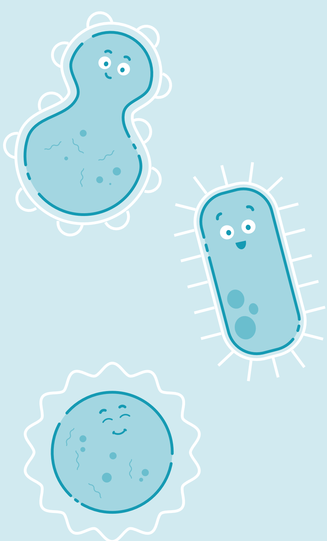
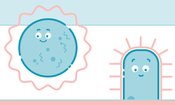
	Essential Gut Health Test	Advanced Gut Health Test
Stool properties		
Colour	✓	✓
Consistency	✓	✓
pH	✓	✓
Biodiversity		
Diversity	✓	✓
Dysbiosis index	✓	✓
Bacterial distribution		
Actinobacteria	✓	✓
Bacteroidetes	✓	✓
Firmicutes	✓	✓
Fusobacteria	✓	✓
Proteobacteria	✓	✓
Verrucomicrobia	✓	✓
Other	✓	✓
Firmicutes/ Bacteroidetes Ratio	✓	✓
Enterotype		
1, 2 or 3	✓	✓
Actinobacteria		
Bifidobacteria	✓	✓
Equol-producing bacteria	✓	✓
Adlercreutzia species		✓
Eggerthella lenta		✓
Slackia species		✓
Bacteroidetes		
Bacteroides	✓	✓
Prevotella	✓	✓
Prevotella copri	✓	✓
Firmicutes		
Butyrate-producing bacteria	✓	✓
Faecalibacterium prausnitzii	✓	✓
Eubacterium rectale	✓	✓
Eubacterium hallii	✓	✓
Roseburia species	✓	✓
Ruminococcus species	✓	✓
Coprococcus	✓	✓
Butyrivibrio species		✓
Cl. butyricum		✓
Total bacterial count	✓	✓
Clostridia	✓	✓
Clostridia total bacterial count	✓	✓
Clostridia cluster 1	✓	✓
Clostridia histolytium		✓
Clostridium perfringens		✓
Clostridium sporenges		✓
Other		✓
Christensenellaceae		✓
Dialister invisus		✓
Fusobacteria		
Fusobacterium species	✓	✓
Verrucomicrobia		
Akkermansia muciniphila	✓	✓





	Essential Gut Health Test	Advanced Gut Health Test
Proteobacteria		
Potentially pathogenic bacteria	✓	✓
Haemophilus	✓	✓
Acinetobacter	✓	✓
Escherichia coli biovare	✓	✓
Proteus species	✓	✓
Proteus mirabilis		✓
Klebsiella species	✓	✓
Klebsiella pneumoniae		✓
Enterobacter species	✓	✓
Serratia species	✓	✓
Hafnia species	✓	✓
Morganella species	✓	✓
Campylobacter species		✓
Providencia species	✓	✓
Citrobacter species	✓	✓
Pseudomonas species	✓	✓
Histamine-producing bacteria	✓	✓
H2S production	✓	✓
Sulphate-reducing bacteria	✓	✓
Desulfovibrio piger		✓
Desulfomonas pigra		✓
Bilophila wadsworthii		✓
Oxalate-degrading bacteria		✓
Oxalobacter formigenes		✓
Archaea		
Methanobrevibacter	✓	✓
Immunogenically effective bacteria		
Escherichia coli	✓	✓
Enterococcus species	✓	✓
Lactobacillus species	✓	✓
Mucin production/ mucosal barrier		
Akkermansia muciniphila	✓	✓
Faecalibacterium prausnitzii	✓	✓
Yeasts/moulds		
Candida albicans	✓	✓
Candida species	✓	✓
Geotrichum candidum	✓	✓
Moulds	✓	✓
Parasites		
Pathobionts	✓	✓
Blastocystis hominis	✓	✓
Dientamoeba fragilis	✓	✓
Helicobacter AG	✓	✓
Pathogenic intestinal protozoa	✓	✓
Giardia lamblia	✓	✓
Entamoeba histolytica	✓	✓
Cryptosporidium species	✓	✓
Cyclospora cayetanensis	✓	✓
Helminths (Ultimate Gut Health Test)		✓
Taenia species		✓
Taenia solium		✓
Taenia saginata		✓
Ascaris species		✓
Enterobius vermicularis		✓
Ancylostoma species		✓
Ancylostoma duodenale		✓
Hymenolepsis species		✓
Hymenolepsis nana		✓
Hymenolepsis diminuta		✓
Trichuris trichiura		✓
Necator americanus		✓
Strongyloides species		✓
Strongyloides stercoralis		✓
Microsporidia		✓
Enterocytozoon species		✓
Encephalitozoon species		✓
Functional markers		
Calprotectin	✓	✓
Haemoglobin in faeces immunologically	✓	✓
Secretory IgA	✓	✓
Pancreatic elastase	✓	✓
Zonulin		✓

