> <li>Faecalibacterium</li> <li>207</li> </ul>	Normal
		<ul> <li>Lachnospira</li> <li>207</li> </ul>	Normal
		<ul> <li>Roseburia</li> <li>88 177 207 208</li> </ul>	Low



Health

### Joint health

$\frown$	Good, easy to improve!
$(\sim)$	<ul> <li>very good</li> <li>e</li> <li>e</li></ul>

Most gut bacteria associated with rheumatoid arthritis are within normal levels. That's good! To continue supporting your bacteria, we have a few suggestions for you in your personalized recommendations.

#### Description

Rheumatoid arthritis is an autoimmune disease that primarily affects the joints. It leads to constant inflammation and destruction of joints and bones because the body's immune system is directed against its own cell structures. The mechanism is very complex and depends on innate and acquired immune responses. The permeability of your intestinal mucosa and microbial imbalances play a role, because they can throw the immune system off balance.<sup>219</sup>

#### **Risk factors**

Rheumatoid arthritis is the result of genetic, environmental and hormonal factors, with bacterial and viral components identified as the most common potential pathogens.

#### Associations

Associated bacteria	Your result	Protective bacteria	Your result
Bacilli 189	Low	Bacteroides 186 196	Low
Collinsella 191 193	Low	<ul> <li>Bacteroides fragilis</li> <li>187 188 190</li> </ul>	Low
Eggerthella	Low	<ul> <li>Bifidobacterium</li> <li>187 188 190</li> </ul>	Low
<ul> <li>Prevotella copri</li> <li>186 192 195 220</li> </ul>	High	<ul> <li>Faecalibacterium prausnitzii</li> <li>189 191</li> </ul>	Normal
		<ul> <li>Flavobacterium</li> <li>189</li> </ul>	Normal
		Roseburia	Low

An increased consumption of coffee (5-10 cups per day) can promote the development of rheumatoid arthritis. A reduction in coffee consumption is therefore beneficial.



# Improvement suggestions

### About the recommendations

We have listed many recommendations for your improvement here. Not all of them will apply to you. Food intolerances and personal preferences have not been taken into account in the recommendations. Try to find out which ones are best for you and which ones you can easily integrate into your everyday life.

# Personal recommendations

#### Eat more L-glutamine (meat, dairy, spinach, parsley) — Intestinal mucosa

L-glutamine helps build up the intestinal mucosa. L-glutamine is included in the following foods: beef, chicken, fish, dairy, beans, parsley and spinach. <sup>255,256</sup>

#### Relieve the inflammation — Irritable bowel syndrome

Try to relieve inflammation in your intestine. The following spices may help you: turmeric, frankincense extract (Boswellia serrata), juniper, chamomile and sage.<sup>324</sup>

#### Tryptophan (pumpkin seeds, dates, avocados) helps — Gut-brain axis

Tryptophan is an essential amino acid that can be converted into serotonin (= neurotransmitter). Tryptophan can help reduce repressive moods, anxiety, and stress and improve performance. Tryptophan is found in the following foods: tuna, pumpkin seeds, amaranth, dates, avocados, strawberries, figs and papayas. <sup>267,268,269</sup>

#### Anthocyanins (grapes, eggplant, red cabbage) support — Gut-heart axis

Anthocyanins are powerful antioxidants. They prevent premature cell aging and help the heart avoid the formation of blood clots. Anthocyanins are present in blue and purple vegetables and fruits, e.g. in blueberries, blackberries, elderberries, grapes, raisins, eggplants, prunes, figs, plums, lavender and red cabbage. <sup>301,302</sup>

#### Choose omega-3 fatty acids (fish, linseed oil, nuts) — Gut-liver axis

Omega-3 fatty acids are unsaturated fatty acids and essential for a healthy liver and healthy blood lipid levels. This reduces cholesterol levels and reduces the risk of hypertension and diabetes. Linseed oil, walnuts and fish are rich in omega-3 fatty acids. <sup>260,262,263,264</sup>

#### Choose food and drinks with high levels of polyphenols — Diversity

Polyphenols are antioxidants that act as fuel for your gut microbes. They help to foster the diversity of your microbes. Examples are nuts, seeds, berries, olive oil, brassicas, coffee and tea – especially green tea. <sup>313,314</sup>

#### Eat more antioxidants (cinnamon, almonds). — Lipid metabolism



Antioxidants such as eugenol, cinnamaldehyde, linalool and camphor protect the body from free radicals and support your metabolism. In addition, they minimize the risk of irritation of the digestive tract. Examples of foods that contain antioxidants are blueberries, cinnamon and almonds. Furthermore, cinnamon stimulates fat burning. Almonds contain a lot of vitamin E and fibre. <sup>252,254</sup>

### Strengthen your vitamin balance (potatoes, beef, leafy vegetables, tomatoes) — Vitamin

#### metabolism

Support your bacteria by giving them certain vitamins. For example, vitamin B6 is found in high amounts in fish, milk, carrots and potatoes. Vitamin B6 helps your body release energy in the form of sugar from stored carbohydrates and form red blood cells. Folic acid is found mainly in beef, liver, peas, spinach and asparagus and is an important factor for well-functioning cell division. Vitamin K, a component of leafy vegetables, soybeans and squash, is needed for blood clotting and bone development. Lipoic acid, which is involved in most enzyme reactions and affects insulin processing, is found mainly in meat products, spinach, broccoli and tomatoes.

### Use coconut oil for cooking — Protein metabolism

Coconut oil is relatively high in medium-chain fatty acids. These can boost your metabolism much better than long-chain fatty acids. However, use coconut oil only in moderation, because it contains many saturated fatty acids. <sup>318,319</sup>

#### Coenzyme Q10 (red meat, soy beans, broccoli) stimulates your metabolism — Sugar metabolism

Coenzyme Q10 is important for your energy production. It is a fat-soluble, body-own substance that can be supplied through the food though is also synthesised by the body itself. Olive oil, beef, sardines, soybeans and broccoli contain a high concentration of coenzyme Q10. <sup>320,321</sup>

### Strengthen your metabolism (green tea, guarana) — Metabolic syndrome

Green tea and guarana can boost your metabolism. In addition, both contain antioxidants that have an additional positive effect on the metabolism. Green tea in particular has also an anti-diabetic effect, positively affecting glucose and lipid metabolism and increasing glucose tolerance.<sup>331</sup>

### Blueberries, ginko and ginseng support you — Insulin balance

Blueberries and ginseng have an anti-diabetic and hypoglycemic effect on your body. Moreover, ginko promotes local microcirculation and hence has a positive effect on your insulin balance. <sup>333,334,335</sup>

### Pay attention to your vitamin C & D levels — Gallstones

Gallstones can often be associated with a reduced absorption of nutrients. In particular, the vitamin household can be affected. A lack of vitamin C can even contribute to the formation of gallstones. Therefore, try to get enough vitamins. <sup>339,340,341</sup>



#### Calcium and manganese support you — Joint health

Calcium is a key nutrient for bone metabolism and is therefore important for the stabilization of your joints. Manganese is a coenzyme of glycosyltransferase. This is involved in the formation of proteoglycans of the cartilage and connective tissue. Calcium is found in broccoli, chard, fennel as well as in in milk and cheese products. Manganese is found in many plant foods, such as cereals, legumes, rice and leeks. <sup>342</sup>

## Enterotype 2 — Enterotypes

You probably eat a diet based primarily on plant-based carbohydrates. Plant-based diets harbor many benefits for your body - for example, a balanced diet rich in fruits, vegetables, and whole grains protects against conditions such as obesity, high blood pressure, and atherosclerosis.

Your enterotype prefers many different vegetables and fruits (the more diverse, the better) Your enterotype needs adequate protein intake - your requirement is 0.8 g protein/kg body weight. Good sources of protein are meat, fish, eggs, dairy products and many plants (especially legumes such as peas, lentils, beans, chickpeas...). Regarding animal products it is important to consider to choose a good quality! According to your enteroytpe, complex carbohydrates (whole spelt bread, wild rice, whole wheat pasta) are preferable to simple carbohydrates (white bread, pasta, rice).

Regarding fat consumption, a diet with more unsaturated fatty acids (nuts, flax oil, avocado) than saturated fatty acids, as found in manufactured products, animal foods and hydrogenated fats, would do your body good. Based on your enterotype, it appears that adequate vitamin B12 (cobalamin) would be important. The more diverse the fruits and vegetables, the better for your enterotype

### Support with B vitamins — Gut-skin axis

B vitamins are essential for the regeneration process of the skin. Mainly, vitamin B6, vitamin B12 and biotin are essential for wound healing and epidermal differentiation processes. Additionally, B vitamins have stimulating effects on the metabolism. The following foods contain high levels of vitamin B: bananas, peas, oranges, red peppers, green vegetables (cabbage sprouts, green beans, lamb's lettuce), whole grain products, bananas, potatoes, soybeans, wheat germ, hazelnuts and walnuts. Try to incorporate those into your daily routine. <sup>329,330</sup>



Improvement suggestions

## **General recommendations**

### **Microbial health**

The following tips will help you to improve your microbial health:

#### Probiotic foods support.

Probiotic foods contain different strains of bacteria that support the regeneration of the intestine. Examples of probiotic foods are buttermilk, kefir, raw cheese, kombucha and natural yoghurt.

#### Prebiotic foods help.

Prebiotic foods help your bacteria because they contain fibres and nutrients, which play an essential role in the regeneration of your intestinal mucosa. Foods considered to be prebiotic are e.g. asparagus, artichoke, banana, chicory, eggplant, honey, leek, onion and Jerusalem artichoke. Try to incorporate them into your daily food intake (of course, only those that you can tolerate!).

