

#AV500L  
**Prep Barrel Compost**

PARCEL

VARIETY

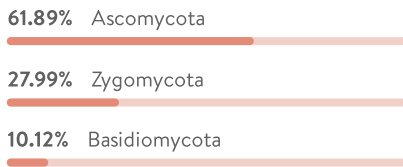
DATE

19-Jun-2019

**MICROBIAL POPULATION**

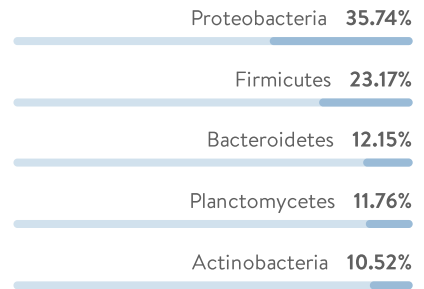
All the information shown in this microbial report is based on the detected presence of **447** different species.

FUNGAL  
PHYLUM DISTRIBUTION



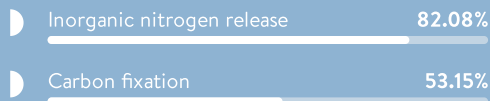
FUNGUS BACTERIA

BACTERIAL  
PHYLUM DISTRIBUTION

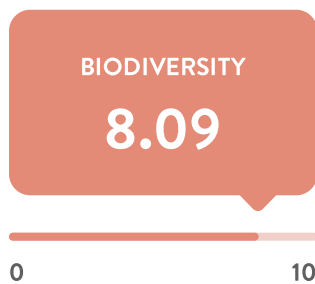


**CONCLUSIONS**

**STRENGTHS**



**BIOSUSTAINABILITY**



Richness, evenness and equilibrium of microbial species



Capability of soil microbial communities to perform multiple functions

## BACTERIAL QUANTIFICATION

### METHODOLOGY

The absolute quantification of bacterial communities using **Next-Gen sequencing** enables the cell number measurements and, thus, the knowledge of the total microbial loads among a sample

The present analysis relies on the application of a **spike-in of exogenous bacterial** with known microbial composition into crude soil amendment samples, under the ZymoBionics Spike-in Control I technology. After sequencing and data processing, the relative abundance of the exogenous bacterial strains and the known Spike-in cell input were used to transform relative abundances of all bacteria strains in the sample to absolute abundance.

Data in this report correspond to the average absolute abundance obtained from three technical replicates.

### LIST OF MAJOR BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

#### IN THIS ORDER OF MAGNITUDE

11 Microorganisms  
38.03% of the whole quantification

e+8

1	Planctomyces sp.	2.13E+08
2	Azospira sp.	1.84E+08
3	Rhodoplanes sp.	1.81E+08
4	Nitrososphaera sp.	1.59E+08
5	Bradyrhizobium sp.	1.54E+08
6	Hyphomicrobium sp.	1.45E+08
7	Clostridium sp.	1.32E+08
8	Bacteroides sp.	1.30E+08
9	Iamia sp.	1.26E+08
10	Ilumatobacter sp.	1.04E+08
11	Hyphomicrobium zavarzinii	1.03E+08

#### IN THIS ORDER OF MAGNITUDE

68 Microorganisms  
50.25% of the whole quantification

e+7

12	Chryseolinea sp.	9.77E+07
13	Rhodobium sp.	9.20E+07
14	Nitrospira sp.	7.55E+07
15	Blastopirellula sp.	6.63E+07
16	Flavobacterium sp.	6.53E+07
17	Methylobacter marinus	5.80E+07
18	Escherichia sp.	5.60E+07
19	Pirellula sp.	5.59E+07
20	Solirubrobacter sp.	5.56E+07
21	Nocardioides sp.	5.34E+07
22	Rhodopirellula sp.	5.22E+07
23	Coproccoccus sp.	4.98E+07

## LIST OF MAJOR BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

24	<i>Mycobacterium sp.</i>	4.80E+07
25	<i>Aquicella sp.</i>	4.71E+07
26	<i>Amaricoccus sp.</i>	4.41E+07
27	<i>Microthrix sp.</i>	4.35E+07
28	<i>Legionella sp.</i>	4.30E+07
29	<i>Sandaracinus sp.</i>	4.15E+07
30	<i>Altererythrobacter sp.</i>	4.08E+07
31	<i>Sedimentibacter sp.</i>	4.04E+07
32	<i>Mariprofundus sp.</i>	3.96E+07
33	<i>Phycisphaera sp.</i>	3.94E+07
34	<i>Novosphingobium sp.</i>	3.87E+07
35	<i>Chthoniobacter sp.</i>	3.80E+07
36	<i>Gemmatimonas sp.</i>	3.66E+07
37	<i>Steroidobacter sp.</i>	3.60E+07
38	<i>Agromyces bauzanensis</i>	3.57E+07
39	<i>Mycobacterium celatum</i>	3.03E+07
40	<i>Xiphinematobacter sp.</i>	2.85E+07
41	<i>Acidovorax sp.</i>	2.77E+07
42	<i>Conexibacter sp.</i>	2.75E+07
43	<i>Ensifer sp.</i>	2.74E+07
44	<i>Mesorhizobium ciceri</i>	2.61E+07
45	<i>Demequina sp.</i>	2.56E+07
46	<i>Pedomicrobium sp.</i>	2.47E+07
47	<i>Gracilibacter sp.</i>	2.46E+07
48	<i>Gemmata sp.</i>	2.44E+07
49	<i>Mesorhizobium sp.</i>	2.39E+07
50	<i>Aquamicrobium sp.</i>	2.33E+07
51	<i>Bryobacter sp.</i>	2.31E+07
52	<i>Butyrivibrio sp.</i>	2.15E+07
53	<i>Mesorhizobium tianshanense</i>	2.11E+07
54	<i>Arenimonas sp.</i>	1.93E+07
55	<i>Ornatilinea sp.</i>	1.87E+07
56	<i>Syntrophomonas sp.</i>	1.77E+07
57	<i>Rubritalea sp.</i>	1.74E+07
58	<i>Haliea sp.</i>	1.57E+07
59	<i>Filimonas sp.</i>	1.53E+07
60	<i>Sedimentibacter hongkongensis</i>	1.47E+07
61	<i>Brassicibacter mesophilus</i>	1.42E+07

