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

External ID

Name		Date of Birth		Order ID	
First Name		Sex	Male	Order Date	03.05.2022
Sampling Date	02.05.2022 00:00	Validation Date		Findings Status	**Final Report**
Sample Material	FE, T909	Validation on	10.05.2022	Findings Date	10.05.2022

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method

Stool Diagnostics

Moleculargenetic Microbiomeanalysis MAXI PLUS

Molecular genetic microbiome analysis 3.0

Stool Properties

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Colour	brown				FE NA) VISU
Consistency	mushy				FE NA) VISU
pH	6,4		5,8 - 6,5 		FE NA) TESTS

Biodiversity

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Diversity	5,70		> 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 **5**

Enterotype

Prevotella

FE
NA) MGSEQ

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

Enterotyp **2**

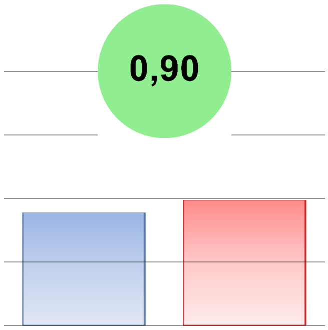
Dysbiosis index

NA) RECHN

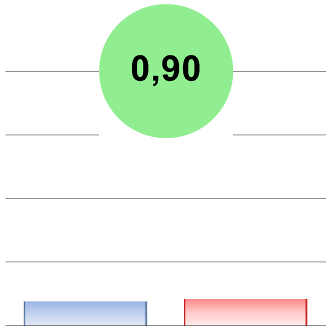
The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.

Index **21**

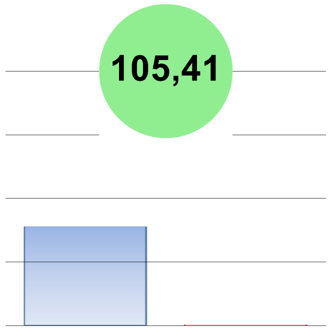
Ratio



Firmicutes / Bacteroidetes
Standard Range: < 1,5



Actinobacteria / Proteobacteria
Standard Range: > 0,5



Prevotella / Bacteroides
Standard Range: > 0,1

FE=stool, T909=stool

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

Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Phyla					
Actinobacteria	1,9	%	1,0 - 5,0		FE NA) MGSEQ
Bacteroidetes	49,4	%	30 - 60		FE NA) MGSEQ
Firmicutes	44,5	%	30 - 60		FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0		FE NA) MGSEQ
Proteobacteria	2,1	%	1,5 - 5,0		FE NA) MGSEQ
Verrucomicrobia	0,0	%	1,5 - 5,0		FE NA) MGSEQ
Other	2,0	%			FE NA) MGSEQ
Metabolome (functional groups)					
Secondary bile acids	-2,6	%			
TMA / TMAO	-30,5	%			
Indoxyl sulfate	-50,0	%			
Phenols	-37,9	%			
Ammonia	-41,4	%			
Histamine	-50,0	%			
Equol	37,3	%			
Beta glucuronidases	-46,0	%			
Bacteria Phyla - most important genera and species					
Actinobacteria					
Bifidobacterium	3,8 x 10^9	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Bifidobacterium longum	97	%			FE NA) MGSEQ
Bacteroidetes					
Bacteroides	3,7 x 10^9	CFU/g faeces	> 1,5 x 10^11		FE NA) MGSEQ
Bacteroides uniformis	16	%			FE NA) MGSEQ
Prevotella	3,9 x 10^11	CFU/g faeces	> 1,0 x 10^10		FE NA) MGSEQ
Prevotella copri	27	%			FE NA) MGSEQ
Firmicutes					
Butyrate producing bacteria					
Total bacteria count	1,9 x 10^11	CFU/g faeces	> 1,2 x 10^11		FE NA) MGSEQ
Faecalibacterium prausnitzii	5,3 x 10^10	CFU/g faeces	> 5,0 x 10^10		FE NA) MGSEQ
Eubacterium rectale	1,5 x 10^10	CFU/g faeces	> 1,0 x 10^10		FE NA) MGSEQ
Eubacterium hallii	2,5 x 10^10	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Roseburia spp.	2,0 x 10^10	CFU/g faeces	> 2,0 x 10^10		FE NA) MGSEQ
Ruminococcus spp.	3,6 x 10^10	CFU/g faeces	> 3,0 x 10^10		FE NA) MGSEQ
Coprococcus spp.	3,0 x 10^10	CFU/g faeces	> 2,0 x 10^10		FE NA) MGSEQ
Butyrivibrio spp.	6,4 x 10^9	CFU/g faeces	> 5,0 x 10^9		FE NA) MGSEQ
Clostridia					
Clostridia total bacteria count	1,7 x 10^8	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	4,8 x 10^8	CFU/g faeces	> 1,0 x 10^9		FE NA) MGSEQ
Dialister spp.	< 1,0 x 10^5	CFU/g faeces	< 4,0 x 10^10		FE NA) MGSEQ