bio|vis DIAGNOSTIK

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DAkkS Deutsche Akkreditierungsstelle D-ML-13188-01-00

External ID 101060329700

Name		Date of Birth	
First Name		Sex	
Order ID			
Order Date			

Test	Result	Unit	Standard Range	Previous Result / Material / Method
Stool Diagnostics				
Microbiome Healthpath Maxi				
Moleculargenetic Microbiomeanalysis MAXI				
Stool Properties				
Colour	brown			FE NA) VISU
Consistency	mushy			FE NA) VISU
pH	8,0		5,8 - 6,5	FE NA) TESTS
Biodiversity				
Diversity	4,30		> 5,0	FE NA) MGSEQ

The bacterial diversity in the intestinal tract may vary considerably from person to person. Antibiotic therapies, infections, increasing age, unbalanced diets or smoking are causes of declining diversity.

Grad **3**

Bacteria Phyla (Distribution)				
Actinobacteria	0,5	%	1,0 - 5	FE NA) MGSEQ
Bacteroidetes	38,7	%	30 - 60	FE NA) MGSEQ
Firmicutes	20,5	%	30 - 60	FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0	FE NA) MGSEQ
Proteobacteria	39,1	%	1,5 - 5,0	FE NA) MGSEQ
Verrucomicrobia	0,4	%	1,5 - 5	FE NA) MGSEQ
Other	0,9	%		FE NA) MGSEQ
Ratio				
Firmicutes/Bacteroidetes	0,53	Quotient	< 1,5	FE NA) RECHN
Enterotype				
Bacteroides				FE NA) MGSEQ

Human intestinal microbiomes can be differentiated into three Enterotypes. Enterotypes are defined by dominant bacterial clusters with distinct metabolic properties.

Enterotyp **1**

Dysbiosis index

FE=Stuhl

* cooperate analytics (R), A) accredited, NA) not accredited

Name		Date of Birth	Order ID
First Name		Sex	Order Date

Test	Result	Unit	Standard Range	Previous Result

The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.

