

GANZIMMUN Diagnostics GmbH - Hans-Böckler-Straße 109 - 55128 Mainz



PROIMMUN d.o.o.
Diagnostik-Zentrum Zagreb
Haulikova 1
HR-10000 Zagreb

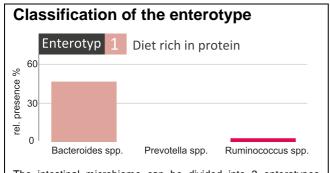


Laboratory report

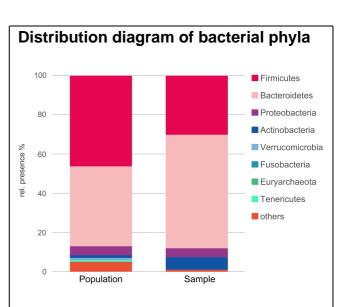
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Sample Material: faeces

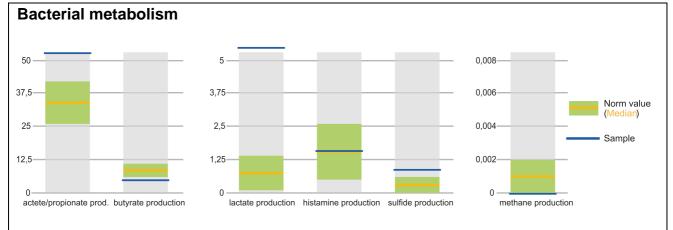
In the context of the microbiome, diversity refers to the diversity of the intestinal bacterial flora. It represents the stability and colonisation resistance.



The intestinal microbiome can be divided into 3 enterotypes based on the predominant bacteria, which allow conclusions to be drawn about long-term eating habits.

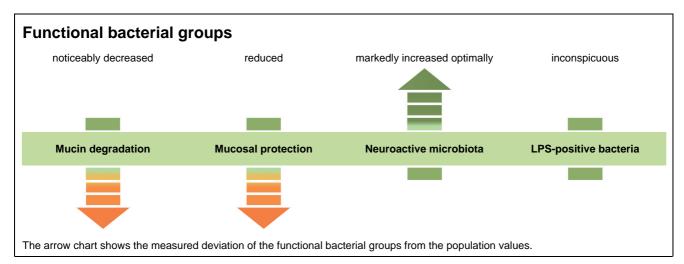


The frequency distribution reflects the proportions amongst the most common bacterial phyla and compares your sample with the average distribution within the population.

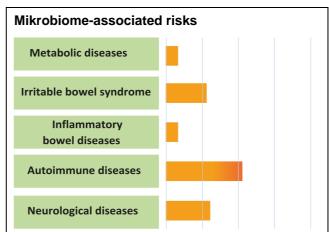


The assignment to the groups was made on the basis of the known predominant metabolic performance of the bacterial species (modified according to Brown et al. 2011).

GANZIMMUN Diagnostics GmbH	Hans-Böckler-Straße 109	55128 Mainz	
T. + 49 (0) 6131 - 7205-0	F. + 49 (0) 6131 - 7205-100	info@ganzimmun.de	www.ganzimmun.de



FODMAP-Index The term FODMAP ("Fermentable Oligosaccharides, Disaccharides, Monosaccharides And Polyols") describes certain short-chain, easily fermentable carbohydrates and sugar alcohols, which are naturally present in numerous foods. 1 2 3 A Low-FODMAP diet is recommended for the improvement of irritable bowel- like or gastrointestinal complaints.



The stated risks **do not represent a diagnosis**, rather the statistical relationships between germs and specific clinical pictures determined in current scientific studies are presented here in relation to the determined microbiome.





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Bioindicators			
pH-value of faeces	7,0		5,5 - 6,5
Biodiversity (Shannon index)**	2,41		> 2,7
Firmicutes / bacteroidetes ratio**	0,5		0,9 - 1,5
Butyrate production**	5,1	%	6,0 - 11,0
Lactate production**	6,3	%	0,1 - 1,4
Acetate / propionate production**	53,0	%	26,0 - 42,0
Mucin degradation**	0.0	%	0,05 - 8,7
LPS-positive bacteria**	0,047	%	< 3,7
Bacterial strains (phyla)			
Firmicutes**	30,134	%	42,0 - 52,0
Bacteroidetes**	57,895	%	34,0 - 45,0
Proteobacteria**	4,558	%	4,0 - 8,8
Actinobacteria**	6,415	%	0,3 - 1,6
Verrucomicrobia**	0,000	%	0,007 - 2,4
Fusobacteria**	0,007	%	< 0,004
Cyanobacteria**	0,010	%	0,02 - 0,6
Euryarchaeota**	0,000	% 🖳	< 0,002
Tenericutes**	0,001	%	0,005 - 0,200
Functional bacterial groups			
Mucin-degrading microbiota			
Akkermansia muciniphila**	0,000	%	0,003 - 2,1
Prevotella spp.**	0,010	%	0,006 - 5,1
Prevotella copri**	0,001	%	< 0,2
Mucosa protective mikrobiota			
Akkermansia muciniphila**	0,000	%	0,003 - 2,1
Faecalibacterium prausnitzii**	0,469	%	1,5 - 5,2
Sulphate-reducing microbiota			
Bilophila wadsworthia**	0,773	%	< 0,3
Desulfobacter spp.**	0,001	%	< 0,004

