tiny health

PRO GUT HEALTH TEST
6104 Old Fredericksburg RD #91622
Austin, TX 78749

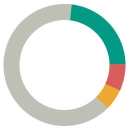
Patient name: **Lindsey Parsons**
DOB: **July 18, 1969**
Sex: **Female**

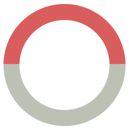
Kit ID: **GEQ343**
Physician: **Dr Taylor Soderborg**
Physician NPI: **1518543321**

Sequence Sample Received: **April 3, 2024**
Sequence Results Ready: **April 18, 2024**

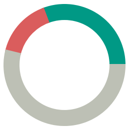
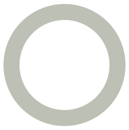
Results Summary

Tiny Health Comprehensive Metagenomics Stool Profiling & Stool Chemistry Markers

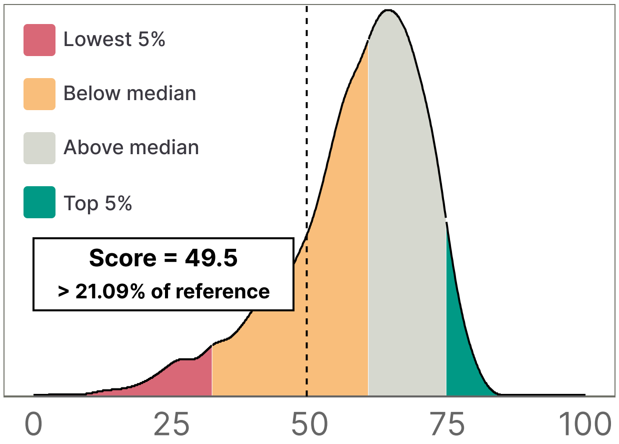
Your sample at a glance		✅ Great results	25/107
		✓ Normal results	69/107
		❗ Can improve	6/107
		⚠ Need support	7/107

	Gut Score	Metrics	Clinical indication examples
Beneficial microbes		✓ Metabolic Health ⚠ Anti-inflammatory Markers ⚠ Beneficial Bifidobacterium ✓ Common Probiotic Species	• Prebiotics / probiotics support • Review Akkemansia promoting supplements • Track and diversify fiber intake • Increase fermented foods • Move and stay physically active
Disruptive microbes		✓ Parasites and Infection ❗ Opportunistic Pathogens ✓ Potential Fungal Overgrowth ✓ Methane Producers ✅ Antibiotic Resistance Signature	• Potential anti-microbial support (e.g. herbs) • Prebiotics / probiotics support • Close monitoring post-antibiotics to track recovery • Nutritional support and therapeutic diet (eg AIP, candida diet, etc) • Review symptoms/conditions • Consider additional testing (e.g. SIBO, OAT, nutritional labs etc)
Gut inflammation markers		✓ Host DNA ✓ Hexa-LPS index ✓ Mucus degradation index ✓ Hydrogen sulfide index ✓ Occult Blood ✅ Calprotectin ✅ Secretory IgA ✅ Lactoferrin ✅ Lysozyme	• Modulate stress levels • Lifestyle changes (eg exercise, sleep) • Nutritional support and therapeutic diet (eg AIP, candida diet, etc) • Support GI motility (eg hydration, pysllium, acacia, pectin, HMOs etc) • GI barrier support (e.g. tumeric, quercetin, L-glutamine) • Soothe mucosal lining (i.e. SBI/ colostrum, marshmallow) • Consider additional testing (e.g. SIBO, OAT, nutritional labs etc)

Note: This microbiome report is exclusively intended to be used for wellness purposes and to educate you about the microbes in your body. The tests we offer are not intended to diagnose or treat disease, or to substitute a physician's consultation.The microbes we talk about in your report, and their associations, are based on emerging scientific research. Feel free to share this with your physician or practitioner. These insights are determined by evaluating current research and may change over time to reflect the most up to date research available.

