

External ID 0400926070

Name - Date of Birth **17.01.1951** Order ID **11393725**
First Name - Sex **Female** Order Date **20.12.2017**

Sampling Date 20.12.2017 00:00 Validation Date Dr. Herbert Schmidt Findings Status **Final Report**
Sample Material FE Validation on 05.01.2018 Findings Date 09.01.2018

Test	Result	Unit	Standard Range	Previous Result
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Stool Diagnostics

Moleculargenetic Microbiomeanalysis MIDI

Stool Properties

Colour	dark brown			braun
Consistency	mushy			breiig
pH	6,5		5,8 - 6,5	6,0

Biodiversity

Diversity	5,29		> 5,0	
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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

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Bacteria Phyla (Distribution)

Bacteroidetes	55,4	%	30 - 60	
Firmicutes	39,3	%	30 - 60	

Ratio

Firmicutes/Bacteroidetes	0,71	Quotient	< 1,5	
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Enterotype

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

Enterotyp

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Dysbiosis index

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

0	5	10	15	20	25	30
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Test	Result	Unit	Standard Range	Previous Result
Bacteria Phyla - most important genera and species				
Actinobacteria				
Bifidobacteria	9,8 x 10^8	CFU/g faeces	> 5,0 x 10^9	FE
Bifidobacterium longum	79	%		NA) MGSEQ
Equol producing bacteria	4,1 x 10^9	CFU/g faeces	> 5,0 x 10^9	FE
				NA) MGSEQ
Bacteroidetes				
Bacteroides	5,0 x 10^11	CFU/g faeces	> 1,5 x 10^11	FE
				NA) MGSEQ
Prevotella	< 1,0 x 10^6	CFU/g faeces	> 1,0 x 10^10	FE
				NA) MGSEQ
Firmicutes				
Butyrate producing bacteria				
Faecalibacterium prausnitzii	5,4 x 10^10	CFU/g faeces	> 5,0 x 10^10	FE
				NA) MGSEQ
Eubacterium rectale	6,5 x 10^9	CFU/g faeces	> 1,0 x 10^10	FE
				NA) MGSEQ
Eubacterium hallii	2,4 x 10^9	CFU/g faeces	> 5,0 x 10^9	FE
				NA) MGSEQ
Roseburia spp.	3,4 x 10^10	CFU/g faeces	> 2,0 x 10^10	FE
				NA) MGSEQ
Ruminococcus spp.	6,2 x 10^10	CFU/g faeces	> 3,0 x 10^10	FE
				NA) MGSEQ
Coprococcus	4,6 x 10^9	CFU/g faeces	> 2,0 x 10^10	FE
				NA) MGSEQ
Total bacterial count	1,9 x 10^11	CFU/g faeces	> 1,3 x 10^11	FE
				NA) MGSEQ
Clostridia				
Clostridia total bacterial count	1,2 x 10^10	CFU/g faeces	< 4,0 x 10^9	FE
				NA) MGSEQ
Clostridia cluster I	1,5 x 10^9	CFU/g faeces	< 2,0 x 10^9	FE
				NA) MGSEQ
Fusobacteria				
Fusobacterium spp.	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^7	FE
				NA) MGSEQ
Verrucomicrobia				
Akkermansia muciniphila	3,6 x 10^7	CFU/g faeces	> 5,0 x 10^9	FE
				NA) MGSEQ
Proteobacteria				
Pathogenic or potentially pathogenic bacteria				
Haemophilus	8,9 x 10^8	CFU/g faeces	< 1,0 x 10^9	FE
				NA) MGSEQ
Acinetobacter	< 1,0 x 10^6	CFU/g faeces	< 1,0 x 10^6	FE
				NA) MGSEQ
Escherichia coli Biovare	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4	< 1,0 x 10^4
				A) KULTAZ
Proteus species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4	< 1,0 x 10^4
				A) KULTAZ
Klebsiella species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4	< 1,0 x 10^4
				A) KULTAZ
Enterobacter species	4,0 x 10^8	CFU/g faeces	< 1,0 x 10^4	4,0 x 10^8
				A) KULTAZ
Serratia species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4	< 1,0 x 10^4
				A) KULTAZ
Hafnia species	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4	< 1,0 x 10^4
				A) KULTAZ
Morganella spp.	< 1,0 x 10^4	CFU/g faeces	< 1,0 x 10^4	FE
				NA) MIB
Histamin Developing Bacteria				
Histaminbildende Bakterien	1,6 x 10^8	CFU/g faeces	< 5,0 x 10^8	FE
				NA) MGSEQ
H2S production				
Sulphate reducing bacteria	5,2 x 10^8	CFU/g faeces	< 2,0 x 10^9	FE
				NA) MGSEQ

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Immunogenicity / Mucus production					
Immunogenically effective bacteria					
Escherichia coli	4,0 x 10^8	CFU/g faeces	10^6 - 10^7	<div><div></div></div>	2,0 x 10^8 FE A) KULTAZ
Enterococcus species	1,0 x 10^8	CFU/g faeces	10^6 - 10^7	<div><div></div></div>	< 1,0 x 10^4 FE A) KULTAZ
Lactobacillus species	1,0 x 10^5	CFU/g faeces	10^5 - 10^7	<div><div></div></div>	4,0 x 10^4 FE A) KULTAZ
Mucin production / Mucosa barrier					
Akkermansia muciniphila	3,6 x 10^7	CFU/g faeces	> 5,0 x 10^9	<div><div></div></div>	FE NA) MGSEQ
Faecalibacterium prausnitzii	5,4 x 10^10	CFU/g faeces	> 5,0 x 10^10	<div><div></div></div>	FE NA) MGSEQ
Yeasts / Molds					
Candida albicans	< 1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3	<div><div></div></div>	< 1,0 x 10^3 FE A) KULTAZ
Candida species	2,0 x 10^4	CFU/g faeces	< 1,0 x 10^3	<div><div></div></div>	4,0 x 10^3 FE A) KULTAZ
Geotrichum candidum	< 1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3	<div><div></div></div>	< 1,0 x 10^3 FE A) KULTAZ
Moulds	negative		negative		negativ FE A) KULTAZ
Parasites					
Giardia lamblia	negative		negative	<div><div></div></div>	negativ FE NA) MOLEK
Entamoeba histolytica	negative		negative	<div><div></div></div>	negativ FE NA) MOLEK
Cryptosporidium spp.	negative		negative	<div><div></div></div>	negativ FE NA) MOLEK
Blastocystis hominis	positive		negative	<div><div></div></div>	positiv FE NA) MOLEK
Dientamoeba fragilis	negative		negative	<div><div></div></div>	negativ FE NA) MOLEK
Cyclospora cayetanensis	negative		negative	<div><div></div></div>	negativ FE NA) MOLEK

Overview - Results and Therapy Options



pH		
Enterotype	1	check vitamin A. E, iron and calcium supply
Biodiversity		
Ratio Firmicutes/Bacteroidetes		
Equol producing bacteria		
Butyrate producing bacteria		prebiotics on the basis of resistant starch* or scFOS/scGOS*
Mucus production		prebiotics (scFOS/scGOS)*
Mucosa integrity		
Milieu stabilising bacteria		milieu stabilizing probiotics*, prebiotics (scFOS/scGOS)*
Immunogenic bacteria		immunogenic effective probiotics*
Clostridia - total bacteria count		
Clostridia cluster I		
H2S producing bacteria (SRB)		
Potentially Pathogenic Bacteria		immunogenic effective / toxin inhibiting probiotics*
Candida (facultive pathogenic)		depending on predisposition: herbal preparations or antimycotics
Oxal decomposing bacteria		