## LIST OF MAJOR BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

62	<i>Blautia sp.</i>	1.39E+07	78	<i>Sorangium sp.</i>	9.90E+06
63	<i>Reyranella sp.</i>	1.37E+07	79	<i>Arthrobacter sp.</i>	8.41E+06
64	<i>Bauldia sp.</i>	1.30E+07	80	<i>Pelotomaculum sp.</i>	8.30E+06
65	<i>Agaricola sp.</i>	1.30E+07	81	<i>Pelagibius sp.</i>	7.82E+06
66	<i>Caldilinea sp.</i>	1.28E+07	82	<i>Luteolibacter sp.</i>	7.76E+06
67	<i>Bacillus coahuilensis</i>	1.28E+07	83	<i>Fodinicola sp.</i>	7.28E+06
68	<i>Haloferula sp.</i>	1.25E+07	84	<i>Anaerostipes sp.</i>	7.25E+06
69	<i>Turicibacter sp.</i>	1.18E+07	85	<i>Ruminococcus sp.</i>	7.12E+06
70	<i>Haliangium sp.</i>	1.17E+07	86	<i>Bacillus sp.</i>	6.71E+06
71	<i>Marmoricola sp.</i>	1.10E+07	87	<i>Rhodococcus sp.</i>	6.18E+06
72	<i>Alysiosphaera sp.</i>	1.09E+07	88	<i>Lautropia sp.</i>	5.29E+06
73	<i>Rhodobacter sp.</i>	1.08E+07	89	<i>Singulisphaera sp.</i>	5.07E+06
74	<i>Bdellovibrio sp.</i>	1.08E+07	90	<i>Anaerovorax sp.</i>	4.63E+06
75	<i>Ilumatobacter fluminis</i>	1.06E+07	91	<i>Dehalobacterium sp.</i>	4.03E+06
76	<i>Pleomorphomonas sp.</i>	1.02E+07	92	<i>Paenibacillus sp.</i>	3.94E+06
77	<i>Sufflavibacter sp.</i>	1.01E+07	93	<i>Marinicella sp.</i>	3.84E+06
			94	<i>Desulfotomaculum sp.</i>	3.66E+06
			95	<i>Pseudomonas sp.</i>	3.49E+06







IN THIS ORDER OF MAGNITUDE

22 Microorganisms  
2.85% of the whole quantification

e+6

## LIST OF MAJOR BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

96	 <i>Alkaliphilus sp.</i>	 2.99E+06
97	 <i>Lysinibacillus sp.</i>	 2.67E+06
98	 <i>Clostridium neonatale</i>	 2.60E+06

## NOTES



Genus predictions ('sp') that have species appearing in the CDFA list provided. (Species might or might not be present)



Species that appears explicitly highlighted in the CDFA list

# PLANT HEALTH IMPROVEMENT

Biocontrol agents, plant growth promoting organisms

## BIOCONTROL



Microbial species grouped according to the type of pest they encounter, capable of preventing pathogenic species from taking hold or proliferation

Fungicide agents

0.04%

Bactericide agents

NOT DETECTED

Insecticide agents

NOT DETECTED

Nematicide agents

NOT DETECTED

## HORMONE PRODUCTION



Microbial species grouped according to the type of phytohormone they generate

Auxin production (IAA)

CELL DIVISION

STEM ELONGATION

9.33%

Cytokinin production (CK)

CELL PROLIFERATION

CELL DIFFERENTIATION

2.79%

Gibberellin production (GA)

STEM ELONGATION

GERMINATION

FLOWERING

1.23%

## STRESS ADAPTATION



Microbial species grouped according to their relationship with the metabolisms linked to the capability to withstand stress conditions

Exopolysaccharide production

NUTRIENT TRAP

SALINITY PROTECT.

DROUGHT PROTECT.

2.10%

ACC deaminase (ACC-d)

PATHOGEN PROTECT.

SALINITY PROTECT.

DROUGHT PROTECT.

2.95%

Heavy metal solubilization

BIOREMEDIATION

DETOXIFICATION

ALLEVIATE HEAVY METAL STRESS

1.01%

Salicylic acid (SA)

DROUGHT PROTECT.

SALINITY PROTECT.

ALLEVIATE HEAVY METAL STRESS

NOT DETECTED

Salt tolerance

SALINITY PROTECT.

ROOT GROWTH PROMOTION

2.37%

Abscisic acid (ABA)

