

Sample

PACIENTE EJEMPLO

XX Years

TT

Requested by Dr. José Perez

Report XXXXXXXX *Sample* 5/12/17

Report Validation and Issue Date 15-12-2017 Lab

Intestinal Disbiosis



PACIENTE EJEMPLO

Report XXXXXXXX

Date 05-12-2017

Orientative Interpretation Results Guide

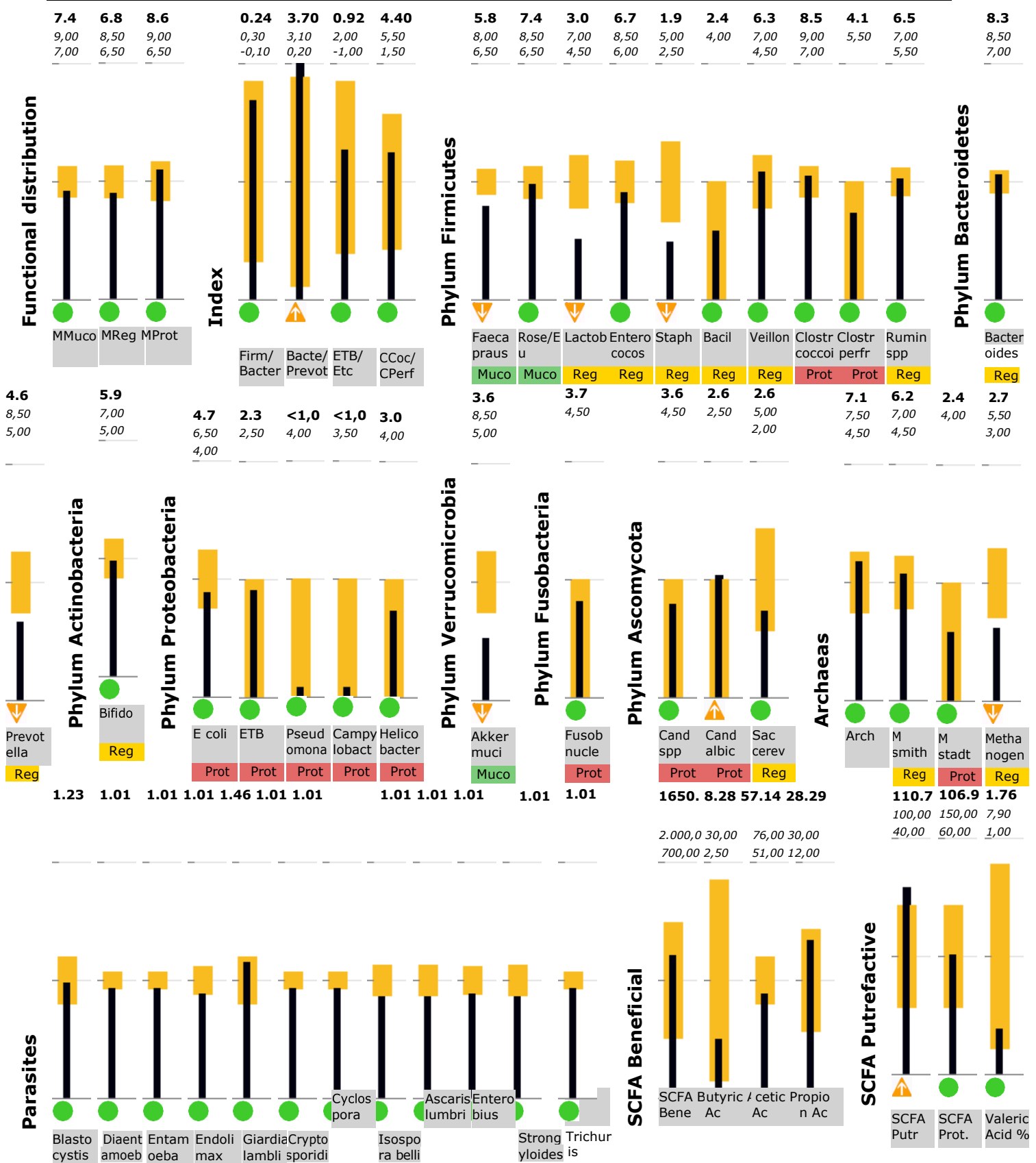
General information

Our organism has evolved to create specific habitats in different parts of the body with a unique system of microorganisms. The set of these commensal, symbiotic and / or pathogenic microorganisms that are part of our system is called Microbioma. The greatest amount of microorganisms is located in the intestine, the skin and the oral cavity. The Microbiome is responsible for enriching our body with glycans, amino acids, xenobiotics, vitamins, isoprenoids and other nutrients that help the development of a good state of health. In addition, it is characterized by evolving over the years and with changes in the diet.

Intestinal Dysbiosis is defined as an alteration of the balance of the Intestinal Microbiome. The microorganisms that make up the intestine have many metabolic functions (production of vitamins, differentiation of intestinal cells, digestion of carcinogenic metabolites, fermentation of non-digestible substrates, production of SCFA ...) and protective (resistance to colonization, intervention in immunity adapted and innate, generation of inflammatory cytokines) and / or structural (production of IgA, intestinal micro-villi and mucosa).

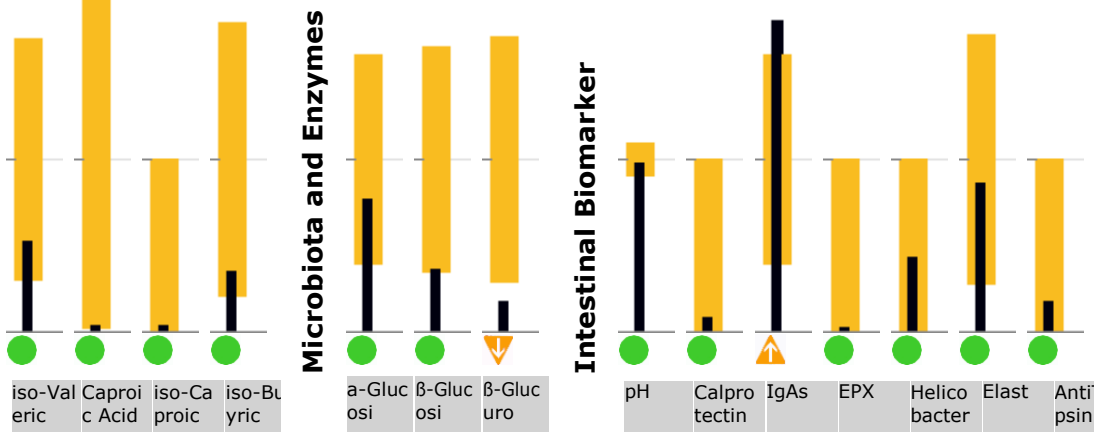
Our R & D team has developed a study of Intestinal Dysbiosis, with a group of Molecular Biology techniques that assess the composition of the Microbiome, Instrumental Techniques for the assessment of SCFA by gas chromatography and metals by ICP-MS and the Department of Immunoassay intestinal markers. The Intestinal Dysbiosis test is of great interest to improve the treatment of diseases directly or indirectly related to the digestive system. It is related to both obesity, diabetes or intestinal inflammatory diseases (Crohn's or Ulcerative Colitis). The causes are very variable from stress, bacterial overgrowth in the small intestine (SIBO), intolerance to sugars, fermentation with production of hydrogen or methane ...

