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AB088884.1 gg_id:78359 termite gut homogenate clone Rs-J14 sp. AB088
AF061347.1 gg_id:3931 Treponema sp. I:Q:AT20 str. AT20 AF061
AB088881.1 gg_id:78047 termite gut homogenate clone Rs-D57 sp. AB088
GQ502611.1 gg_id:582361 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AF068405.1 gg_id:4094 termite gut homogenate clone ZAS89 AF068
EF454213.1 gg_id:220388 termite hindgut clone 290cost002-P3L-1803 EF4542
EF453852.2 gg_id:218658 termite hindgut clone 290cost002-P3L-1216 EF4538
AF023029.1 gg_id:3906 Treponema sp. str. III:13:D94 AF023
AB234361.1 gg_id:150211 termite gut homogenate clone MgMjD-028 AB2343
AB192147.1 gg_id:141512 termite gut homogenate clone RsTz-89 AB192
AB192141.1 gg_id:142334 termite gut homogenate clone RsTz-84 AB192
AB231057.1 gg_id:146440 termite gut wall clone NkW01-009 AB231
EF453913.2 gg_id:218561 termite hindgut clone 290cost002-P3L-1301 EF4539
GQ502615.1 gg_id:536096 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
EF454897.2 gg_id:226681 termite hindgut clone 290cost002-P3L-619 EF4548
EF454832.1 gg_id:217886 termite hindgut clone 290cost002-P3L-484 EF4548
AJ419816.1 gg_id:22449 Spirochaeta sp AJ4198
AB191964.1 gg_id:141888 termite gut homogenate clone M1NP2-77 AB1919
AB088905.1 gg_id:77877 termite gut homogenate clone Rs-A09 sp. AB0889
AB231063.1 gg_id:147373 termite gut wall clone NkW01-044 AB231
AB084952.1 gg_id:69074 termite gut clone NkS1 AB0849
EU794266.1 gg_id:346741 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P10 EU794
AB062832.1 gg_id:31994 termite gut homogenate clone BCf6-15 AB0628
AB360375.1 gg_id:265198 Identification endosymbiotic methanogen and ectosymbiotic spirochetes protists ter AB3603
AF068341.1 gg_id:4087 termite gut homogenate clone RFS41 AF0683
AB088901.1 gg_id:78179 termite gut homogenate clone Rs-C91 sp. AB0889
AM942448.1 gg_id:302412 Evidence multiple Treponema phylotypes involved bovine shown 16rDNA and fluore AM942
EU771469.1 gg_id:354983 Hamadryas Baboon feces clone AFBAB_aai04f02 EU7714
AY571478.1 gg_id:114784 termite gut clone RsaHf303 AY5714
AB088882.2 gg_id:77600 termite gut homogenate clone Rs-P25 sp. AB0888
AF023063.1 gg_id:3947 Treponema sp. str. I:N:D47 AF023
AF068345.1 gg_id:4049 termite gut homogenate clone CFS6 AF0683
AF371928.1 gg_id:68837 swine intestine clone p-2159-s959-3 AF3719
AB192251.1 gg_id:143974 termite gut homogenate clone RPK-14 AB192
EF454122.2 gg_id:220481 termite hindgut clone 290cost002-P3L-1667 EF4541
EF454300.2 gg_id:223993 termite hindgut clone 290cost002-P3L-1914 EF4543
EF454181.2 gg_id:222160 termite hindgut clone 290cost002-P3L-1759 EF4541
AY212749.1 gg_id:105320 equine manure clone wet198 AY2127
EU794214.1 gg_id:316624 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_S39 EU794
EF562545.1 gg_id:251512 stable microbial consortia capable degrading complex organic matter paper pulp colu EF5625

8454.5	7521.1	8200.7	7552.4	7404.7	7255.6	8810.7	6604.1	7894.9	7584.1	7775.7
100.2	608.5	776.2	771.4	390.0	480.2	861.1	930.6	422.7	350.9	742.3
142.4	704.6	1323.7	1923.4	1113.6	798.0	1392.7	1095.2	544.1	282.0	866.9
49.0	107.7	194.7	198.4	189.0	152.6	265.6	140.0	62.8	34.5	71.6
3034.9	3249.0	3764.8	4291.6	4571.3	3324.8	4534.5	4012.8	2140.5	2009.6	3008.9
74.4	138.3	176.4	159.0	88.9	86.2	90.5	111.5	57.3	43.4	94.1
2610.2	3340.9	4058.4	4758.6	3717.2	3514.1	4582.8	4034.8	2954.2	2513.8	3685.7
1471.8	4649.4	4923.8	4284.9	5098.6	4944.0	5533.1	3918.7	6315.6	5464.4	4583.5
235.0	2971.8	4443.8	3629.6	3380.1	3036.9	3590.1	3273.0	1790.2	1012.8	3699.2
39.7	353.7	772.8	669.2	638.7	553.8	540.4	899.2	243.2	53.2	445.0
705.8	1531.3	1498.3	1491.2	1743.1	1864.6	1579.9	1398.9	1095.0	482.8	1235.1
53.5	197.3	484.7	555.4	144.1	263.7	453.2	337.0	106.4	21.9	172.2
35.9	119.6	164.6	181.1	133.5	306.9	94.2	99.9	79.4	275.2	87.9
47.0	29.5	59.2	85.1	45.8	34.5	48.9	45.6	30.5	25.7	39.3
249.3	1033.6	1804.6	2141.6	1481.8	1167.4	2256.4	1285.6	751.1	1164.1	1269.6
1902.9	5074.7	5870.6	6179.4	5073.4	4135.3	3374.8	4446.2	4355.1	4264.0	3969.8
24680.3	5631.5	5688.2	7559.6	5582.8	5697.5	6875.6	5603.9	9035.7	3567.8	8752.1
32.0	30.9	30.3	36.4	31.1	31.5	23.1	25.2	24.8	14.8	29.6
74.2	1855.0	2047.5	2445.2	2405.5	1768.6	3076.9	2372.4	942.3	784.8	1189.3
29.3	104.2	222.6	257.9	61.8	77.5	157.2	144.7	53.5	35.3	87.6
70.7	39.4	50.1	49.2	37.2	43.4	32.2	37.8	31.4	29.6	38.0
41.8	43.5	65.0	47.6	40.7	41.4	54.7	52.7	40.7	24.9	40.0
43.4	26.0	24.5	33.6	26.6	21.9	23.9	23.3	29.0	18.7	22.3
78.0	248.1	273.7	238.4	231.6	327.0	172.4	274.1	231.5	75.5	178.4
44.0	27.5	24.9	28.7	27.6	25.1	27.6	19.9	28.9	23.1	29.4
50.4	37.9	52.3	48.6	42.2	25.4	52.0	34.1	34.4	23.5	33.3
40.6	528.5	1323.6	2095.6	165.7	355.3	843.5	531.0	138.3	109.1	270.5
1621.8	8115.4	8369.9	8109.6	6828.9	7255.8	7875.6	7111.4	8631.5	7401.1	9335.3
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45.4	978.0	1095.9	1599.1	1628.8	696.2	2139.4	936.8	660.0	226.2	978.5
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43.6	1341.1	2206.7	2229.9	1445.1	1557.8	2005.5	2027.7	964.7	246.8	1386.8
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822.0	2304.9	2852.4	3949.5	3270.9	2302.7	3940.9	2729.2	1628.7	1798.4	2521.8
3509.5	3472.8	3330.5	3600.8	3477.8	3488.2	3834.0	3042.9	3744.2	3000.1	4181.5
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8223.6	10567.2	8126.8	12109.0	8870.0	8499.7	10496.6	7722.0	12128.5	10141.7	10038.3
37.8	749.8	1291.6	1449.2	1728.1	1408.6	1307.9	768.1	353.3	75.5	600.6
72.8	29.2	31.6	66.1	48.5	34.0	32.2	26.0	36.2	26.9	44.6
2696.6	5923.9	7086.9	8274.7	7080.9	6173.2	9287.6	6486.2	3719.7	4303.4	6006.8

6941.4	8241.3	8179.1
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857.8	1021.9	2127.9
63.6	214.6	553.6
3859.8	4061.2	4759.8
66.9	122.2	74.1
3521.3	3759.4	4298.1
5272.9	5484.1	5303.2
2725.0	2755.2	3327.1
521.5	417.9	656.5
1443.5	2371.2	2134.6
246.9	275.7	380.5
246.2	159.9	99.1
35.6	38.4	37.1
1398.5	1291.9	2366.9
4403.7	4236.6	4850.8
5133.4	7341.4	5314.3
23.5	34.2	41.1
2238.4	2144.4	3385.3
80.6	69.2	71.5
36.4	47.4	56.6
41.9	48.3	51.9
19.5	26.0	20.0
267.9	328.9	305.9
26.3	18.0	24.9
30.6	27.3	34.3
158.8	227.0	173.9
6855.5	7588.6	7264.6
1962.5	2145.6	2078.2
778.5	869.6	1899.4
3496.7	3810.0	3827.7
1581.0	1384.2	2326.2
75.7	130.4	91.3
46.9	83.1	73.7
2500.4	2922.5	4163.0
2690.9	5601.0	3795.2
2652.4	4135.8	6153.9
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663.1	493.8	443.4
31.9	31.7	36.2
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AB191821.1 gg_id:144329 termite gut homogenate clone M1NP1-80 AB191
AB084965.1 gg_id:74426 termite gut clone NkS50 AB084
GU408735.1 gg_id:557008 Human Oral Microbiome oral cavity GU408
AF023052.1 gg_id:3939 Treponema sp. str. I:G:C1 AF023
AF023053.1 gg_id:3940 Treponema sp. str. I:F:D13 AF023
AF023031.1 gg_id:3908 Treponema sp. str. II:C:T1 AF023
GQ502617.1 gg_id:545719 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
EF454600.2 gg_id:219918 termite hindgut clone 290cost002-P3L-2386 EF4546
AB192144.1 gg_id:142525 termite gut homogenate clone RsTz-02 AB192
AM182455.1 gg_id:146784 Treponema sp. str. SPIT5 AM182
AB360374.1 gg_id:276247 Identification endosymbiotic methanogen and ectosymbiotic spirochetes protists ter AB360
AB062823.1 gg_id:48891 termite gut homogenate clone BCf4-14 AB062
EU358687.1 gg_id:313606 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
AY735103.1 gg_id:102578 Spirochaeta taiwanensis str. K1LY AY735
AB192255.1 gg_id:143026 termite gut homogenate clone RPK-39 AB192
GQ068618.1 gg_id:417534 Topographical and Temporal Human Skin Microbiome skin nare clone nbw152g06c1 GQ068
GU408631.1 gg_id:564057 Human Oral Microbiome oral cavity GU408
AB088908.1 gg_id:78092 termite gut homogenate clone Rs-D13 sp. AB088
AB191856.1 gg_id:144192 termite gut homogenate clone M1NP1-86 AB191
AB191941.1 gg_id:143947 termite gut homogenate clone M2PT2-47 AB191
AB255896.1 gg_id:165815 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2558
EF454002.2 gg_id:220062 termite hindgut clone 290cost002-P3L-1429 EF4540
AB084960.1 gg_id:69104 termite gut clone NkS21 AB084
EF453804.1 gg_id:223738 termite hindgut clone 290cost002-P3L-1157 EF4538
AM980448.1 gg_id:301091 Treponema sp. PT9 PT8 AM980
AF068347.1 gg_id:4118 termite gut homogenate clone CFS121 AF0683
AB062834.1 gg_id:46398 termite gut homogenate clone BCf6-24 AB0628
AF068342.1 gg_id:3984 termite gut homogenate clone RFS6 AF0683
AB189699.1 gg_id:112977 termite gut homogenate clone Tc-69 AB189
EU472054.1 gg_id:294974 francois langur feces clone FL_1aaa01h05 EU472
GQ039064.1 gg_id:441410 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
AB191917.1 gg_id:141191 termite gut homogenate clone M2PB4-42 AB191
AB198448.1 gg_id:135888 termite gut wall fraction clone RsW01-008 AB198
AB192242.1 gg_id:141806 termite gut homogenate clone RPK-17 AB192
AB084968.1 gg_id:69543 termite gut clone NkS83 AB084
GQ502646.1 gg_id:555083 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ502659.1 gg_id:565920 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
EU471602.1 gg_id:295386 Asiatic elephant feces clone AE1_aaa04f01 EU471
EF454215.2 gg_id:226149 termite hindgut clone 290cost002-P3L-1805 EF4542
AB088900.1 gg_id:77591 termite gut homogenate clone Rs-Q78 sp. AB088

67.3	413.7	968.9	1330.3	411.3	357.3	979.5	658.5	199.1	58.8	285.6
48.8	224.3	230.5	215.2	234.7	172.4	303.7	156.5	115.0	63.6	107.7
33.8	25.7	17.5	26.0	27.0	19.4	21.7	19.2	15.0	13.3	16.0
443.6	396.4	1042.1	1440.4	668.1	419.0	423.5	1015.9	422.6	294.4	617.2
1009.6	1763.6	2820.1	4222.2	2414.0	1913.5	2648.5	3539.9	1466.6	302.1	1710.9
38.9	597.3	1132.7	1232.1	844.3	851.5	867.9	997.0	528.9	154.9	789.1
37.1	75.9	148.9	145.2	82.3	66.6	93.4	144.2	31.5	17.4	81.2
578.6	1241.5	1513.9	1747.8	1749.2	1333.9	1922.2	1477.7	1067.6	715.9	1028.0
823.4	4187.9	3777.4	3722.3	3441.0	3024.7	3905.6	3092.1	4148.1	3775.2	3233.5
34.0	79.8	173.7	197.6	74.5	64.2	97.2	109.9	80.7	30.3	61.4
39.4	32.6	45.3	44.4	51.1	36.5	30.6	30.9	29.5	25.5	25.0
92.8	498.8	925.6	1136.8	733.8	603.8	1228.7	729.8	283.3	119.9	417.7
224.2	211.1	555.8	588.6	195.1	169.2	469.5	228.0	129.6	124.5	177.6
2193.2	4842.4	6171.1	6295.6	5990.3	5071.0	5463.0	6429.2	4111.2	2842.1	5332.2
108.8	347.9	615.1	388.3	480.7	278.1	519.0	423.7	150.6	60.5	292.4
43.5	306.0	593.7	760.2	702.8	282.6	906.2	484.8	266.8	106.1	241.8
2248.3	3440.5	4064.5	4981.3	2760.2	3703.6	4328.0	4321.1	2973.9	1852.3	3289.2
1997.0	2377.8	2483.8	2873.9	2176.8	2017.1	2777.2	2130.1	2838.8	1779.1	1915.6
3026.0	1541.9	1636.4	1789.1	2083.3	1399.1	2483.5	1996.2	1271.9	672.9	1625.7
58.5	22.2	24.1	25.6	30.5	25.2	22.3	28.3	26.6	19.3	24.4
44.3	23.1	25.2	22.7	24.3	20.0	23.6	23.3	19.3	14.7	26.6
31.7	291.8	128.8	129.4	144.8	122.7	129.6	276.0	64.1	34.3	126.3
587.2	3432.5	2710.9	3377.2	3415.8	2991.4	4217.0	3080.9	3012.8	2967.5	2627.5
53.0	144.1	214.2	277.6	201.2	212.0	258.6	138.6	76.8	35.4	157.4
773.5	2161.4	2348.5	2210.9	3161.1	2751.7	3338.3	1864.7	1226.3	2006.9	1761.1
2220.0	2265.5	2885.6	3598.3	2016.6	2364.4	2519.5	3100.8	2095.2	929.3	2367.0
76.8	31.9	27.6	37.4	43.8	27.0	40.4	26.9	34.6	20.4	27.9
57.8	50.9	69.2	53.9	61.2	58.5	91.7	40.3	28.5	26.3	50.9
41.1	50.3	54.8	49.5	30.2	45.2	26.8	49.8	25.6	14.6	31.1
59.8	124.1	241.0	292.7	168.2	149.4	288.1	186.5	74.5	56.7	99.0
298.0	1150.7	1197.8	1301.6	832.0	1077.7	1124.2	983.2	849.5	492.1	1066.6
87.6	2078.6	2846.9	3946.7	1869.9	1921.6	2077.1	3079.5	1255.5	448.9	1932.9
85.4	730.4	686.6	805.2	218.5	955.5	436.9	792.2	192.6	114.7	358.5
66.8	170.6	431.0	515.3	266.5	242.1	258.9	500.6	294.3	27.0	291.5
32.6	119.1	180.2	152.9	130.3	156.3	99.5	116.9	66.9	54.3	63.2
43.8	145.6	232.9	422.7	89.9	143.8	181.3	308.1	93.0	53.7	150.1
2918.9	1801.9	2687.7	2727.9	2456.1	1914.4	2975.4	2046.5	1683.6	1000.4	1939.9
53.1	790.4	1213.7	1466.9	1233.3	1180.3	1549.7	1465.6	444.7	212.5	861.5
2197.3	7380.8	6987.3	7706.8	4668.3	6531.1	4992.4	6477.2	6922.2	5201.5	6041.0
477.4	656.4	808.4	849.5	814.1	600.6	711.3	535.1	784.9	762.6	127.2
41.8	92.4	85.5	75.0	55.2	57.4	93.5	62.1	26.7	18.3	39.7

475.4	659.5	482.6
178.8	304.6	187.4
19.5	21.8	20.9
463.8	821.1	869.8
3597.5	2776.5	2648.4
1069.2	717.3	744.0
40.9	109.1	125.0
1350.4	1689.5	1895.7
2588.6	3004.9	3540.7
91.5	136.9	162.2
28.9	41.4	31.7
692.0	640.6	1258.9
79.2	220.3	334.5
5645.9	5158.1	6554.2
281.1	405.9	418.8
383.0	458.3	829.6
4347.2	3742.0	5473.3
1985.1	2139.2	2532.8
1320.2	1625.1	1129.3
28.0	40.0	22.8
23.7	26.6	18.6
81.9	209.0	298.8
2275.2	3811.4	4157.5
100.7	147.1	234.8
2089.6	2596.7	3014.2
2933.9	2753.5	3634.6
25.6	26.8	28.7
41.4	51.5	75.2
61.7	43.0	50.4
87.7	165.4	195.9
822.0	993.8	939.5
2399.1	1996.3	2825.9
594.8	650.3	642.4
409.9	262.6	409.8
92.4	165.5	228.3
212.0	139.8	273.0
1922.5	2751.1	2466.4
1125.4	1306.4	1996.3
5151.1	6216.2	5961.5
625.4	1148.4	756.8
44.1	117.6	174.2

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AB299520.1 gg_id:241126 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
AB231059.1 gg_id:145031 termite gut wall clone NkW01-018 AB2310
EF454250.2 gg_id:217773 termite hindgut clone 290cost002-P3L-1848 EF4542
AF068416.1 gg_id:4098 termite gut homogenate clone RFS52 AF0684
AB088894.1 gg_id:78213 termite gut homogenate clone Rs-A19 AB0888
AB231025.1 gg_id:146570 termite gut wall clone HsW01-020 AB2310
AB088891.1 gg_id:77621 termite gut homogenate clone Rs-B29 sp. AB0888
AB192151.1 gg_id:143612 termite gut homogenate clone RsTz-90 AB1921
NR_029348.1 gg_id:572161 Treponema brennaborense str. DD5/3; DSM 12168 NR_029
EU464306.1 gg_id:295712 hamadryas baboon feces clone AFBAB_aai02c04 EU4643
DQ003618.1 gg_id:124523 human mouth clone MB2_G19 DQ003
EF454942.2 gg_id:225337 termite hindgut clone 290cost002-P3L-730 EF4549
EF453933.2 gg_id:221957 termite hindgut clone 290cost002-P3L-1334 EF4539
AB191865.1 gg_id:142763 termite gut homogenate clone M2PB4-83 AB1918
GU408605.1 gg_id:562976 Human Oral Microbiome oral cavity GU408
EF454221.1 gg_id:223424 termite hindgut clone 290cost002-P3L-1811 EF4542
AB032009.1 gg_id:25824 protist termite clone HsDiSp319 clone AB0320
AB231031.1 gg_id:145132 termite gut wall clone HsW01-012 AB2310
AM420109.1 gg_id:248721 Noma subgingival plaque clone 303F01(oral) AM420
GQ502650.1 gg_id:573443 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AJ419821.1 gg_id:40667 Spirochaeta sp AJ4198
EF454883.2 gg_id:218947 termite hindgut clone 290cost002-P3L-590 EF4548
AB088911.1 gg_id:78206 termite gut homogenate clone Rs-J58 sp. AB0889
EF453968.2 gg_id:225557 termite hindgut clone 290cost002-P3L-1386 EF4539
AB231058.1 gg_id:148743 termite gut wall clone NkW01-016 AB2310
AB191854.1 gg_id:143614 termite gut homogenate clone M1PL1-31 AB1918
AY341822.1 gg_id:93141 Treponema genomosp. P1 AY3418
AF068426.1 gg_id:4127 termite gut homogenate clone RFS18 AF0684
AB299519.1 gg_id:252938 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
EF453971.2 gg_id:222007 termite hindgut clone 290cost002-P3L-1390 EF4539
AB084956.1 gg_id:73924 termite gut clone NkS8 AB0849
AF068346.1 gg_id:4117 termite gut homogenate clone CFS124 AF0683
EU748341.1 gg_id:339907 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07h09 EU7483
AB255898.1 gg_id:171504 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2558
EF454202.2 gg_id:227383 termite hindgut clone 290cost002-P3L-1791 EF4542
AM420288.1 gg_id:239628 Noma subgingival plaque clone 703018(oral) AM420
AB541984.1 gg_id:585733 Spirochaeta stenostrepta str. JCM 16534 AB5419
AF023051.1 gg_id:3938 Treponema sp. str. I:B:C7 AF0230
AB191908.1 gg_id:142284 termite gut homogenate clone M1NP1-85 AB1919
DQ065758.1 gg_id:134428 Treponema zioleckii str. kT DQ065
EF454917.2 gg_id:221675 termite hindgut clone 290cost002-P3L-663 EF4549

129.5	1189.7	1544.3	2163.0	1576.4	1335.9	1574.1	1996.1	866.8	585.1	1086.3
66.6	60.9	68.1	80.7	93.9	86.0	148.4	59.5	93.8	54.3	94.2
7608.7	2611.0	2415.6	2934.7	2171.6	1302.3	2384.7	2012.0	3134.2	2774.3	3219.0
45.1	35.2	31.7	34.5	43.8	27.2	29.8	23.4	18.9	18.2	33.1
502.0	1081.1	1249.6	1621.1	1397.2	999.7	1381.7	1152.5	865.0	482.1	984.9
6008.0	6715.7	6878.1	5671.1	6226.2	5261.7	7796.5	6231.7	9991.0	7736.2	7580.4
46.3	30.6	58.5	55.5	26.8	21.6	33.9	30.0	28.0	18.2	38.0
34.6	74.3	127.5	175.4	42.4	56.3	151.3	174.0	49.7	33.1	56.0
175.3	959.8	1533.7	1794.2	1913.9	1007.4	1846.6	1478.0	1304.7	284.1	774.5
73.0	2180.1	2685.5	3420.8	2502.5	2241.6	3783.7	2924.9	809.7	636.5	1795.4
3406.7	4713.9	3282.1	3571.9	4763.5	3778.5	4792.3	3300.9	2655.5	1373.8	2038.1
8277.5	8071.6	9402.9	8653.5	9942.4	7622.5	8035.4	7332.5	9968.9	6981.9	8324.8
7850.6	4003.4	3632.5	3881.2	4283.3	4608.1	3891.8	4567.6	4655.1	4401.3	5543.0
52.4	828.5	750.4	611.1	503.1	1079.6	1356.7	1085.8	392.3	669.3	522.0
368.5	1618.3	2143.8	2350.3	2482.3	1762.6	3243.5	1872.6	1043.7	36.8	1630.1
1333.8	3940.5	5546.5	4255.8	4331.8	3620.7	4492.6	3682.9	4335.4	4060.4	2349.7
61.5	73.4	85.9	57.4	63.6	64.7	72.8	48.8	25.6	28.3	33.5
55.6	151.1	219.8	302.2	162.9	146.2	230.1	216.9	75.3	36.4	122.5
45.4	159.5	371.9	417.9	337.7	189.1	300.0	258.0	97.2	19.4	161.0
40.0	1562.2	1778.8	2539.1	3019.2	1918.5	3152.4	2267.8	642.0	514.6	989.7
45.9	55.4	56.8	38.3	31.6	21.6	26.7	29.2	36.3	19.4	52.7
2870.6	1445.7	1376.9	1542.1	931.2	1228.6	1294.1	1034.8	1275.4	1116.0	1769.4
173.4	436.5	576.8	721.2	495.0	357.3	695.9	447.2	246.5	95.8	214.9
44.9	26.4	29.5	30.2	23.6	14.0	24.0	16.2	18.6	19.9	16.9
57.8	899.8	1198.5	1462.3	447.5	623.6	752.1	1132.0	312.9	142.3	726.8
37.7	115.5	176.1	259.7	172.9	157.4	196.5	139.4	59.8	26.3	104.0
198.6	756.5	1531.3	1964.7	1178.4	867.4	1539.4	1127.5	612.4	145.9	975.4
58.5	78.1	115.9	126.8	100.5	51.6	118.2	106.2	41.9	33.3	54.8
746.9	2338.8	2155.7	2937.9	2032.1	2773.6	2893.4	3116.5	1764.0	1465.4	1956.1
797.7	3170.5	3302.1	2356.1	3634.4	2956.7	3346.7	2637.5	2476.1	2051.1	2312.9
40.2	33.9	41.2	42.6	49.4	40.0	45.7	34.1	18.2	17.0	33.5
12254.3	1528.6	1501.7	1564.6	1641.9	1198.8	1744.4	1500.1	1791.1	2189.3	2110.8
504.4	1261.7	1924.6	2476.2	1472.0	1667.5	2539.5	1869.4	876.1	859.5	1828.0
65.2	154.3	110.1	135.4	215.8	149.1	160.9	234.8	72.7	40.2	75.0
41.3	276.0	877.3	1629.1	99.2	162.0	446.9	426.6	214.3	37.9	303.6
70.8	1213.4	1797.7	2016.6	1880.6	1417.1	3279.7	1887.6	552.0	242.7	1241.6
108.2	1971.3	2395.8	3123.2	2120.7	1878.4	3056.0	2043.3	2646.7	916.6	1727.6
76.7	1809.5	2752.3	3092.0	1669.6	1972.8	2086.1	2853.1	1217.5	538.5	2081.3
3560.6	1939.5	2337.3	2531.4	2156.0	2218.8	2513.2	2355.7	1419.3	2244.7	2376.1
48.3	44.3	43.6	67.5	58.4	35.2	52.0	66.2	23.4	18.2	41.9
123.0	4902.4	3913.9	4364.9	5508.4	4444.5	4752.5	4414.3	5486.2	2640.0	3801.8

1439.5	1802.7	1737.7
44.0	73.9	54.3
1997.5	3511.5	2347.4
23.9	50.7	27.6
1074.8	1272.0	2462.7
4700.9	6246.2	8212.6
29.2	33.8	25.2
62.1	94.7	58.0
1038.8	1562.5	1865.1
2255.2	1774.0	2776.0
3233.5	3094.8	3695.1
7656.7	8345.6	9415.6
3665.8	6141.0	4393.5
866.2	1081.2	1344.6
1971.5	2022.5	3831.1
3629.1	4571.1	4116.0
32.6	138.2	195.0
307.8	297.4	258.3
150.4	206.8	553.8
1633.5	2022.1	3039.8
21.6	39.4	33.5
892.5	1830.1	922.6
377.2	803.0	524.4
21.1	25.4	37.9
556.6	879.5	600.5
202.7	106.0	170.6
1134.7	1076.5	2133.5
79.7	134.7	89.6
2390.5	2450.5	2553.3
2464.0	3091.4	3611.0
24.4	29.2	32.8
1691.9	2125.9	1823.6
1737.6	1874.4	2793.6
196.2	136.2	181.8
112.6	254.8	575.0
1086.7	1207.7	2053.0
1634.2	2239.5	2642.9
1677.6	1452.3	2308.3
2244.4	2749.2	2477.5
57.1	54.5	35.8
3520.2	5833.7	5750.1

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FJ976395.1 gg_id:571435 Interindividual healthy human oral microbiota mouth clone 24B241 FJ9763
AB191817.1 gg_id:141230 termite gut homogenate clone M1PT4-88 AB1918
AB231061.1 gg_id:149915 termite gut wall clone NkW01-037 AB2310
AY518274.1 gg_id:104346 Treponema sp. str. 14V28 AY5182
AY178844.1 gg_id:104881 Treponema sp. str. Sy24 AY1788
GQ502618.1 gg_id:536459 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AB192139.1 gg_id:142969 termite gut homogenate clone RsTz-33 AB1921
EF453877.2 gg_id:227094 termite hindgut clone 290cost002-P3L-1254 EF4538
AB062839.1 gg_id:27323 termite gut homogenate clone BCf7-24 AB0628
AY369252.1 gg_id:94775 Treponema vincentii str. OMZ 861 AY3692
AF182831.1 gg_id:3955 Treponema sp. str. I:V:AU076 AF1828
AB062840.1 gg_id:38586 termite gut homogenate clone BCf8-03 AB0628
EU473593.1 gg_id:299900 Somali wild ass feces clone WA_aaa02d10 EU4735
EF454129.2 gg_id:226390 termite hindgut clone 290cost002-P3L-1681 EF4541
AB198654.1 gg_id:135860 termite gut fluid and protists fraction clone RsC01-085 AB1986
AM980447.1 gg_id:299619 Treponema sp. PT8 AM980
AY369247.1 gg_id:95168 Treponema sp. str. OMZ 839 AY3692
EF453952.2 gg_id:220850 termite hindgut clone 290cost002-P3L-1363 EF4539
EF454455.2 gg_id:227278 termite hindgut clone 290cost002-P3L-2160 EF4544
GQ502643.1 gg_id:534577 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ502639.1 gg_id:536207 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AB255894.1 gg_id:162987 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2558
FJ976308.1 gg_id:558616 Interindividual healthy human oral microbiota mouth clone 10B549 FJ9763
GQ502652.1 gg_id:591066 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AY571470.1 gg_id:114589 termite gut clone RsaHf241 AY5714
AB085158.1 gg_id:72963 termite gut clone NkS-Dev1 AB0851
AB243262.1 gg_id:149532 acetone-preserved termite gut clone M2PB4a-025 AB2432
DQ307690.1 gg_id:144644 termite intestinal tract clone MTG-91 DQ307
GU304073.1 gg_id:541314 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
EF454406.2 gg_id:222609 termite hindgut clone 290cost002-P3L-2077 EF4544
EF453999.2 gg_id:226973 termite hindgut clone 290cost002-P3L-1424 EF4539
EF454271.2 gg_id:225517 termite hindgut clone 290cost002-P3L-1873 EF4542
AB084973.1 gg_id:73490 termite gut clone NkS97 AB0849
AB191834.1 gg_id:141753 termite gut homogenate clone M1PT4-49 AB1918
AB191848.1 gg_id:142623 termite gut homogenate clone M1NP1-75 AB1918
AB088915.1 gg_id:78017 termite gut homogenate clone Rs-Q13 sp. AB0889
AF068423.1 gg_id:4053 termite gut homogenate clone RFS94 AF0684
AB085166.1 gg_id:69238 termite gut clone NkS-Oxy25 AB0851
GQ502657.1 gg_id:589527 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
DQ003625.1 gg_id:121373 human mouth clone MB4_G11 DQ003
AF357565.1 gg_id:71422 mpn-isolate group 17 AF3575

200.1	872.2	2162.9	3425.0	1472.2	1081.7	1402.7	2246.7	828.5	435.8	1515.2
1134.9	578.4	571.1	505.3	421.1	602.8	490.0	632.0	579.8	500.1	653.3
85.3	298.7	295.6	294.1	345.5	313.1	423.7	254.2	106.8	81.1	145.0
116.1	404.2	520.4	502.8	475.1	456.3	544.1	383.6	273.5	150.2	305.3
44.3	21.8	21.5	28.8	23.2	21.0	25.7	19.9	15.1	19.7	26.2
55.1	584.7	1104.4	1256.8	718.9	822.8	1046.7	1148.3	606.8	207.6	528.8
44.7	25.0	28.5	31.6	26.5	27.9	22.3	27.5	25.7	19.2	24.2
1188.5	2408.2	2284.6	2497.3	3099.6	2083.3	2310.7	2258.4	2459.5	1997.2	3100.9
56.6	132.6	196.7	245.4	86.8	125.0	145.9	145.6	77.7	37.0	137.3
65.3	580.4	1611.3	2523.5	1076.7	740.3	928.0	1707.1	558.8	239.0	1003.8
55.8	886.3	1878.1	2653.3	1667.5	971.1	1336.2	1847.0	616.2	133.3	1151.1
253.6	793.4	1081.7	1031.7	733.5	657.4	1067.2	803.1	527.1	811.7	553.5
11960.0	5061.2	3512.9	4084.1	4110.3	4635.5	4298.2	3786.5	4591.5	5214.7	4443.4
8176.7	8520.4	7388.9	8744.8	8240.8	7783.5	9694.0	8349.1	6818.0	7324.2	10829.4
33.9	31.3	22.5	35.5	43.7	19.0	38.4	38.1	27.0	22.6	20.0
57.6	1075.6	1594.2	1444.6	777.7	1171.6	1041.3	1720.2	1220.7	638.7	1059.3
112.8	134.1	226.0	322.5	299.1	247.4	353.1	240.0	235.8	168.4	256.9
108.5	367.5	595.9	719.9	705.4	440.8	840.0	635.9	232.7	103.8	255.4
56.0	1998.3	2624.5	1851.3	2320.8	2205.3	2613.4	2628.5	1271.7	524.6	1476.2
2295.4	1610.3	2914.9	2884.4	2210.7	1691.7	2508.1	2308.2	985.0	847.5	1522.0
111.3	599.5	1205.2	1847.9	690.7	730.1	1285.6	994.9	578.4	93.3	555.6
572.3	4296.2	4528.3	5953.2	5093.4	4511.5	5552.3	5442.9	3823.3	2732.3	4392.3
12819.4	3510.7	3206.3	4299.1	3481.4	3892.1	4475.1	4897.4	5379.0	4918.7	5006.4
2037.1	2125.3	2445.7	2427.1	2726.9	2234.0	2828.4	3643.6	1315.1	706.9	1720.5
2115.5	1459.9	1667.9	1747.3	1567.8	1324.4	1442.7	1160.2	1523.7	1526.1	2136.7
33.0	35.7	54.3	55.1	39.4	30.7	44.9	35.8	26.5	14.6	31.9
5178.5	2935.4	3601.1	3184.5	2666.9	2571.8	3343.3	3593.2	3847.8	2197.8	3964.1
220.1	865.5	1274.8	1161.5	1365.1	936.9	1890.1	1025.4	484.4	186.5	655.1
31.5	28.8	43.1	41.5	47.3	144.7	126.9	34.7	20.9	23.2	34.8
33689.0	8695.1	8289.6	8964.9	9390.7	8270.3	10340.5	7915.6	13185.7	9305.9	13798.0
4987.6	4558.6	4472.0	4911.8	5972.4	4817.9	6186.3	4451.4	3560.3	3171.4	3718.1
6904.2	3633.9	4145.6	4539.6	4006.6	3423.7	4321.1	3549.2	4742.0	3771.5	3688.1
36.4	91.0	133.0	122.9	115.7	82.7	153.7	86.7	44.9	30.5	49.4
90.5	1573.5	1685.9	2229.3	507.7	1738.2	2327.9	1853.8	711.1	696.8	983.7
38.1	71.4	140.1	115.1	114.5	87.5	61.8	92.1	31.8	101.5	83.8
47.6	140.9	204.8	253.7	82.5	86.3	72.6	340.0	53.1	32.4	72.3
278.9	429.1	852.7	968.2	635.9	501.3	693.1	890.3	247.6	132.1	474.7
49.3	29.8	45.8	50.5	33.5	37.7	38.8	59.9	19.7	16.6	27.3
80.6	288.5	550.9	427.6	385.2	415.9	441.8	563.0	555.9	176.7	472.7
14035.8	8020.9	6656.9	7742.5	6484.1	6691.9	8444.1	7575.0	7594.3	6536.9	9255.9
61.7	61.1	79.7	103.1	89.1	116.4	108.4	67.1	44.7	38.1	62.7

1409.1	1278.3	2658.9
383.7	925.7	480.1
217.1	253.9	443.2
385.5	491.6	554.8
20.6	22.8	20.9
1042.7	778.8	1402.5
24.2	37.6	26.9
2183.4	3363.8	2868.9
75.3	173.3	184.3
981.4	842.3	1915.0
1526.1	1099.4	2391.9
587.8	607.1	60.4
4289.6	4408.4	4072.4
7613.0	8235.9	8597.1
26.6	36.5	45.0
722.6	1120.1	1423.9
208.9	508.1	313.5
416.6	840.7	501.5
2128.9	2303.4	2406.5
2191.3	2612.1	3488.4
1149.1	1233.3	1956.9
4318.6	4641.0	4835.8
3835.2	6468.6	5263.1
2641.0	2691.4	3339.1
1380.5	2061.3	1271.7
25.1	58.0	44.6
2863.5	3687.4	3239.7
783.9	1073.2	1903.8
37.0	44.7	44.5
8266.9	9442.1	8291.5
3791.7	6353.4	7399.2
3095.1	4900.7	5907.0
80.6	116.4	107.7
1544.2	1365.7	2450.3
92.3	143.8	195.2
44.2	96.7	214.3
685.7	1052.9	754.7
34.1	41.0	45.9
945.2	606.8	1209.6
7239.1	7799.3	6868.2
64.4	142.1	202.8

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AB182309.1 gg_id:105400 termite gut clone Rs-SS44 AB182
AB191824.1 gg_id:143359 termite gut homogenate clone M1NP1-15 AB191
AB192253.1 gg_id:143938 termite gut homogenate clone RPK-33 AB192
GQ502658.1 gg_id:590884 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ422733.1 gg_id:565720 Human Oral Microbiome dental plaque GQ422
AY005081.1 gg_id:45933 subgingival dental plaque clone AF068 AY005
AB191928.1 gg_id:144853 termite gut homogenate clone M1PL1-51 AB191
EU464271.1 gg_id:302795 hamadryas baboon feces clone AFBAB_aai01e01 EU464
EU794206.1 gg_id:324511 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_N44 EU794
AB088903.1 gg_id:77948 termite gut homogenate clone Rs-E21 sp. AB088
GQ039162.1 gg_id:400332 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
AB191968.1 gg_id:141054 termite gut homogenate clone M1NP2-94 AB191
EU471558.1 gg_id:291957 Asiatic elephant feces clone AE1_aaa04b06 EU471
AF068336.1 gg_id:4116 termite gut homogenate clone RFS15 AF068
GQ502644.1 gg_id:543504 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ502653.1 gg_id:547244 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AM420275.1 gg_id:240104 Noma subgingival plaque clone 702D05(oral) AM420
AY134898.1 gg_id:59569 oral periodontitis clone EX137 AY134
AB062768.1 gg_id:21434 termite gut homogenate clone BCf1-01 AB062
AF182836.1 gg_id:3922 Treponema sp. str. 3:E:AT013 AF182
GU408692.1 gg_id:546393 Human Oral Microbiome oral cavity GU408
AB088889.1 gg_id:78084 termite gut homogenate clone Rs-A43 sp. AB088
GU428680.1 gg_id:538832 Human Oral Microbiome oral cavity GU428
AB084969.1 gg_id:70817 termite gut clone NkS85 AB084
AB234367.1 gg_id:146849 termite gut homogenate clone MgMjD-036 AB234
AB191868.1 gg_id:144495 termite gut homogenate clone M2PT2-95 AB191
AB032000.1 gg_id:36987 protist termite clone HsPySp16 clone AB032
EF454895.2 gg_id:226214 termite hindgut clone 290cost002-P3L-616 EF454
AB234372.1 gg_id:148779 termite gut homogenate clone MgMjR-079 AB234
AB085163.1 gg_id:70117 termite gut clone NkS-Oxy1 AB085
AB084955.1 gg_id:69510 termite gut clone NkS7 AB084
GQ502640.1 gg_id:539398 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
AB192247.1 gg_id:143443 termite gut homogenate clone RPK-13 AB192
AB084954.1 gg_id:74331 termite gut clone NkS5 AB084
EF559163.1 gg_id:220887 mesophilic anaerobic digester clone G35_D8_L_B_C07 EF559
GQ502642.1 gg_id:584558 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf7- GQ502
GQ426550.1 gg_id:552289 Treponema sp. str. S GQ426
AF275918.1 gg_id:46681 anaerobic digester clone AA14 AF275
AB191836.1 gg_id:143094 termite gut homogenate clone M1NP1-56 AB191
AB088880.1 gg_id:77953 termite gut homogenate clone Rs-B10 sp. AB088
AY337320.1 gg_id:106877 Spirochaeta sp. str. B AY337