GROWTH REGULATION

PLANT RESISTANCE

INCREASE YIELDS

0.05%

Siderophore production

IRON AVAILABILITY

BIOFERTILIZER

34.64%

# NUTRITION

Nutritional status based on the presence and mobilization of certain compounds

## MAJOR COMPOUNDS



### Carbon

#### GAIN

Carbon fixation 53.15%

#### LOSS

Aerobic respiration 75.94%

Fermentation 80.52%

Methanogenesis 44.15%

#### INDIRECT BENEFITS

Organic matter release 26.86%



### Nitrogen

#### NUTRIENT SUPPLY

Inorganic nitrogen release 82.08%

#### NUTRIENT COMPETITION

Inorganic nitrogen consumption 53.83%

#### INDIRECT BENEFITS

Inorganic nitrogen cycle health 158 / 2



### Phosphorus

#### NUTRIENT SUPPLY

Inorganic P solubilization 41.79%

#### NUTRIENT COMPETITION

Inorganic P consumption 61.86%

#### INDIRECT BENEFITS

Organic P assimilation 64.76%



### Potassium

#### NUTRIENT SUPPLY

Potassium solubilization 41.79%

#### NUTRIENT COMPETITION

Potassium consumption 75.47%

## MINOR COMPOUNDS



### Iron

Iron assimilation 35.83%



### Calcium

Calcium transport 76.05%



### Zinc

Zinc transport equilibrium 69.22%



### Copper

Copper export 60.89%



### Manganese

Manganese transport equilibrium 50.92%



### Magnesium

Magnesium transport 64.29%



### Sulfur

Sulfur cycle equilibrium 1.36 / 2



### Chlorine

Chlorine transport 83.99%

# APPENDIX

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

1	<i>Methanoculleus sp.</i>	1.87E+07
2	<i>Bythopirellula sp.</i>	9.62E+06
3	<i>Coxiella sp.</i>	9.13E+06
4	<i>Phenylobacterium sp.</i>	8.62E+06
5	<i>Rubrobacter sp.</i>	8.47E+06
6	<i>Nitrosococcus sp.</i>	8.25E+06
7	<i>Peredibacter sp.</i>	8.22E+06
8	<i>Smithella sp.</i>	7.65E+06
9	<i>Balneimonas sp.</i>	6.77E+06
10	<i>Kaistobacter sp.</i>	6.72E+06
11	<i>Coprothermobacter sp.</i>	6.20E+06
12	<i>Mogibacterium sp.</i>	5.63E+06
13	<i>Saccharimonas sp.</i>	5.47E+06
14	<i>Bradyrhizobium elkanii</i>	5.27E+06
15	<i>Hydrogenoanaerobacterium sp.</i>	4.73E+06
16	<i>Methanomassiliicoccus sp.</i>	4.72E+06
17	<i>Methylotenera sp.</i>	4.72E+06
18	<i>Papillibacter sp.</i>	4.68E+06
19	<i>Achromobacter sp.</i>	4.56E+06
20	<i>Variovorax sp.</i>	4.49E+06
21	<i>Hirschia sp.</i>	4.41E+06
22	<i>Ochrobactrum rhizogenes</i>	4.29E+06
23	<i>Anaeromyxobacter sp.</i>	4.29E+06
24	<i>Alterococcus sp.</i>	4.23E+06
25	<i>Pilimelia sp.</i>	4.22E+06
26	<i>Erythrobacter sp.</i>	4.05E+06
27	<i>Anaerosporobacter sp.</i>	3.95E+06
28	<i>Roseomonas sp.</i>	3.84E+06
29	<i>Bosea enea</i>	3.81E+06
30	<i>Anaerotruncus sp.</i>	3.75E+06
31	<i>Longispora sp.</i>	3.69E+06
32	<i>Isosphaera sp.</i>	3.62E+06
33	<i>Bdellovibrio bacteriovorus</i>	3.40E+06
34	<i>Pedosphaera sp.</i>	3.37E+06
35	<i>Arthrobacter cereus</i>	3.34E+06
36	<i>Oscillospira sp.</i>	3.14E+06
37	<i>Nannocystis exedens</i>	3.12E+06
38	<i>Filomicrobium sp.</i>	3.10E+06



## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

39	<i>Anaerospobacter populeti</i>	3.03E+06
40	<i>Roseibacillus</i> sp.	3.03E+06
41	<i>Thermomonas</i> sp.	2.93E+06
42	<i>Blastocatella</i> sp.	2.80E+06
43	<i>Enhygromyxa</i> sp.	2.79E+06
44	<i>Syntrophobacter</i> sp.	2.78E+06
45	<i>Flavonifactor</i> sp.	2.58E+06
46	<i>Roseimicrobium</i> sp.	2.58E+06
47	<i>Denitratisoma</i> sp.	2.45E+06
48	<i>Thioalkalispira</i> sp.	2.45E+06
49	<i>Lysinibacillus boronitolerans</i>	2.43E+06
50	<i>Desulfotibacter</i> sp.	2.39E+06
51	<i>Methylorosula</i> sp.	2.39E+06
52	<i>Agromyces flavus</i>	2.33E+06
53	<i>Micromonospora</i> sp.	2.32E+06
54	<i>Nordella</i> sp.	2.30E+06
55	<i>Flavobacterium reichenbachii</i>	2.29E+06
56	<i>Iamia majanohamensis</i>	2.28E+06
57	<i>Devosia insulae</i>	2.26E+06
58	<i>Methylomicrobium</i> sp.	2.26E+06
59	<i>Pseudoxanthomonas</i> sp.	2.18E+06
60	<i>Nitrolancea</i> sp.	2.13E+06
61	<i>Entotheonella</i> sp.	2.10E+06
62	<i>Bythopirellula goksoyri</i>	2.08E+06
63	<i>Affella</i> sp.	2.02E+06
64	<i>Sporichthya</i> sp.	2.00E+06
65	<i>Cellulosilyticum</i> sp.	1.88E+06
66	<i>Lysobacter</i> sp.	1.87E+06
67	<i>Anaerolinea</i> sp.	1.87E+06
68	<i>Smaragdicooccus niigatensis</i>	1.85E+06
69	<i>Alkalibacter</i> sp.	1.83E+06
70	<i>Devosia</i> sp.	1.81E+06
71	<i>Catenibacterium</i> sp.	1.80E+06
72	<i>Stella</i> sp.	1.75E+06
73	<i>Longispora albida</i>	1.73E+06
74	<i>Algoriphagus</i> sp.	1.57E+06
75	<i>Citricoccus xinjiangensis</i>	1.50E+06
76	<i>Brachymonas</i> sp.	1.40E+06
77	<i>Phaselicystis</i> sp.	1.37E+06
78	<i>Cellulomonas xylanilytica</i>	1.33E+06