Intestinal Disbiosis

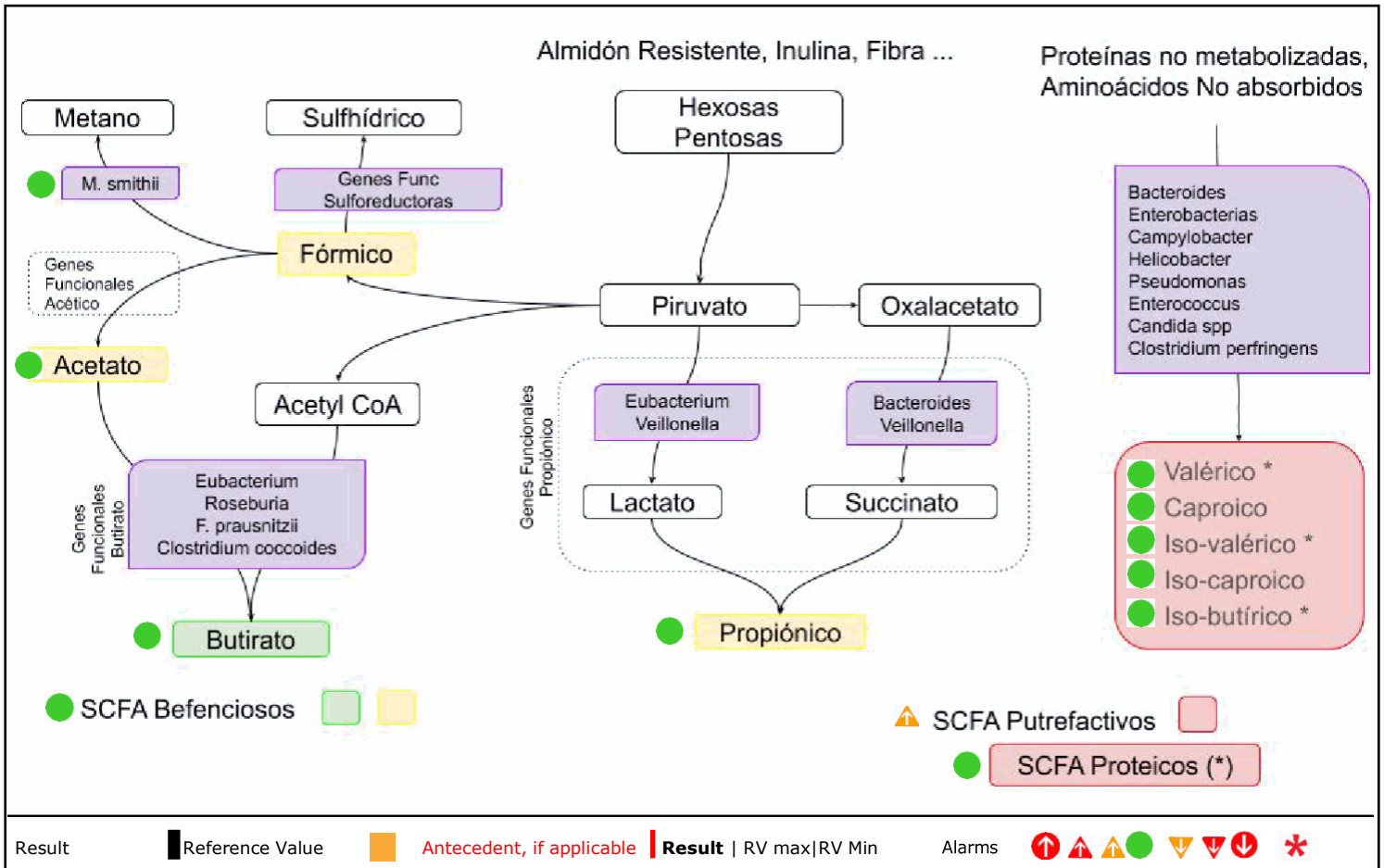


Intestinal Disbiosis

2.30	0.19	0.02	2.01	5.87	1.57	0.39	6.5	<1,0	2297	26	4.4	613	5.84
7,20	7,00	2,60	10,00	12,00	7,00	3,50	7,20	50,00	2.040,0	600,00	10,00	1.200,0	30,00
1,30	0,10		1,20	3,00	1,50	0,60	6,00		510,00			200,00	



Result | Reference Value | Antecedent, if applicable | Result | RV max|RV Min | Alarms (up, down, warning, error icons)








Basic Study

Intestinal Disbiosis

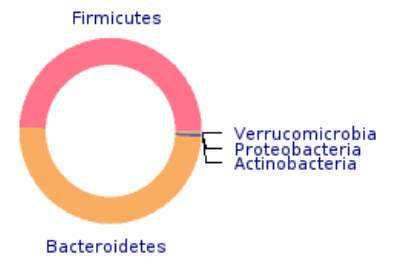
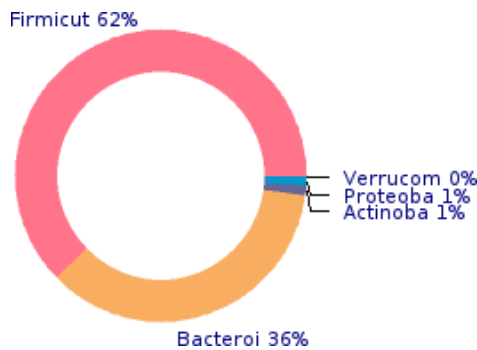
Basic Study

Colour	Marrón
Consistency	Blanda 4 Escala de Bristol
Fecal Occult Blood (FOB)	No se detecta
<i>Urine. Inmunocromatography</i>	



Phyllum distribution

Phylum Firmicutes	8,56 log g.f.u./g	(RV:8,50/11,00log g.f.u./g)	●	
<i>PCR method</i>				
<i>Phylogenetic distribution</i>				
Phylum Bacteroidetes	8,32 log g.f.u./g	(RV:8,00/11,00log g.f.u./g)	●	
<i>PCR method</i>				
<i>Phylogenetic distribution</i>				
Phylum Actinobacteria	6,78 log g.f.u./g	(RV:6,50/9,00log g.f.u./g)	●	
<i>PCR method</i>				
<i>Phylogenetic distribution</i>				
Phylum Proteobacteria	6,81 log g.f.u./g	(RV:3,00/7,00log g.f.u./g)	●	
<i>PCR method</i>				
<i>Phylogenetic distribution</i>				
Phylum Verrucomicrobia	3,89 log g.f.u./g	(RV:5,50/9,00log g.f.u./g)	▼	
<i>PCR method</i>				
<i>Phylogenetic distribution</i>				

Reference Guide



Functional distribution

Muconutritive microbiota [MMuco]	7,4 log g.f.u./g	(RV:7,0/9,0log g.f.u./g)	●	
▼ - Akkermansia muciniphila	3.6 log g.f.u./g			
Regulatory microbiota [MReg]	6,8 log g.f.u./g	(RV:6,5/8,5log g.f.u./g)	●	
▼ - Lactobacillus spp	3.0 log g.f.u./g			
Proteolitic microbiota [MProt]				