Short-chain fatty acids		❗ Butyrate-Producing Capacity ❗ Acetate-Producing Capacity ❗ Propionate-Producing Capacity ⚠ Beta-glucuronidase ⚠ Total SCFA Concentration ⚠ Acetate Percent ✅ Butyrate Concentration ✅ Valerate Percent ✅ Butyrate Percent ✅ Propionate Percent	• Track and diversify fiber intake • Prebiotics / probiotics / postbiotics support • Increase fermented foods • Supportive nutraceuticals (butyrate supplements, spore-based probiotics) • Detoxification supports (calcium d-glucarate, broccoli sprouts, DIM)
Digestion & absorption markers		⚠ Fiber Digestion ⚠ Complex Sugar Digestion ✅ Vitamin Production ✓ Protein Breakdown ✅ Histamine-producing Species ✓ Consistency ✓ Fecal Fats ✓ Color ✓ Muscle fibers ✓ Vegetable fibers ✓ Carbohydrates ✅ pH ✅ Pancreatic Elastase	• Consider balanced, nutrient-dense whole foods diet • Track and diversify fiber intake • Gastric acid optimization (e.g. Betaine HCL, Apple Cider Vinegar) • Digestive enhancement (e.g. digestive bitters, digestive enzymes, bile salts) • Mindful eating habits (e.g. chew well, timing of meals, etc) • Support GI motility (eg hydration, pysllium, acacia, pectin, HMOs etc)
Balance and robustness		✓ Microbiome Diversity ✓ Major Bacterial Phyla ✓ Common Microbiome Members ✓ Gut Ratio	• Track and diversify fiber intake • Increase fermented foods • Use non-toxic cleaners / reduce antimicrobials

Population comparison chart



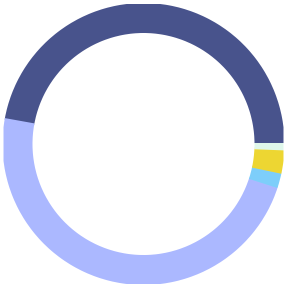
The population score is a reflection of the overall health of your gut microbiome compared to others in a similar age range. This score is determined by assessing various aspects of your gut health, such as the abundance of beneficial bacteria, and comparing these assessments to what is typically observed in a broad range of individuals.

Each aspect of your gut health receives an evaluation, such as whether it's in great condition, normal, could use some improvement, or needs more significant support. These evaluations are then combined in a way that allows us to compare your gut health to that of a reference population—a diverse group of individuals who have shared their gut microbiome data for scientific comparison.

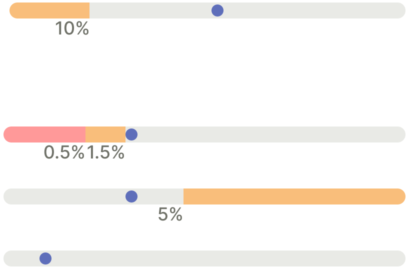
Your population score ranges from 0 to 100, where a score closer to 100 suggests that your gut microbiome is in excellent condition relative to the reference population, and a score closer to 0 indicates that there are more areas for improvement. This scoring system helps us understand how your gut health stacks up against a wide range of individuals.

Major Microbial Members & Ratios

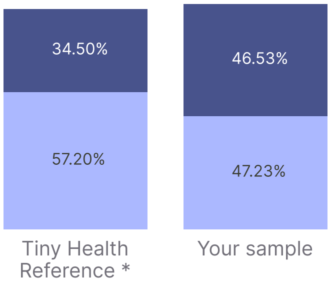
Common Bacterial Phyla



🟦 Bacteroidota	46.53%
🟪 Firmicutes	47.23%
🟦 Actinobacteriota	1.65%
🟨 Proteobacteria	2.62%
🟩 Fusobacteriota	0.60%



Gut Ratio

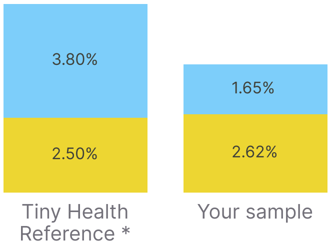


Firmicutes:Bacteroidota Ratio

1.01 (Ideally <30)

Firmicutes and Bacteroidota are the two largest phyla that make up the gut microbiome in humans. Historically and primarily in 16S studies, the ratio of Firmicutes/Bacteroidota has been associated with a number of conditions in adults, including obesity, type 2 diabetes, and inflammation. However, the use of these markers is now considered dated by current microbiome researchers, and the validity of these associations has been called into question.

🟪 Firmicutes 🟦 Bacteroidota

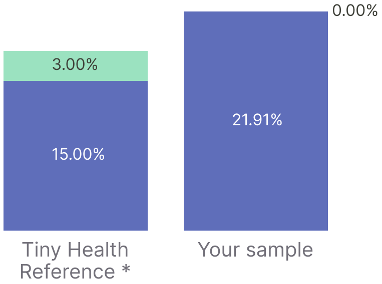


Proteobacteria:Actinobacteriota Ratio

1.59 (Ideally <14)

Aside from Firmicutes and Bacteroidota, Proteobacteria and Actinobacteriota are two common phyla in the gut microbiome in humans. Proteobacteria are widely associated with pathogens, while Actinobacteriota are associated with commensal species. Historically in primarily 16S studies, the ratio of Proteobacteria:Actionbacteriota has been associated with gut inflammation. However, the use of these markers is now considered dated by current microbiome researchers, and the validity of these associations has been called into question.

