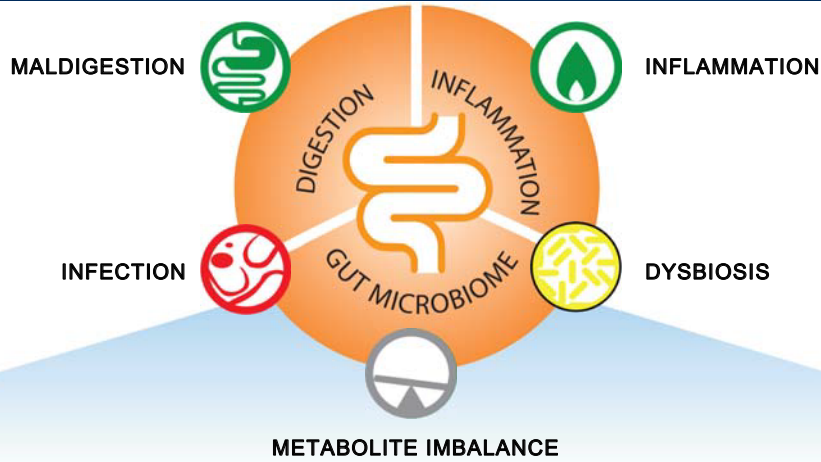


Patient:

2200 GI Effects™ Comprehensive Profile - Stool

Powered by *Genova AI*

**Results Overview**



**Functional Imbalance Scores**

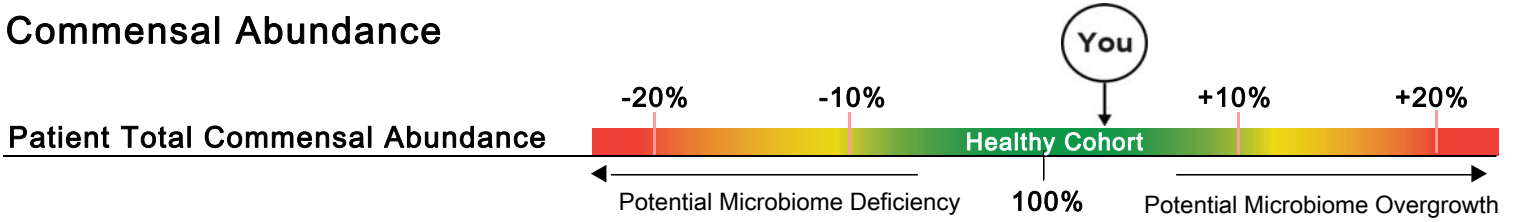
Key **< 2** : Low Need for Support    **2-3** : Optional Need for Support    **4-6** : Moderate Need for Support    **7-10** : High Need for Support

	Need for Digestive Support	Need for Inflammation Modulation	Need for Microbiome Support	Need for Prebiotic Support	Need for Antimicrobial Support
	<b>MALDIGESTION</b>	<b>INFLAMMATION</b>	<b>DYSBIOSIS</b>	<b>METABOLITE IMBALANCE</b>	<b>INFECTION</b>
	<b>0</b>	<b>0</b>	<b>4</b>	<b>2</b>	<b>7</b>
<b>Biomarkers</b>	Products of Protein Breakdown ▼ Fecal Fats ▼ Pancreatic Elastase ●	Secretory IgA ▲ Calprotectin ● Eosinophil Protein X ● Occult Blood ●	PP Bacteria/Yeast ▲ IAD/Methane Score ● Reference Variance ● Total Abundance ●	Total SCFA's ▼ n-Butyrate Conc. ▼ SCFA (%) ● Beta-glucuronidase ●	PP Bacteria/Yeast ▲ Parasitic Infection ▲ Pathogenic Bacteria ● Total Abundance ●
<b>Therapeutic Support Options</b>	<ul style="list-style-type: none"> <li>Digestive Enzymes</li> <li>Betaine HCl</li> <li>Bile Salts</li> <li>Apple Cider Vinegar</li> <li>Mindful Eating Habits</li> <li>Digestive Bitters</li> </ul>	<ul style="list-style-type: none"> <li>Elimination Diet/ Food Sensitivity Testing</li> <li>Mucosa Support: Slippery Elm, Althea, Aloe, DGL, etc.</li> <li>Zinc Carnosine</li> <li>L-Glutamine</li> <li>Quercetin</li> <li>Turmeric</li> <li>Omega-3's</li> <li>GI Referral (If Calpro is Elevated)</li> </ul>	<ul style="list-style-type: none"> <li>Pre-/Probiotics</li> <li>Increase Dietary Fiber Intake</li> <li>Consider SIBO Testing</li> <li>Increase Resistant Starches</li> <li>Increase Fermented Foods</li> <li>Meal Timing</li> </ul>	<ul style="list-style-type: none"> <li>Pre-/Probiotics</li> <li>Increased Dietary Fiber Intake</li> <li>Increase Resistant Starches</li> <li>Increase Fermented Foods</li> <li>Calcium D-Glucarate (for high beta-glucuronidase)</li> </ul>	<ul style="list-style-type: none"> <li>Antibiotics (if warranted)</li> <li>Antimicrobial Herbal Therapy</li> <li>Antiparasitic Herbal Therapy (if warranted)</li> <li><i>Saccharomyces boulardii</i></li> </ul>