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8,6 log g.f.u./g

RV: 6,5/9,0 log g.f.u./g



Intestinal Disbiosis

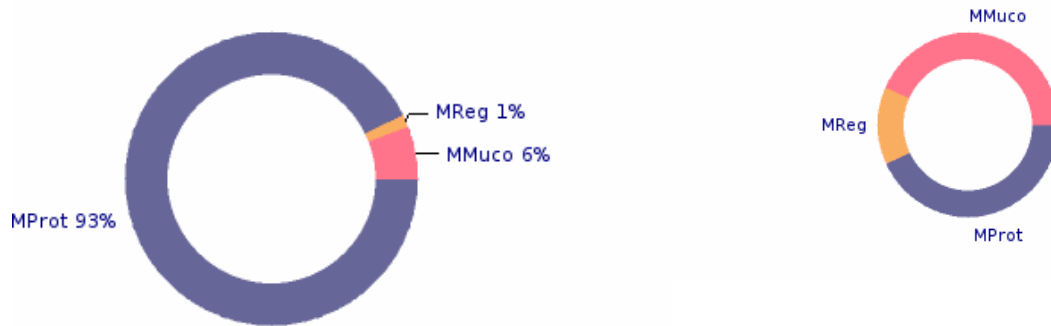
Functional distribution

● - *E. coli* 4.7 log g.f.u./g

Enterotype

The predominant species of ENTEROTIPO 1 are Bacteroides and is characterized by:
- A greater production of biotin by the microbiota.
- A preferred fermentation for carbohydrates and proteins.

Reference Guide



Index

Firmicutes / Bacteroidetes [Firm/ Bacter]	0,24 Ratio	(RV:-0,10/0,30Ratio)	●	
Bacteroides / Prevotella [Bacte/ Prevot]	3,70 Ratio	(RV:0,20/3,10Ratio)	▲	
Enterobacterias / Enterococcus [ETB/ Etc]	0,92 Ratio	(RV:-1,00/2,00Ratio)	●	
Clostridium Coccoides/C perfringens [CCoc/ CPerf]	4,40 Ratio	(RV:1,50/5,50Ratio)	●	
Phylum Firmicutes				
Faecalibacterium prausnitzii [Faeca praus] <i>Muconutritive microbiota</i>	5,8 log g.f.u./g	(RV:6,5/8,0log g.f.u./g)	▼	
Roseburia spp / Eubacterium [Rose/Eu] <i>Muconutritive microbiota</i>	7,4 log g.f.u./g	(RV:6,5/8,5log g.f.u./g)	●	
Lactobacillus spp [Lactob] <i>Regulatory microbiota</i>	3,0 log g.f.u./g	(RV:4,5/7,0log g.f.u./g)	▼	
Enterococos spp <i>Regulatory microbiota</i>	6,7 log g.f.u./g	(RV:6,0/8,5log g.f.u./g)		
Staphylococcus spp [Staph] <i>Regulatory microbiota</i>	1,9 log g.f.u./g	(RV:2,5/5,0log g.f.u./g)		
Bacillus spp [Bacil]	2,4 log g.f.u./g	(RV: ≤4,0log g.f.u./g)	●	

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Regulatory microbiota

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Phylum Firmicutes

Veillonella spp [Veillon] <i>Regulatory microbiota</i>	6,3 log g.f.u./g	(RV: 4,5/7,0 log g.f.u./g)	●	
Clostridium coccoides group [Clostr coccoides] <i>Proteolytic microbiota</i>	8,5 log g.f.u./g	(RV: 7,0/9,0 log g.f.u./g)	●	
Clostridium perfringens group [Clostr perfr] <i>Proteolytic microbiota</i>	4,1 log g.f.u./g	(RV: ≤5,5 log g.f.u./g)	●	
Ruminococcus spp [Rumin spp] <i>Regulatory microbiota</i>	6,5 log g.f.u./g	(RV: 5,5/7,0 log g.f.u./g)	●	

Phylum Bacteroidetes

Bacteroides spp <i>Regulatory microbiota</i>	8,3 log g.f.u./g	(RV: 7,0/8,5 log g.f.u./g)	●	
Prevotella spp <i>Regulatory microbiota</i>	4,6 log g.f.u./g	(RV: 5,0/8,5 log g.f.u./g)	▼	

Phylum Actinobacteria

Bifidobacterium spp [Bifido] <i>Regulatory microbiota</i>	5,9 log g.f.u./g	(RV: 5,0/7,0 log g.f.u./g)	●	
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Phylum Proteobacteria

Escherichia coli [E coli] <i>Proteolytic microbiota</i>	4,7 log g.f.u./g	(RV: 4,0/6,5 log g.f.u./g)	●	
Enterobacteriaceae, excluded E. coli [ETB] <i>Proteolytic microbiota</i>	2,3 log g.f.u./g	(RV: ≤2,5 log g.f.u./g)	●	
Pseudomonas spp <i>Proteolytic microbiota</i>	<1,0 log g.f.u./g	(RV: ≤4,0 log g.f.u./g)	●	
Campylobacter spp <i>Proteolytic microbiota</i>	<1,0 log g.f.u./g	(RV: ≤3,5 log g.f.u./g)	●	
Helicobacter spp <i>Proteolytic microbiota</i>	3,0 log g.f.u./g	(RV: ≤4,0 log g.f.u./g)	●	

Phylum Verrucomicrobia

Akkermansia muciniphila [Akker muc] <i>Muconutritive microbiota</i>	3,6 log g.f.u./g	(RV: 5,0/8,5 log g.f.u./g)	▼	
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Phylum Fusobacteria

Fusobacterium nucleatum [Fusob nucle] <i>Proteolytic microbiota</i>	3,7 log g.f.u./g	(RV: ≤4,5 log g.f.u./g)	●	
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Phylum Ascomycota

Candida spp [Cand spp] <i>Proteolytic microbiota</i>	3,6 log g.f.u./g	(RV: ≤4,5 log g.f.u./g)	●	
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Phylum Ascomycota

Candida albicans [Cand albic] <i>Proteolytic microbiota</i>	2,6 log g.f.u./g	(RV: ≤2,5 log g.f.u./g)	⚠	
Saccharomyces cerevisiae [Sac cerev] <i>Regulatory microbiota</i>	2,6 log g.f.u./g	(RV: 2,0/5,0 log g.f.u./g)	●	

Archaeas

Archaea domain [Arch] <i>PCR method</i>	7,1 log g.f.u./g	(RV: 4,5/7,5 log g.f.u./g)	●	
Methanobrevibacter smithii [M smith] <i>Regulatory microbiota</i>	6,2 log g.f.u./g	(RV: 4,5/7,0 log g.f.u./g)	●	
Methanospaera stadtmanae [M stadt] <i>Proteolytic microbiota</i>	2,4 log g.f.u./g	(RV: ≤4,0 log g.f.u./g)	●	
Methanogens <i>Regulatory microbiota</i>	2,7 log g.f.u./g	(RV: 3,0/5,5 log g.f.u./g)	⚠	

Parasites

Blastocystis hominis	Index 1,23 Índice no significativo	●	
Diaentamoeba fragilis	Index 1,01 AUSENCIA	●	
Entamoeba histolytica	Index 1,01 AUSENCIA	●	
Endolimax nana	Index 1,01 AUSENCIA	●	
Giardia lamblia	Index 1,46 Not significant index	●	
Cryptosporidium parvum	Index 1,01 AUSENCIA	●	
Cyclospora cayetanensis	Index 1,01 AUSENCIA	●	
Isospora belli	Index 1,01 AUSENCIA	●	
Ascaris lumbricoides	Index 1,01 AUSENCIA	●	
Enterobius vermicularis	Index 1,01 AUSENCIA	●	
Strongyloides stercoralis	Index 1,01 AUSENCIA	●	
Trichuris trichiura	Index 1,01 AUSENCIA	●	