🟨 Proteobacteria 🟦 Actinobacteriota



Prevotella:Bacteroides Ratio

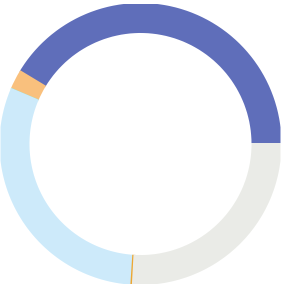
0.00 (Ideally >4)

Prevotella and Bacteroides are two common genera in the gut microbiome in humans. One or the other often dominates the gut microbiome, and can define the Gut Type. Prevotella are widely associated with a high fiber diet, while Bacteroides are associated with a diet high in fat and protein. Historically in primarily 16S studies, the ratio of Prevotella:Bacteroides has been associated with body weight, fat loss, and diet success. However, the use of these markers is now considered dated by current microbiome researchers, and the validity of these associations has been called into question.

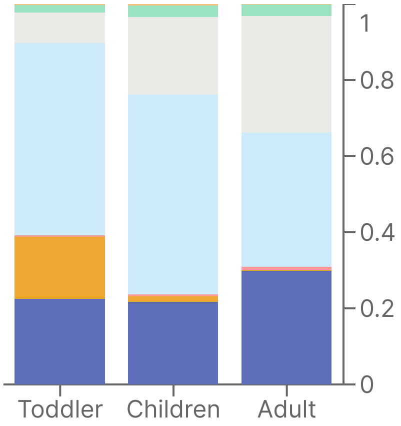
🟦 Bacteroides 🟩 Prevotella

*Tiny Health Reference: This represents a cohort that is free of any acute or chronic conditions, so they may be considered a "healthy" cohort

Gut Type



🟦 Bacteroides	41.35%
🟧 Ruminococcaceae	2.23%
🟩 Prevotella	0.03%
🟦 Lachnospiraceae	30.35%
🟥 Enterobacteriaceae	0.00%
🟧 Bifidobacterium	0.17%
⬜ Other	25.86%



These bars represent the proportion of the different gut types in our database for different age ranges.

The gut type of a sample is determined by the dominant type of microbe in that sample.

Type Bacteroides

The *Bacteroides* gut type is a common type for all ages. As it turns out, this is the most common gut type for people in developed countries. It's often seen in those whose diet is high in animal protein and fats, with lower consumption of plant-based foods.

When compared to the other gut types, the *Bacteroides* gut type has the highest potential to produce vitamin B12 and biotin.

Studies have shown that gut types respond differently to dietary interventions. For example, while foods high in fiber are beneficial for all gut types, if trying to lose weight, the *Bacteroides* gut type may not benefit much from a fiber-rich diet.

Compared to the *Prevotella* gut type, a good thing about the *Bacteroides* gut type is that it tends to have higher levels of *Bifidobacterium* species. In fact, babies with a gut type dominated by *Bifidobacterium* often transition to a *Bacteroides* gut type during toddlerhood.

Compared to other gut types, a *Bacteroides* gut type seems to benefit the most from eating chili peppers, whose content of capsaicin has beneficial effects on the gut microbiome and overall health.

Different gut types also respond differently to supplements. One study found that when people with a *Bacteroides* gut type were given probiotics, there was an improvement in glucose metabolism. Instead, people with a *Prevotella* gut type saw improvement in triglyceride metabolism.

Researchers have identified two subtypes in the *Bacteroides* gut type, named Bact1 and Bact2. The Bact2 subtype has three main characteristics in terms of microbiome composition:

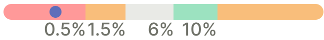
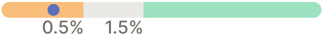
- Top species include *Bacteroides fragilis*, *Phocaeicola vulgatus*, and *Parabacteroides* distasonis
- Has a low diversity
- Has very low levels of *Faecalibacterium prausnitzii*

The Bact2 subtype is more often seen in people with obesity, insulin resistance, or inflammatory conditions such as inflammatory bowel disease and multiple sclerosis.

Detailed Pro Gut Health Test Results

Beneficial microbes

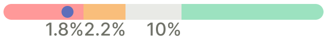
Beneficial Bifidobacterium

⚠ Bifidobacterium	0.17%	
Bifidobacterium longum	0.11%	
Bifidobacterium infantis	0.05%	
! HMO-digesting species	0.16%	

Metabolic Health

✓ Akkermansia	0.06%	

Anti-inflammatory Markers

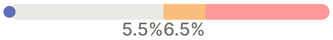
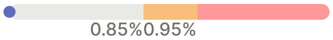
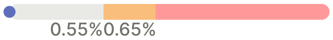
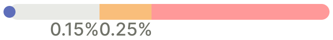
⚠ Faecalibacterium	1.12%	
Faecalibacterium prausnitzii_C	0.11%	
Faecalibacterium prausnitzii_D	0.37%	
Faecalibacterium prausnitzii_G	0.36%	
Faecalibacterium sp900539885	0.10%	
Faecalibacterium sp900539945	0.09%	