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

79	<i>Acidothermus sp.</i>	1.32E+06
80	<i>Roseiflexus sp.</i>	1.31E+06
81	<i>Cryptanaerobacter sp.</i>	1.31E+06
82	<i>Koribacter sp.</i>	1.28E+06
83	<i>Kribbella sp.</i>	1.27E+06
84	<i>Caldicoprobacter sp.</i>	1.25E+06
85	<i>Ohtaekwangia sp.</i>	1.23E+06
86	<i>Opiritutus sp.</i>	1.23E+06
87	<i>Corynebacterium sp.</i>	1.21E+06
88	<i>Rhodococcus tukisamuensis</i>	1.19E+06
89	<i>Ornithinimicrobium pekingense</i>	1.17E+06
90	<i>Truepera sp.</i>	1.16E+06
91	<i>Pelotomaculum schinkii</i>	1.13E+06
92	<i>Leucobacter sp.</i>	1.10E+06
93	<i>Arenibacter sp.</i>	1.09E+06
94	<i>Kaistia sp.</i>	1.08E+06
95	<i>Rubellimicrobium sp.</i>	1.05E+06
96	<i>Luteimonas mephitis</i>	9.80E+05
97	<i>Massilia sp.</i>	9.63E+05
98	<i>Sporocytophaga sp.</i>	9.49E+05
99	<i>Woodsholea sp.</i>	8.98E+05
100	<i>Desulfosporosinus meridiei</i>	8.91E+05
101	<i>Proteiniclasticum sp.</i>	8.74E+05
102	<i>Captivus sp.</i>	8.70E+05
103	<i>Acidiphilium sp.</i>	8.66E+05
104	<i>Adhaeribacter sp.</i>	8.47E+05
105	<i>Acetanaerobacterium sp.</i>	8.29E+05
106	<i>Micromonospora columellifera</i>	8.18E+05
107	<i>Metachlamydia lacustris</i>	8.15E+05
108	<i>Catelliglobospora sp.</i>	8.15E+05
109	<i>Actinotalea sp.</i>	8.08E+05
110	<i>Dehalobacter sp.</i>	8.06E+05
111	<i>Faecalibacterium sp.</i>	7.94E+05
112	<i>Sphingomonas sp.</i>	7.87E+05
113	<i>Pseudomonas flexibilis</i>	7.73E+05
114	<i>Epulopiscium sp.</i>	7.73E+05
115	<i>Acinetobacter sp.</i>	7.56E+05
116	<i>Actinocorallia sp.</i>	7.35E+05
117	<i>Cohnella arctica</i>	7.26E+05
118	<i>Intestinimonas sp.</i>	7.18E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

119	<i>Pseudolabrys sp.</i>	7.17E+05
120	<i>Ruminococcus flavefaciens</i>	7.13E+05
121	<i>Pusillimonas sp.</i>	6.98E+05
122	<i>Aeromicrobium sp.</i>	6.84E+05
123	<i>Rhodomicrobium sp.</i>	6.84E+05
124	<i>Dethiobacter sp.</i>	6.77E+05
125	<i>Nitrosoarchaeum sp.</i>	6.75E+05
126	<i>Nocardioides simplex</i>	6.28E+05
127	<i>Haloplasma sp.</i>	6.08E+05
128	<i>Verrucomicrobium sp.</i>	6.07E+05
129	<i>Oxobacter sp.</i>	6.03E+05
130	<i>Oscillibacter sp.</i>	5.99E+05
131	<i>Waddlia sp.</i>	5.80E+05
132	<i>Niabella sp.</i>	5.60E+05
133	<i>Muricauda sp.</i>	5.59E+05
134	<i>Odyssella sp.</i>	5.53E+05
135	<i>Eilatimonas sp.</i>	5.49E+05
136	<i>Criblamydia sp.</i>	5.39E+05
137	<i>Litorilinea sp.</i>	5.24E+05
138	<i>Novispirillum sp.</i>	5.16E+05
139	<i>Defluviicoccus sp.</i>	5.15E+05
140	<i>Sporosarcina sp.</i>	5.11E+05
141	<i>Quadrisphaera sp.</i>	4.97E+05
142	<i>Acholeplasma sp.</i>	4.97E+05
143	<i>Beutenbergia cavernae</i>	4.83E+05
144	<i>Bosea sp.</i>	4.83E+05
145	<i>Phyllobacterium sp.</i>	4.74E+05
146	<i>Comamonas sp.</i>	4.47E+05
147	<i>Pseudomonas graminis</i>	4.39E+05
148	<i>Pilimelia pattaloongensis</i>	4.28E+05
149	<i>Neochlamydia sp.</i>	4.27E+05
150	<i>Bacillus aryabhatai</i>	4.25E+05
151	<i>Micromonospora hermanusense</i>	4.17E+05
152	<i>Fastidiosipila sp.</i>	4.14E+05
153	<i>Solibacter sp.</i>	4.14E+05
154	<i>Fluviicola sp.</i>	4.07E+05
155	<i>Legionella pneumophila</i>	4.05E+05
156	<i>Pseudospirillum sp.</i>	3.99E+05
157	<i>Paenibacillus alginolyticus</i>	3.93E+05
158	<i>Constrictibacter sp.</i>	3.87E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

159	<i>Caloramator sp.</i>	3.84E+05	179	<i>Oceanobacillus sp.</i>	2.53E+05
160	<i>Reichenbachiella sp.</i>	3.82E+05	180	<i>Pseudomonas luteola</i>	2.51E+05
161	<i>Nocardia coubleae</i>	3.68E+05	181	<i>Christensenella sp.</i>	2.49E+05
162	<i>Haloactinopolyspora sp.</i>	3.55E+05	182	<i>Collinsella sp.</i>	2.46E+05
163	<i>Brevundimonas alba</i>	3.52E+05	183	<i>Planifilum sp.</i>	2.42E+05
164	<i>Chryseobacterium indologenes</i>	3.45E+05	184	<i>Limnobacter sp.</i>	2.38E+05
165	<i>Streptomyces sp.</i>	3.42E+05	185	<i>Blastococcus sp.</i>	2.35E+05
166	<i>Rhizobium etli</i>	3.31E+05	186	<i>Anaerobranca sp.</i>	2.31E+05
167	<i>Byssovorax sp.</i>	3.22E+05	187	<i>Pedosphaera parvula</i>	2.30E+05
168	<i>Methanobrevibacter sp.</i>	3.22E+05	188	<i>Beggiatoa sp.</i>	2.29E+05
169	<i>Rhodococcus equi</i>	3.07E+05	189	<i>Anaerospora sp.</i>	2.29E+05
170	<i>Caulobacter sp.</i>	2.90E+05	190	<i>Acetitomaculum sp.</i>	2.26E+05
171	<i>Atopobium sp.</i>	2.77E+05	191	<i>Halocella sp.</i>	2.25E+05
172	<i>Pseudonocardia halophobica</i>	2.77E+05	192	<i>Pseudomonas azotoformans</i>	2.21E+05
173	<i>Dichotomicrobium sp.</i>	2.76E+05	193	<i>Defluviimonas sp.</i>	2.21E+05
174	<i>Desulfuromonas sp.</i>	2.76E+05	194	<i>Pseudomonas peli</i>	2.10E+05
175	<i>Rhodococcus corynebacterioides</i>	2.69E+05	195	<i>Aeribacillus sp.</i>	2.09E+05
176	<i>Owenweeksia sp.</i>	2.63E+05	196	<i>Agromyces ulmi</i>	2.07E+05
177	<i>Rickettsia sp.</i>	2.62E+05	197	<i>Chlorochromatium sp.</i>	2.07E+05
178	<i>Protochlamydia sp.</i>	2.56E+05	198	<i>Pseudoxanthomonas mexicana</i>	2.07E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