Index **16**

Test	Result	Unit	Standard Range	Previous Result
Bacteria Phyla - most important genera and species				
Actinobacteria				
Bifidobacteria	2,8 x 10^9	CFU/g faeces	> 5,0 x 10^9	
Bifidobacterium adolescentis	88	%		
Equol producing bacteria	1,8 x 10^9	CFU/g faeces	> 5,0 x 10^9	
Adlercreutzia spp.				
Eggerthella lenta				
Slackia. spp.				
Bacteroidetes				
Bacteroides	2,2 x 10^11	CFU/g faeces	> 1,5 x 10^11	
Bacteroides uniformis	6	%		
Prevotella	1,2 x 10^11	CFU/g faeces	> 1,0 x 10^10	
Firmicutes				
Butyrate producing bacteria				
Faecalibacterium prausnitzii	3,6 x 10^10	CFU/g faeces	> 5,0 x 10^10	
Eubacterium rectale	7,1 x 10^9	CFU/g faeces	> 1,0 x 10^10	
Eubacterium hallii	1,9 x 10^9	CFU/g faeces	> 5,0 x 10^9	
Roseburia spp.	4,5 x 10^10	CFU/g faeces	> 2,0 x 10^10	
Ruminococcus spp.	2,8 x 10^10	CFU/g faeces	> 3,0 x 10^10	
Coprococcus	2,5 x 10^9	CFU/g faeces	> 2,0 x 10^10	
Butyrivibrio spp.	4,0 x 10^9	CFU/g faeces	> 5,0 x 10^9	
Cl. butyricum	4,1 x 10^10	CFU/g faeces	> 1,0 x 10^10	
Total bacterial count	1,6 x 10^11	CFU/g faeces	> 1,3 x 10^11	
Clostridia				
Clostridia total bacterial count	2,2 x 10^9	CFU/g faeces	< 4,0 x 10^9	
Clostridia cluster I	2,4 x 10^8	CFU/g faeces	< 2,0 x 10^9	
Clostridium histolyticum	2,4 x 10^8	CFU/g faeces	< 2,0 x 10^9	
Clostridium perfringens	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^8	
Clostridium sporogenes	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^8	
Other				
Christensenellaceae	6,3 x 10^8	CFU/g faeces	> 1,0 x 10^9	
Dialister invisus	< 1,0 x 10^6	CFU/g faeces	< 4,0 x 10^10	
Fusobacteria				
Fusobacterium spp.	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^7	
Verrucomicrobia				
Akkermansia muciniphila	3,5 x 10^9	CFU/g faeces	> 5,0 x 10^9	
Proteobacteria				
Pathogenic or potentially pathogenic bacteria				
Haemophilus	1,0 x 10^8	CFU/g faeces	< 1,0 x 10^9	
Acinetobacter	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^6	

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Name		Date of Birth	Order ID
First Name		Sex	Order Date

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Escherichia coli Biovare	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Proteus species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Klebsiella species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Enterobacter species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Serratia species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Hafnia species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4		FE A) KULTAZ
Morganella spp.	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4		FE NA) MIB
Histamine producing bacteria					
Histamine producing bacteria	5,3 x 10^8	CFU/g faeces	< 5,0 x 10^8		FE NA) MGSEQ
H2S production					
Sulphate reducing bacteria	5,1 x 10^8	CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Desulfovibrio piger	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^9		FE NA) MGSEQ
Desulfomonas pigra	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^9		FE NA) MGSEQ
Bilophila wadsworthii	< 1,0 x 10^6	CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Oxalate degrading bacteria					
Oxalobacter formigenes	2,2 x 10^8	CFU/g faeces	> 1,0 x 10^8		FE NA) MGSEQ
Archaea					
Methanobrevibacter	8,1 x 10^7	CFU/g faeces	< 1,0 x 10^8		FE NA) MGSEQ
Immunogenicity / Mucus production					
Immunogenically effective bacteria					
Escherichia coli	4,0 x 10^8	CFU/g faeces	10^6 - 10^7		FE A) KULTAZ
Enterococcus species	2,0 x 10^7	CFU/g faeces	10^6 - 10^7		FE A) KULTAZ
Lactobacillus species	2,0 x 10^4	CFU/g faeces	10^5 - 10^7		FE A) KULTAZ
Mucin production / Mucosa barrier					
Akkermansia muciniphila	3,5 x 10^9	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Faecalibacterium prausnitzii	3,6 x 10^10	CFU/g faeces	> 5,0 x 10^10		FE NA) MGSEQ
Yeasts / Molds					
Candida albicans	< 1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE A) KULTAZ
Candida species	< 1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE A) KULTAZ
Geotrichum candidum	< 1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE A) KULTAZ
Moulds	negative		negative		FE A) KULTAZ
Parasites					
Pathobionts					
Blastocystis hominis	negative		negative		FE NA) MOLEK
Dientamoeba fragilis	negative		negative		FE NA) MOLEK
Pathogenic intestinal protozoa					
Giardia lamblia	negative		negative		FE NA) MOLEK
Entamoeba histolytica	negative		negative		FE NA) MOLEK
Cryptosporidium spp.	negative		negative		FE NA) MOLEK
Cyclospora cayetanensis	negative		negative		FE NA) MOLEK
Colon Ca early detection					
Calprotectin	<17,9	mg/l	< 50		FE A) ELISA
Hemoglobin in feces immunologically	<10	µg/g	< 10		FE A) ELISA
Special Request					
Secretory IgA	2598,4	µg/ml	510 - 2040		FE A) ELISA

