

External ID

Name	Date of Birth	Order ID
First Name	Sex	Order Date
Sampling Date	Validation by	Findings Status
Sample Material	Validation Date	Findings Date

Test	Result	Unit	Standard Range	Previous Result
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Stool Diagnostics

Moleculargenetic Microbiomeanalysis MIDI

Molecular genetic microbiome analysis 3.0

Stool Properties

Colour	brown			
Consistency	mushy			
pH	6,0		5,8 - 6,5	

Biodiversity

Diversity	5,14		> 5	
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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



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



Dysbiosis index

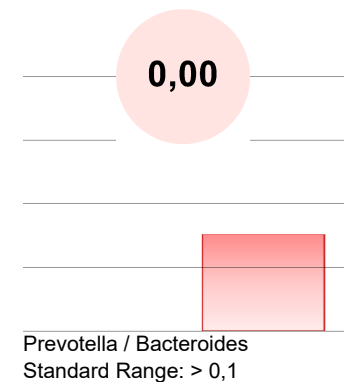
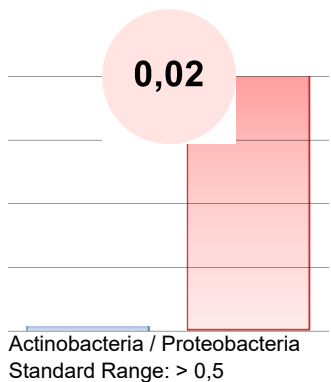
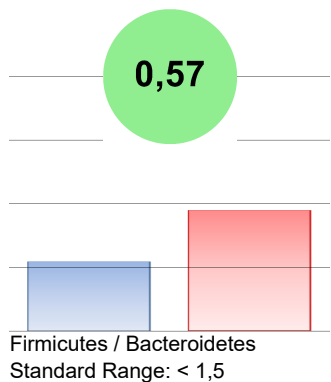
The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.



Index



Ratio



FE=stool

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

Test	Result	Unit	Standard Range	Previous Result
Phyla				
Actinobacteria	0,4	%	1,0 - 5,0	FE NA) MGSEQ
Bacteroidetes	47,5	%	30 - 60	FE NA) MGSEQ
Firmicutes	27,3	%	30 - 60	FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0	FE NA) MGSEQ
Proteobacteria	23,6	%	1,5 - 5,0	FE NA) MGSEQ
Verrucomicrobia	0,0	%	1,5 - 5,0	FE NA) MGSEQ
Other	1,2	%		FE NA) MGSEQ

Metabolome (functional groups)				
Secondary bile acids	-29,2	%		
TMA / TMAO	-43,9	%		
Indoxyl sulfate	-50,0	%		
Phenols	-44,9	%		
Ammonia	-15,9	%		
Histamine	-50,0	%		
Equol	-24,1	%		
Beta glucuronidases	58,9	%		

Bacteria Phyla - most important genera and species

Actinobacteria				
Bifidobacterium	5,8 x 10 ⁸ CFU/g faeces		> 5,0 x 10 ⁹	FE NA) MGSEQ
Bifidobacterium longum	94	%		FE NA) MGSEQ

Bacteroidetes				
Bacteroides	3,8 x 10 ¹¹ CFU/g faeces		> 1,5 x 10 ¹¹	FE NA) MGSEQ
Bacteroides uniformis	15	%		FE NA) MGSEQ
Bacteroides ovatus	11	%		FE NA) MGSEQ
Prevotella	2,8 x 10 ⁸ CFU/g faeces		> 1,0 x 10 ¹⁰	FE NA) MGSEQ

Firmicutes

Butyrate producing bacteria				
Total bacteria count	1,7 x 10 ¹¹ CFU/g faeces		> 1,2 x 10 ¹¹	FE NA) MGSEQ
Faecalibacterium prausnitzii	9,4 x 10 ¹⁰ CFU/g faeces		> 5,0 x 10 ¹⁰	FE NA) MGSEQ
Eubacterium rectale	1,2 x 10 ¹⁰ CFU/g faeces		> 1,0 x 10 ¹⁰	FE NA) MGSEQ
Eubacterium hallii	2,5 x 10 ⁹ CFU/g faeces		> 5,0 x 10 ⁹	FE NA) MGSEQ
Roseburia spp.	3,7 x 10 ¹⁰ CFU/g faeces		> 2,0 x 10 ¹⁰	FE NA) MGSEQ
Ruminococcus spp.	8,3 x 10 ⁹ CFU/g faeces		> 3,0 x 10 ¹⁰	FE NA) MGSEQ
Coprococcus spp.	6,6 x 10 ⁹ CFU/g faeces		> 2,0 x 10 ¹⁰	FE NA) MGSEQ
Butyrivibrio spp.	6,5 x 10 ⁹ CFU/g faeces		> 5,0 x 10 ⁹	FE NA) MGSEQ

Clostridia				
Clostridia total bacteria count	6,3 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

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 ⁷ CFU/g faeces		> 5,0 x 10 ⁹	FE NA) MGSEQ

Proteobacteria

Pathogenic or potentially pathogenic bacteria

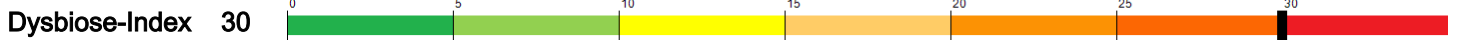
FE=stool * cooperate analytics (R), A) accredited, NA) not accredited



Name	Date of Birth	Order ID				
First Name	Sex	Order Date				
Test	Result	Unit	Standard Range	Visual Scale	Previous Result	Material Method
Haemophilus spp.	1,1 x 10 ⁷ 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.	8,0 x 10 ⁷ CFU/g faeces		< 1,0 x 10 ⁶			FE NA) MGSEQ
Enterobacter spp.	3,2 x 10 ⁸ CFU/g faeces		< 1,0 x 10 ⁶			FE NA) MGSEQ
Serratia spp.	5,7 x 10 ⁶ 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	3,3 x 10 ⁹ 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
Immunogenicity / Mucus production						
Immunogenically effective bacteria						
Escherichia coli	1,1 x 10 ⁹ CFU/g faeces		10 ⁶ - 10 ⁷			FE NA) MGSEQ
Enterococcus spp.	5,7 x 10 ⁶ CFU/g faeces		10 ⁶ - 10 ⁷			FE NA) MGSEQ
Lactobacillus spp.	5,1 x 10 ⁵ CFU/g faeces		10 ⁵ - 10 ⁷			FE NA) MGSEQ
Mucin production / Mucosal barrier						
Akkermansia muciniphila	1,0 x 10 ⁷ CFU/g faeces		> 5,0 x 10 ⁹			FE NA) MGSEQ
Faecalibacterium prausnitzii	9,4 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)	2,1 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 lusitanae (CL)	5,6 x 10 ⁵ CFU/g faeces		< 1,0 x 10 ³			FE NA) QPCR
Parasites						
Pathobionts						
Blastocystis hominis	negative		negative			FE A) MOLEK
Dientamoeba fragilis	negative		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

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Overview - Results and Therapy Options



pH		
Enterotype	1	check vitamin A, E, iron and calcium supply
Biodiversity		
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)		fat and protein reduction, milieu stabilizing probiotics, prebiotics on the basis of resistant starch or scFOS/scGOS
Potentially pathogenic bacteria		immunogenic effective / toxin inhibiting probiotics*
Candida (facultive pathogenic)		depending on predisposition: herbal preparations or antimycotics

Metabolome (functional groups)

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