

External ID 101193217300

Name	Date of Birth	Female	Order ID	25.11.2022
First Name	Sex		Order Date	
Sampling Date	25.11.2022 00:00	Validation Date	Dr. Herbert Schmidt	Findings Status
Sample Material	FE, T909	Validation on	05.12.2022	Findings Date
				<b>Final Report</b> 05.12.2022

Test	Result	Unit	Standard Range	Previous Result
<b>Stool Diagnostics</b>				
<b>Moleculargenetic Microbiomeanalysis MIDI</b>				
<b>Molecular genetic microbiome analysis 3.0</b>				
<b>Stool Properties</b>				
Colour	brown			FE NA) VISU
Consistency	strong			FE NA) VISU
pH	<b>7,3</b>		5,8 - 6,5	FE NA) TESTS
<b>Biodiversity</b>				
Diversity	5,55		> 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



<b>Enterotype</b>				
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



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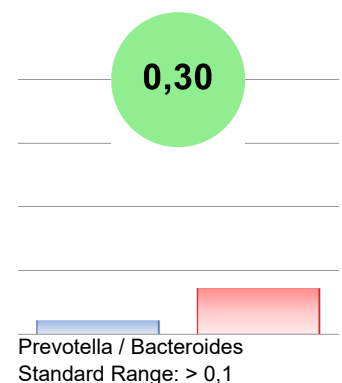
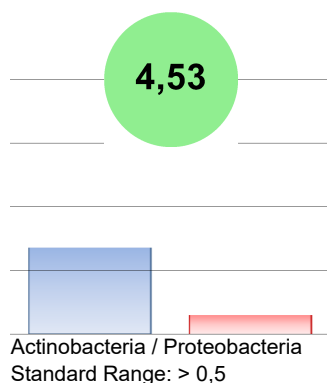
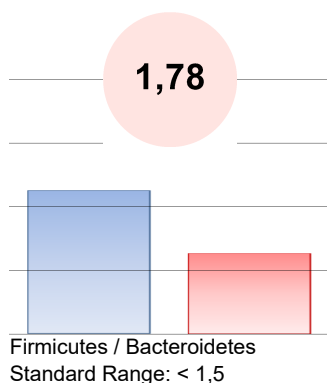
The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.



Index



<b>Ratio</b>				
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Test	Result	Unit	Standard Range	Previous Result	Material Method
<b>Phyla</b>					
Actinobacteria	6,8	%	1,0 - 5,0		FE NA) MGSEQ
Bacteroidetes	31,7	%	30 - 60		FE NA) MGSEQ
Firmicutes	56,4	%	30 - 60		FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0		FE NA) MGSEQ
Proteobacteria	1,5	%	1,5 - 5,0		FE NA) MGSEQ
Verrucomicrobia	0,8	%	1,5 - 5,0		FE NA) MGSEQ
Other	2,9	%			FE NA) MGSEQ

<b>Metabolome (functional groups)</b>					
Secondary bile acids	-35,4	%			
TMA / TMAO	-35,6	%			
Indoxyl sulfate	-50,0	%			
Phenols	-44,8	%			
Ammonia	-42,1	%			
Histamine	-50,0	%			
Equol	-21,2	%			
Beta glucuronidases	-44,7	%			

**Bacteria Phyla - most important genera and species**

<b>Actinobacteria</b>					
Bifidobacterium	5,9 x 10 <sup>10</sup> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Bifidobacterium adolescentis	97	%			FE NA) MGSEQ

<b>Bacteroidetes</b>					
Bacteroides	1,8 x 10 <sup>11</sup> CFU/g faeces		> 1,5 x 10 <sup>11</sup>		FE NA) MGSEQ
Bacteroides uniformis	25	%			FE NA) MGSEQ
Bacteroides fragilis	17	%			FE NA) MGSEQ
Prevotella	5,4 x 10 <sup>10</sup> CFU/g faeces		> 1,0 x 10 <sup>10</sup>		FE NA) MGSEQ