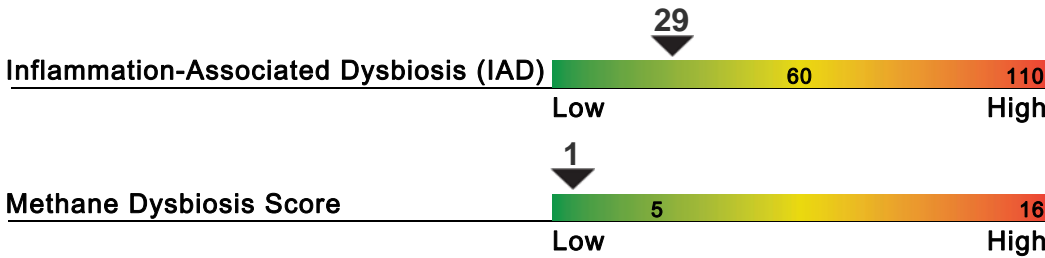
## Commensal Microbiome Analysis

### Commensal Abundance

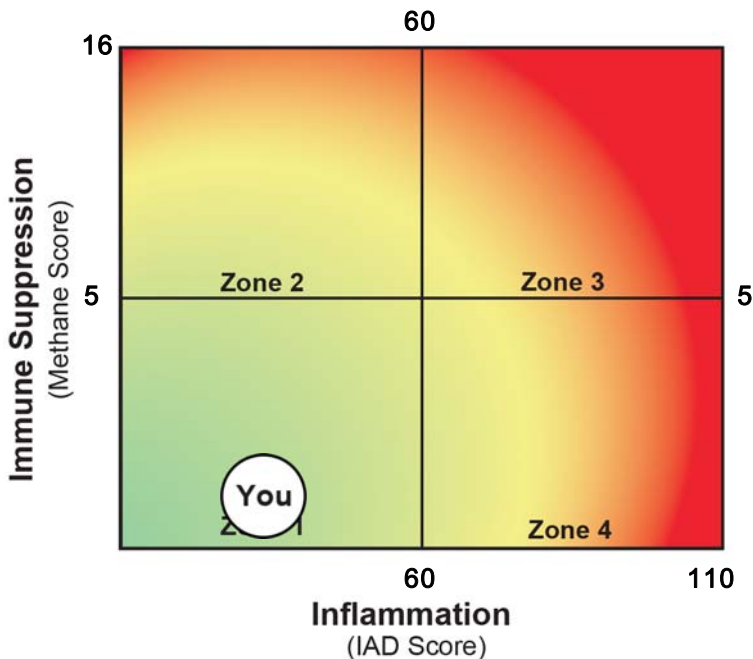


**Total Commensal Balance:** The total commensal abundance is a sum-total of the reported commensal bacteria compared to a healthy cohort. Low levels of commensal bacteria are often observed after antimicrobial therapy, or in diets lacking fiber and/or prebiotic-rich foods and may indicate the need for microbiome support. Conversely, higher total commensal abundance may indicate potential bacteria overgrowth or probiotic supplementation.