#### Eat more fermented foods.

Bacteria in fermented foods support the species richness and variety in your gut: natural yoghurt, fresh sauerkraut, kefir, miso. <sup>236,246,270,271,78,225,226</sup>

### Abdominal pain

For abdominal pain the following recommendations can provide relief:

#### Menthol(peppermint) helps with cramps.

Menthol helps with muscle spasms in the gut and can reduce pain. Menthol stimulates the influx of calcium into smooth muscle cells, thereby relaxing them. In addition, menthol activates an "anti-pain channel" in the walls of the colon. This can dampen the perception of pain by sensitization. Menthol occurs naturally in peppermint. So, try some fresh mint tea. But be careful with the dosage in case you are prone to reflux!

#### Thymol and carvacrol (thyme) have a supporting effect.

Thymol and carvacrol are essential oils that are found mainly in thyme. Thyme also has a high content of lamiacaceous tannins and flavonoids. Thyme has a calming effect on the digestive system and additionally supports the cleansing of your intestines.

#### Alliin (garlic) relieves abdominal pain.

Garlic, a prebiotic with the main active ingredient Alliin, contains essential oils and flavonoids, as well as vitamins and minerals. This bulbous plant not only benefits our immune system, but also ensures the buildup of bacteria in the intestine. Garlic has proven antibiotic, antiviral and anti-inflammatory properties. Even abdominal pain can be reduced. But beware! Garlic also contains Phenprocoumon and warfarin. These substances have an anticoagulant effect! <sup>239,240,241,242,243,244,245,246,247</sup>

### **Flatulences and bloating**



If you regularly suffer from flatulences try these tips:

#### Bitter compounds and essential oils (ginger) have a supporting effect.

Bitter compounds and essential oils are contained in ginger, for example. They activate the intestinal peristalsis and can thus relieve flatulence. In addition, ginger supports your metabolism. Try adding ginger tea or fresh ginger to your meals. Nowadays, ginger roots are readily available in almost every supermarket.

#### Avoid carbonated drinks.

Try to reduce coffee, soft drinks and carbonated drinks. These encourage flatulence and a swollen abdomen.

#### Cuminaldehyde (caraway, fennel) is good for you.

Cuminaldehyde supports the formation of digestive juices, such as saliva, gastric juice, bile secretions and pancreatic juice, which has a positive effect on your digestive processes and thus improves them. Cuminaldehyde thereby alleviates especially flatulence and is found in e.g. caraway, cumin seeds (cumin) or fennel. Dietary fibres, such as legumes, become more digestible by the addition of cumin. <sup>248,252,254,261</sup>

### Constipation

The following tips will help to get constipation under control:

#### Try a stomach massage.

Massage your stomach for at least 5 minutes. Lie on your back and lightly drum your fingertips on your abdomen. This stimulus transfers to the abdominal organs and stimulates the intestinal activity.

#### Oleuropein (olive leaf extract) is good for you.

Oleuropein is an active ingredient which can be found e.g. in olive leaf extracts. It helps calm the stomach and intestines, promotes regular bowel movements and the elimination of toxins.

#### Sea buckthorn is a miracle cure.

Sea buckthorn is a true miracle cure. It contains larger amounts of vitamin B1 and B6, which are needed for a functioning nervous system. A lack of vitamins can cause digestive problems. Sea buckthorn has a strong laxative effect, as it stimulates the intestinal movement. In addition, it detoxifies the mucous membranes and calms it. Just try some delicious sea buckthorn tea or juice! <sup>249,250,251,253,287,288,289</sup>

#### Diarrhea

Diarrhea can significantly affect everyday life, the following recommendations will help:

#### Try water-binding mucilage (psyllium husks, rice, oats).

Water-binding mucilage helps solidify the stool. These can be found e.g. in cooked rice, rusks, oatmeal or in psyllium husks. Avoid a combination with flatulent foods, such as beans or cabbage.

#### Eat more starchy foods (bananas, grated apples).



Improvement suggestions

Starchy foods promote a more solid stool production and can reduce the number of visits to the toilet. Look out for starchy foods that are free of substances that may further irritate your stomach or intestines. Starchy foods include bananas and grated apples.

#### Tannins (St. John's wort, dried blueberries) help.

Tannins cause a contraction of the mucous membranes by binding to proteins. As a result, diarrhea pathogens cannot get into the intestine as easily and less electrolytes are lost. Dried blueberries (and leaves), dried blackberries (and leaves), St. John's Wort and silverweed contain many tannins. From all of these you can brew wonderful teas. Tea leaves for making these teas can be found in most pharmacies. But keep in mind that fresh berries can have the opposite effect and have laxative properties. <sup>290,291,312</sup>



# About the test

# About myBioma

In our digestive system, the microbiome is of particular importance for our health. The microbiome includes all bacteria, viruses, fungi and organisms that are not visible to the naked eye. It trains our immune system from birth and profoundly influences the development of many serious diseases such as diabetes, overweight, irritable bowel syndrome, Parkinson's and even colon cancer.

We - the myBioma team - develop easy to perform stool analysis tests and combine them with intelligent algorithms and a growing knowledge base.

The innovation lies in the unique combination of Next Generation Sequencing (NGS) with a growing knowledge base on the interactions of the microbiome with the human organism.

## Methods & restrictions

With the myBioma self-test, bacterial DNA is extracted, a marker gene present in all bacteria is amplified by polymerase chain reaction (PCR) and subsequently analysed by NGS. The sequence data are processed using a phylogenetic analysis algorithm. This analysis leads to the identification of your bacterial microbiome. Our scientific cooperation partner is the medical university of vienna. The extraction and sequencing steps are performed using a standardized protocol in order to generate comparable data. The development of the analysis test, bioinformatic analysis and interpretation of the data after sequencing is performed by myBioma. That way we ensure a standardization of the process steps, which is essential for the microbial examination and enables comparison with follow-up examinations.



- [1] Costea PI, et al. Towards standards for human fecal sample processing in metagenomic studies, Nat Biotechnol. 35(11):1069-1076 (2017).
- [2] Debelius J, et al. Tiny microbes, enormous impacts: what matters in gut microbiome studies? Genome Biology 17:217 (2016).
- [3] The Integrative HMP (iHMP) Research Network Consortium, The Integrative Human Microbiome Project: Dynamic Analysis of Microbiome-Host Omics Profiles during Periods of Human Health and Disease. Cell Host Microbe, 16(3): 276–289 (2014).
- [4] Knight R, et al. Best practices for analysing microbiomes. Nat Rev Microbiol. 16(7):410-422 (2018).
- [5] Huse SM, et al. A Core Human Microbiome as Viewed through 16S rRNA Sequence Clusters. PLoS ONE 7(6): e34242. (2012).
- [6] Human Microbiome Project Consortium, A framework for human microbiome research, Nature 486(7402):215-221. (2012).
- [7] Donaldson GP, Lee, MS, Mazmanian SK, Gut biogeography of the bacterial microbiota. Nat Rev Microbiol 14, 20–32 (2015).
- [8] Li J, et al. An integrated catalog of reference genes in the human gut microbiome. Nat Biotechnol 32, 834–841 (2014).
- [9] Chatelier E, et al. Richness of human gut microbiome correlates with metabolic markers. Nature 500, 541 (2013).
- [10] Cotillard A, et al. Dietary intervention impact on gut microbial gene richness. Nature 500, 585 (2013).
- [11] Lozupone CA, et al. Diversity, stability and resilience of the human gut microbiota. Nature 489, 220 (2012).
- [12] Yatsunenko T, et al. Human gut microbiome viewed across age and geography. Nature 486, 222 (2012).
- [13] Human Microbiome Project Consortium, Structure, function and diversity of the healthy human microbiome, Nature 486:207-214.
   (2012).
- [14] Masco L, et al. Polyphasic taxonomic analysis of Bifidobacterium animalis and Bifidobacterium lactis reveals relatedness at the subspecies level: reclassification of Bifidobacterium animalis as Bifidobacterium animalis subsp. animalis subsp. nov. and Bifidobacterium lactis as Bifidobacterium animalis subsp. lactis subsp. nov., Int J Syst Evol Microbiol. 54(4):1137-43 (2004).
- [15] O'Callaghan A, et al. Bifidobacteria and Their Role as Members of the Human Gut Microbiota. Front Microbiol. 7: 925 (2016).
- [16] Rivière A, et al. Bifidobacteria and Butyrate-Producing Colon Bacteria: Importance and Strategies for Their Stimulation in the Human Gut. Front Microbiol. 7: 979 (2016).
- [17] Khalif I, et al. Alterations in the colonic flora and intestinal permeability and evidence of immune activation in chronic constipation. Digest Liver Dis 37, 838–849 (2005).
- [18] Malinen E, et al. Association of symptoms with gastrointestinal microbiota in irritable bowel syndrome. World J Gastroentero 16, 4532–4540 (2010).
- [19] Turnbaugh PJ, et al. A core gut microbiome in obese and lean twins. Nature 457, 480 (2008).
- [20] Mayengbam S, et al. Impact of dietary fiber supplementation on modulating microbiota-host-metabolic axes in obesity. J Nutritional Biochem (2018).
- [21] Heeney DD, et al. Intestinal Lactobacillus in health and disease, a driver or just along for the ride? Curr Opin Biotechnol. 49:140-147 (2018).
- [22] Armougom F, et al. Monitoring Bacterial Community of Human Gut Microbiota Reveals an Increase in Lactobacillus in Obese Patients and Methanogens in Anorexic Patients. Plos One 4, e7125 (2009).
- [23] Million M, et al. Obesity-associated gut microbiota is enriched in Lactobacillus reuteri and depleted in Bifidobacterium animalis and Methanobrevibacter smithii. Int J Obesity 36, 817 (2011).
- [24] Marco ML, et al. Health benefits of fermented foods: microbiota and beyond, Curr Opin Biotechnol. 44:94-102. (2017)
- [25] Fouliquie Moreno MR, et al. The role and application of enterococci in food and health, Int J Food Microbiology, 106(1):1-24 (2006)
- [26] Holzapfel WH, et al. Taxonomy and important features of probiotic microorganisms in food and nutrition, American J Clinical Nutrition, 73(2):365S–373 (2001).
- [27] Langille MG, et al. Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology 31:814–821 (2013).
- [28] Gao J, et al. Predictive functional profiling using marker gene sequences and community diversity analyses of microbes in full-scale anaerobic sludge digesters. Bioprocess Biosyst Eng. 39(7):1115-27 (2016).
- [29] Chen L, et al. Assessment of Bacterial Communities and Predictive Functional Profiling in Soils Subjected to Short-Term Fumigation-Incubation. Microb Ecol. 72(1):240-251 (2016).
- [30] Myers L, et al. Isolation of enterotoxigenic Bacteroides fragilis from humans with diarrhea. J Clin Microbiol 25, 2330–3 (1987).
- [31] Sears CL, et al. Association of Enterotoxigenic Bacteroides fragilis Infection with Inflammatory Diarrhea. Clin Infect Dis 47, 797–803 (2008).
- [32] Parthasarathy G, et al. Relationship Between Microbiota of the Colonic Mucosa vs Feces and Symptoms, Colonic Transit, and Methane Production in Female Patients With Chronic Constipation. Gastroenterology 150, 367-379.e1 (2016).
- [33] Pawlowski SW, et al. Diagnosis and Treatment of Acute or Persistent Diarrhea. Gastroenterology 136, 1874–1886 (2009).
- [34] Lopez-Siles M, et al. Mucosa-associated Faecalibacterium prausnitzii phylotype richness is reduced in patients with inflammatory bowel disease. Appl Environ Microbiol. 81(21):7582-92 (2015).
- [35] Jalanka-Tuovinen J, et al. Faecal microbiota composition and host–microbe cross-talk following gastroenteritis and in postinfectious irritable bowel syndrome. Gut 63, 1737 (2014).





