GI360™ Select; stool

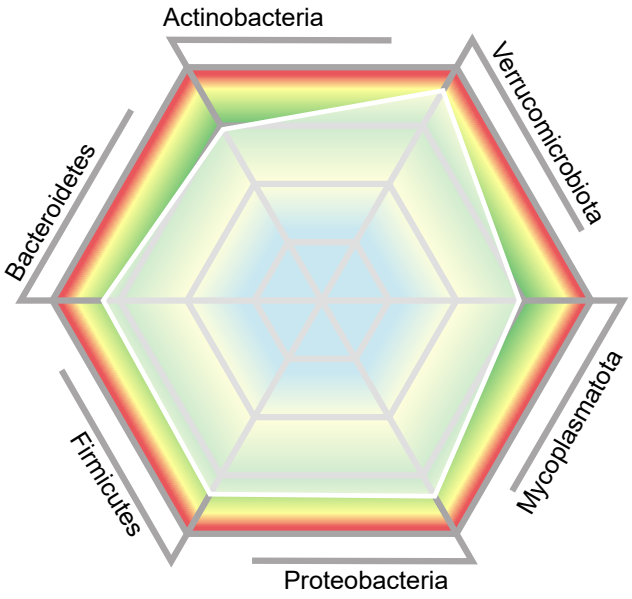
Order: 999999-9999
Client #: 999999
Doctor: Sample Doctor, MD
Doctors Data Inc
123 Main St.
St. Charles, 60174 USA

Patient: Sample Patient
Id: 999999
Age: 60 **DOB:** 00/00/1965
Sex: Female

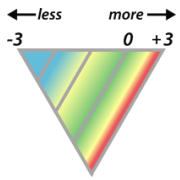
Sample Collection	Date/Time
Date Collected	06/22/2025
Date Received	06/30/2025
Date Reported	07/08/2025

Microbiome Abundance and Diversity Summary

The abundance and diversity of gastrointestinal bacteria provide an indication of gastrointestinal health, and gut microbial imbalances can contribute to dysbiosis and other chronic disease states. The GI360™ Microbiome Profile is a gut microbiota DNA analysis tool that identifies and characterizes more than 45 targeted analytes across six Phyla using PCR and compares the patient results to a characterized normobiotic reference population. The web chart illustrates the degree to which an individual's microbiome profile deviates from normobiosis.



LEGEND



The web image shows the relative diversity and balance among bacteria belonging to the six primary Phyla. The white shaded area represents the patient's results compared to a normobiotic reference population. The center of the web represents less abundance while the outer edges represent more than normobiotic.

Dysbiosis and Diversity Index

These indexes are calculated from the results of the Microbiome Profile, with scores ranging from 1 to 5, and do not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

The Dysbiosis Index the (DI) is calculated strictly from the results of the Microbiome Profile, with scores from 1 to 5. A DI score above 2 indicates dysbiosis; a microbiota profile that differs from the defined normobiotic reference population. The higher the DI above 2, the more the sample deviates from the normobiotic profile. The dysbiosis test and DI does not include consideration of dysbiotic and pathogenic bacteria, yeast, parasites and viruses that may be reported in subsequent sections of the GI360™ test.

A diversity score of 3 indicates an expected amount of diversity, with 4 & 5 indicating an increased distribution of bacteria based on the number of different species and their abundance in the sample, calculated based on Shannon's diversity index. Scores of 1 or 2 indicate less diversity than the defined normobiotic reference population.

Dysbiosis Index

Diversity Score

GI Health Markers

Butyrate producing bacteria	
Gut barrier protective bacteria	
Gut intestinal health marker	
Pro-inflammatory bacteria	
Gut barrier protective bacteria vs. opportunistic bacteria	

= Expected = Imbalanced

Key Findings

Secretory IgA, Very Low
β-glucuronidase, High

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Microbiome Bacterial Abundance;Multiplex PCR

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LEGEND

-3	-2	-1	0	+1	+2	+3
Very Low		Low	Within Reference Interval	High	Very High	

Results are graphed as deviations from a normobiotic population. Normobiosis or a normobiotic state characterizes a composition of the microbiota profile in which microorganisms with potential health benefits predominate in abundance and diversity over potentially harmful ones.