Common Probiotic Species

✓ Bifidobacterium	0.17%
✓ Lactobacillaceae	0.06%
✓ Bifidobacterium infantis	0.05%
✓ Bifidobacterium longum	0.11%

Disruptive microbes

Opportunistic Pathogens

✓ Enterobacteriaceae	0.00%	
✓ Klebsiella	0.00%	
✓ Klebsiella pneumoniae	0.00%	
✓ Klebsiella oxytoca	0.00%	
✓ Salmonella enterica	0.00%	

Disruptive microbes	✓ Escherichia coli	0.00%	2.5% 3.5%
	✓ Escherichia flexneri	0.00%	0.5% 1.5%
	✓ Streptococcus	0.12%	0.5% 1.5%
	Streptococcus anginosus	0.11%	
	✓ Streptococcus agalactiae (GBS)	0.00%	0.05%
	✓ Staphylococcus	0.00%	0.15% 0.25%
	✓ Pseudomonas aeruginosa	0.00%	0.05% 0.1%
	✓ Haemophilus influenzae	0.00%	0.05% 0.1%
	✓ Haemophilus parainfluenzae	0.00%	0.05% 0.1%
	✓ Enterococcus faecium	0.00%	0.45% 0.55%
	✓ Enterococcus faecalis	0.00%	0.15% 0.25%
	! Clostridioides difficile	0.05%	0.05% 0.1%
	✓ Acinetobacter baumannii	0.00%	0.05%
	✓ Campylobacter	0.00%	0.05% 0.1%
	✓ Helicobacter pylori	0.00%	0.05%
	Potential Fungal Overgrowth		
	✓ Candida	0.00%	0.05% 0.1%
	✓ Aspergillus	0.00%	0.05%
	✓ Cryptococcus	0.00%	0.05%
	✓ Saccharomyces	0.00%	0.5%
	✓ Rhodotorula	0.00%	0.05%
	✓ Saprochaete	0.00%	0.05%
	✓ Malassezia	0.00%	0.05%
	✓ Microsporum	0.00%	0.05%
	✓ Trichophyton	0.00%	0.05%

Disruptive microbes

Parasites and Infection

✓ Blastocystis	0.00%	0.08% 0.12%
✓ Cryptosporidium	0.00%	0.05%
✓ Entamoeba histolytica	0.00%	0.05%
✓ Entamoeba dispar	0.00%	0.05%
✓ Giardia	0.00%	0.05%
✓ Yersinia enterocolitica	0.00%	0.05%
✓ Vibrio	0.00%	0.05%
✓ Vibrio cholerae	0.00%	0.05%
✓ Cyclospora cayetanensis	0.00%	