FE=Stuhl

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Name		Date of Birth		Order ID	
First Name		Sex		Order Date	

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Pancreatic elastase	245,13	µg/g	> 200		FE A) ELISA
Zonulin	23,61	ng/ml	< 55		FE A) ELISA
Gastro diagnostics					
Helicobacter AG	negative		negative		FE NA) CLIA

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Overview - Results and Therapy Options

Dysbiose-Index 16

pH	↑	milieu stabilizing probiotics *
Enterotype	1	check vitamin A. E, iron and calcium supply
Biodiversitiy	↓	balanced diet, do without non-essential antibioss
Ratio Firmicutes/Bacteroidetes	●	
Equol producing bacteria	↓	
Butyrate producing bacteria	↓	prebiotics on the basis of resistant starch* or scFOS/scGOS*
Mucus production	↓	prebiotics (scFOS/scGOS)*
Mucosa integrity	↓	prebiotics (scFOS/scGOS)*, phosphytidylcholinr, L-glutamine
Milieu stabilising bacteria	↓	milieu stabilizing probiotics*, prebiotics (scFOS/scGOS)*
Immunogenic bacteria	↓	immunogenic effective probiotics*
Clostridia - total bacteria count	●	
Clostridia cluster I	●	
Fusobacteria	●	
Histamine producing bacteria	↑	
H2S producing bacteria (SRB)	●	
Potentially pathogenic bacteria	●	
Candida (facultive pathogenic)	●	
Oxalate degrading bacteria	●	

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CLIENTS
INVITATIONS
TESTS
SUPPLEMENTS
CONSULTATIONS
FOOD
RESOURCES
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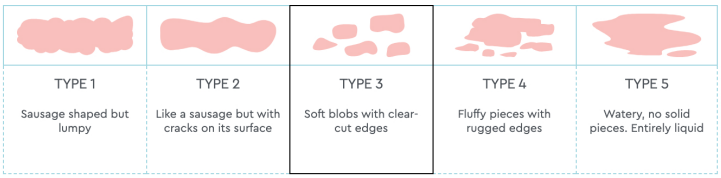
HOW TO

At a glance

PREV

NEXT

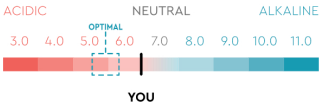
YOU



TYPE 1	TYPE 2	TYPE 3	TYPE 4	TYPE 5
Sausage shaped but lumpy	Like a sausage but with cracks on its surface	Soft blobs with clear-cut edges	Fluffy pieces with rugged edges	Watery, no solid pieces. Entirely liquid

pH

6.5



pH is all about balance. Both very acidic and very alkaline scores represent unhealthy digestive systems.

A LOW pH can indicate that carbohydrates aren't being absorbed properly.

A HIGH pH suggests inadequate acid production and digestion.

Biodiversity

Species richness is thought to be a major marker for gut health. Ideally, we all want high bacterial richness and diversity, as these often reflect ecosystem stability and resilience.

There's also an association between a reduction in the number of species in a person's poop sample and an increased risk of disease.

What can decrease biodiversity? Some factors are transit time, antibiotic therapies, infections, increasing age, unbalanced diets (low in fibre), smoking.

Enterotype

Recent research suggests that the human microbiome can be assigned to three main groups, known as 'enterotypes'.

Enterotype 1

Enriched with Bacteroides and the co-occurring Parabacteroides

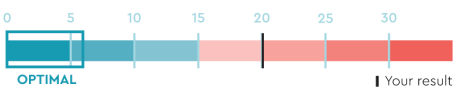
Enterotype 2

Enriched with Prevotella and the co-occuring Desulfovibrio

Enterotype 3

Enriched with Ruminococcus and the co-occurring Akkermansia

Dysbiosis index



The dysbiosis index is a measure of deviations within the microbiome. In other words, if you have too much of one type of bacteria, or not enough of another, it can affect your index.