- [36] Miquel S, et al. Identification of Metabolic Signatures Linked to Anti-Inflammatory Effects of Faecalibacterium prausnitzii. MBio 6:2 (2015).
- [37] Lopetuso LR, et al. Gut Microbiota in Health, Diverticular Disease, Irritable Bowel Syndrome, and Inflammatory Bowel Diseases: Time for Microbial Marker of Gastrointestinal Disorders. Dig Dis. 36(1):56-65 (2018).
- [38] Kleinman SC, et al. The Intestinal Microbiota in Acute Anorexia Nervosa and During Renourishment: Relationship to Depression, Anxiety, and Eating Disorder Psychopathology. Psychosom Med. 77(9):969-81 (2015).
- [39] McGaughey KD, et al. Relative abundance of Akkermansia spp. and other bacterial phylotypes correlates with anxiety- and depressive-like behavior following social defeat in mice. Nature Sci Rep. 9(1):3281 (2019).
- [40] Mearin F, et al. Dyspepsia and Irritable Bowel Syndrome After a Salmonella Gastroenteritis Outbreak: One-Year Follow-up Cohort Study. Gastroenterology 129, 98–104 (2005).
- [41] Andrew M et al. Associations among diet, the gastrointestinal microbiota, and negative emotional states in adults, Nutr Neurosci. 22:1-10 (2019).
- [42] Ferguson JF, et al. Nutrigenomics, the Microbiome, and Gene-Environment Interactions: New Directions in Cardiovascular Disease Research, Prevention, and Treatment. A Scientific Statement from the American Heart Association. Circ Cardiovasc Genet (2016).
- [43] Tang WHW, et al. Dietary metabolism, the gut microbiome, and heart failure. Nat Rev Cardiol. ;16(3):137-154 (2019).
- [44] Jonsson AL, et al. Role of gut microbiota in atherosclerosis. Nat Rev Cardiol. 14(2):79-87 (2017).
- [45] Luedde M, et al. Heart failure is associated with depletion of core intestinal microbiota. ESC Heart Fail. 4, 282–290 (2017).
- [46] Kummen M, et al. The gut microbial profile in patients with primary sclerosing cholangitis is distinct from patients with ulcerative colitis without biliary disease and healthy controls. Gut 66, 611–619 (2017).
- [47] Haro C. et al, The gut microbial community in metabolic syndrome patients is modified by diet. J Nutr Biochem. 27:27-31 (2016).
- [48] Jandhyala SM, et al. Role of the normal gut microbiota. World J Gastroenterol. 21(29):8787-803 (2015).
- [49] Arumugam M, et al. Enterotypes of the human gut microbiome. Nature 473, 174 (2011).
- [50] Wu GD, et al. Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes. Science 334, 105–108 (2011).
- [51] Costea PI, et al. Enterotypes in the landscape of gut microbial community composition. Nat Microbiol 3, 8–16 (2018).
- [52] Schmidt T, et al. The Human Gut Microbiome: From Association to Modulation. Cell 172, 1198–1215 (2018).
- [53] Hayashi, H, et al. Prevotella copri sp. nov. and Prevotella stercorea sp. nov., isolated from human faeces. Int J Syst Evol Micr 57, 941– 946 (2007).
- [54] Ley RE, et al. Microbial ecology: Human gut microbes associated with obesity. Nature 444, 1022 (2006).
- [55] Schloss PD, et al. Status of the Archaeal and Bacterial Census: an Update. Mbio 7, e00201-16 (2016).
- [56] Zhernakova A., et al. Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science 352, 565–569 (2016).
- [57] Cornejo-Pareja I, et al. Importance of gut microbiota in obesity, Nature (2018)
- [58] Hildebrandt MA, et al. High-Fat Diet Determines the Composition of the Murine Gut Microbiome Independently of Obesity. Gastroenterology 137, 1716-1724.e2 (2009).
- [59] Verdam FJ, et al. Human intestinal microbiota composition is associated with local and systemic inflammation in obesity. Obesity 21, E607–E615 (2013).
- [60] Forslund K, et al. Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature 528, 262 (2015).
- [61] Everard A, et al. Cross-talk between Akkermansia muciniphila and intestinal epithelium controls diet-induced obesity. Proc National Acad Sci 110, 9066–9071 (2013).
- [62] Dao M, et al. Akkermansia muciniphila and improved metabolic health during a dietary intervention in obesity: relationship with gut microbiome richness and ecology. Gut 65, 426 (2016).
- [63] Schneeberger M, et al. Akkermansia muciniphila inversely correlates with the onset of inflammation, altered adipose tissue metabolism and metabolic disorders during obesity in mice. Sci Rep-uk 5, srep16643 (2015).
- [64] Zupancic ML, et al. Analysis of the Gut Microbiota in the Old Order Amish and Its Relation to the Metabolic Syndrome. Plos One 7, e43052 (2012).
- [65] Zhu L, et al. Characterization of gut microbiomes in nonalcoholic steatohepatitis (NASH) patients: A connection between endogenous alcohol and NASH. Hepatology 57, 601–609 (2013).
- [66] Raman M, et al. Fecal Microbiome and Volatile Organic Compound Metabolome in Obese Humans With Nonalcoholic Fatty Liver Disease. Clin Gastroenterol H 11, 868-875.e3 (2013).
- [67] Schwiertz A, et al. Microbiota and SCFA in Lean and Overweight Healthy Subjects. Obesity 18, 190–195 (2010).
- [68] Qin J, et al. A metagenome-wide association study of gut microbiota in type 2 diabetes. Nature 490, 55 (2012).
- [69] Lambeth SM, et al. Composition, Diversity and Abundance of Gut Microbiome in Prediabetes and Type 2 Diabetes, J Diabetes Obes, 2(3): 1–7, (2015).
- [70] Zhang X, et al. Human Gut Microbiota Changes Reveal the Progression of Glucose Intolerance. Plos One 8, e71108 (2013).