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Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Cl. butyricum	< 1,0 x 10^5	CFU/g faeces	> 1,0 x 10^8		FE NA) MGSEQ
Fusobacteria					
Fusobacterium	< 1,0 x 10^5	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					
Pathogenic or potentially pathogenic bacteria					
Haemophilus spp.	1,5 x 10^8	CFU/g faeces	< 1,0 x 10^9		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 10^6		FE NA) MGSEQ
Enterobacter spp.	1,1 x 10^8	CFU/g faeces	< 1,0 x 10^6		FE NA) MGSEQ
Serratia spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6		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	6,2 x 10^8	CFU/g faeces	< 2,0 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 wadsworthii	< 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	3,9 x 10^7	CFU/g faeces	10^6 - 10^7		FE NA) MGSEQ
Enterococcus spp.	3,7 x 10^8	CFU/g faeces	10^6 - 10^7		FE NA) MGSEQ
Lactobacillus spp.	4,8 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	5,3 x 10^10	CFU/g faeces	> 5,0 x 10^10		FE NA) MGSEQ
Archaea					
Methanogens					
Methanobrevibacter spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^8		FE NA) MGSEQ
Mycobiome: relevant yeasts					
Candida albicans (CA)	<1,0 x 10^3	CFU/g faeces	<1,0 x 10^3		FE NA) QPCR
Candida krusei (CK)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida glabrata (CG)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida dubliniensis (CD)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida parapsilosis (CP)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida tropicalis (CTp)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Candida lusitaniae (CL)	2,4 x 10^4	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Parasites					

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Test	Result	Unit	Standard Range	Previous Result	Sample Material Method
Pathobionts					
Blastocystis hominis	negative		negative		FE A) MOLEK
Dientamoeba fragilis	borderline		negative		FE A) MOLEK
Pathogenic intestinal protozoa					
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
Helminthiasis					
Helminthen					
Small intestinal roundworms	negative		negative		FE NA) MOLEK
Pinworms	negative		negative		FE NA) MOLEK
Hookworms	negative		negative		FE NA) MOLEK
Threadworms	negative		negative		FE NA) MOLEK
Whipworms	negative		negative		FE NA) MOLEK
Dwarf tapeworms	negative		negative		FE NA) MOLEK
Tapeworms	negative		negative		FE NA) MOLEK
New world hookwoorms	negative		negative		FE NA) MOLEK
Microsporidia					
Microsporidia	negative		negative		FE NA) MOLEK
Maldigestion, malabsorption, MIS					
Digestive Residues					
Quantitative determination of fat	6,10	g/100g	< 3,5		FE NA) PHOT
Quantitative determination of nitrogen	0,60	g/100g	< 1,0		FE NA) PHOT
Quantitative determination of sugar	2,30	g/100g	< 2,5		FE NA) PHOT
Quantitative determination of water	78,00	g/100g	75 - 85		FE NA) PHOT
Determination of Maldigestion					
Pancreatic elastase	168,36	µg/g	> 200		FE A) ELISA
Bile acids in stool	15,50	µmol/l	< 70		FE NA) PHOTO
Detection of Malabsorption					
Calprotectin	<17,90	mg/l	< 50		FE A) ELISA
Alpha1-Antitrypsin	12,9	mg/dl	< 27,5		FE A) ELISA
Special Request					
Secretory IgA	<167,0	µg/ml	510 - 2040		FE A) ELISA
Leaky good: Zonulin, Histamine					
Zonulin	363,76	ng/ml	< 55		FE A) ELISA
Histamine in stool	1646,1	ng/ml	< 959		T909 A) ELISA

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Overview - Results and Therapy Options

Dysbiose-Index 21

pH	●	
Enterotype	2	check vitamin B2, B5, C and biotin supply
Biodiversitiy	●	
Ratio Firmicutes/Bacteroidetes	●	
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	●	
Fusobacteria	●	
H2S producing bacteria (SRB)	●	
Potentially pathogenic bacteria	⬆	immunogenic effective / toxin inhibiting probiotics*
Candida (facultive pathogenic)	⬆	depending on predisposition: herbal preparations or antimycotics
Oxalate degrading bacteria	⬇	low-oxalate diet

Metabolome (functional groups)

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