biovis' DIAGNOSTICS

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

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External ID

Name		Date of Birth		Order ID	
First Name		Sex	Male	Order Date	17.07.2025
Sampling Date	15.07.2025 00:00	Validation by		Findings Status	**Final Report**
Sample Material	FE	Validation Date	24.07.2025	Findings Date	30.07.2025

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Stool Diagnostics					
Microbolome 1.0					
Molecular genetic microbiome analysis 3.0					
Stool Properties					
Colour	olive			braun	FE NA) VISU
Consistency	mushy			breiig	FE NA) VISU
pH	6,5		5,8 - 6,5	6,7	FE NA) TESTS
Biodiversity					
Diversity	5,23		> 5,5		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 **4**

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.

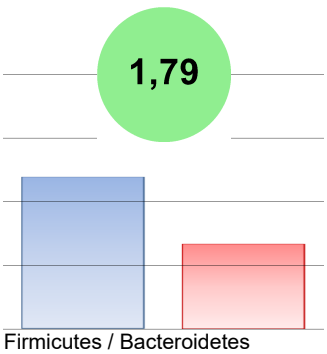
Enterotyp **1**

Dysbiosis index — FE NA) RECHN

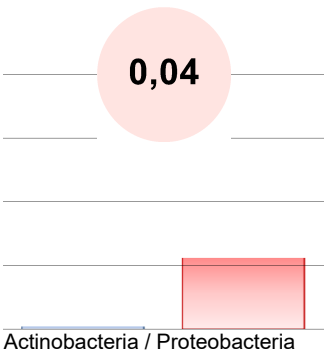
The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.

Index **21**

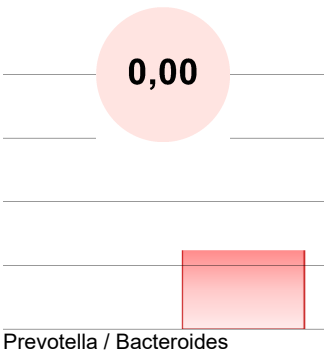
Ratio



Firmicutes / Bacteroidetes
Standard Range: < 3,0



Actinobacteria / Proteobacteria
Standard Range: > 1,0



Prevotella / Bacteroides
Standard Range: > 0,1

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Name		Date of Birth		Order ID	
First Name		Sex	Male	Order Date	17.07.2025

Test	Result	Unit	Standard Range	Previous Result
Phyla				
Actinobacteria	0,2	%	1,5 - 7	FE NA) MGSEQ
Bacteroidetes	33,4	%	20 - 45	FE NA) MGSEQ
Firmicutes	59,8	%	50 - 75	FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0	FE NA) MGSEQ
Proteobacteria	5,6	%	1,0 - 3,5	FE NA) MGSEQ
Verrucomicrobia	0,0	%	1,5 - 5,0	FE NA) MGSEQ
Other	1,0	%		FE NA) MGSEQ
Metabolome (functional groups)				
TMA / TMAO	-32,0	%		
Ammonia	88,1	%		
Equol	69,0	%		
Beta glucuronidases	-17,2	%		
Bacteria Phyla - most important genera and species				
Actinobacteria				
Bifidobacterium	1,0 x 10^9	CFU/g faeces	> 1,0 x 10^10	FE NA) MGSEQ
Bacteroidetes				
Bacteroides	3,1 x 10^11	CFU/g faeces	> 5,0 x10^10	FE NA) MGSEQ
Prevotella	< 1,0 x 10^5	CFU/g faeces	> 1,0 x 10^10	FE NA) MGSEQ
Firmicutes				
Butyrate producing bacteria				
Total bacteria count	2,3 x 10^11	CFU/g faeces	> 2,4 x 10^11	FE NA) MGSEQ
Faecalibacterium prausnitzii	6,4 x 10^10	CFU/g faeces	>1,0 x10^11	FE NA) MGSEQ
Eubacterium rectale	2,3 x 10^10	CFU/g faeces	> 2,0 x 10^10	FE NA) MGSEQ
Eubacterium hallii	1,3 x 10^10	CFU/g faeces	> 1,5 x 10^10	FE NA) MGSEQ
Roseburia spp.	3,2 x 10^10	CFU/g faeces	> 3,0 x10^10	FE NA) MGSEQ
Ruminococcus spp.	1,0 x 10^10	CFU/g faeces	> 5,0 x 10^10	FE NA) MGSEQ
Coprococcus spp.	4,8 x 10^10	CFU/g faeces	> 5,0 x 10^10	FE NA) MGSEQ
Butyrivibrio spp.	3,8 x 10^10	CFU/g faeces	>1,5 x 10^10	FE NA) MGSEQ
Clostridia				
Clostridia total bacteria count	5,9 x 10^9	CFU/g faeces	< 4,0 x 10^9	FE NA) MGSEQ
Clostridia Cluster I	1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9	FE NA) MGSEQ
Clostridium histolyticum	< 1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9	FE NA) MGSEQ
Clostridium perfringens	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^8	FE NA) MGSEQ
Clostridium sporogenes	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^8	FE NA) MGSEQ
Other Firmicutes				
Christensenellaceae	2,2 x 10^7	CFU/g faeces	> 5,0 x 10^9	FE NA) MGSEQ
Dialister spp.	< 1,0 x 10^5	CFU/g faeces	< 4,0 x 10^10	FE NA) MGSEQ
C. butyricum	< 1,0 x 10^5	CFU/g faeces	> 1,0 x 10^8	FE NA) MGSEQ
Fusobacteria				
Fusobacterium	1,1 x 10^8	CFU/g faeces	< 1,0 x 10^7	FE NA) MGSEQ
Verrucomicrobia				
Akkermansia muciniphila	< 1,0 x 10^5	CFU/g faeces	> 5,0 x 10^9	FE NA) MGSEQ
Proteobacteria				

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Name	Date of Birth	Order ID	
First Name	Sex	Male	Order Date	17.07.2025

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Pathogenic or potentially pathogenic bacteria					
Haemophilus spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^8		FE NA) MGSEQ
Acinetobacter spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6		FE NA) MGSEQ
Proteus spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6		FE NA) MGSEQ
Klebsiella spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^7		FE NA) MGSEQ
Enterobacter spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6		FE NA) MGSEQ
Serratia spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^7		FE NA) MGSEQ
Hafnia spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6		FE NA) MGSEQ
Morganella spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6		FE NA) MGSEQ
Citrobacter spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^8		FE NA) MGSEQ
Pseudomonas spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^7		FE NA) MGSEQ
Providencia spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^7		FE NA) MGSEQ
H2S production					
Sulphate reducing bacteria	7,9 x 10^9	CFU/g faeces	< 2,5 x 10^9		FE NA) MGSEQ
Desulfovibrio piger	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^9		FE NA) MGSEQ
Desulfomonas pigra	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^9		FE NA) MGSEQ
Bilophila wadsworthia	< 1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9		FE NA) MGSEQ
Oxalate degrading bacteria					
Oxalobacter formigenes	< 1,0 x 10^5	CFU/g faeces	> 1,0 x 10^8		FE NA) MGSEQ
Immunogenicity / Mucus production					
Immunogenically effective bacteria					
Escherichia coli	6,5 x 10^7	CFU/g faeces	10^6 - 10^7		FE NA) MGSEQ
Enterococcus spp.	5,42 x 10^6	CFU/g faeces	10^6 - 10^7		FE NA) MGSEQ
Lactobacillus spp.	1,6 x 10^6	CFU/g faeces	10^5 - 10^7		FE NA) MGSEQ
Mucin production / Mucosal barrier					
Akkermansia muciniphila	< 1,0 x 10^5	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Faecalibacterium prausnitzii	6,4 x 10^10	CFU/g faeces	>1,0 x10^11		FE NA) MGSEQ
Archaea					
Methanogens					
Methanobrevibacter spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^8		FE NA) MGSEQ

ATTENTION: The new OmicSnap tube and the matrix enable even more effective sample disruption, especially with gram-positive bacteria. This results in slight shifts in the standard ranges. We ask you to take this into account.