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Desiritive microbiota Septiment Sept	Desulfovibrio spp.**	0,129	%	< 0,2
Bifidobacterium adolescentis"	Desulfuromonas spp.**	0,000	%	< 0,001
Bifidobacterium dentium*	Neuroactive microbiota			
Lactobacillus previs** 0,000	Bifidobacterium adolescentis**	0,086	%	0,001 - 0,2
Lactobacillus plantarum** 0,000 %	Bifidobacterium dentium**	0,001	%	> 0,001
Lactobacillus paracasei" 0,000 %	Lactobacillus brevis**	0,000	%	> 0,001
Casilibacter spp." 0.021	Lactobacillus plantarum**	0,000	%	> 0,001
Alistipes spp." 4,957 % 2,2 - 6.7 Methane-producing bacteria Methanobacteria" 0,000 % 0,000 Methanobrevibacter spp." 0,000 % 0,000 LPS-positive microbiota Citrobacter spp." 0,001 % 0,000 Enterobacter spp." 0,001 % 0,000 Escherichia spp." 0,002 % 0,000 Providencia spp." 0,000 % 0,000 Serratia spp." 0,000 % 0,000 Sutterella spp." 0,000 % 0,000 Escherichia spp." 0,000 % 0,000 Sutterella spp." 0,000 % 0,000 Sutterella spp." 0,001 % 0,000 Escherichia spp." 0,000	Lactobacillus paracasei**	0,000	%	> 0,001
Methane-producing bacteria Methane-producing bacteria < 0,000	Oscillibacter spp.**	0,021	%	< 0,3
Methanobacteria** 0,000 %	Alistipes spp.**	4,957	%	2,2 - 6,7
Methanobrevibacter spp." O,000 %	Methane-producing bacteria			
Citrobacter spp." 0,000 %	Methanobacteria**	0.000	%	< 0,002
Citrobacter spp.** 0,000	Methanobrevibacter spp.**	0,000	%	< 0,001
Enterobacter spp.** 0,001	LPS-positive microbiota			
Escherichia spp.** 0,042	Citrobacter spp.**	0,000	% 🔽	< 0,001
Richard Spp.** 0,000 % 0,000 Resolution	Enterobacter spp.**	0,001	%	< 0,007
Providencia spp.** 0,000 % 0,001	Escherichia spp.**	0,042	%	< 0,3
Pseudomonas spp.** 0,001	Klebsiella spp.**	0,000	%	< 0,002
Serratia spp.** 0,000 % < 0,001	Providencia spp.**	0,000	%	< 0,001
Sutterella spp.** 0,003 %	Pseudomonas spp.**	0,001	%	< 0,002
Immunmodulation	Serratia spp.**	0,000	%	< 0,001
Escherichia spp.** Enterococcus spp.** 0,001 % Enterococcus spp.** 0,001 % Eifidobacterium adolescentis** 0,086 % Ruminococcus spp.** 2,881 % 0,001 - 0,01 Eutyrivibrio crossotus** 0,013 % Eubacterium spp.** 1,234 % 1,5 - 5,2 Roseburia spp.** 0,518 % 2,2 - 4,8 Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % Bacteroides vulgatus** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 1,0 - 8,9	Sutterella spp.**	0,003	%	< 2,9
Enterococcus spp.** 0,001 % 0,001 - 0,005 Fiber degrading microbiota Bifidobacterium adolescentis** 0,086 % 0,001 - 0,2 Ruminococcus spp.** 2,881 % 2,2 - 4,8 Butyrate-producing microbiota Butyrivibrio crossotus** 0,013 % 0,001 - 0,01 Eubacterium spp.** 1,234 % 0,2 - 1,6 Faecalibacterium prausnitzii** 0,469 % 1,5 - 5,2 Roseburia spp.** 0,518 % 0,3 - 1,5 Ruminococcus spp.** 2,881 % 2,2 - 4,8 Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % 2,2 - 6,7 Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 % 1,0 - 8,9	Immunmodulation			
Fiber degrading microbiota Bifidobacterium adolescentis** 0,086 % 0,001 - 0,2 Ruminococcus spp.** 2,881 % 2,2 - 4,8 Butyrate-producing microbiota Butyrivibrio crossotus** 0,013 % 0,001 - 0,01 Eubacterium spp.** 1,234 % 0,2 - 1,6 Faecalibacterium prausnitzii** 0,469 % 1,5 - 5,2 Roseburia spp.** 0,518 % 0,3 - 1,5 Ruminococcus spp.** 2,881 % 2,2 - 4,8 Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % 2,2 - 6,7 Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 % 1,0 - 8,9	Escherichia spp.**	0,042	%	< 0,3
Bifidobacterium adolescentis** 0,086 % Ruminococcus spp.** 2,881 % 2,2 - 4,8 Butyrate-producing microbiota Butyrivibrio crossotus** 0,001 - 0,01 Eubacterium spp.** 1,234 % Faecalibacterium prausnitzii** 0,469 % Roseburia spp.** 0,518 % 0,3 - 1,5 Ruminococcus spp.** 2,881 % Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 %	Enterococcus spp.**	0,001	%	0,001 - 0,005
Ruminococcus spp.** 2,881 % 2,2 - 4,8 Butyrate-producing microbiota Butyrivibrio crossotus** 0,013 % 0,001 - 0,01 Eubacterium spp.** 1,234 % 0,2 - 1,6 Faecalibacterium prausnitzii** 0,469 % 1,5 - 5,2 Roseburia spp.** 0,518 % 0,3 - 1,5 Ruminococcus spp.** 2,881 % 2,2 - 4,8 Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % 2,2 - 6,7 Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 % 1,0 - 8,9	Fiber degrading microbiota			
Butyrate-producing microbiota Butyrivibrio crossotus** 0,013 % Eubacterium spp.** 1,234 % 7,201 % Faecalibacterium prausnitzii** 0,469 % 1,5 - 5,2 Roseburia spp.** 0,518 % 0,3 - 1,5 Ruminococcus spp.** 2,2 - 4,8 Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 %	Bifidobacterium adolescentis**	0,086	%	0,001 - 0,2
Butyrivibrio crossotus** 0,013 % Eubacterium spp.** 1,234 % 0,2 - 1,6 Faecalibacterium prausnitzii** 0,469 % Roseburia spp.** 0,518 % 0,3 - 1,5 Ruminococcus spp.** 2,881 % Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % 2,2 - 6,7 Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 %	Ruminococcus spp.**	2,881	%	2,2 - 4,8
Eubacterium spp.** Faecalibacterium prausnitzii** 0,469 Roseburia spp.** 0,518 0,3 - 1,5 Ruminococcus spp.** Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 Bacteroides spp.** 46,696 515,0 - 31,0 Bacteroides vulgatus** 0,2 - 1,6 1,5 - 5,2 0,3 - 1,5 2,2 - 4,8 2,2 - 4,8 4,957 51,0 - 31,0 1,0 - 8,9	Butyrate-producing microbiota			
Faecalibacterium prausnitzii** O,469 Roseburia spp.** O,518 Ruminococcus spp.** Acetate-/ propionate-producing bacteria Alistipes spp.** Bacteroides spp.** 4,957 Bacteroides vulgatus** 6,617 N 1,5 - 5,2 0,3 - 1,5 2,2 - 4,8 2,2 - 4,8 1,5 - 5,2 0,3 - 1,5 2,2 - 4,8 2,2 - 6,7	Butyrivibrio crossotus**	0,013	%	0,001 - 0,01
Roseburia spp.** Ruminococcus spp.** 2,881 Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 Bacteroides spp.** 46,696 515,0 - 31,0 Bacteroides vulgatus**	Eubacterium spp.**	1,234	%	0,2 - 1,6
Ruminococcus spp.*** 2,881 % Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % Bacteroides spp.** 46,696 % Bacteroides vulgatus** 6,617 %	Faecalibacterium prausnitzii**	0,469	%	1,5 - 5,2
Acetate-/ propionate-producing bacteria Alistipes spp.** 4,957 % 2,2 - 6,7 Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 % 1,0 - 8,9	Roseburia spp.**	0,518	%	0,3 - 1,5
Alistipes spp.** 4,957 % 2,2 - 6,7 Bacteroides spp.** 46,696 % 15,0 - 31,0 Bacteroides vulgatus** 6,617 % 1,0 - 8,9	Ruminococcus spp.**	2,881	%	2,2 - 4,8
Alistipes spp.** Bacteroides spp.** 4,997 4,997 5,2-6,7 15,0-31,0 Bacteroides vulgatus** 6,617 1,0-8,9	Acetate-/ propionate-producing bacteria			
Bacteroides vulgatus** 6,617 %	Alistipes spp.**	4,957	%	2,2 - 6,7
	Bacteroides spp.**	46,696	%	15,0 - 31,0
Dorea spp.** 0,141 % 0,08 - 0,2	Bacteroides vulgatus**	6,617	%	1,0 - 8,9
	Dorea spp.**	0,141	%	0,08 - 0,2





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Lactate-producing / saccharolytic mi	crobiota		
Bifidobacterium spp.**	6,231	%	0,07 - 1,3
Bifidobacterium adolescentis**	0,086	%	0,001 - 0,2
Enterococcus spp.**	0,001	%	0,001 - 0,005
Lactobacillus spp.**	0,012	%	0,004 - 0,02
histamine-producing bacteria			
Clostridium spp.**	1,569	%	0,9 - 2,2
Enterobacter spp.**	0,001	%	< 0,007
Hafnia alveii**	0,000	% 🖳	< 0,001
Klebsiella spp.**	0,000	% 🖳	< 0,002
Serratia spp.**	0,000	% 🖳	< 0,001
Escherichia spp.**	0,042	%	< 0,3
Clostridiaceae			
Clostridium spp.**	1,569	%	0,9 - 2,2
Clostridium difficile**	0,010	%	< 0.025
Clostridium scindens**	0,014	%	> 0,001
Other microbiota			
Fusobacterium nucleatum**	0,000	% 🖳	< 0,001
Oxalobacter formigenes**	0,000	% 🖳	> 0,001
Anaerotruncus colihominis**	0,282	%	0,04 - 0,1
Streptococcus spp.**	0,116	%	0,08 - 0,5
Fungi			
Candida spp.**	0,000	%	< 0,005
Candida albicans**	0,000	%	< 0,005
Geotrichum candidum**	0,000	%	< 0,001
Saccharomyces cerevisiae**	0,341	%	< 0,2
Moulds**	negativ		negativ
Gastrointestinal diagnostics			
Digestive residues:			
zigostivo rosidues.			