63.3	61.8	108.1	90.8	148.4	83.6	148.5	79.8	51.4	40.9	52.4
43.5	569.1	738.5	774.0	506.0	668.6	681.6	770.0	151.3	161.4	500.3
223.3	757.7	665.0	588.1	539.5	540.4	497.1	503.8	1066.8	315.0	384.2
2461.1	2605.1	2728.4	2916.0	2937.3	2198.1	2839.1	2773.4	2259.5	2705.6	2601.5
4411.8	2426.2	2554.0	2274.8	4446.0	2576.4	2436.6	2426.6	2437.4	2382.5	2425.6
65.3	526.1	978.7	1169.1	949.0	714.1	965.0	892.6	376.3	91.1	541.5
35.7	223.4	217.2	307.2	356.6	198.1	428.8	254.4	79.2	51.7	93.0
12710.3	5961.4	4598.2	4434.1	4419.6	5676.7	5452.5	4797.8	6942.6	4630.6	5818.5
2258.6	5420.8	6552.3	7850.2	6859.5	5884.2	6825.2	7182.4	4924.3	3575.7	6157.4
37.3	135.5	130.8	119.8	301.2	82.2	160.4	131.4	73.9	31.9	73.5
1650.4	2781.3	3500.5	4207.8	3515.0	2749.4	3257.1	3649.8	2653.1	1298.0	2775.8
36.5	2173.2	2632.8	2720.5	2059.6	1909.5	2098.8	2427.5	1046.2	807.9	1175.3
1187.8	5906.0	6225.3	7919.4	5615.6	5489.9	7253.8	5922.1	6679.1	5319.1	6489.6
32.4	80.3	161.1	119.2	118.4	58.2	100.6	108.1	55.7	48.2	62.8
45.6	148.9	183.5	231.1	153.6	153.2	237.0	214.9	56.1	21.9	162.7
681.7	1049.3	1286.1	1325.1	1306.9	1441.4	1225.9	1244.4	991.7	320.9	1542.9
8186.4	5626.5	7638.2	7697.5	5605.2	5227.1	6136.1	6427.9	6407.5	2892.2	7625.1
53.5	1427.9	1747.8	1625.8	1641.5	1456.4	1616.4	2131.2	1339.6	697.7	1670.9
41.4	99.9	225.5	156.0	60.3	85.6	116.6	98.5	60.5	28.2	52.8
30.6	211.5	604.4	797.3	56.1	147.9	337.5	83.9	47.0	17.1	143.4
43.5	657.6	1441.7	2659.1	913.3	743.3	630.8	1784.8	315.7	263.6	831.5
123.9	251.3	269.7	301.9	336.7	245.6	361.1	190.0	142.9	151.6	235.9
34.5	20.4	42.7	53.8	22.9	28.4	28.2	125.0	96.6	20.5	35.8
38.4	110.2	109.2	192.2	228.9	141.7	202.3	181.3	61.3	23.8	65.3
65.2	731.8	1194.3	1225.5	1475.5	919.1	1941.9	1198.7	636.4	437.7	1101.7
40.2	94.7	267.3	176.8	464.7	88.3	381.3	72.1	59.0	44.6	115.4
12358.9	10548.0	9770.7	9650.2	9945.1	9479.1	10065.3	8845.3	10147.4	12856.3	16014.1
17264.4	8038.4	6714.0	8010.4	9554.6	8830.0	8712.6	8112.8	10325.8	8178.4	7223.4
38.5	127.8	174.3	362.1	130.4	119.6	189.8	138.8	48.4	22.4	100.2
78.7	40.6	43.0	48.9	40.0	33.5	39.9	31.1	31.4	26.6	33.1
58.0	39.1	74.2	67.9	70.4	50.2	70.2	71.9	32.0	27.5	67.2
111.2	1040.0	974.7	1547.6	2342.0	1073.3	1745.0	860.9	763.3	425.6	1232.3
53.1	538.5	1115.5	943.5	537.7	723.4	968.7	1185.1	383.6	104.0	652.2
45.0	34.0	49.8	59.6	25.3	30.2	55.3	42.7	24.7	26.2	47.5
35.9	52.0	126.9	177.4	48.2	51.7	54.8	75.1	108.3	19.6	36.5
2371.8	1106.8	1498.4	1709.7	1617.8	1413.5	1558.1	2038.8	724.9	402.1	865.0
16968.4	7168.3	6666.8	7434.9	6947.4	6533.3	9033.0	5831.1	7593.5	6911.0	9520.1
47.4	45.8	117.0	161.2	27.0	47.5	103.1	43.1	30.9	12.7	55.0
52.5	483.6	645.5	660.9	579.9	487.7	938.1	732.6	190.7	222.1	248.2
86.8	416.0	532.7	414.8	372.4	322.5	328.0	371.4	400.5	167.2	323.0
98.6	90.5	129.5	273.4	153.1	98.9	116.7	119.6	88.2	244.3	83.6

84.5	161.8	215.7
422.1	544.8	1004.1
412.9	637.9	610.6
2385.5	3226.9	2641.8
2229.9	3424.4	2696.7
756.2	713.7	1423.4
195.7	234.0	264.7
3968.8	4947.0	4885.6
6988.0	6650.6	6567.5
98.9	67.6	231.8
3871.8	3533.1	3444.2
1617.2	2478.3	2769.4
5207.8	6230.4	6261.9
89.0	150.1	98.7
108.2	230.0	138.2
886.2	1379.8	1255.0
6413.9	6607.1	5964.7
1366.6	1830.9	1634.7
78.1	79.1	74.6
61.1	101.9	71.0
854.3	927.5	1457.1
165.8	289.5	210.4
147.2	33.7	100.3
95.4	98.9	126.0
1775.8	725.0	2095.4
78.9	122.1	100.8
8220.0	8581.9	10260.0
6973.1	11851.5	8837.6
73.9	162.7	363.1
29.6	41.2	34.9
58.4	65.1	59.9
718.3	999.7	1483.7
1042.5	937.2	1092.0
40.9	50.2	34.2
93.7	285.3	157.9
1737.0	1840.6	2526.8
6284.0	7500.4	6335.9
32.3	44.9	52.2
526.4	1085.8	1814.5
297.2	435.8	239.0
252.7	97.7	75.1

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FJ380060.1 gg_id:586280 Spirochaeta sp. str. SR FJ3800
X93928.1 gg_id:3802 Spirochaeta africana X93928
AY605180.1 gg_id:106187 microbial mat clone LL026 AY605
AY337319.1 gg_id:103241 Spirochaeta sp. str. M6 AY3373
X93926.1 gg_id:3807 Spirochaeta asiatica str. Z-7591 X93926
AF166259.1 gg_id:37803 Spironema culicis str. BR91 AF1662
EU448140.1 gg_id:266509 Spirochaeta sp. str. SIP1 EU448
EU245914.1 gg_id:251213 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-B0 EU245
AB192150.1 gg_id:142321 termite gut homogenate clone RsTz-71 AB192
GQ406200.1 gg_id:583561 Benthic submerged sinkhole ecosystems sediment clone -45-14 GQ406
AB088897.1 gg_id:77774 termite gut homogenate clone Rs-B68 sp. AB088
EU385774.1 gg_id:273317 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU245152.1 gg_id:240123 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-B03 EU245
GU139329.1 gg_id:593443 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
GU139313.1 gg_id:542335 lactate formate propionate hydrogen donors reductive dehalogenation trichloroeth GU139
EF602483.1 gg_id:233469 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
AJ278165.1 gg_id:65483 anaerobic bioreactor clone SHA-116 AJ2781
AF286040.1 gg_id:51888 saltmarsh clone LCP-5 AF286
CU918232.1 gg_id:568533 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AB248650.1 gg_id:146622 mesophilic anaerobic butyrate-degrading reactor clone BHB21 AB248
CU918313.1 gg_id:562644 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU918359.1 gg_id:540776 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU887773.1 gg_id:336104 and RFLP anaerobes Nisargruna biogas plant anaerobic digester clone 8SN EU887
FJ825527.1 gg_id:561904 Microbial during start-up mesophilic biogas plant clone 42B_BS1_4 FJ8255
EF515598.1 gg_id:222084 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
CU917471.1 gg_id:560582 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
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CT574479.1 gg_id:150885 major candidate division within anaerobic sludge digester Evry municipal wastewate CT5744
CT574480.1 gg_id:153806 major candidate division within anaerobic sludge digester Evry municipal wastewate CT5744
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GQ461620.1 gg_id:567190 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial TCE Bioren GQ461

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DQ988271.1 gg_id:203045 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with DQ988
CU927274.1 gg_id:539547 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
AB175393.1 gg_id:99923 mesophilic anaerobic BSA digester clone BSA2B-21 AB1753
EU864445.1 gg_id:335847 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU8644
CU923797.1 gg_id:567700 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
AB513440.1 gg_id:566297 Removal dioxins semi-aerobic fed-batch composting biostimulation 'Dehalococcoide AB5134
AJ306785.1 gg_id:66916 DCP-dechlorinating consortium clone SHA-4 AJ3067
AY426469.1 gg_id:107649 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone E30 AY4264
EF602475.1 gg_id:256047 metabolic planctomycetes anaerobic sulfide- and sulfur-rich zodletone spring oklaho EF6024
EF602476.1 gg_id:227609 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
EU381859.1 gg_id:271582 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
EU474681.1 gg_id:290320 Indian rhinoceros feces clone IR_aaa02b12 EU4746
AB231045.1 gg_id:203507 termite gut wall clone HsW01-043 AB2310
EU283584.1 gg_id:278222 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1104 EU2835
EU101271.1 gg_id:242859 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1012
EU681994.1 gg_id:287458 microflora imbalances intestine dogs inflammatory bowel disease duodenum health EU6819
AF255601.1 gg_id:74652 hot spring clone SRI-24 AF2556
EU635940.1 gg_id:278855 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU6359
CU926426.1 gg_id:573323 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9264
CU926777.1 gg_id:558738 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9267
AF129869.1 gg_id:1641 anaerobic digestor clone BB48 AF1298
NZ_ACJX02000009.1 gg_id:484357 Anaerobaculum hydrogeniformans str. ATCC BAA-1850 NZ_AC
EU878334.1 gg_id:565884 Investigation factors influencing production large-scale municipal biogas plant therm EU8783
NR_028903.1 gg_id:591885 Anaerobaculum mobile str. NGA; DSM13181; ATCC BAA-54 NR_028
U50711.1 gg_id:1634 Anaerobaculum thermoterrnum U50711
EU639374.1 gg_id:343828 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6393
EU276415.1 gg_id:290298 Anaerobaculum thermoterrnum str. YWT-2 EU2764
CU919006.1 gg_id:533770 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9190
GU357466.1 gg_id:574739 Crude biodegraded under thermophilic conditions methanogenic consortia enriched GU357
AB175377.1 gg_id:99359 mesophilic anaerobic BSA digester clone BSA2B-05 AB1753
EU234248.1 gg_id:249038 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
AF069287.1 gg_id:1649 Aminobacterium colombiense AF0692
EF559198.1 gg_id:218020 mesophilic anaerobic digester clone A35_D28_L_B_E01 EF5591
AF234542.1 gg_id:71455 Dethiosulfovibrio marinus str. sr12; DSM 12538 AF2345
AY005466.1 gg_id:72749 Dethiosulfovibrio acidaminovorans str. sr15 (DSM 12590) AY0054
CU917598.1 gg_id:543835 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
AY953224.1 gg_id:114635 anaerobic swine lagoon clone A-2G AY9532
CU925573.1 gg_id:553988 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9255
EF436500.1 gg_id:204216 Jonquetella anthropi str. ADV126 EF4365
CU920428.1 gg_id:539058 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9204
EU462629.1 gg_id:302106 Sumatran orangutan feces clone orang2_aai66c11 EU4626

322.8	2530.8	2231.3	2686.4	2806.9	2523.7	3346.1	2375.2	2327.7	1245.6	2757.2
651.8	1284.4	907.4	1197.6	1135.5	1025.8	1015.9	1476.4	673.9	427.8	880.5
58.8	689.3	832.4	975.6	860.3	682.1	1365.2	654.4	287.6	258.5	474.7
5438.9	9280.7	7651.6	8443.4	8614.6	8981.3	9275.5	9572.5	8966.8	9483.5	9254.4
3899.1	6514.8	6341.8	5983.7	6736.6	6125.0	8385.5	6189.9	6429.3	3410.2	6943.8
49.1	40.5	20.3	22.5	19.4	18.2	21.6	19.8	18.0	14.2	15.6
141.4	312.8	456.2	334.0	287.1	348.2	287.3	286.4	271.2	165.4	219.2
40.0	214.6	347.2	193.2	203.3	123.7	425.9	150.2	56.9	30.7	213.5
433.0	9582.2	7276.0	7351.8	7271.8	7603.7	7583.1	7275.2	7260.5	4532.3	6989.1
1583.3	2081.3	1894.9	2075.8	2125.1	2958.6	1971.5	1992.9	2785.4	692.9	1920.6
14589.7	12200.5	11939.3	12299.4	12947.0	11216.8	14978.4	11176.2	16637.9	13563.6	17378.3
2323.6	6786.7	6227.2	6634.2	6860.3	6216.9	7441.5	6042.5	7102.6	3772.3	6864.4
1205.9	3970.5	4880.0	4874.7	2609.3	3388.6	3572.4	3565.5	4092.8	2399.8	4497.9
904.4	5105.2	5270.9	5352.0	3356.6	4811.6	4874.8	5515.8	2868.4	2762.0	5254.0
13666.5	8718.7	7846.6	8544.5	7815.1	7465.1	8815.7	7194.0	10881.0	9804.4	10058.4
8685.0	11683.8	11122.9	11361.1	10616.3	10414.6	12744.0	9322.5	13881.5	8358.1	11918.7
4690.4	1656.2	1381.7	1427.2	1395.9	1251.2	1707.0	1801.1	1092.8	1713.2	1146.1
288.5	2992.1	2670.4	2827.3	2521.2	2678.4	4190.1	2887.8	1634.1	688.4	1727.7
929.4	1105.9	1167.0	1280.3	1531.6	1087.2	1721.5	1185.8	506.6	309.7	1377.2
63.5	60.5	54.7	59.9	63.6	44.9	60.7	48.5	35.5	52.6	46.1
3661.1	1285.4	1550.6	1533.8	1411.2	1391.1	1747.7	3131.6	998.6	1362.4	1076.8
12189.7	10097.8	9807.2	10461.1	10357.1	9695.8	10152.6	9707.4	11857.9	8311.9	13680.7
9991.7	8320.0	8338.6	8107.2	8921.5	7889.1	6922.2	7994.7	8414.2	8058.0	8900.7
1183.3	6762.8	7499.7	7962.2	8204.5	6897.3	9396.5	7324.8	5306.3	6947.3	6372.7
6773.1	5838.1	5678.5	6313.7	6254.6	5963.6	6653.0	5762.9	7148.0	6081.3	8089.6
966.7	2592.0	2902.1	2532.9	3051.2	2604.1	2931.1	2946.0	1921.9	1900.7	2046.9
4920.8	5152.6	5398.8	5574.1	5438.8	5273.0	6011.2	5255.9	5790.2	4681.3	6730.9
736.2	2581.2	3375.2	2899.7	3060.5	2811.2	3002.6	3447.9	1920.6	1913.3	2641.1
137.9	401.8	439.1	450.0	740.9	335.0	682.6	409.1	276.3	216.2	213.8
47.6	40.0	47.5	37.1	61.9	41.5	71.9	39.0	28.9	20.5	31.1
54.5	170.6	155.4	176.0	217.7	273.8	214.6	157.7	60.2	38.4	111.7
873.8	1669.8	2097.8	2093.4	2304.8	1497.4	1899.2	2363.4	1399.9	394.2	2236.6
9762.8	4409.2	3430.3	3590.3	3520.2	3973.2	2843.9	2763.0	6127.1	5723.2	5103.9
66.3	118.0	261.5	216.8	159.9	114.7	223.0	209.4	85.7	80.1	110.8
3221.2	5549.7	6724.4	5410.3	4750.5	4666.3	5325.8	5206.9	5427.1	3883.3	6311.9
2567.3	6935.2	8258.3	8807.0	9432.8	8097.4	9772.3	8678.8	6288.5	3462.7	7719.3
271.3	4250.9	4243.6	3962.6	4699.6	4140.6	4280.7	3844.2	4729.8	2214.9	2665.9
2036.3	7405.7	7317.7	7834.9	10334.9	7535.8	8988.0	7489.6	8566.7	5202.3	6953.4
53.2	470.4	891.6	957.1	1032.2	687.0	1267.8	819.5	436.9	131.6	493.1
32.6	20.9	18.0	22.0	22.7	15.6	14.9	20.7	20.1	15.7	18.4
859.1	2546.8	2965.1	2556.4	3027.8	2830.7	3074.2	2637.8	2372.4	1511.0	2781.9

2128.1	3204.4	12852.3
1022.6	1739.3	1925.0
681.4	1045.9	4618.8
8321.3	7380.7	9628.5
4920.5	6774.4	10716.3
13.5	70.3	220.0
207.2	366.2	2795.9
181.1	560.7	4184.8
6299.4	7613.9	8454.7
2683.7	2269.7	2086.8
11686.0	12290.5	12096.9
6843.6	6276.8	7481.2
3288.4	4223.2	3278.4
4615.3	4584.5	4215.4
7228.1	8644.7	6997.2
10219.7	10192.3	10739.3
1259.3	1829.5	1689.8
1721.5	3333.0	4057.8
991.8	1518.2	3310.1
37.9	59.2	56.2
1564.0	2043.2	1602.1
9228.9	8568.3	9700.9
7758.6	8758.1	9213.7
7068.0	7421.8	9280.5
5838.0	5810.0	6177.4
2667.4	2985.6	3168.2
5158.5	5269.6	5292.2
2846.9	3427.6	2643.1
367.4	424.7	626.7
45.8	76.2	387.3
110.3	361.3	1130.6
1612.7	2505.0	4121.4
2904.7	4832.2	4591.3
219.5	350.8	234.4
4544.1	5263.3	4005.5
7592.6	7228.3	9053.2
3337.0	3956.9	6600.7
6619.3	8028.2	11142.2
619.7	818.5	1286.3
16.6	27.0	16.9
2461.7	2595.8	4275.7

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k__Bacteria	k__Bacteria	p__Synergistetes	c__Synergistia
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k__Bacteria	k__Bacteria	p__Synergistetes	c__Synergistia
k__Bacteria	k__Bacteria	p__Synergistetes	c__Synergistia
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g__Pyramidobacter
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g__Candidatus Tammella
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g__Candidatus Tammella
g__Cloacibacillus
g__Synergistes
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g__Thermanaerovibrio
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DQ308572.1 gg_id:149439 sheep rumen enrichment clone 196.B09 DQ308
GU303160.1 gg_id:585815 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
AB288913.1 gg_id:199975 termite gut homogenate clone BOf7-16 AB288
DQ085087.1 gg_id:132438 goat rumen clone A13 DQ085
AF125200.1 gg_id:1643 oral cavity clone D084 AF1252
AF125199.2 gg_id:1642 oral cavity clone BH017 AF1251
GU410680.1 gg_id:540821 Human Oral Microbiome oral cavity clone _D059 GU410
AB062819.1 gg_id:19846 termite gut homogenate clone BCf4-02 AB0628
AB062836.1 gg_id:38526 termite gut homogenate clone BCf7-04 AB0628
AB192113.1 gg_id:142452 termite gut homogenate clone M2PB4-76 AB1921
AB192116.1 gg_id:143824 termite gut homogenate clone M1PL1-68 AB1921
AB234551.1 gg_id:149454 termite gut homogenate clone MgMjR-058 AB2345
DQ307691.1 gg_id:144040 termite intestinal tract clone MTG-61 DQ307
AB299560.1 gg_id:254669 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
AB192115.1 gg_id:144260 termite gut homogenate clone M1PL1-49 AB1921
AB231081.1 gg_id:146679 termite gut wall clone NkW01-046 AB2310
AB189694.1 gg_id:113993 termite gut homogenate clone Tc-61 AB1896
AB299558.1 gg_id:237398 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
CU463952.1 gg_id:276742 Cloacibacillus evryensis str. 158 CU4639
EF551160.1 gg_id:230271 Synergistes sp. NML96A088 EF5511
DQ412721.1 gg_id:162959 Synergistes sp. str. RMA 16290 DQ412
CP001818.1 gg_id:523250 Thermanaerovibrio acidaminovorans str. DSM 6589 CP0018
CU927653.1 gg_id:568704 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927
CU924623.1 gg_id:558424 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EU234149.1 gg_id:247916 receiving river and un techniques anaerobic process WWTP treating penicillin G prod EU2341
CU919451.1 gg_id:575488 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9194
EU471574.1 gg_id:296843 Asiatic elephant feces clone AE1_aaa01b03 EU4715
CU920720.1 gg_id:536647 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9207
EU471563.1 gg_id:290654 Asiatic elephant feces clone AE1_aaa04b01 EU4715
CU920536.1 gg_id:552202 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9205
CU923733.1 gg_id:575163 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9237
CT573946.1 gg_id:156047 Evry municipal wastewater treatment plant clone 009G09_B_SD_P15 CT5739
CU926881.1 gg_id:542837 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9268
CU925055.1 gg_id:568648 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9250
FJ189547.1 gg_id:354649 digester anaerobic sludge clone EUB_26 FJ1895
CU927313.1 gg_id:571181 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9273
GQ377129.1 gg_id:547330 structure two reactive PCE degrading enrichment s stimulated OU Duck Pond Norm GQ377
CU920532.1 gg_id:559188 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9205
CU924981.1 gg_id:573012 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9249
CU919042.1 gg_id:563832 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9190
AM933660.1 gg_id:276480 Enrichment dioxin-dehalogenating two-liquid phase s anaerobic enrichment clone M AM933

40.5	27.8	21.6	31.7	27.8	26.2	29.1	22.4	18.1	17.8	23.6
1865.9	4947.4	4904.0	4571.5	5408.7	4229.3	4794.0	3739.5	4359.1	2442.2	3752.9
2137.4	5447.6	5652.3	6901.0	6859.7	6079.0	7337.3	6119.5	5205.2	4664.7	5312.0
48.5	288.0	366.0	430.3	915.3	394.6	535.4	270.5	47.9	36.9	92.9
2890.2	5903.0	5952.9	7238.8	6204.9	5692.3	7135.3	7155.6	4252.6	2496.6	5361.4
10721.1	8512.2	8271.5	9216.0	10593.7	8101.2	10457.6	7831.8	9522.5	10216.1	9314.3
15181.5	10456.5	8953.6	11318.4	10418.1	10484.3	11365.6	9213.7	13255.9	13820.3	13016.9
1960.5	6840.0	6288.9	7499.6	8531.7	6265.8	7479.7	7321.1	6498.6	6117.1	6302.3
37.5	35.5	33.4	28.8	34.1	16.4	33.6	22.2	29.0	17.2	28.4
616.0	1093.1	676.9	740.1	747.1	790.5	807.1	709.8	969.6	473.7	1002.9
472.6	2913.5	3351.2	3025.7	2601.2	2933.3	3501.8	2815.3	1576.3	1599.2	2715.1
169.0	245.6	312.3	274.1	378.7	235.3	370.2	372.2	126.8	48.7	196.6
37.4	64.5	80.9	75.5	94.0	75.9	75.6	95.3	27.7	17.1	73.0
20341.0	6959.4	7474.6	7395.7	6299.6	6032.3	8632.4	6977.6	9254.9	7887.2	9042.1
39.3	135.3	114.8	107.9	87.0	182.0	83.8	129.9	64.6	31.4	78.9
146.9	1577.6	2315.0	1888.5	2452.2	1918.1	2436.2	2668.6	885.5	623.1	2258.8
39.3	22.8	23.1	26.4	24.4	22.3	25.8	22.8	20.9	15.8	24.5
2538.6	3041.9	3700.6	3769.4	4186.7	3204.6	4516.8	4131.7	1891.8	1765.9	3364.2
815.4	4919.1	4533.8	4219.9	5864.1	5368.0	5834.0	5464.4	7779.5	3364.1	4136.5
967.1	5913.0	5098.7	5996.1	6345.1	5662.7	6304.4	5363.5	6283.5	2966.2	4388.3
892.7	5592.0	5418.8	6226.6	5733.6	4383.3	5994.3	4932.4	5256.7	2765.9	4542.0
1548.7	2600.6	3184.3	3104.7	5122.9	3176.5	3768.2	2860.3	1415.0	2256.0	1898.3
828.2	4416.6	4233.4	4593.7	4356.8	3989.4	4660.0	3961.9	4430.5	2735.7	4068.6
2876.9	5326.2	5541.3	5974.6	5117.7	6233.7	5410.0	5279.6	9111.4	6502.4	6599.4
31.0	764.0	622.6	677.2	816.1	665.6	554.2	698.1	597.3	187.2	260.1
20504.7	9265.2	7573.2	9635.3	8504.3	8703.3	9440.1	7991.7	12053.8	10976.0	11492.1
1350.8	5440.5	5847.3	7388.7	5943.0	5765.2	7380.1	6376.5	4111.6	2142.0	4754.6
3999.9	5081.4	4999.2	5229.7	4778.1	5143.6	5617.3	4891.6	5643.1	4897.7	5302.6
22386.8	10375.3	9117.2	11048.8	10044.1	9264.1	11411.5	9005.1	12758.7	9326.4	13920.6
866.7	3466.2	3093.2	3522.3	3913.3	3282.3	3924.0	3357.7	3273.2	1764.1	2971.3
859.0	1666.6	1665.7	2138.3	2146.3	1783.4	2089.3	1758.6	1437.4	2160.6	1434.0
73.0	39.5	44.6	37.5	26.6	52.0	32.3	44.1	20.2	19.7	32.6
1163.2	6079.8	5406.0	5920.6	6414.2	5813.2	6383.4	5256.7	5254.7	3576.1	5268.1
4662.0	7537.6	6666.1	6163.5	8421.3	6735.5	7124.7	7166.3	7404.2	6197.8	5502.5
361.9	4759.3	4056.5	3807.5	3759.1	3373.3	3959.7	3451.6	3503.6	3848.9	2644.1
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37.9	323.9	111.9	112.7	52.8	158.7	49.9	145.2	65.0	24.7	46.8
684.9	6076.0	5428.4	5264.7	4569.4	4927.5	5071.8	5086.9	7203.9	4738.9	5074.1
220.2	3517.8	3143.6	3304.1	3905.3	3189.6	3407.9	3060.9	2962.1	2825.9	2450.7
213.3	2325.1	2401.6	2779.6	2130.0	2251.7	2497.8	2518.1	2466.8	2901.8	2118.6
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9670.2	13438.3	10730.4
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599.4	885.4	898.4
2308.1	2939.7	4218.4
219.5	444.1	432.3
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3859.0	4360.9	5784.3
4738.9	6872.9	5478.9
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30.1	152.5	3569.0
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7672.8	7034.8	7966.9
2967.7	2810.0	4533.6
2512.1	3031.4	4281.3
50.7	160.2	2184.8
4477.0	4853.5	6226.7
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2078.6	2771.7	4145.1
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DQ071273.1 gg_id:143575 Thermovirga lienii str. Cas60314 DQ071
EU721809.1 gg_id:568879 microbial production water Alaskan mesothermic petroleum reservoir two methods EU721
AB195868.1 gg_id:109151 Anaerobic sludge clone N42 AB195
CU918985.1 gg_id:552219 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
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FN563362.1 gg_id:539330 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN5633
AY553945.1 gg_id:114315 Baltimore Harbor sediment clone FA12 AY5539
AB175356.1 gg_id:107021 mesophilic anaerobic BSA digester clone BSA1B-02 AB1753
EU887988.1 gg_id:329262 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU887
EU507776.1 gg_id:266082 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04f03 EU507
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513.9	3548.7	3229.0	3691.8	3638.6	3527.6	4082.3	3111.0	3940.8	2451.6	2919.7
80.4	182.8	233.9	192.9	387.8	242.1	350.8	295.8	181.8	109.6	183.3
45.5	494.2	514.0	105.6	286.2	883.6	118.3	290.4	142.4	74.4	111.1
72.1	162.6	486.0	187.9	350.3	222.9	205.2	220.4	65.1	53.2	132.6
736.6	2792.4	3935.4	2958.5	2672.9	2604.5	3365.2	4904.8	2957.6	3173.0	4579.3
496.1	3927.6	4285.3	3752.9	3005.3	3332.2	4126.7	3708.7	2672.4	3856.0	2475.2
1103.1	3763.8	4253.4	4404.7	3908.2	4204.7	5071.6	4058.7	3061.0	3059.0	3648.7
134.8	383.2	373.8	312.8	507.9	400.9	444.4	474.9	255.5	182.3	158.9
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7866.8	8425.4	8608.5	10347.4	7659.0	8287.6	9499.9	8254.6	10838.5	8275.7	9993.6
16485.9	7212.0	7550.7	7439.4	7488.9	6648.9	7472.2	7741.7	9268.1	5437.2	9289.7
2556.8	2427.9	2550.7	2860.5	2554.5	2308.6	2824.5	2502.0	5350.7	3027.2	2661.3
15195.3	3723.1	4093.8	4453.7	4050.9	4061.1	4180.0	4448.9	4491.5	3622.7	4397.1
1467.3	3691.7	3509.5	3679.2	3632.3	2992.0	3502.5	3658.4	6623.3	2697.4	5195.9
15968.9	5000.4	4698.9	5200.6	4927.7	5098.4	5820.2	4691.6	5736.9	6500.1	4748.0
50.7	341.4	486.4	590.4	344.5	298.2	208.4	259.8	163.0	149.4	111.4
8820.5	5837.1	5081.3	5992.4	5007.3	5237.6	6265.0	5397.6	8020.2	8772.6	8494.2
4742.5	3378.8	3731.2	3713.0	3470.2	3211.8	3249.8	4042.7	5340.4	2310.0	4178.3
5007.6	2507.7	2571.3	2694.4	2650.7	2514.0	2792.4	2371.0	2449.8	2100.9	2870.4
40.5	563.1	581.6	618.5	335.4	435.4	393.8	382.4	626.7	52.1	787.0
8456.3	3589.5	2933.6	3449.6	3880.5	3429.4	3589.6	3652.9	3924.9	3513.3	2798.3
3284.6	2558.7	2888.3	2836.3	2447.0	2412.0	2916.5	2318.5	4104.3	2275.9	4106.6
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275.6	1814.8	2282.6	2620.7	1837.9	1720.1	1802.4	2617.2	2382.2	1468.1	1591.3
11075.0	6090.7	4985.1	5449.4	4977.2	5118.1	5196.8	4621.9	8064.9	6633.9	7655.9
5862.6	1711.5	1297.3	1527.8	1736.7	1441.3	1649.4	1724.3	1747.1	1220.1	1774.3
7389.3	2511.0	2860.3	3109.4	2720.9	2686.3	2590.5	2972.2	2231.5	1505.5	2793.2
84.8	131.3	123.1	148.6	64.9	131.9	131.4	160.0	133.1	67.1	89.7
803.2	1826.2	2199.8	2099.8	1581.0	1746.9	1825.2	2215.1	3199.0	987.3	2562.7
1606.6	6514.0	6400.8	6445.6	8172.8	6253.8	7944.5	5931.6	7876.7	4127.2	6306.1
947.5	2135.1	2500.8	2948.3	2305.6	2332.3	2414.2	2729.3	3365.2	1581.2	2099.3
16234.6	6192.1	6278.6	6312.8	6639.8	6074.5	7101.2	5654.5	6789.9	5822.5	7584.0
525.9	2233.6	2642.2	2720.1	2127.3	1956.2	2307.9	2613.6	2730.9	854.0	1614.2
11958.7	2372.0	2473.8	3043.6	3084.2	2447.5	2724.5	2886.6	2517.2	2882.2	2502.9
55.9	879.3	875.9	1084.5	879.2	848.8	1106.8	845.5	755.7	1196.6	650.3
8504.3	1987.9	2636.2	3198.1	2532.2	2415.3	2619.2	3102.8	2818.6	1814.1	2735.1
9505.6	3147.9	3344.0	3249.1	3286.1	3095.7	3793.0	2946.7	3421.7	3763.0	4033.5
7002.2	3806.5	3921.3	4219.4	3969.9	3819.5	4075.4	4106.5	4511.6	3753.9	3845.5
6405.6	2155.0	2566.5	2774.3	1959.6	2275.3	2329.6	2389.1	2593.8	2476.0	2916.2

410.3	802.3	2155.5
3160.7	3305.2	5288.2
191.4	178.4	1260.6
214.0	224.9	1720.3
139.4	389.1	3279.5
3820.5	4174.2	6412.9
2534.1	3911.7	5211.0
3912.0	4664.0	7336.9
473.4	473.0	406.5
34.8	42.6	96.5
8735.2	9954.1	9859.5
6654.6	8711.4	8220.5
2431.8	3403.7	3072.2
4385.8	5566.8	5647.0
3077.8	4199.9	4792.3
4802.4	5697.7	6176.9
406.8	726.1	697.6
5552.6	6682.0	7336.6
3478.6	5217.3	5631.3
2867.0	2533.3	4176.5
521.9	536.2	1992.6
4059.3	4357.9	3889.1
2367.8	3585.4	3775.1
1682.4	2626.5	5117.8
1633.1	2179.0	3317.2
2721.6	2344.5	2474.9
4981.9	4693.8	5994.6
1574.3	2120.4	1773.4
3055.2	4206.4	4394.3
129.1	412.9	214.9
1943.8	2957.3	3107.3
5817.9	6085.1	8392.6
1840.0	3071.9	2370.1
5826.1	6513.3	6357.6
2044.3	2850.4	3622.8
3724.7	3896.3	5193.1
1061.0	898.6	2124.4
2930.6	3339.9	3674.1
3196.6	3369.9	5465.7
4101.6	5439.6	5530.0
2761.4	3109.7	4537.6

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EU511038.1 gg_id:260292 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01g03
EU505346.1 gg_id:275252 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02h09
EU508553.1 gg_id:259161 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35c08
EU508904.1 gg_id:262026 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap38b10
EU508454.1 gg_id:270956 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33g02
EU507820.1 gg_id:262850 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01d08
EU507901.1 gg_id:261338 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03b11
EU507144.1 gg_id:264111 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa02c04
AY960571.1 gg_id:115098 Clostridium sp. str. ID4
EU503726.1 gg_id:264512 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa03g04
EU507352.1 gg_id:262440 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02a11
EU507705.1 gg_id:276487 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03d12
EU509693.1 gg_id:266803 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak47b12
EU509103.1 gg_id:263498 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap43f09
EU511545.1 gg_id:262139 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak06d02
EU507105.1 gg_id:263436 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01d11
EU511638.1 gg_id:272358 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak08a10
EU507110.1 gg_id:268053 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01f01
EU506770.1 gg_id:276156 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56a06
EU508273.1 gg_id:258736 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa01b03
EF099605.1 gg_id:181334 mouse cecum clone SWPT4_aaa01g04
EU508420.1 gg_id:260325 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33c07
EU507848.1 gg_id:259647 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01h02
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EU508375.1 gg_id:277042 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04c07
EU506604.1 gg_id:261326 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53b10
EU508929.1 gg_id:266817 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39b09
EU508441.1 gg_id:273802 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33e09
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EU507690.1 gg_id:276757 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03c07
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EU505497.1 gg_id:264699 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa01e06
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EU511437.1 gg_id:270460 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20c06
EU507851.1 gg_id:265433 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01h07
EU505321.1 gg_id:274384 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e01

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173.7	873.3	1522.7	1095.3	816.2	714.2	678.6	857.9	928.5	425.6	706.9
8385.4	3931.0	3963.6	3830.1	3938.1	3831.1	4574.5	3489.8	4445.8	5428.4	4520.3
299.2	1908.0	2099.1	1661.8	1821.0	1998.5	1276.1	1816.5	1441.7	544.1	1391.7
271.7	1171.7	1219.7	1308.1	972.4	1059.9	915.2	1402.4	2467.9	610.6	1861.9
7038.4	3733.0	3797.9	3761.9	3272.6	3305.9	3581.0	3687.5	5475.7	3833.9	5279.5
373.1	1717.9	2494.9	2203.7	1991.2	1975.3	2194.1	2292.1	1620.3	3600.9	1726.7
20592.7	5445.8	4760.0	5726.2	4376.7	5366.6	5523.8	4800.8	8939.9	5876.0	9115.3
2665.9	2101.2	2444.4	2081.6	2584.9	2372.1	2342.2	3218.1	2858.0	2671.6	1759.1
22364.2	9548.8	9107.6	10313.5	8307.7	8595.4	9226.8	8046.5	11188.0	8169.1	13034.3
691.1	993.0	1143.0	908.5	796.4	857.1	879.7	1034.1	1128.6	1451.0	783.6
8279.4	2532.0	2770.9	2689.3	2578.9	2560.4	3049.3	2250.8	1611.1	3297.6	2781.7
9492.2	5584.2	5697.4	5233.4	5450.7	4945.2	5217.0	4947.4	6827.5	6213.1	5731.6
714.5	2927.8	2497.5	2414.7	1854.8	2273.8	2072.9	2028.5	3191.3	1776.6	3602.5
46.0	1898.3	1782.4	2056.3	1147.4	1708.7	1607.0	1621.8	1223.7	1263.2	1951.3
825.5	3111.9	4623.7	3883.0	3830.5	3070.1	3770.9	4233.4	2921.3	1678.5	3471.3
3250.0	2299.6	2622.8	2094.5	2029.3	2419.1	2251.0	2675.7	2246.8	3217.7	1648.6
4727.1	2449.3	2490.0	2414.9	2201.3	2301.3	2382.9	2245.0	2426.4	2557.4	2979.4
574.4	1104.6	1406.3	1269.9	1010.6	987.4	902.4	1110.3	1487.8	839.0	1295.3
117.3	969.6	875.5	900.8	667.9	763.1	792.0	680.6	934.0	558.3	827.4
1765.9	3082.8	3071.6	3130.7	3459.0	2863.2	3273.1	3361.9	3993.0	1754.1	3391.4
21008.3	3929.6	4630.6	4869.0	4274.8	4247.1	4449.3	4734.1	5643.3	4673.5	5192.1
4276.9	5083.7	4640.8	4906.1	3381.2	4823.7	4582.8	4208.5	8009.8	6567.6	6757.8
101.8	748.2	795.2	828.4	1017.8	695.5	834.5	539.7	786.8	495.9	935.0
8124.3	3705.8	3927.3	3748.1	3901.8	3822.7	4759.7	3834.0	3693.7	4525.3	3207.1
823.3	1724.2	1959.4	1993.2	1781.4	2253.9	2112.9	2072.4	2411.8	2852.0	1958.9
4630.5	3777.6	3361.1	3872.7	3400.4	3454.3	3624.9	2940.1	3968.1	2487.1	3889.4
11226.8	4966.7	5006.0	4691.6	4758.0	4512.6	5044.6	4625.4	4911.1	4444.5	4691.5
1006.9	1060.0	1300.3	1154.1	825.2	973.4	880.5	1090.8	1049.9	1137.1	1144.3
6130.9	6152.7	6181.5	6203.2	5299.1	5651.9	6116.8	5309.6	8122.7	6767.3	8114.9
9075.7	6844.0	6517.2	6767.3	7715.8	6452.4	8126.8	5939.2	7992.9	7124.3	8194.9
8428.7	2752.3	2702.6	2660.9	2298.8	2406.8	2441.8	2427.7	4297.2	2460.9	3751.2
4846.8	4455.6	4510.1	4449.8	3539.4	4342.1	3964.4	3285.8	4917.7	5486.7	6481.7
4962.8	2054.9	2211.4	2443.1	2155.8	1993.8	1883.0	2793.8	3720.8	895.2	2811.7
6249.9	2931.2	3289.2	4688.2	3579.5	2628.5	3202.4	3046.1	2806.3	312.5	3038.3
10683.1	6709.6	5910.6	6247.1	5128.7	6579.7	6217.0	5485.2	9241.0	6813.4	9034.0
14023.2	4828.2	4004.1	4564.8	4658.0	4397.2	4822.4	4285.0	5771.9	5087.8	7362.1
52.0	1484.9	1310.7	1311.2	783.7	1156.6	998.0	1032.8	1548.1	1416.9	1291.3
11231.6	4215.2	5212.1	4693.5	4450.0	3759.7	4862.7	4553.3	6776.3	3503.1	5083.6
1112.7	3688.7	3899.7	3614.2	4263.3	3670.5	4342.0	3475.0	3872.9	3074.7	3611.3
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3927.0	4512.1	5430.1
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1210.8	1867.2	2785.9
3232.4	5011.1	5805.6
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4888.4	6789.7	7249.4
2591.4	3265.6	2504.9
8405.7	9643.3	9109.4
949.3	1704.9	1568.8
2792.3	2818.1	4641.6
5109.9	6050.9	5746.8
1896.1	2007.1	3527.3
1443.2	1922.6	2318.3
2410.1	3553.9	4593.4
2586.5	2752.4	3491.3
2334.6	2749.2	4875.9
1158.5	1492.3	2070.6
841.0	1079.2	1458.4
2855.5	4043.7	5645.1
4921.5	5704.4	6288.4
3809.3	5430.4	6333.5
769.9	795.5	1849.4
3279.7	4854.4	3839.3
2464.7	2424.1	3189.5
3193.0	4625.7	3920.6
4500.8	4776.7	5321.1
1219.7	1366.2	2581.8
5180.1	7064.3	5928.0
6023.6	6389.3	8610.9
2193.8	3631.9	2393.9
3669.6	4853.2	6225.3
2331.5	3560.5	4396.5
2619.4	2944.9	2976.8
5334.8	6677.2	5643.2
4365.1	5536.9	6592.5
1149.1	1330.9	2767.9
4227.8	5528.8	4678.3
3596.6	3510.6	5647.8
3496.0	4641.1	5785.6

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EU506795.1 gg_id:259351 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56d11
EU508639.1 gg_id:271756 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap36f09
EU506764.1 gg_id:264481 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap55h08
EU510765.1 gg_id:266227 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40h10
EU511037.1 gg_id:259314 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal01g02
EU505265.1 gg_id:260007 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa01e08
EU507268.1 gg_id:273137 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa04g02
EU507889.1 gg_id:259741 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa02g07
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EU505385.1 gg_id:276790 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03f06
EU508763.1 gg_id:260625 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap50f09
EU504373.1 gg_id:276645 cecal contents Mus musculus strain C57BL/6J; CRWD6 clone CRWD6_aaa03c02
EU507092.1 gg_id:268381 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01b08
EU505326.1 gg_id:261861 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e07
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EU505423.1 gg_id:273017 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa04c06
EU504523.1 gg_id:273270 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g09
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EU507094.1 gg_id:275623 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01c02
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EU507233.1 gg_id:258892 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03h12
EU506791.1 gg_id:263684 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap56d05
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EU507701.1 gg_id:267813 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa03d08