Mycobiome: relevant yeasts					
Candida albicans (CA)	<1,0 x 10^3	CFU/g faeces	<1,0 x 10^3		FE NA) PCR
Candida krusei (CK)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) PCR
Candida glabrata (CG)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) PCR
Candida dubliniensis (CD)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) PCR
Candida parapsilosis (CP)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) PCR
Candida tropicalis (CTp)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) PCR
Candida lusitaniae (CL)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) PCR
Parasites					
Pathobionts					
Blastocystis hominis	negative		negative	negativ	FE A) MOLEK
Dientamoeba fragilis	negative		negative	negativ	FE A) MOLEK

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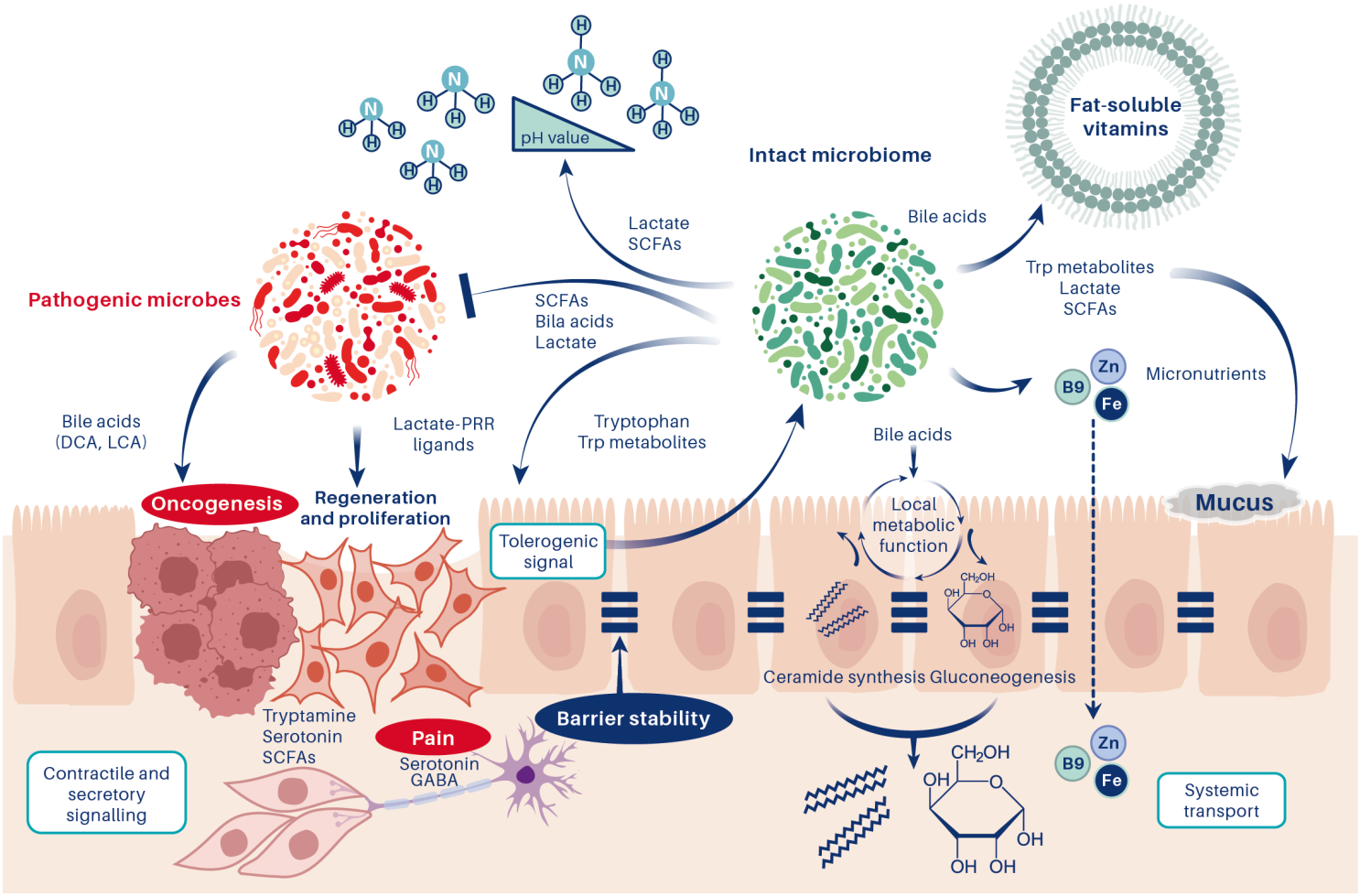
Name		Date of Birth		Order ID	
First Name		Sex	Male	Order Date	17.07.2025

Test	Result	Unit	Standard Range	Previous Result
Pathogenic intestinal protozoa				
Giardia lamblia	negative		negative	negativ
Entamoeba histolytica	negative		negative	negativ
Cryptosporidium species	negative		negative	negativ
Cyclospora cayetanensis	negative		negativ	negativ



Irritable Bowel Relevant Metabolites				
Histamine	<0,3	µmol/l	< 5	FE NA) LCMS
Tryptophan	14,4	µmol/l	> 14,5	FE NA) LCMS
Serotonin	<0,2	µmol/l	0,8 - 4,5	FE NA) LCMS
GABA	20	µmol/l	> 60	FE NA) LCMS
Amino Acids (Precursors)				
Tryptophan	14,4	µmol/l	> 14,5	FE NA) LCMS
Tyrosine	590	µmol/l	> 50	FE NA) LCMS
Phenylalanine	402	µmol/l	> 35	FE NA) LCMS
Toxins				
Tryptamine	2,53	µmol/l	0,05 -19,99	FE NA) LCMS
Indoxyl sulphate	<0,20	µmol/l	< 0,2	FE NA) LCMS
p-Cresol sulphate	<0,15	µmol/l	< 1,5	FE NA) LCMS
Kynurenic acid	< 0,1	µmol/l	0,1 - 7,49	FE NA) LCMS
Composite Parameter				
Toxin- Score	0	Index	< 3	FE NA) LCMS

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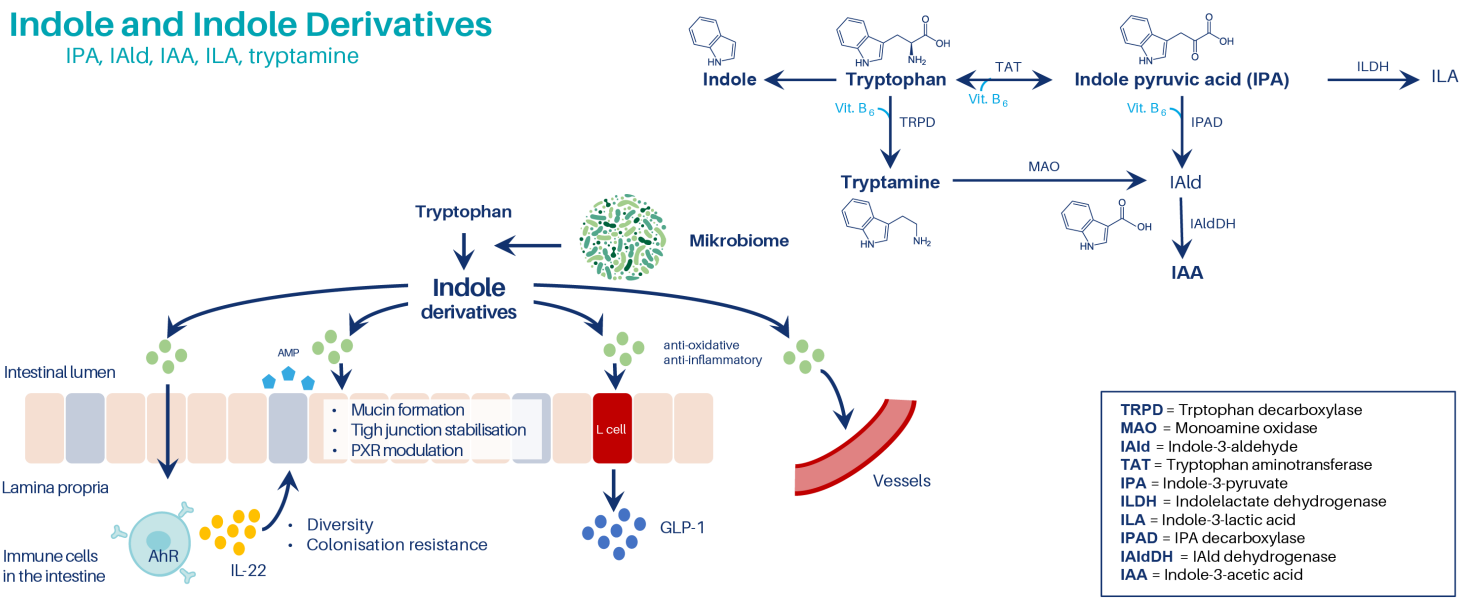
Name	Date of Birth	Order ID	
First Name	Sex	Male	Order Date	17.07.2025

Test	Result	Unit	Standard Range	Previous Result
Indole Derivatives (AhR Agonists)				
Indole propionate (IPA)	1,78	µmol/l	> 3,5	
Indole-3-acetic acid	<0,5	µmol/l	> 3,2	
Indole aldehyde	1,73	µmol/l	> 0,35	
Tryptamine	2,53	µmol/l	0,05 -19,99	
Indole	96,5	µmol/l	> 60	
Indole lactate (ILA)	1,50	µmol/l	> 1,4	
Kynurenic acid	< 0,1	µmol/l	0,1 - 7,49	
AHR score	41	%	> 80	
Bile Acids				
Conjugated/free bile acids	5,1	Ratio	2 - 20	
Deoxycholic acid (DCA)	1280	µmol/l	175 - 2500	
Cytotoxic bile acids / Protective bile acids** **DCA / UDCA	21,16	Ratio	< 67	
Total bile acids	3417	µmol/l	630 - 4125	



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Name	Date of Birth		Order ID	
First Name	Sex	Male	Order Date	17.07.2025

Test	Result	Unit	Standard Range	Previous Result	Sample Material / Method
Erläuterungen und Hinweise:					FE NA)

Detailed information on the recommended therapeutic approaches can be found in the report, including for complex findings. The recommended dosages apply to adults and may vary in individual cases.