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Fecal fat content**	2,1	g/100g		< 5,2
Fecal water content**	74	g/100g		Please mind the altered normal range. 68,5-82,3
			п	Please mind the altered normal range.
Fecal protein content**	1,2	g/100g		< 1,5 Please mind the altered normal range.
Fecal starch content (amylorrhoea)**	7,5	g/100g		2,6 - 10,6
Fecal sugar content**	2,3	g/100g		< 2,3
r oodi oogal oorioni	2,0	g/ 100g		Please mind the altered normal range.
Malabsorption / Inflammation/ Leaky Gut:				
Fecal alpha-1-antitrypsin	14,7	mg/dl		< 27,5
Zonuline in stool	>3200,0	μU/g		< 60.1
Fecal calprotectin	<19.5	μg/g		< 50
Maldigestion:				
Fecal pancreatic elastase	>500,0	μg/g		> 200
Fecal bile acids	24,58	µmol/g		0,46 - 9,96
				Please mind the altered normal range.
Mucosal immunity:				
Fecal secretory IgA	1065,1	μg/ml		510 - 2040
Parasites:				
Native preparation - protozoa:				
Blastocystic hominis	negativ			negativ
Cysts of Giardia lamblia	negativ			negativ
Endolimax nana	negativ			negativ
Amoebic cysts	negativ			negativ
Native preparation - helminths:				
Ascaris lumbricoides	negativ			negativ
Enterobius vermicularis	negativ			negativ
Ancylostoma duodenale (hookworm)	negativ			negativ
Strongyloides	negativ			negativ
Trichuris trichiura	negativ			negativ
Trichostrongylus	negativ			negativ
Diphyllobothrium	negativ			negativ
Hymenolepis	negativ			negativ
tapeworm (T. saginata, T. solium)	negativ			negativ
Clonorchis/Opisthorchis	negativ			negativ
Fasciola/Fasciolopsis	negativ			negativ
Schistosoma	negativ			negativ
Modified Ziehl-Neelsen stain: Cryptosporidium	negativ			negativ
Cyclospora	negativ			negativ
Isospora belli	negativ			negativ

Summary of molecular stool diagnostics, indication of:





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- · Detection of reduced biodiversity
- · disrupted mucosal protection
- · microbiome-associated tendency towards Leaky Gut
- possible bacterial miscolonisation of the small intestine (SIBOS)
- · microbiome-associated health risks

Overview stool diagnostics:

- · Increased digestion residues in case of suspected wrong nutrition?
- · Suspected compensated bile acid loss syndrome
- Currently no worm eggs and protozoan cysts detectable microscopically in the submitted stool sample.

Interpretation of findings intestinal microbiome

Diversity

The diversity of your sample is reduced.

Diversity refers to the diversity of species that occur in a microbiome. Physiologically, the microbiome has a high diversity, ie a high number of different species, and has a great ability to absorb changes and disturbances. Low diversity makes humans highly susceptible for various diseases, such as irritable bowel syndrome, food intolerances, chronic inflammatory bowel diseases and infections. The most important cause for low diversity is the use of antibiotics, the spectrum of which has a direct effect on reducing diversity.

FODMAP-Index

The composition of your intestinal microbiome indicates a FODMAP type 3.

A low FODMAP diet is recommended for type 3 to improve irritable bowel-like or gastrointestinal symptoms.

The term FODMAP ("Fermentable Oligosaccharides, Disaccharides, Monosaccharides And Polyols") describes certain short-chain, easily fermentable carbohydrates and sugar alcohols, which are naturally present in numerous foods. Depending on the composition of their intestinal microbiome, patients with irritable bowel-like or gastrointestinal complaints may benefit from a low-FODMAP diet.

Literature:

Staudacher H. The impact of low fodmap dietary advice and probiotics on symptoms in irritable bowel syndrome: a randomised, placebo-controlled, 2×2 factorial trial. Gut 2015; 64:A51.

Halmos E. P. A diet low in FODMAPs reduces symptoms of irritable bowel syndrome. Gastroenterology. 2014; 146(1):67-75.

Enterotype determination

The enterotype of your stool sample corresponds to type 1.

The intestinal microbiome can be divided into three so-called **enterotypes**. They are independent of age, gender, body weight and nationality. Studies indicate that long-term dietary patterns, e.g. consumption of animal fats and proteins, could cause enterotypes to switch. First associations between enterotype III and artherosclerotic disease have also been described (Karlsson FH et al. (2012) Symptomatic atherosclerosis is associated with an altered gut metagenome. Nat. Commun. 3:1245).

Bioindicators

Firmicutes/Bacteroidetes ratio

With **over 90%**, the Firmicutes and Bacteroidetes strains are the two dominating bacterial groups in the human intestine.

By **breaking down undigested food components**, the intestinal **Firmicutes** bacterial strains can provide the human body with short-chain carbohydrates and fatty acids as an **additional energy source**.

Numerous studies have shown that the ratio between Firmicutes and Bacteroidetes correlates with human body weight. An increased proportion of Firmicutes causes increased resorption of carbohydrates by the human intestinal mucosa.

Mucosaprotective flora

The mucosal protective flora of your sample is **decreased**. A high-fiber diet, prebiotics with inulin and, if dysbiosis is proven, appropriate probiotics can be used to increase the number of mucosal protective germs, *Akkermansia muciniphila* and *Faecalibacterium prausnitzii*.

Akkermansia muciniphila is a gram-negative obligate anaerobic rod. This is a mucin-cleaving bacteria that plays a central role in maintaining Faecalibacterium prausnitzii by metabolic cleavage products, among others. Current studies have shown that this bacteria has beneficial effects on various health factors. Studies were also able to demonstrate that Akkermansia muciniphila has an anti-inflammatory effect and is beneficial for maintaining an intact intestinal barrier.

Faecalibacterium prausnitzii is a gram-negative obligate anaerobic rod of the Firmicutes strain. This bacteria is one of the three most frequent anaerobic bacteria in the intestinal flora. Changes in the specific bacterial species of the intestinal flora were found in patients with inflammatory bowel disease, irritable bowel syndrome and coeliac disease. One of these changes is a reduced count of Faecalibacterium prausnitzii bacteria. Various studies demonstrated that this bacteria has an important effect on cells of the immune system. It is further known that inflammatory processes in the intestines can be significantly reduced by the production of butyric acid. It is known that Faecalibacterium prausnitzii is one of the most abundant butyric-acid producing bacteria in the colon.

Overall, Faecalibacterium prausnitzii reduces intestinal inflammatory processes and is beneficial for inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis.

V

The **enterotype I** is characterised by an abundance of *Bacteroides spp.*. They are involved in generating energy from carbohydrates and proteins by fermentation, and also in the biosynthesis of biotin.