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27756.9	8142.5	7174.2	8193.0	7906.8	7350.2	8517.1	6998.0	8533.7	6511.7	10196.8
11301.9	5498.0	4880.5	5361.4	5222.8	5477.9	5442.9	5194.2	7351.7	5132.8	6480.0
15102.6	6951.9	5922.7	7017.5	6181.8	6448.7	7080.7	6190.5	9940.0	8123.4	8090.3
208.8	1673.5	2358.2	2479.0	2982.9	2015.0	3351.9	2705.2	1903.6	1004.1	2209.2
2758.5	3942.9	3904.8	4269.7	3367.1	3769.1	4225.1	3902.8	4219.8	6037.3	4445.3
1222.5	1911.2	1961.1	2266.4	1930.2	1980.8	1841.1	2331.6	2310.4	1386.6	2344.2
7622.1	4840.5	5084.3	5325.7	4084.3	4422.3	4696.4	4851.4	6582.1	3562.9	8295.7
13491.1	6388.0	5955.7	5713.9	5169.5	5927.0	5821.9	5340.6	8555.9	6391.2	7735.2
321.2	1072.9	1512.3	1505.4	1149.8	1060.6	1058.5	1518.2	2756.5	587.1	1533.8
8145.1	2923.5	2912.8	3261.3	3196.6	2788.1	3234.5	3763.0	4577.2	1397.2	3795.1
7988.8	4004.4	3826.6	3988.9	4196.0	3944.5	3956.2	3634.0	4100.7	5008.5	3953.9
673.2	874.3	988.5	904.1	717.8	806.9	913.2	699.4	784.7	533.9	746.4
242.0	1694.2	2009.7	2153.9	2058.7	1703.6	1712.1	2095.7	3373.6	806.9	2393.9
5372.7	2731.4	2741.4	2654.4	2585.4	2807.5	2575.7	2532.0	3117.9	3771.3	2838.2
5731.0	4849.2	4718.0	5510.4	4741.2	4837.3	5177.8	4588.9	4650.5	5942.8	5150.9
5641.3	2386.1	2649.4	2578.6	2202.1	2406.7	2232.3	2302.5	3283.6	2312.8	3158.8
3912.9	10082.8	8902.5	8530.9	7451.9	8781.7	8332.5	7904.1	15436.7	12085.6	10237.1
7507.2	3551.0	3258.3	3434.6	2656.8	3180.3	3229.2	3129.3	4625.4	4718.1	3946.3
959.5	1734.2	2402.3	2217.9	2248.2	1764.4	1996.8	2343.2	3171.0	822.4	1797.0
1687.7	1774.8	1518.1	1786.6	1502.3	1528.8	1727.4	1521.5	1828.2	1853.2	1837.6
148.6	877.6	1459.5	1198.1	999.0	1083.3	1088.0	1185.2	915.0	1667.6	842.9
746.2	1799.4	1854.7	1764.3	1769.2	1730.6	1581.7	1988.8	2871.8	1058.3	1970.3
9675.6	7100.4	7143.5	8595.1	7127.1	7486.8	7664.4	6664.0	12228.3	6980.4	8146.2
5218.9	5219.9	4419.1	4436.0	3980.6	4923.8	4499.5	4586.9	6290.5	4792.8	6822.6
460.6	3652.4	4092.9	3008.1	4633.8	3412.3	4831.4	3976.8	10145.5	4269.8	4948.7
13504.5	5880.2	5605.5	5909.9	5257.8	4983.6	5588.3	4743.1	5804.0	5247.0	6751.9
18983.0	8547.9	7557.7	7814.9	6611.9	7590.8	7671.0	6917.8	13407.5	9319.1	10119.4
23413.7	6922.0	6152.1	7398.6	6737.6	6239.6	4913.1	5971.3	10834.4	7612.8	10849.3
27394.4	6227.1	5897.5	6572.4	5954.3	6331.8	6524.7	5743.9	10734.1	6396.9	8867.8
266.3	704.1	769.7	669.7	445.4	584.1	549.2	541.6	748.2	642.2	736.6
296.1	233.7	361.3	282.0	331.3	257.8	404.5	270.9	178.0	253.3	183.7
72.6	142.4	215.6	185.7	246.9	159.5	178.9	207.9	115.1	242.6	97.1
9375.9	4002.0	3953.6	3542.5	4066.9	4006.9	4060.6	3742.5	4430.1	5090.5	3279.4
726.7	2726.3	4222.0	3589.6	2401.4	3175.6	2647.2	3372.7	3180.1	3143.6	2609.4
1814.0	2281.4	2464.8	2587.4	2290.8	2372.2	2107.5	3069.6	4273.1	1340.6	3471.0
21169.7	7191.6	6686.1	7205.3	7171.4	6911.8	7231.2	6654.9	8615.5	7755.2	6643.8
1182.7	2463.4	2485.9	2476.3	2314.3	2395.3	2220.5	2777.4	3457.9	1688.4	2940.4
24764.3	6928.2	6217.3	7498.0	6997.7	6371.9	5024.9	6230.6	11653.0	8268.4	9649.5
265.5	401.8	978.4	937.9	839.7	667.2	800.0	681.5	467.2	211.4	662.5
259.7	311.2	525.7	733.1	428.1	301.6	369.8	354.1	249.9	176.8	187.1

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2911.8	2581.8	6012.5
3791.8	4811.6	5767.0
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4039.5	6086.9	5848.2
5122.2	6975.0	6940.0
1380.3	2005.9	1660.2
3058.9	4245.9	4185.6
3817.8	3827.1	4392.9
747.4	1095.8	1348.4
1874.5	2608.0	3848.4
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8379.4	9146.9	11885.6
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1472.0	2366.0	2450.4
1246.0	1288.8	2148.1
1868.0	2634.9	2953.6
6983.0	8605.8	8493.0
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3709.1	4421.6	5742.8
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6762.9	9471.0	9542.8
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675.6	858.1	1160.6
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200.0	337.4	331.9
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3775.7	4224.0	3761.7
2344.4	3943.6	4404.0
6794.0	8375.5	8715.4
2573.3	3085.4	3583.2
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854.0	872.1	1167.3
389.5	555.0	650.8

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EU509085.1 gg_id:271704 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap43c11 EU509
EU509052.1 gg_id:258746 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap42f09 EU509
EU509587.1 gg_id:270157 cecal contents Mus musculus strain C57BL/6J; WD10 clone WD10_aak45c10 EU509
EU511456.1 gg_id:274825 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak20f03 EU511
EU507812.1 gg_id:277029 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa01c03 EU507
EU511344.1 gg_id:276457 cecal contents Mus musculus strain C57BL/6J; WD8 clone WD8_aak18g01 EU511
EU508445.1 gg_id:263759 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap33f03 EU508
EU505392.1 gg_id:259805 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa03g02 EU505
EU508551.1 gg_id:261932 cecal contents Mus musculus strain C57BL/6J; MD2 clone MD2_aap35c06 EU508
EU505649.1 gg_id:261890 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04a10 EU505
EU511197.1 gg_id:273662 cecal contents Mus musculus strain C57BL/6J; WD7 clone WD7_aal04c05 EU511
AJ417075.1 gg_id:98789 Allobaculum stercoricanis str. DSM 13632T AJ417
FJ880109.1 gg_id:404034 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
FJ880453.1 gg_id:385422 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
FJ881278.1 gg_id:371453 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
FJ880804.1 gg_id:438839 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
FJ879085.1 gg_id:454212 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8790
FJ881066.1 gg_id:443722 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8810
DQ113686.1 gg_id:134101 dog colon clone C5-42 DQ113
FJ881120.1 gg_id:389961 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
FJ879538.1 gg_id:396494 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EU503550.1 gg_id:260405 cecal contents Mus musculus strain C57BL/6J; CRWD2 clone CRWD2_aaa01a12 EU503
FJ880589.1 gg_id:393599 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
FJ880248.1 gg_id:409717 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
FJ879685.1 gg_id:386583 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8796
FJ881144.1 gg_id:425371 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8811
AB018187.1 gg_id:42372 Eubacterium cylindroides str. JCM 7787 AB018
FJ681704.1 gg_id:529292 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ681342.1 gg_id:528410 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ805198.1 gg_id:193516 human fecal clone RL249_aaj82h06 DQ805
EU467401.1 gg_id:297126 chimpanzee feces clone CHIMP12_c08_1 EU467
FJ683962.1 gg_id:528905 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
DQ796924.1 gg_id:180379 human fecal clone RL179_aao56e02 DQ796
DQ325889.1 gg_id:150312 Metagenomic gut microbiome healthy human stool clone B703 DQ325
DQ325904.1 gg_id:148077 Metagenomic gut microbiome healthy human stool clone B725 DQ325
DQ796045.1 gg_id:190736 human fecal clone RL202_aai50f11 DQ796
DQ801091.1 gg_id:194446 human fecal clone RL387_aao92a09 DQ801
DQ796640.1 gg_id:195652 human fecal clone RL179aan76d10 DQ796
DQ796955.1 gg_id:184237 human fecal clone RL179_aao56h09 DQ796
FJ673811.1 gg_id:526513 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
FJ675938.1 gg_id:521444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759

143.2	1730.2	1856.9	1805.2	1620.6	1589.9	1627.3	1597.6	1764.5	633.0	2167.6
9390.0	4863.0	4326.6	4960.7	5174.1	4886.5	5574.2	4849.0	6634.6	5855.3	5041.3
625.6	2030.4	2117.5	2327.6	2231.3	2092.8	1705.8	2322.1	3409.1	1351.5	2543.4
9067.8	7885.8	6908.1	7400.7	6243.7	7602.6	6961.2	6815.7	8730.7	7385.5	11656.0
420.9	3162.9	2281.9	2069.7	1909.8	2306.1	1448.6	1818.5	3048.0	1956.4	2238.1
525.6	1295.2	1892.6	1758.6	1536.5	2121.7	1528.0	2053.5	2693.3	1700.2	1353.1
604.2	5081.7	4554.0	3576.5	2846.7	4283.6	2856.9	3774.4	6709.2	6705.8	4134.2
225.3	935.9	1023.5	1123.5	1691.1	975.1	1499.6	1395.3	1388.1	293.3	901.3
7135.7	5477.9	5156.8	5446.8	3889.9	5221.6	4876.2	5706.7	8401.1	4461.3	8398.0
197.5	479.1	734.7	798.8	786.7	875.3	501.8	489.0	252.6	143.6	311.8
3661.7	4483.9	3839.9	4097.5	3629.2	3428.5	5070.7	3725.3	2455.8	2074.2	3771.6
265.4	1615.7	2299.7	2210.9	1488.0	1081.7	1634.3	1428.5	861.1	1633.9	1504.1
12977.7	7956.3	5773.7	7164.1	6554.3	6860.6	7261.5	5438.2	11080.6	8988.6	8111.8
4147.0	1908.3	2271.3	1881.4	1883.7	2118.2	1863.2	2957.0	1695.3	3355.6	2339.0
10333.5	5769.7	5249.9	5609.1	5371.2	5362.4	5980.6	4862.7	8276.5	6751.0	4658.6
180.2	2977.1	3225.4	3921.2	3669.1	3211.0	4103.4	2894.1	2210.3	1708.2	2541.9
12532.7	6896.2	5947.5	5787.2	5550.9	6540.8	6296.4	5270.0	9853.4	7375.3	7215.7
188.9	959.1	1325.3	1336.4	1238.7	1218.4	1313.3	1354.6	1343.0	854.3	989.6
127.1	1265.0	1724.2	1580.8	861.5	1215.7	1004.2	1406.3	428.8	652.5	651.4
6850.0	4090.6	3820.5	4387.0	4367.3	4072.5	4984.6	4400.7	5066.6	5644.9	8304.4
32.1	192.5	150.3	242.5	294.9	241.9	166.3	173.4	35.4	137.7	131.4
40.0	28.4	36.0	38.1	25.9	22.7	25.1	45.3	18.7	11.9	34.0
44.7	392.2	586.6	638.3	818.2	520.0	859.0	694.3	239.5	75.8	328.1
3345.2	2642.9	2214.7	2075.7	2227.0	2341.3	2432.2	1667.4	3461.4	1589.2	2265.7
52.5	615.6	708.3	743.6	628.3	639.9	796.0	624.2	456.8	79.1	401.4
15294.7	4567.3	3728.2	4847.3	5418.4	4698.7	4867.1	4455.8	4341.6	3061.9	4132.6
40.4	269.9	446.9	470.6	239.3	674.1	370.8	375.7	165.0	483.4	184.7
13471.6	8756.7	8043.8	9865.4	9538.0	8225.7	9275.5	9009.7	8885.1	7296.6	10784.8
9415.4	10336.3	9964.0	11137.6	9766.1	9404.3	11130.0	10492.0	12656.8	9615.0	13875.3
199.9	995.8	1240.0	1461.5	804.7	839.2	889.1	1656.3	380.8	164.3	1106.4
93.9	1129.7	1053.5	498.6	457.7	818.4	397.2	667.2	921.4	1230.3	597.5
362.0	3571.7	4287.5	3887.9	3354.1	3522.0	3617.2	3902.6	3229.9	3068.8	3292.4
169.9	1975.3	1993.7	1959.1	1657.7	1615.4	2182.7	1552.8	1670.9	1261.0	2185.4
2840.0	1469.6	1522.3	2330.6	1733.2	1407.4	1739.2	1565.2	839.2	316.8	1250.8
31.1	429.5	968.6	736.2	290.2	763.3	249.2	961.1	305.5	683.5	482.8
9859.5	4237.3	3497.6	3822.8	4006.4	3712.4	3028.8	4140.4	4925.6	5115.8	4831.0
23.4	16.1	17.1	18.1	16.8	12.9	17.8	11.7	16.6	13.1	16.9
53.7	974.5	1215.7	1973.4	648.0	1084.5	1051.1	1330.2	408.7	134.8	680.5
592.3	2446.5	2290.8	2577.4	2389.1	2366.8	3157.8	3103.8	1989.5	1091.1	3101.0
13298.7	4322.9	4481.6	4422.6	3520.6	3964.6	4082.6	4134.5	7317.2	5329.3	6139.8
3995.3	1686.9	2627.3	2105.3	1830.3	1851.4	2049.9	2025.9	1672.8	2505.7	1265.1

1728.3	1743.4	3595.5
4599.7	5839.9	6263.1
2358.9	2946.3	4084.7
6465.1	6772.9	8654.7
2108.7	1527.8	2926.0
2539.8	2817.3	2060.0
3322.7	4851.3	4904.9
1099.3	1650.1	2177.7
4772.3	6848.5	6260.7
513.4	890.3	1233.8
2804.8	3958.7	4556.6
1462.2	2629.7	2067.0
5291.2	6706.5	6674.4
2295.0	2893.5	3370.6
4202.0	5469.7	5436.1
2475.1	3300.7	3438.7
5101.4	5651.7	6401.0
1112.7	1703.9	1756.3
1303.6	1289.0	1544.6
3800.6	5315.0	5061.8
212.7	320.2	635.5
24.9	22.7	83.4
455.8	721.7	800.5
1692.9	1975.7	2252.6
559.1	387.5	560.7
4183.5	4989.0	4713.5
553.6	614.9	662.7
7296.2	8785.7	8483.9
8159.4	9239.0	10031.1
1315.0	1134.6	1156.6
614.5	746.0	1089.7
3455.0	3558.7	4611.2
1572.6	1786.8	4149.6
1866.8	2214.7	2450.2
1074.9	781.7	831.9
4027.4	4952.3	4604.8
13.4	18.5	16.6
1428.5	1755.6	1063.9
2813.5	3080.6	4205.6
3428.9	5212.2	3905.4
1962.3	2789.9	3212.3

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g__Catenibacterium

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s__Catenibacterium mitsuokai	71329
s__Catenibacterium mitsuokai	71367
s__Catenibacterium mitsuokai	71415
s__Catenibacterium mitsuokai	71596

FJ683676.1 gg_id:524279 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
FJ674214.1 gg_id:522991 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
AY977931.1 gg_id:124370 human cecum mucosal biopsy clone LG47 AY977
DQ325818.1 gg_id:150015 Metagenomic gut microbiome healthy human stool clone B551 DQ325
DQ325686.1 gg_id:147618 Metagenomic gut microbiome healthy human stool clone B287 DQ325
DQ796023.1 gg_id:198115 human fecal clone RL202_aai50d06 DQ796
DQ810113.1 gg_id:178347 human fecal clone RL184_aao68c01 DQ810
FJ677579.1 gg_id:529596 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
FJ672990.1 gg_id:522129 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
DQ796744.1 gg_id:198851 human fecal clone RL179_aao53h07 DQ796
EU467482.1 gg_id:292065 Sumatran orangutan feces clone orang1_h04_1 EU467
DQ800165.1 gg_id:184625 human fecal clone RL303_aal69a10 DQ800
DQ326393.1 gg_id:150448 Metagenomic gut microbiome healthy human stool clone C428 DQ326
DQ326047.1 gg_id:148356 Metagenomic gut microbiome healthy human stool clone BA25 DQ326
EU762827.1 gg_id:342647 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
EU474482.1 gg_id:296794 bighorn sheep feces clone BHSD_aaa04h07 EU474
NZ_ADFR01000011.1 gg_id:532556 Bulleidia extructa str. W1219 NZ_AD
Z36271.1 gg_id:15722 Bulleidia extructa str. 1365 Z36271
AF220064.1 gg_id:31844 Bulleidia extructa str. DSM 13220 AF220
FJ833972.1 gg_id:542406 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P2Q202_46F06 FJ8339
EU776314.1 gg_id:323045 Red Kangaroo feces clone KO1_aai41a05 EU776
AB218311.1 gg_id:146880 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgA-88 AB218
DQ325832.1 gg_id:147485 Metagenomic gut microbiome healthy human stool clone B577 DQ325
FJ832913.1 gg_id:559793 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_08H01 FJ8329
EU467125.1 gg_id:302200 mongoose lemur feces clone ML_aae88h01 EU467
FJ832594.1 gg_id:584753 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_12D02 FJ8325
FJ833018.1 gg_id:576628 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q102_85E11 FJ8330
EU462550.1 gg_id:297719 Sumatran orangutan feces clone orang2_aai65a01 EU462
FJ832520.1 gg_id:537476 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q201_73A10 FJ8325
AB031056.1 gg_id:21980 Bulleidia moorei str. JCM 10645 RCA59-74 AB031
EU774283.1 gg_id:340869 Chimpanzee feces clone CHIMP1_a07_1 EU774
EU344272.1 gg_id:275128 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU344303.1 gg_id:260783 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ976219.1 gg_id:582816 Interindividual healthy human oral microbiota mouth clone 3688 FJ9762
AF371517.1 gg_id:54730 swine intestine clone p-2772-24E5 AF371
EU344300.1 gg_id:259168 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
DQ015346.1 gg_id:132391 mouse cecum clone M2_1g10_3 DQ015
AB030223.1 gg_id:33198 Catenibacterium mitsuokai str. JCM 10608 AB030
AB030222.1 gg_id:27171 Catenibacterium mitsuokai str. JCM 10607 AB030
AB030225.1 gg_id:21138 Catenibacterium mitsuokai str. JCM 10610 AB030
AB030221.1 gg_id:46764 Catenibacterium mitsuokai str. JCM 10606 AB030

24455.7	8111.1	8682.8	7635.1	7574.0	7306.2	8484.7	6777.5	10343.1	9233.1	9843.9
53.9	1124.8	1917.9	2142.5	882.9	1227.9	1597.1	895.3	499.8	127.2	797.0
627.0	2387.0	3406.4	2439.0	1929.4	2401.4	1689.5	2694.5	1400.9	1051.8	1891.8
1558.5	1847.1	3470.8	3316.4	2502.2	3314.5	2580.1	3753.7	3177.6	4295.4	2657.1
7429.9	1560.5	2050.2	2139.7	1817.2	1669.5	1887.8	1977.5	1569.9	2462.5	1549.5
46.0	419.9	455.5	395.5	412.8	379.1	559.0	485.2	236.3	240.7	453.1
123.9	849.3	1441.6	1218.6	1031.0	1197.0	505.5	1612.0	608.7	315.8	747.5
4893.4	4602.0	5248.1	4073.6	3394.9	4225.7	4022.4	3946.1	6714.4	6324.2	5447.6
115.8	2870.1	2686.6	1650.0	1392.8	2176.1	1532.0	1886.8	3118.7	2683.1	1719.1
1074.9	2487.5	2194.3	2257.6	1411.8	2280.3	2312.6	2178.7	1616.1	1351.2	2385.6
136.3	1246.4	1530.4	1471.9	879.8	1390.4	843.9	1879.7	721.5	1337.9	1817.9
239.0	1708.1	1819.6	2254.3	2179.0	2433.6	2122.4	2988.3	1583.2	3888.8	1380.3
11538.9	4153.4	4426.2	4417.8	3754.8	3049.2	3750.1	3852.6	5660.0	4828.7	5399.9
821.7	804.3	1369.5	1077.3	863.7	764.8	880.0	807.7	427.7	165.0	672.6
3503.3	753.7	1403.0	1632.2	1849.3	1127.6	1614.9	1325.0	875.3	814.1	935.4
8909.2	8973.4	8228.1	7800.7	7587.4	8073.0	7065.0	7832.2	9991.2	6469.8	7700.7
1765.4	1584.7	1484.4	1773.3	1450.3	1529.6	1604.5	1340.5	1387.5	840.1	1419.4
4227.3	3451.6	3183.8	3376.9	3116.6	2884.5	3381.1	3194.2	4804.0	3505.3	3967.0
5553.0	4544.6	3827.7	4075.9	4557.5	4687.5	4146.2	4645.9	3614.8	4249.2	4722.8
3092.5	4683.9	3954.8	4113.1	4248.6	4087.4	3644.7	4068.2	4167.4	3887.3	3711.6
201.6	4322.4	6075.2	5714.1	3535.1	5023.9	6006.4	4851.6	2413.0	2571.7	4001.3
228.0	2501.6	2928.8	2978.5	2382.8	2998.6	3609.1	2949.8	1608.6	2008.8	2624.9
40.4	13.7	7.6	10.2	9.8	9.6	8.2	7.5	14.7	8.9	9.2
1701.5	6942.6	6496.1	6342.0	8103.7	6249.6	7662.9	6094.5	6601.8	5154.1	6762.3
6965.1	7058.2	6161.4	5993.4	5715.8	6220.5	6413.7	6667.6	4873.0	6326.1	5955.4
7515.5	6052.1	5933.9	5530.7	5923.2	5395.5	6216.9	5366.4	5841.0	4551.3	6169.9
1258.5	3854.1	3925.1	4103.4	4720.8	4133.0	4315.0	3510.2	3208.5	2310.6	3051.6
2366.4	4215.2	4112.0	4270.9	5847.0	4171.9	5642.6	3840.5	4600.0	3058.5	4292.6
3086.6	6995.9	6356.7	6819.8	8859.1	6601.2	8317.9	6249.1	5903.6	4085.5	6713.3
70.3	281.0	404.6	406.5	301.4	329.0	277.1	389.8	163.6	398.5	225.6
8464.3	5030.3	4683.4	4938.0	5486.3	5068.5	6103.6	4588.7	4555.8	4768.2	4299.1
323.5	2624.7	3331.1	3820.8	2810.6	2781.5	4022.1	3371.8	3059.8	1810.2	2627.3
423.7	3918.1	4080.3	4556.3	4478.8	3765.0	3774.0	4850.5	2267.6	2739.5	3573.8
731.9	4245.3	4768.3	4788.9	4549.8	3560.8	4435.2	4491.5	2541.5	3131.1	4441.6
367.1	2540.6	3923.2	2334.3	1448.1	2569.6	1844.5	3010.5	1642.0	932.0	2696.5
110.7	2837.7	2216.3	2735.6	2142.6	2013.1	1664.2	2846.4	2644.2	2206.6	2885.0
57.5	38.9	39.4	45.4	50.9	39.9	48.4	45.7	41.5	43.4	48.0
8744.3	5701.3	6875.2	5885.6	6089.1	6101.8	7113.9	7396.6	5457.9	7301.3	8528.6
4331.5	4442.8	5247.6	5050.7	4663.6	4672.0	4848.5	5793.6	4249.8	4867.6	5388.6
15733.9	6906.9	7066.8	7085.6	8025.8	7031.3	8137.0	8167.5	7258.4	7113.2	11622.3
2955.8	3745.4	4405.3	4304.9	3908.4	3957.3	4083.4	4889.1	3103.6	2997.6	4093.2

6982.5	7741.7	8088.7
2427.9	1318.1	1335.8
2612.4	1961.2	2441.0
3523.1	3616.6	3472.7
2263.2	3010.2	2352.3
359.0	590.8	784.2
1506.0	907.5	1085.9
3989.3	4737.1	4892.4
1841.6	2030.9	2691.5
1569.2	2349.1	2192.8
1729.5	2263.2	1538.6
3594.7	2477.0	2936.4
3396.7	3972.1	3704.5
720.0	1068.1	542.0
1704.2	2313.0	1803.5
7009.7	7353.9	8499.0
1253.7	1745.1	1748.1
2844.3	4318.9	3551.4
5000.7	6261.0	6182.3
3246.9	4989.0	6472.0
4494.0	4273.6	9537.3
2999.1	3268.0	3200.5
9.0	7.2	10.3
6232.6	6538.7	8853.1
6252.9	6590.9	6406.3
4984.7	6238.8	6381.8
3662.5	3835.0	5145.1
4254.7	4995.2	6923.9
6514.6	6421.6	8887.9
361.5	707.2	993.7
4427.4	6020.3	7693.9
3042.1	3592.9	4711.6
5533.6	5222.8	7479.9
3879.6	4448.6	6424.0
2643.8	2659.0	4015.0
2429.6	3972.4	6031.4
46.7	50.6	40.1
5897.8	7177.0	7023.3
4876.3	4850.1	5467.5
6565.7	8753.3	7546.7
4075.6	4159.6	4892.1

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k__Bacteria	k__Bacteria	p__Tenericutes	c__Erysipelotrichi

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AB030226.1 gg_id:40839 Catenibacterium mitsuokai str. JCM 10611 AB030
DQ326116.1 gg_id:145343 Metagenomic gut microbiome healthy human stool clone BB76 DQ326
DQ326286.1 gg_id:145169 Metagenomic gut microbiome healthy human stool clone C247 DQ326
DQ325906.1 gg_id:150498 Metagenomic gut microbiome healthy human stool clone B730 DQ325
DQ325656.1 gg_id:150173 Metagenomic gut microbiome healthy human stool clone B225 DQ325
EU773418.1 gg_id:309852 Black lemur feces clone BKLE_g06_1 EU773
EU461777.1 gg_id:287510 mongoose lemur feces clone ML_aaj28g12 EU461
DQ325879.1 gg_id:146207 Metagenomic gut microbiome healthy human stool clone B679 DQ325
EU469507.1 gg_id:289377 black lemur feces clone BKLE_b06_2 EU469
EU459789.1 gg_id:295705 ring-tailed lemur feces clone RT_aai12h06 EU459
AY978040.1 gg_id:122153 human cecum mucosal biopsy clone LH84 AY978
EU530322.1 gg_id:274970 mucosa adherent and invasive microbes profile adenoma colorectal cancer clone M4 EU530
AY978152.1 gg_id:125309 human cecum mucosal biopsy clone LJ38 AY978
NZ_ACCK01000460.1 gg_id:469918 Catenibacterium mitsuokai str. DSM 15897 NZ_AC
EU469487.1 gg_id:298026 black lemur feces clone BKLE_g01_1 EU469
DQ325735.1 gg_id:146738 Metagenomic gut microbiome healthy human stool clone B383 DQ325
AY976273.1 gg_id:124283 human ascending colon mucosal biopsy clone LX20 AY976
DQ326095.1 gg_id:145882 Metagenomic gut microbiome healthy human stool clone BB39 DQ326
NR_026495.1 gg_id:550248 Clostridium cocleatum str. I50; DSM 1551 NR_02
NR_029247.1 gg_id:590150 Clostridium ramosum str. 113-1; DSM 1402 NR_02
EU462941.1 gg_id:300521 southern three-banded armadillo feces clone arma_aaj55d03 EU462
NZ_ABIK02000003.1 gg_id:259777 Clostridium spiroforme str. DSM 1552 NZ_AB
ABIK02000013.1 gg_id:270245 Clostridium spiroforme str. DSM 1552 ABIK02
X75908.1 gg_id:15715 Clostridium spiroforme str. ATCC 29900 X75908
X73441.1 gg_id:15716 Clostridium spiroforme str. DSM 1552 X73441
DQ825115.1 gg_id:193907 human fecal clone RL185_aan85e10 DQ825
FJ673628.1 gg_id:528507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ100445.1 gg_id:142563 Clostridium sp. str. SDG-Mt85-3Db DQ100
AJ576394.1 gg_id:100232 midgut homogenate Pachnoda ephippiata larva clone PeM34 AJ5763
GQ897372.1 gg_id:571478 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ897
EU542496.1 gg_id:274239 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
FJ364978.1 gg_id:368625 feces adult twins and mothers; TS1 clone TS1_a01d09 FJ3649
DQ808012.1 gg_id:199138 human fecal clone RL180_aan70f06 DQ808
AB288920.1 gg_id:200664 termite gut homogenate clone BOf9-07 AB288
DQ793967.1 gg_id:187634 human fecal clone RL176_aah45h09 DQ793
FJ365022.1 gg_id:368528 feces adult twins and mothers; TS1 clone TS1_a01h09 FJ3650
DQ326867.1 gg_id:149994 Metagenomic gut microbiome healthy human stool clone E349 DQ326
FJ363684.1 gg_id:357024 feces adult twins and mothers; TS14 clone TS14_a02b01 FJ3636
FJ676587.1 gg_id:516871 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
EU134663.1 gg_id:251385 tallgrass prarie soil clone FFCH17703 EU134
FJ678331.1 gg_id:515661 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783

2960.3	3749.8	4704.4	4305.2	3941.8	3955.6	4090.1	4569.1	3112.3	2998.6	4385.4
14732.1	5189.0	5050.0	5791.8	5305.1	5170.0	6251.2	6949.9	7981.6	6266.1	9967.4
124.6	1939.1	2464.1	2840.4	2222.6	2408.5	2422.0	4239.8	1963.3	3197.9	2634.3
509.2	1723.5	2146.4	1795.6	1322.5	1942.2	1328.8	2244.0	1797.7	3836.9	1833.6
47.4	129.6	220.3	253.1	130.4	143.7	173.8	337.4	26.2	15.2	128.3
1834.1	950.2	1775.1	1101.6	1378.1	999.8	1146.0	3442.1	340.5	429.3	2029.4
335.5	1828.1	2100.5	2373.0	1980.7	1635.1	1925.5	2077.4	1730.6	1645.6	2110.9
156.2	3247.1	3192.6	3017.9	2423.0	3227.4	2522.5	4219.7	2863.1	4237.7	3252.0
9988.4	5240.3	5039.9	6093.5	4938.0	5288.6	5269.4	5560.7	6691.2	5882.9	7154.5
3272.4	2491.4	3014.5	3151.4	2700.5	2485.4	3160.2	2746.3	2650.8	2406.7	3749.1
1282.9	3244.6	3310.0	4142.8	3850.9	3670.6	3570.0	5518.6	3629.6	4486.8	4728.2
142.9	1562.5	2590.7	2104.0	1280.1	2150.8	2147.8	3123.3	1025.7	728.1	1778.4
196.6	1059.8	1658.6	1147.0	1454.0	1274.0	1392.0	1974.3	1746.3	1785.0	1396.7
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15288.3	7734.7	8168.7	9247.7	8366.0	7675.5	8721.9	8251.6	12678.7	10230.0	9394.2
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120.4	63.9	75.4	94.8	126.9	77.3	95.2	100.6	45.6	27.5	52.5
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207.6	3196.2	3182.0	3193.9	2583.6	3034.1	2923.3	3184.4	2622.3	1757.7	3029.5
92.9	489.8	610.1	806.4	656.6	584.4	595.2	722.8	545.9	512.3	369.2
112.2	417.7	494.3	507.2	453.9	373.1	461.2	511.5	204.3	376.1	258.6
217.3	2584.7	2213.3	2332.1	2183.1	2110.7	2206.7	2535.9	1474.3	1029.6	1515.0
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1354.8	1447.6	1778.8	1663.5	1638.5	1541.2	1642.8	1746.0	1151.6	1822.6	1294.6

4076.3	4439.8	4895.0
4499.7	5411.1	5137.4
2719.3	1831.8	3214.1
1915.6	2315.8	1661.0
155.6	237.7	261.8
2272.5	1051.1	2189.3
1854.7	2041.4	3618.6
3116.2	2269.5	4092.4
4765.2	6219.7	4920.6
2590.5	2830.9	2443.4
3556.7	3558.4	3939.9
2215.4	2161.6	3409.6
1297.7	1918.4	2202.9
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7561.8	9249.0	8185.6
3353.9	4663.0	3801.8
4786.6	5575.0	5233.4
3808.6	5429.5	4499.9
92.6	142.6	127.3
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707.0	886.8	1500.8
419.3	632.0	1475.5
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4071.7	3483.3	5133.4
3115.3	3808.0	3453.4
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59.1	74.4	106.7
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2339.9	2385.3	4184.1
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1381.8	2261.4	2713.4
6434.2	5797.6	6211.3
1090.7	1162.2	1857.9
2138.6	2845.1	2990.2
4413.9	6680.1	5672.9
3823.9	5777.3	4383.2
3754.6	5378.8	4806.5
4926.3	6897.8	5395.7
680.0	556.5	302.4
1754.4	2047.1	2493.5

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DQ326852.1 gg_id:149140 Metagenomic gut microbiome healthy human stool clone E331 DQ326
FJ370952.1 gg_id:358786 feces adult twins and mothers; TS5 clone TS5_a03b10 FJ3709
DQ794080.1 gg_id:183083 human fecal clone RL176_aan57g03 DQ794
AY982801.1 gg_id:115534 human descending colon mucosal biopsy clone KZ46 AY982
FJ677018.1 gg_id:516022 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ441352.1 gg_id:191030 human intestinal biopsy clone CD101 DQ441
DQ057480.1 gg_id:136526 str. ic1391 DQ057
GQ492588.1 gg_id:580597 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ798465.1 gg_id:181284 human fecal clone RL181_aan97a10 DQ798
FJ679216.1 gg_id:521524 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6792
FJ678731.1 gg_id:514684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
GQ898739.1 gg_id:570735 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ898
GQ491637.1 gg_id:588666 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF071177.1 gg_id:190872 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
DQ798576.1 gg_id:178236 human fecal clone RL181_aan98e03 DQ798
AY975735.1 gg_id:116787 human ascending colon mucosal biopsy clone Y182 AY975
DQ797930.1 gg_id:180338 human fecal clone RL302_aal93e08 DQ797
FJ372126.1 gg_id:360238 feces adult twins and mothers; TS9 clone TS9_a02a08 FJ3721
FJ371039.1 gg_id:370335 feces adult twins and mothers; TS5 clone TS5_a04c01 FJ3710
AJ576387.1 gg_id:104610 midgut homogenate Pachnoda ephippiata larva clone PeM18 AJ5763
GQ046231.1 gg_id:427628 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ046
FJ370907.1 gg_id:362830 feces adult twins and mothers; TS5 clone TS5_a02f06 FJ3709
DQ327268.1 gg_id:145872 Metagenomic gut microbiome healthy human stool clone E812 DQ327
FJ370787.1 gg_id:363246 feces adult twins and mothers; TS5 clone TS5_a01c07 FJ3707
FJ370764.1 gg_id:362087 feces adult twins and mothers; TS5 clone TS5_a01a04 FJ3707
FJ369674.1 gg_id:360605 feces adult twins and mothers; TS51 clone TS51_a03e03 FJ3696
DQ797079.1 gg_id:194170 human fecal clone RL386_aao86g03 DQ797
FJ368379.1 gg_id:359304 feces adult twins and mothers; TS3 clone TS3_a03f08 FJ3683
FJ368229.1 gg_id:358899 feces adult twins and mothers; TS3 clone TS3_a01g05 FJ3682
FJ678559.1 gg_id:516982 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
DQ327312.1 gg_id:145134 Metagenomic gut microbiome healthy human stool clone E859 DQ327
FJ366410.1 gg_id:359009 feces adult twins and mothers; TS26 clone TS26_a02g07 FJ3664
FJ370922.1 gg_id:358586 feces adult twins and mothers; TS5 clone TS5_a02h01 FJ3709
AM277455.2 gg_id:229069 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
DQ804182.1 gg_id:198054 human fecal clone RL187_aah69h03 DQ804
GQ492759.1 gg_id:587530 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ440561.1 gg_id:156898 Clostridium innocuum str. Ulm 12 DQ440
GQ492977.1 gg_id:586813 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AB030220.1 gg_id:21822 Coprobacillus cateniformis str. JCM 10605 AB030
DQ803568.1 gg_id:177504 human fecal clone RL251_aaj87e08 DQ803

4749.7	2717.0	2653.4	3505.5	3457.7	2593.1	2800.2	3175.8	4561.9	1628.7	3108.3
262.7	761.1	1394.0	973.0	898.1	963.3	723.4	1366.8	888.2	1258.6	964.1
11584.4	6504.7	6231.1	7502.6	6285.8	5910.3	6595.0	6425.4	8666.6	7117.2	6990.6
134.4	911.7	888.6	997.2	1228.6	879.8	1119.5	1155.6	472.8	640.8	750.3
6931.2	3598.5	3773.8	4075.2	4002.6	3606.7	3823.8	3141.9	6147.5	3917.3	4556.7
2649.8	2951.4	3354.5	2796.4	3032.0	3209.0	3392.0	3213.4	3312.9	2443.6	2299.2
146.7	2098.3	2103.2	1909.9	1767.7	2162.4	1624.4	1943.8	2658.2	1201.9	1356.5
43.8	77.1	114.7	62.1	50.4	53.9	57.2	41.8	49.9	35.7	66.4
195.1	2182.1	2093.4	2045.2	1657.2	2021.6	1706.3	2211.8	1350.7	670.6	1905.5
293.2	2286.7	2702.3	1921.5	1950.5	2130.4	1786.0	2144.5	3174.0	2686.9	1950.7
46.3	3300.2	3315.1	1395.2	852.3	1929.7	1607.9	1963.5	2782.9	2122.7	1505.3
309.8	957.7	1584.6	1163.6	899.0	1260.3	1115.5	1689.7	827.3	1835.1	1306.1
13765.1	6754.2	6233.1	4948.3	4392.9	5760.3	5083.2	5319.2	6497.7	5949.1	6528.5
161.8	2258.4	2338.4	2498.2	1904.3	2142.7	2062.3	2086.5	2118.4	1375.4	2361.0
49.9	1491.5	2592.2	1061.8	497.1	1187.7	1163.3	1444.7	1064.3	640.3	790.4
11188.4	5702.5	4819.0	4950.6	4472.2	5112.4	5490.0	4347.9	7872.5	7254.2	6997.8
79.4	1839.2	1706.2	974.1	1652.9	1808.1	1638.2	1773.8	2865.7	2051.5	1580.6
162.2	1029.0	1053.0	1337.6	721.2	1154.9	665.3	1342.6	642.5	945.4	618.5
131.7	688.5	971.8	756.3	613.7	675.9	601.9	1180.0	385.2	410.9	422.6
199.9	1814.4	1982.6	1876.5	1045.5	1552.4	1226.8	1719.9	989.5	295.9	2001.6
54.8	1706.5	2053.5	2030.8	2193.4	1816.1	2314.3	1847.2	993.5	667.3	2003.9
12485.3	6538.4	6352.7	6144.2	5816.0	6095.7	6915.9	5834.1	8763.7	7358.0	7740.9
98.0	951.3	942.6	827.8	724.8	914.2	1009.7	991.0	1636.7	1532.1	886.9
121.4	883.8	867.4	978.0	777.5	1068.4	798.3	707.8	373.4	172.2	682.5
618.3	1703.5	1097.2	968.8	1252.3	1003.9	1260.4	1126.6	1346.2	556.9	803.7
60.7	225.8	260.5	251.5	339.5	190.0	309.2	286.7	106.6	128.5	143.2
238.1	900.5	1853.4	791.4	852.6	962.2	472.8	1547.2	422.2	1525.4	916.2
1666.8	4858.8	5358.9	4639.6	5215.9	5141.2	5726.1	5015.5	4223.4	5097.8	5792.3
3397.1	861.5	1206.6	1338.0	1392.2	1815.9	1543.4	2208.8	490.8	609.8	1136.6
160.3	1038.6	1945.4	1541.8	1242.1	1814.5	1599.0	2639.8	808.2	1262.4	1423.4
381.2	678.9	923.1	878.1	963.1	767.1	948.4	711.8	542.4	435.9	627.7
825.4	3069.7	2930.7	2899.5	2777.9	2737.3	3144.2	3011.1	1976.8	2503.8	2753.8
58.4	348.9	593.0	522.0	616.4	771.7	781.2	991.2	242.3	455.2	397.0
30192.8	6173.5	4726.4	5782.6	5338.4	3518.5	6355.7	5109.6	7874.0	7381.1	8369.8
34.0	19.7	17.4	22.0	18.4	17.7	13.5	18.4	11.7	22.9	18.5
16373.2	5114.3	4652.3	5653.2	5172.4	4588.1	5472.5	5170.8	8711.6	5735.5	8520.5
7862.1	4984.8	4956.1	6081.7	6390.9	4584.9	7020.3	4469.3	6055.8	6480.4	7368.5
49.4	267.0	576.3	369.8	206.5	350.9	257.2	337.1	138.6	64.4	383.7
16956.6	5904.7	5733.2	5815.0	6314.0	5550.7	5863.9	5843.0	9651.8	6471.9	9366.0
34.5	94.0	142.0	85.8	139.0	282.0	166.2	132.4	43.1	21.6	86.1
468.5	785.6	1091.7	866.0	1061.8	952.4	890.1	1016.0	711.7	669.5	993.2

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3219.1	4122.0	4807.6
3385.4	3711.0	3897.3
1603.8	2404.5	3269.8
63.7	97.9	243.6
2318.2	1791.4	3018.8
1880.9	2670.9	3432.3
1286.2	1209.4	1956.6
1947.6	2086.8	2405.7
4689.7	5876.6	6014.0
2138.4	2123.0	2722.2
1095.6	1058.9	1819.8
4191.2	5631.6	5316.2
1637.6	1860.9	1390.2
1227.5	1231.4	2788.4
1158.9	867.3	1757.6
1346.4	1716.0	1799.7
1680.3	2091.5	1877.2
6635.9	6919.3	5378.2
951.4	1523.2	1157.9
819.8	930.6	1719.7
1151.3	1467.3	1684.3
371.0	404.0	455.4
915.8	1694.0	3065.2
5425.7	6750.0	7076.8
1192.0	2007.8	1946.2
1692.7	1863.3	3183.6
1015.7	1233.6	1331.7
2334.0	3150.8	3053.9
623.9	751.7	1082.8
5054.6	6030.6	5563.8
21.0	28.3	18.6
3355.9	6295.8	4722.7
4162.5	5202.4	6653.2
382.8	285.0	387.4
4781.8	6991.8	5467.4
179.4	203.6	225.4
884.7	1375.2	1018.6

