

Accession Number: Reference Number:

Sample Report Patient: Sex: Female Age: 60

Date of Birth:

Date Collected: 6/23/09 6/24/09 Date Received: Report Date: 7/15/09

Telephone: (425) 271-8689 Fax: (425) 271-8674

Reprinted: Comment:

# 2100 Gastrointestinal Function Profile

Methodology: DNA Analysis, GC/MS, Microscopic, Colorimetric, Automated Chemistry, ELISA

Consistency = Not Given



#### (E+007) E+007 **Predominant Bacteria** Obligate anaerobes 1.6 Bacteroides sp. 3.6 >= 1.3 1.5 6.2 Clostridia sp. 9.8 1.6 6.2 Prevotella sp. 14.7 1.6 7.4 Fusobacteria sp. 13.7 1.6 5.8 Streptomyces sp. 5.6 62 17 Mycoplasma sp. 16.6 **Facultative anaerobes** Lactobacillus sp. 6.7 2.3 Bifidobacter sp. 9.6 **Obligate aerobes** Escherichia coli 16.9 Opportunistic Bacteria

# **Units and Reference Ranges**

Organisms are detected by DNA analysis. One colony forming unit (CFU) is equivalent to one bacterium. Each genome detected represents one cell, or one CFU. Results are expressed in scientific notation, so an organism reported as 2.5 E7 CFU/gram is read as 25 million colony forming units per gram of feces. The cutoff for significance of Opportunistic Bacteria has been set at 1.0E+ 005 (100,000). These are levels above which clinically significant growth may be present. Rather than reporting semi-quantitative +1 to +4 levels, the new methodology provides full quantitative analysis.

Predominant Bacteria play major roles in health. They provide colonization resistance against potentially pathogenic organisms, aid in digestion and absorption, produce vitamins and SCFA's, and stimulate the GI immune system. DNA probes allow detection of multiple species (sp.) within a genus, so the genera that are reported cover many species.

Opportunistic Bacteria may cause symptoms and be associated with disease. They can affect digestion and absorption, nutrient production, pH and immune state. Antibiotic

sensitivity tests will be performed on all opportunistic bacteria found, although clinical history is usually considered to determine treatment since the organisms are not generally considered to be pathogens.

3.8E+008 H <=1.0E+005 Yersinia sp.



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#### 2100 Gastrointestinal Function Profile 95% Reference Pathogenic Bacteria Range <=1.0E+005 Helicobacter pylori 4.5E+005 H <=1.0E+005 Clostridium difficile < 0.01 E.H.E. coli < 0.01 <=1.0E+005 Campylobacter sp. < 0.01 <=1.0E+005 Yeast/Fungi Candida sp. +1 => 100 pg DNA/g specimen Neg

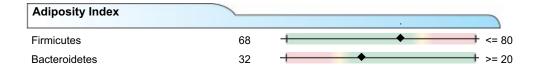
# **Parasites**

Parasite present; taxonomy unavailable.

**Positive** 

Neg

A taxonomy unavailable finding likely indicates an ingested protozoan and not a human parasite. It does not indicate treatment unless patient symptoms and other inflammatory markers are consistent with parasite infection.



# Drug Resistance Genes aacA, aphD Pos gyrB, ParE Neg mecA Neg PBP1a, 2B Neg vanA, B, and C Neg

#### Yeast/Fungi

Yeast overgrowth has been linked to many chronic conditions, in part because of antigenic responses in some patients to even low rates of yeast growth. Potential symptoms include diarrhea, headache, bloating, atopic dermatitis and fatigue. Positives are reported as +1, +2, +3 or +4 indicating >100, >1000, >10000 or >100000 pg DNA/g.

## Parasites

Parasite infections are a major cause of non-viral diarrhea. Symptoms may include constipation, gas, bloating, increased allergy response, colitis, nausea and distention.

The **Adiposity Index** is derived by using DNA probes that detect multiple genera of the phyla Firmicutes and Bacteroidetes. Abnormalities of these phyla may be associated with increased caloric extraction from food.