Several current studies have demonstrated a positive relationship between high counts of **Akkermansia muciniphila** bacteria and the following conditions:

- Low body weight
- Low body fat proportion
- ► Reduced metabolic endotoxaemia by bacterial lipopolysaccharides
- ► Reduced adipose tissue inflammation
- ► Reduced insulin resistance (type II diabetes)



Several studies determined the following immunological effects of *F. prausnitzii*:

- ► Inhibition of transcription factor NF-KB → inhibition of the pro-inflammatory interleukin 8 (IL-8)
- ► Production of butyric acid, which further inhibits NF-KB
- Differentiation of regulatory T cells → increasing the anti-inflammatory interleukin 10 (IL-10), reducing the pro-inflammatory interleukin 12 (IL-12)

Microbiome-associated health risks

The specified risks represent **no diagnosis**, rather the statistical relationships between germs and specific clinical pictures taken from current scientific studies in relation to the determined microbiome.



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Metabolic diseases	Irritable bowel syndrome	Inflammatory bowel diseases	Autoimmune diseases	Neurological diseases
Obesity	Irritable bowel	Chronic-inflammatory bowel diseases	Coeliac disease	Depression
Type 2 diabetes mellitus	Leaky Gut syndrome	Colorectal carcinoma	Rheumatoid arthritis	Chronic fatigue syndrome
Cardiovascular diseases	Histamine intolerance	Dysbiosis	Psoriasis	Autism spectrum disorder
Non-alcoholic steatohepatitis	Food intolerance	Colonisation resistance	Allergy / asthma	Parkinson's disease
Alcoholic steatohepatitis	SIBOS	Gastrointestinal susceptibility to infections	Type 1 diabetes mellitus	Alzheimer's disease

Metabolic diseases

Non-alcoholic steatohepatitis - NASH

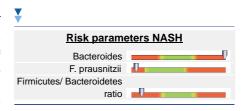
Several studies already observed a correlation between intestinal bacteria and the development of non-alcoholic steatohepatitis. A shift in the metabolic function of intestinal bacteria is predominantly caused by dysbiosis. In the intestine, it leads to an increase in the permeability of intestinal mucosa for lipopolysaccharides (LPS) and ultimately causes chronic inflammation. The extent of LPS permeability can be determined by measuring the soluble LPS receptor protein sCD14 in the serum. It was further determined that the concentration of bacterial metabolites in the blood, such as trimethylamine which is metabolised in the liver to trimethylamine-N-oxide (TMAO) correlates with the severity of steatohepatitis.

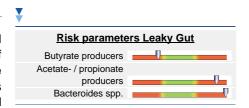
According to studies, the relative frequency of the bacteria *Bacteroides spp.* and *Ruminococcus spp.* correlated with NASH. A similar effect was observed when *Prevotella spp.* and *Faecalibacterium prausnitzii* were reduced.

Leaky Gut syndrome

Irritable bowel syndrome

The scientific findings on the causes and consequences of increased intestinal mucosa permeability are playing an important role in the diagnostics and therapy of gastrointestinal complaints. The transfer of bacterial antigens is believed to be involved in metabolic processes or autoimmune diseases. The new findings demonstrate that a balanced ratio between butyric acid-producing and mucin-degrading bacteria (mucosa protection ratio) plays an important role. When the balance is disrupted and the diversity reduced, bacterial lipopolysaccharides (LPS) can enter the human circulatory system and lead to pathological conditions. The regulatory protein zonulin is a suitable marker to better assess the permeability of the intestinal mucosa.





Food intolerance

Current research results on the causes and consequences of a reduced intestinal barrier show that under physiological conditions most food antigens are resorbed by the intestinal epithelium and are intracellularly degraded into small peptides by its digestive enzymes without triggering pathological immune reactions. If the physiological conditions are disrupted, as in cases with reduced diversity and a strong increase in bacteria of the *Escherichia, Klebsiella* and *Pseudomonas* genus, incompletely digested food components can transfer into the circulatory system where they can trigger potentially pathogenic immune reactions. An example is non-coeliac gluten sensitivity (NCGS), whose clinical manifestation is very similar to that of coeliac disease. In contrast, important protective mechanisms of mucosal integrity are supported by the muco-protective flora, such as *Akkermansia muciniphila* and *Faecalibacterium prausnitzii*.

Small Intestinal Bacterial Overgrowth Syndrome (SIBOS)

The term SIBOS summarises an intolerance to certain carbohydrates or proteins. In cases with lactose or fructose intolerance, an analysis using the hydrogen breath test can support a diagnosis. According to studies, the causes can be non-physiological conditions of the bacteria colonising the intestine. Thus, a significantly elevated relative frequency of *Eschericha spp., Klebsiella spp.* and *Pseudomonas spp.* in the intestine may cause SIBOS. The diagnosis is supported when in addition obligate anaerobic bacteria, such as *Bacteroides spp.* and various species of the genus *Clostridium*, are strongly increased and diversity decreased.

T

Further diagnostics for the risk area irritable bowel syndrome

Due to the identified risk of irritable bowel syndrome, the following **additional laboratory diagnostic tests** are recommended:

- Parasites (immunologic) in the stool
- Histamine metabolite in urine
- PreScreen allergy in serum
- Breath test (fructose and lactose)

Inflammatory bowel diseases and susceptibility to infection

Gastrointestinal susceptibility to infections

Campylobacter infections

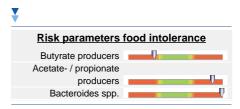
The different susceptibility for an infection with *Campylobacter* depends on the species composition of the intestinal microbiome. People with a higher variety (diversity) of their microbiome and with a high frequency of bacteria from the genuses of *Dorea* and *Coprococcus* are significantly more resistant against a *Campylobacter* infection than people with a low diversity and low frequency of these bacteria. On the other hand, bacteria such as *Bacteroides, Escherichia coli* and *Streptococcus* increase sensitivity towards such infections.

The analysis of your sample reveals **reduced resistance** of your microbiome **against infections by enteropathogenic** *Campylobacter* species.

Infections with rota virus and noro virus

In studies, microbiota analysis showed a significant negative correlation between the sensitivity against infections with noro viruses and rota viruses and the frequency of *Ruminococcus spp.* and *Faecalibacterium prausnitzii*. On the other hand, a positive correlation between these infections and the frequency of *Akkermansia muciniphila* was determined.

The analysis of your sample reveals a **reduced resistance** of your microbiome against infections with noro viruses and rota viruses.











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Further diagnostics for the risk area inflammatory bowel diseases

Due to the identified risk of inflammatory bowel diseases, the following **additional laboratory diagnostic tests** are recommended:

- Haemoglobin-haptoglobin complex
- M2PK
- Blood in the stool

Autoimmune diseases

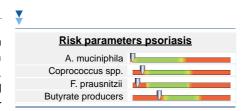
Coeliac disease

Coeliac disease is one of the most frequent autoimmune diseases in children and adults. The research group around Cheng et al. (BMC Gastroenterology 2013, 13:113) determined a significant accumulation of *Prevotella spp.* and *Serratia spp.* in affected people and a strongly reduced diversity in the faecal samples. In contrast, the samples from the healthy population were high in Clostridium spp. and Ruminococcus spp. If coeliac disease seems unlikely because of the absence of a genetic predisposition, non-coeliac gluten sensitivity (NCGS) could be present, which is accompanied by very similar symptoms.

Risk parameter coeliac disease Bacteroides spp. Staphylococcus spp. Butyrate producers

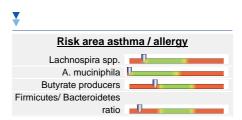
Psoriasis

Psoriasis is an inflammatory systemic autoimmune disease primarily visible through skin changes that also affects joints, ligaments, vessels and other organs. In analogy to other autoimmune diseases, a genetic predisposition is often present. The risk of developing one of the psoriasis forms can be increased by a reduced mucosa-protective and butyric acid-producing bacterial intestinal flora and by lower diversity. In a study that included patients and healthy subjects, a significant relationship between the frequency of the bacteria *Coprococcus spp.*, *Akkermansia muciniphila* and *Ruminococcus spp.* was observed in stool samples (Arthritis Rheumatol. 2015 January; 67(1): 128–139).