199	<i>Ammoniphilus</i> sp.	2.05E+05	219	<i>Paracoccus chinensis</i>	1.38E+05
200	<i>Roseburia</i> sp.	2.04E+05	220	<i>Luedemannella helvata</i>	1.35E+05
201	<i>Rhabdochlamydia</i> sp.	2.00E+05	221	<i>Shimazuella</i> sp.	1.35E+05
202	<i>Spirochaeta</i> sp.	1.93E+05	222	<i>Microcunatus</i> sp.	1.34E+05
203	<i>Rickettsiella</i> sp.	1.93E+05	223	<i>Chitinophaga</i> sp.	1.31E+05
204	<i>Nakamurella</i> sp.	1.84E+05	224	<i>Flavisolibacter</i> sp.	1.31E+05
205	<i>Methylovirgula ligni</i>	1.84E+05	225	<i>Litorilinea aerophila</i>	1.31E+05
206	<i>Desulfovibrio africanus</i>	1.80E+05	226	<i>Tsukamurella pulmonis</i>	1.31E+05
207	<i>Georgenia satyanarayanai</i>	1.80E+05	227	<i>Promicromonospora sukumoe</i>	1.29E+05
208	<i>Azoarcus</i> sp.	1.73E+05	228	<i>Amoebophilus</i> sp.	1.25E+05
209	<i>Kiloniella</i> sp.	1.69E+05	229	<i>Methylotenera mobilis</i>	1.25E+05
210	<i>Ignavibacterium</i> sp.	1.52E+05	230	<i>Parvibaculum</i> sp.	1.25E+05
211	<i>Methylacidiphilum</i> sp.	1.52E+05	231	<i>Sphingopyxis</i> sp.	1.25E+05
212	<i>Pseudonocardia</i> sp.	1.48E+05	232	<i>Dongia</i> sp.	1.25E+05
213	<i>Terrabacter</i> sp.	1.45E+05	233	<i>Sporobacter</i> sp.	1.25E+05
214	<i>Dietzia maris</i>	1.41E+05	234	<i>Pasteuria</i> sp.	1.19E+05
215	<i>Euzebya</i> sp.	1.38E+05	235	<i>Flavobacterium succinicans</i>	1.16E+05
216	<i>Methanobacterium</i> sp.	1.38E+05	236	<i>Streptococcus</i> sp.	1.13E+05
217	<i>Turneriella parva</i>	1.38E+05	237	<i>Catellatospora citrea</i>	1.10E+05
218	<i>Criblamydia sequanensis</i>	1.38E+05	238	<i>Taibaiella</i> sp.	1.10E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

239	<i>Clostridium perfringens</i>	1.09E+05	259	<i>Parvularcula</i> sp.	7.60E+04
240	<i>Tepidamorphus gemmatus</i>	1.01E+05	260	<i>Salana</i> sp.	7.60E+04
241	<i>Propionicicella</i> sp.	9.65E+04	261	<i>Sneathiella</i> sp.	7.60E+04
242	<i>Caldanaerocella</i> sp.	9.22E+04	262	<i>Thalassobaculum</i> sp.	7.60E+04
243	<i>Chelatococcus</i> sp.	9.22E+04	263	<i>Actinoplanes</i> sp.	7.24E+04
244	<i>Comamonas composti</i>	9.22E+04	264	<i>Chryseobacterium</i> sp.	6.88E+04
245	<i>Portibacter</i> sp.	9.17E+04	265	<i>Enterorhabdus</i> sp.	6.88E+04
246	<i>Thermincola</i> sp.	9.17E+04	266	<i>Fimbriimonas</i> sp.	6.88E+04
247	<i>Alicyclobacillus</i> sp.	8.98E+04	267	<i>Glycomyces mongolensis</i>	6.88E+04
248	<i>Chloroflexus</i> sp.	8.74E+04	268	<i>Methylobacillus flagellatus</i>	6.88E+04
249	<i>Elioraea tepidiphila</i>	8.74E+04	269	<i>Planctomyces maris</i>	6.88E+04
250	<i>Rhizobium</i> sp.	8.74E+04	270	<i>Garciella</i> sp.	6.56E+04
251	<i>Flavobacterium gelidilacus</i>	8.57E+04	271	<i>Williamsia faeni</i>	6.56E+04
252	<i>Blastococcus aggregatus</i>	8.31E+04	272	<i>Singulisphaera acidiphila</i>	6.39E+04
253	<i>Geobacillus</i> sp.	8.30E+04	273	<i>Anaerofustis</i> sp.	6.23E+04
254	<i>Arthrobacter nitroguajacolicus</i>	8.28E+04	274	<i>Caulobacter henricii</i>	6.23E+04
255	<i>Anaerosinus</i> sp.	7.74E+04	275	<i>Desulfobulbus</i> sp.	6.23E+04
256	<i>Blastomonas</i> sp.	7.60E+04	276	<i>Geobacter humireducens</i>	6.23E+04
257	<i>Longilinea</i> sp.	7.60E+04	277	<i>Glycomyces arizonensis</i>	6.23E+04
258	<i>Parachlamydia acanthamoebae</i>	7.60E+04	278	<i>Thermaerobacter marianensis</i>	6.23E+04