### Dysbiosis Patterns



**Dysbiosis Patterns:** Genova's data analysis has led to the development of unique dysbiosis patterns, related to key physiologic disruptions, such as immunosuppression and inflammation. These patterns may represent dysbiotic changes that could pose clinical significance. Please see Genova's published literature for more details: <https://rdcu.be/bRhzv>



**Zone 1:** The commensal profile in this zone does not align with profiles associated with intestinal inflammation or immunosuppression. If inflammatory biomarkers are present, other causes need to be excluded, such as infection, food allergy, or more serious pathology.

**Zone 2:** This pattern of bacteria is associated with impaired intestinal barrier function (low fecal sIgA and EPX). Patients in this zone have higher rates of opportunistic infections (e.g. *Blastocystis spp.* & *Dientamoeba fragilis*) as well as fecal fat malabsorption. Commensal abundance is higher in this group suggesting potential bacterial overgrowth.

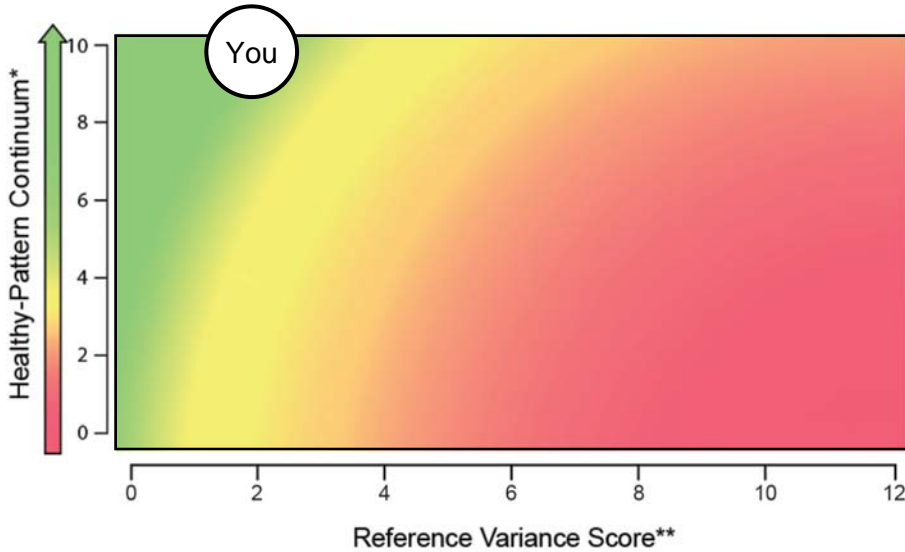
**Zone 3:** Patients in this zone may have more inflammation compared to those in zone 4. However, commensal abundance is usually higher making use of antimicrobial therapy relatively safer. Patients in this zone may have higher rates of pathogenic infections.

**Zone 4:** This commensal profile is associated with increased intestinal inflammation. IBD patients are more likely to have this pattern of bacteria. Commensal abundance is lower in this zone; therefore, antibiotic use for GI potential pathogens should be used with caution. In addition to standard treatment for intestinal inflammation, modulation of the commensal gut profile is encouraged.



## Commensal Microbiome Analysis

### Commensal Balance



Balanced	Represents 95% of healthy individuals
Borderline	Represents 5% of healthy individuals
Imbalanced	Represents 60% of unhealthy individuals

\*A progressive ranking scale based on a Genova proprietary algorithm that differentiates healthy and unhealthy commensal patterns.

\*\*The total number of Commensal Bacteria (PCR) that are out of reference ranges for this individual.