Antibiotic Resistance Signature

✓ Abundance index	0.00	0.1 0.25 0.35
✓ Richness index	0.02	0.1 0.28 0.32

Methane Producers

✓ Methanobrevibacter smithii	0.00%	0.05% 0.45% 0.55%

Gut inflammation markers

Hexa-LPS index

✓ Hexa-LPS index	9.57	8 11.8 12.2

Mucus degradation index

✓ Mucus degradation index	11.50	8 11.8 12.2

Hydrogen sulfide index

✓ Hydrogen sulfide index	10.36	8 11.8 12.2

Host DNA

✓ Host DNA	3.74%	10%

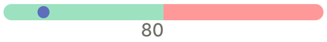
Secretory IgA

✓ Secretory IgA	43.70 mg/dL	30 275

Gut inflammation markers

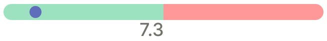
Calprotectin

✓ Calprotectin 20.00 ug/g



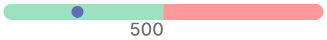
Lactoferrin

✓ Lactoferrin 1.40 ug/mL



Lysozyme

✓ Lysozyme 229.00 ng/mL



Occult Blood

✓ Occult Blood Positive

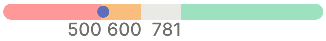
Short-chain fatty acids

Butyrate-Producing Capacity

! Butyrate 970.07 rpkm

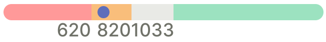
Propionate-Producing Capacity

! Propionate 501.85 rpkm



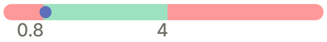
Acetate-Producing Capacity

! Acetate 678.54 rpkm



Butyrate Concentration

✓ Butyrate Concentration 0.85 mg/mL



Butyrate Percent

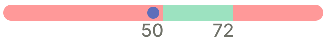
✓ Butyrate Percent 19.70

Propionate Percent

✓ Propionate Percent 28.50

Acetate Percent

⚠ Acetate Percent 46.90

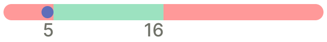


Valerate Percent

✓ Valerate Percent 4.90

Total SCFA Concentration

⚠ Total SCFA Concentration 4.30 mg/mL



Short-chain fatty acids

Beta-glucuronidase

⚠	Beta-glucuronidase	9788.20 U/h*g	4000 9400

Digestion & absorption markers

Muscle fibers

✓	Muscle fibers	None

Vegetable fibers

✓	Vegetable fibers	Rare

Fiber Digestion

✓	Cellulose	1246.48 rpkm	900 1100
⚠	Resistant starch	2466.83 rpkm	2550 2750
✓	Chitin	658.27 rpkm	448
✓	Pectin	586.89 rpkm	230 270

Complex Sugar Digestion

✓	Fructooligosaccharides	618.89 rpkm	400 600
!	Galactooligosaccharides	1069.94 rpkm	900 1100
✓	Xylooligosaccharides	349.00 rpkm	150 250
⚠	Isomaltooligosaccharides	0.00 rpkm	9 11

Protein Breakdown

✓	Protein breakdown	450.42 rpkm	444 600 700

Color

✓	Color	Brown

Consistency

✓	Consistency	Soft

Pancreatic Elastase

✓	Pancreatic Elastase	285.00 ug/g	200

Fecal Fats

✓	Fecal Fats	Few

Digestion & absorption markers

Carbohydrates

✓ Carbohydrates	Negative	

pH

✓ pH	6.50	5.8 7

Vitamin Production

✓ Vitamin B2	977.05 rpkm	938
✓ Vitamin B7	571.67 rpkm	351
✓ Vitamin B9	295.66 rpkm	263
✓ Vitamin B12	1939.36 rpkm	1524
✓ Vitamin K	407.52 rpkm	183

Histamine-producing Species

✓ Histamine-producing species	0.00%	0.05% 0.5% 1.5%

Balance and robustness

Major Bacterial Phyla

✓ Bacteroidota	46.53%	10%
✓ Firmicutes	47.23%	
✓ Actinobacteriota	1.65%	0.5% 1.5%
✓ Proteobacteria	2.62%	5%
✓ Fusobacteriota	0.60%	

Microbiome Diversity

✓ Shannon diversity	5.81	5.1 5.5 6.3

Common Microbiome Members

✓ Bacteroides	21.91%	
✓ Bacteroides fragilis	0.19%	
✓ Prevotella	0.00%	0.5% 40%
✓ Ruminococcus	3.49%	4% 15%

Balance and robustness	✓ Ruminococcus gnavus	1.52%	
	✓ Blautia	12.95%	1%
	✓ Roseburia	0.57%	0.1%
	✓ Phocaeicola dorei	4.36%	
	Gut Ratio		
	✓ Firmicutes / Bacteroidota ratio	1.01	30
	✓ Proteobacteria / Actinobacteriota ratio	1.59	12
	✓ Prevotella / Bacteroides ratio	0.00	

Your Microbiome Breakdown

This shows what was detected in the sample, but is not meant to provide an evaluation if your levels are optimal.

● Beneficial 40% ● Variable 42% ● Unfriendly 0% ● Unknown 18%

Top 20 species

Metric	Result	Description
● **Bacteroides stercoris**	12.09%	*B. stercoris* appears to be an unfriendly *Bacteroides* species. Studies suggest it may have something to do with type 1 diabetes and Crohn's disease. Outside of the gut, it can cause infection.
● **Phocaeicola vulgatus**	10.88%	*P. vulgatus* is one of the most abundant bacteria in the human gut, detected very early in babies. People with cardiovascular disease have low levels of *P. vulgatus* which could indicate it is a beneficial bacterium. But women with polycystic ovary syndrome have high levels of it. And *P. vulgatus* has been associated with Crohn's disease and ulcerative colitis, although the effects depend on the strain. Also, when in high numbers throughout the first two years of life, it may contribute to the development of Type 1 diabetes.
● **Phocaeicola dorei**	4.36%	*P. dorei* are very common in the gut of adults and babies. Some studies have found that in children with a family history of type 1 diabetes (T1D), high levels of *P. dorei* may be associated with T1D development. In babies, it's been found that the risk of developing T1D increases when *P. dorei* levels are high, *Bifidobacterium* are low, and *Enterobacteriaceae* are absent to train the baby's immune system. When present at levels higher than ideal, this will be flagged in the Balance and Robustness category of your results.

Note: This microbiome report is exclusively intended to be used for wellness purposes and to educate you about the microbes in your body. The tests we offer are not intended to diagnose or treat disease, or to substitute a physician's consultation.The microbes we talk about in your report, and their associations, are based on emerging scientific research. Feel free to share this with your physician or practitioner. These insights are determined by evaluating current research and may change over time to reflect the most up to date research available.