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s__Eubacterium dolichum	71459
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s__Erysipelothrix rhusiopathiae	71515
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EU771920.1 gg_id:326369 Southern three-banded armadillo feces clone arma_aaj56h10 EU771
GQ448197.1 gg_id:585386 Microbiome neonatal calves: shedding microorganisms fecal clone calf32_6wks_grp GQ448
GQ175408.1 gg_id:509861 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
AM275546.2 gg_id:231985 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
FJ368343.1 gg_id:368662 feces adult twins and mothers; TS3 clone TS3_a03b11 FJ3683
AM275478.2 gg_id:233953 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
DQ801017.1 gg_id:191700 human fecal clone RL387_aao91a01 DQ801
EU507257.1 gg_id:276227 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa04e02 EU507
FJ676717.1 gg_id:510237 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
NZ_ABAW02000024.1 gg_id:470381 Eubacterium dolichum str. DSM 3991 NZ_AB
FJ680914.1 gg_id:515268 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
FJ681460.1 gg_id:519377 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
FJ681610.1 gg_id:512366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
M23728.1 gg_id:15730 Erysipelothrix rhusiopathiae M2372
DQ462571.1 gg_id:157405 Erysipelothrix muris DQ462
AB055910.1 gg_id:78143 Erysipelothrix rhusiopathiae str. KG-BB2 AB055
AB540983.1 gg_id:581050 Erysipelothrix tonsillarum str. JCM 8533 AB540
AJ550617.1 gg_id:88075 Erysipelothrix inopinata str. 143-02 AJ5506
EU748014.1 gg_id:306059 neotropical folivorous flying bird adult hoatzin crop clone hoa12_36D05 EU748
Y11466.1 gg_id:15728 Holdemania filiformis str. ATCC 51649 Y11466
FJ369019.1 gg_id:367215 feces adult twins and mothers; TS4 clone TS4_a03c12 FJ3690
EU761816.1 gg_id:341803 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7618
FJ371255.1 gg_id:366464 feces adult twins and mothers; TS6 clone TS6_a02g10 FJ3712
EU461496.1 gg_id:296385 black rhinoceros feces clone RH_aaj91a04 EU461
FJ833665.1 gg_id:583224 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_90B12 FJ8336
EU471859.1 gg_id:292053 Asiatic elephant feces clone AE3_aaa04h07 EU4718
FJ364883.1 gg_id:356807 feces adult twins and mothers; TS19 clone TS19_a04c08 FJ3648
EU771726.1 gg_id:309403 African elephant feces clone AFYEL_aaj65d04 EU771
DQ353900.1 gg_id:149744 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z2 DQ353
EU470295.1 gg_id:293994 Grevy's zebra feces clone GZ_aaa03h02 EU470
DQ353909.1 gg_id:149927 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z22 DQ353
EU470473.1 gg_id:299480 Grevy's zebra feces clone GZ_aaa01g09 EU470
EU462969.1 gg_id:297568 southern three-banded armadillo feces clone arma_aaj55h06 EU462
EU467550.1 gg_id:294524 southern three-banded armadillo feces clone arma_h07 EU467
AJ629069.1 gg_id:188919 Eubacterium sp. Pei061 AJ6290
AY953174.1 gg_id:114580 anaerobic swine lagoon clone B-1F AY953
EU981243.1 gg_id:332976 sulfate reducing living bench scale aquifer packed bed clone D7_FB EU981
FJ382687.1 gg_id:562083 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3826
EU104057.1 gg_id:355578 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ382255.1 gg_id:513876 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
AY297808.1 gg_id:89878 waterlogged archaeological wood clone pACH93 AY2978

42.3	117.7	235.0	163.5	128.4	218.9	126.6	170.0	48.8	49.1	96.7
1007.6	2295.6	2524.8	2395.2	2947.7	2274.7	2863.4	2523.2	2070.0	1757.6	2260.4
75.7	202.3	216.5	156.1	262.1	170.8	230.5	201.7	145.8	49.5	149.0
30.8	31.9	37.5	32.6	38.9	76.3	33.0	38.3	30.2	23.0	46.1
7320.4	3387.9	3378.6	2928.6	3525.5	2070.9	3632.1	2865.9	2335.6	4661.4	3173.9
61.9	342.7	516.6	442.8	367.6	498.0	440.5	585.6	980.0	154.4	176.5
168.0	593.3	1406.1	308.9	401.0	586.1	235.0	950.2	272.3	1223.0	578.9
36.1	55.2	86.3	63.5	114.4	62.4	67.5	65.6	36.5	24.9	50.9
5962.6	6936.6	6699.9	6970.2	7095.7	6628.0	7317.3	6693.5	11271.7	7003.6	8020.8
297.9	2804.8	3689.3	3121.1	2621.6	2556.4	3263.6	3125.8	1968.4	1385.2	2655.2
11179.9	8969.5	9104.7	9507.7	8222.0	9177.0	9781.0	7942.3	13840.3	10645.0	10838.8
3657.0	6244.7	6931.6	7165.9	5528.4	6053.5	6865.7	6838.9	7114.3	8933.8	7204.6
11652.3	6240.6	6256.6	6689.7	5934.6	5801.5	6726.8	5822.3	8305.5	5149.6	6986.1
909.2	2955.7	2858.6	2893.3	2390.1	2480.8	2440.6	2888.3	2076.2	1665.8	2769.6
742.7	2621.5	2512.6	2538.2	2145.3	2185.5	2123.5	2523.1	1894.1	1637.4	2573.9
604.8	2164.6	2077.5	2305.3	2790.1	2214.5	2572.3	2069.9	1453.5	1069.1	2142.0
713.6	2562.3	2560.3	2539.6	2153.9	2151.3	2107.2	2571.2	1799.5	1634.6	2570.3
135.7	2120.2	2546.2	3148.7	2578.7	2293.7	2576.6	2349.4	1927.9	1530.6	2388.4
235.0	3712.1	5217.4	4478.7	3517.7	3898.4	5423.5	4613.9	3662.0	3671.2	3460.1
437.6	3499.5	4344.4	4441.3	3256.1	3829.2	3828.3	3853.2	1689.0	5420.6	2436.2
43.6	122.9	360.1	239.0	63.8	197.5	104.2	177.6	56.8	31.2	110.0
256.3	3801.3	3695.6	4289.8	3545.5	3955.7	4742.0	4540.6	2490.6	3318.5	3868.9
1364.3	598.1	1314.9	757.2	286.0	764.9	604.1	493.9	524.7	357.6	489.4
8294.0	9226.1	8176.7	8959.9	7735.7	8099.0	8402.5	8601.9	8511.9	7215.6	10563.6
8056.1	9554.3	8875.8	10083.7	10691.0	8938.1	11191.3	9330.3	9606.1	7422.6	11045.0
876.6	6774.8	5792.6	5725.4	5233.0	5515.9	5796.7	5902.9	6192.5	7118.7	5735.3
50.8	101.5	119.4	156.8	86.3	106.5	87.6	100.4	66.8	82.8	72.2
699.0	2872.1	3543.5	3404.9	3776.2	2729.0	3812.8	3143.9	2453.0	2018.6	3198.2
55.4	145.9	154.7	136.3	212.3	175.5	167.4	153.7	85.5	70.5	106.6
736.1	2677.6	2850.2	2960.0	2568.2	2430.2	2492.4	3458.0	1679.2	1039.3	1780.0
446.9	1786.0	2705.4	2730.6	2549.3	2373.2	2754.4	3057.4	1351.4	949.1	2049.2
1521.5	4030.3	4195.2	5064.0	4325.2	3633.5	4754.5	5613.2	5922.5	960.6	4509.7
2496.7	4053.8	3740.7	3844.8	3886.9	3697.2	4461.3	4821.2	4784.4	5162.0	4814.4
2980.0	3872.8	3140.3	3328.9	3102.9	2970.4	3369.9	3027.8	4108.0	1780.9	3689.3
56.5	307.8	630.0	333.9	167.1	432.6	180.9	254.6	196.4	143.4	421.0
643.5	4896.7	2858.5	4278.4	4280.9	4931.5	3983.1	5813.5	2555.0	5580.6	4371.9
537.1	2479.7	2357.4	2252.5	2299.6	2212.9	2551.4	2613.9	1546.7	2721.3	2596.9
897.3	4934.4	4910.0	4779.9	4128.5	3877.6	4684.8	4323.2	3447.2	2767.1	4754.4
4688.5	4335.4	4661.3	4566.0	3969.5	3872.0	4371.7	4434.2	2835.1	1691.7	3658.0
7314.4	5035.4	4998.6	5684.0	4734.6	5281.6	6289.6	4782.7	6662.4	7461.6	7384.8
17581.6	8757.2	8141.3	8767.4	7826.0	8004.1	8496.5	7371.7	10642.6	8814.5	12026.1

260.1	267.1	338.0
2687.3	3265.7	3461.4
208.6	432.4	762.4
29.9	45.1	30.1
2878.4	3684.6	3869.7
397.6	782.4	808.6
854.1	1417.6	1462.1
52.8	84.7	64.4
6458.5	8573.7	7338.3
2306.6	3489.4	3408.7
7799.5	10962.5	9349.1
6403.1	7008.5	8490.6
5601.7	7096.1	8970.5
2781.6	3277.8	6242.7
2380.5	2748.5	5516.7
2256.7	2810.6	5551.3
2409.4	2746.2	5491.3
2443.1	2978.3	6370.9
4485.1	4944.4	6691.8
4049.6	4506.3	5757.8
186.4	158.3	288.1
3675.3	3936.1	6358.5
689.8	832.2	942.9
8374.6	8892.9	8313.0
8979.0	9317.0	13081.2
5674.4	5426.4	8080.4
129.2	149.4	83.9
2764.4	4211.7	4331.1
146.3	259.5	234.2
2539.9	3455.1	3083.3
4017.4	3222.1	4012.8
3937.9	6926.5	5701.7
3477.3	3562.3	5375.3
2771.5	2984.1	6002.1
461.2	520.0	837.5
5033.5	5712.7	8318.7
2355.6	2965.7	4793.9
3961.8	3457.5	5100.6
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5028.9	6528.6	5836.6
6772.6	8714.6	8955.9

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DQ266900.1 gg_id:142208 Cloning and microorganism genes alkaline soil clone pGXAR27 DQ266
AY128088.1 gg_id:60757 phototrophic sludge clone PSB-M-3 AY128
AY953244.1 gg_id:114755 anaerobic swine lagoon clone B-4D AY953
FM178530.1 gg_id:350518 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
AB210825.1 gg_id:168842 Lactobacillus vitulinus str. JCM 1143 AB210
EU458708.1 gg_id:300437 Goeldi's marmoset feces clone CAL_g06 EU458
EU458757.1 gg_id:289892 Goeldi's marmoset feces clone CAL_e12_1 EU458
EU458790.1 gg_id:290793 Goeldi's marmoset feces clone CAL_f07_1 EU458
EU458745.1 gg_id:295903 Goeldi's marmoset feces clone CAL_c04_2 EU458
EU458772.1 gg_id:295432 Goeldi's marmoset feces clone CAL_b05_2 EU458
EU458780.1 gg_id:299091 Goeldi's marmoset feces clone CAL_c08_2 EU458
EU772354.1 gg_id:328719 Babirusa feces clone BARB_aaa02c06 EU772
EU773547.1 gg_id:324232 Goeldi's Marmoset feces clone CAL_f12_1 EU773
EU458750.1 gg_id:297734 Goeldi's marmoset feces clone CAL_d06_1 EU458
EU772358.1 gg_id:351169 Babirusa feces clone BARB_aaa03g09 EU772
EU458715.1 gg_id:287857 Goeldi's marmoset feces clone CAL_b06_1 EU458
AJ621549.1 gg_id:129426 Lactobacillus catenaformis str. DSM 20559 AJ6215
AB192060.1 gg_id:200153 termite gut homogenate clone M2PT2-44 AB192
AB018186.1 gg_id:49837 Eubacterium cylindroides str. JCM 7786 AB018
FJ371145.1 gg_id:360344 feces adult twins and mothers; TS6 clone TS6_a01e02 FJ3711
DQ353903.1 gg_id:148303 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z5 DQ353
GQ016276.1 gg_id:493391 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016
AF371514.1 gg_id:49369 swine intestine clone p-1763-b3 AF3715
EU510761.1 gg_id:276677 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40h01 EU510
AM405127.2 gg_id:565289 percent G+C fraction libraries number Actinobacteria human faecal clone AP11K.78 AM405
EU461077.1 gg_id:288677 red kangaroo feces clone KO1_aai43g04 EU461
EU458788.1 gg_id:289655 Goeldi's marmoset feces clone CAL_e07_2 EU458
GQ175443.1 gg_id:539382 Chicken intestinal microbiota modulations various feed supplementations DGGE anc GQ175
EU504762.1 gg_id:262375 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01g05 EU504
L34683.1 gg_id:15729 Eubacterium tortuosum L34683
EF071180.1 gg_id:195355 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
EU850490.1 gg_id:346727 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF257 EU850
AB009222.1 gg_id:15714 rumen clone RFN74 bacterium AB009
EU009857.1 gg_id:256237 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_Y12 EU009
GQ377117.1 gg_id:585892 structure two reactive PCE degrading enrichment s stimulated OU Duck Pond Norm GQ377
EU459459.1 gg_id:294991 capybara feces clone CAP_aah97e09 EU459
CU922014.1 gg_id:541244 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
EU009820.1 gg_id:248473 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_J26 EU009
EU407216.1 gg_id:259697 household biogas digester clone GW-33 EU407
EF445265.1 gg_id:211927 dairy cow rumen clone NED5E6 EF4452
EU473447.1 gg_id:297865 Somali wild ass feces clone WA_aaa02f10 EU473

1988.8	3507.8	2949.8	2411.0	2412.4	2830.7	2357.3	2042.4	3425.2	2127.2	3594.0
638.4	4929.8	4099.8	4699.4	4001.0	3809.3	3281.0	5151.3	5799.7	3238.7	5619.7
10108.6	6279.8	5590.2	6117.4	6734.0	6256.2	6887.3	7080.1	4306.5	4617.2	6793.6
1271.8	3198.1	3859.5	4054.3	3026.0	3252.8	3093.8	3386.3	2485.9	3457.3	4360.7
49.3	43.2	67.7	58.5	44.3	44.8	43.1	44.1	27.5	53.9	39.1
3814.3	1458.9	1906.8	2231.7	2503.7	2290.5	2233.8	2194.5	1721.1	843.8	3224.8
50.4	1105.5	1560.9	1789.5	864.1	1131.6	1402.0	1467.8	517.9	1033.3	867.6
3469.3	2830.8	3199.1	3018.3	3017.4	2748.5	3287.8	2710.6	2814.1	2971.9	4981.2
279.4	948.7	1638.9	1013.3	931.1	1002.2	1524.7	988.2	574.6	782.4	1077.0
3339.2	4616.1	4827.0	4657.6	4641.0	4225.8	6282.2	4181.9	5964.5	8853.5	6714.3
10526.2	5286.3	5489.9	5079.4	5128.5	4504.5	6775.9	4297.9	5315.7	7661.3	6892.4
82.3	3091.2	2476.9	2027.2	1778.8	2393.8	1914.1	2336.2	2617.6	3438.3	1727.7
48.6	1080.4	2082.5	1279.7	809.6	1308.2	1306.5	1583.8	847.8	1015.8	1069.2
2916.5	3104.2	3472.1	3180.1	3314.8	3361.7	2954.6	3430.1	3953.1	2819.4	6718.0
54.9	906.6	1010.4	990.5	1070.4	867.3	1154.4	918.4	918.5	543.8	551.2
44.8	23.3	33.2	23.8	30.2	22.1	21.7	18.0	22.0	16.1	21.1
53.7	49.6	40.6	49.4	44.7	47.2	47.0	57.5	35.1	42.6	36.8
1857.3	4573.4	5426.5	5252.3	4868.2	4624.3	5672.1	4335.8	4924.5	5317.6	6002.0
77.2	39.8	43.3	56.9	53.7	46.2	72.1	62.6	36.9	36.6	42.5
30.3	41.9	73.6	79.5	118.2	67.2	48.6	63.4	31.3	44.0	38.3
61.3	52.0	104.3	121.8	48.0	107.9	56.2	89.5	28.5	40.3	52.0
1812.8	4227.8	4029.1	4899.5	4620.1	4480.1	4222.1	4627.1	4860.4	4482.9	4223.2
53.2	154.0	149.4	155.7	178.0	113.0	123.6	175.6	69.3	100.1	110.6
39.1	34.1	38.4	29.2	38.5	38.9	27.7	42.9	44.2	32.3	26.0
73.5	121.7	396.8	407.6	193.2	335.5	738.9	598.3	242.7	82.6	268.8
1633.2	5298.5	5731.2	5426.3	5498.8	5830.8	5654.2	6821.6	4429.8	5614.7	5343.2
2458.4	1192.2	1837.9	1382.2	1530.6	1389.1	1466.8	1556.4	887.0	1555.8	1131.0
36.6	31.1	48.4	30.2	31.6	29.5	32.2	30.0	29.4	28.9	37.1
4560.8	4702.5	4698.9	4725.5	4436.9	4362.4	5532.1	4410.7	4106.5	3459.4	4309.5
3993.0	7419.0	6304.0	6698.4	5869.0	6284.8	6379.5	6566.2	6793.7	5954.2	7485.1
50.1	40.3	73.5	68.6	91.6	85.2	53.7	66.3	48.4	70.1	68.8
744.4	4548.9	5107.9	4786.0	4296.9	3892.2	4957.7	5001.4	2430.3	1123.8	4213.7
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583.4	557.8	680.1	886.7	1041.9	742.8	808.8	876.2	409.3	377.1	391.3
765.1	3932.2	4197.3	3993.7	4807.6	3940.3	4919.6	4376.6	4697.6	2380.2	4536.1
840.8	5957.8	5768.4	5702.5	6928.4	5740.0	7958.7	5908.5	4521.1	3329.9	4404.3
46.0	24.2	29.1	31.9	43.4	32.9	25.3	28.2	30.9	22.9	26.2
7449.3	3536.2	2848.6	2819.1	3071.5	2822.7	3058.7	2927.9	2849.5	2247.5	1845.6
379.0	3361.5	3764.9	4359.2	2999.9	3765.2	4006.8	4096.2	2265.0	2627.1	2858.5
36.0	42.0	54.1	41.3	65.4	74.1	46.5	70.6	49.9	27.1	51.4
3016.2	5128.1	4751.6	5600.4	5787.0	4606.4	6449.8	5250.3	5810.2	4730.9	5632.4

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3372.8	4217.4	3846.0
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1949.7	1375.9	1087.6
2486.1	3001.9	3058.8
1036.8	1554.7	1528.4
3696.9	4219.9	4885.3
4431.5	4909.0	4697.9
2185.8	2568.4	3168.8
1126.8	1402.2	1878.6
3003.9	2764.3	2429.4
809.2	1549.0	1422.6
18.1	18.9	22.6
59.5	58.0	75.6
4825.3	4594.7	5775.5
55.4	66.4	102.6
82.2	85.4	94.2
143.9	100.7	94.0
3641.8	4093.6	4666.3
222.7	246.5	145.8
49.3	52.1	29.7
508.5	171.1	84.6
6631.0	5548.2	6668.7
1521.9	1449.6	2364.2
26.8	36.1	26.1
4041.1	5882.3	7351.7
6209.2	7214.3	7436.5
101.0	86.9	127.0
4842.2	4346.5	4617.6
872.0	1067.0	1569.0
673.5	1153.2	1014.3
4534.2	3289.8	4714.4
5407.1	6190.9	7891.0
47.2	35.3	73.2
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EU463746.1 gg_id:301292 domesticated horse feces clone horsej_aai92a12 EU463
EU871344.1 gg_id:346271 Genetic Bovine (Bos taurus) Rumen Thailand clone CF16 EU871
FJ681865.1 gg_id:529472 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
EU842625.1 gg_id:352686 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EF515475.1 gg_id:221660 Electricigen Enrichment MFC upf microbial fuel cell anode clone 24h04 EF5154
DQ456144.1 gg_id:158774 pre-adolescent turkey cecum clone CFT114H9 DQ456
EU464340.1 gg_id:293385 hamadryas baboon feces clone AFBAB_aai03a08 EU464
FJ680789.1 gg_id:518054 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ205803.1 gg_id:335171 microbial integrating library sequences and metagenome data obtained 454-pyroseq FJ2058
EU794282.1 gg_id:317703 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_K38 EU794
FJ684918.1 gg_id:530177 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU219944.1 gg_id:257268 study prokaryotic approach landfill soil 5.5 ft. depth clone C81B EU219
FJ717180.1 gg_id:511931 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7171
EU050916.1 gg_id:236166 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_07_32 EU050
EU142042.1 gg_id:243175 Methyl sulfides intermediates anaerobic oxidation methane seep sediment clone SR EU142
EU570894.1 gg_id:545311 transition and zone within near-shore anoxic basin: Nitinat Lake depth 13 m clone Ni EU570
FJ366283.1 gg_id:360268 feces adult twins and mothers; TS25 clone TS25_a04h01 FJ3662
EF434374.1 gg_id:204256 human infant gastrointestinal tract microbiota stool mother babies 13 and 14 7 mont EF4343
FJ366026.1 gg_id:366738 feces adult twins and mothers; TS25 clone TS25_a01h02 FJ3660
CU924120.1 gg_id:551818 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
CU921361.1 gg_id:552601 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
AJ853619.1 gg_id:110120 landfill leachate clone GZKB127 AJ8536
FN436127.1 gg_id:559693 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
AY862794.2 gg_id:160460 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon AY8627
AF507895.1 gg_id:62666 Mono Lake at depth 2m station 6 July 2000 clone ML602J-25 G+C AF5078
EU778068.1 gg_id:313232 feces clone RL117_aae91b10 EU778
AM947541.1 gg_id:268726 Minor changes detected microbial structure and after three week thermophilic dige AM947
AM947531.1 gg_id:265685 Minor changes detected microbial structure and after three week thermophilic dige AM947
GU196243.1 gg_id:581038 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
GQ448397.1 gg_id:588815 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_6wks_gr GQ448
AF412968.1 gg_id:21971 Acholeplasma axanthum str. S-743(T) AF412
FJ226570.1 gg_id:355090 Acholeplasma laidlawii str. Haig 179L FJ2265
AY257485.1 gg_id:83638 Mesoplasma pleciae str. ATCC 49582; PS-1 AY2574
CP000896.1 gg_id:243946 Acholeplasma laidlawii str. PG-8A CP000
U14905.1 gg_id:15691 Acholeplasma laidlawii str. PG8 ATCC 23206 U1490
AY785356.1 gg_id:108386 Acholeplasma sp. str. CODA 1G AY7853
FJ590762.1 gg_id:568272 Acholeplasma sp. DM-2009 str. Lorelei FJ5907
EU517562.1 gg_id:274442 methanogenic microbial consortia mature oil sands tailings clone 12-7C EU517
DQ337019.1 gg_id:145365 subsurface water clone EV818CFSSAHH219 DQ337

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14375.4	4564.7	3906.6	4825.0	3993.7	4520.8	5177.5	5306.4	5210.4	4786.3	5566.1
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s__Candidatus Phytoplasma pini	73934
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s__Candidatus Phytoplasma solani	73731
s__Cassava frogskin disease phytoplasma	73310
s__Cassava frogskin disease phytoplasma	73414
s__Cassava frogskin disease phytoplasma	74305

AY538166.1 gg_id:103660 Acholeplasma granularum str. BTS-39 AY538
AY538163.1 gg_id:103238 Acholeplasma brassicae str. 0502 AY538
AM950255.1 gg_id:540644 Sulphide oxidation elemental sulphur membrane bioreactor: Performance and selec AM950
L33734.1 gg_id:15688 Acholeplasma palmae str. ATCC49389; J233 L33734
AY538168.1 gg_id:103956 Acholeplasma morum str. 72-043 AY538
FJ876262.1 gg_id:556175 Acholeplasma oculi str. Panangala 59 FJ8762
FJ825517.1 gg_id:542107 Microbial during start-up mesophilic biogas plant clone 86_BS1_21 FJ8255
AM982581.2 gg_id:278258 microbial and slurry pig saw dust spent bedding clone PISD-AIG02 AM982
DQ337046.1 gg_id:148755 subsurface water clone EV818EB5CPSAJJ46 DQ337
AY538170.1 gg_id:107774 Acholeplasma parvum str. H23M AY538
EF586009.1 gg_id:252219 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D8_L EF586
AB369182.1 gg_id:235282 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
AY538167.1 gg_id:103806 Acholeplasma hippikon str. C1 AY538
AY538164.1 gg_id:103388 Acholeplasma cavigenitalium str. GP3 AY538
DQ989179.1 gg_id:235828 Artemisia witches'-broom phytoplasma II DQ989
AF411592.1 gg_id:60512 Erigeron witches'-broom phytoplasma str. RPWB phytoplasma AF411
AY180931.1 gg_id:100768 Aster yellows phytoplasma str. OnionD2 AY180
AY180930.1 gg_id:100615 Aster yellows phytoplasma str. RgwdD1 AY180
AY180925.1 gg_id:105275 Aster yellows phytoplasma str. C..13 AY180
AY265216.1 gg_id:102638 Plantago virescence phytoplasma str. PVM AY265
AY180941.1 gg_id:105824 Aster yellows phytoplasma str. PLD1 AY180
AY180936.1 gg_id:101585 Aster yellows phytoplasma str. BtsvCarD6 AY180
AY180933.1 gg_id:101087 Aster yellows phytoplasma str. CarD4 AY180
AY180948.1 gg_id:106919 Aster yellows phytoplasma str. OnionD1 AY180
EU099556.1 gg_id:275610 Cactus witches'-broom phytoplasma str. YN11 EU099
EU099557.1 gg_id:271658 Cactus witches'-broom phytoplasma str. YN12 EU099
EU099549.1 gg_id:273742 Cactus witches'-broom phytoplasma str. YN04 EU099
EU099563.1 gg_id:275567 Cactus witches'-broom phytoplasma str. YN18 EU099
EU099555.1 gg_id:275102 Cactus witches'-broom phytoplasma str. YN10 EU099
EU099569.1 gg_id:274000 Cactus witches'-broom phytoplasma str. YN24 EU099
EU099566.1 gg_id:272756 Cactus witches'-broom phytoplasma str. YN21 EU099
AY377868.1 gg_id:106270 Strawberry virescence phytoplasma 3101 AY377
AB052872.1 gg_id:106149 Brachiaria grass white leaf phytoplasma str. BraWL-KK AB052
X68339.1 gg_id:15630 Phytoplasma sp str. ash yellows X68339
NC_011047.1 gg_id:345428 Candidatus Phytoplasma mali NC_01
AJ310849.2 gg_id:53611 Candidatus Phytoplasma pini str. PinG AJ3108
X68374.1 gg_id:15654 Phytoplasma sp str. German peach X68374
GQ403235.1 gg_id:561370 Grapevine stolbur phytoplasma str. GrIRAN08 GQ403
FJ376625.1 gg_id:582084 Poinsettia branch-inducing phytoplasma str. PoiBI-JR1 FJ3766
AY731819.1 gg_id:102742 Solanum quitoense machorreo phytoplasma AY731
AY081817.1 gg_id:58989 Chinaberry yellows phytoplasma AY081

103.4	1194.0	1285.8	1038.2	759.1	1403.9	591.5	1430.7	539.2	320.4	828.7
41.5	31.5	51.8	43.5	40.4	33.9	33.4	47.9	26.5	18.9	32.9
81.5	802.4	816.3	986.2	838.7	729.8	1068.5	1009.6	490.3	725.8	646.3
65.2	273.7	360.2	238.2	112.2	249.1	162.0	365.7	131.6	43.3	192.4
64.8	54.3	76.8	67.7	41.5	51.0	35.5	69.1	50.9	62.6	69.9
202.3	1597.1	1499.1	1451.8	1347.5	1547.1	1454.7	1631.5	911.2	627.2	1212.3
1867.4	2661.0	2698.0	2898.7	2402.7	2666.5	2628.5	2255.8	2108.3	2486.6	2166.0
204.5	3166.6	3550.0	2833.6	2368.2	2624.7	2820.2	2899.8	2103.7	2221.2	2334.4
7205.8	5643.1	4570.6	4652.2	4766.6	4862.1	4644.2	4344.0	7374.5	4620.1	4721.8
105.3	2011.3	2752.2	1794.0	1569.1	1463.7	2292.0	2129.7	2329.7	880.1	1943.9
1998.3	5151.6	5668.1	5433.0	3930.2	4135.6	5169.9	4708.8	5817.5	3067.0	5758.8
3545.1	2624.6	2688.9	3310.5	2593.2	2304.8	2980.7	2791.0	3285.5	1853.6	3815.0
4851.4	5541.6	5699.0	5780.1	5165.4	5273.9	4979.5	5422.9	7378.6	5415.8	7295.9
6336.9	4700.1	4631.8	5097.4	5300.5	4810.1	5282.5	4547.4	3394.8	3466.6	4249.1
11583.3	7000.8	6034.3	7350.8	6098.1	6936.3	6883.8	6381.2	8814.2	8047.0	9011.5
5579.0	7181.3	7116.3	7403.0	6701.1	7668.2	7424.4	7738.2	8435.9	7031.0	9150.9
11052.6	5094.3	5376.7	5609.2	5084.7	4940.0	5917.8	5390.3	6577.6	5360.3	7050.0
6486.5	3385.9	3533.6	3669.6	3281.0	3198.8	4072.9	3629.3	3920.3	2970.4	4340.1
14263.8	3264.1	3341.3	3674.5	3578.5	3266.5	3729.9	3582.9	4361.7	3004.8	5567.7
21524.6	5513.4	5384.7	5873.8	4886.7	5120.8	6116.8	4869.7	7475.1	7217.9	8792.8
12150.4	5013.2	5206.8	5444.7	4980.1	4779.7	6226.1	5115.9	6502.3	5018.0	7477.2
5722.2	3686.1	3958.5	4167.6	3628.8	3552.3	4386.2	3975.6	4981.7	3956.3	5818.4
8545.4	2900.7	3339.2	3250.4	2866.6	2802.9	3841.6	3078.6	3542.3	2494.2	3943.2
7453.0	4079.3	3986.1	4661.8	4183.8	4335.9	4690.6	5024.2	5463.8	5160.7	5435.3
199.1	3175.7	1896.7	2568.7	3353.9	2262.7	3798.9	2271.1	4481.0	1131.9	1489.1
60.5	377.6	454.7	582.1	1009.6	320.4	579.8	590.5	377.4	491.6	341.0
73.3	877.1	695.5	1088.9	1158.8	920.2	662.3	1128.4	411.9	144.2	501.0
59.8	378.0	455.3	581.8	946.5	320.5	579.3	590.8	376.4	491.6	341.5
54.5	365.5	442.6	610.3	993.9	308.5	568.3	582.3	343.7	488.7	333.5
65.8	883.6	962.2	1015.8	1317.0	966.7	1129.7	1142.9	752.2	595.1	759.6
7871.3	4545.5	4345.0	5313.3	5802.1	3910.5	5034.3	3700.8	5547.4	5530.5	4778.8
692.9	1995.9	2737.7	1819.2	2099.7	2142.1	2260.1	2099.8	1514.7	408.2	3137.1
50.9	463.3	642.9	504.4	636.9	623.4	667.5	757.6	405.2	162.8	316.1
13225.6	6851.5	6154.6	6238.0	5963.8	6762.4	6747.0	6004.4	8019.2	6278.4	8398.7
12099.4	2807.7	3074.2	3734.7	3249.1	2855.0	3441.2	3276.7	3146.1	2184.1	2443.5
164.1	985.8	938.1	1250.0	1550.8	1127.6	700.2	1794.1	815.1	1316.3	805.9
6188.5	6714.6	6886.0	7356.1	7130.3	6596.1	8305.6	7089.2	6777.1	6612.9	9857.6
6754.9	2769.0	2084.8	2319.5	1836.0	2137.2	1978.1	2048.4	2669.0	2713.5	3380.8
665.6	669.8	754.5	941.7	398.0	538.0	799.5	760.2	427.8	438.1	620.5
1473.7	1705.5	1734.7	1946.7	1398.2	1722.1	1948.9	1750.9	2335.2	1273.4	1800.8
1382.4	2257.2	2224.3	2599.4	1782.0	2259.9	2420.9	2284.5	2909.8	2042.6	2317.8

1290.9	1745.5	2338.3
40.8	46.0	93.9
699.3	961.7	2803.6
189.8	292.5	737.3
65.4	85.7	374.8
1599.5	2023.0	1985.5
2083.6	2699.4	3503.1
2506.0	2804.8	5443.2
3847.4	6098.0	5109.1
2093.6	2428.0	2766.4
4192.6	5157.1	6481.3
2632.8	3193.4	5611.2
4886.6	5776.9	8405.1
4257.4	5628.3	6765.1
5775.9	7534.8	7457.9
7703.4	9093.4	9038.3
5498.9	5772.1	7869.4
3685.4	4079.5	5968.0
3731.5	4468.6	5281.2
5212.0	7234.8	5762.9
5131.5	5950.0	7430.9
3997.1	4433.8	6195.7
2830.2	4225.8	5382.6
4903.4	6139.3	6624.0
2161.4	1756.2	3459.9
586.9	522.9	1932.1
1129.8	929.5	1301.7
586.7	523.3	1933.1
580.2	500.0	1917.8
1019.0	1023.6	2624.4
4159.2	4512.4	4335.1
1621.8	1932.4	857.3
875.7	640.5	814.4
5667.3	6613.8	7108.8
3845.7	4066.0	3789.8
1755.0	1341.6	3738.6
6732.1	7576.7	7522.9
2127.6	2977.7	2434.8
710.6	774.9	566.1
1362.2	2086.1	1887.0
1813.0	2761.5	2593.2

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s__Cassava frogskin disease phytoplasma	74424
s__Chinaberry yellows phytoplasma	73831
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s__Lethal yellowing phytoplasma	74266
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s__Lethal yellowing phytoplasma	74440
s__Lethal yellowing phytoplasma	74521
s__Loofah witches-broom phytoplasma	73268
s__Onion yellows phytoplasma	74599

FJ376627.1 gg_id:566603 Goldenrod yellows phytoplasma str. GRY-GR1	FJ3766
AF495882.1 gg_id:67193 Chinaberry yellows phytoplasma str. CbY1	AF4958
DQ444264.1 gg_id:201671 Chinaberry yellows phytoplasma ChTYXIII-4	DQ444
AY787141.2 gg_id:108981 Morinda yellows phytoplasma	AY7871
DQ640501.1 gg_id:230702 Poa stunt phytoplasma str. PoaS	DQ640
DQ640502.1 gg_id:229957 Poa stunt phytoplasma str. PoaS	DQ640
AY669063.1 gg_id:137793 Ribes rubrum phytoplasma	AY6690
AY265218.1 gg_id:102937 Clover phyllody phytoplasma str. KVG	AY2652
DQ452416.1 gg_id:157195 Glycine tomentella witches'-broom phytoplasma str. WBGT	DQ452
EF193357.1 gg_id:202717 Sesame phyllody phytoplasma str. SEPN	EF1933
EU513212.1 gg_id:267241 Cleome witches'-broom phytoplasma str. ClWB-Hnsy	EU5132
AB257290.1 gg_id:183185 Jasmine witches'-broom phytoplasma	AB2572
EF990734.1 gg_id:256711 Pigeon pea witches'-broom phytoplasma M2	EF9907
GU184178.1 gg_id:583290 Jujube witches'-broom phytoplasma str. Yingbuluo	GU184
GU184173.1 gg_id:561436 Jujube witches'-broom phytoplasma str. Fupingdazao	GU184
AY197659.1 gg_id:86835 Cherry lethal yellows phytoplasma str. CLY-5	AY1976
GU184174.1 gg_id:591979 Jujube witches'-broom phytoplasma str. Dongzao	GU184
GU184185.1 gg_id:565984 Jujube witches'-broom phytoplasma str. Jinsimizao	GU184
GU184175.1 gg_id:575585 Jujube witches'-broom phytoplasma str. Pozao	GU184
GU184177.1 gg_id:538789 Jujube witches'-broom phytoplasma str. Baizao	GU184
GU184186.1 gg_id:584389 Jujube witches'-broom phytoplasma str. OT	GU184
EF661582.1 gg_id:242473 Jujube witches'-broom phytoplasma str. DL1	EF6615
DQ842529.1 gg_id:163675 Lethal yellowing phytoplasma M3	DQ842
EU026213.1 gg_id:245559 Lethal yellowing phytoplasma SN	EU0262
DQ286706.1 gg_id:149401 Lethal yellowing phytoplasma str. DJ7	DQ286
DQ286704.1 gg_id:148438 Lethal yellowing phytoplasma str. DJ10	DQ286
DQ842525.1 gg_id:173631 Lethal yellowing phytoplasma S4	DQ842
DQ842531.1 gg_id:167990 Lethal yellowing phytoplasma M2	DQ842
DQ842527.1 gg_id:172269 Lethal yellowing phytoplasma M4	DQ842
DQ286702.1 gg_id:148239 Lethal yellowing phytoplasma str. DJ4	DQ286
AY572031.1 gg_id:102515 Coconut lethal yellowing phytoplasma str. Jamaica	AY5720
AY572030.1 gg_id:102350 Coconut lethal yellowing phytoplasma	AY5720
DQ842528.1 gg_id:173235 Lethal yellowing phytoplasma C1	DQ842
DQ842532.1 gg_id:171211 Lethal yellowing phytoplasma M1	DQ842
DQ286707.1 gg_id:145483 Lethal yellowing phytoplasma str. DJ5	DQ286
DQ286701.1 gg_id:147292 Lethal yellowing phytoplasma str. DJ8	DQ286
DQ286705.1 gg_id:146262 Lethal yellowing phytoplasma str. DJ2	DQ286
AY572029.2 gg_id:108988 Coconut lethal yellowing phytoplasma	AY5720
DQ842530.1 gg_id:169291 Lethal yellowing phytoplasma M6	DQ842
AF248956.1 gg_id:69018 Loofah witches'-broom phytoplasma str. LfWB phytoplasma	AF2489
DQ321822.2 gg_id:145208 Ragweed yellows phytoplasma str. RwY	DQ321

2752.3	4401.4	4876.7	5334.5	4002.5	4436.1	6681.7	5321.6	3474.3	1789.7	6615.9
74.5	413.6	422.1	380.5	298.2	398.0	458.5	575.8	304.7	338.5	296.2
73.7	427.2	330.9	333.0	259.9	454.3	527.4	496.4	246.6	64.4	225.9
4764.3	3859.4	5143.6	4906.5	3112.0	3836.1	4455.1	4846.0	3701.6	1845.2	4723.6
7711.8	2757.2	3093.6	3189.6	2813.9	2764.0	3478.1	3289.3	3328.7	2536.4	3766.3
5398.4	3955.7	4177.5	4406.3	3890.5	3764.9	4701.0	4171.4	5323.8	4109.5	6212.7
11049.1	5090.8	5373.6	5604.2	5077.2	4936.7	6325.7	5388.1	6572.7	5357.4	7549.6
11049.7	4995.2	5145.7	5408.3	4949.1	4772.6	6142.5	5048.9	6505.0	5319.5	7435.7
5895.8	3302.2	3031.1	3183.7	2892.1	1755.6	3084.4	3177.2	3731.2	2858.9	4351.8
12172.6	4458.8	4094.0	4316.3	3938.2	3975.8	4932.2	4588.1	5625.6	4693.0	5637.2
511.9	960.3	908.2	845.3	759.3	1015.8	855.8	1024.9	586.2	452.3	792.2
477.6	932.7	898.1	831.5	797.3	1007.9	844.3	1015.2	581.5	451.0	780.8
517.7	905.5	988.9	1007.0	904.4	1110.9	1007.7	1057.3	584.0	454.5	818.0
1718.4	4226.5	4471.6	4465.8	4443.7	3770.3	4484.8	4026.6	4152.7	3819.4	4446.2
13286.4	5868.4	7124.0	6419.1	8176.4	5754.8	7063.5	6032.2	5975.8	7327.9	6657.3
1711.5	5585.2	5263.2	5469.8	5679.1	4990.2	6312.0	5200.5	5197.3	3559.3	5099.8
1821.0	5136.9	4724.2	5033.7	5156.7	4791.5	5711.5	4684.3	4949.2	3472.7	4826.2
1801.3	5598.8	5297.7	5345.5	6274.8	4900.2	6114.3	5030.6	5384.4	4070.6	5247.6
1727.8	4149.3	4337.3	4356.6	4433.5	3691.2	4460.4	3904.8	4124.1	3509.3	4315.9
1932.0	5041.3	5200.6	5254.3	5712.8	4674.4	5652.9	4775.8	4703.5	4856.8	5140.0
620.2	4344.0	4506.4	4362.4	4249.5	3775.6	4240.8	3916.0	4259.3	3828.2	3935.1
1702.1	4424.5	4584.8	4524.1	4367.1	3845.4	4467.2	4134.1	4489.4	3739.3	4634.1
8301.9	7446.5	6874.9	7021.5	6266.2	7630.0	6512.6	6686.6	8867.8	7763.9	8151.1
823.2	3641.6	4106.2	4037.0	3577.7	4091.7	3781.5	4147.9	2771.6	2477.3	3909.7
2525.4	3499.1	4251.4	4061.5	3777.7	3889.7	3536.1	4753.9	3179.9	5640.7	3443.4
183.6	1839.1	1835.9	1696.4	1319.8	1737.9	1321.9	1883.0	1244.4	1028.2	1349.2
4795.9	6603.8	7262.4	6088.7	5166.1	6277.8	5691.9	6269.7	7818.0	8427.4	7068.9
680.3	1743.3	1893.2	1624.6	1437.9	1591.9	1487.5	1852.1	1626.9	1331.7	1452.8
4506.1	3432.9	2934.1	2691.6	2331.6	3456.1	2733.8	3142.4	4038.0	3371.4	2593.6
3624.0	4977.8	5725.4	5403.2	5035.1	5522.1	6320.1	6454.6	3742.1	2567.8	6795.3
7802.4	7478.2	6593.1	6784.5	5375.2	6614.4	6076.2	6088.7	8632.7	8462.4	7838.4
143.4	1453.8	1381.3	1161.8	991.9	1330.0	815.9	1435.4	874.7	700.5	902.8
725.7	1750.2	1996.9	1745.0	1576.9	1705.3	1670.6	1991.0	1708.8	1616.9	1549.7
176.6	1822.5	1871.2	1643.4	1336.5	1356.2	1282.8	1631.5	1274.3	1119.3	1307.2
434.4	2633.0	2906.7	3254.6	2869.2	2910.9	2733.3	3480.8	1670.7	1323.2	2414.1
2084.9	1978.7	2820.2	2608.5	2390.3	1779.0	1938.7	2562.8	1872.4	1068.6	1953.0
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31852.7	9038.3	8725.2	9591.2	8877.1	8530.1	9571.0	7910.8	12384.5	12220.0	12649.2
515.5	1960.9	2102.1	1919.2	1896.8	1804.6	1856.9	2001.9	1348.4	1513.8	1796.9
3407.3	4091.0	3562.8	3124.9	4732.9	3504.6	4630.5	4079.0	3137.2	5151.0	4122.0
7773.8	2921.9	3354.2	3257.0	2882.7	2828.7	3573.4	3122.4	3600.9	2510.4	3691.7