Actinobacteria	Result	Reference Interval
Actinobacteria	0	0
Actinomycetales	0	0
Bifidobacterium family	0	0

Bacteroidetes	Result	Reference Interval
Alistipes spp.	0	0
Alistipes onderdonkii	0	0
Bacteroides fragilis	0	0
Bacteroides spp. & *Prevotella* spp.	0	0
Bacteroides spp.	0	0
Bacteroides pectinophilus	0	0
Bacteroides stercoris	+1	0
Bacteroides zoogleoformans	0	0
Parabacteroides johnsonii	0	0
Parabacteroides spp.	0	0

Firmicutes	Result	Reference Interval
Firmicutes	0	0
Bacilli Class	0	0
Catenibacterium mitsuokai	0	0

Notes:
The gray-shaded area of the bar graph represents reference values outside the reporting limits for this test.
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Methodology: Multiplex PCR

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Firmicutes	Result	-3 -2 -1 0 +1 +2 +3	Reference Interval
Clostridia Class	0		0
Clostridium methylpentosum	0		0
Clostridium L2-50	0		0
Coprobacillus cateniformis	0		0
Dialister invisus	0		0
Dialister invisus & Megasphaera micronuciformis	0		0
Dorea spp.	-1		0
Holdemanella biformis	0		0
Anaerobutyricum hallii	-1		0
Agathobacter rectalis	0		0
Eubacterium siraeum	+2		0
Faecalibacterium prausnitzii	0		0
Lachnospiraceae	0		0
Ligilactobacillus ruminis & *Pediococcus acidilactici*	0		0
Lactobacillus family	-1		0
Phascolarctobacterium spp.	0		0
Ruminococcus albus & R. bromii	0		0
Mediterraneibacter gnavus	0		0
Streptococcus agalactiae & Agathobacter rectalis	0		0
Streptococcus salivarius ssp. *thermophilus & S. sanguinis*	0		0

Notes:
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Firmicutes	Result	-3 -2 -1 0 +1 +2 +3	Reference Interval
Streptococcus salivarius ssp. *thermophilus*	0		0
Streptococcus spp.	0		0
Veillonella spp.	0		0

Proteobacteria	Result	-3 -2 -1 0 +1 +2 +3	Reference Interval
Proteobacteria	0		0
Enterobacteriaceae	0		0
Escherichia spp.	+1		0
Acinetobacter junii	0		0

Mycoplasmatota	Result	-3 -2 -1 0 +1 +2 +3	Reference Interval
Metamycoplasma hominis	0		0

Verrucomicrobiota	Result	-3 -2 -1 0 +1 +2 +3	Reference Interval
Akkermansia muciniphila	+1		0

Microbiome Abundance Information:

- The GI360™ Microbiome Profile is a focused gut microbiota DNA analysis tool that identifies more than 45 targeted analytes across six phyla using a CE-marked multiplex PCR system. Patient results are compared to a highly defined normobiotic reference population (n > 1,100). The white shadowed web plot within the hexagonal diagram illustrates the degree to which an individual's microbiome profile deviates from normobiosis. The center of the diagram represents less bacterial abundance while the outer edges represent greater than normobiosis. Deviation from a hexagon-shaped plot indicates variant diversity of the microbial community. Key findings for patient's microbiome profile are summarized in the table below the diagram, and detailed results for all of the analytes are presented on the next 3 pages of the report. Detailed results for the specific bacteria are reported as -3 to +3 standard deviations, as compared to the normobiotic reference population.

Notes:
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Methodology: Multiplex PCR

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GI Pathogens;Multiplex PCR; stool

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Viruses	Result
Adenovirus F40/41	Negative
Norovirus GI/GII	Negative
Rotavirus A	Negative

Pathogenic Bacteria	Result
Campylobacter (*C. jejuni*, *C. coli* and *C. lari*)	Negative
Clostridioides difficile (Toxin A/B)	Negative
Escherichia coli O157	Negative
Enterotoxigenic *Escherichia coli* (ETEC) lt/st	Negative
Salmonella spp.	Negative
Shiga-like toxin-producing *Escherichia coli* (STEC) stx1/stx2	Negative
Shigella (*S. boydii*, *S. sonnei*, *S. flexneri* & *S. dysenteriae*)	Negative
Vibrio cholerae	Negative

Parasites	Result
Cryptosporidium (*C. parvum* and *C. hominis*)	Negative
Entamoeba histolytica	Negative
Giardia duodenalis (AKA *intestinalis & lamblia*)	Negative

GI Pathogen information:

- This specimen exhibited inhibition of the PCR reaction. Additional processing steps including dilution and repeat testing were taken to overcome the inhibitors.