¹ Fermented foods not in cases of histamine intolerance or elevated histamine levels in the stool.elevated histamine levels in the stool.

* Tryptophan rich foods, classified by fat content, for use as part of a low-fat or a diet balanced in fat content (see below!).
In cases of intolerance to the listed foods, tryptophan can also be supplemented as a dietary supplement.

Low fat tryptophan-rich foods: turkey breastsoy beans, lentils, low-fat quark
Higher-fat tryptophan-rich foods: nuts, cheese,eggs, salmon
** Tyrosine-rich foods, categorized by fat content. In cases of intolerance, tyrosine can also be supplemented.

Low-fat tyrosine-rich foods: chicken breast, tofu, low-fat yogurt, beans.
Higher-fat tyrosine-rich foods: Parmesan, avocado, almonds, pork.

Note: In the presence of toxins, such as p-cresol or indoxyl sulfate, protein-rich foods should generally be consumed with caution, and plant-based alternatives should be preferred instead.

*** If a low-histamine diet is not feasible, antihistamines may also be used.

Overview - Results and Therapy Options

Dysbiosis Index 21

pH	●	
Enterotype	1	
Biodiversity	↓	
Ratio Firmicutes/Bacteroidetes	●	
Butyrate producing bacteria	↓	
Mucus production	↓	
Mucosa integrity	↓	
Milieu stabilising bacteria	↓	
Immunogenic bacteria	↑	
Clostridia - total bacteria count	↑	
Clostridia cluster I	●	
Fusobacteria	↑	
H2S producing bacteria (SRB)	↑	
Potentially pathogenic bacteria	●	
Candida (facultive pathogenic)	●	
Oxalate degrading bacteria	↓	

Metabolome (functional groups)

TMA / TMAO	●	
Beta glucuronidases	●	
Ammonia	↑	
Equol	●	

Irritable Bowel Relevant Metabolites

Histamine	●	
Tryptophan	↓	
Serotonin	↓	5-HTP (50-150 mg/day) + cofactors (e.g. vit. B6)*

GABA		GABA (0,4-0,8 g in the evening), probiotics (GABA-producing: e.g. SAH Hista-Care, OB SR9)*
Amino Acids (Precursors)		
Tryptophan		
Tyrosine		
Phenylalanine		
Toxins		
Toxins		
AHR Agonists		
AHR agonists		Tryptophan-rich foods**, cruciferous vegetables (e.g. broccoli, cauliflower), fermented foods[1], tryptophanase prod. Probiotics (e.g. LGG, SAH Hista-Care)*
Bile Acids		
Conjugated/free bile acids		
Deoxycholic acid (DCA)		
Cytotoxic/protective bile acids		
Total bile acids		

Order ID
Order Date 17.07.2025 00:00:00
Name
First Name
Date of Birth

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Therapy options with prebiotics and probiotics in overview

Changes of Microbiome
- Diversity
- Inflammation (α1AT, CP, Ly)
- Leaky Gut (Zonulin, Histamine)
- Mucus formation
- Butyrate formation
- Flora

Probiotics: Requirement
- Not necessary

Prebiotics: Requirement
- Not necessary

Nutrition
- healthy, vegetable-rich
- Flatulence:FODMAP
- Obesity:Low Carb

Changes of Microbiome
- Diversity
- Inflammation (α1AT, CP, Ly)
- Leaky Gut (Zonulin, Histamin)
- Mucus formation
- Butyrate formation
- Flora

Probiotics: Requirement
- Mastzellstabilisierung
- Milieustabilisierung
- Promotion GKZ,Diversity

Prebiotics: Requirement
- Mucin formation
- Mucosa protection
- Butyrate formation
- Förderung GKZ,Diversität
- Bifidogenic effect

Prebiotics
- 2-Fucosyllactose
- scFOS/scGOS,FOS
- Acacia fibres

Probiotics
- OB SR-9
- AB Compens
- SAH Hista-Care
- AB Sensitive

Changes of Microbiome
- Pathogenic Bacteria
- and/or Clostridum difficile
- and/or Clostridum Cluster I
- and/or potentially path. Bact.

Probiotics: Requirement
- Toxin-Inhibition
- Immunogenically effective

Probiotics
- Omni-Biotic 10***
- AB akut / AB Premium***
- Lactobact AAD

- * age related: Omni-Biotic Active / OB Panda
- ** age related: Lactobact 60plus
- *** in combination with other probiotics

Therapy options based on results of pElastase, inflammation marker, sIgA and / or zonulin / histamine

Exocrine Pancreatic Insufficiency / -insuffizienz *pElastase*	**Inflammation +/++** *(α1-AT and/or CP)*	**Mucosa Immune System -** *(sIgA)*	**Leaky gut** *(Zonulin and/or Histamine)*	**Food Intolerance** *Fructose / Lactose / Allergy: Typ I, III, Pseudo allergy / ATI / Celiac Disease / DPP4-Defekt / EPX*
Approach: Digestion enzymes 20.000 - 80.000 E / meal* Children see explanation	**Approach:** • Phosphatidylcholin • L-Glutamine • Myrrh, Chamomile	**Approach:** • microbiological therapy • Zinc / Echinacea / Colostrum • Autohaemotherapy	**Approach:** • Phosphatidylcholin • Humic acids • Zeolite	**Approach:** • Reduction or avoidance of incompatible foods • Enzyme substitution: Lactase, DAO, DPP4
Compound: • Pancreatin • Creon • Pankreon	**Compound:** • SAH Mucosa-Care • Aminoplus Glutamin • Myrrhinil-Intest	**Compound:** • Symbioflor I / II, Mutaflor • Arktibiotic Strong **** • Omni-Biotic 6 ***	**Compound:** • SAH Mucosa-Care • Activomin • cAMPD30 / Zeolite*****	
Dietary Therapy: Fat- and fibrereduced Diet (fat < 70 g / day)	**Dietary therapy:** Light food / diet Light bland diet**			

* **Dosage** depending on fat content in stool, for **children** age and weight related dosages apply. In case of slightly reduced pElastase values but normal fatty residues: possible administration of vegetable enzyme mixtures (e.g. Digest, Full Spectrum Digest, Combizym).
** in case of α1-antitrypsin values > 100 mg / dl and/or calprotectin > 150 mg / l
*** MIS-activating probiotics (alternatively see table „probiotics acc. to effects“)
**** contains Colostrum
***** prescription only, prescribed by a doctor or therapist (powder mixture of zeolite, CAMP D30 and CA and Mg carbonate)

Microbolome 1.0

Introduction

The **intestinal microbiome** (entirety of all bacteria living in the intestinal tract) has considerable influence on health or illness of humans. It modulates the immune defence, supplies the organism with vitamins (vitamin B1, B2, B6, B12, and K), participates in the digestion of food components, supplies intestinal epithelia with energy via developing short-chain fatty acids and stimulates intestinal peristalsis. The microbiome also plays an important role in the scope of xenobiotic detoxification. Shifts within the microbiome are causally relevant factors for diseases like adiposity, non-alcoholic fatty liver disease, diabetes, coronary heart disease or cancer. After the composition of the human intestinal microbiome was studied in more detail, alterations can be detected and counteracted with well-aimed measures.

Result Evaluation
With the help of the **molecular genetic stool analysis**, the intestinal microbiome was analysed in order to assess the composition and to determine possible shifts. The evaluation yielded the **following results:**

Evaluation of Stool Consistency, Color and pH-Value

General viewing of the stool sample showed **mushy consistency**. Healthy stool should be mushy and formed. Liquid or slurry stool indicates accelerated, doughy or solid stool samples delayed intestinal passage.

The color of the analysed stool sample was olive. The **pH-value** was **within normal range** at 6,5.

Evaluation of the Intestinal Diversity

More important than individual bacteria species or types is the interaction of the bacteria present in the microbiome. Manifold tasks of the intestinal flora require adequate diversity. The intestinal **diversity** of humans may vary considerably.

In the microbiome of healthy people one finds **300 to 500 bacteria species**, in sick persons there are often a lot less. Causes for reduced diversity are manifold. They are for example repeated **antibiotic therapies, infections, increasing age, unbalanced diet or smoking**.