Allergy / Asthma

Allergic reactions can start as early as in childhood, remain in later years, disappear or reappear with increased intensity. Several studies emphasised the protective importance of a previous colonisation of the intestinal flora with *Lactobacillus spp.*, *Lachnospira spp.*, *Veillonella spp.* and *Bifidobacterium spp.* In contrast, a reduced diversity and the predominance of bacteria from the Proteobacteria strain and the gram-negative anaerobic *Bacteroides spp.* promote the development of inflammatory and allergic reactions.



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Type 1 diabetes mellitus

Type I diabetes mellitus is considered to be an autoimmune disease. In studies with affected patients, a clear correlation between the disease and the relative frequency of bacteria from the genuses of *Prevotella, Clostridium, Veilonella, Bifidobacterium, Lactobacillus* and *Bacteroides* was determined (Murri et al. BMC Medicine 2013, 11:46). In a different study, researchers determined other correlations relating to the diversity and the ratio between short-chain fatty acid-producing bacteria (*Faecalibactrium, Ruminococcus, Bacteroides*) and mucin-degrading bacteria (*Prevotella* and *Akkermansia*) (PLOSONE October 2011, Volume 6, Issue 10, e25792).

Risk parameters type 1 diabetes mellitus Acetate- / propionate producers Bacteroides spp. F. prausnitzii A. muciniphila



Further diagnostics for the risk area autoimmune diseases

Due to the identified risk of autoimmune diseases, the following **additional laboratory diagnostic tests** are recommended:

- Gluten sensitivity in serum
- DQ2/DQ8
- HLA-B27
- · Large rheumatoid profile
- · Autoimmune screen
- · Asthma/rhinitis seasonal or year-round

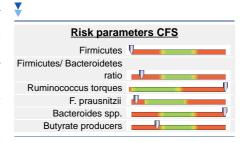
Neurological disorders

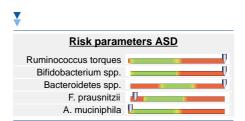
Chronic Fatigue Syndrome – CFS

Chronic fatigue syndrome, also called myalgic encephalomyelitis, is a disease pattern that is often not sharply defined and is characterised by mental and physical fatigue and in some cases muscle ache after only minor exertion. The causes for this mental illness are mostly complex in nature and are attributed to immunology, post infection or to the bacterial composition of the intestinal flora and its metabolites, such as short-chain fatty acids. A study including affected and healthy subjects frequently observed the relationship between CFS and irritable bowel syndrome (IBS). The intestinal flora of affected patients was characterised by a low frequency of bacterial species, such as Faecalibacterium prausnitzii, Eubacterium spp. and Odoribacter spp., while Clostridium spp. and Ruminococcus torques were markedly increased. A correlation between the severity of the symptoms was even established for some bacteria. A low number of the Alistipes genus was connected to higher vitality and motivation, while the symptoms were significantly more severe when the frequency of Faecalibacterium prausnitzii was low (Nagy-Szakal et al. Microbiome (2017) 5:44).

Autism Spectrum Disorder - ASD

The autism spectrum disorder comprises early childhood autism, Asperger's syndrome, and several rare atypical forms. An early diagnosis can help the patient develop compensation mechanisms that can overcome shortcomings in social communication. In a study including patients and healthy control subjects, a significant correlation was observed between the permeability of the intestinal mucosa, measured by means of zonulin in the serum, and the degree of the Autism Rating Score (Esnafoglu et al. J Pediatr. 2017 May 11). The integrity of the intestinal mucosa is significantly influenced by the intestinal bacteria. Thus, a strong reduction in butyric acid-producing bacteria such as Faecalibacterium prausnitzii can cause an insufficient regeneration of colonocytes and promote the permeability of the intestinal mucosa. Predominance of Proteobacteria, and in particular a higher density of the Sutterella genus, is often observed in autistic patients. A 10-fold amount of Ruminococcus torques from the Firmicutes strain was recorded in samples of affected patients compared to samples from healthy subjects (Wang et al. Molecular Autism 2013, 4:42). Another study observed a significantly lower number of mucin-degrading Akkermasia muciniphila and the short-chain fatty









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acid-producing Bifidobacterium spp. in children with autism.



Further diagnostics for the risk area neurological disorders

Due to the identified risk of neurological disorders, the following **additional laboratory diagnostic tests** are recommended:

- · Adrenal stress index in saliva
- Large hormone profile (female/male)
- Thyroid profile
- Total T3/reverse T3 ratio
- Q10
- Oxidative stress
- Vitamins B1, B2, B3, B5
- · Methylmalonic acid in urine

Other risks

Calcium oxalate urinary stones

According to a study by the group from the Slone Epidemiology Centre of Boston University, the Harvard Medical School and the Neurological Clinic of Duke University, the intestinal tract bacteria *Oxalobacter formigenes* can reduce the risk for developing kidney stones by up to 70%. The researchers report that the protective effect is most likely based on the metabolisation of oxalate in the digestive tract. In contrast, the absence of this bacteria can increase the risk for forming these kidney stones.

Butyrate-producing bacteria

Butyrate-producing bacteria include mainly Faecalibacterium prausnitzii, Eubacterium spp., Roseburia spp., Ruminococcus spp. and Butyrivibrio crossotus. These types of bacteria reduce intestinal inflammatory processes by promoting the formation of regulatory T cells and by inhibiting the production of pro-inflammatory cytokines by macrophages and dendritic cells. Butyrate also increases the oxygen consumption of colonocytes and exacerbates the phenomenon of mucosal "physiological hypoxia", which contributes to supporting the intestinal barrier function. It inhibits proliferation of cancer cells and induces apoptosis.

A reduction in the number of butyrate-producers can promote inflammatory processes, increase intestinal mucosal permeability (Leaky Gut), and promote the manifestation of inflammatory diseases (Crohn's disease, ulcerative colitis), irritable bowel syndrome, food intolerances and coeliac disease.

Mucin-degrading bacteria

Mucin-degrading bacteria include mainly *Akkermansia muciniphila* and *Prevotella* species. These types of bacteria can degrade mucin and are essential for the regeneration of the physiological mucin layer. In this way, they support the maintenance of an intact intestinal barrier by butyrate-producing bacteria, such as *Faecalibacterium prausnitzii*.

Sulphate-reducing bacteria

GANZIMMUN Diagnostics GmbH	Hans-Böckler-Straße 109	55128 Mainz	
T. + 49 (0) 6131 - 7205-0	F. + 49 (0) 6131 - 7205-100	info@ganzimmun.de	www.ganzimmun.de

Sulphate-reducing bacteria, such as *Desulfovibrio spp., Desulfomonas spp.* and *Desulfobacter spp.*, are anaerobic bacteria that produce energy via sulphate reduction and form large amounts of sulphides. The metabolite of these bacteria is hydrogen sulphate, which has cytotoxic properties. Hydrogen sulphate can inhibit butyrate oxidation that is essential to supply energy to colonocytes. Proliferation of sulphate-reducing bacteria can result in chronic inflammation of the intestinal epithelium.

Methane-producing bacteria

Methane-producing bacteria, such as *Methanobrevibacter spp.* and *Methanobacterium spp.* are part of the Archaea domain. They are characterised by their ability to convert primary and secondary bacterial fermentation products, such as hydrogen and carbon dioxide, into methane. They therefore play a significant role in optimising the energy balance. In addition, methane has an inhibitory effect on intestinal motility, which can lead to worsening of chronic constipation. These bacteria can also activate dendritic cells in the gut mucosa and induce the production of TNF alpha and other pro-inflammatory cytokines.