- [71] Pedersen H, et al. Human gut microbes impact host serum metabolome and insulin sensitivity. Nature 535, 376 (2016).
- [72] Murri M, et al. Gut microbiota in children with type 1 diabetes differs from that in healthy children: a case-control study. Bmc Med 11, 46 (2013).
- [73] Moreno-Indias I, et al. Insulin resistance is associated with specific gut microbiota in appendix samples from morbidly obese patients. Am J Transl Res 8, 5672–5684 (2016).
- [74] Wu X, et al. Molecular Characterisation of the Faecal Microbiota in Patients with Type II Diabetes. Curr Microbiol 61, 69–78 (2010).
- [75] Larsen N, et al. Gut Microbiota in Human Adults with Type 2 Diabetes Differs from Non-Diabetic Adults. Plos One 5, e9085 (2010).
- [76] Clarke SF, et al. The gut microbiota and its relationship to diet and obesity. Gut Microbes 3, 186–202 (2012).
- [77] Santacruz A, et al. Gut microbiota composition is associated with body weight, weight gain and biochemical parameters in pregnant women. Brit J Nutr 104, 83–92 (2010).
- [78] Clarke SF, et al. Exercise and associated dietary extremes impact on gut microbial diversity. Gut 63, 1913 (2014).
- [79] Karlsson FH, et al. Gut metagenome in European women with normal, impaired and diabetic glucose control. Nature 498, 99 (2013).
- [80] Cani PD, Human gut microbiome: hopes, threats and promises. Gut; 67(9): 1716–1725 (2018).
- [81] Sohail MU, et al. Role of the Gastrointestinal Tract Microbiome in the Pathophysiology of Diabetes Mellitus. Journal of Diabetes Research 2017:9631435, 9 (2017).
- [82] Wang N, et al. Proteomics, metabolomics and metagenomics for type 2 diabetes and its complications. Life Science 1;212:194-202 (2018).
- [83] Maslowski KM, et al. Regulation of inflammatory responses by gut microbiota and chemoattractant receptor GPR43. Nature 461, 1282 (2009).
- [84] Mokhtari Z, et al. Nonalcoholic Fatty Liver Disease, the Gut Microbiome, and Diet. Adv Nutr. 8(2):240-252 (2017).
- [85] Nistal E, et al. An altered fecal microbiota profile in patients with non- alcoholic fatty liver disease (NAFLD) associated with obesity. Rev Esp Enferm Dig. 111(4):275-282 (2019).
- [86] Madi A, et al. Pseudomonas fluorescens alters epithelial permeability and translocates across Caco-2/TC7 intestinal cells. Gut Pathog 2, 16 (2010).
- [87] Hiippala K, et al. Mucosal Prevalence and Interactions with the Epithelium Indicate Commensalism of Sutterella spp. Front Microbiol 7, 1706 (2016).
- [88] David LA, et al. Diet rapidly and reproducibly alters the human gut microbiome. Nature 505, 559 (2014).
- [89] Mu Q, et al. Leaky Gut As a Danger Signal for Autoimmune Diseases. Front Immunol; 8:598 (2017).
- [90] Sicard JF, et al. Interactions of Intestinal Bacteria with Components of the Intestinal Mucus. Front Cell Infect Microbiol;7:387 (2017).
- [91] Cruz-Aguliar RM, et al. An Open-Labeled Study on Fecal Microbiota Transfer in Irritable Bowel Syndrome Patients Reveals Improvement in Abdominal Pain Associated with the Relative Abundance of Akkermansia Muciniphila. Digestion 1–12 (2018).
- [92] Turroni F, et al. Role of sortase-dependent pili of Bifidobacterium bifidum PRL2010 in modulating bacterium–host interactions. Proc National Acad Sci 110, 11151–11156 (2013).
- [93] Fanning, S. et al. Bifidobacterial surface-exopolysaccharide facilitates commensal-host interaction through immune modulation and pathogen protection. Proc National Acad Sci 109, 2108–2113 (2012).
- [94] Coyne MJ, et al. Human Symbionts Use a Host-Like Pathway for Surface Fucosylation. Science 307, 1778–1781 (2005).
- [95] Huang JY, et al. The human commensal Bacteroides fragilis binds intestinal mucin. Anaerobe 17, 137–141. (2011).
- [96] Ley RE, Gut microbiota in 2015: Prevotella in the gut: choose carefully. Nat Rev Gastroenterology Hepatology 13, 69–70 (2016).
- [97] Png CW, et al. Mucolytic bacteria with increased prevalence in IBD mucosa augment in vitro utilization of mucin by other bacteria. Am J Gastroenterol., 105(11):2420-8 (2010).
- [98] Crost EH, et al. Utilisation of mucin glycans by the human gut symbiont Ruminococcus gnavus is strain-dependent. PLoS One;8(10):e76341 (2013).
- [99] Jeffery IB, et al. An irritable bowel syndrome subtype defined by species-specific alterations in faecal microbiota. Gut 61, 997 (2012).
- [100] Peter J, et al. A Microbial Signature of Psychological Distress in Irritable Bowel Syndrome, Psychosom Med., 80(8): 698–709 (2018).
- [101] Rajilić-Stojanović M, et al. Intestinal Microbiota And Diet in IBS: Causes, Consequences, or Epiphenomena? Am J Gastroenterology 110, 278 (2015).
- [102] Rajilić–Stojanović M, et al. Global and Deep Molecular Analysis of Microbiota Signatures in Fecal Samples From Patients With Irritable Bowel Syndrome. Gastroenterology 141, 1792–1801 (2011).
- [103] Frank DN, et al. Disease phenotype and genotype are associated with shifts in intestinal-associated microbiota in inflammatory bowel diseases. Inflamm Bowel Dis 17, 179–184 (2011).
- [104] Kassinen A, et al. The Fecal Microbiota of Irritable Bowel Syndrome Patients Differs Significantly From That of Healthy Subjects. Gastroenterology 133, 24–33 (2007).
- [105] Lyra A, et al. Diarrhoea-predominant irritable bowel syndrome distinguishable by 16S rRNA gene phylotype quantification. World J Gastroentero 15, 5936–5945 (2009).





- [106] Hynönen U, et al. Isolation and whole genome sequencing of a Ruminococcus-like bacterium, associated with irritable bowel syndrome. Anaerobe 39, 60–67 (2016).
- [107] Salonen A, de Vos, W. M., & Palva, A. Gastrointestinal microbiota in irritable bowel syndrome: present state and perspectives. Microbiology, 156(11), 3205–3215 (2010).
- [108] Kerckhoffs AP, et al. Lower Bifidobacteria counts in both duodenal mucosa-associated and fecal microbiota in irritable bowel syndrome patients. World J Gastroentero 15, 2887–2892 (2009).
- [109] Sokol H, et al. Faecalibacterium prausnitzii is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients. Proc National Acad Sci 105, 16731–16736 (2008).
- [110] Mangiola F, et al. Gut microbiota in autism and mood disorders. World J Gastroentero 22, 361–368 (2016).
- [111] Jiang, H, et al. Altered fecal microbiota composition in patients with major depressive disorder. Brain Behav. Immun. 48, 186–194 (2015).
- [112] Valles-Colomer M, et al. The neuroactive potential of the human gut microbiota in quality of life and depression. Nature Microbiology (2019).
- [113] Huang Y, et al. Possible association of Firmicutes in the gut microbiota of patients with major depressive disorder, Neuropsychiatric Disease and Treatment 14 3329–3337 (2018).
- [114] Messaoudi M, et al. Assessment of psychotropic-like properties of a probiotic formulation (Lactobacillus helveticus R0052 and Bifidobacterium longum R0175) in rats and humann subjects, British Journal of Nutrition 105:5 755-764 (2011).
- [115] Taverniti V, et al. health-promoting properties of Lactobacillus helveticus, Frontiers in Mircobiology 3:392 (2012).
- [116] Pedersen N, et al. Ehealth: Low FODMAP diet vs Lactobacillus rhamnosus GG in irritable bowel syndrome, Gastroenterology 20:43 16215 (2014).
- [117] Aizawa E, et al. Possible association of Bifidobacterium and Lactobacillus in the gut microbiota of patients with major depressive disorder, Journal of Affective Disorders (2016).
- [118] Bolca, S. & Verstraete, W. Microbial equal production attenuates colonic methanogenesis and sulphidogenesis in vitro. Anaerobe 16, 247–252 (2010).
- [119] Vaughn AR, et al. Skin-gut axis: The relationship between intestinal bacteria and skin health. World J Dermatol. 6(4): 52-58 (2017).
- [120] Jalanka-Tuovinen J, et al. Intestinal Microbiota in Healthy Adults: Temporal Analysis Reveals Individual and Common Core and Relation to Intestinal Symptoms. Plos One 6, e23035 (2011).
- [121] Manichanh C, et al. Anal gas evacuation and colonic microbiota in patients with flatulence: effect of diet. Gut 63, 401 (2014).
- [122] Mancabelli L, et al. Unveiling the gut microbiota composition and functionality associated with constipation through metagenomic analyses. Sci Rep-uk 7, 9879 (2017).
- [123] Chassard C, et al. Functional dysbiosis within the gut microbiota of patients with constipated-irritable bowel syndrome. Aliment Pharm Therap 35, 828–838 (2012).
- [124] Zhao Y, Yu, YB Intestinal microbiota and chronic constipation. Springerplus 5, 1130 (2016).
- [125] Bajaj JS, et al. Linkage of gut microbiome with cognition in hepatic encephalopathy. Am J Physiol-gastr L 302, G168–G175 (2012).
- [126] Bajaj JS, et al. Colonic mucosal microbiome differs from stool microbiome in cirrhosis and hepatic encephalopathy and is linked to cognition and inflammation. Am J Physiol-gastro 303, G675–G685 (2012).
- [127] Henao-Mejia J, et al. Inflammasome-mediated dysbiosis regulates progression of NAFLD and obesity. Nature 482, 179 (2012).
- [128] Jiang, W, et al. Dysbiosis gut microbiota associated with inflammation and impaired mucosal immune function in intestine of humans with non-alcoholic fatty liver disease. Sci Rep-uk 5, 8096 (2015).
- [129] Boursier J, et al. The severity of nonalcoholic fatty liver disease is associated with gut dysbiosis and shift in the metabolic function of the gut microbiota, Hepatology, 63(3):764-75 (2016).
- [130] Mouzaki M, et al. Intestinal microbiota in patients with nonalcoholic fatty liver disease. Hepatology 58, 120–127 (2013).
- [131] Stern JM, et al. Evidence for a distinct gut microbiome in kidney stone formers compared to non-stone formers. Urolithiasis 44, 399– 407 (2016).
- [132] Stewart CS, et al. Oxalobacter formigenes and its role in oxalate metabolism in the human gut. Fems Microbiol Lett 230, 1–7 (2004).
- [133] Sidhu H, et al. Absence of Oxalobacter formigenes in cystic fibrosis patients: a risk factor for hyperoxaluria. Lancet 352, 1026–1029 (1998).
- [134] Duncan SH, et al. Oxalobacter formigenes and Its Potential Role in Human Health. Appl Environ Microb 68, 3841–3847 (2002).
- [135] Barnett C, et al. The Presence of Oxalobacter formigenes in the Microbiome of Healthy Young Adults. J Urology 195, 499–506 (2016).
- [136] Mehta M, et al. The role of the microbiome in kidney stone formation. Int J Surg 36, 607–612 (2016).
- [137] Whisner CM, et al. Diet, physical activity and screen time but not body mass index are associated with the gut microbiome of a diverse cohort of college students living in university housing: a cross-sectional study. BMC Microbiol.;18(1):210 (2018).
- [138] Del Chierico F, et al. Gut Microbiota Markers in Obese Adolescent and Adult Patients: Age-Dependent Differential Patterns. Front Microbiol. 9:1210 (2018).