Research revealed that numerous diseases come along with reduced diversity and thus presumably promote disease manifestation. Very often reduced diversity is found in patients suffering from **adiposity, fatty liver (NAF), diabetes type 2, Alzheimer disease, chronic inflammatory bowel disease, intestinal cancer or irritable colon syndrome**. Due to decreasing diversity the intestinal microbiome no longer grants adequate protection against endogenic infections. Obese patients with reduced diversity tend to gain more weight, respond worse to diets and there are often already indications of fat metabolism disorders or insulin resistance. In patients suffering from chronic inflammatory bowel disease (CIBD) reduced diversity promotes recurrence and chronicity. Research data are also available for the irritable bowel syndrome, the manifestation of which is promoted by reduced diversity.

Results

The **diversity** analysis indicated **reduced biodiversity**.

Determination of the Enterotype

Recent research showed that the human microbiome can be assigned to **three main groups-** so-called enterotypes. Intestinal bacteria develop – depending on the enterotype – stable, clearly different clusters with typical metabolic properties (9). **Enterotype 1** is characterized by high **bacteroides counts** and **enterotype 2** by strong **Prevotella** population. **Enterotype 3** is only found rarely – in hardly more than 5 % of the analysis. This type shows strong **Ruminococcus** flora.

The described enterotypes show significantly differing **metabolic performance.** The bacteroides dominated flora (enterotype 1) is optimally adjusted to the utilisation of **fat, fatty acids, protein and amino acids**. **Carbohydrates**, however, are metabolized significantly worse than by Prevotella dominated flora (enterotype 2)

Result

The microbiome analysis indicates **enterotype 1** with dominating **bacteroides flora** and clearly less present Prevotella and Ruminococcus sp.

A bacteroides dominated flora is specialized in energy generation from **oligosaccharides**, **animal proteins** and **saturated fatty acids.** Enterotype 1 is therefore mainly only found in persons, who regularly eat meat. Bacteroides only rarely dominate in vegetarians and fruit and vegetable enthusiasts. Bacteroides species are on one hand able to **synthesize vitamins** (biotin, riboflavin (B2), pantothenic acid (B5), folic acid (B9) and vitamin C); on the other hand the enterotype also influences intestinal **nutrient absorption.** The latter is significantly lower than in Prevotella dominated enterotype 2.

Determination of relevant ratios

Firmicutes-Bacteroidetes ratio

Firmicutes and Bacteroidetes are the most common bacterial phyla in adults. Patients with **irritable bowel syndrome** or **obesity** often show a high proportion of Firmicutes.

Studies have examined the influence of the microbiome on the development of obesity. It has been found that **Firmicutes** are able to ferment **complex, indigestible carbohydrates** in such a way that short-chain fatty acids (SCFA) are formed, which are absorbed through the intestinal mucosa and serve as additional energy suppliers for the host. By fermenting indigestible carbohydrates through Firmicutes, **10 – 12 % more energy** is available.

Bacteroidetes are unable to utilize complex carbohydrates. If Firmicutes dominate over Bacteroidetes in the microbiome, one speaks of an increased Firmicutes-Bacteroidetes ratio. In patients with irritable bowel syndrome, an increased **Firmicutes-Bacteroidetes ratio** is often associated with meteorism, flatulence or increased pain symptoms.

Result

The microbiome analysis shows a balanced ratio of Firmicutes to Bacteroidetes. The **Firmicutes-Bacteroidetes ratio is normal**.

Actinobacteria-Proteobacteria ratio

Actinobacteria and Proteobacteria make up around 5 – 10 % of the total intestinal microbiota. The proportion of Proteobacteria should not exceed 5 % in healthy adults. Numerous bacterial species from this phylum have **facultative pathogenic properties** and produce metabolites such as histamine, indoles, phenols, TMA and hydrogen sulfide, which are directly or indirectly harmful to the intestinal mucosa or other organs.

Decreased Actinobacteria-Proteobacteria ratios have been demonstrated in numerous intestinal and extraintestinal diseases, most of which have an **inflammatory component**. For example, a greater proportion of Proteobacteria was found in Crohn's disease patients with a severe course than a mild course.
An decreased ratio can also occur as a result of antibiotic therapies and intestinal symptoms such as severe flatulence and constipation can be increasingly evident.

Result

The microbiome analysis shows **clear predominance** of Proteobacteria over Actinobacteria. The **Actinobacteria-Proteobacteria ratio** is **decreased**.

Prevotella-Bacteroides ratio

Prevotella and Bacteroides are the two most prevalent genera of bacteria in the intestine. Their share in the microbiome is the basis for the assignment to the enterotypes 1 (Bacteroides) and 2 (Prevotella). Furthermore the Prevotella-Bacteroides ratio is associated with development of metabolic disease and weight changes.

Result

The microbiome analysis shows a **clear predominance** of Bacteroides over Prevotella. The **Prevotella-Bacteroides ratio** is **decreased**.

Frequency Scale of the Most Important Bacteria Phyla

The colon is populated by bacteria, which reach a total density of approximately 1011-1012 bacterial cells/ml colon content. This dense community of bacteria consists mainly of three or four large bacteria phyla: **Bacteroidetes, Firmicutes, Actinobacteria and Proteobacteria**. Other phyla (Verrucomicro-bia, Fusobacteria) show smaller shares.

Result

The distribution of the bacteria-phyla shows an increase of:

- Proteobacteria

The distribution of the bacteria-phyla shows a reduction of:

- Actinobacteria
- Verrucomicrobia

Metabolome (functional groups)

TMA formation

The present findings indicate an unsuspicious number of TMA forming bacteria.
The metabolite bacteria Trimethylamine (TMA) can be produced by certain bacterial species primarily from choline, but also from betaine or L-carnitine. TMA is the precursor of the TMAO (trimethyl-N-oxide) formed in the liver.

TMAO is a key molecule in the pathogenesis of cardiovascular diseases. It influences cholesterol and bile acid metabolism and promotes inflammation of the vascular walls.

Ammonia formation

The present finding shows an increased number of ammonia-producing bacteria.
Ammonia is produced by the breakdown of amino acids. The anaerobic flora is also an important producer of ammonia. In the case of dysbiosis and an alkaline intestinal environment ammonia is increasingly absorbed through the intestinal wall.
Ammonia is a cytotoxin and can negatively affect both nerve cells and mitochondrial function.

Equol

The current findings indicate a sufficient number of equol-forming bacteria.
To clarify whether the existing bacteria really produce equol, a quantitative equol diagnostic is recommended.
As a bacterial metabolic product, equol is mainly synthesized upon consumption of soy products.
Its binding affinity to oestrogen receptors has been associated with beneficial effects in menopausal disorders and may protect against artherosclerosis, osteoporosis or neuroinflammatory diseases.
Mainly species such as Adlercreutzia, Eggerthella and Slackia are able to form equol. The bacterial formation, however, varies greatly between individuals. While in Europe, only about 20 – 30 % of the population is able to form equol, in Asia it is 50 – 60 %.

β-Glucuronidase formation

The present findings indicate a normal number of β-glucuronidase-bearing bacteria.
β-glucuronidases are enzymes formed in the course of human metabolism, as well as by various bacterial genera. The microbial β-glucuronidase activity in the intestine ensures that inactivated hormones, active ingredients or toxins are released again as conjugate.
Depending on the intensity of the activity, this has a physiologically important effect, but may also promote a wide range of diseases.

Actinobacteria

Bifido bacteria are the most important genre in the scope of actinobacteria. They are gram-positive anaerobic rod-shaped bacteria, which utilize starch, but mainly oligosaccharides. Mostly acetic and lactic acid are developed. Common representatives are B. adolescentis, B. breve and B. longum.

Reduced bifido bacteria are often found after repeatedly applied antibiotic therapies, in case of irritable colon syndromes, chronic-inflammatory intestinal diseases or colorectal carcinoma. They mainly come along with reduced diversity in the intestines. By developing short-chained fatty acids and related pH-value reduction in the intestinal lumen bifido bacteria do not only counteract proliferation of pathogenic bacteria (**colonisation resistance**), they also have **anti-inflammatory effects.**

Result

In case of Mr. ___ the **bifido bacteria count is below the norm.** Reduced bifido bacteria promote endogenic infections. Inflammation inhibiting properties are not at all or only little effective.

Bacteroidetes

Bacteroides is the most common genus in the microbiome of many people, regularly reaching >40% of the total intestinal microbiota. As distinct biomarkers of nutrition, they define enterotypes 1 and 2.

Results

In case of Mr. ___ 30,9 % are of these genus, which equals a normal bacteria count.

Also high **prevotella** bacteria counts can be reached, especially in case of vegetarians. But here it is with < 1,0 x 10^5 CFU / g stool **below normal range**.