Saccharolytic bacteria

Saccharolytic bacteria in the intestine are responsible for cleaving complex polyand oligosaccharides, such as resistant starch. The lactic acid formed during cleavage is used by other bacteria such as *Ruminococcus bromii* or *Faecalibacterium prausnitzii* as the basis for producing butyric acid. *Bifidobacterium adolescentis* thereby plays a key role, which was investigated in a study with healthy subjects (Venkataraman et al. Microbiome 2016).

LPS-bacteria

LPS-positive bacteria are gram-negative bacteria that carry lipopolysaccharide (LPS) as a so-called endotoxin and, after penetrating into the intestinal mucosa, activate inflammatory processes, as is the case with Leaky Gut. The activation of the immune system can result in low-grade chronic inflammation ("silent Inflammation").





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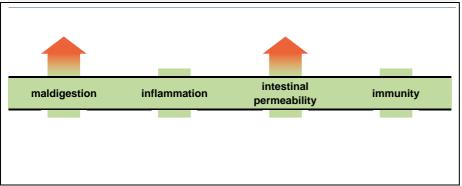
Neuroactive Microbiota

Neuroactive microbiota are microbiota that participate in the metabolism of neuroactive substances or form such substances.

Because **tryptophan** is the **precursor** of **serotonin**, the increased microbial count of Alistipes may interfere with the balance of the serotonergic system in the gut.

Oscillibacter produces valeric acid as the main metabolite. Valeric acid has a structural similarity to gamma-aminobutyric acid (GABA) and can like GABA bind to and inhibit the GABAa receptor. Bacteria that can form the neuroactive gamma-aminobutyric acid (GABA) include: Bifidobacterium adolescentis, Bifidobacterium dentium, Lactobacillus brevis, Lactobacillus plantarum and Lactobacillus paracasei.

Stool diagnostics - diagnosis interpretation



Digestion residues

Sugar content in the stool

Increased sugar excretion in the stool can occur with increased dietary intake.

If a carbohydrate intolerance is suspected based on the patient's clinical symptoms (diarrhea, flatulence and abdominal discomfort), the following breath gas analyses may be useful:

- · H2 breath test, lactose intolerance
- · H2 breath test, fructose intolerance
- H2 breath test, sorbitol intolerance

The determination of the bile acids and fats in the stool is used to diagnose a **bile acid deficiency syndrome** or **bile acid loss syndrome**. In the stool sample examined, the concentration of bile acids is increased and the concentration of fat is normal

There is an indication of a compensated bile acid loss syndrome. This means that the enteral loss of bile acids is compensated for by an increase in the hepatic bile acid synthesis, fat digestion is still undisturbed. A typical symptom is **chologene diarrhea** without **simultaneous steatorrhea** (fatty stools). The diarrhea is mostly watery and is caused by the laxative effect of the bile acids in the large intestine.

Therapeutic aspects:

There are different approaches to therapy options (see therapy recommendations):

- The **causal therapy** of the underlying disease (e.g. blind sack syndrome, crohn's disease) should be in the foreground.
- **Drug therapy** through the administration of **Colestyramine** or **Colestipol** (both prescription drugs that prevent the permeability-increasing effect of bile acids in the colon) can effectively treat compensated chologene diarrhea will.
- Nutritional therapy: See therapy recommendations.

A follow-up in 2-3 months is recommended.



Further information on bile acid deficiency syndrome and bile acid loss syndrome can be found in the specialist information "Bile acid loss syndrome - an underestimated disease" (FIN 0146) and "Irritable bowel syndrome - A guide to diagnosis and therapy" (FIN 0066) at www.ganzimmun.de

Malabsorption / Inflammation

Fecal calprotectin

Calprotectin is a protein that is increasingly produced by neutrophillic granulocytes in case of **inflammatory intestinal diseases**. Increased calprotectin levels are especially prominent in case of chronic inflammatory intestinal diseases. The extent of the calprotectin level correlates with the inflammatory activity and is therefore an ideal progression parameter for diseases like M. Crohn or Colitis ulcerosa. Calprotectin levels as of approx. 400 mg/l with verified CED indicate an acute attack. Elevated calprotectin levels of an unknown origin should be cleared up in any case.

Zonulin in the stool

A **strongly increased zonulin concentration** indicates a disturbed function of the tight junctions. It can be assumed that there is increased mucosal permeability in the sense of a "leaky gut". This process is associated with an increased risk of inflammatory reactions in the area of the intestinal mucosa (increased calprotectin, a1-AT). In addition, the influx of antigenic material into the circulation associated with this process carries the risk of systemic inflammation, so that pro-inflammatory processes can also develop in other body compartments.

Zonulin is a human protein that is produced in the enterocytes of the intestinal mucosa. It serves to regulate the intercellular "tight junctions", which are located between the individual intestinal epithelial cells. Their task is to seal the cell structure. By binding to a specific receptor on the enterocyte surface, zonulin induces a cascade of biochemical processes that regulate or open the tight junctions. Excessive release of zonulin therefore results in the risk of leaky gut.



Recommended further diagnostics:

- ► Microbiome Analysis
- Gut check inflammation
- ► Micronutrient profile with checking of the fat-soluble vitamins A, D, E and K in the serum
- Fatty acids in stool
- ► Vitamin B12 in the serum
- Gliadin-IgG- and IgA-AK and transglutaminase-IgG and IgA-AK as well as zonulin and FABP-2 in the serum with suspected gluten intolerance
- Clarification of carbohydrate intolerance (fructose, sorbitol and lactose intolerance, overgrowth syndrome / SIBOS)
- ► Colon carcinoma early detection: sensitive combination test



Further diagnostics:

- ► Alpha-1-Antitrypsin
- ►LPS (endotoxin)
- ► Intestinal check-up inflammation
- ► Mucosa protective gut flora
- ► Short-chain fatty acids in the stool

Please refer to

our specialist brochures "Prebiotics and secondary plant substances", "Leaky gut syndrome" and "Gut-brain axis" as well as the nutritional recommendation for your patients "Proper nutrition for a stable intestinal microbiome":

www.ganzimmun.de/service/download-center





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According to recent studies, the release of zonulin is not only influenced by dietary components (gliadin), but also by microbial endotoxins. Certain changes in the composition of the intestinal microbiota are considered to be the cause of increased zonulin synthesis. The short-chain fatty acid buytrate appears to play a special role here, as reduced intestinal butyrate levels result in increased zonulin release.

In addition, there is a connection between an increased zonulin concentration and dysautonomia of the autonomic nervous system. Decreased vagal tone, which often occurs in connection with long-term stress, leads to a loss of the stabilizing influence of the vagus nerve on the microbiome and the intestinal mucosa. This promotes pro-inflammatory processes in the intestinal mucosa and reduces occludin synthesis, which ultimately leads to an increase in intestinal permeability. This can trigger an increased expression of tight-junction deregulating proteins and increase zonulin synthesis.

Clinical studies have also shown that zonulin-triggered increased intestinal permeability can occur in patients with chronic inflammatory bowel disease, coeliac disease, diabetes mellitus and other autoimmune diseases, as well as after antibiotic-induced dysbiosis.

The latest studies also show an association between an increased zonulin concentration and an increased risk of developing symptomatic rheumatoid arthritis (RA).

In many cases, a therapeutic reduction in zonulin levels has a positive effect on intestinal inflammation and the severity of existing RA. The short-chain fatty acid butyrate is an important regulator of zonulin synthesis, which is formed in particular by the fermentation of soluble fiber with the help of mucosaprotective flora. Positive stimulation of the vagus nerve through lifestyle changes (e.g. relaxation exercises) also regulates zonulin levels. synthesis.