- [139] Xu J, et al. Evolution of symbiotic bacteria in the distal human intestine. PLoS Biol. 5(7):e156 (2007).
- [140] Wang K, et al. Parabacteroides distasonis Alleviates Obesity and Metabolic Dysfunctions via Production of Succinate and Secondary Bile Acids. Cell Rep.26(1):222-235 (2019).
- [141] Haro C, et al. The gut microbial community in metabolic syndrome patients is modified by diet. J Nutr Biochem. 27:27-31 (2016).
- [142] DaSilva HE, et al. Nonalcoholic fatty liver disease is associated with dysbiosis independent of body mass index and insulin resistance. Sci Rep. 8(1):1466 (2018).
- [143] Jiang W, et al. Dysbiosis gut microbiota associated with inflammation and impaired mucosal immune functionin intestine of humans with non-alcoholic fatty liver disease. Sci Rep. 5:8096 (2015).
- [144] Zhu L, et al. Characterization of gut microbiomes in nonalcoholic steatohepatitis (NASH) patients: a connection between endogenous alcohol and NASH. Hepatology 57(2):601-9 (2013).
- [145] Del Chierico F, et al. Gut microbiota profiling of pediatric nonalcoholic fatty liver disease and obese patients unveiled by an integrated meta-omics-based approach. Hepatology, 65(2):451-464 (2017).
- [146] Khlevner J, et al. Brain-Gut Axis: Clinical Implications. Gastroenterol Clin North Am. 47(4):727-739 (2018).
- [147] Hwang N, et al. Genes and Gut Bacteria Involved in Luminal Butyrate Reduction Caused by Diet and Loperamide. Genes (Basel) 28;8(12) (2017).
- [148] Lin HX, et al. The long term effect of metabolic profile and microbiota status in early gastric cancer patients after subtotal gastrectomy. PLoS One.;13(11):e0206930 (2018).
- [149] Medina-Vera I, et al. A dietary intervention with functional foods reduces metabolic endotoxaemia and attenuates biochemical abnormalities by modifying faecal microbiota in people with type 2 diabetes. Diabetes Metab.: S1262-3636(18)30175-7 (2018).
- [150] Díaz-Rizzolo DA, et al. Healthy dietary pattern and their corresponding gut microbiota profile are linked to a lower risk of type 2 diabetes, independent of the presence of obesity. Clin Nutr.: S0261-5614(19)30089-5 (2019).
- [151] Wie S, et al. Intermittent administration of a fasting-mimicking diet intervenes in diabetes progression, restores  $\beta$  cells and reconstructs gut microbiota in mice. Nutr Metab ;15:80 (2018).
- [152] Hod K, et al. The effect of a multispecies probiotic on microbiota composition in a clinical trial of patients with diarrheapredominant irritable bowel syndrome. Neurogastroenterol Motil. 30(12):e13456 (2018).
- [153] Cheung SG, et al. Systematic Review of Gut Microbiota and Major Depression. Front Psychiatry. 10:34 (2019).
- [154] Hadizadeh F, et al. Faecal microbiota composition associates with abdominal pain in the general population. Gut 67(4):778-779 (2018).
- [155] Baron E, Bilophila wadsworthia: a Unique Gram-negative Anaerobic Rod. Anaerobe 3, 83–86 (1997).
- [156] Suarez F, et al. Identification of gases responsible for the odour of human flatus and evaluation of a device purported to reduce this odour. Gut 43, 100 (1998).
- [157] Mari A, et al. Bloating and Abdominal Distension: Clinical Approach and Management. Adv Ther. 2019 (2019).
- [158] Malagelada JR, et al. Bloating and Abdominal Distension: Old Misconceptions and Current Knowledge. Am J Gastroenterol. 112(8):1221-1231 (2018).
- [159] Zhang H, et al. Human gut microbiota in obesity and after gastric bypass. Proc Natl Acad Sci U S A 106(7):2365-70 (2009).
- [160] Gianchecchi E, Fierabracci A, Recent Advances on Microbiota Involvement in the Pathogenesis of Autoimmunity. Int. Journal of Mol Science 20(283) (2019).
- [161] Safari Z, Gerard P, The links between the gut microbiome and non-alcoholic fatty liver disease (NAFLD), Cellular and Molecular Life Sciences 76(8):1541-1558, (2019).
- [162] Salem I, et al. The Gut Microbiome as a Major Regulator of the Gut-Skin Axis. Front. Microbiol. 9:1459 (2019).
- [163] Chiu CM, et al. Systematic Analysis of the Association between Gut Flora and Obesity through High-Throughput Sequencing and Bioinformatics Approaches. BioMed Research International 2014: 906168 (2014).
- [164] Kim YA, et al. Probiotics, prebiotics, synbiotics and insulin sensitivity. Nutrition Research Reviews 2017: 1-17 (2017).
- [165] Al-Otaibi FE, Al-Mohizea MM, Non-vertebral Veillonella species septicemia and osteomyelitis in a patient with diabetes: a case report and review of the literature, J Med Case Rep, 8:365 (2014).
- [166] Lippert K, et al. Gut microbiota dysbiosis associated with glucose metabolism disorders and the metabolic syndrome in older adults. Benef Microbes. 8(4):545-556 (2017).
- [167] Barreau F, Hugot J, Intestinal barrier dysfunction triggered by invasive bacteria. Curr Opin Microbiol 17, 91–98 (2014).
- [168] Mazzawi T, et al. The kinetics of gut microbial community composition in patients with irritable bowel syndrome following fecal microbiota transplantation. PLoS ONE 13(11): e0194904 (2018).
- [169] Dunlop SP, et al. Relative importance of enterochromaffin cell hyperplasia, anxiety, and depression in postinfectious IBS. Gastroenterology 125, 1651–1659 (2003).
- [170] Spiller RC, Role of infection in irritable bowel syndrome. J Gastroenterol 42, 41–47 (2007).
- [171] Simren M, et al. Intestinal microbiota in functional bowel disorders: a Rome foundation report. Gut 62(1):159–176 (2013).