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Results - out of range

Show detailed description Yes

DOWNLOAD LAB REPORT

PREV NEXT

Bacterial distribution — Out of range

Actinobacteria — Borderline low

Actinobacteria help to maintain balance in the gut. They produce special substances called short-chain fatty acids, which reduce the pH within the intestines. A lower pH is a good thing because it helps to prevent the growth of bad bacteria.

Low levels of Actinobacteria may predispose a person to intestinal inflammation. Low levels of Bifidobacteria (a type of Actinobacteria) are seen in IBS, IBD and colon cancer. Taking antibiotics can reduce Bifidobacteria.

Proteobacteria — Borderline high

Proteobacteria are normal residents of the gut microbiome.

High levels of Proteobacteria may indicate dysbiosis. Excess Proteobacteria has also been associated with IBS.

Verrucomicrobia — Borderline low

There's only one type of Verrucomicrobia found in human stools: Akkermansia muciniphila. This species correlates with a healthier, more diverse gut microbiome.

Low levels of Akkermansia muciniphila are associated with leaky gut.

Actinobacteria — Out of range

Bifidobacteria — Borderline low

Bifidobacteria play an important role in breaking down fibre that humans can't digest on their own. They also help to train the immune system.

Taking several courses of antibiotics can lead to a low levels of Bifidobacteria. Low levels are also more common in obese people.

Eqoul-producing bacteria — Borderline low

These bacteria turn compounds found in soy into a substance called equol. This may explain the health benefits of soy, as higher levels of equol are associated with reduced menopausal symptoms and reduced risk of chronic disease.

These bacteria turn compounds found in soy into a substance called equol. This may explain the health benefits of soy, as higher levels of equol are associated with reduced menopausal symptoms and reduced risk of chronic disease.

Bacteroidetes — Out of range

Bacteroides — Borderline low

Bacteroides are immune-modulating bacteria. They're believed to be involved in microbial balance, the integrity of the gut wall and neuroimmune health.

People with low levels of Bacteroides may be more likely to experience gut inflammation.

Prevotella — Extreme low

Prevotella are gram-negative bacteria. They're considered to be normal residents of the gut microbiome.

Low levels of Prevotella indicate dysbiosis due to loss of overall bacterial diversity.

Firmicutes — Out of range

Butyrate-producing bacteria

Eubacterium rectale — Borderline low

Eubacterium rectale (E. rectale) produces butyrate—a short-chain fatty acid that helps to reduce inflammation and heal the gut.

E. rectale has been found to be lower in people who suffer from ulcerative colitis.

Eubacterium hallii — Borderline low

Eubacterium hallii (E. hallii) is considered an important indicator of metabolic balance within the intestines. It produces butyrate—a short-chain fatty acid that helps to reduce inflammation and heal the gut. E. hallii also helps to produce vitamin B12, though it's unlikely much of this is absorbed by the body.

Low levels of E. hallii indicate dysbiosis due to loss of overall bacterial diversity.

Roseburia species — Borderline low

Roseburia species produce butyrate—a short-chain fatty acid that helps to reduce inflammation and heal the gut. Appropriate levels of Roseburia species have also been associated with weight loss and improved glucose tolerance.

Lower levels of Roseburia species have been observed in people suffering from inflammatory bowel disease and/or kidney disease.

Coprococcus — Borderline low

Coprococcus species are key fermenting bacteria, meaning they help to break down carbohydrates. They produce butyrate—a short-chain fatty acid that helps to reduce inflammation and heal the gut.

Low Coproccocus has been seen in autistic children, though this it thought to be a result of restrictive diets.

Total bacterial count — Borderline low

This is the total amount of butyrate-producing bacteria.

A low level of butyrate-producing bacteria may indicate leaky gut.

Faecalibacterium prausnitzii — Borderline low

Appropriate levels of Facecalibacterium prausnitzii (F.prausnitzii) are generally seen as a marker of health. It's a key producer of butyrate—a short-chain fatty acid that helps to reduce inflammation and heal the gut.

Low levels of F. prausnitzii are seen in intestinal and metabolic disorders such as inflammatory bowel disease, irritable bowel syndrome, colorectal cancer, obesity and coeliac disease.