Parasites in the stool

Since the excretion of worm eggs and protozoan cysts varies, the submission of two further stool samples for microscopic and immunological parasite detection at intervals of 1 to 3 days is recommended in case of persisting clinical suspicion.

Medically validated by Dr. med. Sabine Emrich

All parameters marked with an * are tested at our laboratory partners.
** study not accredited

 GANZIMMUN Diagnostics GmbH
 Hans-Böckler-Straße 109
 55128 Mainz

 T. + 49 (0) 6131 - 7205-0
 F. + 49 (0) 6131 - 7205-100
 info@ganzimmun.de
 www.ganzimmun.de

Basic principles of microbiome therapy

The development, diversity and stability of the intestinal microbiome are sensitive to peoples' lifestyle and dietary habits. Therefore, the intestinal microbiome must always be viewed as a product of lifestyle. The opposite conclusion can be derived from the fact that long-term stabilisation of the intestinal microbiome is only possible when improper nutrition and other unfavourable living conditions are eliminated.

Microbiome therapy is therefore not only based on **long-term dietary changes** but also on the administration of **prebiotic preparations**. This therapy biologically stabilises intestinal environmental conditions. At the same time, it results in the desired adaptation of the microbiome. This clearly shows that the focus should not be on the administration of viable microbes in form of **probiotics**, but that a suitable presentation of substrates for the desired modulation of the microbiota should be prioritised instead.

The prerequisite for a highly diverse physiological intestinal microbiome is therefore a long-term, varied, low-fat, fibre-rich diet containing secondary plant substances that corresponds, for example, to a vegetarian whole food diet!

According to the *German Society of Nutrition* [Deutsche Gesellschaft für Ernährung] (DGE) vegetarian food with lots of fruit, vegetables and whole-grains – if possible organically farmed - is recommended in any case. At the same time, "microbiome-healthy nutrition" is characterised by avoiding artificial food additives, such as preservatives, food stabilisers, artificial flavours, dyes etc. as much as possible.

Factors that disrupt the development of a "healthy" microbiome

This is in contrast to the more unfavourable nutritional habits in our populations, which often start as early as in infancy by use of formula. In adolescence and adulthood stress, this is followed by a disrupted sleep-wake rhythm, excess consumption of industrially-produced food, excess consumption of carbohydrate-rich food and the regular intake of additives, such as artificial flavours, dyes, sugar substitutes and food stabilizers. Alcohol and various toxic residues in food also prevent the development of a healthy microbiome. Moreover, unnecessary antibiotic therapies are often an important cause for the development of dysbioses. Preventative, probiotic or symbiotic therapy should therefore be given during and after antibiotics administration.



You can find additional information on therapy in the specialist brochure **Intestinal** microbiome in our download centre at www.ganzimmun.de

Fibres

Fibres are indigestible carbohydrates of plant-derived food that benefit only the microbiome and are not a substrate for humans. This simple fact permits the direct deduction that an insufficient intake of fibres will inevitably result in "supply disruptions" for the microbiome, which cause major and exclusively harmful changes to the entire gastrointestinal microbiota, ultimately affecting the host at a correspondingly level.



Substrates promoting a **physiological microbiome Fibres** (prebiotics) such as:

- * Psyllium husks
- * Flaxseed
- * Acacia fibres
- * Wheat bran
- * Resistant starches (e.g. resistant dextrin)
- * Fructo-/galacto oligosaccharides
- * Amylopectin / citruspectin
- * Whole-grain millet
- * Buckwheat
- * Buckwheat
- * Baobab fruit (African monkey bread tree)

Secondary plant ingredients from the polyphenol group such as:

- * (Epi)catechin (green tea)
- * Procyanidines (red grapes)
- * Flavanoles (cocoa)
- * Tannins (tea)



Substrates that promote a non-physiological microbiome:

- ➤ Too much protein (irrespective of the source; inflammatory proteins are also available as a substrate for the putrefying flora)
- Too much fat
- ► Refined carbohydrates/starch





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Prebiotics are components of food that are part of the soluble fibre group. They are composed of indigestible and natural fructooligosaccharides (FOS) or galactooligosaccharides (GOS), are stable in gastric acid and - corresponding to the above-mentioned principles about fibres - are available to the microbiome and non-human organisms as growth substrates. Thus, prebiotics selectively affect the growth and the metabolic performance of the intestinal microbiome in the colon. They therefore have a significant health-maintaining effect. Mixtures of different prebiotics as present in finished formulations in various combinations have proven effective.



Prebiotic oligosaccharides - the most important group of the prebiotics - are also contained in breast milk. They are the prerequisite for the development of a healthy microbiome in the child. This clearly demonstrates that the use of prebiotics can be appropriate even in childhood.

🕓 Secondary plant ingredients

Secondary plant ingredients are part of a substance group that is formed by plants among other things as defence substrates against pesticides and diseases, as growth regulators or as dyes. From the evolutionary perspective, it can be assumed that bioactive substances from plants play an essential role in maintaining and promoting human health and physical performance. This also appears to be true for the intestinal microbiome, which is modulated in particular by polyphenols. Substances such as procyanidins, and dyes such as flavonoids and anthocyanins are part of the group of polyphenols. A varied diet rich in fresh vegetables and fruit contains sufficiently high concentrations of secondary plant nutrients.

A current study* also proves the importance of secondary plant ingredients for the species Akkermansia muciniphila. Polyphenols confer important substrates to Akkermansia, resulting in a survival advantage and thus contributing to its stabilisation and proliferation.



Literature:

Anonye, B. O. 2017. Commentary: Dietary Polyphenols Promote Growth of the Gut Bacterium Akkermansia muciniphila and Attenuate High-Fat Diet-Induced Metabolic Syndrome. Front Immunol.



Probiotics

Probiotics are viable, metabolically active microorganisms that survive the passage through the stomach due to their acid resistance and unfold specific and nonspecific effects in the intestine. They strengthen a patient's own physiological flora through their metabolic activity so that undesired bacterial species can be displaced. They inhibit putrefying bacteria, such as histamine producers, by competing for substrate and stabilising a physiological microbial intestinal environment.

The administration of probiotics during microbiome therapy serves to supplement the above-mentioned prebiotic measures in order to optimise the environmental conditions. With the help of the various bacterial compositions available today, the measures can be varied depending on the findings and the clinical symptoms.



Daily doses of highly concentrated probiotics (at least 1x 10°) and the highest possible variety of bacterial species, like in the so-called multi-species probiotics, are required to achieve an efficient probiotic effect.

Therapy recommendations





Following recommendations are directed exclusivley to the treating doctor or threapist and are not intended for distribution to the patient.

Please note, that the recommendations include alternative products from different manufacturers, that are similar in terms of active ingredients, administration and indication. As a guide, please pay attention to the information in the corresponding columns, which are lagrely identical for alternative pharmaceuticals.