● **Blautia_A wexlerae**	4.01%	*B. wexlerae* is one of the most abundant *Blautia* species in humans. Along with a healthy diet high in fiber, it may contribute to healthy metabolism. High levels of *B. wexlerae* may protect against obesity, insulin resistance, eczema and inflammation.
● **Fusicatenibacter saccharivorans**	3.23%	*F. saccharivorans* is a beneficial bacterium that produces short-chain fatty acids and promotes the production of anti-inflammatory molecules. People with active ulcerative colitis or rheumatoid arthritis have low levels of *F. saccharivorans*.
● **Bacteroides xylanisolvens**	2.98%	*B. xylanisolvens* is very good at digesting soluble fiber from fruits and insoluble fiber from cereals. It contributes to gut health by transforming fiber into beneficial short-chain fatty acids. We don't know for sure, but it may be protective against certain diseases. People with atherosclerosis and children with type 1 diabetes have low levels of *B. xylanisolvens* in their gut.
● **Parabacteroides merdae**	1.97%	*Parabacteroides merdae*, previously known as *Bacteroides merdae* are a variable species found in the human gut. This means this species can either disrupt your health or benefit it. Some studies have associated high numbers of *P. merdae* to a variety of health conditions, such as: • Ulcerative colitis • Cardiovascular disease • Parkinson's disease On the good side, *P. merdae* has been associated with longevity. Luckily, having *P. merdae* in your gut isn't much of a concern unless its populations grow out of balance.
● **Agathobacter rectalis**	1.85%	*A. rectalis* is a beneficial bacterium found in the gut of many people. It's a butyrate producer whose levels increase when babies start eating solid foods. According to one study, very low levels of *A. rectalis* may contribute to inflammatory bowel syndrome. But too much of it may be associated with obesity. So better to keep *A. rectalis* at that sweet spot. If you need to give it a boost, you can add more fiber to your diet.
● **Ruminococcus_A sp003011855**	1.84%	*Ruminococcus_A sp003011855* is also known as *Oliverpabstia intestinalis*. This is a newly described species so we don't know much about it. We can tell you that these bugs belong to the *Lachnospiraceae* family. Bacteria from this family help you digest carbohydrates and produce short-chain fatty acids (SCFAs) that protect against inflammation.

🟠 **Bacteroides caccae**	1.80%	*B. caccae* is a variable bacterium in your gut microbiome. Laboratory experiments suggest that it contributes to gut health by protecting the gut barrier from unfriendly bacteria. However, if your *B. caccae* levels are too high, you may get into trouble. High amounts of *B. caccae* may contribute to inflammation and development of: • Type 2 diabetes • Inflammatory bowel disease • Obesity Rarely, it can cause serious blood infections. Luckily, you can keep your levels of *B. caccae* in the sweet spot by eating a healthy anti-inflammatory diet.
🟢 **Blautia_A wexlerae_A**	1.72%	*B. wexlerae* is one of the most abundant *Blautia* species in humans. Along with a healthy diet high in fiber, it may contribute to healthy metabolism. High levels of *B. wexlerae* may protect against obesity, insulin resistance, eczema and inflammation.
🟠 **Parabacteroides distasonis**	1.62%	*P. distasonis* is a variable species found in the gut microbiome of many healthy people. The species can disrupt your health or benefit it. Scientists have linked it to a variety of health conditions, when in high counts and outside of the gut, including: • Inflammatory bowel disease • Cardiovascular disease • Autoimmune disease • Diabetes and gestational diabetes • Abscesses However, the species may play a protective role against colorectal cancer and obesity. Luckily, having *P. distasonis* in your gut isn't much of a concern unless its populations grow out of balance.
🟠 **Ruminococcus_B gnavus**	1.52%	*R. gnavus* can be part of a healthy gut microbiome. But when its numbers go up, it may become a problem. Too much *R. gnavus* can break down the protective gut mucus layer and induce strong inflammation. In adults, high levels of *R. gnavus* have been associated with: • Crohn's disease • Ulcerative colitis • Type 1 and type 2 diabetes • Celiac disease In babies, high levels of *R. gnavus* have been associated with the atopic march and allergic diseases. Research shows that the probiotic species *Bifidobacterium infantis* can help decrease the levels of *R. gnavus*. However, *R. gnavus* are variable bugs because low levels seem to offer protection against eczema symptoms in babies. As it turns out, some *R. gnavus* strains seem to be friendly and don't cause high inflammation.
🟢 **Blautia sp003287895**	1.39%	This is a newly detected species of *Blautia* so we don't know much about it. Like most *Blautia*, it probably thrives on plant-based foods and provides benefits to your gut.