Proteobacteria — Out of range

Potentially pathogenic bacteria

Haemophilus — Borderline high

Haemophilus is a group of bacteria, but we don't yet know whether it has a positive or negative effect on health.

High levels of Haemophilus species have been found in people with multiple sclerosis and colon cancer.

Enterobacter species — Extreme high

Enterobacter species are gram-negative bacteria. They're closely related to E. coli.

High levels of Enterobacter species can indicate increased inflammation in the intestines. Two specific strains of Enterobacter—E. aerogenes and E. cloacae—have been identified as antibiotic-resistant superbugs in hospitals.

Citrobacter species — Extreme high

Species of Citrobacter don't tend to cause problems, but they can become pathogenic if given the opportunity.

High levels of Citrobacter species have been associated with bloating and IBS. They have also been associated with gastroenteritis, although this is rare.

Pseudomonas species — Extreme high

Pseudomonas species are opportunistic pathogens. They're especially problematic in people who have compromised immune systems or weak beneficial bacteria.

One species of Pseudomonas, Pseudomonas aeruginosa, is known to cause hospital-acquired infections. The gut can be a reservoir for Pseudomonas aeruginosa. It may not cause problems in the gut itself, but it can lead to infection elsewhere in the body.

HS2 production

Sulphate-reducing bacteria — Borderline high

Sulphate-reducing bacteria—including Desulfovibrio piger, Desulfomonas pigra and Bilophila wadsworthii—turn sulphate the toxic metabolic byproduct, hydrogen sulphide.

Too many sulphate-reducing bacteria can produce a high concentration of hydrogen sulphide, which damages the large intestine. Reducing meat intake may help to reduce the number of sulphate-reducing bacteria.

Oxalate-degrading bacteria

Oxalobacter formigenes — Extreme low

Oxalobacter formigenes is a bacterium that works in symbiosis with humans. It produces oxalyl-coA-decarcarboxylase—a special enzyme that breaks down calcium oxalate. Oxalobacter formigenes is present in most people.

People with low oxalobacter formigenes may not be able to break down calcium oxalate effectively. This can promote the development of calcium-containing kidney stones—although more research is needed to confirm this.

Histamine producing bacteria

Histamine-producing bacteria — Medium high

Histamine is a pro-inflammatory signalling molecule. Bacteria that produce histamine include: Hafnia alvei, Klebsiella pneumoniae, Morganella morganii

High levels of histamine in the gut are associated with inflammatory disorders that affect mucous membranes, such as asthma. Signs of histamine intolerance include diarrhoea, headaches, nose and eye irritation, low blood pressure, irregular heartbeat, hives, itchy skin and flushing. Children may also experience chronic intermittent vomiting.

Archaea — Out of range

Methanobrevibacter — Medium high

These are species of archaea found in the gut, mouth, vagina and skin. They are 'methanogens', which means they consume hydrogen and produce methane. They are helpful at healthy levels because they favour the growth of fibre-fermenting bacteria and encourage short-chain fatty acid production.

High levels of methanobrevibacter may lead to the production of too much methane. This can reduce intestinal motility and promote constipation-dominant IBS. High methane has also been seen in diverticulitis.

Immunogenically effective bacteria — Out of range

Escherichia coli — Borderline high

Escherichia coli (E. coli) is a species of gram-negative bacteria. It's a normal part of the gut microbiome, and most strains don't cause problems in humans.

Some pathogenic E. coli strains can cause diarrhoea. High levels of E. coli may also indicate intestinal inflammation.

Enterococcus species — Medium low

These species of bacteria are a normal part of a gut microbiome, and most don't cause problems in humans.

Low levels of Enterococcus species indicate dysbiosis due to loss of overall bacterial diversity.

Lactobacillus species — Medium low

These species of bacteria are a normal part of the gut microbiome. They produce antimicrobial substances that stop the growth of bad bacteria.

Low levels of Lactobacillus may be a result of low carbohydrate or low salt intake. Depletion of Lactobacillus species is frequently associated with disease.

Parasites — Out of range

Pathobionts

Dientamoeba fragilis — Borderline

Dientamoeba fragilis is transmitted through the faecal-oral route, so personal hygiene is important. You're more likely to get it if someone you live with is infected.

