

External ID

Table with 6 columns: Name, First Name, Muster, Date of Birth, Sex, Order ID, Order Date, Findings Status, Findings Date, Final Report. Includes sample material FE and validation date 26.07.2024.

Table with 6 columns: Test, Result, Unit, Standard Range, Previous Result, Sample Material. Rows include Microbiome Healthpath, Molecular genetic microbiome analysis 3.0, Stool Properties (Colour, Consistency, pH), Biodiversity (Diversity 5,42).

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



Table with 2 columns: Enterotype, 1=2. Includes sample material FE NA) MGSEQ.

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

Enterotyp



Table with 1 column: 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.



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Table with 6 columns: Ratio, Firmicutes/Bacteroidetes, 1,01, Quotient, < 3,0, Sample Material. Includes a color scale for the ratio.

Table with 6 columns: Phyla, Actinobacteria, Bacteroidetes, Firmicutes, Fusobacteria, Proteobacteria, Verrucomicrobia, Other, Results, Sample Material. Includes horizontal bar charts for each phylum.

Test	Result	Unit	Standard Range	Previous Result	Sample Material	Method
Bacteria Phyla - most important genera and species						
Actinobacteria						
Bifidobacterium	5,4 x 10^7	CFU/g faeces	> 1,0 x 10^10		FE	NA) MGSEQ
Bifidobacterium longum	60	%			FE	NA) MGSEQ
Bifidobacterium adolescentis	30	%			FE	NA) MGSEQ
Equol producing bacteria	7,2 x 10^9	CFU/g faeces	> 5,0 x 10^9		FE	NA) MGSEQ
Adlercreutzia spp.					FE	NA) MGSEQ
Eggerthella lenta					FE	NA) MGSEQ
Slackia spp.					FE	NA) MGSEQ
Bacteroidetes						
Bacteroides	1,5 x 10^11	CFU/g faeces	> 5,0 x10^10		FE	NA) MGSEQ
Bacteroides ovatus	34	%			FE	NA) MGSEQ
Bacteroides uniformis	12	%			FE	NA) MGSEQ
Prevotella	8,5 x 10^10	CFU/g faeces	> 1,0 x 10^10		FE	NA) MGSEQ
Firmicutes						
Butyrate producing bacteria						
Total bacteria count	1,8 x 10^11	CFU/g faeces	> 2,4 x 10^11		FE	NA) MGSEQ
Faecalibacterium prausnitzii	1,2 x 10^11	CFU/g faeces	>1,0 x10^11		FE	NA) MGSEQ
Eubacterium rectale	6,8 x 10^9	CFU/g faeces	> 2,0 x 10^10		FE	NA) MGSEQ
Eubacterium hallii	4,6 x 10^9	CFU/g faeces	> 1,5 x 10^10		FE	NA) MGSEQ
Roseburia spp.	7,8 x 10^9	CFU/g faeces	> 3,0 x10^10		FE	NA) MGSEQ
Ruminococcus spp.	9,3 x 10^9	CFU/g faeces	> 5,0 x 10^10		FE	NA) MGSEQ
Coprococcus spp.	1,8 x 10^10	CFU/g faeces	> 5,0 x 10^10		FE	NA) MGSEQ
Butyrivibrio spp.	1,1 x 10^10	CFU/g faeces	>1,5 x 10^10		FE	NA) MGSEQ
Clostridia						
Clostridia total bacteria count	4,3 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 10^5	CFU/g faeces	> 5,0 x 10^9		FE	NA) MGSEQ
Proteobacteria						
Pathogenic or potentially pathogenic bacteria						
Haemophilus spp.	1,6 x 10^7	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.	3,3 x 10^9	CFU/g faeces	< 1,0 x 10^6		FE	NA) MGSEQ
Serratia spp.	5,4 x 10^6	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.	7,2 x 10^9	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						

FE=stool

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