Firmicutes

Formation of Butyrate and Short-Chain Fatty Acids by Firmicutes

Carbohydrate fermentation in the colon leads to formation of short-chain fatty acids (SCFA) (37) and gases (H2, CO2, methane). SFCA detectable in stool samples are mainly **formic acid**, **acetic acid**, **propionic acid** and **butyric acid**. Dietary changes lead to altered production rates of short-chain fatty acids. **Low-carb diets** lead to reduction of the butyrate formation to one quarter (Duncan et al. 2007) while **prebiotic agents** or **increased fibre consumption** lead to butyrate and propionate increases (39), the acetate levels decrease.

Short-chain fatty acids have positive influence on health. They stimulate intestinal motility and reduce inflammatory reactions. **Butyrate** is the most important **energy source** for colonocytes, it has an anti-inflammatory effect (40, 41, 42), protects against cell degeneration and also has **preventive influence** in regard to colorectal carcinoma.

Intestinal butyrate formation is mainly carried out by **firmicutes**. Among firmicutes mostly **Eubacterium spp.**, **Roseburia spp.**, **Ruminococcus spp.** and **Butyrivibrio species** as well as **Cl. butyricum** are potent butyrate formers. The strongest butyrate former, however, is **Faecalibacterium prausnitzii**, which in contrast to the other listed butyrate forming species, cannot utilize starch (Rios-Covian et al., 2015). As butyrate is quickly absorbed via the intestinal mucosa, measurements in stool only provide unreliable results. Important information about butyrate formation can be obtained with the aid of quantitative analysis of butyrate forming bacteria.

Result

The molecular genetic microbiome analysis on butyrate-forming bacteria showed **deficits in several important butyrae formers**:
The **total bacteria count** of the butyrate formers was also **reduced**.

Deficits in several important butyrate formers and a reduced total bacteria count indicate an **insufficient butyrate formation**.

E. hallii is a bacterium that can convert acetate to butyrate. The butyrate source is not available, or only to a limited extent, when the number of microorganisms is low. A butyrate deficiency can result.

Evaluation of the Clostridia Flora (Total Bacteria Count, Toxin Development)

Clostridia belong to the group of firmicutes. They are obligatory anaerobic bacteria and develop spores. Pathogens belong to the clostridia species, but also apathogenic, useful bacteria, which have an immune modulating effect and lead to an increase of IL-10. Mainly Clostridium botulinum, Clostridium tetani or Clostridium difficile belong to the group of pathogenic representatives. In regard to their favoured energy sources clostridia can be assigned to two groups: **proteolytic** and **saccharolytic species**.

Proteolytic clostridia utilize protein and amino acids. Saccharolytic species on the other hand ferment carbohydrates, starch or fibres. During this process butyrate, acetone, butanol, CO2 and hydrogen are developed. Dominance of proteolytic species often indicates so-called **"putrescence dyspepsia",** which frequently comes along with increased pH-values in stool. If the pH-value is – in spite of high counts of proteolytic species – within the norm or reduced, this is mostly due to accelerated intestinal passage. High clostridia counts may also come along with "**fermentative dyspepsia**". In this case, however, they are saccharolytic species.

Some clostridia groups – so-called **Cluster I-Clostridia** contain **toxin developing species**, like for example C. perfringens, C. sporogenes or C. histolyticum. Cluster I clostridia are often found in diseases of the autistic spectrum disorders and are not rarely the cause of **autism associated intestinal** and frequently also **extra-intestinal complaints.**

Results

The microbiome analysis of Mr. ___ showed **increased clostridia counts**.

Toxin developing clostridia (Cluster I) could not be detected during sequencing. But only the most important representatives C. perfringens, C. sporogenes und C. histolyticum are considered.

Additional Relevant Firmicutes

Christensenella

The genus Christensenella, which was recently discovered in 2012, contains gram-negative, obligate anaerobic bacteria, which can be isolated from human feces. As extensive investigations on twins showed, the occurrence of Christensenella is to a large extent inherited. Especially twins with a **low BMI** showed high bacterial counts (Goodrich et al., 2014, Hamazelou, 2016). Animal experiments suggest that Christensenella is **counteracting obesity** (Waters et al., 2016). Christsensenella is often found in feces of very old people (Kong et al., 2016).

Result

In the case of Mr. ___ Christensenella are not present or only present in low bacterial counts.

Dialister invisus

The Dialister species are part of the Firmicutes. Their share of the total microbiome is about 1-1.5% (Van Zanten et al., 2014). 5 species belong to this generic group of which 3 can be determined in stool. Before all Dialister invisus is of importance – a gram-negative, obligate anaerobic bacterium – which may be involved in **oral cavity infections** (periodontitis, gingivitis) (Morio et al., 2007). Only little is known so far about the function of Dialister invisus in the intestines. They are not of physiological significance. High bacteria counts should be regarded as in indication of dysbiosis.

Result

In case of Mr. ___ the bacteria count of Dialister invisus is within normal range.

Proteobacteria

Like microbiome analyses show there is decreasing digestive performance in older age, which often leads to an increase of Enterobacteriaceae (**Escherichia coli**, **Klebsiella**, **Enterobacter**, **Proteus**) or pasteurellaceae (e.g. **Haemophilus**). There are also alterations of the obligatory anaerobic flora. An increase of **Clostridia** is suspicious. **Bifidobacteria** and **Lactobacilli** on the other hand reduce.

The described alterations can also be caused by other factors. Repeated **antibiotic therapies** lead to increasing Enterobacteriaceae, Enterococci and Clostridia counts as well as to significantly decreasing bifido bacteria. (62). Similar can be observed in case of **chronic inflammatory bowel diseases or irritable colon syndromes** (63, 64).

Determination of Pathogenic or Potentially Pathogenic Bacteria

No potentially pathogenic Proteobacteria could be found in the microbiome of Mr. ___.

Archea

Methanobrevibacter spp.

Methanogens such as Methanobrevibacter spp. belong to the domain of the archaea and are not bacteria. In humans, a stable colonization is found in the gastrointestinal tract and oral cavity, in the vagina and on the skin. There, methanogens form a syntropic community with other microorganisms. The most common representative in the gastrointestinal tract with >90% is Methanobrevibacter smithii.

Methanogens are able to reduce CO2 under H2 consumption, as well as secondary bacterial metabolites like acetate to methane. The frequency of methanogens is related to various diseases. Increased methanogenesis can reduce intestinal motility and promote constipation-type irritable bowel syndrome. Increased methanogenesis is also reported for Diverticulosis patients. However, by consuming H2, methanogens also favor the growth of fiber-fermenting bacteria and thus SCFA production.

Result

In the present case, **Methanobrevibacter spp. were found only in minor bacterial counts or not at all**.

Mucosa-relevant bacterial groups

Damage of the Intestinal Mucosa due to Hydrogen Sulphide Development (H2S)

Hydrogen sulphide is a toxic metabolic product, which – in case of higher concentrations – leads to damage of intestinal epithelia and such promotes the occurrence of cellular atypia. H2S is produced in the colon by **sulphate reducing bacteria** – mainly by **Bilophila wadsworthii**, **Desulfomonas pigra** and **Desulfovibrio piger**. Meat is an important source of sulphur, which promotes the growth of sulphate reducing bacteria. The **cancer promoting potential** of hydrogen sulphide is based on the formation of **free radicals** (oxidative stress) and up-regulation of **cyclooxygenase-2** activity in the epithelial cells.

Result

The total bacteria count of **sulphate reducing bacteria is increased** indicating increased **H2S production**.

Oxalobacter formigenes

Oxalobacter formigenes is an oxalate decomposing anaerobic bacterium, which is often found in the colon flora. Oxalobacter formigenes lives in symbiosis with humans. If this bacterium is not or only available in insufficient counts, the primary source for the enzyme oxalyl-CoA-decarboxylase is missing. This enzyme decomposes **calcium oxalate**. Oxalyl-CoA-carbolase deficiency promotes the development **calcium oxalate containing kidney stones**.

Result

Missing evidence of **Oxalobacter formigenes**– like in case of Mr. ___ – promotes development of **calcium oxalate kidney stones.**

Bacteria with an Immunogenic Effect

E. coli and enterococci have an **immunogenic effect** and are in interaction with other bacteria mainly responsible for the **immune modulating effect of the microbiota**.
And at last **lactobacilli** together with enterococci are the main representatives of the small intestine flora. Furthermore they have an **immunogenic effect**, are **anti-inflammatory** and **stabilize the milieu.** They are able to develop substances similar to antibiotics (**bacteriocins**), which counteract proliferation of endogenic pathogens.

Result

We found normal **lactobacilli and enterococci counts** in the microbiome of Mr. ___.