**Firmicutes**

<b>Butyrate producing bacteria</b>					
Total bacteria count	1,9 x 10 <sup>11</sup> CFU/g faeces		> 1,2 x 10 <sup>11</sup>		FE NA) MGSEQ
Faecalibacterium prausnitzii	1,1 x 10 <sup>11</sup> CFU/g faeces		> 5,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Eubacterium rectale	4,2 x 10 <sup>9</sup> CFU/g faeces		> 1,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Eubacterium hallii	2,5 x 10 <sup>10</sup> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Roseburia spp.	7,0 x 10 <sup>9</sup> CFU/g faeces		> 2,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Ruminococcus spp.	1,3 x 10 <sup>10</sup> CFU/g faeces		> 3,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Coprococcus spp.	2,6 x 10 <sup>10</sup> CFU/g faeces		> 2,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Butyrivibrio spp.	4,2 x 10 <sup>9</sup> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ

<b>Clostridia</b>					
Clostridia total bacteria count	1,3 x 10 <sup>9</sup> CFU/g faeces		< 4,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Clostridia Cluster I	1,0 x 10 <sup>5</sup> CFU/g faeces		< 2,0 x 10 <sup>9</sup>		FE NA) MGSEQ

<b>Fusobacteria</b>					
Fusobacterium	4,1 x 10 <sup>7</sup> CFU/g faeces		< 1,0 x 10 <sup>7</sup>		FE NA) MGSEQ

<b>Verrucomicrobia</b>					
Akkermansia muciniphila	7,6 x 10 <sup>8</sup> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ

<b>Proteobacteria</b>					
<b>Pathogenic or potentially pathogenic bacteria</b>					












FE=stool, T909=stool

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

Test	Result	Unit	Standard Range	Visual Scale	Previous Result	Material Method
Haemophilus spp.	1,5 x 10 <sup>8</sup>	CFU/g faeces	< 1,0 x 10 <sup>9</sup>		FE	NA) MGSEQ
Acinetobacter spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE	NA) MGSEQ
Proteus spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE	NA) MGSEQ
Klebsiella spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE	NA) MGSEQ
Enterobacter spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE	NA) MGSEQ
Serratia spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE	NA) MGSEQ
Hafnia spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE	NA) MGSEQ
Morganella spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE	NA) MGSEQ
Citrobacter spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 5,0 x 10 <sup>8</sup>		FE	NA) MGSEQ
Pseudomonas spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 5,0 x 10 <sup>7</sup>		FE	NA) MGSEQ
Providencia spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 5,0 x 10 <sup>7</sup>		FE	NA) MGSEQ
<b>H2S production</b>						
Sulphate reducing bacteria	3,6 x 10 <sup>8</sup>	CFU/g faeces	< 2,0 x 10 <sup>9</sup>		FE	NA) MGSEQ
Desulfovibrio piger	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>9</sup>		FE	NA) MGSEQ
Desulfomonas pigra	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 1,0 x 10 <sup>9</sup>		FE	NA) MGSEQ
Bilophila wadsworthii	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	< 2,0 x 10 <sup>9</sup>		FE	NA) MGSEQ
<b>Immunogenicity / Mucus production</b>						
<b>Immunogenically effective bacteria</b>						
Escherichia coli	5,2 x 10 <sup>7</sup>	CFU/g faeces	10 <sup>6</sup> - 10 <sup>7</sup>		FE	NA) MGSEQ
Enterococcus spp.	< 1,0 x 10 <sup>5</sup>	CFU/g faeces	10 <sup>6</sup> - 10 <sup>7</sup>		FE	NA) MGSEQ
Lactobacillus spp.	7,4 x 10 <sup>6</sup>	CFU/g faeces	10 <sup>5</sup> - 10 <sup>7</sup>		FE	NA) MGSEQ
<b>Mucin production / Mucosal barrier</b>						
Akkermansia muciniphila	7,6 x 10 <sup>8</sup>	CFU/g faeces	> 5,0 x 10 <sup>9</sup>		FE	NA) MGSEQ
Faecalibacterium prausnitzii	1,1 x 10 <sup>11</sup>	CFU/g faeces	> 5,0 x 10 <sup>10</sup>		FE	NA) MGSEQ
<b>Archaea</b>						
<b>Methanogens</b>						
Methanobrevibacter spp.	2,2 x 10 <sup>8</sup>	CFU/g faeces	< 1,0 x 10 <sup>8</sup>		FE	NA) MGSEQ
<b>Mycobiome: relevant yeasts</b>						
Candida albicans (CA)	<1,0 x 10 <sup>3</sup>	CFU/g faeces	<1,0 x 10 <sup>3</sup>		FE	NA) QPCR
Candida krusei (CK)	<1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		FE	NA) QPCR
Candida glabrata (CG)	<1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		FE	NA) QPCR
Candida dubliniensis (CD)	<1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		FE	NA) QPCR
Candida parapsilosis (CP)	<1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		FE	NA) QPCR
Candida tropicalis (CTp)	<1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		FE	NA) QPCR
Candida lusitanae (CL)	<1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		FE	NA) QPCR
<b>Parasites</b>						
<b>Pathobionts</b>						
Blastocystis hominis	negative		negative		FE	A) MOLEK
Dientamoeba fragilis	negative		negative		FE	A) MOLEK
<b>Pathogenic intestinal protozoa</b>						
Giardia lamblia	negative		negative		FE	A) MOLEK
Entamoeba histolytica	negative		negative		FE	A) MOLEK
Cryptosporidium species	negative		negative		FE	A) MOLEK
Cyclospora cayetanensis	negative		negative		FE	A) MOLEK
<b>Maldigestion, malabsorption, MIS</b>						