The most common symptoms resemble IBS: intermittent diarrhoea, abdominal pain and chronic mental and physical fatigue. However, some people can have it and experience no symptoms.

Functional markers — Out of range

Pancreatic elastase — Medium low

Elastase is an enzyme that digests protein. It's produced in the pancreas, which means it can be measured to assess pancreatic function.

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Bacterial distribution

Bacteroidetes — Optimal

Bacteroidetes help us to break down food, enabling us to extract more energy from it.

Firmicutes — Optimal

Several species of Firmicutes break down complex carbohydrates to produce a short-chain fatty acid called butyrate. Butyrate nourishes the intestinal lining, helping to prevent leaky gut.

Fusobacteria — Optimal

Once considered friendly bacteria, Fusobacteria strains are now thought to be pathogenic. They colonise mucous membranes and have been associated with periodontal disease and skin ulcers.

Firmicutes/Bacteroidetes ratio — Optimal

This is the ratio between two major categories of bacteria in the gut microbiome: Firmicutes and Bacteroidetes.

Firmicutes

Butyrate-producing bacteria

Ruminococcus species — Optimal

Ruminococcus bacteria play a major role in helping us digest resistant starches—the complex carbohydrates found in high-fibre foods such as lentils, beans and unprocessed whole grains. They may help to reduce the risk of diabetes and colon cancer, and they can alleviate infectious diarrhoea.

Butyrivibrio species — Optimal

Butyribivrio bacteria produce butyrate—a short-chain fatty acid that helps to reduce inflammation and heal the gut.

Cl. Butyricum — Optimal

Clostridia butyricum (Cl. Butyricum) modulates gut bacteria and their production of short-chain fatty acids, including butyrate. These short-chain fatty acids provide energy for intestinal cells, and they also have anti-inflammatory properties.

Clostridia

Clostridia total bacterial count — Optimal

Clostridia can be both friendly and unfriendly. Friendly types help to maintain overall gut function by supporting the immune system and producing butyrate. The not-so-friendly types of Clostridia have been associated with various conditions, from diarrhoea to autism.

Clostridia cluster I — Optimal

Some clostridia groups, such as Cluster I-Clostridia, include toxin-developing species. Examples of these species are C. perfringens, C. sporogenes and C. histolyticum.

Clostridium histolyticum — Optimal

In healthy adults, Clostridia histolyticum (Cl. Histolyticum) makes up no more than 1% of the total bacteria.

Clostridium perfringens — Optimal

This species can be a normal part of the gut microbiome at appropriate amounts.

Clostridium sporogenes — Optimal

Clostridia sporogenes only colonises the gut in certain people.

Other

Hemoglobin test — Optimal

test for HBFE marker

Christensenellaceae — Optimal

Christensenella is a genus (group) in the Christensenellaceae family. The amount of Christensenella in our guts is largely inherited. Animal studies suggest that it may help to counteract obesity.

Dialister invisus — Optimal

Although Dialister invisus may play a role in oral cavity infections, little is known of its function in the intestines.

Fusobacteria

Fusobacterium species — Optimal

Fusobacteria species are part of the normal ecosystem of the mouth, gut and vagina.

Verrucomicrobia

Akkermansia muciniphila — Optimal

Appropriate levels of Akkermansia muciniphila (A. muciniphila) have been associated with greater metabolic health. This bacterium breaks down mucins (a part of mucous in the intestines) to produce short-chain fatty acids. These short-chain fatty acids help to feed the host (that's you!) as well as other bacteria in the intestines.

Proteobacteria

Potentially pathogenic bacteria

Acinetobacter — Optimal

This group of bacteria is found in lots of places: drinking water, soil, sewage and various types of food. Healthy people are unlikely to be infected with Acinetobacter.

Escherichia coli biovare — Optimal

Escherichia coli is one of the first types of bacteria to colonise infants, and it generally sticks around for life. Non-pathogenic strains help us to produce vitamin K and vitamin B12.

Proteus species — Optimal

Proteus species are gram-negative bacteria. They're part of a normal gut microbiome.