Product	Ingredients and administration	Indication	Note
ColonBalance® Company / manufacturer: Biogena Naturprodukte GmbH & Co. KG Dosage:1 x daily. 1 ML Supplier: www.biogena.com	Ingredients: resistant dextrin, pregelatinised waxy maize starch (amylopectin), acacia fiber (Fibregum™), citrus pectin Administration: Stir 1 measuring spoon (10 g) in about 100 ml of liquid and drink immediately, or stir into cereals, yoghurt, etc.	 to increase the fiber intake. Serves as a substrate for the health-promoting bacterial strains and thus contributes to colonization resistance to yeasts and other pathogens. Binds cholesterol and bile acids in the intestine and thus promotes their excretion. 	
Darm Formula Plus Company: Biogena Naturprodukte GmbH & Co. KG Dosage: 3 capsules per day Supplier: www.biogena.com	Ingredients: black cumin seed extract, Curcuma longa extract, black pepper extract, inulin (fructooligosaccharide), niacin and vitamin B2 Administration: take with plenty of liquid	 to increase fiber intake and thus modulate and strengthen the microbiome. for inflammatory processes and diseases in the gastrointestinal tract 	
GluteZym® Hersteller/Vertrieb: Biogena Naturprodukte GmbH & Co. KG Dosage: up to 3 Caps. to the meals Bezugsquelle: www.biogena.com	Ingredients: Aspergillus niger-prolylendopeptidase, calcium, vitamine B2 Usage: Take with plenty of liquid with a meal. To achieve optimum results, the dose can be increased and adjusted individually if necessary.	 To improve gluten tolerance in the case of gluten sensitivity (recognizable e.g. by increased zonulin). 	Does not replace a gluten-free diet if this is indicated (e.g. in the case of celiac disease).
Lactobin® N Company / manufacturer: Dr. Wolz Zell GmbH Dosage: Adults: 1 x per day 10-20 g (1ML = 3,3g) Supplier: pharmacy Drug code (PZN): 03777611 (70g)	Ingredients: Colostrum concentrate from New Zealand grass-fed cows, vitamin B6, vitamin B12 Administration: The daily dose can be taken all at once or taken apart from meals throughout the day. To do this, stir the powder into cold drinks or consume it together with cold food (e.g. yoghurt). Do not mix with hot foods.	 To lower elevated zonulin levels and maintain the intestinal barrier. As dietary fiber, lactoferrin - a component of colostrum - promotes the growth of the healthy microbiota, which produces short-chain fatty acids such as butyrate and can thus reduce zonulin production and intestinal permeability. 	

mucozink®

Company / manufacturer:

nutrimmun GmbH

Dosage:

Children from 4-10 years: 1 x 7 g (1 heaped tsp.)

Children from 11-14 years: 1 x 13 g (2 heaped tsp) daily

Adults: 1 x 20 g (2 level measuring spoon or 1 sachet) daily

Supplier:

Pharmacy

PZN: 02766108 (15 daily servings, 300 g powder) PZN: 02019819 (30 daily servings, 600 g powder) PZN: 12901553 (30 daily servings, 30 x 20 g

powder)

Ingredients:

Vitamins (A, C, E, B1, B2, B6, B12, D, niacin, pantothenic acid, folic acid, biotin), minerals (magnesium, zinc, selenium, copper, chromium), as well as L-glutamine and taurine.

Application:

Pour the powder into an empty glass and dissolve in approx. 200 ml of still water while stirring. Drink with or after a meal.

Alternatively, the daily portion can also be divided into two meals.

Duration of application:

Long-term use is possible.

- For Leaky Gut Syndrome: Vitamin A and D increase the stability of the intestinal barrier and support a reduction in high zonulin levels.
- For regeneration of the intestinal mucosa, e.g. in the context of inflammatory processes.

The consumption of foods with emulsifiers and thickeners (e.g. carboxymethylcellulose, polysorbate, carrageenan, lecithin) should be severely restricted or avoided in patients with increased intestinal permeability and inflammatory diseases such as IBD. An appropriate change in diet supports mucosal regeneration. *

MyBIOTIK®LIFE+

Company / manufacturer:

nutrimmun GmbH

Dosage: Adults and children from 11 years: 1 x

daily 1 sachet and 2 caps. **Supplier:** pharmacy

PZN:16537481 (30 daily servings)

Ingredients:

Combination of probiotics and specific micronutrients: the powder contains the bacterial cultures Bifidobacterium longum R0175 and Lactobacillus helveticus R0052. The capsule contains vitamin B1, vitamin B2, niacin, pantothenic acid, vitamin B6, biotin, folic acid, vitamin B12, vitamin D, magnesium and zinc

Administration:

Pour the powder (1 sachet) into an empty glass and dissolve in approx. 100 ml of still water while stirring. Drink on an empty stomach at least 15 minutes before a meal. Take the two capsules with a meal with some liquid, e.g. B. a glass of water.

- To reduce an increased cortisol level as a result of chronic stress.
- For neuropsychiatric disorders such as depression or CFS.

OPC Polymax® 250/30

Company / manufacturer:

Biogena Naturprodukte GmbH & Co. KG

Dosage: 2 capsules per day **Supplier:** www.biogena.com

Ingredients:

grape seed extract 145 mg, grape extract 117 mg, green-tee extract 140 mg, pomegranate-extrakt 140 mg, olive leaf-extract 120 mg, oligomere Proanthocyanidine (OPC) 60 mg, polyphenole (total) 500 mg

Administration:

take with plenty of liquid

- As a prebiotic to improve the composition and activity of the intestinal microbiome.
- Inhibits potentially pathogenic bacteria such as Clostridium difficile
- To improve the antioxidant status of oxidative stress, cardiovascular diseases, arteriosclerotic changes and increased blood fat levels (triglycerides, cholesterol and LDL).

MyBIOTIK®PREALASAN

Company / manufacturer:

nutrimmun GmbH

Dosage:

Children from 6-14 years: 1 x daily 1.5 st. ML

Ingredients:

Fibre mix of ground psyllium husks, resistant maize dextrin and baobab fruit powder, as well as calcium.

Anwendung:

Pour the daily portion of powder into an empty glass and dissolve

 Nourishes the physiological microbiota (especially lactobacilli and bifidobacteria), especially in the case of a low-fibre diet, and thus contributes to resistance to colonisation by fungi and other pathogens. Make sure you drink plenty of fluids so that the fibre can swell up in the intestine.

^{*} Quelle: Gubatan, J. et al. (2023). Dietary exposures and interventions in inflammatory bowel disease: Current evidence and emerging concepts. Nutrients, 15(3), 579.

Therapy recommendations





Following recommendations are directed exclusivley to the treating doctor or threapist and are not intended for distribution to the patient.

Please note, that the recommendations include alternative products from different manufacturers, that are similar in terms of active ingredients, administration and indication. As a guide, please pay attention to the information in the corresponding columns, which are lagrely identical for alternative pharmaceuticals.

Product	Ingredients and administration	Indication	Note
From 15 years: 1 x daily 3 st. ML Supplier: pharmacy Drug code (PZN): 18706120 (15 daily portions) Drug code (PZN): 18033129 (30 daily portions)	in approx. 200 ml of still water while stirring. Drink the solution throughout the day before or with a meal. Depending on your preference, the powder can also be stirred into other drinks (e.g. tea, juice) or food (e.g. yoghurt, muesli). Administration: At least 1 month. Regular intake is recommended.	 Increases the production of short-chain fatty acids. 	
Sanaglu® Laves Company / manufacturer: Laves Arzneimittel GmbH Dosage: Adolescents from 12 years and adults: 1-2 caps. per meal containing gluten Supplier: pharmacy 10793088 (30 Cps.) 10793094 (60 Cps.)	Ingredients: Gluten-degrading enzyme mixture of endo- and exopeptidases with an effectiveness of: Protease 3.0: 500 SAPU, protease mixture: 75,000 HTU, dipeptidyl peptidase IV: 125 DPPIV. Administration: Immediately before consuming foods containing gluten, swallow them with a little liquid. Maximum dose: 5 caps/d	 To aid gluten digestion. For gluten intolerance, especially in connection with increased zonulin values. 	Kein Ersatz für eine strikt glutenfreie Ernährungsweise bei Zöliakie.