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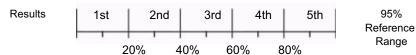
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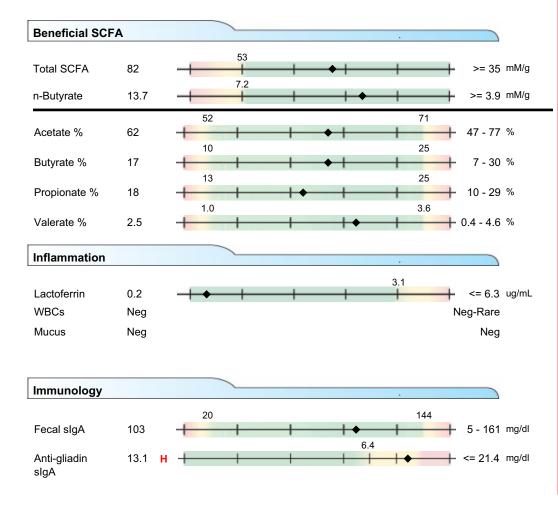
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# **2100 Gastrointestinal Function Profile**

Methodology: DNA Analysis, GC/MS, Microscopic, Colorimetric, Automated Chemistry, ELISA

# Percentile Ranking by Quintile





#### **Beneficial SCFA**

Short chain fatty acids (SCFA) are produced by bacterial fermentation of dietary polysaccharides and fiber. The product, N-butyrate, is taken up and used to sustain the normal activity of colonic epithielial cells. Butyrate has been shown to lower the risk of colitis and colorectal cancer. A healthy balance of GI microbes depends on production of SCFA by one specie to allow the normal growth of another one in a complex cross-feeding network.

# Inflammation

Lactoferrin, an iron-binding glycoprotein, is released in IBD but not in non-inflammatory IBS. High levels are found in Crohn's, UC or infection. WBC's are elevated in general inflammation/infection. Mucus is often visualized in acute GI inflammation.

## Immunology

High fecal sIgA indicates immune system reactions to the presence of antigens from bacteria, yeast or other microbes. Low sIgA can result from stress or malnutrition. Anti-gliadin sIgA is a screening marker for gluten sensitivity.



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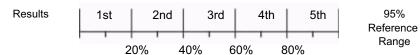
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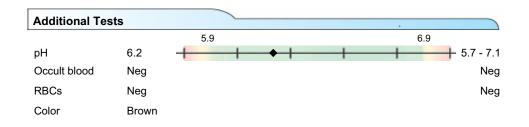
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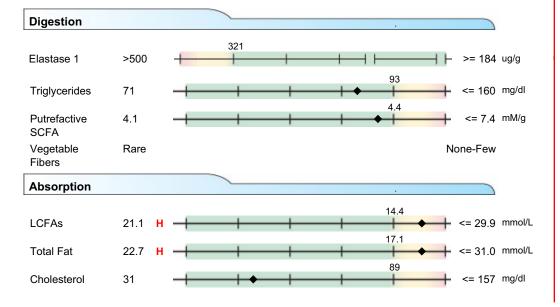
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# **Percentile Ranking by Quintile**







### Additional Tests

**pH** is influenced by numerous factors, but it is strongly related to the bacterial release of pH-lowering organic acids and pH-raising ammonia. Positive **occult blood** can signify GI tract bleeding, as can elevated **RBCs. Color** (other than brown) abnormalities can be due to upper GI bleeding, or bile duct blockage, steatorrhea or antibiotic use.

## Digestion

Pancreatic elastase 1 levels below the reference limits are strongly correlated with pancreatic insufficiency. High triglycerides signify fat maldigestion. Putrefactive SCFA are a result of bacterial fermentation of undigested protein. High numbers of vegetable fibers indicate maldigestion.

## Absorption

High **LCFA** indicates fat malabsorption due to pancreatic or biliary insufficiency, or acute bacterial infection that produces intestinal cell destruction. High total fat usually signals malabsorption, as does elevated fecal cholesterol.

UC\*\* = Unable to Calculate

These test results are not for the diagnosis of disease. They are intended to provide nutritional guidelines to qualified healthcare professionals with full knowledge of patient history and concerns to assist in their design of an appropriate healthcare program.