- References
- [172] Niccolai E, et al. The Gut–Brain Axis in the Neuropsychological Disease Model of Obesity: A Classical Movie Revised by the Emerging Director "Microbiome". Nutrients 11:156 (2019).
- [173] Duncan SH, et al. Proposal of Roseburia faecis sp. nov., Roseburia hominis sp. nov. and Roseburia inulinivorans sp. nov., based on isolates from human faeces. Int. J. Syst. Evol. Microbiol. 56, 2437–2441 (2006).
- [174] Louis P, Flint HJ, Formation of propionate and butyrate by the human colonic microbiota. Environ. Microbiol. 19, 29–41 (2017).
- [175] Forbes JD, et al. A comparative study of the gut microbiota in immune-mediated inflammatory diseases—does a common dysbiosis exist? Microbiome 6:221 (2018).
- [176] Caussy C, et al. A gut microbiome signature for cirrhosis due to nonalcoholic fatty liver disease. Nat Commun. 10(1):1406 (2019).
- [177] Tana C, et al. Altered profiles of intestinal microbiota and organic acids may be the origin of symptoms in irritable bowel syndrome. Neurogastroenterol Motil. 22(5):512-9, e114-5 (2010).
- [178] Lopes-Siles M, et al. Alterations in the Abundance and Co-occurrence of Akkermansia muciniphila and Faecalibacterium prausnitzii in the Colonic Mucosa of Inflammatory Bowel Disease Subjects. Front Cell Infect Microbiol. 8:281 (2018).
- [179] Qin N, et al. Alterations of the human gut microbiome in liver cirrhosis. Nature 513:59–64 (2014).
- [180] Zheng P, et al. Gut microbiome remodeling induces depressive-like behaviors through a pathway mediated by the host's metabolism. Mol Psychiatry. 21(6):786-96 (2016).
- [181] Mack I, et al. Weight gain in anorexia nervosa does not ameliorate the faecal microbiota, branched chain fatty acid profiles, and gastrointestinal complaints. Sci. Rep, 6:26752 (2016).
- [182] Allen AP, et al, Bifidobacterium longum 1714 as a translational psychobiotic: Modulation of stress electrophysiology annd neurocognition in health volunteers. Translational Psychiatry 6:11 e939 (2016).
- [183] Guyonnet D, et al, Effect of a fermented milk containing Bifidobacterium animalis DN-173 010 on the health-related quality of life and symptoms in irritable bowel syndrome in adults in primary care: a multicenter, randomized, double-blind, controlled trial. Alimentary Pharmacology & Therapeutics 26:3 475-486 (2007).
- [184] Codoñer FM, et al. Gut microbial composition in patients with psoriasis. Sci. Rep. 8:3812 (2018).
- [185] Loomba R, et al. Gut microbiome-based metagenomic signature for non-invasive detection of advanced fibrosis in human nonalcoholic fatty liver disease. Cell Metab 25(5):1054–1062.e1055 (2017).
- [186] Scher JU, et al. Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis. Elife 2, e01202 (2013).
- [187] Kimura Y, et al. Periodontal pathogens participate in synovitis in patients with rheumatoid arthritis in clinical remission: a retrospective case–control study. Rheumatology 54, 2257–2263 (2015).
- [188] Yeoh, N, et al. The role of the microbiome in rheumatic diseases. Curr. Rheumatol. Rep. 15 (2013).
- [189] Picchianti-Diamanti A, et al. Analysis of Gut Microbiota in Rheumatoid Arthritis Patients: Disease-Related Dysbiosis and Modifications Induced by Etanercept. Int. J. Mol. Sci. 19:2938. (2018).
- [190] Mclean MH, Dieguez D, Miller LM, Young HA. Does the microbiota play a role in the pathogenesis of autoimmune diseases?. Gut, 64(2):332-41 (2015).
- [191] Chen J, et al. An expansion of rare lineage intestinal microbes characterizes rheumatoid arthritis. Genome Med. 8:43 (2016).
- [192] Alpizar-Rodriguez D, et al. Prevotella copri in individuals at risk for rheumatoid arthritis. Ann Rheum Dis 78(5):590-593 (2019).
- [193] Horta-Baas G, et al. Intestinal dysbiosis and rheumatoid arthritis: a link between gut microbiota and the pathogenesis of rheumatoid arthritis. J Immunol Res. 2017:1–13 (2017).
- [194] Forbes JD, et al. A comparative study of the gut microbiota in immune-mediated inflammatory diseases-does a common dysbiosis exist? Microbiome 6(1):2212 (2018).
- [195] Pianta, A. et al. Evidence of the Immune Relevance of Prevotella copri, a Gut Microbe, in Patients With Rheumatoid Arthritis. Arthritis Rheumatol 69, 964–975 (2017).
- [196] Moen K, et al. Immunoglobulin G and A Antibody Responses to Bacteroides forsythus and Prevotella intermedia in Sera and Synovial Fluids of Arthritis Patients. Clin Diagn Lab Immun 10, 1043–1050 (2003).
- [197] Eppinga H, et al. Similar depletion of protective Faecalibacterium prausnitzii in psoriasis and inflammatory bowel disease, but not in Hidradenitis suppurativa. J. Crohn's Colitis (2015).
- [198] Scher JU, et al. Decreased bacterial diversity characterizes the altered gut microbiota in patients with psoriatic arthritis, resembling dysbiosis in inflammatory bowel disease. Arthritis Rheumatol. 67, 128–139 (2015).
- [199] Santacruz A, et al. Interplay between weight loss and gut microbiota composition in overweight adolescents. Obesity (Silver Spring) 17(10):1906-15 (2009).
- [200] Song, H, et al. Faecalibacterium prausnitzii subspecies-level dysbiosis in the human gut microbiome underlying atopic dermatitis. J. Allergy Clin. Immunol. 137, 852–860 (2016).
- [201] Vich Vila A, et al. Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. Sci. Transl. Med. 10, eaap8914 (2018).
- [202] Karlsson FH, et al. Symptomatic atherosclerosis is associated with an altered gut metagenome. Nat Commun 3, 1245 (2012).
- [203] Jie Z, et al. The gut microbiome in atherosclerotic cardiovascular disease. Nat Commun. 8(1):845 (2017).



- [204] Kasahara K, et al. Interactions between Roseburia intestinalis and diet modulate atherogenesis in a murine model. Nat. Microbiol. 3:1461–1471 (2018).
- [205] Kelly TN, et al. Gut Microbiome Associates With Lifetime Cardiovascular Disease Risk Profile Among Bogalusa Heart Study Participants. Circ Res 119, 956–964 (2016).
- [206] Johnson DI, Yersinia spp. In: Bacterial Pathogens and Their Virulence Factors. Springer, Cham 407-421 (2018).
- [207] Wu et al. Gut microbiota dysbiosis and bacterial community assembly associated with cholesterol gallstones in large-scale study. BMC Genomics 14:669 (2013).
- [208] Keren N, et al. Interactions between the intestinal microbiota and bile acids in gallstones patients. Environ Microbiol Rep 7:874 880 (2015).
- [209] Konikoff T, et al. Oscillospira: a Central, Enigmatic Component of the Human Gut Microbiota. Trends Microbiol. 24(7):523-524 (2017).
- [210] Qin J, et al. A human gut microbial gene catalogue established by metagenomic sequencing: commentary. Inflamm. Bowel Dis. Monit. 11:28 (2010).
- [211] Patterson AM, et al. Human Gut Symbiont Roseburia hominis Promotes and Regulates Innate Immunity. Front Immunol. 8: 1166 (2017).
- [212] Rodríguez NE, et al. Eosinophils and mast cells in leishmaniasis. Immunol. Res. 59, 129–141 (2014).
- [213] Tamanai-Shacoori Z,et al., Roseburia spp.: a marker of health?, Future Microbiol.,12:157-17 (2017).
- [214] Haro C, et al. Intestinal Microbiota Is Influenced by Gender and Body Mass Index. Plos ONe 11, e0154090 (2016).
- [215] von Ossowski, I. et al. Mucosal Adhesion Properties of the Probiotic Lactobacillus rhamnosus GG SpaCBA and SpaFED Pilin Subunits. Appl Environ Microb 76, 2049–2057 (2010).
- [216] Torres J, et al. The features of mucosa-associated microbiota in primary sclerosing cholangitis Aliment Pharmacol Ther. 43(7):790-801 (2016).
- [217] Chiang YL, et al. Bile Acid Metabolism in Liver Pathobiology. Gene Expression, The Journal of Liver Research 18(2):71-87(17) (2018).
- [218] DiCiaula A, et al. An update on the pathogenesis of cholesterol gallstone disease. Curr Opin Gastroenterol. 34(2):71-80 (2018).
- [219] Campbell AW et al. Autoimmunity and the Gut, Autoimmune Diseases (2014).
- [220] Scher JU, et al. Expansion of intestinal Prevotella copri correlates with enhanced susceptibility to arthritis. eLife; 2: e01202 (2013).
- [221] Pierantonelli I, et al. Nonalcoholic Fatty Liver Disease: Basic Pathogenetic Mechanisms in the Progression From NAFLD to NASH. Transplantation. 103(1):e1-e13 (2019).
- [222] Ramakrishna BS, Role of the gut microbiota in human nutrition and metabolism. J Gastroenterol Hepatol 28 Suppl 4:9-17 (2013).
- [223] Biesalski HK, Nutrition meets the microbiome: micronutrients and the microbiota. Ann NY Acad Sci 1372, 53–64 (2016).
- [224] Galanakis C, Trends in Personalized Nutrition. American Press, 1st Edition, ISBN 9780128164037 (2019).
- [225] Allen JM, et al. Exercise alters gut microbiota composition and function in lean and obese humans. Med Sci Sports Exerc. 50(4):747– 57 (2018).
- [226] Mitchell CM, et al. Does Exercise Alter Gut Microbial Composition? A Systematic Review. Med Sci Sports Exerc. 51(1):160-167 (2019).
- [227] Sleep and Circadian Alterations and the Gut Microbiome: Associations or Causality?
- [228] "St-Onge MP, et al. Reciprocal Roles of Sleep and Diet in Cardiovascular Health: a Review of Recent Evidence and a Potential Mechanism. Curr Atheroscler Rep. 21(3):11 (2019).
- [229] Tetel MJ, et al. Steroids, stress and the gut microbiome-brain axis. J Neuroendocrinol. (2019)
- [230] Allen AP, et al. A psychology of the human brain-gut-microbiome axis. Soc Personal Psychol Compass. 11(4): e12309 (2017).
- [231] Savin Z, et al. Smoking and the intestinal microbiome. Arch Microbiol. 200(5):677-684 (2018).
- [232] Capurso G, Lahner E, The interaction between smoking, alcohol and the gut microbiome. Best Pract Res Clin Gastroenterol. 31(5):579-588 (2017).
- [233] Tingirikari JMR, Microbiota-accessible pectic poly- and oligosaccharides in gut health. Food Funct. 9(10):5059-5073 (2018).
- [234] Vital M et al. Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. Appl Environ Microbiol. 84(23) (2018).
- [235] Sheflin AM, et al. Linking dietary patterns with gut microbial composition and function. Gut Microbes. 8(2):113-129 (2017).
- [236] Maier TV, et al. Impact of Dietary Resistant Starch on the Human Gut Microbiome, Metaproteome, and Metabolome. American Soc. Microbiology mBio 8:e01343-17 (2017).
- [237] Filippis F, et al. High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. Gut 65, 1812 (2016).
- [238] Hjorth MR, et al. Pre-treatment microbial Prevotella-to-Bacteroides ratio, determines body fat loss success during a 6-month randomized controlled diet intervention. Int J Obes (Lond). 42(3):580-583 (2018).