Mucin Development and Mucosa Barrier

In the healthy large intenstine a layer of mucosa mucus (**mucin layer**) protects the epithelial cells. If the mucin layer is damaged or insufficient mucin is formed, pathogens, pollutants or allergens can come into direct contact with the mucosa and lead to inflammation. Mucin formation and mucosal barrier are therefore closely connected. The maintenance of an intact mucosal barrier protects against bacterial translocation (LPS) and thus against inflammation. Bacteria such as **A. muciniphila** are significantly involved in maintaining the mucin layer. They emit mediator substances that stimulate the goblet cells to form mucosal mucus.

Result

Reduced Akkermansia muciniphila counts in the microbiome of Mr. ___ indicate **insufficient mucin** formation.

We found **reduced Faecalibacterium prausnitzii counts** in the stool of Mr. ___. **Inflammation intensity and F. prausnitzii bacterial count** often correlate inversely with each other. Low F. prausnitzii bacterial counts therefore often indicate **inadequate butyrate supply of the mucosa** and existing **inflammatory mucosa alterations**.

Mycological Stool Analysis

No yeasts could be found in the stool sample of Mr. ___.

Determination of Parasites or Parasitic Enteritis Pathogens

There was no indication of Blastocystis hominis,Dientamoeba fragilis,Giardia lamblia,Entamoeba histolytica,Cryptosporidium spp.,Cyclospora cayetanensis in stool.

Therapeutic Approaches

The results of the microbiome analysis require therapeutic approaches, which protect the microflora against negative consequences or ease existing complaints by supporting the microflora.

Successful therapies, however, also take basics into consideration, which practicably apply for everyone and often already lead to significant improvement of ailments. These basic therapies are based on decade-long experiences. They are listed in short form below and can be found under .

Basics for healthy intestines:

Diet
Healthy diets consist of a plentiful breakfast, a main meal at lunch and a modest dinner. It should be varied and diverse.

Giving Psyllium seed husks (dosage 1 – 2 tablespoons) should lead to 1 – 2 formed stools per day. They are tolerated well and may also be given in case of obstipation or diarrhoea.

Wheat
Avoid or significantly reduce wheat. Wheat is often not tolerated well, even if there is no evidence of intolerance. This is caused by amylase-trypsin inhibitors (ATI), which inhibit digestive enzymes and promote mucosa irritations.

Sugar
Radical reduction of sugar consumption

Chewing
Thoroughly chewing and salivating of food is the first step to healthy digestion and nutrient absorption. Chewing 30 – 40 times leads to optimal preparation of food for intestinal processes.

Exercise
Adequate moderate exercise

Relaxation
Keep adequate resting phases

Detoxification
Drink enough (2-3 l water / unsweetened herbal teas) – this provides for improved intestinal passage and excretion of foreign matters. Possibly drainage of toxic substances via zeolite and/ or humic acids may be sensible.

Substitution
Consumption high-value herbal oils (e.g. linseed oil) and/or fish, possibly curcumin or aloe vera, which have an anti-inflammatory effect respectively promote butyrate development.

Note

As part of the metabolome analysis, which builds on the microbiome findings, you will receive personalised recommendations for optimising nutritional therapy, along with guidance on further therapeutic measures. The analysis provides insight into current metabolic processes and highlights potential strategies for targeted interventions.

Diversity

The microbiome analysis indicates reduced **diversity**. Only adequate biodiversity provides protection against endogenic infections. If the diversity is adequate, the intestinal microbiota can fully unfold their immune modulating and anti-inflammatory activities and only then they can fulfil their function as important supporter of the mucosa barrier.

Biodiversity can be influenced by **prebiotics** and **probiotics** but also by **dietary factors**. The treatment should be based on the type of determined alterations. Well aimed measures based on findings and medical history are described below.

Please make sure to keep a **balanced diet** to provide for the maintenance of the microbiome diversity. An antibiotic therapy should always be accompanied by taking **probiotics.** They not only counteract proliferation of resistant pathogens, but also further reduction of bacteria diversity. Please keep in mind that also **smoking, aging, imbalanced high-fat diets** ("Western Diet") or diseases coming along with inflammatory mucosa irritations ("**low grade inflammation**") or medication (NSAR) lead to biodiversity decline. Therefore therapies should always start here and fight against the causal factors.

Enterotype

The patient has **enterotype 1** dominated by strong bacteroides flora. Bacteroides species are able to synthesize vitamins (biotin, riboflavin, pantothenic acid, folic acid and vitamin C), but intestinal **nutrient resorption** of enterotype 1 – with the exception of some B-vitamins (B1, B2, B3) – is significantly **worse** than that of Prevotella dominated enterotype 2.

Consequence:
Enterotype 1 patients should therefore make sure their **micronutrient supply** is **adequate.** This before all applies for:

- **Vitamin A**
- **Vitamin E**
- **Iron**
- **Calcium**

Individual prebiotic or probiotic therapies

Prebiotics

Prebiotics can promote diversity and achieve targeted changes in the composition and metabolism of the gut microbiota. Prebiotics consist of hard-todigest carbohydrates, such as **resistant starches**, which lead to the proliferation of firmicutes and some bifidobacteria. **Oligosaccharides** such as XOS, AXOS, FOS, GOS or acacia fibers also show a bifidogenic effect. They too lead to an increase in butyrate formers. In addition, Faecalibacterium prausnitzii or Akkermansia muciniphila can be propagated via FOS / GOS or acacia fibers, resulting in a stabilization of the mucus layer and the mem-brane barrier. Recently, 2-fucosyllactose has also become available, an oligosaccharide that leads to a particularly strong proliferation of bifidobacteria and can also noticeably enrich Akkermansia muciniphila (SAH Fukosyllaktose, Arktis Feed).

Probiotics

Probiotics are selected, living microorganisms that positively affect the environment in the intestine. Above all, strains of bifidobacteria and lactobacilli, but also E. coli, and enterococci are used. Whereas in the past it used to work predominantly with individual strains, it is now known that com-binations of several potentiating probiotic strains can achieve significantly stronger effects. **Modern multispecies probiotics** can stimulate the mucosal immune system or have an immunomodulating effect. Depending on the selection and composition of the strains used, probiotics can stabilize the mucosal barrier in the intestine by stabilizing mast cell membranes and counteract a leaky gut. Modern multispecies probiotics have an anti-inflammatory effect and lead to a significant reduction of proinflammatory cytokines.

Pre- and probiotics should be used as specifically as possible in order to achieve an optimal effect. The selection is based on the following criteria:

- Patient age
- Complaint image
- Diversity
- Mikrobiota changes
- Butyrate and mucin formation
- Existing pathogenic / potential-pathogenic germs
- Existing facultatively pathogenic yeasts
- Inflammatory mucosal changes
- Leaky Gut (disturbed mucous membrane barrier)
- Mucosal immune system
- Incompatibilities / intolerances
- Overweight or underweight

Nutritional forms, such as **FODMAP or low carb** have an impact on diversity and microbiota composition. Therefore, they are also taken into account in the following compilations.

Pre- and probiotics should be used as **specifically** as possible in order to achieve an **optimal effect**. The following tables allow you to determine suitable pre- and probiotics according to fixed criteria. If prebiotics can easily be restricted to the naming of active substances, this is practically impossible with probiotics, since even the same named bacterial species can vary greatly in their abilities. Even if products are named for these reasons, a claim for completeness cannot be guaranteed due to the large number of products offered. However, attempts were made above all to include probiotics which

can substantiate the indication and efficacy with studies. If the listing is based only on similar parent compositions or indications by the manufacturer, this is marked in color. For further explanations, please refer to the tables.

Microbiological Therapy

Increased **E.coli** bacteria counts are often caused by insufficient activity of the mucosa immune system (MIS). In the scope of **microbiological therapies** preparations with viable (Symbioflor I, II, Mutaflor) or inactivated bacteria (ProSymbioflor) are applied because they activate the mucosa immune system. Preparations with viable bacteria principally have stronger simulating effects than those with inactivated bacteria.

Dietetic Treatment

The microbiome composition is significantly influenced by the diet. Long-term change of diets alter the bacteria-phyla distribution (e. g. of firmicutes or bacteroidetes) as well as the bacteria count of those bacteria species, which are important for intestinal health.

Please note:

The recommended dietetic treatment may lead to flatulence in the beginning. If this is the case starch or oligo-saccharide containing foods have to be increased gradually.

Additional Therapeutic Approaches

Most kidney stones consist of calcium oxalate – a salt of oxalic acid. If there is an *Oxalobacter formigenes* deficiency the primary source for the enzyme oxalyl-CoA-decarboxylase is missing. This enzyme metabolizes calcium oxalate. Therefore the development of **calcium oxalate containing kidney stones** is promoted.

By **keeping low oxalate diets** one can counteract kidney stone development. Hazelnuts, almonds, amaranth, sesame, chard, spinach, rhubarb, black or green tea, mineral waters with high calcium content (more than 100 mg calcium per litre) and alcoholic drinks should be avoided. Also cocoa and wood sorrel contain a lot of oxalic acid.