5281.4	5917.1	7509.7
305.1	650.3	638.5
302.9	1110.5	1574.6
4131.1	4996.0	8131.4
3260.2	3881.3	5442.6
4162.7	4739.2	6016.2
5494.7	6150.4	7374.3
5016.3	5925.3	7312.3
2450.1	3292.7	2874.3
4024.2	5383.5	4305.3
781.5	893.0	1313.1
773.3	865.7	1128.2
847.9	939.6	1344.0
3837.8	5033.5	6492.5
6335.5	8306.4	7247.1
4926.2	5673.8	6626.7
4291.4	5184.1	6384.7
4949.9	5877.4	7818.6
3740.4	4882.2	6405.8
4651.6	5854.2	6321.0
3905.9	4644.7	6639.4
4026.9	5046.1	6513.8
6733.3	7693.5	8528.0
3753.0	4543.0	5011.7
5147.9	5189.8	6269.3
1761.0	2201.6	2731.4
5838.8	6995.8	7922.0
1656.0	2243.9	2443.8
2850.9	4637.6	4031.7
5987.3	7189.7	6977.4
6397.0	7177.8	8142.1
1338.8	1694.1	1874.7
1710.0	2393.9	2902.0
1526.8	1949.7	3402.3
2708.8	3773.2	3384.5
2702.7	2968.0	4930.4
4240.2	4098.7	5725.9
8314.6	9599.0	9175.2
1856.0	2182.5	2607.6
3097.2	3564.5	4060.9
2842.6	3975.1	5402.8

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g__Candidatus Phytoplasma
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s__Paulownia witches-broom phytoplasma	73282
s__Pigeon pea witches-broom phytoplasma	74396
s__Rubus stunt phytoplasma	73171
s__Rubus stunt phytoplasma	73317
s__Rubus stunt phytoplasma	73347
s__Russian potato purple top phytoplasma	73243
s__Russian potato purple top phytoplasma	73727
s__Russian potato purple top phytoplasma	74428
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AY192577.1 gg_id:79786 Paulownia witches'-broom phytoplasma AY1925
EF186824.1 gg_id:183787 Pigeon pea witches'-broom phytoplasma str. PPWBpr EF1868
AY197649.1 gg_id:86755 Rubus stunt phytoplasma str. Rus400 AY1976
AY197648.1 gg_id:87980 Rubus stunt phytoplasma str. RuS AY1976
AY197654.1 gg_id:87732 Hemp dogbane yellows phytoplasma str. HD1 AY1976
EU333400.1 gg_id:278893 Russian potato purple top phytoplasma str. Rus103-7 EU3334
EU333397.1 gg_id:278326 Russian potato purple top phytoplasma str. Rus103-2 EU3333
EU333398.1 gg_id:279421 Russian potato purple top phytoplasma str. Rus103-4 EU3333
EU003536.1 gg_id:244948 Sweet potato little leaf phytoplasma 14c EU0035
EU003537.1 gg_id:243480 Sweet potato little leaf phytoplasma 7E EU0035
EF474451.2 gg_id:235777 Identification Allocasuarina fraseriana little phytoplasma disease Allocasurina Kings P EF4744
X80117.1 gg_id:15647 Phytoplasma sp str. Coconut lethal yellowing disease X80117
FJ226072.1 gg_id:575096 Sweet pepper purple vein phytoplasma str. SwPPV3 FJ2260
AY197643.1 gg_id:86864 Flavescence doree phytoplasma str. FD70 AY1976
AB010425.2 gg_id:32876 -group I phytoplasma~synonym:Japanese Hydrangea phyllody phytoplasma japonicur AB0104
AB242433.1 gg_id:169824 Henon bamboo witches'-broom phytoplasma AB2424
Y18052.1 gg_id:15588 Knautia arvensis phyllody phytoplasma Y18052
DQ459438.1 gg_id:157077 Sugarcane grassy shoot phytoplasma Bidar DQ459
AF370120.1 gg_id:66821 Dandelion virescence phytoplasma str. DanVir AF3701
DQ286953.1 gg_id:144993 Broadbeam phytoplasma DQ286
AY863003.1 gg_id:109692 chinaberry yellows phytoplasma str. Vietnam AY8630
EU375834.1 gg_id:259943 Periwinkle little leaf phytoplasma EU3758
EU371934.1 gg_id:260301 Malaysian periwinkle virescence phytoplasma EU3719
EF050071.1 gg_id:177441 Sandal spike phytoplasma Karnataka EF0500
DQ645635.1 gg_id:161008 Coconut lethal yellowing phytoplasma str. LYC347 DQ645
AY204549.1 gg_id:107635 Periwinkle witches'-broom phytoplasma str. PerWB-FL AY2045
GU361756.1 gg_id:538151 Goosegrass yellows phytoplasma str. GGY1 GU361
AY180950.1 gg_id:101862 Aster yellows phytoplasma str. Btsv4C..2b AY1809
AY180946.1 gg_id:106611 Aster yellows phytoplasma str. ParsD4 AY1809
AY075038.1 gg_id:55023 Mulberry dwarf phytoplasma str. MD-ko AY0750
EF534205.1 gg_id:258469 Iranian safflower phyllody phytoplasma EF5342
AF305198.1 gg_id:69629 Virginia creeper phytoplasma str. VC-Fl AF3051
DQ286574.1 gg_id:142079 Parthenium histrophorus phytoplasma DQ286
AY270156.1 gg_id:82781 Centaurea solstitialis virescence phytoplasma CSV virescence AY2701
EF493020.1 gg_id:226498 Poinsettia flower distortion phytoplasma EF4930
AY685055.1 gg_id:98886 Peanut yellows phytoplasma AY6850
DQ164212.1 gg_id:170032 Dictamnus stunt phytoplasma str. DitS DQ164
AF244363.1 gg_id:17222 Black locust witches'-broom phytoplasma str. BLWB witches'-broom AF2443
EF529494.1 gg_id:219241 Chrysanthemum witches'-broom phytoplasma EF5294
FJ376629.1 gg_id:572583 Alaska potato purple top phytoplasma str. PPT-AK6 FJ3766
AF521672.1 gg_id:64303 Weeping tea tree witches'-broom phytoplasma tree AF5216

5926.6	3356.3	3327.5	3531.4	3716.9	3296.9	4352.8	3200.5	4623.1	3804.3	5345.5
3409.0	5936.3	5293.2	4835.8	5668.5	5182.5	6286.4	5553.2	6422.7	3559.8	5354.5
2082.8	4449.5	4552.0	4544.8	4656.5	3989.4	4673.9	4121.3	4300.8	3868.6	4579.0
298.8	4321.4	4122.3	4417.3	5151.3	4223.8	5111.9	3879.4	3933.1	2866.7	3543.8
277.6	2560.8	3055.8	3001.3	3081.3	3236.6	2748.9	3251.3	2223.4	3560.7	1939.9
2299.0	2652.7	2835.6	2575.1	3617.4	2413.8	3064.0	2434.6	2801.8	2858.4	2580.5
2295.0	2662.8	2837.6	2568.5	3620.0	2429.2	3060.4	2470.1	2682.3	2871.2	2584.0
2136.7	2591.9	2811.4	2550.3	3598.5	2347.0	3043.1	2419.4	2721.0	2853.7	2558.3
16477.3	5310.1	4509.0	5235.7	5022.4	4839.8	5730.8	5775.6	7709.1	6266.1	6454.9
81.7	466.2	567.7	575.8	538.7	597.4	662.8	597.7	264.6	147.1	320.1
72.1	454.7	469.8	421.3	468.4	520.8	536.1	490.2	248.0	129.9	280.7
794.3	3901.4	4494.5	5152.8	4149.8	3578.4	5429.5	3983.3	3586.4	2937.4	5464.2
176.2	1651.1	1991.5	1772.0	2473.1	1642.5	2251.4	1617.6	1567.8	2131.4	1902.3
973.3	5250.3	6154.6	5824.3	6265.8	5609.2	6064.9	5665.6	4998.0	4997.2	4909.3
33.4	66.5	78.2	66.3	52.4	70.6	59.3	102.6	103.4	32.0	62.5
9487.7	2934.0	3405.7	3342.4	2888.6	2939.3	3731.2	3137.3	3569.6	2817.0	3702.8
3526.1	4884.3	4746.4	4429.6	5243.2	4786.5	5092.0	4919.9	5985.7	4872.7	5392.6
150.4	2227.4	2173.9	1808.1	2474.2	1633.1	2522.7	1843.5	875.8	949.9	1769.8
246.3	523.7	614.8	827.1	296.2	327.8	678.4	564.1	246.8	182.6	319.8
2626.2	1393.2	1452.8	1455.3	1491.2	1144.3	1765.5	1327.5	1383.3	723.9	1431.6
7128.7	2922.0	3131.1	3255.8	2883.4	2829.3	3573.4	3120.4	3600.8	2510.7	3692.1
6584.9	3045.9	3263.1	3386.8	3299.6	2975.4	3718.6	3215.6	3632.5	2703.3	3534.9
3439.2	5110.6	4150.4	4453.5	4234.0	3953.2	4030.5	5148.3	5301.5	3917.4	4588.2
7765.9	2416.7	2828.8	2711.2	2906.7	2592.5	3494.2	2706.2	2908.7	2395.8	3024.8
438.2	3210.3	3185.4	3077.8	2651.2	2875.6	2830.4	3145.9	2797.2	2898.7	3095.1
47.4	1050.2	1354.3	1343.8	747.8	954.1	1155.7	1332.3	538.5	146.0	702.3
7770.2	2839.9	3313.2	3225.6	2847.6	2736.2	3817.5	3063.5	3466.6	2489.5	3917.8
29173.5	4401.1	4535.1	5079.7	4858.9	4583.5	5315.8	5149.6	4815.1	5785.7	5346.9
6602.1	3951.2	3805.2	4142.5	3747.7	3664.3	4533.2	3885.5	5034.5	3846.8	4803.9
8534.4	2656.1	2923.4	2879.5	2617.3	2556.5	3454.9	2751.7	3313.7	2340.9	3617.9
8500.9	4745.7	3759.0	5493.9	4307.2	4595.0	5101.0	4410.8	5781.1	5447.7	5865.4
666.3	5115.1	4115.9	4331.2	4616.2	4213.2	5008.7	4192.1	5446.1	2384.9	3562.1
86.8	36.6	24.5	37.5	47.0	37.3	36.9	44.6	25.5	14.2	33.0
5764.6	2893.2	2887.0	3609.9	2558.2	2930.0	3548.4	2981.2	4233.3	2568.3	3484.7
382.6	1293.1	1031.2	1386.7	974.4	1076.1	1310.6	1643.0	701.3	514.4	1453.5
20432.0	6265.9	6328.9	7073.3	6661.7	5935.6	7049.4	6731.1	7481.1	6159.8	7468.0
3374.2	5759.0	4599.1	5396.5	4564.3	4752.1	5174.7	5481.3	5061.8	3089.8	8579.8
1472.5	2228.6	2195.3	2558.7	1665.2	2223.5	2587.2	2226.9	2899.4	2039.8	2294.9
10134.3	5094.1	5041.1	5608.0	5085.4	4940.6	5917.8	5388.3	6577.5	5360.7	7050.3
9270.0	9086.2	8132.0	8626.2	8745.1	8712.5	9887.2	7591.4	10760.0	9613.1	12041.6
77.7	1689.8	1626.6	2221.5	1053.5	1913.5	1495.0	2161.5	666.7	816.4	2241.9

3053.0	3808.9	3641.2
4608.3	5806.3	6819.0
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4088.0	4030.6	5019.3
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2493.5	2921.5	5032.8
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2484.2	2862.4	5037.2
4584.2	6179.5	5852.1
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389.5	595.3	1137.1
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1700.9	2132.4	3855.7
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3913.3	5627.8	5626.8
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573.2	886.8	1128.3
1152.0	1976.5	3578.5
2842.6	4234.1	5328.5
2930.5	4032.7	5503.4
3245.1	5068.5	4817.0
2450.8	3435.1	3598.0
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2821.0	4162.8	5386.9
5638.6	6421.9	7151.6
3526.9	5301.6	6270.2
2608.6	3911.6	4968.4
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4171.4	4280.5	5567.9
39.4	62.9	33.8
2793.3	4233.3	4064.2
1424.6	1894.6	1905.0
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4707.8	5662.0	5210.8
1786.3	2710.5	2562.5
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AY495702.1 gg_id:99151 polystachya phytoplasma str. Aphanamixis yellows
EF432569.1 gg_id:254955 Bischofia polycarpa witches'-broom phytoplasma
AF455039.1 gg_id:68807 Almond witches'-broom phytoplasma str. AlmWB4 phytoplasma
AJ289192.2 gg_id:69575 Stylosanthes little leaf phytoplasma
AJ289191.1 gg_id:41747 Pigeon pea little leaf phytoplasma
EU999740.1 gg_id:328637 Jujube witches'-broom phytoplasma str. ZY1
FN257485.1 gg_id:544411 Chandigarh periwinkle phytoplasma
AJ548787.2 gg_id:150071 Flavescence doree phytoplasma str. FD1487
AF438413.1 gg_id:60303 Omani alfalfa witches'-broom phytoplasma
DQ305979.2 gg_id:546804 Leptodelphax dymas phytoplasma
FJ432664.1 gg_id:369928 Salt cedar witches'-broom phytoplasma str. SCWB1
AY389822.2 gg_id:100290 Aster yellows phytoplasma str. AY-BD2
DQ286577.1 gg_id:143334 Ocimum basilicum phytoplasma
DQ321821.1 gg_id:145420 Carludovica palmata leaf yellowing phytoplasma str. CPY
X76560.1 gg_id:15602 Mycoplasma sp str. FD flavescence doree
AJ289195.1 gg_id:25555 Vigna little leaf phytoplasma
Y16390.1 gg_id:15625 Italian alfalfa witches-broom phytoplasma
AY725211.2 gg_id:103733 Bolivia alfalfa phytoplasma
EF634457.1 gg_id:246840 Chrysanthemum yellows phytoplasma str. CY
AY725231.2 gg_id:200942 Conyza phytoplasma
AY265212.1 gg_id:102027 Aster yellows phytoplasma str. CVB
EU375835.1 gg_id:277015 Periwinkle yellows phytoplasma str. Hainan
X92869.1 gg_id:15651 Phytoplasma sp.
DQ302722.1 gg_id:144066 Garden beet witches'-broom phytoplasma str. YCH500
EU999741.1 gg_id:351684 Jujube witches'-broom phytoplasma str. TA1
DQ318241.1 gg_id:145644 Coconut lethal yellowing phytoplasma str. CLY-DR
EU549768.1 gg_id:263110 Coconut lethal yellowing phytoplasma str. M-182
EF050085.1 gg_id:180292 Periwinkle virescence phytoplasma str. CICY7
EF186822.1 gg_id:181552 Lethal yellowing phytoplasma str. LYja
DQ431843.1 gg_id:151644 Sesamum phyllody phytoplasma
AB076404.1 gg_id:80823 Potato witches'-broom phytoplasma
X83432.1 gg_id:15624 mollicute str. FAB (faba bean phyllody)
AY742330.1 gg_id:107557 Sorghum phytoplasma
AF147708.1 gg_id:54260 Candidatus Phytoplasma brasiliense
DQ378279.1 gg_id:151592 Coconut lethal yellowing phytoplasma str. Nevis (LYN 18-3)
AY197644.1 gg_id:87547 Flavescence doree phytoplasma str. FD-D
FN257484.1 gg_id:568424 Himachal periwinkle phytoplasma
AY204548.1 gg_id:107488 Sweet potato little leaf phytoplasma str. SPLL-Uga
AY147038.1 gg_id:106863 Argentinian alfalfa witches'-broom phytoplasma str. 16SrVII-C
EU099559.1 gg_id:277355 Cactus witches'-broom phytoplasma str. YN14
DQ431842.1 gg_id:153316 Chrysanthemum witches'-broom phytoplasma

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EF6344
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AY2652
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232.1	3621.0	4189.0	5252.0	5079.5	3707.8	4675.3	4475.6	2594.0	2855.7	3709.5
3408.3	4888.8	4551.5	4215.9	4083.8	4115.0	3989.5	3966.1	4280.3	2925.5	4813.1
4699.3	4907.9	4081.2	4748.3	5140.0	4234.3	4842.2	4293.2	5463.6	5131.7	5972.7
120.9	1720.6	1770.4	2463.7	1718.0	1553.5	2017.0	1804.5	1080.1	708.7	1736.6
1821.4	5092.2	4681.7	5048.2	4790.5	4691.5	5425.9	4681.7	4932.8	3216.6	5093.8
7129.8	2921.3	3357.3	3259.0	2880.8	2833.9	3566.8	3155.6	3647.0	2508.4	3696.8
758.5	6734.1	5900.5	6113.8	7105.8	5822.1	7036.6	5709.4	6746.4	4671.6	4902.3
5160.2	2393.5	2486.2	2946.1	2985.8	2375.8	2521.2	2697.4	3353.9	1926.4	2463.4
26575.7	7963.5	6775.1	7139.6	7453.9	7212.4	8696.6	6604.5	10968.1	10527.4	8713.8
2607.1	2423.3	2925.4	2904.9	2471.5	2638.2	2802.2	2962.0	2124.2	2503.4	3504.6
6558.2	3317.9	3431.1	3399.2	3299.9	3024.5	3825.0	3148.8	3917.2	2752.7	3937.8
27533.4	7711.4	7207.3	7875.5	7612.8	7390.4	8657.8	7498.1	9088.5	7807.2	8007.4
244.4	1906.8	2327.8	2292.2	1914.4	1813.5	1943.9	2363.4	1061.2	495.4	1751.5
718.1	6235.4	5245.1	5635.1	5851.5	5229.2	6245.0	5254.8	6340.8	3365.9	4583.4
71.1	1166.6	1017.1	711.6	978.1	1034.7	713.6	1245.8	1052.9	637.9	783.0
76.5	1474.6	1474.3	2006.0	1682.2	1395.9	1283.5	1433.1	1602.9	1288.1	1496.2
5427.1	1767.2	1747.0	1927.0	1702.1	1589.1	1953.3	1792.1	1792.8	1208.1	2114.1
12974.0	6810.9	6619.1	6448.6	6722.1	6619.8	6705.7	7220.8	7366.1	8078.7	7931.2
2440.3	4048.4	3859.4	3003.6	3406.7	3667.7	3599.6	4165.2	3180.1	2937.8	4730.7
4748.5	4124.9	4349.3	4751.2	4137.5	3824.6	4372.5	4533.6	4631.7	2748.3	4701.8
283.8	4957.1	4462.8	4985.3	4957.6	4189.9	5615.8	4781.7	4691.0	2230.5	3870.7
4690.8	1736.2	1627.0	1978.8	1866.5	1682.2	1937.1	2033.2	2268.9	1356.0	1312.6
16266.8	5728.3	5356.5	5433.1	5146.6	5161.7	5684.0	5783.9	7664.8	5994.7	7735.1
3160.9	3112.6	3667.5	3530.1	5436.2	3133.3	4316.8	3528.9	3380.2	2329.2	2986.6
188.2	1673.2	1960.6	1794.3	1436.4	1842.8	1485.6	1995.0	1221.7	1289.3	1424.9
3057.4	3149.1	2663.5	2705.1	2729.9	3425.6	2754.1	2595.4	4357.1	3238.5	3569.6
2100.1	2761.4	2776.9	2683.3	4018.5	2517.1	3222.3	2502.7	2830.8	3070.8	2644.5
743.5	3516.6	3537.1	3412.3	3086.3	3330.9	3127.1	3560.2	3269.2	2165.6	3658.1
5719.7	3836.2	3518.2	3997.4	3139.8	3164.7	3420.9	3184.8	4671.9	3324.1	5192.6
2548.9	5064.2	4350.7	5168.0	4086.9	4774.0	5079.6	5008.7	7429.0	5138.5	4965.7
80.5	317.8	365.0	507.1	399.4	227.0	333.9	454.3	251.6	218.9	308.3
580.2	3203.0	3509.5	2717.0	2946.7	3256.9	2861.5	2919.3	2570.3	966.8	5057.7
46.7	68.4	88.9	98.1	97.0	62.7	63.2	186.9	55.5	30.2	55.8
169.9	1216.3	1270.2	970.8	987.0	986.6	917.9	1222.5	835.0	826.8	723.0
686.2	5361.1	4915.1	5034.8	5495.0	4679.0	5473.4	4558.3	5927.8	4177.7	4336.6
5786.8	3869.7	4289.4	4234.6	3708.3	3634.3	4479.6	3816.5	5261.3	3857.2	5609.7
108.6	5419.7	5930.1	5440.5	5049.9	6498.0	4892.6	5758.4	4157.8	2069.4	6356.3
7442.4	9117.6	8247.5	8588.4	7923.3	9500.2	9087.9	8145.2	11219.2	11076.8	10429.3
80.9	364.1	422.8	527.0	450.3	289.0	372.3	539.0	422.7	250.4	343.0
4409.2	5219.2	4737.8	5433.6	4731.4	4282.0	5124.6	4764.5	5040.3	3417.0	4886.7

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2667.1	3855.8	4641.8
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1075.7	1440.5	1946.0
4571.9	5177.8	5915.6
3536.7	4485.8	6177.1
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8412.3	9650.3	10311.4
392.7	545.8	1546.6
4536.1	5266.7	8878.6

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Y16395.1 gg_id:15608 Rubus stunt phytoplasma Y16395
Y16391.1 gg_id:15674 Bindweed yellows phytoplasma Y16391
EF363314.1 gg_id:573100 Cotton virescence phytoplasma EF3633
EF153634.1 gg_id:186762 Solanum malacoxylon new natural host stolbur phytoplasma R16F2n R16R2; _primer EF1536
FJ226076.1 gg_id:550833 Montana potato purple top phytoplasma str. PPT-MT117-3 FJ2260
FJ226074.1 gg_id:566707 Montana potato purple top phytoplasma str. PPT-MT117-1 FJ2260
EU333395.1 gg_id:278466 Coneflower phyllody phytoplasma str. ConPh MD3 EU3333
AF248960.1 gg_id:55663 Mexican periwinkle virescence phytoplasma str. MPV virescence AF2489
AF147706.1 gg_id:54971 Chayote witches'-broom phytoplasma str. ChWBIII(Ch10) phytoplasma AF1477
AY265220.1 gg_id:106715 Blueberry stunt phytoplasma str. BBS1 AY2652
EU999742.1 gg_id:326955 Jujube witches'-broom phytoplasma str. ZZH1 EU9997
GU361757.1 gg_id:551933 Persian violet stunt phytoplasma str. PVS1 GU361
AY197647.1 gg_id:87317 Alder yellows phytoplasma str. ALY1068 AY1976
GU113147.1 gg_id:589201 Periwinkle little leaf phytoplasma str. PLL-Hn1 GU113
EU057983.1 gg_id:237448 Lethal yellowing phytoplasma EU0579
EU241515.1 gg_id:254449 Coconut lethal yellowing phytoplasma str. BCT-C6 EU2415
Y16393.1 gg_id:15581 Picris echioides phyllody phytoplasma Y16393
EF186828.1 gg_id:181939 Lime witches'-broom phytoplasma str. LWB EF1868
DQ318244.1 gg_id:147021 Coconut lethal yellowing phytoplasma str. CLY-Hon DQ318
AY739024.1 gg_id:100418 Lethal wilt oil palm phytoplasma str. PC2.1014R AY7390
AY180953.1 gg_id:102314 Aster yellows phytoplasma str. DillD2 AY1809
AF331973.1 gg_id:112027 Cactus witches'-broom phytoplasma str. CWB1 AF3319
DQ318242.1 gg_id:147649 Coconut lethal yellowing phytoplasma str. CLY-Mexl DQ318
AY265210.1 gg_id:101708 Primrose virescence phytoplasma str. PRIVC AY2652
FJ217385.1 gg_id:340797 Tanzania coconut lethal disease phytoplasma str. LDT FJ2173
GU113145.1 gg_id:568778 Chinese periwinkle phyllody phytoplasma str. PP-Hn1 GU113
AF173558.1 gg_id:15599 Clover yel edge phytoplasma str. CYE-L AF1735
AY787136.4 gg_id:201507 Candidatus Phytoplasma lycopersici new phytoplasma species causing Morrenia littl AY7871
AY180944.1 gg_id:106289 Aster yellows phytoplasma str. Btsv2C..17 AY1809
AY377876.1 gg_id:102155 Napier grass phytoplasma 2002/19-5 AY3778
EU333396.1 gg_id:279028 Russian potato purple top phytoplasma str. Rus103-1 EU3333
AM180882.1 gg_id:187579 Sweet potato little leaf phytoplasma Aus1 AM180
DQ384857.1 gg_id:151119 Coconut lethal yellowing phytoplasma str. LYN 14-1 DQ384
X68373.1 gg_id:15687 Phytoplasma sp str. American aster yellows X68373
DQ321820.1 gg_id:145945 Carludovica palmata leaf yellowing phytoplasma str. CPY DQ321
AF279271.1 gg_id:21611 Paulownia witches'-broom phytoplasma AF2792
Y08173.1 gg_id:15618 Phytoplasma sp Y08173
AY180954.1 gg_id:102473 Aster yellows phytoplasma str. ParsD1 AY1809
AF509322.1 gg_id:63017 Sorghum bunchy shoot phytoplasma AF5093
AY265213.1 gg_id:102179 Blueberry stunt phytoplasma str. BBS3 AY2652
EF042898.1 gg_id:176840 Strawberry multiplier phytoplasma str. SMP-FL EF0428

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80.8	190.2	450.1	334.4	182.2	252.7	200.6	417.5	153.7	193.7	215.6
96.3	2032.3	1984.4	2509.4	2009.0	1783.9	1885.4	1921.9	975.6	1113.8	2033.7
1176.7	2845.9	2747.3	2111.6	3420.0	2467.6	3546.9	2529.9	2174.0	1861.4	2888.3
2664.1	5999.1	5813.7	6327.3	5875.2	5726.6	6954.6	5772.1	6496.4	4906.8	8685.8
4144.6	5416.6	5558.7	5773.5	6506.5	5431.5	7384.6	5288.0	6861.0	8621.9	8314.2
2292.9	2044.6	2227.2	1904.0	3237.4	2055.1	2611.6	1966.9	2090.5	2586.7	1892.5
59.2	1798.7	1877.7	1971.8	1135.1	1603.8	1470.9	2031.2	800.3	211.5	1002.4
676.1	620.3	698.8	819.7	352.4	515.4	731.4	719.5	421.3	423.7	596.6
7775.4	2903.2	3345.6	3257.4	2872.1	2811.4	3575.3	3114.5	3593.3	2494.9	3689.0
2000.5	4078.7	4048.7	4354.9	4235.0	3868.5	4473.5	3807.5	4023.8	3425.6	4232.1
265.5	1708.8	1566.0	1738.5	1979.5	1592.9	2172.5	1524.5	1975.1	1415.5	2300.5
2923.3	2365.9	2627.3	2621.4	2846.0	2034.8	2005.4	1814.9	2413.9	2882.1	2925.3
13401.6	8082.5	7494.4	7631.2	6792.4	7662.8	8022.5	7454.9	10148.0	9185.2	9059.1
774.3	1935.7	2079.6	2088.1	1652.3	1777.1	1647.5	2151.9	1756.7	1478.6	1571.0
373.0	2084.4	2351.5	2409.3	2303.1	2284.2	3059.3	3509.3	1303.7	759.3	2388.5
71.7	1174.7	1254.4	1700.5	1096.3	1154.9	1195.6	1362.0	1255.7	761.8	1150.1
66.3	924.4	910.0	1193.7	856.6	1008.4	1123.7	954.7	372.7	775.8	620.5
546.5	3574.8	3470.8	3519.7	2831.3	3149.3	3081.7	3403.2	3033.5	3123.0	3460.9
15103.5	6021.3	5881.9	6385.8	5339.0	4874.3	5785.9	4826.3	7644.4	6285.6	8507.6
7062.6	3932.2	3795.9	4115.9	3721.4	3615.8	4830.3	3858.2	5025.1	3840.6	5474.7
59.8	714.1	767.9	1082.4	982.6	633.4	1025.3	1027.1	862.1	375.5	701.3
542.0	3612.4	3596.7	3522.9	2967.0	3225.6	3133.9	3537.4	3195.6	3110.5	3616.8
25363.6	8918.1	8209.0	9013.6	8198.5	8004.3	9386.3	8004.7	11832.2	9352.4	10962.1
15037.3	7190.9	7948.7	8683.7	7797.4	7007.5	9297.8	7168.7	7808.7	8163.0	9456.9
2892.1	1514.0	1834.7	1815.4	1426.9	1441.0	1743.7	1707.7	2005.0	1194.2	2220.3
963.7	1096.4	1233.0	1535.6	881.0	1024.3	1453.6	1201.8	1154.3	808.1	1232.8
12926.6	6320.1	6113.7	6312.0	6465.1	6289.6	6814.5	6462.7	7127.3	6892.8	7428.9
13330.4	3092.5	3074.5	3378.1	2880.9	2676.1	2888.1	3220.2	3510.3	2883.4	3125.9
3155.7	5445.0	5719.7	5801.6	5816.2	4881.1	6059.8	5299.2	6418.3	5413.6	6484.4
11463.2	5588.9	4423.9	5903.1	4119.0	4930.8	5893.4	5434.8	5952.4	4814.2	5900.8
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9314.6	5703.6	6178.5	5587.6	5005.9	4556.6	5857.9	5034.0	6437.6	6340.2	6453.5
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7550.6	6561.9	6543.8	6766.1	6836.1	6436.5	7374.8	6726.4	7330.6	5300.9	8234.5
6554.7	3550.6	3825.6	3737.0	3349.9	3263.5	4168.2	3462.4	4192.4	2917.3	4227.2
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2591.4	1371.2	1462.5	1586.2	1665.2	1288.0	1677.6	1454.4	1749.4	1103.5	1980.3
452.4	6030.9	6960.0	6511.5	8080.6	6426.9	8128.2	6812.0	5123.5	6775.5	7475.2

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5635.1	6047.5	8676.8
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1934.1	1953.2	2820.4
567.5	647.2	535.5
2839.3	3982.8	5386.7
3398.0	4746.1	5319.1
1512.5	1889.2	1950.8
2011.0	3371.8	1883.3
7049.5	8457.8	9580.1
1860.2	2640.5	2942.0
3086.3	3597.8	3893.8
1367.0	1536.9	3005.6
943.9	1303.4	2697.3
3326.6	3844.4	4617.7
5161.0	6968.1	7948.7
3505.9	5271.6	5460.4
817.6	732.5	2028.4
2808.7	3769.9	4601.2
8104.0	9899.4	11310.4
8065.8	8585.2	8471.6
1434.7	2517.4	3734.1
1107.0	1542.6	1366.3
6522.1	6830.7	8319.1
3662.4	4778.6	5769.3
4435.1	5516.4	5682.4
5420.1	6264.1	9911.9
3566.6	3061.3	4498.1
5025.4	5927.0	5861.2
6490.3	8582.1	10637.7
5650.3	7407.6	5826.3
3241.2	4160.9	5928.3
3616.9	4423.8	4769.1
2667.0	3797.8	3886.1
66.9	79.5	309.6
1297.1	1928.9	3135.3
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EU170353.1 gg_id:239724 Sweet potato little leaf phytoplasma 2&3Vtrio EU170
FJ154847.1 gg_id:312556 Jujube witches'-broom phytoplasma str. ZQ FJ1548
U16758.1 gg_id:15696 Mycoplasma feliminutum str. ATCC 25749 U16758
EU006252.1 gg_id:257027 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU456203.1 gg_id:314291 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU456
FJ681157.1 gg_id:529539 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
EU794312.1 gg_id:354444 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_L44 EU7943
EF604794.1 gg_id:228310 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EU774401.1 gg_id:315971 mammals their gut microbes Eastern Black and White Colobus feces clone COL_aai1! EU7744
M25050.1 gg_id:15703 Anaeroplasma abactoclasticum M2505
EF604918.1 gg_id:231986 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
EU344682.1 gg_id:262497 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
EU794279.1 gg_id:305348 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_G18 EU7942
FJ683969.1 gg_id:528228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6839
GQ897174.1 gg_id:555555 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
DQ797091.1 gg_id:185593 human fecal clone RL386_aao86h04 DQ797
DQ797049.1 gg_id:179979 human fecal clone RL386_aao86c09 DQ797
NR_028691.1 gg_id:591314 Entomoplasma freundtii str. BARC318; ATCC 51999 NR_028
GQ275106.1 gg_id:581987 gut symbionts are tightly linked herbivory ants extract single ant clone #130 GQ275
AE017263.1 gg_id:100309 Mesoplasma florum L1 str. L1; ATCC 33453 AE0172
AY187288.1 gg_id:79099 Mesoplasma tabanidae str. BARC 857; ATCC 49584 AY1872
AF042194.1 gg_id:15792 Mycoplasma monodon str. Australiain AF0421
AY168929.2 gg_id:75831 Mesoplasma corruscae str. ATCC 49579 AY1689
AY166704.1 gg_id:76006 Mesoplasma chauliocola str. ATCC 49578 AY1667
DQ157864.1 gg_id:139255 Mycoplasma capricolum str. 700 DQ157
U26055.1 gg_id:15786 Mycoplasma putrefaciens str. KS-1 U26055
AY155670.1 gg_id:75155 Entomoplasma luminosum str. ATCC 49195; PIMN-1 AY1556
GQ275109.1 gg_id:568610 gut symbionts are tightly linked herbivory ants extract single ant clone #133 GQ275
GQ275144.1 gg_id:555846 gut symbionts are tightly linked herbivory ants extract single ant clone #168 GQ275
AY538169.1 gg_id:104104 Acholeplasma multilocale str. PN525 AY5381
AF303132.1 gg_id:71794 Mesoplasma lactucae str. 831-C4; ATCC 49193 ATCC AF3031
DQ861915.1 gg_id:168652 Spiroplasma cantharicola str. Q-6 DQ861
X63781.1 gg_id:15803 Spiroplasma citri str. R8A2HP X63781
DQ112020.1 gg_id:130516 Spiroplasma citri str. Car6 DQ112
AJ006775.1 gg_id:41072 Spiroplasma sp AJ0067
NR_025706.1 gg_id:534716 Spiroplasma lampyridicola str. PUP-1; ATCC 43206 NR_025
AY189309.1 gg_id:99424 Spiroplasma syrphidicola str. ATCC 33826; EA-1 AY1893
AY189132.1 gg_id:101796 Spiroplasma helicoides str. ATCC 51746; TABS-2 AY1891
AY345990.1 gg_id:93470 Entomoplasma melaleucae str. M1 AY3459
AY189125.1 gg_id:106072 Spiroplasma alleghenense str. ATCC 51752; PLHS-1 AY1891
EF151267.1 gg_id:202191 Spiroplasma sp. str. CRW-1 EF1512

847.7	2117.5	1998.6	2132.0	1981.2	1717.7	1903.1	1953.6	2120.3	1026.7	2337.0
1678.6	4905.8	4402.0	4704.7	5082.3	4623.2	5394.7	4479.2	4860.8	3387.6	4648.9
59.2	928.3	796.6	709.0	724.3	838.9	699.7	713.8	209.0	248.2	573.5
648.2	2180.3	1839.8	2259.2	2921.1	2159.8	2088.7	2364.7	1291.1	1592.3	1111.8
11815.0	6509.8	6013.6	6424.8	7366.3	5917.2	6422.5	5799.5	8514.5	7506.4	7063.9
2595.3	5458.0	7009.2	6381.0	5343.2	5055.0	5502.2	5772.5	5584.0	4464.3	5623.1
1063.9	2768.9	3366.3	3843.8	2177.6	2296.4	2432.7	3938.6	1752.8	1538.8	2834.2
4049.5	3315.6	2716.1	2680.3	2888.1	2723.5	2789.8	3491.4	2682.6	1885.6	2909.0
36.6	1369.2	2459.8	2178.3	1211.0	1411.6	1335.3	2106.0	707.6	496.2	1294.3
28.1	23.6	26.6	28.8	22.1	18.6	24.3	26.2	17.7	17.1	32.9
12630.9	8222.8	7397.6	7803.3	8627.6	7209.7	8062.9	6557.4	9891.6	6802.2	9892.3
8020.5	4724.0	3514.2	5379.3	3986.2	4180.8	4937.8	4473.7	2953.2	4627.5	5681.5
6006.9	8699.7	8625.2	9640.1	7930.2	8512.9	9638.1	8432.3	7498.8	5542.1	8931.4
208.5	622.3	870.5	859.1	185.9	691.9	857.9	749.7	403.8	435.0	691.1
3993.4	3053.3	4285.8	4274.1	2998.7	3188.0	3255.3	3010.4	3655.7	1877.2	4071.6
7758.6	5648.4	6122.7	5182.6	4075.2	6718.1	4804.0	5001.6	7756.7	6111.2	7224.6
10284.4	7161.0	6627.5	6258.7	6403.6	8546.0	6170.7	5577.7	11583.3	8701.1	9755.3
69.6	195.7	318.0	289.6	382.9	294.7	395.7	245.3	84.0	52.3	140.2
487.9	3922.4	4352.6	4062.7	3452.6	3779.2	3586.7	3542.7	4412.4	2391.9	4528.7
1360.1	2040.6	2066.3	2167.1	2201.0	1494.9	2217.9	2377.5	2310.4	1482.6	1941.6
1461.3	2041.8	2070.1	2043.0	2184.4	1517.6	2214.0	2491.4	2354.9	1383.4	1975.3
51.9	190.8	186.1	206.2	169.4	185.9	165.0	293.2	59.2	40.5	96.5
4808.8	4480.4	3988.6	3960.3	4006.7	3632.0	2983.9	4039.3	3843.9	2994.3	3614.4
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795.4	3407.2	3187.3	2933.5	2195.4	3005.4	2457.3	3307.8	2019.0	3402.0	2462.4
351.3	348.5	520.0	447.8	293.7	442.1	495.1	478.3	738.9	114.2	477.9
8238.8	4347.1	4448.0	5607.7	3574.4	4338.7	4604.1	5012.1	4845.4	3951.6	5698.4
65.8	2840.6	2192.6	2211.4	2699.8	2279.5	2444.3	3120.6	1223.8	1805.2	2143.0
34.5	369.5	138.8	146.6	195.5	194.5	194.8	140.2	113.6	47.8	66.4
77.7	84.6	75.2	65.6	35.3	86.7	28.0	127.1	65.3	25.3	41.1
6977.3	3232.7	3611.4	3161.5	3732.0	4039.5	3765.5	4210.8	3229.7	2701.7	4101.3
11147.7	4303.2	4743.3	5290.2	5777.0	4775.1	5571.2	5491.5	7209.4	4136.8	4356.7
11551.4	5554.4	4563.1	5035.3	4311.6	5095.9	4936.5	4728.1	5855.6	4667.8	5248.7
61.4	115.7	176.6	109.8	115.8	133.9	108.8	143.8	52.1	62.2	66.4
671.0	2045.7	2740.8	2297.2	1756.4	2030.7	1466.7	2425.6	1714.5	1700.4	1342.3
4530.1	3921.2	3555.9	4143.3	3133.0	3500.8	4390.1	3775.5	3224.9	2478.8	3980.4
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AY189133.1 gg_id:101955 Spiroplasma insolitum str. ATCC 33502; M55 AY1891
DQ917756.1 gg_id:258655 Spiroplasma mirum DQ917
GQ051079.1 gg_id:429439 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ051
GQ275102.1 gg_id:558391 gut symbionts are tightly linked herbivory ants extract single ant clone #126 GQ275
AY772395.1 gg_id:108248 Spiroplasma phoeniceum str. P40 AY7723
AY189318.1 gg_id:104368 Spiroplasma sp. str. TIUS-1 AY1893
AY189129.1 gg_id:106700 Spiroplasma culicicola str. ATCC 35112; AES-1 AY1891
DQ860101.1 gg_id:166158 Spiroplasma platyhelix str. PALS-1 DQ860
AY189305.1 gg_id:107782 Spiroplasma leptinotarsae str. ATCC 43213; LD-1B AY1893
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NR_025709.1 gg_id:565097 Spiroplasma montanense str. HYOS-1; ATCC 51745 NR_025
AY189310.1 gg_id:103192 Spiroplasma turonicum str. ATCC 700271; Tab-4c AY1893
NR_025713.1 gg_id:561932 Spiroplasma velocicrescens str. MQ-4; ATCC 35262 NR_025
GQ129114.1 gg_id:526608 Prevalence geographical canine hemotropic mycoplasma infections Mediterranean GQ129
EF424082.1 gg_id:209237 Mycoplasma sp. China-1 EF4240
AY831867.1 gg_id:133123 Mycoplasma sp. 'feline hemotropic Switzerland' AY8318
DQ825454.1 gg_id:222355 Worldwide occurrence feline hemoplasma infections wild felid species Tanzania DQ825
NC_009497.1 gg_id:233772 Mycoplasma agalactiae str. PG2 NC_009
AF332745.1 gg_id:73703 Mycoplasma agalactiae str. 396/12 AF3327
AF332751.1 gg_id:70015 Mycoplasma agalactiae str. 35 AF3327
AF060821.1 gg_id:15907 Mycoplasma agassizii str. K120 AF0608
NR_025985.1 gg_id:565268 Mycoplasma alvi str. Isley; NCTC 10157 NR_025
AY531656.1 gg_id:111859 Mycoplasma amphoriforme str. M5572 AY5316
FJ226575.1 gg_id:326725 Mycoplasma amphoriforme str. A39 FJ2265
NR_029180.1 gg_id:550692 Mycoplasma gateae str. ATCC 23392 NR_029
CP001047.1 gg_id:308649 Mycoplasma arthritidis str. 158L3-1 CP0010
AF340023.1 gg_id:74000 Mycoplasma canis str. PG14 AF3400
AF412973.1 gg_id:70402 Mycoplasma citelli str. RG-2C(T) AF4129
FJ226571.1 gg_id:310264 Mycoplasma conjunctivae str. Goat 655 FJ2265
GU227404.1 gg_id:579318 Mycoplasma flocculare str. USP9T GU227
L08896.4 gg_id:15854 Mycoplasma gallisepticum str. A5969 L08896
AF412980.1 gg_id:72545 Mycoplasma gallopavonis str. WR1(T) AF4129
AY466443.1 gg_id:107609 Mycoplasma genitalium str. M2288 AY4664
DQ825438.1 gg_id:217964 Mycoplasma haemofelis 111 DQ825
EU930823.1 gg_id:340543 Mycoplasma haemofelis Porto Alegre EU9308
AY150985.1 gg_id:58418 Mycoplasma haemofelis UK no. 6 AY1509
AY150973.1 gg_id:71517 Mycoplasma haemocanis Germany Munich no. 1 AY1509