Notes:
Methodology: Multiplex PCR

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Stool Chemistries

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Digestion / Absorption	Result	Unit	Reference Interval
Elastase	357	µg/g	> 200
Fat Stain	None		None – Moderate
Carbohydrates†	Negative		Negative

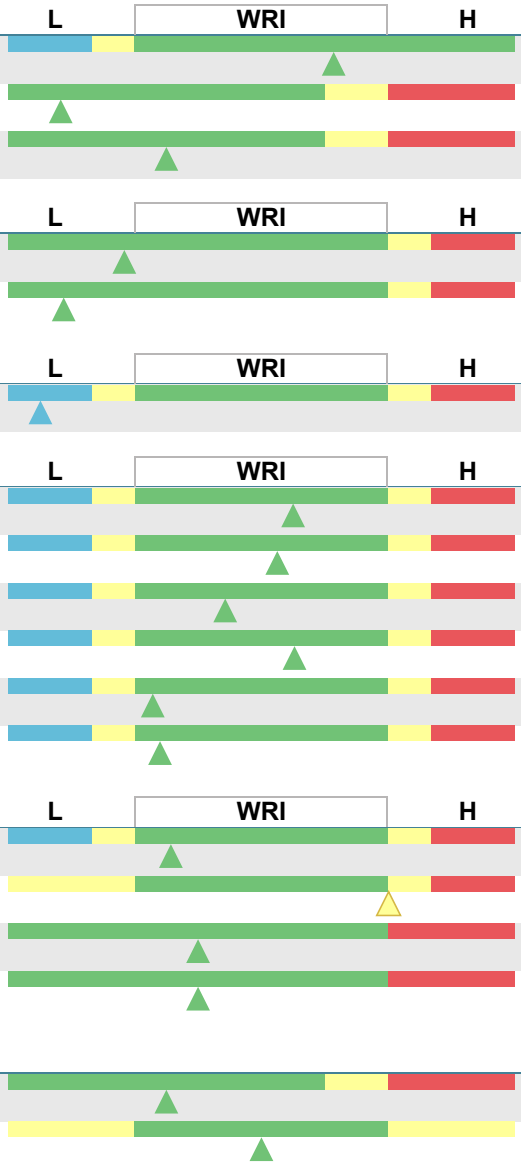
Inflammation	Result	Unit	Reference Interval
Lysozyme*	160	ng/mL	≤ 500
Calprotectin	16	µg/g	< 80

Immunology	Result	Unit	Reference Interval
Secretory IgA*	7.7	mg/dL	30 – 275

Short Chain Fatty Acids	Result	Unit	Reference Interval
% Acetate‡	63	%	50 – 72
% Propionate‡	18	%	11 – 25
% Butyrate‡	16	%	11 – 32
% Valerate‡	3.3	%	0.8 – 5.0
Butyrate‡	0.90	mg/mL	0.8 – 4.0
Total SCFA's‡	5.8	mg/mL	5.0 – 16.0

Intestinal Health Markers	Result	Unit	Reference Interval
pH	6.0		5.8 – 7.0
β-glucuronidase*	8020	U/h*g	2800 – 8000
Occult Blood	Negative		Negative
Helicobacter pylori	Negative		Negative

Macroscopic Appearance	Result	Unit	Reference Interval
Color	Brown		Brown
Consistency	Soft		Soft



Notes:
RI= Reference Interval, L (blue)= Low (below RI), WRI (green)= within RI, Yellow= moderately outside RI, L or H, H (red)= High (above RI)

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†This test has been modified from the manufacturer's instructions and its performance characteristics determined by Doctor's Data Laboratories in a manner consistent with CLIA requirements.