Probiotics Indications	OB Panda Ec. Panda OF Start Lb. Junior[2)] AB Start	OB 6[4)] Lb. omni FOS OF Plus pb pur	OB Aktiv Sb. Vital Lb. 60plus OF Senior	OB 10[4)] Ec. AAD[4)] pb protect Lb. AAD AB Akut	OB Stress OB SR9 Ec. 825 AB Compens Lb. Forte[1)]	OB Power Ec. Perform.	OB Hetox Ec. Barrier[5)]	OB Hetox light Ec. Barrier Ec. Sense	OB Flora plus+ OF Fem
Babies	+ + +	Wo 5 - 12			Wo 1 - 4				
Children	+ + +[2)]			*/+ +		*	*	*	
Adults		+ + +	+	+ +	+ +	+ +	+ +	+ +	+ +
Seniors		+	+ + +	+ +	+ +	+ +	+ +	+ +	+ +
Antibiotics				+ + +					
Lack of Butyrate					+ + +	+ +			
C. albicans	+	+ +		+ +					+ +
C. krusei /glabrata		+		+					+ + +
Diversity low	+ +[3)]				+ +		+ +	+	
Inflammation					+ + + +[1)]	+ +	+ +	+ +	
Flora (pH +)		+ + +	+ + +		+	+			
MIS-Activity - [6)]	+ +	+ + +	+ +	+ +	+	+ + +	+ +	+	
Lack of Mucin									+ +
Leaky Gut	+ +[3)]				+ + +	+ + +		+ + + +	
PO / PPO		+		+ + + +	+ +			+	
SRB		+ + +	+ +		+				

Notes

+ + + / + + + + Method of choice | + + appropriate | + slight effect detectable | * from 8 years on
1) Lb. Forte: Indication: inflammatory mucosa reactions, CED (Interval); 2) from 2nd year on life; 3) detected for OB Panda and Ec. Panda; 4) OB 6, OB 10, Ec. AAD also for children from 2nd year of life on, until 3 years half of dosage; 5) Ec. Barrier double dosage; 6) see introductory paragraph
OB: Omni-Biotic | Ec.: Ecologic | Lb.: Lactobact | OF: Orthica Flora / Orthiflor | pb: Probiotik | AB: Arktibiotic
MIS: Mucosal immune system | PO / PPO: pathogens / potentially pathogenic bacteria | SRB: sulfate-reducing bacteria

Important:

Information based on scientific studies or on indication statements of manufacturers. Due to the large quantity of probiotics available, there is no claim for completeness. **Black**: based on study | Violet: manufacturer´s specification

Stool Analysis for Direct Detection of Bacterial Metabolites

Functional Bacterial Groups vs. Direct Metabolite Detection: What Sets Them Apart?

Functional bacterial groups refer to different groups of bacteria that carry out similar metabolic functions. These groups can be identified through genetic analysis (e.g. 16S rRNA sequencing). The actual formation of metabolites depends on various influencing factors, including nutrient availability, environmental conditions (such as pH), chemical signals (e.g. quorum sensing molecules), and genetic and epigenetic factors, among others.

In **metabolite detection**, on the other hand, **actual bacterial metabolites** are directly measured in the stool.
The key distinction is that functional groups represent the **potential** of bacteria to produce health-relevant metabolites, without confirming whether they are actually being produced. Only through the direct detection of metabolites in the patient's stool are we able to determine whether specific metabolic pathways are actively utilised and whether metabolites are being formed.

Microbolome - Bacterial Metabolites as Key Components of Good Gut Health

The following findings not only utilise functional groups to assess the metabolic potential of the gut microbiota, but also - for the first time - employ direct metabolite detection in the stool to evaluate the impact of central metabolic pathways on the current disease process. Thus, instead of potential risks, **actual changes** and their consequences are revealed.
The following metabolites are measured directly in the patient's stool:

Tryptophan metabolism	Phe/Tyr metabolism	Neurotransmitters	Bile acids
Tryptophan	Phenylalanine	Serotonin	CA
Serotonin	Tyrosine	GABA	UDCA
Indole	p-Cresol	Histamine	Conjugated bile acids
Indole proprionate (IPA)			Free bile acids
Indole lactate (ILA)			Total bile acids
Indole aldehyde (IAId)			
Indoleacetic acid (IAA)			
Tryptamine			
Kynurenic acid			
Indoxyl sulphate			

Result

The metabolites analysed in the stool of Mr. ___ reveal significant **abnormal findings** that suggest changes in bacterial metabolism or underlying diseases, warranting diagnostic or therapeutic action.
The abnormal findings include:

- a **lack of AhR agonists** and diminished AhR score
- an **insufficient supply of amino acids**
- **Kynurenic acid levels** outside the normal range

Background Information

This section provides background details on **abnormal** metabolites or metabolite groups in a **concise format**.

AhR (Aryl Hydrocarbon Receptor) Activators

Indole and its protective derivatives act as AhR agonists. A **deficiency in AhR agonists** should be addressed, as an adequate supply of these metabolites offers several beneficial effects. Activation of the aryl hydrocarbon receptor (AhR) leads to:

- Reduction of **inflammation** and **autoimmunity** through increased release of Treg cells and IL-10.
- Boosting the **gut barrier** through increased expression of tight junction proteins.
- Increased **mucus production**, providing an additional protective layer.
- Promotion of **colonisation resistance** through the formation of antimicrobial peptides.

Kynurenic Acid

Kynurenic acid (KYNA), a tryptophan metabolite, exerts **dose-dependent** effects in the gut:
At physiological levels, it supports anti-inflammatory activity, immune regulation, intestinal barrier protection, and antioxidant defense. However, elevated levels may inhibit AhR receptors, potentially triggering intestinal inflammation. High KYNA levles are also associated with neurotoxic effects. For this reason, it's crucial to maintain levels within the **physiological range**.

Amino Acid Precursors

The amino acids **tryptophan**, **tyrosine**, and **phenylalanine** function as precursors in the production of neurotransmitters. Tryptophan is converted into serotonin, which affects mood and sleep. In the intestine, it regulates peristalsis and pain perception. Tyrosine is a precursor for dopamine, noradrenaline, and adrenaline, all of which are crucial for mood, motivation, and energy. Lastly, phenylalanine can be converted into tyrosine. Tryptophan can also be used to form protective indole derivatives in the intestine, which have anti-inflammatory and antioxidant properties. A deficiency in these amino acids in the gut may lead to mood disturbances, sleep disorders, digestive issues, low energy, or neurological disorders.

Therapeutic Approaches for Addressing Altered Stool Metabolomics

Warning for histamine intolerance and food intolerances
The following treatment recommendations consider bacterial bile acid and tryptophan metabolism, toxins, environmental factors, and potential inflammatory changes to the mucous membrane. However, individual **food intolerances or histamine intolerance are not taken into account**.

In the case of histamine intolerance, **fermented foods** such as sauerkraut, kimchi, and yoghurt should be avoided, as they are high in histamine and can exacerbate symptoms. With regards to **probiotics**, please make sure that the strains they don't contain histamine-producing strains.

Influence on Tryptophan Metabolism and the Formation of Toxins

The following is a list of measures that can influence the intestinal environment, tryptophan metabolism, and the formation of toxins. To achieve optimal results, it is recommended to combine as many independent approaches as possible.

Diet
If there is a deficiency in indole or its protective derivatives, attemshould be made to raise their levels to support gut health. This can be achieved through dietary measures, particularly by consuming foods high in **tryptophan**, such as meat, fish, dairy products, eggs, soybeans, pumpkin, or bananas.

Cruciferous vegetables such as broccoli, cauliflower, and Brussels sprouts are also important as they contain **indole-3-carbinol (I3C)**, which is directly converted into indole in the gut.

Fermented foods such as sauerkraut, kimchi, or kefir lead to changes in the intestinal environment and contain lactobacilli and bifidobacteria. Both factors favor an increased formation of indole and indole derivatives.

Dietary supplements
In cases of more pronounced deficiencies or existing intolerances, taking tryptophan supplements (0.5–1.5 g/day) can initially raise tryptophan levels in the gut and thereby support kynurenic acid formation. However, there should be **no significant inflammation** present, as this can activate IDO or KMO and enhance tryptophan degradation.

Probiotics
Indole is produced by various Gram-positive and Gram-negative bacteria, including Escherichia coli and Bacteroides. Probiotics can also enhance the formation of indole and protective indole derivatives in the gut by providing enzymes involved in the conversion of tryptophan to indole. This is particularly true for probiotic strains capable of expressing the enzyme **tryptophanase**. These include, among others:

- Escherichia coli Nissle 1917 (e.g. Mutaflor©)
- Lb. reuteri, Lb. rhamnosus(e.g. SAH Hista-Care©, AB Sensitive©, BiGaia©)
- Lb. rhamnosus GG (LGG)(e.g. LGG© Lb. rhamnosus GG, PureGG 25B©)
- Lactobacillus plantarum 299v(e.g. MyBIOTIK© BALANCE RDS, Smebiocta LP299V©)

Prebiotics

Prebiotics such as **2-fucosyllactose** (e.g. Arktis Feed©), **acacia fibre**, inulin, or FOS support the growth of bacteria involved in the conversion of tryptophan into indole. Through the production of lactate, acetate, and butyrate, they help regulate the intestinal environment (by lowering pH levels), which promotes the formation of protective metabolites and inhibits the production of harmful degradation products.