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Name	Date of Birth	Order ID		
First Name	Sex	Female	Order Date	25.11.2022
Test	Result	Unit	Standard Range	Previous Result
<b>Digestive Residues</b>				
Quantitative determination of fat	<b>8,20</b>	g/100g	< 3,5	 FE NA) PHOT
Quantitative determination of nitrogen	<b>1,10</b>	g/100g	< 1,0	 FE NA) PHOT
Quantitative determination of sugar	<b>3,20</b>	g/100g	< 2,5	 FE NA) PHOT
Quantitative determination of water	<b>67,30</b>	g/100g	75 - 85	 FE NA) PHOT
<b>Determination of Maldigestion</b>				
Pancreatic elastase	274,86	µg/g	> 200	 FE A) ELISA
Bile acids in stool	67,00	µmol/l	< 70	 FE NA) PHOTO
<b>Detection of Malabsorption</b>				
Calprotectin	<b>76,00</b>	mg/l	< 50	 FE A) ELISA
Alpha1-Antitrypsin	<b>91,3</b>	mg/dl	< 27,5	 FE A) ELISA
<b>Special Request</b>				
Secretory IgA	<b>2139,8</b>	µg/ml	510 - 2040	 FE A) ELISA
Histamine in stool	<b>1521,6</b>	ng/ml	< 959	 T909 A) ELISA
Zonulin	<b>322,22</b>	ng/ml	< 55	 FE A) ELISA

## Overview - Results and Therapy Options



pH	↑	milieu stabilizing probiotics *
Enterotype	1	check vitamin A, E, iron and calcium supply
Biodiversity	●	
Ratio Firmicutes/Bacteroidetes	↑	Low Carb Diet, prebiotics (scFOS/scGOS)*
Butyrate producing bacteria	↓	prebiotics on the basis of resistant starch* or scFOS/scGOS*
Mucus production	↓	prebiotics (scFOS/scGOS)*
Mucosa integrity	●	
Milieu stabilising bacteria	●	
Immunogenic bacteria	↓	immunogenic effective probiotics*
Clostridia - total bacteria count	●	
Clostridia cluster I	●	
Fusobacteria	↑	
H <sub>2</sub> S producing bacteria (SRB)	●	
Potentially pathogenic bacteria	●	
Candida (facultive pathogenic)	●	

## Metabolome (functional groups)

Secondary bile acids	●
TMA / TMAO	●
Beta glucuronidases	●
Indoxyl sulfate	●
Phenols	●
Ammonia	●
Histamine	●
Equol	↓