### Relative Commensal Abundance

	-50%	-25%	Healthy Cohort	+25%	
Bacteroidetes Phylum	[Bar from -50% to ~-15%]				Increase in <i>Bacteroides</i> spp. and <i>Odoribacter</i> spp. seen in animal-based diets; <i>Prevotella</i> increased with plant-based diet
Firmicutes Phylum	[Bar from -50% to ~+15%]				Contains many butyrate-producers; most species responsive to plant-based diets; <i>Faecalibacterium</i> spp. is anti-inflammatory
Actinobacteria Phylum	[Bar from -50% to ~-10%]				<i>Bifidobacterium</i> is increased with plant-based diets; <i>Collinsella</i> may be proinflammatory, and is elevated with a Western-diet
Proteobacteria Phylum	[Bar from -50% to ~-10%]				Some species may be proinflammatory; <i>E. coli</i> consumes simple sugars and is lower in individuals on plant-based diets
Euryarchaeota Phylum ***	NR				<i>Methanobrevibacter smithii</i> is associated with methane production and with diets high in carbohydrates
Fusobacteria Phylum ***	NR				Certain <i>Fusobacterium</i> spp. may be proinflammatory and increased on low fiber, high fat diets
Verrucomicrobia Phylum	[Bar from -50% to ~-15%]				<i>Akkermansia</i> spp. is involved in gut membrane integrity and may be increased with polyphenols and prebiotics

**Relative Abundance:** The relative abundance compares the quantity of each of 7 major bacterial phyla to a healthy cohort. This can indicate broader variances in the patient's gut microbiome profile. Certain interventions may promote or limit individual phyla when clinically appropriate. Please refer to Genova's Stool Testing Support Guide for more information on modulation of commensal bacteria through diet & nutrient interventions. \*\*\*Approximately 70% of the healthy cohort had below detectable levels of *Methanobrevibacter smithii*. Approximately 90% of the healthy cohort had below detectable levels of *Fusobacterium* spp.

### Physician Notes/Recommendations

## 2200 GI Effects™ Comprehensive Profile - Stool

Methodology: GC-FID, Automated Chemistry, EIA

		QUINTILE DISTRIBUTION					Reference Range
		1st	2nd	3rd	4th	5th	
<b>Digestion and Absorption</b>							
Pancreatic Elastase 1 †	>500						>200 mcg/g
Products of Protein Breakdown (Total*) (Valerate, Isobutyrate, Isovalerate)	2.2						1.8-9.9 micromol/g
Fecal Fat (Total*)	6.6						3.2-38.6 mg/g
Triglycerides	0.7						0.3-2.8 mg/g
Long-Chain Fatty Acids	4.6						1.2-29.1 mg/g
Cholesterol	0.8						0.4-4.8 mg/g
Phospholipids	0.5						0.2-6.9 mg/g
<b>Inflammation and Immunology</b>							
Calprotectin †	<16						<=50 mcg/g
Eosinophil Protein X (EPX)†	<DL						<=2.7 mcg/g
Fecal secretory IgA	683						<=2,040 mcg/mL
<b>Gut Microbiome Metabolites</b>							
<b>Metabolic</b>							
Short-Chain Fatty Acids (SCFA) (Total*) (Acetate, n-Butyrate, Propionate)	29.3						>=23.3 micromol/g
n-Butyrate Concentration	6.7						>=3.6 micromol/g
n-Butyrate %	22.9						11.8-33.3 %
Acetate %	59.2						48.1-69.2 %
Propionate %	18.1						<=29.3 %
Beta-glucuronidase	1,547						368-6,266 U/g

\*Total value is equal to the sum of all measurable parts.

†These results are not represented by quintile values.

Tests were developed and their performance characteristics determined by Genova Diagnostics. Unless otherwise noted with \*, the assays have not been cleared by the U.S. Food and Drug Administration.