- [239] Cappello G, et al. Peppermint oil (Mintoil) in the treatment of irritable bowel syndrome: a prospective double blind placebo-controlled randomized trial. Dig Liver Dis. 39(6):530-6 (2007).
- [240] Khanna R, et al. Peppermint oil for the treatment of irritable bowel syndrome: a systematic review and meta-analysis. J Clin Gastroenterol. 48(6):505-12 (2014).
- [241] Beißner F, et al. Therapeutische Empfehlungen, Akupunkt 61: 2 (2018).
- [242] Schmid CM, Characterization of agonistic (aroma-active and physiologically active) compounds in thyme, oregano and marjoram, Techn Univ München (2018).
- [243] Martín-Peláez, S, et al. Effect of virgin olive oil and thyme phenolic compounds on blood lipid profile: implications of human gut microbiota. Eur J Nutr 56: 119 (2017).
- [244] Europäisches Arzneibuch (http://www.edqm.eu)
- [245] Ried K, et al. Potential of garlic (Allium sativum) in lowering high blood pressure: mechanisms of action and clinical relevance. Integr Blood Press Control. 7:71-82 (2014).
- [246] Pallister T, Spector TD, Food: a new form of personalised (gut microbiome) medicine for chronic diseases? J R Soc Med. 109(9):331-6 (2016).
- [247] Sahebkar A, et al. Effect of garlic on plasma lipoprotein(a) concentrations: A systematic review and meta-analysis of randomized controlled clinical trials. Nutrition. 32(1):33-40. (2016).
- [248] Capili B, Addressing the Role of Food in Irritable Bowel Syndrome Symptom Management. J Nurse Pract. 12(5):324-329. (2016).
- [249] Gentile L, et al. Oleuropein: Molecular Dynamics and Computation. 24(39):4315-4328 (2017).
- [250] Gavahian M, et al. Health benefits of olive oil and its components: Impacts on gut microbiota antioxidant activities, and prevention of noncommunicable diseases Trends in Food Sc. & Tech. 88:220-227 (2019).
- [251] Pacheco C, et al. Retention and pre-colon bioaccessibility of oleuropein in starchy food matrices, and the effect of microencapsulation by using inulin. J. Funct. Foods 41:112-117 (2018).
- [252] Rowland I, et al. Gut microbiota functions: metabolism of nutrients and other food components. Eur J Nutr 57: 1 (2018).
- [253] López de las Hazas MC, et al. Differential absorption and metabolism of hydroxytyrosol and its precursors oleuropein and secoiridoids. J Funct Foods 22: 52-63 (2016).
- [254] Tianthong W, Phupong V. A randomized, double-blind, placebo-controlled trial on the efficacy of ginger in the prevention of abdominal distention in post cesarean section patients. Sci Rep. 8(1):6835 (2018).
- [255] Achamrah N et al. Glutamine and the regulation of intestinal permeability: from bench to bedside. Curr Opin Clin Nutr Metab Care. 20(1):86-91. (2017).
- [256] Burrin DG, Stoll B, Metabolic fate and function of dietary glutamate in the gut. Am J Clin Nutr. 90(3):850S-856S (2009).
- [257] Mahida YR, et al. Enhanced production of interleukin 1-beta by mononuclear cells isolated from mucosa with active ulcerative colitis of Crohn's disease. Gut. 30(6):835-8 (1989).
- [258] Di Sabatino A, et al. Transforming growth factor beta signalling and matrix metalloproteinases in the mucosa overlying Crohn's disease strictures. Gut. 58(6):777-89 (2009).
- [259] Basilisco, G. & Coletta, M. Chronic constipation: A critical review. Digest Liver Dis 45, 886–893 (2013).
- [260] Menni C, Omega-3 fatty acids correlate with gut microbiome diversity and production of N-carbamylglutamate in middle aged and elderly women Sci Rep. 7: 11079 (2017).
- [261] Singh RP, et al. Cuminum cyminum A Popular Spice: An Updated Review. Pharmacogn J. 9(3):292-301 (2017).
- [262] Robertson RC, et al. Omega-3 polyunsaturated fatty acids critically regulate behaviour and gut microbiota development in adolescence and adulthood. Brain Behav Immun. 59:21-37 (2017).
- [263] Mocking RJT, et al. Meta-analysis and meta-regression of omega-3 polyunsaturated fatty acid supplementation for major depressive disorder. Transl Psychiatry. 6(3): e756. (2016).
- [264] Calder PC, Omega-3 polyunsaturated fatty acids and inflammatory processes: nutrition or pharmacology? Br J Clin Pharmacol. 75(3):645-62 (2013).
- [265] Hayek N, Chocolate, gut microbiota, and human health. Front Pharmacol. 4:11 (2013).
- [266] Brickman AM, et al. Enhancing dentate gyrus function with dietary flavanols improves cognition in older adults. Nat Neurosci. 17(12):1798–1803 (2014).
- [267] Waclawiková B, El Aidy S, Role of Microbiota and Tryptophan Metabolites in the Remote Effect of Intestinal Inflammation on Brain and Depression. Pharmaceuticals (Basel). 11(3): 63 (2018).
- [268] O'Mahony SM, et al. Serotonin, tryptophan metabolism and the brain-gut-microbiome axis. Behav Brain Res. 277:32-48 (2015).
- [269] Lindseth G, et al. The Effects of Dietary Tryptophan on Affective Disorders. Arch Psychiatr Nurs. 29(2):102–107 (2015).
- [270] Tillisch K, et al. Consumption of Fermented Milk Product With Probiotic Modulates Brain Activity. Gastroenterology. 144(7):10.1053/j.gastro.2013.02.043 (2013).
- [271] Schmidt K, et al. Prebiotic intake reduces the waking cortisol response and alters emotional bias in healthy volunteers. Psychopharmacology 232(10): 1793–1801 (2015).



- [272] Jørgensen PB, et al. A possible link between food and mood: dietary impact on gut microbiota and behavior in BALB/c mice. PLoS One 9(8):e103398 (2014).
- [273] Owen L, et al. The role of diet and nutrition on mental health and wellbeing. Proc Nutr Soc. 76(4):425-426 (2017).
- [274] Noble EE, et al. Gut to Brain Dysbiosis: Mechanisms Linking Western Diet Consumption, the Microbiome, and Cognitive Impairment. Front Behav Neurosci. 11:9 (2017).
- [275] Oriachad CS, et al. Food for thought: The role of nutrition in the microbiota-gut-brain axis. Clin Nut Experimental 6:25-38 (2016).
- [276] Ndeh D, et al. Complex pectin metabolism by gut bacteria reveals novel catalytic functions. Nature 544(7648):65-70 (2017).
- [277] Reddel S, et al. The Impact of Low-FODMAPs, Gluten-Free, and Ketogenic Diets on Gut Microbiota Modulation in Pathological Conditions. Nutrients. 11(2) (2019).
- [278] Heianza Y, et al. Changes in Gut Microbiota-Related Metabolites and Long-term Successful Weight Loss in Response to Weight-Loss Diets: The POUNDS Lost Trial. Diabetes Care. 41(3):413-419 (2018).
- [279] Altobelli E, et al. Low-FODMAP Diet Improves Irritable Bowel Syndrome Symptoms: A Meta-Analysis. Nutrients 9(9) (2017).
- [280] Haupt-Jorgensen M, et al Possible Prevention of Diabetes with a Gluten-Free Diet. Nutrients ;10(11) (2018)
- [281] Korakas E, et al. Dietary Composition and Cardiovascular Risk: A Mediator or a Bystander? Nutrients 10(12) (2018).
- [282] Costabile A, et al. Whole-grain wheat breakfast cereal has a prebiotic effect on the human gut microbiota: A double-blind, placebocontrolled, crossover study. Br J Nutr 99:110–120 (2008).
- [283] Zhang S, et al. Curcumin attenuates atherosclerosis in apolipoprotein-E knockout mice by inhibiting Toll-like receptor 4 expression. J. Agric. Food Chem. 66:449–456 (2018).
- [284] McNulty H, et al. Biologic activity of carotenoids related to distinct membrane physicochemical interactions. Am. J. Cardiol. 101:20– S29 (2008).
- [285] Foerster J, The influence of whole grain products and red meat on intestinal microbiota composition in normal weight adults: a randomized crossover intervention trial. PLoS One. 9(10):e109606 (2014).
- [286] Ejtahed, H. S. et al. Probiotic yogurt improves antioxidant status in type 2 diabetic patients. Nutrition 28, 539–543 (2012).
- [287] Zielińska A, Nowak I, Abundance of active ingredients in sea-buckthorn oil. Lipids Health Dis. 16: 95 (2017).
- [288] Olas B, The beneficial health aspects of sea buckthorn (Elaeagnus rhamnoides (L.) A.Nelson) oil. J Ethnopharmacol. ;213:183-190 (2018).
- [289] Yang B, Kortesniemi M, Clinical evidence on potential health benefits of berries. Curr Op Food Science 2:36-42 (2015).
- [290] Dreher ML, et al. Starch digestibility of foods: a nutritional perspective. Crit Rev Food Sci Nutr. 20(1):47-71. (1984)
- [291] Lin AH, Structure and Digestion of Common Complementary Food Starches. J Pediatr Gastroenterol Nutr. 66 Suppl 3:S35-S38 (2018).
- [292] Abu-Elsaad NM, et al. Modified citrus pectin stops progression of liver fibrosis by inhibiting galectin-3 and inducing apoptosis of stellate cells. Can J Physiol Pharmacol. 94(5):554-62 (2016).
- [293] Lascala A, et al. Analysis of proautophagic activities of Citrus flavonoids in liver cells reveals the superiority of a natural polyphenol mixture over pure flavones. J Nutr Biochem. 58:119-130 (2018).
- [294] Cardinal S, Anti-inflammatory properties of quebecol and its derivatives. Bioorg Med Chem Lett. 26(2):440-444 (2016).
- [295] Gaiz AA, et al. Potential of Anthocyanin to Prevent Cardiovascular Disease in Diabetes. Altern Ther Health Med. 24(3):40-47.
   (2018).
- [296] Celli GB, et al. Gastroretentive systems a proposed strategy to modulate anthocyanin release and absorption for the management of diabetes. Drug Deliv. 23(6):1892-901 (2016).
- [297] Tulini F, et al. Development of solid lipid microparticles loaded with a proanthocyanidin-rich cinnamon extract (Cinnamomum zeylanicum): Potential for increasing antioxidant content in functional foods for diabetic population. Food Res Int. 85:10-18 (2016).
- [298] Loo R, et al. Characterization of metabolic responses to healthy diets and association with blood pressure: application to the Optimal Macronutrient Intake Trial for Heart Health (OmniHeart), a randomized controlled study. Am J Clin Nutr. 107(3):323-334 (2018).
- [299] Fraga CG, The effects of polyphenols and other bioactives on human health. Food Funct. 10(2):514-528 (2019).
- [300] Kunnumakkara AB, et al. Curcumin, the golden nutraceutical: Multitargeting for multiple chronic diseases. Br. J. Pharmacol 174, 1325–1348 (2017).
- [301] Goszcz K, et al. Bioactive polyphenols and cardiovascular disease: Chemical antagonists, pharmacological agents or xenobiotics that drive an adaptive response? Br. J. Pharmacol. 174, 1209–1225 (2017).
- [302] De Bruyne T, et al. Dietary Polyphenols Targeting Arterial Stiffness: Interplay of Contributing Mechanisms and Gut Microbiome-Related Metabolism. Nutrients. 11:3 (2019).
- [303] Deutsche Rheuma-Liga e.V. Bundesverband: Merkblatt 5.2 Ernährung bei Rheuma. 9. Auflage (2018).
- [304]Kuno habil Hottenrott, Präventionsstudie: Evaluation des Gesundheitsfastens nach dem Konzept der Deutschen Fastenakademie.<br/>Zeitschrift für Komplementärmedizin 08(02): 63-68 (2016).
- [305] Höfer S, Sprengart P, Praktische Diätetik. Wissenschaftl. Verlagsgesellschaft Stuttgart, XII (2018).
- [306] Felson DT, Bischoff-Ferrari HA, Dietary fatty acids for the treatment of OA, including fish oil. Ann Rheum Dis 75:1–2 (2016).