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

279	<i>Clostridium bowmanii</i>	6.13E+04	299	<i>Geodermatophilus sp.</i>	4.59E+04
280	<i>Tissierella sp.</i>	6.12E+04	300	<i>Jatrophihabitans sp.</i>	4.59E+04
281	<i>Atopococcus sp.</i>	5.79E+04	301	<i>Nitriliruptor sp.</i>	4.59E+04
282	<i>Herpetosiphon sp.</i>	5.79E+04	302	<i>Nocardia rhamnosiphila</i>	4.59E+04
283	<i>Granulosicoccus sp.</i>	5.53E+04	303	<i>Simiduia areninigrae</i>	4.59E+04
284	<i>Pelosinus fermentans</i>	5.50E+04	304	<i>Skermanella sp.</i>	4.59E+04
285	<i>Trichococcus sp.</i>	5.50E+04	305	<i>Sporomusa sp.</i>	4.49E+04
286	<i>Achromobacter xylooxidans</i>	5.07E+04	306	<i>Acinetobacter lwoffii</i>	4.37E+04
287	<i>Brachybacterium conglomeratum</i>	5.07E+04	307	<i>Paenibacillus aestivum</i>	4.24E+04
288	<i>Chelativorans sp.</i>	5.07E+04	308	<i>Inquilinus sp.</i>	4.15E+04
289	<i>Georgenia sp.</i>	5.07E+04	309	<i>Methyloversatilis sp.</i>	4.15E+04
290	<i>Prosthecobacter sp.</i>	5.07E+04	310	<i>Niastella sp.</i>	4.15E+04
291	<i>Streptosporangium roseum</i>	5.07E+04	311	<i>Rhizobacter globosum</i>	4.15E+04
292	<i>Thiothrix sp.</i>	5.07E+04	312	<i>Rhodocytophaga aerolata</i>	4.15E+04
293	<i>Paenibacillus taihuensis</i>	4.99E+04	313	<i>Ruminococcus albus</i>	4.15E+04
294	<i>Paenibacillus taiwanensis</i>	4.99E+04	314	<i>Variovorax quadricarinatus</i>	4.15E+04
295	<i>Desulfosporosinus sp.</i>	4.91E+04	315	<i>Cohnella sp.</i>	4.14E+04
296	<i>Sphaerisporangium rubeum</i>	4.83E+04	316	<i>Lutispora sp.</i>	4.14E+04
297	<i>Brachymonas denitrificans</i>	4.59E+04	317	<i>Bacillus alkalitelluris</i>	4.01E+04
298	<i>Crossiella sp.</i>	4.59E+04	318	<i>Dietzia sp.</i>	3.80E+04

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

<b>319</b>	<i>Halarsenatibacter sp.</i>	3.80E+04	<b>339</b>	<i>Halomonas sp.</i>	2.53E+04
<b>320</b>	<i>Pedobacter sp.</i>	3.80E+04	<b>340</b>	<i>Alcanivorax indicus</i>	2.49E+04
<b>321</b>	<i>Pontibacter sp.</i>	3.80E+04	<b>341</b>	<i>Arthrobacter alkaliphilus</i>	2.49E+04
<b>322</b>	<i>Agrobacterium tumefaciens</i>	3.44E+04	<b>342</b>	<i>Bavariicoccus seileri</i>	2.49E+04
<b>323</b>	<i>Myxococcus sp.</i>	3.44E+04	<b>343</b>	<i>Desemzia sp.</i>	2.49E+04
<b>324</b>	<i>Streptomyces serianimatus</i>	3.44E+04	<b>344</b>	<i>Pseudobutyrvibrio sp.</i>	2.49E+04
<b>325</b>	<i>Acidocella sp.</i>	3.12E+04	<b>345</b>	<i>Rickettsiella viridis</i>	2.49E+04
<b>326</b>	<i>Gluconobacter oxydans</i>	3.12E+04	<b>346</b>	<i>Terrimonas sp.</i>	2.49E+04
<b>327</b>	<i>Hamadaea yuxiensis</i>	3.12E+04	<b>347</b>	<i>Kocuria rhizophila</i>	2.29E+04
<b>328</b>	<i>Ochrobactrum latifolia</i>	3.12E+04	<b>348</b>	<i>Sporotomaculum sp.</i>	2.29E+04
<b>329</b>	<i>Plantactinospora sp.</i>	3.12E+04	<b>349</b>	<i>Symbiobacterium thermophilum</i>	2.29E+04
<b>330</b>	<i>Noviherbaspirillum sp.</i>	3.07E+04	<b>350</b>	<i>Paenibacillus sepulcri</i>	2.23E+04
<b>331</b>	<i>Atopostipes sp.</i>	3.04E+04	<b>351</b>	<i>Bacillus clausii</i>	2.17E+04
<b>332</b>	<i>Flaviumibacter sp.</i>	3.04E+04	<b>352</b>	<i>Brevibacillus agri</i>	2.08E+04
<b>333</b>	<i>Flavisolibacter ginsengisoli</i>	3.04E+04	<b>353</b>	<i>Microbispora sp.</i>	2.08E+04
<b>334</b>	<i>Pricia sp.</i>	3.04E+04	<b>354</b>	<i>Tumebacillus sp.</i>	2.08E+04
<b>335</b>	<i>Caldalkalibacillus sp.</i>	2.90E+04	<b>355</b>	<i>Acinetobacter johnsonii</i>	1.97E+04
<b>336</b>	<i>Ferruginibacter sp.</i>	2.75E+04	<b>356</b>	<i>Proteiniborus sp.</i>	1.97E+04
<b>337</b>	<i>Methylobacterium sp.</i>	2.75E+04	<b>357</b>	<i>Kroppenstedtia eburnea</i>	1.90E+04
<b>338</b>	<i>Thermobacillus sp.</i>	2.75E+04	<b>358</b>	<i>Tepidimicrobium ultunense</i>	1.78E+04



## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

359	<i>Pelosinus sp.</i>	1.75E+04
360	<i>Thermoflavimicrobium sp.</i>	1.56E+04
361	<i>Bacillus firmus</i>	1.52E+04
362	<i>Bacillus gibsonii</i>	1.25E+04
363	<i>Paenibacillus koleovorans</i>	1.17E+04
364	<i>Paenibacillus edaphicus</i>	1.06E+04
365	<i>Paenibacillus turicensis</i>	9.58E+03
366	<i>Acetivibrio sp.</i>	0.00E+00
367	<i>Acidiferrobacter sp.</i>	0.00E+00
368	<i>Acinetobacter ursingii</i>	0.00E+00
369	<i>Actinopolymorpha cephalotaxi</i>	0.00E+00
370	<i>Adhaeribacter terreus</i>	0.00E+00
371	<i>Adlercreutzia sp.</i>	0.00E+00
372	<i>Aequorivita sp.</i>	0.00E+00
373	<i>Agrobacterium sp.</i>	0.00E+00
374	<i>Alistipes sp.</i>	0.00E+00
375	<i>Alkanibacter sp.</i>	0.00E+00
376	<i>Alteromonas sp.</i>	0.00E+00
377	<i>Amycolatopsis pigmentata</i>	0.00E+00
378	<i>Aneurinibacillus sp.</i>	0.00E+00
379	<i>Arcticibacter sp.</i>	0.00E+00
380	<i>Ardenscatena sp.</i>	0.00E+00
381	<i>Arenicella sp.</i>	0.00E+00
382	<i>Armatimonas sp.</i>	0.00E+00
383	<i>Arthrospira sp.</i>	0.00E+00
384	<i>Asticcacaulis biprosthecium</i>	0.00E+00
385	<i>Asticcacaulis solisilvae</i>	0.00E+00
386	<i>Aureimonas phyllosphaerae</i>	0.00E+00
387	<i>Azospirillum sp.</i>	0.00E+00
388	<i>Bacillus decolorationis</i>	0.00E+00
389	<i>Bacillus thermolactis</i>	0.00E+00
390	<i>Bacteriovorax sp.</i>	0.00E+00
391	<i>Brevundimonas bullata</i>	0.00E+00
392	<i>Brevundimonas diminuta</i>	0.00E+00
393	<i>Brevundimonas sp.</i>	0.00E+00
394	<i>Caenimonas sp.</i>	0.00E+00
395	<i>Cellvibrio sp.</i>	0.00E+00
396	<i>Cerasicoccus sp.</i>	0.00E+00
397	<i>Chitinophaga soli</i>	0.00E+00
398	<i>Coprobacillus sp.</i>	0.00E+00

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

399	<i>Croceibacter sp.</i>	0.00E+00
400	<i>Cryomorpha sp.</i>	0.00E+00
401	<i>Cryptosporangium sp.</i>	0.00E+00
402	<i>Cytophaga sp.</i>	0.00E+00
403	<i>Desulfocapsa sp.</i>	0.00E+00
404	<i>Dokdonella sp.</i>	0.00E+00
405	<i>Ensifer meliloti</i>	0.00E+00
406	<i>Ferrovibrio sp.</i>	0.00E+00
407	<i>Fontimonas thermophila</i>	0.00E+00
408	<i>Gemicoccus sp.</i>	0.00E+00
409	<i>Gluconobacter cerinus</i>	0.00E+00
410	<i>Gracilibacillus sp.</i>	0.00E+00
411	<i>Granulicella sp.</i>	0.00E+00
412	<i>Halorhodospira sp.</i>	0.00E+00
413	<i>Hymenobacter sp.</i>	0.00E+00
414	<i>Lactococcus lactis</i>	0.00E+00
415	<i>Limnobacter thiooxidans</i>	0.00E+00
416	<i>Luteibacter sp.</i>	0.00E+00
417	<i>Luteimonas composti</i>	0.00E+00
418	<i>Lutibacterium sp.</i>	0.00E+00
419	<i>Marinoscillum sp.</i>	0.00E+00
420	<i>Melghirimyces thermohalophilus</i>	0.00E+00
421	<i>Methanosphaera cuniculi</i>	0.00E+00
422	<i>Microtetraspora malaysiensis</i>	0.00E+00
423	<i>Mycobacterium hassiacum</i>	0.00E+00
424	<i>Nafulsella sp.</i>	0.00E+00
425	<i>Neptunomonas sp.</i>	0.00E+00
426	<i>Nitrosomonas sp.</i>	0.00E+00
427	<i>Nitrososphaera gargensis</i>	0.00E+00
428	<i>Nitrospira defluvii</i>	0.00E+00
429	<i>Nocardioides koreensis</i>	0.00E+00
430	<i>Oceanibaculum sp.</i>	0.00E+00
431	<i>Oenococcus oeni</i>	0.00E+00
432	<i>Paenibacillus darangshiensis</i>	0.00E+00
433	<i>Panacagrmonas sp.</i>	0.00E+00
434	<i>Pantoea sp.</i>	0.00E+00
435	<i>Parasegetibacter sp.</i>	0.00E+00
436	<i>Pedobacter roseus</i>	0.00E+00
437	<i>Pelagibacterium halotolerans</i>	0.00E+00
438	<i>Pelagicoccus sp.</i>	0.00E+00

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

439	<i>Phaeosporillum fulvum</i>	0.00E+00	459	<i>Sphingobium</i> sp.	0.00E+00
440	<i>Pleomorphomonas diazotrophica</i>	0.00E+00	460	<i>Sphingomonas dokdonensis</i>	0.00E+00
441	<i>Porifericola</i> sp.	0.00E+00	461	<i>Sphingomonas wittichii</i>	0.00E+00
442	<i>Pseudomarcicurvus</i> sp.	0.00E+00	462	<i>Sphingopyxis alaskensis</i>	0.00E+00
443	<i>Pseudomonas litoralis</i>	0.00E+00	463	<i>Stenotrophomonas acidaminiphila</i>	0.00E+00
444	<i>Pseudoxanthomonas spadix</i>	0.00E+00	464	<i>Stenotrophomonas</i> sp.	0.00E+00
445	<i>Rheinheimera aquimaris</i>	0.00E+00	465	<i>Subsaxibacter</i> sp.	0.00E+00
446	<i>Rhizomicrobium</i> sp.	0.00E+00	466	<i>Tepidimicrobium ferriphilum</i>	0.00E+00
447	<i>Rhodanobacter</i> sp.	0.00E+00	467	<i>Tepidimicrobium</i> sp.	0.00E+00
448	<i>Rickettsia prowazekii</i>	0.00E+00	468	<i>Thalassospira</i> sp.	0.00E+00
449	<i>Roseococcus</i> sp.	0.00E+00	469	<i>Thauera</i> sp.	0.00E+00
450	<i>Roseomonas frigidaquae</i>	0.00E+00	470	<i>Thermopolyspora</i> sp.	0.00E+00
451	<i>Rubricoccus</i> sp.	0.00E+00	471	<i>Thiobacillus</i> sp.	0.00E+00
452	<i>Saccharomonospora azurea</i>	0.00E+00	472	<i>Tistlia consotensis</i>	0.00E+00
453	<i>Sandarakinorhabdus</i> sp.	0.00E+00	473	<i>Umezawaea tangerina</i>	0.00E+00
454	<i>Simiduia</i> sp.	0.00E+00	474	<i>Undibacterium</i> sp.	0.00E+00
455	<i>Solimonas</i> sp.	0.00E+00	475	<i>Weeksella</i> sp.	0.00E+00
456	<i>Sphaerobacter</i> sp.	0.00E+00	476	<i>Xanthomonas</i> sp.	0.00E+00
457	<i>Sphingobacterium multivorum</i>	0.00E+00			
458	<i>Sphingobacterium</i> sp.	0.00E+00			