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230.3	2782.0	3660.3	3741.2	3240.2	3144.9	3562.3	3985.2	2174.5	1894.7	3119.7
21701.5	10274.7	10135.2	10062.9	10150.4	9623.6	11261.5	9716.2	10599.0	8893.2	12363.1
8871.5	5087.6	4862.7	5075.1	4252.6	4731.6	5022.3	5113.5	5915.6	5196.3	5595.4
2296.0	6557.6	6826.4	6444.3	5583.6	5955.5	6632.6	6402.4	8159.2	7575.6	8325.9
14654.1	8361.7	8395.1	9151.1	8205.4	8363.1	9382.0	8937.1	8686.0	7038.8	10549.4
66.6	268.1	633.6	430.2	369.1	394.6	833.7	299.2	165.3	168.3	182.0
1721.8	4126.5	4313.1	4298.8	5044.5	3955.2	5443.6	4750.2	3028.4	2291.1	3940.2
54.1	122.2	49.8	97.6	20.7	110.3	99.8	126.3	47.9	15.2	25.4
112.5	33.4	43.6	42.3	28.9	32.9	42.1	30.7	36.1	28.5	48.9
683.9	2884.3	2675.9	2039.8	1986.2	2105.2	2429.7	1847.6	3612.6	2259.9	3224.1
880.2	4559.9	3850.9	3550.3	3072.6	3934.6	3341.6	4322.1	3210.6	3295.9	4002.6
282.2	3250.8	2955.5	3028.8	2804.0	3502.6	3612.2	3322.0	2679.8	1905.3	3064.5
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4919.2	5845.8	6065.7	5601.6	6354.8	5207.1	7180.2	4961.7	5529.1	4008.5	4878.0
7894.5	5073.8	4565.0	5125.9	5520.3	4757.5	5808.4	5525.3	3775.6	3643.9	5974.1
165.0	1733.2	1703.8	1573.0	2005.0	1634.6	2065.8	2035.9	682.3	944.8	1543.5
56.9	43.7	67.1	51.1	58.5	43.5	62.8	55.9	27.6	21.3	28.3
210.5	157.0	162.3	174.1	209.9	156.4	242.8	186.8	119.2	54.2	162.6
7172.4	2069.7	2157.5	1845.5	2082.4	2334.7	1967.2	1919.2	2314.9	2136.7	3224.2
614.9	3846.9	3436.7	2704.3	2442.0	4296.9	2158.7	2854.9	4230.7	4811.7	3562.3
4090.6	1386.2	1453.7	1676.7	1450.7	1450.1	1670.7	1588.5	2897.4	1113.8	2203.9
1861.9	283.4	464.3	458.3	566.9	290.1	619.9	434.8	224.2	46.2	227.7
3932.3	1802.6	1570.3	1937.1	1606.7	1510.9	1839.5	1627.9	3212.2	1561.9	2376.6
70.8	1816.8	2567.9	2500.0	1416.0	2505.5	1761.1	1922.6	716.4	351.3	1326.4
487.2	5819.1	5404.5	7012.5	6800.5	5543.5	7939.4	6547.8	3528.7	6741.8	6784.5
813.9	739.9	932.5	926.7	952.0	850.9	1179.5	1051.8	719.0	720.2	532.7
2576.0	2785.5	3505.2	3320.7	3155.1	2985.2	3991.0	3693.6	2584.7	3049.7	2926.7
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62.3	148.0	169.1	173.1	75.3	113.1	127.5	266.2	89.1	28.5	99.4
345.6	2985.5	3404.9	2279.4	1849.6	2492.6	2614.0	2461.8	2303.0	1902.8	1591.2
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619.2	1825.7	2080.2	982.7	2327.3	1897.8	2645.2	2187.6	3608.2	610.0	2087.1
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203.3	923.0	966.6	1275.0	1146.7	1036.0	1280.9	1151.3	772.0	1822.1	828.1
193.5	923.6	967.8	1277.1	1061.0	1036.8	1085.5	1150.5	773.6	1683.2	703.4
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3393.9	4363.5	5504.4
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4630.0	7070.9	9062.8
5738.8	6210.1	7879.8
7250.6	10368.5	10272.4
236.4	339.2	374.1
4376.4	4462.2	5271.5
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2515.9	3649.0	4215.2
1367.4	1874.2	1561.1
447.5	670.1	418.2
1431.0	1955.8	1624.2
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684.7	957.8	820.2
2999.1	3767.6	4012.5
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5991.3	7805.1	6146.7
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23.1	30.3	29.3
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EU643797.1 gg_id:278892 Mycoplasma hyorhinis LuSIV EU643
AF121890.1 gg_id:15878 Mycoplasma hyorhinis str. ATCC VR-2580 AF1218
GU227374.1 gg_id:593611 Mycoplasma hyorhinis str. USP10T GU227
NR_025064.1 gg_id:562555 Mycoplasma iners str. PG30; ATCC 19705 NR_02
EF447273.1 gg_id:210500 Mycoplasma iowae str. HTL04-4846A EF4472
AF221116.1 gg_id:47885 Mycoplasma maculosum PG15(T) AF221
U22415.1 gg_id:15832 Mycoplasma microti str. IL-372 U22415
AE017308.1 gg_id:103527 Mycoplasma mobile str. 163K AE0173
FJ655919.1 gg_id:565101 Mycoplasma neurolyticum str. T15 FJ6559
AF538961.1 gg_id:71629 Mycoplasma opalescens str. MHS408 AF5389
U44771.1 gg_id:15870 Mycoplasma ovipneumoniae str. Y-98 U4477
BA000026.2 gg_id:107845 Mycoplasma penetrans str. HF-2 BA000
DQ840513.1 gg_id:166698 Mycoplasma phocicerebrale str. CSL 5195S2 DQ840
EU827597.1 gg_id:349932 Mycoplasma phocidae str. CSL 7498-2 EU8275
EU827598.1 gg_id:315295 Mycoplasma phocirhinis str. CSL 7475-4 EU8275
NC_000912.1 gg_id:108728 Mycoplasma pneumoniae str. M129 NC_00
AL445565.1 gg_id:58394 Mycoplasma pulmonis str. UAB CTIP AL4455
AF538684.1 gg_id:59733 Mycoplasma spumans AF5386
FJ263944.1 gg_id:316748 Mycoplasma suis str. HN FJ2639
AE017245.1 gg_id:200524 Mycoplasma synoviae str. 53 AE0172
U19768.1 gg_id:202917 Mycoplasma str. H3110 U19768
EU367963.1 gg_id:258287 Mycoplasma wenyonii cattle no. 48 EU3679
DQ530428.1 gg_id:233952 Mycoplasma zalophi str. CSL 5195 DQ530
AY571416.1 gg_id:114530 termite gut clone RsaHf232 AY5714
GQ502581.1 gg_id:590759 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf4- GQ502
AB089055.1 gg_id:78062 termite gut homogenate clone Rs-G80 AB089
U09788.1 gg_id:15851 Mycoplasma str. ATCC 43263 U09788
NR_029165.1 gg_id:567958 Mycoplasma pirum str. 70-159; ATCC 25960 NR_02
AB089054.1 gg_id:77956 termite gut homogenate clone Rs-B54 AB089
AB192228.1 gg_id:142809 termite gut homogenate clone RsTu1-65 AB192
AF125879.1 gg_id:15849 Mycoplasma cavipharyngis str. 117C(T) AF1258
AB089057.1 gg_id:77895 termite gut homogenate clone Rs-E42 AB089
AY571419.1 gg_id:114509 termite gut clone RsaHf283 AY5714
EU859984.1 gg_id:344923 Mycoplasma sp. str. CSL7529-conjunctiva EU8599
AF221113.1 gg_id:71570 Mycoplasma columbinum MMP-1(T) AF221
L24105.1 gg_id:15949 Mycoplasma gallinarum str. PG16 L24105
FM165074.1 gg_id:329837 Mycoplasma sp. C3T str. C3 FM165
AF221119.1 gg_id:19645 Mycoplasma spermatophilum AH159(T) AF221
AM182894.1 gg_id:199102 Mycoplasma sp. str. 15CL2 AM182
AF221111.1 gg_id:73061 Mycoplasma caviae G122(T) AF221

2857.0	6982.4	6545.4	6871.4	5606.0	6046.5	6418.9	5977.6	6078.6	6247.2	6831.2
15976.0	2870.3	2848.4	3022.0	3083.8	2982.2	2830.9	3473.0	3487.6	2990.8	3618.6
6573.6	4756.1	3933.2	4378.2	4721.5	4916.8	4398.5	4816.6	7545.5	5700.7	5799.8
60.0	76.7	81.5	85.9	81.8	73.8	72.3	200.3	74.4	57.8	104.5
2301.0	1250.0	1517.8	850.5	814.0	1431.6	955.4	1241.3	1011.8	1130.9	1379.2
1213.7	6697.6	5683.5	5805.8	5432.3	4983.8	6797.8	5283.5	4686.2	5220.1	6173.3
1036.4	8575.9	9422.7	8297.1	6956.0	7709.1	7110.9	6847.1	11149.4	12244.0	7851.7
1974.4	4777.4	5751.0	6257.1	2868.5	4155.2	4892.9	3658.5	2888.3	1991.9	5206.4
5843.6	6195.1	6261.6	6748.0	6241.7	5816.9	7460.0	6532.4	6693.7	5164.3	8539.4
54.1	90.5	95.6	71.5	53.7	57.9	57.7	52.5	19.3	38.4	69.3
33.4	36.9	57.7	40.0	35.7	39.8	32.8	30.2	30.7	26.1	25.3
4671.9	3993.5	4042.2	4507.8	3901.9	4212.4	4726.3	4552.4	3213.8	3176.0	3760.1
40.9	123.2	102.4	78.5	111.2	123.3	80.5	124.2	38.7	36.9	77.7
4601.9	5172.3	4176.4	4128.8	3674.8	3893.0	4741.3	4470.7	3509.5	4130.3	3278.8
4515.9	8616.6	7437.1	7690.1	6340.6	6816.1	7029.3	6863.5	7231.7	7910.6	7021.4
55.4	670.4	795.9	760.4	624.9	750.1	679.9	728.3	278.4	340.3	802.5
692.3	1970.5	2096.5	1988.4	2022.4	2200.2	2080.7	2276.5	1843.4	1444.9	2424.7
371.4	2844.8	3143.7	3025.0	2898.9	2714.5	3165.0	2921.0	2625.5	1076.9	3122.1
1443.4	5362.8	4602.1	4787.7	4646.8	4644.4	5201.0	4585.9	4761.6	4478.9	3958.3
18257.5	5736.3	5351.8	6100.4	5825.0	5404.9	5897.6	4924.5	7072.0	6173.7	8248.1
31.9	49.3	51.7	61.0	45.1	37.5	33.6	41.6	35.5	27.5	38.4
8324.6	4015.9	4002.3	5450.6	4300.9	4023.9	5238.8	4866.5	3820.6	2876.7	3878.2
5037.1	2108.4	2155.4	2089.8	2010.2	2056.0	2075.7	2010.7	2885.0	2163.4	2696.5
2923.8	4380.3	5044.5	5536.1	3064.1	4381.4	4215.2	4771.9	5682.5	2124.3	5526.9
9634.3	5230.8	5228.7	5677.0	6358.7	5124.1	5161.1	6095.9	4878.9	4286.6	5202.6
19768.8	5435.2	4758.7	5775.2	5494.2	4853.7	5315.2	5080.0	5956.5	5103.5	7033.0
265.8	729.0	503.2	450.7	615.2	687.3	538.6	722.0	313.2	277.8	276.2
37.8	27.1	26.9	41.7	82.6	32.3	60.5	32.3	19.2	23.0	26.3
81.2	1301.1	1445.6	1416.4	964.9	1337.3	2578.6	1434.3	1062.7	995.2	1615.9
44.9	98.3	106.7	117.1	95.9	118.2	79.9	190.8	73.5	39.4	66.1
28.3	33.6	39.4	38.0	36.1	22.1	26.5	31.1	17.0	20.2	25.7
119.8	748.9	576.7	503.9	336.9	746.0	422.4	655.2	289.6	168.6	748.0
46.3	205.0	311.1	367.9	339.6	223.0	364.4	354.6	98.2	53.4	162.6
35.4	33.3	27.0	45.4	42.0	38.9	36.3	45.0	15.5	17.3	19.6
77.7	3455.7	3802.3	3264.6	1838.1	4170.1	1905.4	3064.4	1915.5	1185.4	5371.3
30.8	35.7	69.7	25.0	24.3	48.4	19.9	43.6	18.2	16.2	24.1
802.2	1173.1	1223.7	960.8	833.3	1233.1	704.3	1367.4	1185.0	1617.6	1357.0
157.9	1100.8	859.7	1112.3	931.3	925.4	796.8	1162.2	1114.4	270.7	660.2
263.3	491.2	938.5	304.3	192.0	441.4	195.3	292.3	282.1	183.5	494.4
22953.4	10887.1	10239.7	10817.5	10059.2	10194.7	11610.7	9481.9	15213.0	11003.2	13687.4
35.0	36.6	27.1	36.1	36.6	37.3	33.6	28.4	31.1	48.2	30.9

5478.7	6579.9	6326.3
3344.1	4433.2	3015.6
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187.2	160.8	122.0
983.3	1388.5	963.3
4384.0	5549.0	6140.1
8652.4	9441.9	10552.9
2804.9	3705.5	4201.7
5756.7	6209.5	5946.7
55.4	83.8	183.3
37.1	37.7	26.4
3976.8	5140.9	5523.7
67.5	192.8	146.4
3885.2	4741.6	4343.9
6191.8	7250.5	7020.3
589.5	819.6	737.2
1835.3	2696.3	2356.9
2329.4	3350.7	2746.2
4367.4	5085.1	5103.1
4658.2	6715.0	4861.1
36.5	73.5	46.0
4427.5	6077.4	5765.4
1635.2	2855.7	1687.6
3971.8	4882.8	4227.7
6429.5	7158.8	6693.0
4946.9	7076.2	5701.0
557.0	802.0	937.7
44.7	53.2	36.4
1147.8	1597.6	1041.7
130.4	119.0	130.2
30.8	34.3	24.6
303.6	794.8	756.2
254.5	470.3	532.0
28.9	51.1	145.7
2810.3	3356.4	1379.1
22.5	27.1	20.8
1050.0	1140.7	1421.4
883.2	1441.0	1170.5
226.1	381.1	298.9
9513.2	11515.3	11252.4
35.8	37.6	40.4

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U16759.1 gg_id:15916 Mycoplasma leonicaptivi str. ATCC 49890 U16759
GU227407.1 gg_id:579601 Mycoplasma hyopneumoniae str. USP14P GU227
AF412977.1 gg_id:32469 Mycoplasma crocodyli str. MP145(T) AF4129
EF510696.1 gg_id:220331 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
DQ223546.1 gg_id:144780 Mycoplasma sp. str. Ms02 DQ223
EF510778.1 gg_id:224463 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5107
AF221118.1 gg_id:48246 Mycoplasma primatum HRC292(T) AF2211
DQ223545.1 gg_id:142935 Mycoplasma sp. str. Ms01 DQ223
U44768.1 gg_id:15865 Mycoplasma bovoculi str. M165/69 U44768
U22013.1 gg_id:15920 Mycoplasma sturni str. UC/MF U22013
EF036469.1 gg_id:179109 Mycoplasma cricetuli str. CH EF0364
EF510860.1 gg_id:225935 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5108
AF412970.1 gg_id:71789 Mycoplasma anatis str. 1340(T) AF4129
AF332757.1 gg_id:73175 Mycoplasma bovis str. 422/88 AF3327
AF332748.1 gg_id:73746 Mycoplasma agalactiae str. L9 AF3327
NR_024978.1 gg_id:548556 Mycoplasma equirhinis str. M432/72; ATCC 29420 NR_02
AM182896.1 gg_id:186205 Mycoplasma sp. str. 10T4 AM182
EF510818.1 gg_id:217758 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5108
FJ959657.1 gg_id:555715 bottlenose dolphin upper respiratory tract blowhole clone D896_262 FJ9596
U67943.1 gg_id:15941 Mycoplasma adleri str. G145 U67943
L08054.1 gg_id:15918 Mycoplasma corogypsi str. BV1 L08054
U73903.1 gg_id:15913 Mycoplasma edwardii str. PG24 U73903
NR_024981.1 gg_id:573950 Mycoplasma subdolum str. TB; ATCC 29870 NR_02
AY121109.1 gg_id:72631 Mycoplasma bovigenitalium 398/87 AY1211
FJ226566.1 gg_id:349001 Mycoplasma sp. str. LR5794 FJ2265
FM165076.1 gg_id:325252 Mycoplasma sp. 2F1AT str. 2F1A FM165
U58997.1 gg_id:15931 Mycoplasma hyopharyngis U5899
EF510714.1 gg_id:224150 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5107
EU859973.1 gg_id:328570 Mycoplasma iguanae str. 2327 EU8599
NR_029183.1 gg_id:594001 Mycoplasma hyosynoviae str. S-16; ATCC 25591 NR_02
AF538681.1 gg_id:56134 Mycoplasma collis str. 58B AF5386
FM165075.1 gg_id:344619 Mycoplasma sp. A1802T str. A1802 FM165
AF221112.1 gg_id:70343 Mycoplasma columbinasale 694(T) AF2211
AM774638.1 gg_id:239999 Mycoplasma canimucosale str. 1642 AM774
AY246564.1 gg_id:85218 Mycoplasma sp. str. VJC358 AY2465
L24104.1 gg_id:15922 Mycoplasma gallinaceum str. DD L24104
FM878637.1 gg_id:553341 Mycoplasma sp. str. 38104 FM878
DQ340199.1 gg_id:147129 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo DQ340
U44766.1 gg_id:15912 Mycoplasma bovirhinis str. PG43 U44766
AM182891.1 gg_id:184771 Mycoplasma sp. str. 13CL AM182

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46.3	248.3	324.2	371.8	172.7	245.0	298.9	366.5	83.9	62.4	297.2
4610.1	3614.5	3896.2	4207.9	3709.8	3824.3	4732.6	4208.3	2952.7	2820.7	3452.3
46.8	26.4	32.9	27.7	25.0	24.0	22.8	22.0	33.1	17.7	25.4
1268.9	2140.7	2002.8	2361.1	1551.4	1778.0	1512.4	2101.5	1321.9	2015.3	1572.8
445.5	1897.4	1916.7	2037.9	1889.8	1817.6	2313.8	2260.5	1474.9	737.5	1568.8
1030.9	4852.4	4735.7	4615.0	4123.5	4302.0	4880.3	4064.8	3560.1	4427.4	4861.0
60.2	791.7	1393.5	1518.7	993.8	1073.0	1286.3	1415.9	1899.7	551.1	784.9
197.1	2063.0	978.7	1091.0	980.3	1116.8	1181.9	1892.7	1096.4	1816.0	831.2
7158.5	6223.5	6225.1	5575.9	4659.6	5485.0	5319.2	6896.9	4811.5	5902.6	6280.7
42.5	54.5	76.6	88.6	66.5	48.6	52.0	58.0	39.9	33.7	24.4
746.3	3474.0	3403.0	2741.5	3516.5	3264.9	3528.2	2497.2	6152.6	4091.9	3076.5
731.5	6136.2	5376.8	4319.0	3418.5	4915.9	3537.7	4442.5	4878.3	5088.9	4690.6
50.1	44.6	155.3	167.6	125.6	82.5	155.5	188.4	134.0	31.2	52.2
59.7	288.8	320.1	366.2	273.4	420.4	335.3	433.6	352.9	180.2	253.2
71.5	421.6	567.5	670.3	425.3	530.0	610.0	692.8	990.4	189.1	398.0
1620.3	5783.8	5719.3	6034.3	4727.6	5299.5	6005.5	5501.4	4132.8	3896.8	5415.5
12305.5	6895.5	6502.2	7365.9	7572.8	7571.9	7659.4	6716.8	11750.8	6684.1	8294.7
30740.6	10992.7	10114.0	11419.0	9644.7	9535.5	10418.6	9365.1	12245.6	10845.1	15571.8
146.6	879.5	1554.8	1334.8	1037.1	967.8	1240.7	1348.4	1482.6	653.2	1105.6
3220.3	4849.9	6054.2	5405.4	4601.5	6262.1	5593.5	5358.0	5887.8	4020.5	5700.4
4061.8	5573.1	5646.5	5756.4	6754.2	6785.1	7234.0	5680.0	8106.8	3838.4	6090.9
269.1	1145.3	1374.5	972.0	1364.2	1400.2	1968.4	1266.9	1439.2	602.6	1051.4
930.3	7152.4	6513.5	5635.8	4589.4	5635.9	4848.5	5873.7	5385.2	5122.9	5540.4
177.2	646.1	610.1	753.2	731.9	895.6	650.2	665.7	182.9	553.0	550.3
114.2	1329.8	1180.3	1369.7	936.5	1248.1	826.2	1455.2	1390.8	477.6	782.4
287.9	1475.8	1391.8	1785.8	1536.0	1838.8	2121.5	1897.9	1819.5	665.3	1531.9
47.6	110.4	238.1	178.7	105.7	157.9	127.5	235.5	83.0	71.2	114.9
10170.0	6037.7	5360.1	5204.4	4735.1	5416.5	5319.7	5057.6	6687.9	6361.6	6099.9
46.3	14.2	17.2	20.6	19.1	19.7	15.5	16.3	16.1	10.0	17.5
1541.9	8717.7	7915.6	8273.5	6555.9	7876.9	8011.5	7933.3	7025.4	6424.5	8024.3
3142.1	3310.6	3359.9	3961.2	3588.6	3474.5	3758.1	3084.8	5748.4	2848.4	4772.6
1737.2	4029.8	4691.3	4812.8	5235.1	4396.4	4789.4	4060.1	3201.1	2522.6	3676.6
28.3	15.1	25.4	26.0	36.6	16.6	28.3	21.8	15.5	19.3	24.3
2361.6	2641.9	2970.8	2829.7	3364.1	2762.4	3758.6	2799.6	2283.1	2518.5	2552.5
2924.2	4431.3	4416.0	4725.7	3482.7	5161.9	5123.7	5109.6	3696.2	2003.2	4964.7
1221.7	912.6	977.9	734.1	600.1	723.9	428.2	731.6	749.8	388.2	668.5
222.8	912.2	786.4	818.9	585.4	1299.4	622.6	1195.4	564.3	563.1	783.4
105.5	1181.8	1050.7	1061.9	980.6	1131.4	861.5	1300.0	1390.4	1605.1	1476.6
52.3	22.5	21.7	28.2	30.4	17.1	39.4	26.8	26.9	13.7	27.8
1975.2	5252.3	4445.7	4391.7	3745.5	4066.6	4525.3	4405.0	3454.1	3776.3	3792.8

4996.2	5371.6	4272.2
315.1	274.8	418.2
3625.8	4712.0	4892.1
22.9	37.1	24.6
1849.3	2133.4	1576.8
1703.3	2644.5	1720.0
3298.1	4790.3	5033.6
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1192.9	1617.5	1071.3
5258.9	6593.9	6166.3
58.6	52.7	36.7
3310.8	3672.8	3381.5
4316.9	4308.9	5204.5
306.6	155.9	63.8
424.9	379.5	450.2
568.1	920.6	563.2
4745.3	6398.4	5808.9
6916.9	7903.2	7127.1
9092.4	10740.5	9253.1
704.9	1532.7	1274.0
4189.2	5224.5	4734.7
4868.5	6855.5	5379.1
1287.5	1607.1	920.5
5270.2	5826.3	4854.8
684.1	1145.8	650.2
1928.6	1959.2	1578.8
1378.8	1823.8	1592.7
152.5	362.2	342.0
4830.3	6490.8	5233.0
19.2	16.6	17.4
6959.5	8467.9	8537.7
3318.5	5244.3	3668.3
4025.6	4914.0	3565.8
23.9	27.8	26.1
2758.6	3382.1	3328.0
3849.7	5271.4	4623.9
577.2	728.7	388.9
2251.8	1590.1	1193.3
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24.6	29.4	27.1
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NR_025186.1 gg_id:543508 Mycoplasma moatsii str. MK405; ATCC 27625 NR_02
AF412974.1 gg_id:28253 Mycoplasma collis str. 58B(T) AF412
AY050170.1 gg_id:60547 Mycoplasma timone AY050
AF412989.1 gg_id:28733 Mycoplasma verecundum str. GIH(T) AF412
FM878042.1 gg_id:557236 Mycoplasma sp. str. 51CL FM878
EF510815.1 gg_id:219506 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5108
AF125591.1 gg_id:15897 Mycoplasma falconis str. H/T1(T) AF125
DQ340198.1 gg_id:146814 Dominance Mycoplasma guts Long-Jawed Mudsucker Gillichthys mirabilis five Califo DQ340
AF150495.1 gg_id:15925 Mycoplasma sp. str. 94630 AF150
AF412981.1 gg_id:70918 Mycoplasma glycophilum str. 486(T) AF412
NR_024982.1 gg_id:567316 Mycoplasma gypis str. B1/T1; ATCC 51370 NR_02
NR_025914.1 gg_id:557285 Mycoplasma meleagridis str. 17529; ATCC 25294 NR_02
EF510816.1 gg_id:227513 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5108
AF412971.1 gg_id:69777 Mycoplasma buteonis str. BbT2g(T) AF412
M24582.1 gg_id:15954 Mycoplasma californicum M2458
U15795.1 gg_id:15943 Mycoplasma felifaucium str. ATCC 43428 U1579
EF510786.1 gg_id:220695 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aeru EF5107
FM196534.1 gg_id:331374 Mycoplasma sp. str. Zaradi2 FM196
U09787.1 gg_id:15917 Mycoplasma felis str. ATCC 23391 U0978
AM182893.1 gg_id:190324 Mycoplasma sp. str. 11CL2 AM182
U16760.1 gg_id:15944 Mycoplasma leopharyngis str. ATCC 49889 U1676
AF170102.1 gg_id:15921 Mycoplasma capricolum AF170
AF221115.1 gg_id:19295 Mycoplasma lipofaciens R171(T) AF221
NR_025182.1 gg_id:555208 Mycoplasma dispar str. 462/2; ATCC 27140 NR_02
AY492086.1 gg_id:136766 Mycoplasma suis str. Guangdong AY492
AF178676.1 gg_id:51934 Candidatus Mycoplasma haemodidelphidis Illinois AF178
AF306346.1 gg_id:136331 Candidatus Mycoplasma haemolamae str. Michigan AF306
EU165510.1 gg_id:339052 Mycoplasma ovis Mo-Hu-3-05.2007 EU165
AY171918.1 gg_id:87318 Mycoplasma coccoides AY171
EF221880.1 gg_id:206167 Mycoplasma wenyonii str. CGXD EF2218
U82963.1 gg_id:15860 Mycoplasma haemomuris str. Shizuoka U8296
EU134687.1 gg_id:255073 tallgrass prarie soil clone FFCH10627 EU134
GU293201.1 gg_id:568172 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EF516576.1 gg_id:219640 grassland soil clone FCPT702 EF5165
AY500249.1 gg_id:102371 Candidatus Hepatoplasma crinochetorum clone 48 AY500
EU646193.1 gg_id:285164 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor EU646
EU646198.1 gg_id:280566 Host-specificity transmitted Mycoplasma-like isopod symbionts hepatopancreas clor EU646
AF001173.1 gg_id:15899 Candidatus Mycoplasma ravipulmonis AF001
U62937.2 gg_id:15831 Ureaplasma gallorale str. ATCC 43346 U6293
GU227393.1 gg_id:580923 Ureaplasma sp. str. USP S/N GU227

72.5	333.1	352.1	397.7	242.6	272.9	228.7	543.4	169.1	76.2	415.8
40.4	282.9	381.2	438.4	232.3	344.3	295.4	313.4	133.8	59.6	184.8
2424.5	6132.2	5770.0	6679.0	5408.6	5265.7	5624.5	5456.3	6716.4	3564.6	5845.4
4246.7	7556.8	6074.8	5994.9	5866.4	5790.7	6307.2	6010.8	6537.7	7457.3	6377.6
34.2	8.3	19.5	19.9	15.6	13.9	14.5	97.9	33.6	19.0	26.5
311.7	3338.3	2809.3	2249.7	2667.2	2167.2	2451.8	2639.3	2116.0	2102.7	2232.1
9870.9	6982.9	6531.3	7044.6	5506.6	5995.8	5900.8	5861.2	6698.3	6386.4	7911.9
5156.6	3506.3	3332.3	3503.9	3471.3	3501.8	4182.4	3619.0	1782.8	2779.5	3144.6
5072.7	3106.2	3043.9	3528.6	3431.8	3154.5	4636.3	3408.4	3193.5	2680.8	3242.2
74.8	306.6	386.8	444.9	672.1	485.9	632.1	499.6	221.7	116.0	186.0
1970.9	6141.8	5163.4	6378.4	6470.4	4370.0	6800.7	5585.7	6552.7	1336.9	5660.6
6254.1	9374.0	9072.8	8818.9	6744.4	8570.2	6992.6	8618.3	8605.3	6668.5	11191.5
67.8	515.2	551.3	757.6	607.5	598.9	587.6	614.0	666.5	1105.3	467.5
7577.1	7895.8	6705.5	7307.2	6081.9	6358.3	7171.7	6627.6	6960.7	7013.0	7756.4
2899.3	5886.9	6192.4	6869.6	7520.0	5386.6	7516.8	6430.6	7935.9	5503.7	7379.4
36.0	16.2	17.1	22.8	17.8	19.0	16.3	18.6	16.6	16.2	18.2
571.7	3319.2	3659.5	4019.6	3158.8	3706.2	3678.0	3697.4	4259.6	3570.1	3672.6
806.3	3789.5	3163.5	2754.7	2091.5	2849.3	2389.0	2617.0	3139.1	2367.9	2765.3
3708.4	4760.8	4109.8	4010.1	3989.0	3842.8	4912.0	3540.3	3499.4	5409.6	4660.7
438.9	3325.4	3921.4	4099.0	3636.3	3808.2	4167.3	4040.0	4928.4	3071.4	4223.1
970.2	5531.7	6118.5	5826.9	5151.2	5623.6	5682.0	4942.7	8463.6	6788.9	5875.9
7528.3	6473.4	6865.8	6103.1	6079.9	5899.2	5788.7	5406.2	9558.5	8293.1	6168.0
29.3	99.3	133.4	111.6	48.7	69.7	102.4	79.5	59.6	20.0	66.9
30.9	19.3	23.1	19.0	21.8	17.0	26.1	22.6	16.0	15.2	18.9
4953.3	3328.9	3592.4	3906.7	3490.6	3563.6	4385.5	3946.5	2795.4	2708.1	3237.3
3221.6	1317.0	1321.7	1424.6	1457.2	1381.3	1491.5	1408.9	1860.8	1738.1	1858.5
168.8	172.9	170.2	163.3	172.7	176.1	172.7	207.3	106.3	36.6	165.8
59.5	386.4	480.4	473.8	629.1	538.8	593.8	488.9	316.0	28.4	170.1
7977.0	2841.8	2822.1	2822.0	2827.4	2680.8	2856.6	2770.6	4124.0	2840.8	3641.8
100.6	2383.9	1933.5	1901.9	1832.8	2325.8	1928.2	2256.7	2274.2	2106.2	2070.1
14846.0	5742.2	5710.2	5725.1	5100.1	5767.8	5534.3	4928.4	7073.0	5767.2	7735.4
64.4	51.0	34.4	105.8	83.7	50.8	57.5	59.6	51.6	25.8	40.3
16833.0	9126.9	8924.7	9877.6	8063.0	8948.5	10298.0	8706.0	11611.5	8339.5	12642.5
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46.3	35.2	21.0	65.8	42.9	27.7	88.5	96.1	29.7	20.8	19.3
5591.2	3695.7	3215.4	3924.3	4197.1	3642.1	4726.7	3803.7	5150.6	5845.7	5086.2
1123.1	3940.1	4766.5	5408.5	4253.9	4389.9	3584.6	5160.7	4285.8	6943.1	5315.7
3223.4	6054.4	7440.6	5805.0	4003.8	5363.9	4860.2	6442.2	6492.7	4728.1	7322.8
39.9	161.5	257.6	242.0	114.6	199.3	175.4	217.4	90.8	58.8	124.9
8608.1	3717.8	3501.5	4123.7	3942.2	3541.8	4071.9	3568.8	4602.0	2695.2	4768.5
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2196.5	2043.4	2065.3
5657.7	6952.8	5504.5
3503.9	3281.7	3389.7
3280.2	3708.2	3245.3
552.9	630.8	889.3
5727.1	5976.8	4193.6
7261.7	9226.0	7820.7
640.2	1564.9	900.4
5767.0	7302.6	6071.6
6961.8	7173.5	6112.0
16.5	23.5	25.0
3447.6	3379.9	3724.7
2264.5	2934.4	2806.9
3857.2	4555.6	3486.9
3433.0	4616.0	3583.2
5319.4	5880.0	5792.1
6470.9	8514.5	8577.3
101.7	135.4	76.8
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3406.4	4335.1	4608.9
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128.8	270.4	306.9
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2304.4	3928.8	2379.5
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L08642.1 gg_id:15811 Ureaplasma urealyticum str. 27 L08642
U06097.1 gg_id:15816 Ureaplasma urealyticum str. 354 (serovar 5) U0609
EU844042.1 gg_id:310545 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
EU459553.1 gg_id:294314 capybara feces clone CAP_aah99g08 EU459
FJ172803.1 gg_id:348767 Qinghai Yak Ruminal and Fungi China rumen clone RB-3C9 FJ1728
EU382038.1 gg_id:268757 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
FJ366886.1 gg_id:370110 feces adult twins and mothers; TS28 clone TS28_a01a06 FJ3668
FJ671998.1 gg_id:521062 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
AF371530.1 gg_id:21652 swine intestine clone p-1735-b3 AF371
DQ805924.1 gg_id:175271 human fecal clone RL306aal92g01 DQ805
GQ167173.1 gg_id:567437 Effects Hydraulic Retention Time on Anaerobic Hydrogenation Performance Microbi GQ167
GQ897787.1 gg_id:578177 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
GQ448417.1 gg_id:576850 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
GU303669.1 gg_id:561959 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AM275414.2 gg_id:234959 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
EF445243.1 gg_id:207023 dairy cow rumen clone NED5C1 EF4452
FJ681340.1 gg_id:519348 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
AM275475.2 gg_id:233848 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
GQ896843.1 gg_id:569244 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ896
FJ673493.1 gg_id:515507 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ684684.1 gg_id:529404 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
GQ897386.1 gg_id:585199 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do s GQ897
EU474506.1 gg_id:292635 bighorn sheep feces clone BHSD_aaa03h12.Contig2 EU474
GU303586.1 gg_id:566240 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU850597.1 gg_id:311889 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF427 EU850
AY985740.1 gg_id:117030 human stool clone C771 AY985
GQ451187.1 gg_id:513605 Fecal Yunnan snub-nosed monkey feces clone J19 GQ451
FJ673434.1 gg_id:518672 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
EF445272.1 gg_id:213966 dairy cow rumen clone NED4E12 EF4452
DQ057362.1 gg_id:131450 chicken ileum/cecum clone cc106 DQ057
EU773287.1 gg_id:306877 BigHorn sheep feces clone BH1_aao27e05 EU773
DQ326418.1 gg_id:148285 Metagenomic gut microbiome healthy human stool clone C469 DQ326
FJ673790.1 gg_id:515508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
EU844544.1 gg_id:325403 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ680415.1 gg_id:515855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ673176.1 gg_id:527857 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU344185.1 gg_id:277047 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU475428.1 gg_id:297545 springbok feces clone SBSD_aaa04g12 EU475
EU850542.1 gg_id:342412 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF336 EU850

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2423.2	3485.6	3276.8	3408.1	3046.0	3242.8	3438.7	3192.9	2671.6	1821.6	3103.7
37140.8	12178.8	11622.7	11935.6	11906.9	11345.3	12773.6	10935.4	16517.9	14183.1	17382.4
3564.4	1822.8	1690.2	2082.8	1934.6	1706.0	1839.0	1831.3	2561.0	849.1	1983.2
2231.3	6400.5	6155.2	6755.7	5964.5	6815.0	7676.2	6650.7	5278.7	5050.4	7062.3
2680.5	5898.0	5246.0	5824.7	5019.8	5095.3	5643.4	6055.1	5656.3	2485.4	5346.4
264.6	2077.5	2206.6	1848.3	1702.1	2054.5	1935.5	1962.6	1714.2	1342.4	1514.0
1065.7	3167.4	3607.7	4034.5	4175.0	3178.1	3287.3	3352.4	2896.3	2757.5	3286.5
2289.2	3695.4	3892.9	3995.8	3061.2	3201.4	4020.8	4173.3	4287.6	2128.7	3260.6
9074.3	5597.3	6588.2	6091.8	6297.4	5478.8	6941.2	5438.1	7183.4	6734.5	7556.2
51.8	32.2	79.4	38.4	33.0	27.9	27.0	31.2	22.0	20.8	46.1
3379.2	1833.3	1801.8	2192.9	1523.3	1878.4	1703.0	1821.3	2297.7	1608.6	1957.5
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148.5	1570.8	2374.4	1845.9	2009.7	1273.5	1642.6	1504.7	1115.2	1187.6	1205.4
7928.3	5424.6	4939.5	5025.0	4413.5	4494.6	5400.7	4466.7	5936.3	6861.5	6427.6
517.2	1318.3	1740.4	1768.1	1336.9	1397.2	1307.5	2001.4	689.0	553.0	1109.7
51.5	395.0	364.6	336.4	452.5	290.7	487.9	506.4	772.8	168.7	280.9
517.7	2492.9	2058.4	1989.8	1878.5	1777.8	1600.8	1943.5	1482.7	1334.0	2110.5
8942.5	8351.2	9685.2	9733.7	8961.4	8710.5	9559.9	8432.1	11931.1	8843.5	9876.1
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FJ367190.1 gg_id:367962 feces adult twins and mothers; TS28 clone TS28_a04e12 FJ3671
FJ678613.1 gg_id:531345 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
AY916353.1 gg_id:114378 human stool clone D051 AY9163
EU381774.1 gg_id:265197 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ832322.1 gg_id:558715 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P1Q301_19C03 FJ8323
EU463631.1 gg_id:303133 domesticated horse feces clone horsej_aai90a12 EU463
FJ440078.1 gg_id:567506 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
FJ682646.1 gg_id:513042 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
EU844825.1 gg_id:327546 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8448
EU871410.1 gg_id:324570 Genetic Bovine (Bos taurus) Rumen Thailand clone CF378 EU8714
DQ456306.1 gg_id:158491 pre-adolescent turkey cecum clone CFT211G6 DQ456
EU381733.1 gg_id:265925 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
DQ353915.1 gg_id:146314 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z32 DQ353
EU843681.1 gg_id:325563 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU844239.1 gg_id:327857 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8442
AF001742.1 gg_id:15698 rumen clone RF9 AF0017
GQ451225.1 gg_id:545091 Fecal Yunnan snub-nosed monkey feces clone J128 GQ451
AM277561.2 gg_id:229533 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
GU303762.1 gg_id:580081 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU622737.1 gg_id:279179 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
AY916186.1 gg_id:114444 human ascending colon biopsy clone LW88 AY9161
EU344299.1 gg_id:271356 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
FJ833479.1 gg_id:591398 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q201_78F10 FJ8334
EU871378.1 gg_id:304971 Genetic Bovine (Bos taurus) Rumen Thailand clone CF203 EU8713
EF406725.1 gg_id:211308 mouse colon clone infected_14days-B9 EF4067
EU842453.1 gg_id:316729 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
AY986020.1 gg_id:127092 human stool clone D332 AY9860
EU764308.1 gg_id:341905 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU7643
FJ172880.1 gg_id:352691 Qinghai Yak Ruminal and Fungi China rumen clone RB-2D1 FJ1728
EU844758.1 gg_id:347587 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8447
GU476604.1 gg_id:522127 microbial biogas fermentation enrichment clone BBMC-4 GU476
GU208279.1 gg_id:537538 Study on Sediment Dongping Lake sediment clone 6F1-3 GU208
EU358689.1 gg_id:325820 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3586
GQ458248.1 gg_id:513979 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
AB192099.1 gg_id:143019 termite gut homogenate clone M1NP1-24 AB1920
AB192110.1 gg_id:144845 termite gut homogenate clone M1PT4-30 AB1921
AB255930.1 gg_id:164433 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
EF454354.2 gg_id:220027 termite hindgut clone 290cost002-P3L-1996 EF4543
EF454970.2 gg_id:227321 termite hindgut clone 290cost002-P3L-828 EF4549
AB243293.1 gg_id:149384 acetone-preserved termite gut clone M2PB4a-088 AB2432
FJ202893.1 gg_id:317953 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028