Short Chain Fatty Acid (SCFA)

Intestinal Disbiosis

Short Chain Fatty Acid (SCFA)

SCFA Total	1.761,72 µmol/g sample	(RV: ≥740,00µmol/g sample)	●	
SCFA Beneficial	1.650,96 µmol/g sample	(RV: 700,00/2.000,00µmol/g sample)	●	93,7 %
SCFA Putrefactives	110,76 µmol/g sample	(RV: 40,00/100,00µmol/g sample)	●	6,3 %

Reference Guide



SCFA Beneficial

SCFA Beneficial [SCFA Bene]	1.650,96 µmol/g sample	(RV: 700,00/2.000,00µmol/g sample)	●	
Butyric Acid % [Butyric Ac]	8,28 %	(RV: 2,50/30,00%)	●	
Acetic Acid % [Acetic Ac]	57,14 %	(RV: 51,00/76,00%)	●	
Propionic Acid % [Propion Ac]	28,29 %	(RV: 12,00/30,00%)	●	

SCFA Putrefactive

SCFA Putrefactive [SCFA Putr]	110,76 µmol/g sample	(RV: 40,00/100,00µmol/g sampl.)	⚠	
SCFA protein breakdown [SCFA Prot.]	106,98 µmol/g sample	(RV: 60,00/150,00µmol/g sampl.)	●	
Valeric Acid %	1,76 %	(RV: 1,00/7,90%)	●	
iso-Valeric Acid %	2,30 %	(RV: 1,30/7,20%)	●	
Caproic Acid %	0,19 %	(RV: 0,10/7,00%)	●	
iso-Caproic Acid %	0,02 %	(RV: ≤2,60%)	●	
iso-Butyric Acid %	2,01 %	(RV: 1,20/10,00%)	●	

Microbiota and Enzymes

Alpha glucosidase [α-Glucosi]	5,87 IU / 100 mg Protein	(RV: 3,00/12,00IU / 100 mg Protein)	●	
<i>Enzyme Method</i>				
Beta-glucosidase [β-Glucosi]	1,57 IU / 100 mg Protein	(RV: 1,50/7,00IU / 100 mg Protein)	●	
<i>Enzyme Method</i>				

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Microbiota and Enzymes

Beta glucuronidase [β-Glucuro] <i>Enzyme Method</i>	0,39 IU / 100 mg Protein	(RV: 0,60/3,50 IU / 100 mg Protein)	▼	
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Intestinal Biomarker

pH <i>Selective electrode Intestinal Markers</i>	6,5 or. pH	(RV: 6,0/7,2 or. pH)	●	
Calprotectin <i>EIA Intestinal Markers</i>	<1,0 mg/Kg	(RV: ≤50,00 mg/Kg)	●	
sIgA Secretory [IgAs] <i>EIA Intestinal Markers</i>	2.297 µg/mL	(RV: 510/2.040 µg/mL)	⚠	
Eosinophil Protein X [EPX] <i>Stool. EIA Intestinal Markers</i>	26 ng/mL	(RV: ≤600 ng/mL)	●	
Helicobacter Pylori. Antigen <i>Stool. EIA Intestinal Markers</i>	4,4 ng/mL No significativo	(RV: ≤10,0 ng/mL)	●	
Pancreatic elastase 1 [Elast] <i>EIA Intestinal Markers</i>	613 µg/g stool	(RV: 200/1.200 µg/g stool)	●	
Alpha-1 antitrypsin [AntiTrypsin] <i>EIA Intestinal Markers</i>	5,84 mg/g	(RV: ≤30,00 mg/g)	●	

Guidance for the Result Interpretation

Basic Study

- **Colour** Marrón
- **Fecal Occult Blood (FOB)** No se detecta

The presence of occult blood in the stool is an indicator of abnormal bleeding in the gastrointestinal tract.

Phylum distribution

- **Phylum Firmicutes** 8,56 *log g.f.u./g* (8,50 / 11,00 *log g.f.u./g*)

The Phylum Firmicutes is very abundant in the gastrointestinal tract. It contributes most of the bacterial diversity, since its microorganisms are part of the three types of microbiota (muconutritive, regulating and proteolytic).

- **Phylum Bacteroidetes** 8,32 *log g.f.u./g* (8,00 / 11,00 *log g.f.u./g*)

Phylum Bacteroidetes is formed by anaerobic bacteria with regulatory functions. They are related to the protection of the muconutritive microbiota and are indicators of the type of diet (carnivora or vegetarian).

- **Phylum Actinobacteria** 6,78 *log g.f.u./g* (6,50 / 9,00 *log g.f.u./g*)

Saccharolytic germs present in different mucous membranes. pH regulating and protective functions against external flora.

- **Phylum Proteobacteria** 6,81 *log g.f.u./g* (3,00 / 7,00 *log g.f.u./g*)

Group enterobacteria fermenters and other germs. aerobic bacteria / facultative anaerobes.

- ▼ **Phylum Verrucomicrobia** 3,89 *log g.f.u./g* (5,50 / 9,00 *log g.f.u./g*)

Belong to the stable intestinal flora must, both in the gut and in the mouth, vagina. Produce lactic acid and short chain fatty acids (Omega), bactericides, and acidification of the medium. In growth hiben putrefaction bacteria (proteolytic). Reduce the formation of carcinogenic substances.

Intestinal Disbiosis

Functional distribution

- **Muconutritive microbiota [MMuco]** 7,4 log g.f.u./g (7,0 / 9,0 log g.f.u./g)

The muconutritive microbiota is responsible for maintaining the mucus that is part of the intestinal mucosa. These bacteria help digestion, absorption and synthesis of many nutrients, such as butyric acid.

- **Regulatory microbiota [MReg]** 6,8 log g.f.u./g (6,5 / 8,5 log g.f.u./g)

The regulatory microbiota has two functions:

- The immunological function that regulates the performance of the immune system. They prevent most potentially antigenic substances from triggering a specific immune reaction.
- The protective function creates a physical and immunological barrier. They maintain physiologically acidic pH in the intestinal lumen and preserve the integrity of intestinal permeability.

- **Proteolytic microbiota [MProt]** 8,6 log g.f.u./g (6,5 / 9,0 log g.f.u./g)

The proteolytic microbiota behaves as facultative pathogens. They alkalize the intestinal environment and generate potentially toxic substances, such as amines (protein hydrolysis).

Intestinal Disbiosis

Index

- Firmicutes / Bacteroidetes [Firm/
Bacter]** 0,24 Ratio (-0,10 / 0,30Ratio)

The Firmicutes / Bacteroidetes ratio reflects the majority distribution of the flora and decreases with age due to a decrease in the biodiversity of the intestinal flora.

Calculation: $\log \text{ Ph Firmicutes} - \log \text{ Ph Bacteroidetes}$

- Bacteroides / Prevotella [Bacte/
Prevot]** 3,70 Ratio (0,20 / 3,10Ratio)

The ratio Bacteroides / Prevotella (Bacteroidetes phylum bacteria) is closely related to diet, increases in carnivorous diets and decreases in vegetarian diets.

Calculation: $\log \text{ Bacteroides} - \log \text{ Prevotella}$

- Enterobacterias / Enterococcus
[ETB/ Etc]** 0,92 Ratio (-1,00 / 2,00Ratio)

The Enterobacteria / Enterococcus ratio reflects the balance between the proteolytic and regulatory microbiota together with the main functionality of Escherichia coli.