## Gastrointestinal Microbiome (PCR)

Commensal Bacteria (PCR)	Result CFU/g stool	QUINTILE DISTRIBUTION					Reference Range CFU/g stool
		1st	2nd	3rd	4th	5th	
<b>Bacteroidetes Phylum</b>							
<i>Bacteroides uniformis</i>	3.5E8						<=9.5E8
<i>Phocaeicola vulgatus</i>	2.8E8						<=8.3E8
<i>Barnesiella spp.</i>	3.6E7						3.0E6-2.9E8
<i>Odoribacter spp.</i>	<DL						<=9.5E7
<i>Prevotella spp.</i>	1.2E9						6.6E7-3.8E9
<b>Firmicutes Phylum</b>							
<i>Anaerotruncus colihominis/massiliensis</i>	1.6E7						<=2.0E7
<i>Butyrivibrio crossotus</i>	<DL						<=3.3E7
<i>Clostridium spp.</i>	<DL						<=1.5E7
<i>Coprococcus eutactus</i>	<DL						<=1.2E8
<i>Faecalibacterium prausnitzii</i>	2.4E8						1.1E6-1.1E9
<i>Lactobacillus spp.</i>	5.6E3						<=1.6E6
<i>Pseudoflavonifractor spp.</i>	1.4E6						1.3E4-2.9E7
<i>Roseburia spp.</i>	7.4E7						3.6E5-4.6E8
<i>Ruminococcus bromii</i>	4.6E8						<=1.5E9
<i>Veillonella spp.</i>	4.6E5						<=4.1E6
<b>Actinobacteria Phylum</b>							
<i>Bifidobacterium spp.</i>	5.0E7						4.6E5-2.6E8
<i>Bifidobacterium longum subsp. longum</i>	<DL						<=1.3E8
<i>Collinsella aerofaciens</i>	<DL						<=1.3E8
<b>Proteobacteria Phylum</b>							
<i>Desulfovibrio piger</i>	<DL						<=5.4E7
<i>Escherichia coli</i>	2.1E4						<=7.5E6
<i>Oxalobacter formigenes</i>	<DL						<=1.1E7
<b>Euryarchaeota Phylum</b>							
<i>Methanobrevibacter smithii</i>	<DL						<=2.0E7
<b>Fusobacteria Phylum</b>							
<i>Fusobacterium spp.</i>	<DL						<=1.8E5
<b>Verrucomicrobia Phylum</b>							
<i>Akkermansia muciniphila</i>	5.9E5						>=8.5E3

The gray-shaded portion of a quintile reporting bar represents the proportion of the reference population with results below detection limit.

Commensal results and reference range values are displayed in a computer version of scientific notation, where the capital letter "E" indicates the exponent value (e.g., 7.3E6 equates to 7.3 x 10<sup>6</sup> or 7,300,000).

The methodology for the PCR Commensal Bacteria has been updated to qPCR. The reference ranges have been updated accordingly.

The names of some of the bacteria have been updated as a result of taxonomy changes and method improvements.



## Gastrointestinal Microbiome (Culture)

Human microflora is influenced by environmental factors and the competitive ecosystem of the organisms in the GI tract. Pathogenic significance should be based upon clinical symptoms.

Microbiology Legend			
<b>NG</b>	<b>NP</b>	<b>PP</b>	<b>P</b>
<b>No Growth</b>	<b>Non-Pathogen</b>	<b>Potential Pathogen</b>	<b>Pathogen</b>

### Additional Bacteria

**Non-Pathogen:** Organisms that fall under this category are those that constitute normal, commensal flora, or have not been recognized as etiological agents of disease.

**Potential Pathogen:** Organisms that fall under this category are considered potential or opportunistic pathogens when present in heavy growth.

**Pathogen:** The organisms that fall under this category have a well-recognized mechanism of pathogenicity in clinical literature and are considered significant regardless of the quantity that appears in the culture.