4786.9	3840.4	4506.1	4411.3	3431.3	3899.5	4151.0	4839.1	4416.8	3495.2	3799.0
2818.3	2778.4	3157.4	3520.8	2572.8	2815.8	3393.1	3487.1	2301.0	1421.3	3135.5
73.4	710.2	1016.4	702.1	592.2	633.7	393.7	716.2	349.7	234.4	492.3
1229.0	6063.4	6143.8	5852.2	5285.3	5068.7	5909.2	5144.6	5454.3	5553.2	5830.0
614.8	2991.3	4225.5	3837.3	2905.9	3041.7	3227.8	4547.8	6341.6	3604.8	2806.9
92.1	506.6	557.1	663.1	462.8	448.7	577.4	682.7	351.4	118.0	353.4
1716.2	4475.5	4887.8	5538.1	4497.3	4033.9	5620.9	3930.9	2561.4	2393.6	4080.5
112.4	621.9	708.8	656.1	241.4	433.7	395.2	622.4	174.5	120.4	434.7
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9540.5	6253.3	8925.0	8205.1	6432.0	7747.8	7881.1	8510.8	7050.8	5988.8	9104.1
73.6	43.3	57.4	72.9	58.1	40.9	60.1	36.0	32.4	31.0	36.2
183.0	2422.4	3224.7	3133.5	3243.5	2399.9	3751.9	3653.5	1595.6	1008.6	2761.0
44.2	698.1	879.8	818.9	626.0	724.1	1190.3	663.6	270.8	470.4	684.2
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2349.9	2239.0	2606.5	2522.4	3722.7	2595.6	5063.9	2475.8	1781.0	1125.3	2433.9
59.0	798.6	623.4	684.8	489.3	734.8	538.9	850.4	192.0	206.7	447.5
6511.4	5161.8	4982.3	4790.9	4588.7	5805.7	4982.1	4642.1	5029.4	4974.2	5149.9
50.3	341.3	391.3	386.9	273.5	303.3	341.8	305.3	208.3	77.9	165.6
240.2	3044.0	3067.6	3252.8	2148.5	2608.5	2494.1	2715.1	2383.1	1961.8	2777.5
4147.2	3256.0	2914.2	3044.5	3619.6	2692.5	3327.8	3005.4	3113.1	5102.6	2876.6
4348.9	4729.5	3998.9	3804.3	4446.1	3863.6	4026.3	4785.2	5795.8	3913.1	3860.3
729.1	3494.2	4797.8	5032.5	2781.2	3921.9	3920.8	5368.8	2713.1	1548.3	4327.3
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5946.1	2387.2	3303.5	3205.7	3305.4	2904.8	3353.8	3880.4	2663.2	2253.8	3586.9
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5731.2	4732.3	4717.9	4829.1	4607.2	4313.1	4820.7	4156.8	4559.1	5610.7	4691.8
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1542.8	2363.4	2160.0	2119.5	2073.8	1051.2	1895.8	2107.5	1470.7	1561.9	2160.3
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86.9	3145.7	3306.6	3682.0	3151.4	2969.7	3823.9	3105.9	4426.2	3115.6	1900.4
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7510.4	7015.3	10413.4
43.2	63.7	125.0
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4572.8	6195.3	6567.4
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2817.3	3456.8	2855.2
3413.4	4196.1	3676.6
3795.4	4694.5	6330.0
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3845.6	4049.5	3124.1
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4545.0	5642.4	5036.4
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415.9	845.8	594.9
9260.3	9993.6	11015.1
7912.2	10659.8	8743.4
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GQ348358.1 gg_id:560472 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AY876379.1 gg_id:111757 Deinococcus deserti str. VCD117 AY8763
AJ585983.1 gg_id:97958 Deinococcus sp. str. AA752 AJ5859
AJ585981.1 gg_id:97107 Deinococcus sp. str. AA692 AJ5859
NZ_AAHE01000002.1 gg_id:131883 Deinococcus geothermalis str. DSM 11300 NZ_AA
AAHE01000005.1 gg_id:134272 Deinococcus geothermalis str. DSM 11300 AAHE0
AY743256.1 gg_id:138843 Deinococcus hohokamensis str. KR-40 AY7432
AY743275.1 gg_id:138931 Deinococcus maricopensis str. KR-1 AY7432
AB264133.1 gg_id:171820 Deinococcus sp. str. TDMA-21 AB2641
AY743280.1 gg_id:138834 Deinococcus papagonensis str. KR-241 AY7432
AE000513.1 gg_id:146329 Deinococcus radiodurans str. R1 AE0005
AY743284.1 gg_id:138790 Deinococcus sonorensis str. KR-90 AY7432
GQ043868.1 gg_id:461798 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
EF141348.1 gg_id:247857 Deinococcus peraridilitoris str. KR-200 EF1413
AY743267.1 gg_id:139200 Deinococcus apachensis str. KR-32 AY7432
AM988777.1 gg_id:568744 Deinococcus sp. str. K4.1 AM988
AF385541.1 gg_id:136570 Prevalent species and phylotypes advanced noma lesions Deinococcus oral clone CB(AF3855
DQ532354.2 gg_id:168505 Geographical Variation Microbial Burden and Spacecraft Assembly Kennedy Space C DQ532
EU834252.1 gg_id:347125 Deinococcus aquaticus str. DS27 EU8342
DQ883809.1 gg_id:163551 Deinococcus cellulolytica str. 5516J-15 DQ883
NR_026403.1 gg_id:562641 Deinococcus radiopugnans str. ATCC 19172 NR_02
EU029127.1 gg_id:238409 Deinococcus sp. str. 2A2 EU0291
EF635408.1 gg_id:285250 Deinococcus alpinitundrae str. ME-04-04-52 EF6354
GQ357648.1 gg_id:546802 Deinococcus sp. str. YIM 75723 GQ357
GQ441240.1 gg_id:556010 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
EU029130.1 gg_id:250755 Deinococcus sp. str. 3A5 EU0291
AB374383.1 gg_id:271722 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss(AB3743
M21413.1 gg_id:1418 Deinococcus radiodurans M2141
EU626561.1 gg_id:282134 Deinococcus xinjiangensis str. X-82 EU6265
DQ022077.1 gg_id:136712 Truepera radiovictrix str. TU-8 DQ022
EU622978.1 gg_id:279041 Deinococcus sp. str. 5516T-9 EU6229
EU427464.1 gg_id:264010 Deinococcus sp. str. I-0 EU4274
GQ058151.1 gg_id:406491 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ058
AY743279.1 gg_id:138901 Deinococcus yavapaiensis str. KR-236 AY7432
EU362143.1 gg_id:332198 and Mesquite Flats Site Death Valley dune sand clone 14 EU3621
EF522236.1 gg_id:219134 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS01(EF5222
GQ058104.1 gg_id:395808 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ058
AM283039.1 gg_id:159842 Deinococcus sp. str. Han23 AM283
GQ072152.1 gg_id:389682 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw192g11 GQ072
AM292065.1 gg_id:249433 Deinococcus radiodurans zf-69-II AM292
GQ130053.1 gg_id:435637 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130

4318.1	7293.6	7743.8	6383.0	4859.2	5713.4	5687.7	6141.2	6975.8	5498.8	6146.6
1184.5	6535.3	7716.7	6549.1	5927.5	6725.2	6161.2	6568.9	6567.2	5516.3	6980.2
6846.3	7644.9	8000.3	8362.6	8140.2	7759.2	8361.4	8976.4	9950.2	10467.1	8195.2
9018.0	6718.0	6633.5	6833.1	7017.5	6525.1	7422.9	6329.6	8958.4	7362.6	7176.2
61.6	38.8	41.4	42.4	41.1	31.0	36.0	35.6	33.4	31.6	33.6
190.0	1389.2	1422.5	1111.0	1287.7	1304.8	1536.5	1034.5	1292.2	993.9	1050.9
5606.9	2568.0	3575.7	2886.1	2687.4	2875.0	1967.6	2954.7	3241.3	3002.0	3611.0
6123.8	9183.2	8628.4	8370.9	9090.1	8847.3	9706.1	7882.2	10119.9	5742.2	7048.2
15000.7	5920.6	7833.4	6100.4	5716.3	5255.1	5884.3	5029.4	6899.4	4943.2	6666.1
116.2	474.1	448.7	488.8	726.0	418.0	930.7	616.0	848.7	126.2	290.8
25496.9	11262.3	12460.7	12250.3	11982.6	12574.0	13052.6	10853.9	15947.7	12515.4	13809.4
3716.2	2182.5	2940.8	2803.5	3100.1	2919.1	3624.7	2888.7	3952.1	740.9	1571.8
58.8	552.4	447.0	242.2	267.0	382.1	225.1	349.5	450.7	567.0	161.5
168.4	3309.4	4038.4	4268.8	4367.6	3729.5	6494.7	5184.6	1680.0	1380.4	4084.7
46.0	54.4	45.0	43.2	44.6	25.8	42.4	39.6	25.5	13.7	31.4
5447.9	8917.5	7892.1	7625.7	8571.6	8111.8	9206.4	6948.6	9301.0	7341.4	7602.3
51.5	611.0	747.6	538.4	308.1	470.7	282.0	510.6	402.0	210.5	476.1
5775.3	1620.7	1725.3	1731.9	1965.2	1875.2	1654.5	2001.9	1762.5	1970.2	1261.0
4804.6	4520.7	4943.0	4617.6	5041.9	4315.3	5234.9	4715.5	5828.3	4046.2	6247.7
27.4	1156.4	734.0	687.0	309.2	19.8	24.9	595.3	28.6	37.5	96.1
8998.7	6587.6	6653.7	7224.8	6782.0	6258.9	7643.1	6424.6	7438.0	4007.3	9386.3
4343.0	6473.5	6371.1	6796.6	6830.0	5897.2	6562.4	7467.6	6846.1	5524.1	7768.0
3363.4	4084.1	5334.1	4619.6	5264.4	3701.4	7062.9	4935.4	4382.2	2432.0	4250.0
929.7	2931.6	2950.8	3070.6	2680.1	3372.0	2862.2	2887.8	2011.7	1783.3	3151.1
13979.8	8061.8	8004.7	8488.5	8041.8	7799.0	8678.5	8356.8	9922.5	7317.9	9190.8
1442.4	3756.2	3555.5	3423.6	4188.0	3526.2	4598.8	3901.8	4190.2	1262.0	2191.0
1298.7	3809.6	4225.7	4156.0	5158.0	3939.6	4806.6	4765.4	2692.5	2882.0	3313.0
17540.7	10360.8	10133.3	10039.9	10370.3	10041.8	9639.3	9082.6	13553.1	10223.1	11664.7
1032.2	2642.7	2844.6	2351.8	2583.4	3133.0	2560.3	2486.8	3812.3	4556.1	2049.9
43.9	45.5	44.5	44.3	198.1	47.6	46.7	39.0	37.7	20.2	41.3
2134.6	4332.7	5542.9	4861.3	4846.9	4357.4	4763.9	5579.0	5096.4	4237.4	5277.4
193.7	4159.8	4494.6	4041.7	5183.8	4285.8	4906.5	3832.8	3611.2	1870.0	2419.6
244.6	221.4	697.9	262.4	463.1	281.2	192.9	331.3	562.6	96.5	199.8
182.3	1137.5	841.0	1367.4	1343.1	1240.8	1251.1	1128.1	462.1	190.3	975.6
1905.0	4660.9	4368.8	4923.2	6060.0	4696.5	4825.2	4517.4	5124.6	1644.9	3676.6
4731.4	7990.8	8968.0	8510.7	8808.8	7337.1	8292.3	8662.9	8398.5	7088.1	8797.3
1823.8	4158.7	4994.1	3053.0	4227.8	3879.5	3942.3	3288.5	4669.2	2724.7	3325.9
68.0	59.7	96.1	85.6	106.3	66.8	78.6	68.1	107.4	35.7	59.0
17145.9	8886.9	8935.8	9627.5	9504.4	8925.9	9814.0	9902.4	10364.4	11621.2	12077.0
22676.4	5868.2	6371.0	5758.4	5681.5	6016.7	4992.4	4965.0	8923.1	5614.6	6714.5
57.9	50.2	63.9	70.5	68.7	34.3	67.0	33.7	27.2	20.3	42.8

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6039.0	6915.0	5419.6
8538.0	8955.1	8573.2
6343.2	7021.8	7379.0
36.1	39.4	41.8
1155.9	1212.9	1127.2
2788.2	4206.2	3199.8
8655.9	7547.0	6412.9
5201.1	7168.2	5208.1
301.1	701.5	600.5
10574.8	13565.8	14000.0
3498.0	2818.6	1775.1
499.2	325.7	291.0
2995.2	2933.0	4668.3
34.4	28.5	41.3
6974.1	7487.5	7831.1
496.9	868.1	692.8
1981.9	2202.4	2107.5
3933.3	5386.8	4453.4
28.2	30.0	618.5
6398.3	7418.1	6850.0
6028.9	6883.3	5943.3
5716.0	5003.9	5187.2
2932.9	3237.7	2978.8
8091.0	8538.5	8158.6
3531.5	3063.5	2906.1
4895.7	4578.7	4051.5
8940.9	10134.5	9251.4
2781.2	3378.9	3561.7
44.0	50.3	70.6
4657.4	5707.7	4527.1
2949.5	3490.1	3894.9
284.7	556.0	187.1
1251.7	1413.2	1014.8
4344.5	5849.8	6247.3
7770.0	8364.4	7480.2
3811.0	6245.0	4609.6
96.6	105.0	74.4
9209.2	9920.2	9949.7
5497.8	7137.1	5448.6
51.6	42.2	50.0

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g__Deinococcus
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s__Thermus igniterrae	53760

DQ336980.1 gg_id:146805 subsurface water clone EV818CFSSAHH23 DQ336
DQ130032.1 gg_id:138316 microbial biota normal forearm human skin clone GL109 DQ130
DQ847439.1 gg_id:170011 human forearm skin clone GL2-41 DQ847
DQ366016.1 gg_id:152980 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone 21 DQ366
EU622979.1 gg_id:279558 Deinococcus sp. str. 5516T-11 EU622
AB473897.1 gg_id:568788 sequences endolithic and archaea Weissenstein (white rock) / Albula pass few millim AB473
DQ883808.1 gg_id:169628 Deinococcus aeria str. 5516J-6 DQ883
GQ130015.1 gg_id:405062 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ130
FJ444684.1 gg_id:562787 Cotton Rhizosphere cotton rhizosphere clone 2y-56 FJ4446
FJ176238.1 gg_id:307654 Deinococcus sp. str. ZLM-202 FJ1762
GQ026439.1 gg_id:453803 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
EU029134.1 gg_id:250725 Deinococcus sp. str. 5A5 EU029
AM940971.1 gg_id:263628 Deinococcus aquatilis str. CCUG 53370 AM940
AJ585985.1 gg_id:95404 Deinococcus sp. str. AA69 AJ5859
GQ052823.1 gg_id:377731 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ052
DQ223543.2 gg_id:171337 Deinococcus sp. X2 DQ223
FM872722.1 gg_id:365101 occupant source house floor dust clone FB01A10 FM872
AY743278.1 gg_id:139150 Deinococcus pimensis str. KR-242 AY743
AY250871.1 gg_id:86556 lichen-dominated Antarctic cryptoendolithic community clone FBP266 bacterium AY250
GU214174.1 gg_id:593108 and biota slimes Canadian paper mills slime mill taken wet section around papermal GU214
DQ366015.1 gg_id:153959 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3 DQ366
DQ130037.1 gg_id:137532 microbial biota normal forearm human skin clone GR66 DQ130
GQ023518.1 gg_id:486153 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319e11 GQ023
DQ683348.1 gg_id:172621 Deinococcus piscis str. 3ax DQ683
NR_026421.1 gg_id:555743 Meiothermus cerbereus str. GY-1 NR_02
DQ916146.1 gg_id:167558 Meiothermus rosaceus str. WQBGR2-3 DQ916
NR_027614.1 gg_id:543137 Meiothermus ruber 1279 str. DSM 1279; ATCC 35948 NR_02
AJ871173.1 gg_id:114851 Meiothermus ruber str. SPS-242 AJ8711
X84211.1 gg_id:1405 Meiothermus silvanus str. V1-R2 X84211
AF418002.1 gg_id:20802 Meiothermus taiwanensis str. WR-220 AF418
AF418001.1 gg_id:26209 Meiothermus taiwanensis str. WR-30 AF418
AJ871171.1 gg_id:114643 Meiothermus timidus str. RQ-12 AJ8711
DQ899883.1 gg_id:238702 structure receiving long-term augmentations chromium contaminated wastes landfi DQ899
NR_026244.1 gg_id:540285 Meiothermus chliarophilus str. ALT-8; ATCC 700543; BCRC 17113 NR_02
AJ871172.1 gg_id:114775 Meiothermus ruber str. SPS-241 AJ8711
L37521.1 gg_id:1398 Thermus sp str. ac-2 L37521
FN178497.1 gg_id:573829 Meiothermus sp. str. CAL-12 FN178
EU249978.1 gg_id:239060 Polyphasic description Pocillopora mucus secreted Pacillopora meandrina coral color EU249
AB107956.1 gg_id:85579 Oceanithermus desulfurans str. St55B AB107
Y18412.1 gg_id:35343 Thermus antranikianii str. HE-5 Y18412
NR_026501.1 gg_id:533728 Thermus igniterrae str. RF-4; DSM 12459 NR_02

56.7	131.2	235.7	200.6	222.8	208.0	173.5	243.1	461.2	73.2	117.4
185.1	1193.9	1740.9	2149.8	1078.3	1160.7	867.8	1513.1	907.7	430.2	1188.4
7591.4	9424.1	8273.3	7887.9	7821.1	8167.1	8307.3	7017.6	10093.9	4714.9	8902.7
10359.1	7032.6	5857.8	7338.9	7481.5	6800.6	7574.9	6685.1	8766.8	7365.0	10051.3
710.5	2820.9	3186.4	2296.8	2220.7	3054.6	2286.2	2715.2	3420.2	2678.0	2334.9
40.9	86.3	75.5	66.1	139.0	74.9	104.9	63.9	74.5	67.8	52.7
1559.0	4771.7	4697.8	4813.3	4973.5	5206.8	5006.9	4482.0	6722.4	5552.6	3762.3
6406.4	4134.9	5313.1	5086.5	4949.1	5043.1	5448.4	5014.9	5640.2	5625.6	4907.1
69.2	1655.6	1255.5	1228.3	1747.0	1175.5	1498.0	1163.1	1640.0	300.0	842.2
3483.7	4846.4	5486.2	6277.4	7553.6	5387.6	6992.1	7294.3	5065.2	1957.3	4881.6
4274.8	8667.8	8785.9	9980.9	9233.2	8425.9	10076.2	8769.8	9730.2	9523.7	9610.3
274.9	2419.9	2597.1	2537.8	2610.7	2460.6	2640.6	3062.6	2844.4	1295.7	2943.1
4556.4	5595.1	6083.3	5820.8	6483.9	5110.4	6117.6	6206.8	5939.8	4734.5	5880.6
2254.8	5311.3	6133.7	5544.4	6149.4	4999.2	6298.3	6181.6	6521.5	5550.6	6126.8
6981.1	4864.3	5759.2	4413.1	5186.3	5015.6	5098.1	4715.1	8506.4	6604.0	5000.1
1219.2	3543.9	4662.4	3867.8	3677.4	3958.1	3927.5	3798.0	4776.1	3715.1	3897.3
2014.1	7082.0	6797.7	7233.3	7658.2	6360.5	7011.7	7940.2	6256.0	5155.8	6090.7
38.9	179.3	132.6	128.9	383.5	260.6	154.2	121.9	35.7	34.6	72.5
8932.3	4823.9	5673.3	4600.5	4934.3	4112.0	5696.5	4571.9	6798.7	5382.1	5850.8
161.5	3053.8	3338.4	3054.4	3886.1	2366.4	3480.4	3227.6	1896.7	776.8	2932.9
7825.4	5719.6	6299.3	6361.9	6615.3	5806.8	6942.8	5914.5	6926.6	5985.2	8741.3
19880.6	7712.4	7638.9	7571.1	8673.8	7317.6	7562.6	6852.8	8702.0	8028.0	15220.8
75.4	2863.9	4109.2	3083.2	2893.1	3393.3	3976.1	3710.4	2721.9	4264.2	2922.8
21600.1	9734.7	9728.1	10511.2	10832.8	9689.8	11688.8	9495.4	11262.2	9382.8	11285.2
2023.9	1603.7	1433.3	1802.1	1700.2	1526.1	1744.9	1715.2	2122.3	1438.8	1667.7
1955.4	2468.8	1891.5	2445.5	2590.3	2425.3	2853.3	2595.9	2823.6	2359.8	2230.0
2296.2	3120.9	2401.2	2879.7	3277.7	3242.6	3347.3	4046.2	3350.6	2645.9	3029.4
18017.8	6948.9	5921.1	6458.7	7078.7	6144.3	7478.7	6670.4	10100.4	8045.6	8450.1
136.3	772.9	609.1	651.1	474.1	631.3	521.3	758.7	328.8	180.8	547.5
12103.3	6281.7	5025.0	6241.7	5517.3	6591.1	5588.6	5246.6	6057.5	6766.2	6008.7
1827.8	2471.2	1885.1	2288.9	2624.0	2331.2	2668.5	3008.3	2823.3	2177.4	2218.0
298.9	1634.1	1237.2	1477.0	2009.0	1819.4	1560.0	1579.5	1892.3	484.3	1096.1
590.0	3015.7	3066.6	3230.0	3573.8	2708.0	3593.9	2948.1	2916.7	2350.2	3490.5
65.4	88.8	106.1	90.3	187.6	91.1	196.7	86.3	63.0	66.5	67.0
2456.4	3123.1	2409.0	2884.6	3277.7	3240.8	3347.9	4059.7	3350.2	2647.9	3030.5
1881.0	1491.9	1426.4	1799.1	1577.5	1521.7	1863.5	1860.6	2115.7	1314.4	1663.7
9530.9	10735.7	9789.1	11437.3	11561.6	10118.6	14601.5	11801.6	8098.2	10780.0	10626.8
120.8	942.7	885.0	934.2	1433.8	919.2	1080.0	825.3	659.3	536.8	719.8
43.2	121.7	113.6	82.9	73.3	103.3	119.9	132.1	51.2	48.0	79.0
26.9	39.0	44.1	21.4	131.4	46.9	47.0	37.2	22.8	32.8	29.3
710.0	1794.4	2303.1	2034.2	1975.7	1551.8	1713.7	1589.9	1236.7	1663.0	1550.0

167.5	316.1	205.4
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7025.1	7567.3	7182.0
7128.1	7378.9	7056.8
2296.6	2948.6	1625.2
75.7	106.9	100.8
4831.6	5452.9	6406.8
5172.9	6206.2	6203.6
1179.3	1207.2	1706.6
6603.9	5607.7	5225.1
8237.5	9394.5	10984.4
2790.0	2190.4	2701.3
5423.5	6117.3	4813.5
5278.7	6215.0	5233.1
4688.9	7093.0	6120.2
4007.2	4948.6	3356.9
7409.3	8238.9	6021.1
118.1	178.1	128.2
4592.4	5851.8	4819.1
2146.8	2097.0	3460.9
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6607.0	9070.7	8147.0
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10024.2	11189.9	11467.7
1530.1	1661.5	1755.8
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5999.3	5873.9	6103.1
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5152.9	5300.4	4853.1
2301.7	2176.1	2164.1
1703.5	1846.7	1642.5
2845.5	3440.4	3350.3
143.2	145.3	221.1
3177.4	2829.4	3188.4
1537.7	1767.0	1742.0
9827.0	9943.5	11592.2
842.7	1089.0	957.4
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39.4	54.9	230.7
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s__Thermus thermophilus	53194
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EU214609.1 gg_id:323841 Thermus thermophilus yb60g EU214
EU616794.1 gg_id:273039 Thermus thermophilus str. WG EU616
AY557603.1 gg_id:105041 Thermus yunnanensis AY557
NR_025901.1 gg_id:535809 Thermus filiformis str. Wai33; ATCC 43280 NR_02
Y18409.1 gg_id:30085 Thermus brockianus str. 15038T Y18409
Y18416.1 gg_id:45920 Thermus oshimai str. SPS-17T Y18416
AF018197.1 gg_id:1324 temperature clone env.OPS 15 AF018
L09663.1 gg_id:1345 Thermus aquaticus L09663
AF331969.1 gg_id:41572 Thermus rehai str. RH99-02 AF331
FJ638543.1 gg_id:511615 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
GU233838.1 gg_id:537430 effects temperature pH salinity and sinter growth rate on microbial Icelandic waters GU233
AY861866.1 gg_id:112463 Obsidian Pool prime community clone OPPB146 AY861
AF020205.1 gg_id:1335 Thermus scotoductus str. SA-01 AF020
EU701067.3 gg_id:290466 Thermus sp. str. K-39 EU701
Y18408.1 gg_id:47782 Thermus igniterrae str. GE-2 Y18408
EU924248.1 gg_id:326104 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8C EU924
AB071811.1 gg_id:24092 Thermus kawarayuensis str. KW11 AB071
EU753248.1 gg_id:352672 Thermus sp. str. PRI-2268 EU753
AY028380.1 gg_id:67904 Thermus sp. str. C4 AY028
AF521188.1 gg_id:63588 Thermus sp. str. RH-1514 AF521
L77877.1 gg_id:106875 Thermothrix thiopara L77877
L37522.1 gg_id:1357 Thermus sp str. ac-7 L37522
AF255591.1 gg_id:17962 Thermus sp. str. SRI-248 AF255
Y18410.1 gg_id:26144 Thermus scotoductus str. ITI-252T Y18410
AJ507298.1 gg_id:60062 Vulcanithermus mediatlanticus str. TR AJ5072
DQ832056.1 gg_id:165232 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
DQ832059.1 gg_id:165655 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
NR_028639.1 gg_id:540517 Marinithermus hydrothermalis str. T1; JCM 11576 NR_02
DQ832060.1 gg_id:173448 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
DQ924664.1 gg_id:177658 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
DQ924670.1 gg_id:189281 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
EU435435.1 gg_id:273276 Thermodesulfatator sp. str. AT1325 EU435
AJ969460.1 gg_id:157635 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AY280428.1 gg_id:102075 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
AB282756.1 gg_id:230931 Thermosulfidobacterium lithotrophicum str. ABI70S6 (= JCM13301 = DSM 17441 AB282
EU635930.1 gg_id:279109 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU635
EF077228.1 gg_id:253157 Anaerobic oxidation short-chain hydrocarbons marine sulphate-reducing Guaymas B EF0772
AM712345.1 gg_id:247140 detection and ly microbial Brothers Seamount Kermadec Arc New Zealand biofilm h AM712
NR_025146.1 gg_id:570497 Thermodesulfobacterium hydrogeniphilum str. SL6; DSM 14290 NR_02
FJ638609.1 gg_id:537018 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6386
AF419676.1 gg_id:25647 Guaymas Basin hydrothermal sediment clone a2b002 AF419

3092.3	3199.3	2962.0	3613.6	3822.8	3636.6	5320.6	4358.0	3827.5	3528.4	4332.2
2183.8	1937.7	2471.3	1575.1	2046.8	2259.5	2299.3	2808.4	1535.9	2251.5	1933.2
1005.8	2867.5	2965.7	3496.4	3439.2	2537.1	2841.9	2394.3	1174.0	1523.9	2164.1
258.2	564.7	730.2	798.2	829.3	721.1	740.2	631.5	399.7	469.0	527.2
56.7	450.9	438.4	440.0	657.2	384.2	505.4	789.8	129.9	70.0	419.6
56.4	183.8	296.4	369.3	416.9	270.1	766.2	321.6	100.4	48.5	141.2
452.7	1639.8	1818.6	2006.5	2466.3	1610.7	2265.7	1813.9	797.6	1402.7	227.0
2266.2	4637.1	3657.1	4348.7	5670.5	4058.1	4731.1	3733.2	2738.5	2952.2	2946.4
45.7	319.3	434.1	408.8	518.0	374.7	511.6	518.8	88.6	76.7	161.1
44.6	70.1	102.6	74.4	189.5	68.2	99.3	91.8	37.8	40.6	59.2
4786.8	1950.5	1627.4	1969.5	1639.2	1549.2	1549.7	1672.7	2561.0	2138.5	2285.6
11111.8	5453.9	5204.9	5958.5	5542.3	4861.9	4579.0	4813.2	5087.2	6137.8	6205.7
75.6	306.9	531.0	534.2	716.9	479.5	490.6	452.3	138.6	173.1	211.1
72.2	254.8	257.1	333.2	331.1	295.4	622.9	300.5	77.9	81.5	154.3
329.9	1377.7	1731.1	1727.7	1915.5	1182.3	1119.3	1421.8	1058.5	1739.4	1082.8
1681.8	3760.6	4156.8	3421.3	2220.8	3367.6	4194.0	2917.4	3518.8	3159.4	4059.7
1099.9	2368.5	2398.4	2829.5	3687.2	2595.9	3579.1	2600.8	1291.2	1064.0	1610.0
989.9	1395.6	1370.4	1549.0	2061.1	1627.5	2893.0	1551.2	1024.6	770.4	995.0
41.2	70.9	93.0	114.8	64.6	97.0	41.7	88.1	47.2	30.3	67.6
49.3	1402.9	976.7	800.5	663.6	891.6	504.0	1683.3	373.3	1856.6	1018.6
2405.0	484.7	772.9	546.4	701.9	558.3	493.7	910.1	457.2	232.8	956.1
87.6	961.8	1109.1	1166.0	862.1	957.0	882.8	1291.5	368.8	631.0	126.8
1089.8	5278.1	3558.3	4387.3	4815.4	4200.1	5817.3	4252.1	2114.4	1903.4	3230.3
51.2	27.3	25.3	33.4	36.9	29.5	33.1	24.1	34.7	43.6	24.7
120.5	727.2	597.3	651.5	765.1	551.3	762.6	567.8	333.0	148.2	372.7
6746.8	2707.0	2660.6	3050.5	2706.1	2814.4	2884.9	2709.6	3370.4	2799.5	2867.7
85.3	452.0	1234.8	1531.0	1371.1	1202.6	1515.6	1372.7	583.4	1256.9	645.4
58.0	104.2	121.1	122.6	159.4	146.2	345.0	135.6	46.7	44.2	110.3
5958.7	2775.8	3033.7	2929.8	2709.6	2828.3	2994.8	2897.2	3073.3	3564.8	3376.5
70.3	489.2	587.2	512.5	954.1	667.5	864.7	499.3	153.6	71.6	236.2
44.5	27.7	39.1	38.0	36.1	29.4	30.7	37.6	25.8	20.3	40.3
36.3	18.0	18.1	27.5	24.2	13.1	21.2	20.9	24.2	14.9	24.0
48.2	92.0	117.5	118.3	157.4	121.6	187.4	233.6	131.5	46.1	103.9
42.3	62.9	49.9	70.7	48.3	62.1	41.3	35.7	36.1	35.0	47.6
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4668.5	9695.7	10332.5	10853.0	12576.3	10232.9	12951.8	9573.3	10498.8	9343.3	10932.1
2232.3	4686.3	5830.1	5375.2	4954.7	4854.1	5966.8	4561.5	4433.6	5572.5	5368.7
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78.2	127.8	125.3	115.1	153.5	137.3	144.8	125.7	67.5	75.8	91.6
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2840.7	3012.6	3103.3
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419.9	689.1	759.9
214.6	153.5	96.3
1362.5	1553.6	1736.6
2777.8	3418.0	3464.2
2172.0	3306.1	5221.4
1179.7	1688.5	2143.7
34.7	68.1	35.2
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484.2	1531.1	212.5
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632.2	920.4	705.3
2222.3	3193.6	3100.1
1174.5	1725.5	2196.7
104.0	133.9	210.9
2597.0	3665.9	3519.9
422.7	548.8	787.7
31.9	38.5	30.2
18.1	18.9	24.3
93.8	198.6	501.4
62.4	48.9	86.3
6534.1	8747.9	10169.6
8977.1	10301.6	11882.3
4235.9	4498.8	6890.5
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s__Fervidobacterium nodosum	54571
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CU924090.1 gg_id:565047 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
Z49117.1 gg_id:1227 Fervidobacterium gondwanense Z49117
EU851047.2 gg_id:325520 Fervidobacterium sp. str. 1445t EU851
AF509468.1 gg_id:66261 Geotoga aestuarianus str. T3B AF5094
EU245202.1 gg_id:245616 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-A11 EU245
DQ080153.1 gg_id:128210 sediment clone BFA-T46 DQ080
DQ080178.1 gg_id:128351 sediment clone A2 DQ080
DQ080154.1 gg_id:133990 sediment clone BFA-K27 DQ080
CP001634.1 gg_id:422862 Kosmotoga olearia str. TBF 19.5.1 CP001
CU918298.1 gg_id:557400 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
EU542473.1 gg_id:258468 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
FJ901103.1 gg_id:540611 Polymorphism microbial reservoirs water cut stage oil field clone Z-49 FJ9011
AB530678.1 gg_id:539611 Kosmotoga sp. str. S304 AB530
AJ431250.1 gg_id:107334 Thermotogales str. Dex60-136 AJ4312
AJ250439.1 gg_id:1220 Marinitoga camini MV1075 AJ2504
FM253687.1 gg_id:341893 Marinitoga sp. str. MC3 FM253
AJ431249.1 gg_id:79381 Thermotogales str. Dex60-32 AJ4312
DQ834030.1 gg_id:167691 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ834
CP000879.1 gg_id:256420 Petrotoga mobilis str. SJ95 CP000
EU999020.1 gg_id:321922 Predominance Methanolobus and Methanoculleus spp. Archaeal Saline Gas Field Fo EU999
GQ385331.1 gg_id:575997 Petrotoga sp. str. AR80 GQ385
NR_029058.1 gg_id:590603 Petrotoga mexicana str. Met-12; DSM 14811; CIP 107371 NR_02
EU878330.1 gg_id:550151 Investigation factors influencing production large-scale municipal biogas plant therm EU878
EU639044.1 gg_id:325788 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EU639299.1 gg_id:338480 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EU639355.1 gg_id:316749 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
AB274516.1 gg_id:210440 packed-bed reactor clone CFB-27 AB274
EU638581.1 gg_id:326331 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU638
EU639024.1 gg_id:337040 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
EU639041.1 gg_id:315077 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
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EU639209.1 gg_id:338914 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
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EU639281.1 gg_id:336042 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU639
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CP000716.1 gg_id:243559 Thermosipho melanesiensis str. BI429 CP000
AJ272022.2 gg_id:40837 Thermosipho geolei str. DSM 13256 AJ2720
AF491334.1 gg_id:83498 Thermosipho ferriphilus str. GB21 AF4913
AJ577471.1 gg_id:90392 Thermosipho atlanticus str. DV1140 AJ5774
AB024932.1 gg_id:1231 Thermosipho japonicus str. IHB1 AB024

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58.0	43.8	54.7	38.1	72.8	39.2	32.3	58.5	32.7	23.2	35.1
43.4	176.1	313.1	305.4	179.0	288.5	322.4	398.4	156.4	136.6	208.9
63.0	672.4	589.0	677.6	1246.4	780.7	1183.3	536.2	256.1	117.7	390.4
785.7	2739.1	3077.1	2832.2	2246.4	2441.1	3144.2	3278.2	2094.5	1734.8	2716.0
171.7	1674.7	1791.3	1790.1	2149.5	1737.2	2043.6	2341.5	1127.9	790.0	2065.8
148.2	1958.7	1564.9	1918.8	1216.6	1578.4	2197.9	1699.6	656.9	423.8	1446.1
1047.7	2543.3	2315.3	3510.5	2271.3	1973.4	4597.0	2083.4	3147.9	2644.2	2439.4
6847.7	4538.8	3827.3	6266.9	4160.1	4362.7	5978.1	4253.2	6944.3	4231.7	6180.2
329.9	930.1	846.9	758.8	1020.2	857.8	884.2	829.3	656.9	413.0	507.4
1375.5	3844.4	3073.9	3587.6	2943.2	3422.2	3343.1	2951.2	3939.0	2872.9	3738.8
76.2	275.9	278.8	264.1	276.5	263.3	371.1	343.8	30.6	207.7	276.8
124.1	1136.8	1163.5	1280.9	1153.6	1433.4	1496.4	1684.4	805.5	271.3	1109.6
6606.2	6384.2	6677.5	6249.9	5125.2	5715.9	6564.3	5704.4	6992.6	3938.4	5444.9
36.2	40.1	53.0	59.0	39.2	31.8	39.2	43.5	35.0	29.9	35.9
48.2	435.8	224.2	203.8	186.5	232.1	238.5	277.7	127.8	103.1	192.4
5896.9	5386.1	5941.3	7269.6	6990.4	5566.0	7212.0	6074.8	5765.0	4975.5	5948.8
1762.6	5814.1	6462.2	6924.7	5478.5	5758.0	6164.0	6154.7	5116.8	4947.8	6919.7
53.5	76.9	226.5	91.3	99.0	98.1	123.6	103.8	53.2	30.6	58.5
2093.7	2018.9	2237.7	2414.0	2626.1	2216.3	2574.3	2648.4	1852.0	2399.4	3151.5
44.5	307.6	344.3	303.8	289.4	264.5	312.2	379.7	212.9	142.9	217.4
1029.1	1545.5	1399.4	1456.0	1443.0	1437.1	1594.0	2094.3	1303.0	1545.3	1511.8
631.9	902.3	763.0	964.9	1010.5	807.7	1189.3	846.5	717.6	438.9	971.0
3425.7	3245.9	3562.1	3309.3	3181.9	3093.7	3722.9	3363.1	5761.9	1113.6	4225.5
8709.4	7972.6	8678.3	8009.0	7816.0	7460.3	8445.1	7571.3	12703.2	6575.4	9915.5
743.2	2074.7	2892.1	3264.2	2466.9	2615.3	2607.0	2637.6	2152.7	2354.0	2045.9
75.4	2074.7	2778.9	3523.2	2470.4	2606.5	2587.2	2598.0	1816.7	2033.6	2022.8
724.3	1192.9	2010.9	2481.1	1838.8	1988.9	1838.7	2083.5	1904.3	2321.9	1843.2
304.8	2038.4	2488.4	3192.3	2346.8	2387.9	2444.2	2281.7	1844.7	1902.5	1972.4
7251.5	3515.4	4547.3	3864.5	3448.8	3112.6	4037.3	3877.1	6068.1	2016.4	3502.4
542.1	2461.5	2916.7	2712.2	2372.5	2456.2	2788.0	2857.3	2058.8	1311.8	2558.7
7482.3	6097.5	6011.6	5761.1	5359.7	5407.7	5809.0	5340.6	10534.6	3746.2	8033.3
23720.6	12398.1	12210.5	12140.8	11393.1	10727.7	12736.8	10382.2	19729.8	10208.7	16098.1
3414.6	3723.5	3794.4	3276.3	3155.1	3284.1	3556.2	3282.0	6787.9	1134.9	4246.4
2941.3	4262.3	4899.3	4818.8	4254.9	4219.6	4784.6	4405.2	5725.9	2705.2	5519.6
71.1	871.2	968.6	969.3	1279.0	851.9	1396.6	1334.5	292.7	416.3	900.5
68.3	130.1	138.5	84.7	74.3	103.6	115.5	249.8	71.6	85.6	215.1
108.4	3734.0	4100.2	3970.5	5887.2	4617.8	7422.8	3857.9	1539.7	1010.6	3248.7
1835.4	3082.8	3732.7	4239.8	3722.1	3043.0	3860.5	2882.7	2188.7	596.2	1600.8
117.4	2614.7	2674.4	2780.5	2656.7	2747.2	3854.3	2781.5	1466.2	818.4	1949.7
65.5	386.8	416.1	358.4	489.6	369.7	541.1	532.1	186.6	224.2	422.7

21.5	34.5	52.3
41.7	50.1	44.1
224.6	457.5	392.2
385.5	885.6	1975.8
2151.7	3193.4	2854.8
1747.5	2150.5	1545.5
1136.0	1400.5	2139.9
1873.0	2319.7	2507.1
4115.0	5090.8	5230.0
539.1	1491.4	905.1
2905.5	3222.2	5103.9
172.2	378.8	2822.5
1174.8	1609.2	3216.3
5539.4	6250.0	6591.1
36.2	36.1	34.2
241.8	419.1	377.6
6398.5	6544.9	6373.5
6096.0	5884.7	6542.4
69.9	106.1	124.5
2784.6	2446.6	2835.0
249.3	325.0	310.2
1654.7	1892.8	1671.1
938.5	667.5	939.3
2785.7	4091.8	3751.6
7265.8	8994.3	8107.8
1945.4	3075.0	3113.8
1844.4	2593.1	3184.0
1426.8	1840.9	2565.9
1787.4	2430.3	3166.2
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74.9	135.1	208.4
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2149.4	2834.7	3915.1
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U22664.1 gg_id:1233 "Thermotoga subterranea" U2266
AB039768.1 gg_id:41353 Thermotoga neapolitana str. DSM 4359 AB039
AJ401020.1 gg_id:32773 Thermotoga neapolitana str. LA10 AJ401
AAWB01000011.1 gg_id:187003 Thermotoga petrophila str. RKU-1 AAWB
EU924246.1 gg_id:303956 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8 EU924
AJ401017.1 gg_id:72408 Thermotoga maritima str. SL7 AJ401
AY526506.1 gg_id:136778 Microbial thermophilic anaerobic sludge methanol-fed lab scale bioreactor clone H8 AY526
AJ401021.1 gg_id:24284 Thermotoga maritima str. FJSS3-B.1 AJ401
AJ401016.1 gg_id:35101 Thermotoga neapolitana str. NES AJ401
AJ431248.1 gg_id:79590 Thermotogales str. BHI80-139 AJ431
FN429790.1 gg_id:588200 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN429
DQ676372.1 gg_id:226370 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
DQ676349.1 gg_id:225336 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AF268992.1 gg_id:32172 obtained sequencing batch reactor and sequenced Paul Burrell clone SBRH58 AF268
GQ402738.1 gg_id:592512 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
CU921813.1 gg_id:556480 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
EF530679.1 gg_id:225631 Extremely acidic pendulous biofilms Frasassi cave system Italy microbial biofilm clone EF5306
AF507714.1 gg_id:65675 forest soil clone S1198 AF507
AY261809.1 gg_id:82807 UASB reactor granular sludge clone PD-UASB-12 AY261
AJ387898.1 gg_id:50582 TCB-dechlorinating consortium? clone C1-3 AJ3878
AJ009448.1 gg_id:10538 chlorobenzene-degrading consortium clone SJA-4 AJ0094
U81641.2 gg_id:10536 anaerobic sludge clone vadinBA07 U8164
EU038004.1 gg_id:238619 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and c EU038
EU038003.1 gg_id:236698 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and c EU038
DQ499222.1 gg_id:159620 acidic cave snottite biofilm clone DSJB94 DQ499
EF020241.1 gg_id:212070 aspen rhizosphere clone Elev_16S_1745 EF0202
DQ811945.1 gg_id:164866 mangrove soil clone MSB-4E11 DQ811
GQ101240.1 gg_id:417532 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw49 GQ101
GQ402806.1 gg_id:513096 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY661981.1 gg_id:137499 uranium-contaminated groundwater clone 300I-B02 AY661
DQ404590.1 gg_id:156555 contaminated sediment clone 656034 DQ404
GU208307.1 gg_id:586450 Study on Sediment Dongping Lake sediment clone Ftt4-19 GU208
DQ499213.1 gg_id:159549 acidic cave snottite biofilm clone DSJB30 DQ499
EU037998.1 gg_id:247518 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and c EU037
EF516771.1 gg_id:226009 grassland soil clone FCPN632 EF5167
EU135363.1 gg_id:242950 tallgrass prarie soil clone FFCH1293 EU135
AY043958.1 gg_id:61307 forest soil clone NMW3.210WL AY043
GQ402802.1 gg_id:576700 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EU386052.1 gg_id:259809 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386