- Clostridium Coccoides/C perfringens
[CCoc/ CPerf]** 4,40 Ratio (1,50 / 5,50Ratio)

The Clostridium coccoides / Clostridium perfringens ratio reflects the balance between beneficial and pathogenic bacteria within the proteolytic microbiota group.

Intestinal Disbiosis

Phylum Firmicutes

- ▼ **Faecalibacterium prausnitzii [Faeca praus]** **5,8** *log g.f.u./g* (6,5 / 8,0 *log g.f.u./g*)

The *Faecalibacterium prausnitzii* is one of the components of the muconutritive microbiota. It is a bacterium producing short chain fatty acids (SCFA), mainly butyric acid (energy source for the intestinal mucosa and modulator of the microbiota). It is distributed throughout the gastrointestinal tract and is considered an indicator of intestinal health.

- **Roseburia spp / Eubacterium [Rose/Eu]]** **7,4** *log g.f.u./g* (6,5 / 8,5 *log g.f.u./g*)

Roseburia intestinalis is one of the components of the muconutritive microbiota. It is specifically responsible for stabilizing the mucosa and repairing its permeability.

The *Eubacterium* species are one of the components of the regulatory microbiota. They are associated with *Roseburia* species, helping in their growth and protecting the intestinal mucosa.

The bacteria that are detected are *Eubacterium rectale*, *E. oxidoreducens*, *Roseburia intestinalis*, *R. cecicola*, *R. faecis*, *R. hominis*.

- ▼ **Lactobacillus spp [Lactob]** **3,0** *log g.f.u./g* (4,5 / 7,0 *log g.f.u./g*)

The *Lactobacillus* species are part of the stable and obligate regulatory microbiota. They are producers of lactic acid (precursor of the SCFA, of short chain fatty acids) and bactericides. They are also responsible for acidifying the medium in such a way that they inhibit the growth of proteolytic bacteria.

The bacteria that are detected are *Lactobacillus acidophilus*, *L. amylovorus*, *L. delbrueckii* subsp. *bulgaricus*, *L. delbrueckii* subsp. *delbrueckii*, *L. delbrueckii* subsp. *lactis*, *L. amylolyticus*, *L. acetotolerans*, *L. crispatus*, *L. amylophilus*, *L. johnsonii*, *L. gasseri*, *L. fermentum*, *L. pontis*, *L. reuteri*, *L. mucosae*, *L. vaginalis*, *L. panis*, *L. oris*, *L. pentosus*, *L. plantarum*, *L. collinoides*, *L. alimentarius*, *L. farciminis*, *L. brevis*, *L. buchneri*, *L. kefir*, *L. fructivorans*, *L. mali*, *L. animalis*, *L. murinus*, *L. ruminis*, *L. agilis*, *L. salivarius* subsp. *salicin*, *L. aviarius* subsp. *aviarius*, *L. sharpeae*, *L. manihotivorans*, *L. rhamnosus*, *L. casei* subsp. *casei*, *L. zaeae*, *L. paracasei* subsp. *paracasei*, *L. paracasei* subsp. *tolerans*, *L. coryniformis* subsp. *coryniformis*, *L. bifermentans*, *L. perolens*, *L. sakei* subsp. *sakei*, *L. casei* subsp. *fusiformis*, *Pediococcus pentosaceus*, *P. parvulus*, *P. acidilactici*, *P. dextrinicus*, *Weissella halotolerans*, *W. confusus*, *W. Paramesenteroides*, *W. hellenica*, *W. viridescens*, *W. kandleri*, *W. minor*, *Leuconostoc Lactis*

Intestinal Disbiosis

Phylum Firmicutes

● **Enterococos spp** 6,7 log g.f.u./g (6,0 / 8,5 log g.f.u./g)

The Enterococcus species is one of the components of the regulatory microbiota. They are considered opportunistic pathogens and they are also very resistant to bile acids and antibiotics in general. Acidify the intestinal tract providing numerous antibacterial substances, both bactericidal and bacteriostatic.

The bacteria that are detected are Enterococcus faecalis, E. faecium, E. asini, E. saccharolyticus, E. casseliflavus, E. gallinarum, E. dispar, E. flavescens, E. hirae, E. durans, E. pseudoavium, E. raffinosus, E. avium, E. malodoratus, E. mundtii, E. azikeevi, E. canis, E. gilvus, E. haemoperoxidus, E. hermanniensis, E. moraviensis, E. pallens, E. phoeniculicola, E. villorum, E. rottae

▼ **Staphylococcus spp [Staph]** 1,9 log g.f.u./g (2,5 / 5,0 log g.f.u./g)

Staphylococcus species are part of the regulatory microbiota. They are present in the intestinal mucosa and in the skin of humans. They have several virulence factors such as teichoic acids and peptidoglycans.

The bacteria that are detected are Staphylococcus aureus, S. caprae, S. epidermidis, S. haemolyticus, S. saprophyticus

● **Bacillus spp [Bacil]** 2,4 log g.f.u./g (≤4,0 log g.f.u./g)

The Bacillus species are part of the stable but transient regulatory microbiota. Its presence is an indicator of a greater microbiological biodiversity in the intestine.

The bacteria that are detected are: Bacillus cereus, B. pumilus, B. licheniformis, B. clausii, B. subtilis, B. megaterium, B. mediterraneensis, B. thuringiensis, B. coagulans, B. natto, B. stearothermophilus, B. alkalophilus, B. aquaemaris, B. brevis, B. firmus.

● **Veillonella spp [Veillon]** 6,3 log g.f.u./g (4,5 / 7,0 log g.f.u./g)

The Veillonella species are part of the regulatory microbiota. They are related to problems of sensitivity and / or food intolerance. In some cases it is related to oral pathologies since it is a habitual resident of the oral microbiota.

The bacteria that are detected are Veillonella alcalescens, V. parvula, V. criceti, V. ratti, V. atypica, V. caviae, V. denticariosi, V. dispar, V. infantium, V. magna, V. montpellierensis, Veillonella. rodentium, V. rogosae, Veillonella seminalis, V. tobetsuensis.

Intestinal Disbiosis

Phylum Firmicutes

- **Clostridium coccoides group [Clostr coccoides]** 8,5 log g.f.u./g (7,0 / 9,0 log g.f.u./g)

The Clostridios coccoides group is part of the proteolytic microbiota and are common residents. They belong to the active microbiota, helping the intestinal cells to modulate the physiological, metabolic and immune processes.

The bacteria detected are Clostridium coccoides, Cl. Proteoclasticum, Cl. Aminophilum, Cl. Symbiosum, Cl. Sphenoides, Cl. Celerecrescens, Cl. Aerotolerans, Cl. Xylanolyticum, Cl. Clostridiform, Cl. Fusiformis, Cl. Nexile, Cl. Oroticum, Cl. populeti, Cl. aminovalericum, Cl. indolis, C. herbivorans, Cl. polysaccharolyticum, Eubacterium xylanophilum, E. ruminantium, E. saburreum, E. fissicatena, E. hadrum, E. rectale, E. ramulus, E. contortum, E. elegns, E. hallii, E. formicigenerans, E. cellulosolvans, Ruminococcus productus, R. obeum, R. schinkii, R. hydrogenotrophicus, R. hansenii, R. torques, R. lactaris, R. gnavus, Butyrivibrio fibrisolvans, B. crossotus, B. fibrisolvans, Desulfotomaculum guttoideum, Roseburia cecicola, Pseudobutyribrio ruminis, Lachnospira multipara, Lachnospira pectinoschiza, Acetitomaculum ruminis, Catonella morbi

- **Clostridium perfringens group [Clostr perfr]** 4,1 log g.f.u./g ($\leq 5,5$ log g.f.u./g)

The Clostridios perfringens group is part of the proteolytic microbiota and are transient residents. It is composed of pathogens widely distributed in the environment. They are spore formers and can produce the release of thermolabile enterotoxins.