## NOTES

# APPENDIX

## RELATIVE FUNGAL ABUNDANCE

The relative abundance of the fungal communities is reported in %. Data in this report correspond to the average relative abundance obtained from three technical replicates. The absolute quantification of fungal communities using amplicon sequencing has not yet been validated at Biome Makers, Inc.

#	Genus & Species	Percentage	#	Genus & Species	Percentage
1	<i>Cochliobolus geniculatus</i>	28.3039%	19	<i>Aspergillus austroafricanus</i>	0.6301%
2	<i>Mortierella ambigua</i>	12.2703%	20	<i>Lewia infectoria</i>	0.5776%
3	<i>Choanephora cucurbitarum</i>	9.9072%	21	<i>Wallemia sebi</i>	0.5426%
4	<i>Stagonospora</i> sp.	7.4742%	22	<i>Phialophora</i> sp.	0.5251%
5	<i>Trematosphaeria pertusa</i>	6.4765%	23	<i>Penicillium chrysogenum</i>	0.5076%
6	<i>Mortierella</i> sp.	4.8311%	24	<i>Pilobolus sphaerosporus</i>	0.4551%
7	<i>Cryptococcus aerius</i>	3.3608%	25	<i>Cortinarius</i> sp.	0.3501%
8	<i>Phialosimplex caninus</i>	3.3082%	26	<i>Chrysosporium</i> sp.	0.3326%
9	<i>Coprinellus bisporus</i>	2.4856%	27	<i>Acremonium</i> sp.	0.2976%
10	<i>Aspergillus</i> sp.	2.3280%	28	<i>Chrysosporium vallenarense</i>	0.2801%
11	<i>Pyrenochaeta keratinophila</i>	2.2930%	29	<i>Aspergillus felis</i>	0.2801%
12	<i>Trichosporon</i> sp.	1.8554%	30	<i>Cephalotheca sulfurea</i>	0.2626%
13	<i>Sagenomella</i> sp.	1.5754%	31	<i>Scedosporium prolificans</i>	0.2451%
14	<i>Phaeosphaeria</i> sp.	1.4703%	32	<i>Mortierella elongata</i>	0.2451%
15	<i>Penicillium corylophilum</i>	1.0852%	33	<i>Mortierella elongatula</i>	0.2276%
16	<i>Cryptococcus terreus</i>	1.0327%	34	<i>Gymnostellatospora frigida</i>	0.2100%
17	<i>Chloridium</i> sp.	0.8227%	35	<i>Lophiostoma</i> sp.	0.2100%
18	<i>Chrysosporium lobatum</i>	0.8227%			

## RELATIVE FUNGAL ABUNDANCE

The relative abundance of the fungal communities is reported in %. Data in this report correspond to the average relative abundance obtained from three technical replicates. The absolute quantification of fungal communities using amplicon sequencing has not yet been validated at Biome Makers, Inc.

#	Genus & Species	Percentage	#	Genus & Species	Percentage
36	<i>Penicillium glabrum</i>	0.2100%	55	<i>Microascus</i> sp.	0.0350%
37	<i>Aspergillus penicillioides</i>	0.1925%	56	<i>Mortierella oligospora</i>	0.0350%
38	<i>Coprinopsis clastophylla</i>	0.1750%	57	<i>Penicillium roseopurpureum</i>	0.0350%
39	<i>Cryptococcus podzolicus</i>	0.1400%	58	<i>Corynespora smithii</i>	0.0350%
40	<i>Penicillium monsgalena</i>	0.1400%	59	<i>Paecilomyces</i> sp.	0.0350%
41	<i>Penicillium sizovae</i>	0.1225%	60	<i>Coniothyrium sidae</i>	0.0350%
42	<i>Cryptococcus diffluens</i>	0.1050%	61	<i>Mortierella dichotoma</i>	0.0175%
43	<i>Cephalosporium serrae</i>	0.0875%	62	<i>Penicillium</i> sp.	0.0175%
44	<i>Mariannaea superimposita</i>	0.0875%	63	<i>Lysurus cruciatus</i>	0.0175%
45	<i>Penicillium brevicompactum</i>	0.0875%	64	<i>Pyrenochaeta</i> sp.	0.0175%
46	<i>Arthrospis hispanica</i>	0.0700%	65	<i>Aspergillus insuetus</i>	0.0175%
47	<i>Scutellinia torrentis</i>	0.0525%	66	<i>Helicoma</i> sp.	0.0175%
48	<i>Cryptococcus laurentii</i>	0.0525%	67	<i>Fusarium pseudensiforme</i>	0.0175%
49	<i>Aspergillus melleus</i>	0.0525%			
50	<i>Podospora</i> sp.	0.0525%			
51	<i>Penicillium cyclopium</i>	0.0350%			
52	<i>Aspergillus candidus</i>	0.0350%			
53	<i>Trichoderma citrinoviride</i>	0.0350%			
54	<i>Aspergillus ruber</i>	0.0350%			

## NOTES

Genus predictions ('sp') that have species appearing in the CDFA list provided. (Species might or might not be present)

Species that appears explicitly highlighted in the CDFA list

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