‡This test was developed and its performance characteristics determined by Doctor's Data Laboratories in a manner consistent with CLIA requirements. The U.S. Food and Drug Administration (FDA) has not approved or cleared this test; however, FDA clearance is not currently required for clinical use.

Methodology: Turbidimetric immunoassay, Microscopy, Colormetric, Elisa, Gas Chromotography, Enzymatic, Guaiac, Enzyme Immunoassay, Macroscopic Observation

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Stool Chemistries

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Chemistry Information:

- **Elastase** findings can be used for assessing pancreatic exocrine function and insufficiency.
- **Fat Stain:** Microscopic determination of fecal fat using Sudan IV staining is a qualitative procedure utilized to assess fat absorption and to detect steatorrhea.
- **Carbohydrates:** The presence of reducing substances in stool specimens can indicate carbohydrate malabsorption.
- **Lactoferrin** and **Calprotectin** are reliable markers for differentiating organic inflammation (IBD) from function symptoms (IBS) and for management of IBD. Monitoring levels of fecal lactoferrin and calprotectin can play an essential role in determining the effectiveness of therapy, are good predictors of IBD remission, and can indicate a low risk of relapse.
- **Lysozyme** is an enzyme secreted at the site of inflammation in the GI tract and elevated levels have been identified in IBD patients.
- **Secretory IgA** (sIgA) is secreted by mucosal tissue and represents the first line of defense of the GI mucosa and is central to the normal function of the GI tract as an immune barrier. Elevated levels of sIgA have been associated with an upregulated immune response.
- **Short chain fatty acids (SCFAs):** SCFAs are the end product of the bacterial fermentation process of dietary fiber by beneficial flora in the gut and play an important role in the health of the GI as well as protecting against intestinal dysbiosis. Lactobacilli and bifidobacteria produce large amounts of short chain fatty acids, which decrease the pH of the intestines and therefore make the environment unsuitable for pathogens, including bacteria and yeast. Studies have shown that SCFAs have numerous implications in maintaining gut physiology. SCFAs decrease inflammation, stimulate healing, and contribute to normal cell metabolism and differentiation. Levels of **Butyrate** and **Total SCFA** in mg/mL are important for assessing overall SCFA production, and are reflective of beneficial flora levels and/or adequate fiber intake.
- **pH:** Fecal pH is largely dependent on the fermentation of fiber by the beneficial flora of the gut.
- **Occult blood:** A positive occult blood indicates the presence of free hemoglobin found in the stool, which is released when red blood cells are lysed.
- **β-glucuronidase** is an enzyme that breaks the tight bond between glucuronic acid and toxins in the intestines. The binding of toxins in the gut is protective by way of blocking their absorption and facilitating excretion.

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Introduction

This analysis of the stool specimen provides fundamental information about the overall gastrointestinal health of the patient. When abnormal microflora or significant aberrations in intestinal health markers are detected, specific commentaries are presented. If no significant abnormalities are found, commentaries are not presented.

The majority of reference intervals are established from adult populations. Results may differ in pediatric populations and care should be taken when interpreting these values.

Microbiome Abundance Information

Actinobacteria (phylum)

Actinobacteria is one of the largest bacterial phyla, comprised of Gram-positive bacteria. This phylum includes a wide range of species, with different morphological and physiological characteristics. Significant groups in the human colon include Actinomycetales and Bifidobacteriales. Actinomycetales were inversely associated with clinically significant depression in IBS patients, suggesting these bacteria may be depleted in depressed IBS patients. A strict vegetarian diet may increase the total count of *Actinomyces* spp. compared to following a Western diet.

Bacteroidetes (phylum)

Bacteroidetes make up approximately 28% of the gut microbiota in healthy human adults. They are early colonizers of the infant gut and are amongst the most stable, at a species and strain level, in the host. A low preponderance of Bacteroidetes in relation to Firmicutes has been associated with obesity, though this can increase with weight loss and restricted calorie intake.