### Bacteriology (Culture)

*Lactobacillus spp.*

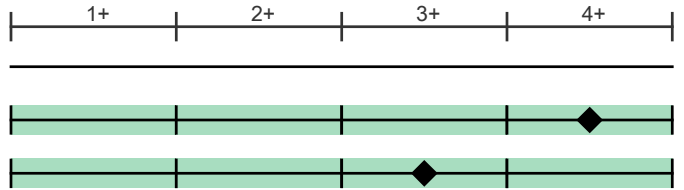
NG

*Escherichia coli*

4+ NP

*Bifidobacterium (Anaerobic Culture)*

3+ NP



### Additional Bacteria

*Salmonella spp.*

NG

*Shigella spp.*

NG

*Klebsiella pneumoniae*

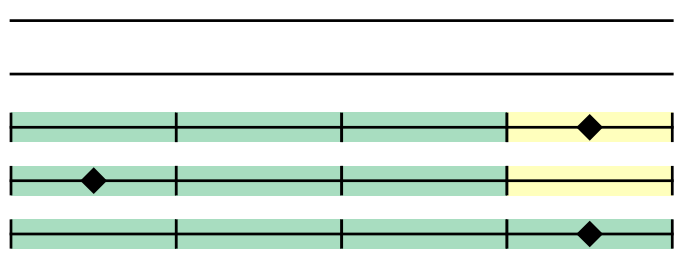
4+ PP

*Bacillus species*

1+ NP

*Enterococcus faecium*

4+ NP



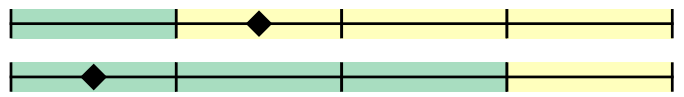
### Mycology (Culture)

*Candida kruseii*

2+ PP

*Yeast, not Candida albicans*

1+ NP





## Parasitology

### Microscopic O&P Results

Microscopic O&P is capable of detecting all described gastrointestinal parasites. The organisms listed in the box represent those commonly found in microscopic stool analysis. Should an organism be detected that is not included in the list below, it will be reported in the Additional Results section. These results were obtained using wet preparation(s) and trichrome stained smear. For an extensive reference of all potentially detectable organisms, please visit [www.gdx.net/product/gi-effects-comprehensive-stool-test](http://www.gdx.net/product/gi-effects-comprehensive-stool-test)

Genus/species	Result
<b>Nematodes - roundworms</b>	
<i>Ancylostoma/Necator</i> (Hookworm)	Not Detected
<i>Ascaris lumbricoides</i>	Not Detected
<i>Capillaria philippinensis</i>	Not Detected
<i>Enterobius vermicularis</i>	Not Detected
<i>Strongyloides stercoralis</i>	Not Detected
<i>Trichuris trichiura</i>	Not Detected
<b>Cestodes - tapeworms</b>	
<i>Diphyllobothrium latum</i>	Not Detected
<i>Dipylidium caninum</i>	Not Detected
<i>Hymenolepis diminuta</i>	Not Detected
<i>Hymenolepis nana</i>	Not Detected
<i>Taenia</i> spp.	Not Detected
<b>Trematodes - flukes</b>	
<i>Clonorchis/Opisthorchis</i> spp.	Not Detected
<i>Fasciola</i> spp./ <i>Fasciolopsis buski</i>	Not Detected
<i>Heterophyes/Metagonimus</i>	Not Detected
<i>Paragonimus</i> spp.	Not Detected
<i>Schistosoma</i> spp.	Not Detected
<b>Protozoa</b>	
<i>Balantidium coli</i>	Not Detected
<i>Blastocystis</i> spp.	<b>Many Detected</b>
<i>Chilomastix mesnili</i>	Not Detected
<i>Cryptosporidium</i> spp.	Not Detected
<i>Cyclospora cayetanensis</i>	Not Detected
<i>Dientamoeba fragilis</i>	Not Detected
<i>Entamoeba coli</i>	Not Detected
<i>Entamoeba histolytica/dispar</i>	Not Detected
<i>Entamoeba hartmanii</i>	Not Detected
<i>Entamoeba polecki</i>	Not Detected
<i>Endolimax nana</i>	Not Detected
<i>Giardia</i>	Not Detected
<i>Iodamoeba buetschlii</i>	Not Detected
<i>Cystoisospora</i> spp.	Not Detected
<i>Trichomonads</i> (e.g. <i>Pentatrichomonas</i> )	Not Detected
<b>Additional Findings</b>	
White Blood Cells	Not Detected
Charcot-Leyden Crystals	Not Detected
<b>Other Infectious Findings</b>	

One negative specimen does not rule out the possibility of a parasitic infection.