🟠 **Sutterella wadsworthensis_A**	1.35%	*S. wadsworthensis* doesn't seem to induce inflammation on its own, but it may negatively affect the antibacterial immune response in the gut. For people with ulcerative colitis, high levels of *S. wadsworthensis* predict poor outcomes after surgery or after fecal microbiota transplantation. However, people with inflammatory bowel syndrome have lower levels of *S. wadsworthensis* than healthy people. So the role of this bacterium in inflammatory gut diseases is not totally clear.
🟢 **Anaerostipes hadrus_B**	1.30%	*A. hadrus* is a beneficial bacterium in your gut that produces butyrate. It has been associated with a healthy weight and with high cholesterol levels, but of the good one (HDL). You can increase *A. hadrus* levels by eating inulin. However, if you have an inflammatory bowel disease, you may want to keep its levels on the low side.
🟢 **Bacteroides uniformis**	1.28%	Lots of healthy people have *B. uniformis* in their gut. This bacterium is very good at digesting a wide range of plant-based foods. It has anti-inflammatory properties that keep your gut healthy. It may also have a role in reducing binge eating and anxiety. Breastfeeding is a good way to boost *B. uniformis* levels in babies.
⚪ **KLE1615 sp900066985**	1.23%	Scientists don't know enough about this species to classify it or tell you anything about it. This shows how new microbiome research really is! We will keep updating our information as research advances.
🟢 **Blautia_A massiliensis**	1.17%	*B. massiliensis* was first isolated from human feces in 2017. Although most *Blautia* species are known to contribute to a healthy gut this one may have a different role. One study showed that a plant-based diet increased the levels of *Blautia obeum* and *Blautia faecis*. Instead, the levels of *B. massiliensis* decreased. Therefore, it may be that *B. massiliensis* is not as fond of fiber as other *Blautia* species.
🟢 **Blautia_A sp003480185**	1.16%	This is a newly detected species of *Blautia* so we don't know much about it. Like most *Blautia*, it probably thrives on plant-based foods and provides benefits to your gut.

All species

🟢 Anaerostipes hadrus	1.11%	🟢 Barnesiella intestinihominis	1.10%
🟠 Mediterraneibacter torques	1.09%	🟠 Bacteroides ovatus	1.02%
🟠 Catenibacterium sp000437715	0.90%	⚪ CAG-495 sp001917125	0.89%
⚪ UBA1691 sp900544375	0.88%	🟢 Blautia_A faecis	0.86%
🟢 Dysosmobacter welbionis	0.85%	🟢 Anaerobutyricum hallii	0.75%
🟢 Blautia_A caecimuris	0.74%	🟢 Lachnospira rogosae_A	0.71%
🟠 Alistipes putredinis	0.71%	🟢 Alistipes shahii	0.71%
⚪ Desulfovibrio piger_A	0.71%	🟢 Blautia_A obeum	0.68%
🟢 Bacteroides faecis	0.66%	🟠 Flavonifractor plautii	0.66%
🟢 Bacteroides thetaiotaomicron	0.64%	🟢 Alistipes onderdonkii	0.63%
🟢 Megamonas funiformis	0.62%	⚪ Fusobacterium_B sp900545035	0.58%
⚪ UBA9502 sp900538475	0.57%	🟢 Odoribacter splanchnicus	0.55%
🟢 Paraprevotella clara	0.48%	⚪ Megasphaera stantonii	0.46%
🟢 Ruminiclostridium_E siraeum	0.43%	🟢 Ruthenibacterium lactatiformans	0.42%
⚪ Amedibacterium intestinale	0.41%	🟢 Butyricimonas paravirosa	0.39%
🟠 Enterocloster bolteae	0.38%	🟢 Eubacterium_I ramulus	0.38%
🟢 Faecalibacterium prausnitzii_D	0.37%	🟢 Dorea formicigenerans	0.37%
🟢 Faecalibacterium prausnitzii_G	0.36%	🟢 Bacteroides cellulosilyticus	0.36%
🟢 Blautia_A sp003471165	0.36%	🟢 Flavonifractor sp000508885	0.36%
🟢 Dorea_A longicatena	0.35%	⚪ UMGS1375 sp900066615	0.32%
🟢 Bacteroides finegoldii	0.32%	🟢 Roseburia inulinivorans	0.30%
🟢 Blautia_A schinkii	0.30%	⚪ Agathobaculum sp003481705	0.29%
⚪ Evtepia gabavorous	0.27%	⚪ Anaerotignum sp001304995	0.26%
🟢 Mediterraneibacter faecis	0.26%	⚪ CAG-41 sp900066215	0.26%
⚪ Emergencia timonensis	0.25%	⚪ Enterocloster sp001517625	0.25%
⚪ UMGS1071 sp900542375	0.25%	🟢 Dorea_A longicatena_B	0.25%
⚪ Bilophila sp900550745	0.24%	🟢 Bariatricus comes	0.22%
⚪ CAG-81 sp000435795	0.22%	🟠 Sutterella wadsworthensis	0.22%
🟢 Phocaeicola sp002493165	0.21%	⚪ Faecalimonas umbilicata	0.21%