↑ ***Bacteroides* (species)**

Species in the genus *Bacteroides* carry out broad metabolic functions, including degradation of complex plant polysaccharides, proteolytic activities, de-conjugation of bile acids, mucosal barrier integrity, short chain fatty acid production, fatty acid storage and glucose metabolism. *Bacteroides* spp. are maintained at a higher abundance in breastfed individuals into adulthood. *Bacteroides fragilis* plays an important role in the prevention of intestinal inflammation. An energy-restricted diet has been shown to increase *B. fragilis* in overweight adolescents. An increase in *B. stercoris* has been associated with higher risk of colon cancer. Decreased levels of *Bacteroides* spp. have been reported in association with multiple sclerosis, rheumatoid arthritis and Parkinson's disease.

Firmicutes (phylum)

The phylum Firmicutes constitutes the most diverse and abundant group of gastrointestinal microbiota which are grouped into four classes, Bacilli, Clostridia, Erysipelotrichia, and Negativicutes. They constitute about 39% of gut bacteria in healthy adults, but may increase to as high as 80% in an imbalanced microbial community.

↓ ***Dorea* (genus)**

Dorea is a genus within the *Lachnospiraceae* family that is in the Firmicutes phylum. *Dorea* species are known to produce hydrogen and carbon dioxide as end-products of glucose fermentation and may be associated with bloating. Decreased levels of *Dorea* spp. were observed in patients with Parkinson's disease. Recent studies have identified increased levels of *Dorea* spp. in patients diagnosed with IBS, nonalcoholic fatty liver disease and non-alcoholic steatohepatitis, multiple sclerosis and colorectal cancer.

↓ ***Anaerobutyricum hallii* (species)**

Anaerobutyricum hallii and *Agathobacter rectalis* (*Eubacterium rectale*) are both part of the Lachnospiraceae family that is in the Firmicutes family *A. hallii* and *A. rectalis* produce butyrate that is a key regulator of mucosal barrier integrity and function. Decreased levels of *Anaerobutyricum*/Agathobacter spp have been associated with very high protein diets. *Anaerobutyricum hallii* is capable of metabolizing glucose products with antimicrobial properties.

↓ ***Lactobacillus* (genus)**

Decreased and normal levels of *Lactobacillus* spp. have been reported in patients with irritable bowel syndrome. *Lactobacillus* spp. abundance was shown to be lower in the active phase of ulcerative colitis. *Lactobacillus* levels were shown to be increased after inulin consumption, but decreased after consumption of maltodextrin. Polyphenols derived from chocolate, green tea, blackcurrant, red wine and grape seed extracts have been shown to increase *Lactobacillus* species. The increased abundance of *Lactobacillus* species has been associated with amelioration of inflammation.

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Microbiome Abundance Information continued...

Proteobacteria (phylum)

Proteobacteria include a wide variety of pathogens, including species within the *Escherichia*, *Shigella Salmonella*, *Vibrio*, and *Helicobacter* genera. The phylum includes a number of species that are permanent residents of the microbiota and capable of inducing nonspecific inflammation and diarrhea when their presence is increased. Proteobacteria make up approximately 2% of the gut microbiota in healthy adults.

***Escherichia* (genus)**

Clinically, *Escherichia* has been reported to contribute to irritable bowel syndrome. *Escherichia* spp. are commonly recovered from inflamed tissues of both Crohn's disease and ulcerative colitis patients. Untreated inflammatory bowel disease patients were shown to have higher abundance of *Escherichia* and lower abundance of *Faecalibacterium prausnitzii*. Increased levels of *Escherichia* were observed in colorectal cancer patients. Patients diagnosed with nonalcoholic steatohepatitis have higher abundance of *Escherichia*. Consumption of a Western diet is positively associated with *Escherichia* levels. Increased levels of *E. coli* were observed in people on a gluten-free diet. A non-pathogenic strain of *Escherichia*, *Escherichia nissle*, is a widely used probiotic for treating gut related diseases such as chronic constipation.

Mycoplasmatota (Tenericutes) (phylum)

Mycoplasmatota are cell wall-less bacteria that do not synthesize precursors of peptidoglycan. Mycoplasmatota consist of four main clades designated as the *Acholeplasma*, *Spiroplasma*, *Pneumoniae* and *Hominis* clusters. Mycoplasmatotas are typically parasites or commensals of eukaryotic hosts.