Klebsiella species — Optimal

Klebsiella species are gram-negative bacteria. They're mostly considered part of a normal gut microbiome.

Serratia species — Optimal

Serratia species are opportunistic, gram-negative bacteria. They're not usually part of a healthy microbiome.

Hafnia species — Optimal

Hafnia species are opportunistic, gram-negative bacteria.

Morganella species — Optimal

Morganella species are gram-negative bacteria. They're a part of a normal gut microbiome in humans, mammals and reptiles.

Providencia species — Optimal

The three known Providencia species—Providencia rettgeri, Providencia rustigiani and Providencia stuartii—are common in the gastrointestinal tract.

HS2 production

Desulfovibrio piger — Optimal

Sulphate-reducing bacteria—including Desulfovibrio piger, Desulfomonas pigra and Bilophila wadsworthii—turn sulphate the toxic metabolic byproduct, hydrogen sulphide.

Desulfomonas pigra — Optimal

Sulphate-reducing bacteria—including Desulfovibrio piger, Desulfomonas pigra and Bilophila wadsworthii—turn sulphate the toxic metabolic byproduct, hydrogen sulphide.

Bilophila wadsworthii — Optimal

Sulphate-reducing bacteria—including Desulfovibrio piger, Desulfomonas pigra and Bilophila wadsworthii—turn sulphate the toxic metabolic byproduct, hydrogen sulphide.

Yeasts/moulds

Candida albicans — Optimal

These are several species of yeast. They're a normal part of the gut microbiome and are generally benign.

Candida species — Optimal

Candida albicans is a friendly yeast, though it has the potential to turn pathogenic if a person's immune system is compromised in some way.

Geotrichum candidum — Optimal

These are several species of yeast. They're a normal part of the gut microbiome, though they can turn pathogenic if a person's immune system is compromised in some way.

Moulds — Optimal

Some types of mould—particularly a type called Aspergillus—are found in the gut. They don't present a problem unless someone's immune system is compromised, such as in critically ill patients. Moulds can also become problematic if someone has a 'weak' (not very diverse) microbiome. They can contribute to brain fog, fatigue and other non-specific symptoms.

Parasites

Pathobionts

Blastocystis hominis — Negative

We have discovered 17 different types of Blastocystis so far, and not all of them cause symptoms. The faecal-to-oral route is the most common mode of infection, which means we typically get it through drinking contaminated water or through poor hygiene practices.

Helicobacter AG — Negative

This is a species of bacteria that's usually found in the stomach.

Pathogenic intestinal protozoa

Giardia lamblia — Negative

Giardia lamblia is the leading cause of infectious gastroenteritis worldwide. Most people believe that foreign travel—especially in developing countries—is the most common reason for infection, but it's just as easy to pick up the parasite in the UK. Things that increase the likelihood of infection are changing children's nappies, swallowing contaminated water (e.g. from swimming pools), eating raw food, sexual activity and owning a dog.

Entamoeba histolytica — Negative

Entamoeba histolytica infection can occur if we drink water contaminated by faeces or eat food that contains Entamoeba histolytica cysts. Infection is most common in tropical and subtropical areas. It can also be transmitted sexually, as well as being passed between people who live together.

Cryptosporidium species — Negative

Along with Blastocystis and Giardia, Cryptosporidium species are believed to play a role in the development of IBS. We can pick Cryptosporidium species up from animals, other humans, water and food.

Cyclospora cayetanensis — Negative

This parasite is mostly found in tropical waters, and seems most prevalent in travellers returning from Mexico. It can also be found in contaminated food.

Functional markers

Calprotectin — Optimal

Calprotectin is a marker of gut inflammation. It's used to distinguish between cases of IBS and IBD (which includes Crohn's disease and ulcerative colitis).

Secretory IgA — Optimal

Secretory IgA is an antibody that helps to reduce inflammation. The immune system releases it into the gut in response to infections.

Zonulin — Optimal

The biomarker zonulin serves as a measure for properdin—a protein that activates cell-to-cell messaging pathways. Along with other proteins in the zonulin family, properdin plays a key role in regulating the gaps between intestinal cells (a.ka. preventing leaky gut). Appropriate levels of zonulin indicate stable and tight gaps between cells.