The bacteria that are detected are Clostridium perfringens, Cl. Homopropionicum, Cl. Cadaveris, Cl. Putrificum, Cl. Botulinum, Cl. Difficile, Cl. Tetani, Cl. Septicum, Cl. Leptum, Cl. Novyi, Cl. Sporogenes, Cl. tyrobutyricum, Cl. kluverii, Cl. ljunghdahlia, Cl. scatologenes, Cl. acetireducens, Cl. subterminale, Cl. estertheticum, Cl. argentinense, Cl. sardiniensis, Cl. paraputrificum, Cl. longisporum, Cl. septicum, Cl. cellulovorans, Cl. Barati, Cl. Absonum, Cl. Chauvoei, Cl. Carnis, Cl. Butyricum, Cl. Beijerinckii, Cl. Kainantoi, Cl. Corinoforum, Cl. Puniceum, Cl. Histolyticum, Cl. Proteolyticum, Cl. Limosum, Cl. paraputrificum, Eubacterium budayi E. nitritogenes, E. moniliforme, E. multiforme

- **Ruminococcus spp [Rumin spp]** 6,5 log g.f.u./g (5,5 / 7,0 log g.f.u./g)

Intestinal Disbiosis

Phylum Bacteroidetes

● **Bacteroides spp** 8,3 log g.f.u./g (7,0 / 8,5 log g.f.u./g)

Bacteroides species are one of the most abundant components of the regulatory microbiota. It has a low metabolic activity but potentiates the resistance against the pathogenic flora.

The bacteria that are detected are Bacteroides fragilis, B. stercoris, B. vulgatus, B. eggerthii, B. acidofaciens, B. caccae, B. ovatus, B. uniformis, B. thetaiotaomicron, B. distasonis, B. merdae, B. forsythus, Prevotella tanneriae, P. bryantii, P. ruminicola, P. heparinolytica, P. zooglyphiformans, P. brevis, P. loescheii, P. buccae, P. oralis, P. enoeca, P. melaninogenica, P. veroralis, P. intermedia, P. albensis, P. nigrescens, P. corporis, P. disiens, P. bivia, P. pallens, P. denticola, Porphyromonas canoris, P. gingivalis, P. asaccharolytica, P. levii, P. cangingivalis, P. endodontalis, P. macacae, P. circumdentaria, P. cationiae

▼ **Prevotella spp** 4,6 log g.f.u./g (5,0 / 8,5 log g.f.u./g)

The Prevotella species are part of the regulatory microbiota and are found in the mucous membranes of the upper tract. They are sensitive to bile and participate in the resistance against the pathogenic microbiota.

The bacteria that are detected are Prevotella corporis, P. denticola, P. melaninogenica, P. veroralis, P. buccalis, P. intermedia, P. melaninogenica, P. oralis, P. loescheii, P. oris, P. ruminicola.

Phylum Actinobacteria

● **Bifidobacterium spp [Bifido]** 5,9 log g.f.u./g (5,0 / 7,0 log g.f.u./g)

The Bifidobacterium species are major components of the regulatory microbiota and are distributed throughout the entire intestine. Its levels reduce over the years. They are associated with a lower epidemiological incidence of allergies and can even prevent the growth of tumors.

The bacteria that are detected are Bifidobacterium longum, B. minimum, B. angulatum, B. catenulatum, B. pseudocatenulatum, B. dentium, B. ruminantium, B. thermophilum, B. subtile, B. bifidum, B. boum, B. lactis, B. animalis, B. choerinum, B. gallicum, B. pseudolongum subsp. globosum, B. pseudolongum subsp. pseudolongum, B. magnum, B. infantis, B. indicum, B. gallinarum, B. pullorum, B. saeculare, B. suis

Intestinal Disbiosis

Phylum Proteobacteria

- **Escherichia coli [E coli]** 4,7 log g.f.u./g (4,0 / 6,5 log g.f.u./g)

Escherichia coli represents less than 0.1% of the intestinal microbiota and its functions can be as a regulatory or proteolytic microbiota.

- **Enterobacteriaceae, excluded E. coli [ETB]** 2,3 log g.f.u./g (≤2,5 log g.f.u./g)

Enterobacteria is one of the main representatives of the proteolytic microbiota. They are usually transit bacteria that come from food in general.

The bacteria that are detected are different species of Alishewanella, Alterococcus, Aquamonas, Aranicola, Arsenophonus, Azotivirga, Blochmannia, Brenneria, Buchnera, Budvicia, Buttiauxella, Cedecea, Citrobacter, Dickeya, Edwardsiella, Enterobacter, Erwinia, Escherichia, Ewingella, Grimontella, Hafnia, Klebsiella, Kluyvera, Leclercia, Leminorella, Moellerella, Morganela, Obesumbacterium, Pantoea, Paracolobactrum, Pectobacterium, Phlomobacter, Photorhabdus, Plesiomonas, Pragia, Proteus, Providence, Rahnella, Raoultella, Salmonella, Samsonia, Serratia, Shigella, Sodalis, Tatumella, Trabulsiella, Wigglesworthia, Xenorhabdus, Yersinia, Yokenella.

- **Pseudomonas spp** <1,0 log g.f.u./g (≤4,0 log g.f.u./g)

Pseudomonas species are part of the proteolytic microbiota and are considered opportunistic pathogens. Normally, they are transit bacteria that come from the intake.

The bacteria that are detected are Pseudomonas aeruginosa, P. putida

- **Campylobacter spp** <1,0 log g.f.u./g (≤3,5 log g.f.u./g)

Campylobacter species are part of the proteolytic microbiota and are looked for as an indicator of intestinal infection (causes acute diarrhea).

The bacteria that are detected are Campylobacter jejuni subsp. jejuni, C. gracilis, C. sputorum, C. hyointestinalis, C. fetus, C. showae, C. rectus, C. curvus, C. lanienae, C. coli, C. lari, C. helveticus, C. concisus, C. jejuni subsp. doylei, C. hominis, C. upsaliensis, C. faecalis, C. mucosalis

- **Helicobacter spp** 3,0 log g.f.u./g (≤4,0 log g.f.u./g)

The Helicobacter species are part of the proteolytic microbiota. It is sought as an indicator of infection in the stomach.

The bacteria that are detected are Helicobacter pylori, H. pullorum, H. pametensis, H. trogontum, H. bizzozeronii, H. felis, H. salomonis, H. heilmannii, H. hepaticus, H. rodentium, H. mesocricetus, H. rodentium, H. suis, H. mustelae, H. suncus, H. muridarum, H. bile, H. cholecystus, H. cinaedi, H. canis, Flexispira rappini, Wollinella succinogenes

Intestinal Disbiosis

Phylum Verrucomicrobia

- ▼ Akkermansia muciniphila [Akker mucu] 3,6 log g.f.u./g (5,0 / 8,5 log g.f.u./g)

The Akkermansia muciniphila is the main representative of the muconutritive microbiota. It is responsible for the formation of mucosa to correct intestinal permeability and help in the absorption of nutrients.