## Parasitology

### PCR Parasitology - Protozoa

Methodologies: DNA by PCR

Organism	Result	Units		Expected Result
<i>Blastocystis</i> spp.	<2.14e2	femtograms/microliter C&S stool	Detected	Not Detected
<i>Cryptosporidium parvum/hominis</i>	<1.76e2	genome copies/microliter C&S stool	Not Detected	Not Detected
<i>Cyclospora cayetanensis</i>	<2.65e2	genome copies/microliter C&S stool	Not Detected	Not Detected
<i>Dientamoeba fragilis</i>	<1.84e2	genome copies/microliter C&S stool	Not Detected	Not Detected
<i>Entamoeba histolytica</i>	<9.64e1	genome copies/microliter C&S stool	Not Detected	Not Detected
<i>Giardia</i>	<1.36e1	genome copies/microliter C&S stool	Not Detected	Not Detected

## Additional Results

Methodology: Fecal Immunochemical Testing (FIT)

	Result	Expected Value
Fecal Occult Blood♦	Negative	Negative
Color††	Brown	
Consistency††	Formed/Normal	

††Results provided from patient input.

Tests were developed and their performance characteristics determined by Genova Diagnostics. Unless otherwise noted with ♦, the assays have not been cleared by the U.S. Food and Drug Administration.



## Bacteria Sensitivity

### Prescriptive Agents

<i>Klebsiella pneumoniae</i>	R	I	S-DD	S	NI
Ampicillin	R				
Amox./Clavulanic Acid				S	
Cephalothin				S	
Ciprofloxacin				S	
Tetracycline				S	
Trimethoprim/Sulfa				S	

### Natural Agents

<i>Klebsiella pneumoniae</i>	LOW INHIBITION	HIGH INHIBITION
Berberine		
Oregano		
Uva-Ursi		

#### Prescriptive Agents:

The R (Resistant) category implies isolate is not inhibited by obtainable levels of pharmaceutical agent.

The I (Intermediate) category includes isolates for which the minimum inhibition concentration (MIC) values usually approach obtainable pharmaceutical agent levels and for which response rates may be lower than for susceptible isolates.

The S-DD (Susceptible-Dose Dependent) category implies clinical efficacy when higher than normal dosage of a drug can be used and maximal concentration achieved.

The S (Susceptible) column implies that isolates are inhibited by the usually achievable concentrations of the pharmaceutical agent.

NI (No Interpretive guidelines established) category is used for organisms that currently do not have established guidelines for MIC interpretation.

Refer to published pharmaceutical guidelines for appropriate dosage therapy.

#### Natural Agents:

In this assay, inhibition is defined as the reduction level on organism growth as a direct result of inhibition by a substance. The level of inhibition is an indicator of how effective the substance was at limiting the growth of an organism in an in vitro environment. High inhibition indicates a greater ability by the substance to limit growth, while Low Inhibition a lesser ability to limit growth. The designated natural products should be considered investigational in nature and not be viewed as standard clinical treatment substances.



## Mycology Sensitivity

### Candida Susceptibility Profile for Azoles\*

Organism	Number of Isolates	% Sensitive	
		Fluconazole	Voriconazole
<i>Candida albicans</i>	25561	99.19%	99.51%
<i>Candida parapsilosis</i>	8777	98.64%	99.33%
<i>Candida kruseii</i>	3420	0.23%	97.79%
<i>Candida tropicalis</i>	1076	93.22%	90.57%
<i>Candida glabrata</i>	2898	27.1%	90.9%

**\*Results of pharmaceutical sensitivities against certain yeast species are based on internal Genova data pertaining to the frequency of susceptibility of the specific yeast to the listed antifungal agent. The pharmaceutical results are not patient-specific. Conversely, the results of inhibition to nystatin and natural agents are patient-specific.**

### Non-absorbed Antifungals

<i>Candida kruseii</i>	LOW INHIBITION	HIGH INHIBITION
Nystatin		

### Natural Agents

<i>Candida kruseii</i>	LOW INHIBITION	HIGH INHIBITION
Berberine		
Caprylic Acid		
Garlic		
Undecylenic Acid		
Uva-Ursi		

#### Nystatin and Natural Agents:

Results for Nystatin are being reported with natural antifungals in this category in accordance with laboratory guidelines for reporting sensitivities. In this assay, inhibition is defined as the reduction level on organism growth as a direct result of inhibition by a natural substance. The level of inhibition is an indicator of how effective the substance was at limiting the growth of an organism in an in vitro environment. High inhibition indicates a greater ability by the substance to limit growth, while Low Inhibition a lesser ability to limit growth. The designated natural products should be considered investigational in nature and not be viewed as standard clinical treatment substances.