Verrucomicrobiota (Verrucomicrobia) (phylum)

Verrucomicrobiota is a less common phylum in the human microbiota, but one with increasing recognition with regards to health. Verrucomicrobiota includes *Akkermansia muciniphila*. The obligate anaerobe *A. muciniphila* constitutes 3-5% of total bacteria in a healthy microbiome, and has a protective or anti-inflammatory role in the intestinal mucosa.

***Akkermansia muciniphila* (genus)**

Higher abundance of *Akkermansia muciniphila* has been associated with a milder disease course in newly discovered ulcerative colitis patients. Archaea and *Akkermansia* were significantly more prevalent after weight reduction. A Low FODMAP diet has been shown to decrease the abundance of *A. muciniphila* leading to recommendations against long-term use of such a diet. *A. muciniphila* is a mucolytic specialist that has potent anti-inflammatory effects in part associated with a specific surface coat protein (Amuc- 1100).

GI Pathogens

Introduction

The GI Pathogen profile is performed using an FDA-cleared multiplex PCR system. It should be noted that PCR testing is much more sensitive than traditional techniques and allows for the detection of extremely low numbers of pathogens. PCR testing does not differentiate between viable and non-viable pathogens and should not be repeated until 21 days after completion of treatment or resolution to prevent false positives due to lingering traces of DNA. PCR testing can detect multiple pathogens in the patient's stool but does not differentiate the causative pathogen. All decisions regarding the need for treatment should take the patient's complete clinical history and presentation into account.

Stool Chemistries

Secretory IgA (sIgA) Low

The concentration of sIgA is abnormally low in this fecal specimen. Secretory IgA represents the first line of defense of the gastrointestinal (GI) mucosa and is central to the normal function of the GI tract as an immune barrier. Immunological activity in the gastrointestinal tract can be accessed via fecal sIgA levels in a formed stool sample. However, sIgA may be artefactually low due to fluid dilution effects in a watery or loose/watery stool sample.

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Stool Chemistries continued...

Chronic mental and physical stress as well as inadequate nutrition have been associated with low fecal sIgA concentrations. This includes dietary restrictions, excessive alcohol intake, body mass loss, negative moods, and anxiety. One study found decreased levels of sIgA in malnourished children, particularly protein malnourishment, which responded well to nutritional rehabilitation with a significant increase in sIgA. A possible explanation for this may be the synthesis and expression of sIgA requires adequate intake of the amino acid L-glutamine. An increase of dietary L-glutamine may restore GI immune function by protection of cells that synthesize sIgA. *Saccharomyces boulardii* is a nonpathogenic yeast that has been used for the treatment of acute infectious enteritis and antibiotic-associated diarrhea. Restored levels of sIgA and subsequent enhanced host immune response have been found following *S. boulardii* administration (animal models). With low sIgA one might consider a salivary cortisol test.

β-glucuronidase

A high level of fecal β-glucuronidase (β-G) may promote enterohepatic reabsorption of toxins and steroid hormones that the body has conjugated to glucuronic acid for elimination via the biliary-fecal route of excretion. B-glucuronidase is an enzyme, produced by the intestinal epithelium and certain intestinal bacteria, which breaks down the tight bond between glucuronic acid and many different chemical entities. Observational studies have indicated a correlation between high β-G activity and certain cancers, but a definitive causal relationship has not been established. Higher levels of β-G have been associated with higher circulating estrogens and lower fecal excretion of estrogens in premenopausal women. A potential dietary carcinogen derived from cooked meat and fish induces high β-G and prolongs internal exposure to the toxin in an animal model.

Diet and intestinal bacterial imbalance modulate β-G. High fat, high protein and low fiber diets are associated with higher β-G compared to vegetarian or high soluble fiber diets. Higher β-G may be associated with an imbalanced intestinal microbiota profile. Some major bacterial producers of fecal β-G include *Bifidobacterium*, *Lactobacillus*, *Escherichia coli*, *Clostridium*, *Bacteroides fragilis* and other *Bacteroides* species, *Mediterraneibacter gnavus*, and species that belong to the genera *Staphylococcus* and *Eubacterium*.

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