Phylum Fusobacteria

- Fusobacterium nucleatum [Fusob nucle] 3,7 log g.f.u./g (≤4,5 log g.f.u./g)

Fusobacterium nucleatum is a bacterium that is part of the proteolytic microbiota and is related to cancer pathologies. In women, their presence may indicate problems during pregnancy.

Phylum Ascomycota

- Candida spp [Cand spp] 3,6 log g.f.u./g (≤4,5 log g.f.u./g)

Candida species are part of the intestinal mycological microbiota and can lead to intestinal and / or vaginal candidiasis. It is usually found in low levels helping to maintain intestinal balance, to eliminate remains of poorly absorbed carbohydrates, to absorb heavy metals to prevent them from entering our blood ...

Candida albicans, C. auris, C. glabrata, C. kefyr, C. krusei, C. parapsilosis, C. tropicalis, C. utilis are detected

- ▲ Candida albicans [Cand albic] 2,6 log g.f.u./g (≤2,5 log g.f.u./g)
- Saccharomyces cerevisiae [Sac cerev] 2,6 log g.f.u./g (2,0 / 5,0 log g.f.u./g)

The Saccharomyces cerevisiae is part of the mycological microbiota of the intestine. It mostly comes from diet and in some cases the intake of probiotics. It is used as an indicator of excess intake of probiotics.

Intestinal Disbiosis

Archaeas

● Archaea domain [Arch]	7,1 log g.f.u./g	(4,5 / 7,5 log g.f.u./g)
● Methanobrevibacter smithii [M smith]	6,2 log g.f.u./g	(4,5 / 7,0 log g.f.u./g)
● Methanosphaera stadtmanae [M stadt]	2,4 log g.f.u./g	(≤4,0 log g.f.u./g)
▼ Methanogens	2,7 log g.f.u./g	(3,0 / 5,5 log g.f.u./g)

Intestinal Disbiosis

Parasites



Interpretation of results:

- ABSENCE: NEGATIVE result, DNA is not detected.
- NON-SIGNIFICANT INDEX: unfeasible DNA is detected.
- PARASITES IN TRANSIT: low levels of DNA are detected.
- PARASITOSIS: high levels of DNA are detected.

There is little correlation between optical microscopy and DNA detection by Molecular Biology techniques.



Blastocystis hominis

1,23 *Index*

Índice no significativo

Blastocystis hominis is a parasite that initially can be asymptomatic. Causes diarrhea, nausea, vomiting and / or stomach spasms. It has been linked to irritable bowel syndrome and atritis.



Diaentamoeba fragilis

1,01 *Index*

AUSENCIA

Dientamoeba fragilis is a parasite that can be asymptomatic or cause gastrointestinal pain and chronic diarrhea with bloody stools, mucus and pus at times. It can cause eosinophilia.



Entamoeba histolytica

1,01 *Index*

AUSENCIA

Entamoeba histolytica is a parasite that causes invasive amebiasis. It affects the liver (excess of collagenase activity), the immune system (excess proteases) and intestinal cells (osmotic shock). Normally, it causes liver abscesses.



Endolimax nana

1,01 *Index*

AUSENCIA

Endolimax nana is an exclusive commensal parasite of the human intestine. Sometimes it can cause chronic diarrhea or enterocolitis or hives.



Giardia lamblia

1,46 *Index*

Not significant index

Giardia lamblia is a parasite that is fixed in the intestinal epithelium altering the microvilli, causing malabsorption problems. It is usually asymptomatic and very common.

Intestinal Disbiosis

Parasites

- **Cryptosporidium parvum** 1,01 *Index*
AUSENCIA
- Cryptosporidium parvum a parasite that gives rise to acute infection of short duration usually in immunosuppressed patients. It can come from untreated water.
- ABSENCE: Index 1.00 - 1.01
 - NON-SIGNIFICANT INDEX: Index 1.01 - 1.15
 - PARASITES IN TRANSIT: Index 1.15 - 1.30
 - PARASITOSIS: Index Higher than 1.30
- **Cyclospora cayetanensis** 1,01 *Index*
AUSENCIA
- Cyclospora cayetanensis is a parasite that causes acute diarrhea and weight loss.
- **Isospora belli** 1,01 *Index*
AUSENCIA
- Isospora belli is a parasite that causes diarrhea, malabsorption, eosinophilia and weight loss.
- **Ascaris lumbricoides** 1,01 *Index*
AUSENCIA
- Ascaris lumbricoides is a parasitic nematode of the small intestine of man that causes abdominal pain, malabsorption, intestinal obstruction, biliary colic ...
- **Enterobius vermicularis** 1,01 *Index*
AUSENCIA
- Enterobius vermicularis is a parasitic nematode that causes pruritus due to perianal migration; and in children: insomnia, nervousness, irritability, nightmares and seizures.
- **Strongyloides stercoralis** 1,01 *Index*
AUSENCIA
- Strongyloides stercoralis is a parasitic nematode that can cause intestinal symptoms (diarrhea, anorexia, nausea, vomiting, malabsorption ...), cutaneous (purple angioderma, erythroderma ...) or pulmonary.
- **Trichuris trichiura** 1,01 *Index*
AUSENCIA
- Trichuris trichiura is a parasitic nematode that causes abdominal pain, diarrhea, colitis, rectal prolapse and / or eosinophilia.

Intestinal Disbiosis

Short Chain Fatty Acid (SCFA)

SCFA Total 1.761,72 $\mu\text{mol/g}$ ($\geq 740,00 \mu\text{mol/g sample}$)
sample

Fatty acids derived from bacterial fermentation of carbohydrates, especially of non-digestible fibers.

They are beneficial for supporting colon epithelial cells of the colon and improve bacterial colonization and decreasing absorption of ammonia.

Levels may be increased in situations:

Increasing dietary fiber

By regulating the transit time

Bacterial overgrowth in the small intestine

Increasing the intake of Probiotics and Prebiotics. Lactobacilli and bifidobacteria produce lactic acid, precursor of SCFA by fermentation.

Acetic / Propionic / Butyric:: 60/25/20 ratio is recommended.

Diet and flora influence the relationship.

SCFA Beneficial 1.650,96 $\mu\text{mol/g}$ (700,00 / 2.000,00 $\mu\text{mol/g}$)
sample sample)
93,7 %

The beneficial SCFA are acetic, propionic and butyric acid, the latter being the most important. Its proportions must be 60/25/20 in a balanced situation.

SCFA Putrefactives 110,76 $\mu\text{mol/g}$ (40,00 / 100,00 $\mu\text{mol/g}$)
sample sample)
6,3 %

The putrefactive SCFA are fatty acids that come from the bacterial fermentation of undigested proteins. Specifically, they are valeric, iso-valeric, caproic, iso-caproic and iso-butyric acids.

Intestinal Disbiosis

SCFA Beneficial

● SCFA Beneficial [SCFA Bene]	1.650,96 $\mu\text{mol/g}$ sample	(700,00 / 2.000,00 $\mu\text{mol/g}$ sample)
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fatty acids from bacterial fermentation of carbohydrates, especially of the nondigestible fibers, and lactic acid fermentation.

They are beneficial for colon support colon epithelial cells and enhance bacterial colonization and reduce the absorption of ammonia. Increase mucin production, regulating the permeability.

Levels may be increased in situations:

- Increasing dietary fiber
- Regulating transit time
- bacterial overgrowth in the small intestine

Increasing the intake of probiotics and prebiotics. Lactobacilli and bifidobacteria generate lactic acid, the precursor of SCFA by fermentation.