⚪ Lawsonibacter sp902363045	0.20%	⚪ Clostridium_Q sp000435655	0.19%
⚪ CAG-145 sp000435715	0.18%	🟠 Collinsella sp003466125	0.16%
🟢 Phocaeicola sp900554435	0.16%	🟢 Gemmiger qucibialis	0.15%
⚪ Dysosmobacter sp014297375	0.15%	🟢 Butyricimonas faecihominis	0.15%
🟠 Collinsella sp900759435	0.15%	🟠 Bacteroides fragilis	0.14%
⚪ Bacteroides salyersiae	0.14%	⚪ Schaedlerella glycyrrhizinilytica	0.14%
🟢 Butyricimonas virosa	0.14%	🟢 Faecalimonas phoceensis	0.13%
🟢 Roseburia sp900552665	0.13%	⚪ Agathobacter sp900317585	0.12%
⚪ Romboutsia timonensis	0.12%	🟢 Blautia_A sp900120195	0.12%
⚪ Phascolarctobacterium_A succinatutens	0.12%	🟢 Faecalibacterium prausnitzii_C	0.11%
🟢 Bifidobacterium longum	0.11%	🔴 Streptococcus anginosus	0.11%
🟠 Alistipes finegoldii	0.11%	🟠 Bilophila wadsworthia	0.11%
🟢 Bacteroides intestinalis	0.11%	🟢 Faecalibacterium sp900539885	0.10%
⚪ Lawsonibacter sp000177015	0.10%	⚪ Slackia_A piriformis	0.10%
🟠 Clostridium_AQ innocuum	0.10%	⚪ GCA-900066135 sp900543575	0.10%
⚪ Schaedlerella sp900066545	0.10%	⚪ Bacteroides sp003463205	0.09%
🟢 Roseburia intestinalis	0.09%	🟢 Agathobaculum butyriciproducens	0.09%
🟢 Agathobacter faecis	0.09%	🟢 Phocaeicola plebeius_A	0.09%
🟢 Faecalibacterium sp900539945	0.09%	⚪ Enterocloster sp000431375	0.08%
🟠 Erysipelatoclostridium ramosum	0.08%	⚪ Agathobacter sp900546625	0.08%
🟠 Eggerthella lenta	0.08%	⚪ Gordonibacter urolithinfaciens	0.08%
🟠 Collinsella aerofaciens_G	0.08%	🟢 Eubacterium_G sp900556905	0.08%
🟢 Eubacterium_G sp000435815	0.08%	🟢 Lachnospira eligens_A	0.08%
⚪ CAG-317 sp900543415	0.08%	⚪ Clostridium_Q sp003024715	0.08%
🟢 Acetatifactor sp900066565	0.08%	⚪ Lawsonibacter sp900066645	0.08%
⚪ Victivallis sp002998355	0.08%	⚪ Erysipelatoclostridium spiroforme	0.08%
🟢 Lachnospira sp900316325	0.08%	⚪ Bacteroides sp900066265	0.07%
⚪ Catenibacterium sp900540685	0.07%	⚪ UBA9502 sp900540335	0.07%
⚪ Ruminococcus_A faecicola	0.07%	⚪ Anaerobutyricum sp900554965	0.07%
🟠 Collinsella sp003487125	0.07%	🟢 Hungatella effluvii	0.07%
🟢 Anaerobutyricum soehngenii	0.07%	🟢 Eubacterium_F sp003491505	0.07%

🟠 Collinsella sp900549355	0.06%
⚪ Holdemania sp900120005	0.06%
🟢 Alistipes senegalensis	0.06%
🟠 Enterocloster clostridioformis	0.06%
🟢 Blautia_A wexlerae_B	0.06%
⚪ TF01-11 sp001414325	0.05%
🟢 Blautia sp001304935	0.05%
🟠 Collinsella sp002232035	0.05%
⚪ Succinivibrio sp000431835	0.06%
🟢 Intestinimonas butyriciproducens	0.06%
🟢 Catenibacterium mitsuokai	0.06%
⚪ Paraprevotella sp900548345	0.06%
⚪ UBA9475 sp900549885	0.06%
🟢 Bifidobacterium infantis	0.05%
⚪ Catenibacillus sp900553975	0.05%
⚪ UMGS1670 sp900548595	0.05%

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