Caution: It is recommended to begin with a **low dose** of prebiotics and increase it gradually to minimise potential side effects such as flatulence or diarrhoea.

Lifestyle Interventions: Sports, Exercise, and Stress Management

Regular **physical activity** can positively influence tryptophan metabolism, promoting an increase in indole, indole derivatives, and kynurenic acid. The same holds true for effective **stress management**, as chronic stress also alters tryptophan metabolism.

Minimising Exposure to Chemicals and Toxins

Certain heavy metals (such as mercury, lead, and cadmium), chemicals (e.g. PCBs, benzpyrene), and pesticides (e.g. DDT) can act as AhR antagonists. Therefore, it is important to avoid or minimise exposure to these substances.

Irritable Bowel Syndrome and Metabolome

Irritable bowel syndrome (IBS) is probably the most common disease of the gastrointestinal tract. Around 50% of patients who consult a GP because of **gastrointestinal complaints** suffer from it. Typical signs of irritable bowel syndrome are chronic **abdominal pain**, which can occur in conjunction with **constipation**, **diarrhea**, and **flatulence**. The symptoms can be significantly influenced by bacterial metabolites. These include in particular **tryptophan**, **serotonin**, **GABA** and **histamine**.

Here is some crucial background information on **noteworthy** irritable bowel-related test parameters. Further details are available in our specialist brochure "**Irritable Bowel Syndrome IBS**" on our website.

Serotonin (5-HT)

Serotonin (5-HT) is crucial for regulating both pain perception and intestinal motility.

Pain Perception: 5-HT_3 receptors, which are ligand-gated ion channels, are involved in modulating pain signals in the gut. Reduced serotonin levels can lead to inadequate activation of these receptors, thereby increasing pain sensitivity.

Intestinal transit time: Serotonin influences intestinal motility by binding to 5-HT_4 receptors. Disruptions in this signaling pathway can result in motility disorders, such as constipation or diarrhea.

Tryptophan

Tryptophan is an essential amino acid and a functions as a **precursor** in the synthesis of serotonin. A tryptophan deficiency or a disruption in tryptophan metabolism can reduce serotonin production which may affect symptoms of irritable bowel syndrome.

Some intestinal bacteria use tryptophan as a nutrient source, metabolizing it into **bioactive compounds** that support microbial diversity, enhance the intestinal barrier, and exert anti-inflammatory effects. A deficiency in tryptophan can therefore reduce the formation of these beneficial metabolites—such as indole derivatives and AhR agonists.

GABA (Gamma-Aminobutyric Acid)

As the primary inhibitory neurotransmitter in the central nervous system, GABA plays a key role in modulating pain perception. In irritable bowel syndrome (IBS) patients, a GABA deficiency may lead not only to increased **visceral pain sensitivity**, but also to increased anxiety and stress responses. Both factors can further worsen IBS symptoms, as stress and anxiety affect bowel function and motility, promoting abdominal pain, bloating, and altered bowel habits.

Result

The analysis of irritable bowel syndrome-related metabolites, such as tryptophan, serotonin, GABA, and histamine, showed significant findings for Tryptophan,Serotonin,GABA.

Supplementary Measures for Abnormal Irritable Bowel-Related Metabolites

When **metabolites relevant to irritable bowel syndrome** are detected in pathological concentrations, additional therapeutic steps are crucial; these are outlined below.

Serotonin and Tryptophan Deficiency

When faecal **tryptophan and serotonin levels are diminished**, the underlying causes should first be identified. Could there be malabsorption or mucosal inflammation (e.g., low-grade inflammation) triggering the activation of tryptophan-degrading enzymes such as IDO or KMO? This may be assessed by measuring inflammatory markers like **alpha1-antitrypsin** or **calprotectin**.

To address **serotonin deficits**, **5-HTP** (e.g., in the form of**Griffonia**) can be administered, as it is almost entirely converted into serotonin within EC cells. This helps restore serotonin activity at 5-HT receptors. 5-HTP is typically taken between meals at an initial dose of 50–150 mg/day, divided into 2–3 doses. Gradual dosing is recommended, with additional cofactors (especially vitamin B6) if needed.

A mild **tryptophan deficiency** can be corrected, as noted above, by consuming **tryptophan-rich foods** such as meat, fish, dairy, eggs, soybeans, or bananas. In cases of intolerance or severe deficiency, **supplementation** is also an option (500–1500 mg Trp/day). However, this should only be done in the **absence of inflammation**, which can activate IDO or KMO and accelerate tryptophan breakdown. If inflammation is present, it must be addressed—e.g., with combinations of **phosphatidylcholine** and **glutamine** (like SAH Mucosa-Care®, Colon Guard Plus®), supported by **anti-inflammatory probiotics** (OB SR9®, AB Compens®, Lactobact Forte®) or **omega-3 fatty acids** (EPA, DHA: 2–3 g/day).

Important notes:
Therapy with 5-HTP or tryptophan is contraindicated when medications affecting the serotonergic system (e.g., SSRIs or serotonin reuptake inhibitors) are used concurrently.

Gamma-Aminobutyric Acid (GABA) Deficiency

If **decreased gamma-aminobutyric acid (GABA) levels** are associated with visceral pain, GABA supplementation can be considered. A typical dosage of 0.4 to 0.8 g **GABA** in the evening, taken outside of meals, is effective. However, it is becoming increasingly clear that certain probiotic strains can also synthesize neurotransmitters and help address GABA deficiencies. Specifically, strains carrying the Gad B gene are capable of converting glutamate into GABA. Therefore, we recommend using probiotics that contain GABA-producing strains, such as SAH Hista-Care®, Omni-Biotic SR9®, or Synbiosis Spasmodia®, to support low GABA levels.

Therapeutic Approaches for Irritable Bowel Syndrome (IBS)	Therapeutic approaches after clarification of causes	Probiotic strains / probiotics
Histamine excess Typical symptoms: diarrhoea, abdominal pain, cramps, flatulence	• Histamine-free diet DAO substitution • Cofactors (DAO) • Histamine-blocking probiotics • Classical: mast cell stabilizers (e.g. Colimune®, Allergoval®)	L. reuteri B. longum B. infantis *Probiotics:* e.g. SAH Hista-Care®, AB Sensitive®, BiGaia®
Tryptophan Deficiency	Cause clarification: • Malabsorption* (alpha-1-antitrypsin, calpreotectin) • IDO activation, fructose malabsorption *Therapeutic approaches:* • TRP administration* + TRP-forming probiotics	B. infantis *Probiotics:* e.g. SAH Hista-Care®, SB Spasmodia®
Serotonin Deficiency Constipation, abdominal pain	• Tryptophan-* or 5-HTP** substitution • Serotonin-producing probiotics	L. plantarum, L. brevis, L reuteri, L rhamnosus GG *Probiotics:* e.g. SAH Hista-Care®, BiGaia®, OB Power®
Serotonin Excess Diarrhea	• *Classic:* 5-HT_4 antagonist	
GABA Deficiency visceral pain	GABA substitution**** - GABA-forming probiotics	L. plantarum, L. brevis, Lc. Lactis, B. longum *Probiotics:* e.g. SB Spasmodia®, OB SR9®, AB Sensitive®, SAH Hista-Care®, Aflorex®

Explanations:

AB Arktibiotic, OB Omni-Biotic, SAH Sinavita Adler Health, SB Synbiosys
Dosages for Adults: *L-tryptophan: 0.5-1.5 g/d; ** 5-HTP (Griffonia): 50-150 mg/d (creep in); *** GABA: 0.4-0.8 g/d (evening)

With kind regards

Your Biovis-Diagnostik

Attention: *The recommendations given are only advice based on the compiled findings and possible clinical information. They are exclusively addressed to the therapist/physician and are* ***not intended*** *for direct transfer to the patient. They cannot replace diagnosis and therapy of the treating therapist. The recommendations for therapy are a suggestion. The responsibility for the final selection/measure/dosage lies with the medical professional/therapist responsible for each individual case. Please also note that there may be contraindications/interactions associated with the recommended medication/nutritional supplements for pre-existing primary diseases and when taking certain medication. These must be investigated by the medical professional/therapist before starting therapy.*

To achieve a special medical purpose, the dosing recommendations for individual substances may be higher than those of EU Regulation 2016/128.