Germes involved: Flora muconutritiva (F. prausnitzii, Akkermansia m, Roseburia.), Prevotella, Lactobacillus and Bifidobacterium.

Acetic / Propionic / Butyric: 60/25/20 ratio is recommended.

Diet, flora and transport conditions of the sample influence the relationship.

● Butyric Acid % [Butyric Ac]	8,28 %	(2,50 / 30,00%)
● Acetic Acid % [Acetic Ac]	57,14 %	(51,00 / 76,00%)
● Propionic Acid % [Propion Ac]	28,29 %	(12,00 / 30,00%)

Intestinal Disbiosis

SCFA Putrefactive







 SCFA Putrefactive [SCFA Putr]	110,76 $\mu\text{mol/g}$ <i>sample</i>	<i>(40,00 / 100,00</i> $\mu\text{mol/g}$ <i>sample)</i>
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Fatty acids from bacterial fermentation of undigested proteins.

An increase suggests hipoclohidria, protein malabsorption, bacterial overgrowth (SIBO), gastro intestinal diseases and / or rapid transit.

Germes involved: Enterobacteriaceae, Firmicutes (except Roseburia and F. praus.)

The relationship Bacteroides <Prevotella reduces spoilage SCFA. Betaine, the complex carbohydrates and digestive enzymes SCFA reduce spoilage.

 SCFA protein breakdown [SCFA Prot.]	106,98 $\mu\text{mol/g}$ <i>sample</i>	<i>(60,00 / 150,00</i> $\mu\text{mol/g}$ <i>sample)</i>
 Valeric Acid %	1,76 %	<i>(1,00 / 7,90%)</i>
 iso-Valeric Acid %	2,30 %	<i>(1,30 / 7,20%)</i>
 Caproic Acid %	0,19 %	<i>(0,10 / 7,00%)</i>
 iso-Caproic Acid %	0,02 %	<i>(\leq2,60 %)</i>
 iso-Butyric Acid %	2,01 %	<i>(1,20 / 10,00%)</i>

Microbiota and Enzymes

 Alpha glucosidase [α-Glucosi]	5,87 IU / 100 mg <i>Protein</i>	<i>(3,00 / 12,00</i> IU / 100 mg <i>Protein)</i>
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Alpha-glucosidase is an enzyme that is synthesized mostly by most bacterial species .. Its main function is the hydrolysis of glycosides to aglycones and other sugary components, especially alpha bonds.

 Beta-glucosidase [β-Glucosi]	1,57 IU / 100 mg <i>Protein</i>	<i>(1,50 / 7,00</i> IU / 100 mg <i>Protein)</i>
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Beta-glucosidase is an enzyme that is synthesized mostly by the species of Bacteroides, Clostridium and / or Enterococcus faecalis. Its main function is the hydrolysis of glycosides to aglycones and other sugary components.








 Beta glucuronidase [β-Glucuro]	0,39 IU / 100 mg <i>Protein</i>	<i>(0,60 / 3,50</i> IU / 100 mg <i>Protein)</i>
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The glucuronide acid is a substance that binds to different metabolites in the liver and allows the elimination of these through the digestive tract (hepatic detoxification phase II).

Beta-glucuronidase is an enzyme that is found in the digestive tract in high concentrations and is produced by some of the intestinal bacteria. Its function is to separate the metabolites of glucuronide acid to make them resorbable.

Intestinal Disbiosis

Intestinal Biomarker

- | | | | |
|--|--|---------------------------|--------------------------------|
|  | pH | 6,5 <i>or. pH</i> | <i>(6,0 / 7,2or. pH)</i> |
| The pH reflects the overall metabolic activity of the colon, the microbial composition of the intestine and the dietary habit. It is not related to gastric acidity, since bile salts neutralize it. | | | |
|  | Calprotectin | <i><1,0 mg/Kg</i> | <i>(≤50,00 mg/Kg)</i> |
| Calprotectin is a non-specific and stable marker of intestinal inflammation. | | | |
|  | slgA Secretory [IgAs] | 2.297 <i>µg/mL</i> | <i>(510 / 2.040µg/mL)</i> |
| Secretory IgA is a marker of the immune response of the gastrointestinal system, whether due to inflammatory, infectious or intestinal permeability problems. | | | |
|  | Eosinophil Protein X [EPX] | <i>26 ng/mL</i> | <i>(≤600 ng/mL)</i> |
| EPX or X protein of eosinophils is a marker of parasitic infection and / or allergic reaction. | | | |
|  | Helicobacter Pylori. Antigen | <i>4,4 ng/mL</i> | <i>(≤10,0 ng/mL)</i> |
| No significativo | | | |
|  | Pancreatic elastase 1 [Elast] | <i>613 µg/g stool</i> | <i>(200 / 1.200µg/g stool)</i> |
| Elastase is a marker of pancreatic exocrine or secretory function. The causes of a pancreatic insufficiency can be prolonged stress and insulin resistance. | | | |
|  | Alpha-1 antitrypsin [AntiTrypsin] | <i>5,84 mg/g</i> | <i>(≤30,00 mg/g)</i> |
| Alpha 1 anti-trypsin is a protein of hepatic synthesis. It is an inhibitor of the proteolysis of polymorphonuclear leukocytes in inflammatory processes. It is also a marker of intercontinental permeability. | | | |

It is advisable that the preparation of individualized treatment is carried out by a professional, who must take into account the analytical results obtained in this test and associate the individual treatment according to each patient's pathology.

Intestinal Disbiosis

Test Report

Report XXXXXXXXX2



Laboratory Director: Jose M^a Mestres. Pharmacist Specialist Clinical Analysis. COFB 12.195

Summary Deviations

34043611 GIVAN CAICEDO, ALDANA; Date: 5/12/19;

Intestinal Disbiosis

▼ Faecalibacterium prausnitzii [Faeca praus]	5,8 log g.f.u./g	(6,5/8,0)
▲ Bacteroides / Prevotella [Bacte/ Prevot]	3,70 Ratio	(0,20/3,10)
▼ Lactobacillus spp [Lactob]	3,0 log g.f.u./g	(4,5/7,0)
▼ - Akkermansia muciniphila	3,6 log g.f.u./g	(5,0/8,5)
▼ Staphylococcus spp [Staph]	1,9 log g.f.u./g	(2,5/5,0)
▼ - Lactobacillus spp	3,0 log g.f.u./g	(4,5/7,0)
▼ Methanogens	2,7 log g.f.u./g	(3,0/5,5)
▼ Prevotella spp	4,6 log g.f.u./g	(5,0/8,5)
▼ Prevotella spp	2.297 µg/mL	(510/2.040)
▲ sIgA Secretory [IgAs]	3,6 log g.f.u./g	(5,0/8,5)
▼ Akkermansia muciniphila [Akker muc]	2,6 log g.f.u./g	(<2,5)
▲ Candida albicans [Cand albic]	3,89 log g.f.u./g	(5,50/9,00)
▼ Phylum Verrucomicrobia	0,39 IU / 100 mg Protein	(0,60/3,50)
▼ Beta glucuronidase [β-Glucuro]	110,76 µmol/g sample	(40,00/100,00)
▼ Beta glucuronidase [β-Glucuro]	110,76 µmol/g sample	(40,00/100,00)
▲ SCFA Putrefactive [SCFA Putr]	6,3 %	
▲ SCFA Putrefactives		