- References
- [307] Kale-Pradhan PR, et al. Role of Lactobacillus in the Prevention of Antibiotic-Associated Diarrhea: A Meta-analysis. Pharmacother J Hum Pharmacol Drug Ther 30:119–126 (2010).
- [308] Carroll IM, et al. Alterations in composition and diversity of the intestinal microbiota in patients with diarrhea-predominant irritable bowel syndrome. Neurogastroenterol Motil. 24(6):521-30, e248 (2012).
- [309] Malinen E, et al. Analysis of the Fecal Microbiota of Irritable Bowel Syndrome Patients and Healthy Controls with Real-Time PCR. Am J Gastroenterology 100, ajg200561 (2005).
- [310] Labus JS, et al. Evidence for an association of gut microbial Clostridia with brain functional connectivity and gastrointestinal sensorimotor function in patients with irritable bowel syndrome, based on tripartite network analysis. Microbiome, 7:45 (2019).
- [311] Rizzello F, Dietary geraniol ameliorates intestinal dysbiosis and relieves symptoms in irritable bowel syndrome patients: a pilot study. BMC Complement Altern Med. 18: 338 (2018).
- [312] Stargrove, M. B. et al. Herb, Nutrient and Drug Interactions: Clinical Implications and Therapeutic Strategies, 1. Auflage. St. Louis, Missouri: Elsevier Health Sciences, 2008.
- [313] Tomas-Barberan, FA et al., Advances in Health-Promoting Food Ingredients. J. Agric. Food Chem., 67, 33, 9121-9123 (2019)
- [314] Duda-Chodak A, et al, Interaction of dietary compounds, especially polyphenols, with the intestinal microbiota: a review, Eur J Nutr, 54(3):325-41 (2015)
- [315] Alfa MJ, et al, A randomized trial to determine the impact of a digestion resistant starch composition on the gut microbiome in older and mid-age adults, Clinical Nutrition 37, 797e807 (2018)
- [316] Braune A, et al, Bacterial species involved in the conversion of dietary flavonoids in the human gut, Gut Microbes. 7(3):216-34 (2016)
- [317] Aherne S A, et al, Dietary flavonols: chemistry, food content, and metabolism, Nutrition ;18(1):75-81 (2002)
- [318] Wallace TC, Health Effects of Coconut Oil-A Narrative Review of Current Evidence, J Am Coll Nutr. 2019 Feb;38(2):97-107 J Am Coll Nutr. ;38(2):97-107 (2019)
- [319] Santos HO, Coconut oil intake and its effects on the cardiometabolic profile A structured literature review, Prog Cardiovasc Dis., 62(5):436-443 (2019)
- [320] Xu Y, et al, Coenzyme Q10 Improves Lipid Metabolism and Ameliorates Obesity by Regulating CaMKII-Mediated PDE4 Inhibition, Sci Rep.;7(1):8253 (2017)
- [321] Samiento A, et al, Coenzyme Q10 Supplementation and Exercise in Healthy Humans: A Systematic Review, Curr Drug Metab.;17(4):345-58 (2016)
- [322] Franco EAN, et al, syllium (Plantago ovata Forsk): From evidence of health benefits to its food application, Trends in Food Science & Technology (2020)
- [323] Mullin G, et al, Integrative Gastroenerology, Oxford University Press, ISBN 9780190933074 (2020)
- [324] Kunnumakkara AB, et al, Chronic diseases, inflammation, and spices: how are they linked?, J Transl Med. 16(1):14 (2018)
- [325] Burri BJ, et al, Absorption, metabolism, and functions of  $\beta$ -cryptoxanthin, Nutr Rev. 74(2): 69–82 (2016)
- [326] Franco R, et al, The central role of glutathione in the pathophysiology of human diseases. Medycyna pracy. 113(4-5):234-58 (2007)
- [327] Innes KJ, et al, Omega-6 fatty acids and inflammation, Prostaglandins Leukot Essent Fatty Acids.;132:41-48 (2018)
- [328] Simopoulos AP, The importance of the ratio of omega-6/omega-3 essential fatty acids. Biomed Pharmacother;56(8):365-79. (2002)
- [329] Millsop JW, et al, Diet and psoriasis, part III: role of nutritional supplements, J Am Acad Dermatol. 71(3):561-9 (2014)
- [330] Del Duca E, et al, Superiority of a vitamin B12-containing emollient compared to a standard emollient in the maintenance treatment of mild-to-moderate plaque psoriasis. Int J Immunopathol Pharmacol. 30(4):439-444 (2017)
- [331] Bortolin RC, et al, Guarana supplementation attenuated obesity, insulin resistance, and adipokines dysregulation induced by a standardized human Western diet via brown adipose tissue activation. Phytother Res. 33(5):1394-1403 (2019)
- [332] Lips P, et al, Vitamin D and type 2 diabetes. J Steroid Biochem Mol Biol.;173:280-285 (2017)
- [333] Chen W, et al, Review of Ginseng Anti-Diabetic Studies. Molecules.;24(24) (2019)
- [334] Satija A, et al, Plant-Based Dietary Patterns and Incidence of Type 2 Diabetes in US Men and Women: Results from Three Prospective Cohort Studies. PLoS Med ;13(6):e1002039 (2016)
- [335] Różańska D, et al, The significance of anthocyanins in the prevention and treatment of type 2 diabetes. Adv Clin Exp Med.;27(1):135-142 (2018)
- [336] Eisner BH, et al, High dietary magnesium intake decreases hyperoxaluria in patients with nephrolithiasis. Urology. 80(4):780-3 (2012)
- [337] Ticinesi A, et al, Salt and nephrolithiasis. Nephrol Dial Transplant.;31(1):39-45 (2016)
- [338] Afsar B, ET AL, The role of sodium intake in nephrolithiasis: epidemiology, pathogenesis, and future directions. Eur J Intern Med.;35:16-19 (2016)
- [339] Walcher T, et al, Vitamin C supplement use may protect against gallstones: an observational study on a randomly selected population. BMC Gastroenterol.;9:74 (2009)
- [340] Shabanzadeh DM, et al, Vitamin D and gallstone disease-A population-based study. Endocrine.;54(3):818-825 (2016)



- [341] Gaby AR, et al, Nutritional approaches to prevention and treatment of gallstones. Altern Med Rev. 14(3):258-67. (2009)
- [342] Fernandez-Moreno M, et al, Mitochondrial DNA (mtDNA) haplogroups and serum levels of anti-oxidant enzymes in patients with osteoarthritis. BMC Musculoskelet Disord.; 12: 264. (2011)