228.1	1969.5	1986.3	2004.1	2923.2	2324.1	2625.6	2012.3	2657.1	2091.5	2245.4
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35.1	31.5	43.8	46.6	39.6	33.7	44.7	42.4	23.8	18.3	26.7
4413.6	2952.0	3183.7	3786.2	4308.0	3304.6	4658.0	3320.8	2311.0	3428.5	2716.4
4382.5	2542.9	3167.9	3505.6	3683.7	2921.3	4677.4	2992.8	2473.9	2677.4	2764.7
2280.5	2887.7	3585.9	3982.7	4543.4	3449.2	5439.9	4182.9	2124.0	3096.6	2861.0
66.2	114.9	103.4	81.5	133.8	105.6	160.3	75.7	59.6	40.6	45.3
10152.5	4311.9	4578.4	5080.6	5691.9	4501.6	5715.6	4608.2	3565.4	4003.6	4433.2
38.0	69.9	89.4	88.7	72.8	61.1	83.7	69.9	79.8	41.0	60.8
20975.8	7268.0	7078.3	7622.1	8777.7	6926.5	8703.6	6939.8	8055.8	7627.6	10187.8
4410.8	2895.7	3341.3	3726.3	4005.7	3153.6	5296.3	3671.3	2285.8	3232.8	2698.7
58.8	362.6	411.7	563.6	317.9	326.9	350.7	554.4	176.3	71.7	213.8
2567.8	2970.8	3894.0	4496.0	4266.2	3282.3	5130.5	4429.4	9450.3	1415.5	4020.2
3146.6	3919.6	4211.5	3394.8	3326.8	4190.8	3789.8	4262.2	3297.8	2976.4	4328.1
214.2	1571.2	1659.6	1401.4	1334.8	1816.0	1779.0	2017.6	1281.9	803.4	1486.5
54.4	240.7	740.3	228.6	241.3	122.5	90.5	99.5	96.2	56.4	75.1
131.5	3575.8	2533.9	2145.7	2883.1	3960.8	5239.2	3886.0	1274.9	860.9	2253.6
2565.7	7016.7	5906.6	6717.4	5482.0	6665.6	7914.4	6595.7	4766.2	4100.6	7051.7
1220.0	7279.1	6581.0	6156.4	4270.6	7290.5	6044.9	7602.1	5341.8	4275.1	6818.2
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251.2	3607.8	3271.4	1643.0	1509.7	4256.2	2107.0	4580.8	2442.1	934.8	2569.2
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33340.1	10611.4	9241.4	10543.9	9762.5	10216.5	12542.9	9719.3	13727.5	11321.9	13629.9
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1383.0	8617.9	7427.2	8473.1	7715.5	8869.1	8558.6	8685.2	7545.0	5821.9	8958.5
255.9	5797.5	4858.6	5169.9	5912.5	5592.7	5964.8	6013.7	5804.8	3332.7	4047.2
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2468.3	7740.4	5370.9	4999.3	6467.0	7518.9	4967.7	6371.1	5711.0	3341.7	5106.6
626.5	6582.7	5484.9	5882.0	6999.1	6873.6	7247.0	7163.4	4998.4	3867.8	5494.5
119.1	2208.1	1711.5	1441.7	1913.8	2542.9	2986.7	2851.0	1237.9	1059.0	1641.4
1440.8	1280.3	1272.0	945.8	862.3	1643.1	969.3	1675.0	657.8	780.6	1028.5
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123.3	773.6	744.9	419.8	583.4	920.9	919.0	875.2	373.3	245.3	591.7
359.1	4082.7	3536.9	3560.9	5436.2	4737.6	4068.5	4141.2	2784.7	2479.5	3061.8
31.9	304.7	360.1	188.5	162.5	708.9	208.2	456.1	53.4	126.1	160.6
1924.7	4811.0	4732.7	4358.1	3706.4	5280.6	4275.6	5188.0	4915.8	6776.9	4786.6
80.0	3419.5	1847.7	1224.3	1378.8	3522.7	1036.9	2931.6	1405.9	633.7	1561.2
373.6	5933.0	4898.7	4823.0	4259.2	5655.6	6158.2	5398.3	3976.1	1762.0	4300.2
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3551.6	3326.3	4974.9
73.9	73.7	120.9
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6936.6	7793.8	8617.9
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AB257652.1 gg_id:260396 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB257
AY945884.1 gg_id:148869 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal AY945
FJ466109.1 gg_id:571249 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4661
FJ542881.1 gg_id:528972 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
GU172187.1 gg_id:555087 Microbial Eucalyptus plantation soil clone DSM-R15 GU172
DQ395404.1 gg_id:154700 deep-sea octacoral clone ctg_BRRAA28 DQ395
EU385703.1 gg_id:272615 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
FJ478536.1 gg_id:576754 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EU332802.1 gg_id:366100 FACS assist identification TFO present aerobic enhanced biological phosphorus remo EU332
DQ811946.1 gg_id:162674 mangrove soil clone MSB-5E11 DQ811
EU038006.1 gg_id:239453 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc EU038
X97099.1 gg_id:10543 peat bog clone TM6 X97099
DQ070831.1 gg_id:146798 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
DQ394954.1 gg_id:153947 harbor sediment clone VHS-B3-63 DQ394
EF019831.1 gg_id:212739 aspen rhizosphere clone Elev_16S_1183 EF0198
DQ404638.1 gg_id:152373 contaminated sediment clone 654967 DQ404
FM209162.1 gg_id:546081 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd FM209
EU135398.1 gg_id:257656 tallgrass prarie soil clone FFCH4275 EU135
AM935187.1 gg_id:557742 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY345503.1 gg_id:91512 Lake Waiau sediment clone W4-B20 AY3455
AY571850.1 gg_id:107654 hydrocarbon-contaminated soil clone 342B AY5718
EU861950.1 gg_id:316001 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
GQ396865.1 gg_id:532665 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts GQ396
AF507687.1 gg_id:111978 forest soil clone C129 AF5076
EU135387.1 gg_id:248392 tallgrass prarie soil clone FFCH16289 EU135
EU104333.1 gg_id:321742 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
DQ906081.1 gg_id:223958 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-G10 DQ906
AM991156.1 gg_id:279572 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
GU444063.1 gg_id:520918 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
AF507688.1 gg_id:65695 forest soil clone C1105 AF5076
FJ542918.1 gg_id:515209 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
EU703288.1 gg_id:566066 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF688335.1 gg_id:238281 soil clone F1-127 EF6883
GU444078.1 gg_id:518809 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
DQ640696.1 gg_id:234110 full-scale EBPR sludge clone Skagenf80 DQ640
DQ451478.1 gg_id:156885 forest soil clone FAC39 DQ451
DQ404603.1 gg_id:153216 contaminated sediment clone 656047 DQ404
AJ318136.1 gg_id:26128 Waste-gas biofilter clone BIgi18 AJ3181
DQ404740.1 gg_id:154332 contaminated sediment clone 655080 DQ404
EU381500.1 gg_id:275085 Rumen eubacterial implicates Bacteroidetes major particulate phylum rumen liquid EU381
EU381884.1 gg_id:258263 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381

237.5	6571.5	5371.8	5120.1	5114.0	6831.9	6015.4	7125.5	4214.3	3305.4	5929.3
45.2	1393.1	480.9	254.4	242.9	1063.4	344.1	771.0	268.7	187.4	375.7
1184.5	2629.2	1946.4	2087.7	2589.9	3445.4	2301.5	2893.4	2266.8	1611.8	1962.0
16855.9	9540.6	8525.8	8155.3	7980.2	9818.3	9347.7	9442.1	9852.2	7578.3	10055.7
2430.5	5336.5	4635.5	4259.8	3543.9	5611.7	4275.9	5055.0	4608.3	2753.7	5449.9
6650.6	7791.1	6789.4	7202.1	6639.0	7693.7	6873.6	7395.3	6011.7	3289.9	6895.7
339.8	5391.3	5660.5	5407.0	4848.8	4890.9	4323.5	5574.1	4894.2	1340.5	3838.1
759.4	6257.5	4613.1	4790.0	5039.9	6225.7	5089.8	6265.7	3360.7	2518.7	5140.4
14624.4	6885.2	6509.6	6309.3	5988.4	7437.4	6266.6	8273.7	6782.3	6067.8	7787.3
426.6	2920.4	2814.9	2049.6	3032.6	3436.6	3350.8	5151.7	1607.5	704.5	2169.9
3071.2	4258.4	4259.8	4437.0	2875.3	5517.8	2758.0	4847.9	3776.2	2012.5	3896.3
94.9	2800.6	2207.8	1671.0	2209.5	4726.4	1882.4	4611.1	1695.9	2424.5	2634.3
16457.5	10931.8	11321.1	11753.2	11317.2	11114.7	14032.1	10451.6	12117.3	8939.3	14033.1
57.4	3939.1	3368.1	3526.5	2158.4	3666.4	2996.2	5446.5	3097.3	2559.7	2875.0
5741.7	5453.5	4615.2	3974.0	4294.4	4775.1	5636.5	4418.1	6635.4	3539.8	3800.8
36.0	205.2	98.4	68.3	173.3	174.5	58.9	168.5	41.5	23.1	35.4
544.3	4628.1	3913.0	4278.5	4977.1	4460.5	5032.5	4150.9	1676.3	3679.1	3777.9
8409.9	7234.6	5248.8	6040.8	7470.4	6347.4	7346.1	6110.9	3141.0	2437.1	5328.5
9139.0	10340.1	7680.6	8384.0	10092.7	8933.0	10817.5	8021.4	6202.7	5724.5	9082.4
45.7	284.1	286.2	279.0	446.9	290.6	365.1	348.5	45.8	70.9	160.2
67.6	190.7	193.2	231.7	359.4	278.5	161.5	184.6	72.2	48.2	147.4
628.2	3874.3	2719.9	3264.9	3692.6	3269.2	3439.4	3294.8	1668.9	859.6	2461.6
204.0	3482.8	3072.5	3449.7	3549.6	3992.9	4319.2	4465.3	2795.8	1946.5	3108.9
97.3	1471.9	738.3	795.3	1511.9	1135.0	1714.2	991.5	188.0	219.0	513.1
3900.8	4215.7	2103.2	2276.6	3036.9	3242.1	3651.1	2527.7	1704.5	1160.7	2094.0
1462.2	4064.0	3592.3	4292.8	4227.6	3746.5	5364.6	3704.1	1837.1	2775.6	2779.1
65.6	844.7	604.2	491.3	453.0	1247.9	1173.9	387.6	116.7	114.7	342.8
573.2	5172.9	4022.5	3624.9	5444.0	4294.0	4405.1	3497.8	907.9	1053.0	2346.7
56.9	2882.0	1552.3	1423.3	2453.5	3650.2	1322.0	1273.5	318.0	517.9	1172.9
39.2	193.7	274.5	219.1	197.5	488.2	175.2	176.9	134.7	62.9	155.5
142.1	6510.3	3417.9	3679.0	4572.9	5140.9	6464.5	4417.9	1545.6	1603.0	3269.8
1253.7	5315.3	3665.5	4620.8	4706.9	5886.2	4809.7	4558.5	4507.5	2905.1	5498.1
884.3	5431.0	3450.0	2973.9	3758.2	4131.0	3188.2	2773.4	2148.7	2367.1	2910.9
1126.9	6545.0	5262.6	5615.0	4727.7	5276.9	5450.0	4724.6	8678.5	7262.1	6728.4
3577.6	5172.1	3946.4	3353.3	4304.2	4160.1	5118.6	3805.4	4857.8	2894.8	3395.0
38.5	72.9	107.0	107.8	69.2	65.8	64.1	171.8	57.8	45.3	65.5
974.5	2225.2	2042.9	2077.4	1997.9	1991.1	2611.1	2191.0	995.0	651.8	1493.7
45.1	909.2	962.3	976.6	644.4	766.5	874.0	570.3	206.4	128.3	470.9
855.4	1968.2	2281.8	1957.8	1765.6	2073.0	2632.1	2416.6	1435.3	1434.9	1456.2
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110.8	1773.9	1285.0	2046.3	1391.9	1297.3	998.9	1496.5	751.4	757.2	735.0

7472.7	6671.8	9733.1
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7330.9	8580.7	10687.6
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6476.3	6673.1	9191.9
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4169.1	4523.2	8562.4
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8283.9	8497.3	9199.2
127.6	279.1	636.7
133.3	173.9	283.0
1648.8	2533.5	3523.3
3613.8	3690.0	3558.5
757.9	750.4	1056.6
2400.5	2836.9	3538.3
3281.4	3763.4	4235.5
686.4	582.0	942.9
3341.3	3566.9	3079.1
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136.9	346.8	401.1
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4421.4	5513.7	4845.2
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AF385506.1 gg_id:39443 tongue dorsa clone CW040 AF3855
EU475226.1 gg_id:290144 bonobo feces clone BNO_aaa02b03 EU4752
FJ881207.1 gg_id:397321 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8812
DQ815554.1 gg_id:169081 mouse cecum clone aab42f07 DQ815
AM932658.1 gg_id:573677 microbiota Toll-like receptor 2 deficient mice exhibits lineage specific modifications AM932
DQ815839.1 gg_id:169901 mouse cecum clone aab23a06 DQ815
AF432141.1 gg_id:17020 oral clone FR058 AF4321
EU431764.1 gg_id:575675 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
EU431761.1 gg_id:552692 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
DQ309369.1 gg_id:149506 high salinity effluent treatment plant clone HKT135 DQ309
GQ035442.1 gg_id:450572 Topographical and Temporal Human Skin Microbiome skin back clone nbu372b12c1 GQ035
AJ318200.1 gg_id:34261 Waste-gas biofilter clone BIxi1 AJ3182
AY005446.1 gg_id:72347 oral cavity clone BE109 AY0054
GQ057266.1 gg_id:377444 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ057
AF507686.1 gg_id:65697 arid soil clone C026 AF5076
DQ378246.1 gg_id:151868 oil-polluted soil clone M26_Pitesti DQ378
AJ583163.1 gg_id:95008 radioactive site ground water clone S15B-MN121 AJ5831
GQ009422.1 gg_id:500243 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU431832.1 gg_id:564738 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
AF513102.1 gg_id:65419 activated sludge foam clone 71 AF5131
DQ640707.1 gg_id:235238 full-scale EBPR sludge clone Skagenf9 DQ640
DQ521555.1 gg_id:197766 Antarctic lake ice cover clone ANTLV9_C10 DQ521
GU451214.1 gg_id:519665 adult gut male clone A6H6M10 GU451
EU244101.1 gg_id:360054 16SrRNA probes river Leine sediment clone sl1394 EU2441
GQ009543.1 gg_id:500117 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AY005448.1 gg_id:21239 oral cavity clone BS003 AY0054
CU919840.1 gg_id:555590 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9198
GQ009402.1 gg_id:500262 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AY349415.1 gg_id:93147 human oral cavity clone HD027 AY3494
AB200304.1 gg_id:113976 lab-scale sequencing batch reactor clone UTFS-OF09-d22-29 AB2003
EU104285.1 gg_id:338215 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1042
GQ113945.1 gg_id:449146 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ113
GQ115439.1 gg_id:434423 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685f06 GQ115
AY571500.1 gg_id:114578 termite gut clone RsaM67 AY5715
DQ666092.1 gg_id:165179 human vaginal epithelium clone Y2 DQ666
FJ470446.1 gg_id:537729 Chinese human cavities healthy oral cavity clone A_D_01_89 FJ4704
EU979068.1 gg_id:340964 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU9790
CU917574.1 gg_id:569517 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
CU924524.1 gg_id:571106 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9245
EU861856.1 gg_id:341554 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
AF352537.1 gg_id:16693 hot spring clone BH81 AF3525

123.5	1528.6	1332.1	2547.6	789.3	633.5	1240.1	892.6	301.8	173.4	556.5
359.7	5723.5	6040.7	6217.9	6203.2	5857.9	5841.8	6302.5	5941.6	4564.7	5261.9
3772.6	4301.8	4200.7	5008.2	2921.4	4236.5	4694.5	3811.2	3715.2	3180.7	4809.3
55.9	56.3	193.2	136.9	31.6	50.9	32.6	47.3	21.5	19.7	27.9
46.8	683.5	650.4	1535.7	94.1	249.9	375.7	308.8	52.8	36.0	157.7
44.8	33.0	32.5	32.8	32.8	30.2	33.8	26.7	21.4	28.1	22.5
29.2	1108.8	983.8	1079.9	649.4	938.4	1024.8	796.6	169.7	181.6	665.1
14980.4	4961.3	5490.1	6005.0	4353.8	4379.9	4362.4	4706.6	5706.7	4034.7	5757.0
3456.3	5437.8	4689.1	6105.9	4783.2	4602.8	5413.4	4688.2	2532.2	4969.8	4741.4
1098.4	5575.7	5007.5	4955.6	5876.1	5181.4	7474.7	5224.7	2122.4	6131.5	5060.3
13167.4	8576.5	8519.8	10028.2	10017.6	8146.5	8776.7	8894.1	10188.0	4802.7	11438.1
31.1	761.1	801.4	991.7	999.1	629.0	877.6	833.8	69.4	94.0	383.7
36.1	331.9	198.7	155.4	102.3	209.3	237.8	149.8	37.3	27.4	98.7
1135.8	3519.9	3811.5	4087.7	3654.2	3239.5	3838.9	3482.0	1819.9	1757.4	3620.2
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18657.7	3115.8	2608.7	3084.6	3859.3	3503.0	3372.1	3124.8	2852.4	3158.9	2220.1
150.7	4231.6	4952.9	5354.6	3950.7	4418.5	4404.7	5245.1	2356.8	2389.0	3997.1
100.5	993.7	784.4	733.4	396.6	711.7	355.3	586.2	153.5	149.8	345.0
82.7	825.1	769.3	796.2	708.7	706.6	1080.2	880.4	192.9	164.1	486.3
118.4	3412.9	2540.1	2996.0	3090.7	3011.0	3715.2	2727.2	1737.4	1417.4	2447.3
1760.9	4430.7	4371.2	4999.7	4109.9	4270.5	3997.6	3874.3	3164.0	3174.6	4079.4
1242.9	4504.5	4415.0	5578.8	4692.6	3310.5	4776.4	4886.7	3468.2	2504.2	3505.2
4983.6	7151.6	7046.7	8328.8	9231.3	8411.9	8152.0	7232.7	6514.1	8410.0	8114.7
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637.9	4574.2	3418.1	4689.0	4257.6	3946.7	4317.9	4447.4	3384.9	1198.9	2736.0
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70.7	1840.6	1974.7	2521.1	1318.3	1662.3	1938.2	2215.4	338.8	314.8	1116.5
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EU043224.1 gg_id:239967 uncultivated soil clone BJ-169 EU043
EU386046.1 gg_id:265422 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
AF015925.1 gg_id:13724 hot spring clone OctSpA1-106 AF015
AF419683.1 gg_id:112352 Guaymas Basin hydrothermal sediment clone CS_B017 AF419
EU385715.1 gg_id:267027 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
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GQ340316.1 gg_id:550625 Prokaryotic Marathonas Reservoir Greece water column clone K08-115-BAC GQ340
FJ466437.1 gg_id:536133 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
EF520638.1 gg_id:230312 structure lakes: what controls ? acid-impacted lake clone ADK-SGe02-31 EF5206
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EU419167.1 gg_id:274373 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
EU419166.1 gg_id:266894 Microbial and ecology selected andesitic hydrothermal acidic hydrothermally modifi EU419
FJ638587.1 gg_id:511517 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
AJ229235.1 gg_id:1561 Opitutus terrae str. PB90-1 AJ2292
X99391.1 gg_id:1558 Opitutus sp. str. VeCb1 X99391
X99392.1 gg_id:1559 Opitutus sp. str. VeSm13 X99392
AM162468.1 gg_id:153174 and situ identification acidic sphagnum peat bog clone B70 AM162
AY922067.1 gg_id:114313 farm soil clone AKYG804 AY922
FJ478682.1 gg_id:567922 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
FM866301.1 gg_id:357272 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-182 FM866
AY661974.1 gg_id:136998 uranium-contaminated groundwater clone 300G-H06 AY661
AM162467.1 gg_id:156120 and situ identification acidic sphagnum peat bog clone B36 AM162
EU800822.1 gg_id:350772 It's all ranking aquatic Delaware Bay NJ clone 2C229041 EU800
EF516172.1 gg_id:231447 grassland soil clone FCPT606 EF5161
AY297806.1 gg_id:89313 archaeological wood clone? pACH90 AY297
FJ769447.1 gg_id:553713 Changes Methanogenic Microbial After Sludge Pre-treatment full-scale municipal ana FJ7694
AB240503.1 gg_id:144089 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB240
GQ339177.1 gg_id:526112 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
AB369167.1 gg_id:237121 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
AJ575730.1 gg_id:96609 lake water clone SW59 AJ5757
GQ264061.1 gg_id:566392 Structure Simulated Level Waste Site simulated level waste site clone WC3_16 GQ264
AB369179.1 gg_id:245910 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
GQ502665.1 gg_id:542290 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9- GQ502
AY820718.1 gg_id:109053 drilling fluid clone CCSD_DF2030_B14 AY820
DQ833492.1 gg_id:167091 detected analyses depth sediment Guanting Reservoir clone 35-54 DQ833
AY587231.1 gg_id:106739 termite gut clone AY587

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59.4	5679.2	3699.0	3806.0	2337.4	4975.5	3694.1	4842.7	974.9	1394.6	4383.0
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9423.5	6805.3	7098.5	6714.9	6736.1	6478.0	7137.3	6542.5	8726.0	5196.5	9043.0
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63.6	113.6	92.7	104.2	121.8	100.5	48.0	104.3	60.2	16.1	52.3
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46.6	43.3	54.5	40.7	103.6	40.8	61.0	55.1	33.2	19.6	31.5
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7443.2	6095.9	6457.6	7355.4	7317.0	6999.4	8275.8	7581.2	6196.6	8924.7	7459.5
37498.0	14303.5	13644.2	15053.4	14926.8	13949.5	16311.0	12937.1	20821.0	17434.6	19593.5
415.0	6526.9	6737.3	6338.1	6640.6	6282.7	7427.0	6702.7	5418.2	4031.3	5347.3
211.1	3646.4	4979.2	5113.5	5352.4	4503.9	6293.3	5730.1	2325.2	1343.1	3990.7
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FJ169213.1 gg_id:327499 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1692
FJ444768.1 gg_id:587631 Cotton Rhizosphere cotton rhizosphere clone 4y-121 FJ4447
AJ633978.1 gg_id:114788 host's accessory nidamental gland clone I1ANG45 AJ6339
EU015115.1 gg_id:253831 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
AB286360.1 gg_id:216828 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AB062814.1 gg_id:18774 termite gut homogenate clone BCf3-05 AB0628
EU135529.1 gg_id:246267 tallgrass prarie soil clone FFCH9358 EU135
AY622244.1 gg_id:107299 subsurface soil clone B-I12 AY622
DQ097276.1 gg_id:160664 Encapsulating and growing '' Majority mucus coral Fungia granulosa clone RS.Sph.0C DQ097
AB299563.1 gg_id:247779 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
DQ539046.1 gg_id:161645 Puniceibacter vermicola str. IMCC1545 DQ539
AB299565.1 gg_id:241161 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
GQ502667.1 gg_id:578464 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf9- GQ502
EU803670.1 gg_id:338096 It's all ranking aquatic Lake Gatun clone 5C231275 EU803
DQ302114.1 gg_id:153206 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
FM242275.1 gg_id:341545 sequences sediment clone 13bis T0h-oil FM242
GQ347889.1 gg_id:585626 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
U81738.2 gg_id:1556 anaerobic digestor clone vadinHA64 U81738
AY695840.1 gg_id:105129 Opitutus sp. str. SA-9 AY6958
FM242391.1 gg_id:310512 sequences sediment clone 89 T12d-oil FM242
EF574171.1 gg_id:235121 site S25 near Coco's Island marine clone S25_515 EF5741
AJ240909.1 gg_id:74031 marine clone CHAB-II-49 AJ2409
EU617885.1 gg_id:332206 Seasonal variation microbial Yel Sea sediment clone D13S-153 EU617
FJ202864.1 gg_id:353683 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2028
AB198611.1 gg_id:135899 termite gut fluid and protists fraction clone RsC01-040 AB198
EU283474.1 gg_id:278788 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A210 EU2834
AB299566.1 gg_id:256775 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
AB073978.1 gg_id:41135 Fucophilus fucoidanolyticus str. SI-1234 AB073
EU328081.1 gg_id:278462 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU328
FJ745063.1 gg_id:545467 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7450
GQ984310.1 gg_id:588321 surface water Northern Bering Sea clone DBS1a9 GQ984
AB192188.1 gg_id:143442 termite gut homogenate clone RsTz-69 AB192
FJ516822.1 gg_id:513750 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm FJ5168
AF075271.2 gg_id:9675 Alterococcus agarolyticus str. ADT3; CCRC17102 AF075
FJ717327.1 gg_id:535151 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
FJ717277.1 gg_id:511489 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FJ717325.1 gg_id:510475 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
AY114312.1 gg_id:72268 anoxic marine sediment clone LD1-PA15 AY1143
AB189371.1 gg_id:114335 cold seep sediment clone JT75-134 AB189
AF449255.1 gg_id:61856 vent worm clone R76-B128 AF449

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620.7	3453.7	4572.6	4597.5	3493.8	3999.5	3836.0	4964.3	2892.6	1354.7	5618.8
916.8	4159.8	5965.5	5834.8	4131.8	5405.2	5124.6	7187.9	5211.9	4620.9	5668.1
48.2	344.9	443.2	490.6	311.5	359.1	492.6	542.4	203.9	72.4	291.4
25855.7	9261.2	9091.7	9886.1	10058.2	8581.5	10705.1	8997.2	11421.4	8940.7	11788.5
413.6	4410.3	5605.7	5718.0	6428.4	4719.2	7525.3	5581.4	2944.5	708.0	3911.0
39.0	50.2	67.6	53.9	36.1	41.4	49.2	123.9	45.5	14.1	64.7
40.1	400.0	561.0	570.0	483.8	492.9	473.4	583.9	420.6	121.6	321.8
11032.9	7169.2	7849.9	8231.1	8334.4	6973.4	8669.7	7469.8	8325.2	4879.8	9148.0
29.7	192.5	491.6	613.7	466.8	487.4	434.9	563.0	513.7	25.6	398.4
901.4	2782.1	2917.0	3016.7	2484.3	2487.6	3279.3	3613.1	1940.7	2394.2	2205.9
370.4	1646.0	1451.6	1303.5	1071.3	1469.1	1027.8	1240.1	947.1	687.5	1007.6
1091.7	3769.3	3680.4	4724.9	4114.6	4493.0	4940.3	4365.0	3391.2	5056.2	4246.7
4458.4	4414.2	4573.2	4842.9	4648.4	4396.4	5538.6	4898.2	5231.5	2917.3	5012.8
72.1	1073.8	1038.2	847.2	750.6	921.1	1197.0	1144.2	552.5	220.6	564.8
34.8	278.6	382.1	222.2	124.5	232.3	98.8	168.0	198.1	89.7	218.7
115.1	1376.2	2111.6	2389.2	2396.4	1690.7	2351.7	1983.9	780.6	423.1	816.6
714.5	4104.9	4331.5	5425.7	4314.6	3684.1	4437.1	3653.5	4115.7	1594.5	3201.8
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59.0	377.9	375.6	532.0	50.4	320.6	424.0	429.2	121.3	35.6	310.5
487.4	4403.2	4567.9	3721.2	3886.1	4409.1	5462.6	4269.6	4976.1	3716.0	2770.2
2089.0	2633.7	2266.2	2508.3	1637.4	2718.2	2807.3	2532.4	2879.1	1480.8	3186.2
35.9	1459.0	1466.8	1527.0	743.8	1031.1	895.1	1261.3	319.2	98.1	877.5
9192.1	11737.6	11029.6	12169.7	12065.9	11028.6	13256.6	10788.1	12753.0	8375.8	13335.5
36.3	31.7	33.2	24.5	48.3	28.8	33.2	28.8	26.3	28.6	24.6
104.2	1642.9	1037.8	1101.3	1296.8	1265.9	1824.2	1243.4	1252.1	613.0	1195.3
6031.7	4924.9	5557.3	4546.3	5408.5	5012.6	6500.2	4750.9	5251.5	5621.9	4023.7
9847.5	6691.1	7050.0	7401.3	6489.7	6024.7	9205.6	8384.3	4575.1	4907.8	5006.2
58.3	157.5	169.5	137.7	174.8	517.2	164.9	161.9	72.8	29.1	113.9
814.5	3032.9	4749.8	4383.7	4590.0	4651.8	3887.4	5869.0	3060.8	1158.3	4359.8
54.4	152.6	232.5	249.5	245.8	156.5	166.8	272.2	590.3	112.3	141.2
2750.8	3608.6	4025.8	4516.7	4084.9	4633.8	4116.7	4626.2	5493.2	4994.1	4579.5
405.6	4664.0	5087.1	5152.5	5379.2	4745.2	5641.9	6048.7	3944.5	1635.6	5481.7
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62.7	523.6	692.1	720.5	753.3	584.5	971.6	850.9	466.7	77.8	761.6
5321.5	4537.6	6261.4	5361.7	5019.0	5753.4	5112.3	5506.9	5624.4	5203.0	4243.8
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2701.0	6913.1	7911.9	8689.5	6352.4	7328.7	6239.0	6694.0	7646.8	5462.6	5553.3
30.1	233.1	464.6	257.5	365.9	265.4	321.5	377.6	281.3	78.6	253.9
46.2	97.2	374.3	297.4	109.1	311.2	75.5	776.0	38.4	35.6	178.8
6870.2	5818.0	5607.1	6106.9	5458.4	6116.8	6805.5	5462.4	12308.9	8428.9	6879.9

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3875.0	3529.4	3806.9
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885.3	1036.3	1007.6
10103.0	10858.8	11730.4
30.1	39.4	37.2
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414.1	351.3	173.6
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5393.0	5725.5	6396.4
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732.1	524.8	727.9
4033.9	5885.0	5299.2
4327.9	7059.1	8795.3
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272.3	501.7	257.7
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FJ717308.1 gg_id:535176 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
AF449257.1 gg_id:61853 Riftia pachyptila's tube clone R76-B18 AF4492
EU287160.1 gg_id:240419 Pacific arctic surface sediment clone P13-67 EU287
FJ717273.1 gg_id:510216 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FJ717296.1 gg_id:510340 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FJ717311.1 gg_id:572386 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7173
FJ717270.1 gg_id:568860 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
FM165269.1 gg_id:564018 seep chitineous tube vestimentiferan tubeworm Lamellibrachia sp. cold seeps clone FM165
FJ717291.1 gg_id:548455 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7172
EU804364.1 gg_id:341372 It's all ranking aquatic 250 miles Panama City clone 6C232274 EU8043
DQ513023.1 gg_id:160321 Microbial life fluids ridge flank crustal fluid clone FS142-12B-02 DQ513
AY222315.1 gg_id:113883 host hindgut caecum clone Ver 1 AY2223
EF520620.1 gg_id:232855 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-31 EF5206
AJ575731.1 gg_id:97376 lake water clone NE06 AJ5757
EU703279.1 gg_id:554393 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
EF520637.1 gg_id:231528 structure lakes: what controls ? acid-impacted lake clone ADK-HDh02-03 EF5206
AY752089.1 gg_id:99083 lake water clone P38.12 AY752
FJ543046.1 gg_id:519253 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
FJ543079.1 gg_id:527379 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
AJ863245.1 gg_id:127649 poplar tree microcosm, bulk soil, flooded clone 21BSF50 AJ8632
EF516165.1 gg_id:221896 grassland soil clone FCPP479 EF5161
FJ612408.1 gg_id:535790 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.22 FJ6124
AY792308.1 gg_id:123679 Humic Lake clone CrystalBog1B6 AY7923
AB369162.1 gg_id:256945 Microbiological Assessment Circulation Mud Fluids During First Operation Drilling De AB369
AY388649.1 gg_id:108024 Chthoniobacter flavus AY3886
DQ450786.1 gg_id:160871 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated saturat DQ450
EF516096.1 gg_id:224503 grassland soil clone FCPT710 EF5160
EF515981.1 gg_id:220364 grassland soil clone FCPT465 EF5159
EF516968.1 gg_id:223379 grassland soil clone FCPS729 EF5169
FJ822655.1 gg_id:588551 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
AY960766.1 gg_id:115027 Detection and Cultivation Soil Verrucomicrobia Ellin503 AY9607
EU135441.1 gg_id:251499 tallgrass prarie soil clone FFCH5517 EU1354
AB486453.1 gg_id:588961 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSBARC AB4864
AB374368.1 gg_id:270180 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
GQ402701.1 gg_id:541789 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF516529.1 gg_id:221334 grassland soil clone FCPN729 EF5165
FJ822636.1 gg_id:535268 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
GQ397058.1 gg_id:538238 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
FM877557.1 gg_id:358664 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-321 FM877
AY960770.1 gg_id:114998 Detection and Cultivation Soil Verrucomicrobia Ellin507 AY9607

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6952.1	4477.2	4297.1	5292.5	5204.5	5118.8	6727.1	4767.5	3962.1	2457.2	5206.4
3000.0	3616.8	4701.3	3308.4	3178.8	3742.2	3485.2	3763.0	3398.3	1464.8	2774.4
28207.9	7017.2	9081.8	9615.1	6456.5	7491.3	7522.9	7483.4	11381.1	6409.2	9837.2
5685.3	5048.7	7218.5	6480.2	5691.7	6622.3	5926.8	5917.4	6906.6	6287.3	5085.0
531.2	2118.5	2625.3	2075.0	2094.9	2086.9	2072.4	1723.9	2397.1	1319.3	736.7
8128.3	7732.1	7861.1	7570.4	8233.9	8478.0	9214.5	7621.6	7444.8	7051.7	7621.1
2579.3	3404.4	4231.9	4130.6	4254.6	4060.2	5359.6	4150.3	2028.0	1411.8	2697.9
15818.5	11220.9	9189.8	11048.8	10246.9	10222.4	10660.5	8874.8	12310.2	9860.4	12471.1
66.0	402.0	438.2	424.7	272.8	737.0	546.9	598.6	276.0	130.2	134.6
1460.6	3258.0	3777.3	3271.3	3942.9	3770.4	4624.6	3563.0	3622.8	1373.5	1395.6
133.9	3908.9	4227.0	4528.6	4484.9	3982.8	5053.1	4382.5	2853.4	1199.6	3720.3
57.5	966.3	1632.7	1244.8	578.2	624.3	1224.7	1798.5	146.1	90.2	669.7
353.5	3883.6	3122.4	3054.4	5048.5	3940.2	4018.1	3811.7	2644.9	885.4	2118.6
5251.6	7418.5	7029.1	7740.5	8345.5	8072.5	9622.9	6339.5	7676.5	3394.1	6416.3
83.7	3725.4	3766.9	3533.0	5800.1	4136.5	5316.2	4014.9	2106.4	950.0	2513.1
38.0	55.4	168.8	269.3	21.4	572.2	188.6	599.2	69.4	104.8	319.7
1817.7	3187.6	3640.8	4211.7	4069.5	4463.8	3877.9	4289.5	3215.4	6301.1	3639.5
2581.5	6279.9	6696.6	7342.6	5995.2	6816.4	6984.2	6681.3	5005.6	5976.5	7921.2
81.5	777.8	697.2	521.9	667.2	501.9	1131.6	795.9	190.2	66.1	340.6
86.7	4912.4	4317.3	4397.9	5716.4	5223.2	6194.7	4786.3	2657.6	2222.3	4188.7
57.7	471.6	263.7	195.8	515.0	279.1	370.6	460.9	181.8	70.8	185.3
235.1	5131.9	4606.4	3617.2	6290.7	5225.8	5172.3	4357.1	3892.9	4012.3	3680.6
4890.1	10319.6	9700.0	10480.1	12353.2	9837.2	11958.0	9362.3	9744.4	5666.4	10108.0
42.9	1404.0	1589.6	1106.2	3551.2	1500.3	2702.8	1001.2	766.6	475.7	492.5
238.9	702.2	696.3	509.7	1883.6	859.1	1072.6	725.4	399.5	431.4	443.2
134.6	555.4	587.5	551.8	606.5	698.4	831.4	606.2	217.3	189.2	236.1
52.1	1373.7	1440.8	1248.0	3567.1	1681.8	2731.5	1842.1	834.6	272.4	645.2
43.9	457.5	586.2	474.6	1368.1	525.3	1373.5	663.9	356.8	207.7	176.1
263.3	4060.9	3969.7	3170.5	6477.9	4467.3	4682.4	3798.9	2776.6	1348.1	2046.3
39.4	167.1	357.7	246.7	447.7	271.5	343.0	163.3	103.5	62.8	98.7
59.6	3809.1	4141.6	3359.9	8527.7	3566.7	7135.4	3922.9	2448.3	1132.3	2358.3
63.2	1238.2	1152.8	969.8	1778.7	1521.5	1334.9	1592.2	790.1	188.1	494.2
39.7	2746.1	2848.6	2397.0	4997.7	3199.9	3847.2	2923.4	2260.8	548.0	1199.0
263.2	4753.1	4391.0	3844.9	6724.9	4572.9	5643.7	4017.0	3434.7	1574.4	2879.0
43.9	1859.7	2068.1	2196.9	5162.3	2018.6	3490.6	1680.2	682.5	1862.0	617.7
116.3	2242.8	2079.1	1811.9	2869.8	2307.6	3037.1	2232.3	1267.5	854.9	1452.5
4054.8	7528.7	7493.5	8123.8	7837.4	6941.9	6649.7	7095.0	6113.4	2146.8	9024.2
257.9	2804.8	2857.3	2985.3	4560.6	2923.6	3562.8	2909.7	2586.3	2164.6	2375.6
602.5	5176.8	5050.2	4932.5	8249.5	4792.1	7210.5	4760.7	4132.7	3010.2	4182.0

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4086.5	4638.0	6870.2
3149.7	4487.2	4964.9
6003.0	9506.2	8719.2
4643.2	6243.7	5906.8
1175.3	2231.4	3116.9
6445.6	7232.9	7306.7
2862.0	4352.6	6444.9
8725.3	9434.1	8982.3
431.4	660.8	1635.1
3201.8	3643.1	5563.1
3207.8	3902.7	6560.3
667.2	1130.0	1247.7
4036.7	3311.8	6414.2
6023.7	6552.8	8269.4
3812.7	3265.5	5996.6
546.1	524.1	1252.4
3738.1	4418.4	3871.2
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628.4	584.1	1273.5
4135.4	3600.1	6652.8
181.6	359.7	293.9
4357.0	3672.6	6200.8
9675.6	8648.9	11368.3
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488.5	905.7	679.1
494.6	946.6	597.8
1208.7	1015.0	1566.7
362.0	280.2	376.4
3762.8	3114.9	3380.5
118.0	272.3	176.4
3316.0	2649.4	4293.5
1094.7	1112.9	1195.6
2692.7	2209.0	2125.4
3717.4	3654.0	4111.5
1549.8	1765.4	1938.5
1798.2	1755.3	1741.4
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3130.5	3665.7	3225.5
4721.5	4726.0	5181.8

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AY960764.1 gg_id:114899 Detection and Cultivation Soil Verrucomicrobia Ellin501 AY960
EU131041.1 gg_id:236458 alkaline China coal mine soil clone SIP CM42 EU131
EU644180.1 gg_id:286072 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
EF018510.1 gg_id:214306 aspen rhizosphere clone Amb_16S_1148 EF0185
EF018524.1 gg_id:207125 aspen rhizosphere clone Amb_16S_784 EF0185
GQ264267.1 gg_id:511817 Structure Simulated Level Waste Site simulated level waste site clone WW1_b71 GQ264
FJ822653.1 gg_id:554650 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8226
DQ228393.1 gg_id:142335 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EU135556.1 gg_id:249859 tallgrass prarie soil clone FFCH4930 EU135
AY212589.1 gg_id:104784 water 10 m downstream manure clone 139ds10 AY212
FM253596.1 gg_id:325609 Rock gold mine unusually microbial biofilm clone D07-1 FM253
AY960769.1 gg_id:115085 Detection and Cultivation Soil Verrucomicrobia Ellin506 AY960
EU881176.1 gg_id:354713 Karst region natural restoration land soil clone KNR200711-119 EU881
AY395330.1 gg_id:100320 pasture soil clone EB1011 AY395
AY326520.1 gg_id:136989 Amazon soil clone 28-1 AY326
AY218772.1 gg_id:82424 penguin droppings sediments clone KD6-84 AY218
AY395325.1 gg_id:104976 pasture soil clone EB1006 AY395
EF018259.1 gg_id:213922 aspen rhizosphere clone Amb_16S_615 EF0182
EF516966.1 gg_id:223148 grassland soil clone FCPS574 EF5169
EF494340.1 gg_id:222682 Nunnock River granitic landscape clone NR.1.035 EF4943
EF516048.1 gg_id:222701 grassland soil clone FCPS405 EF5160
FJ592654.1 gg_id:557191 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
Y07576.1 gg_id:1624 grassland soil clone DA101 Y07576
DQ298012.1 gg_id:143982 Microbial hydrocarbon contaminated soil clone UA4 DQ298
EU881274.1 gg_id:335630 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EF018412.1 gg_id:213519 aspen rhizosphere clone Amb_16S_1028 EF0184
EU861826.1 gg_id:320598 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU861
EU881282.1 gg_id:320201 (long-term grazing and burned annual) Karst region serious disturbance field soil clor EU881
EF494343.1 gg_id:227202 Nunnock River granitic landscape clone NR.1.076 EF4943
DQ404689.1 gg_id:154629 contaminated sediment clone 655902 DQ404
FJ822650.1 gg_id:582528 and metagenomic Verrucomicrobia former agricultural grassland rhizosphere soil clor FJ8226
EF019688.1 gg_id:214739 aspen rhizosphere clone Elev_16S_849 EF0196
EF516045.1 gg_id:217322 grassland soil clone FCPN578 EF5160
DQ395984.1 gg_id:155782 deep-sea octacoral clone ctg_CGOGA62 DQ395
EF019129.1 gg_id:212017 aspen rhizosphere clone Amb_16S_1762 EF0191
EF516305.1 gg_id:225899 grassland soil clone FCPN716 EF5163
EU335341.1 gg_id:241683 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EF019121.1 gg_id:206632 aspen rhizosphere clone Amb_16S_1750 EF0191
FM877556.1 gg_id:359072 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-107 FM877
EF018766.1 gg_id:206493 aspen rhizosphere clone Amb_16S_1227 EF0187
EF516889.1 gg_id:220177 grassland soil clone FCPO660 EF5168

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32.2	1185.1	1279.7	977.5	3744.6	1276.9	2256.8	1247.3	653.7	236.3	373.2
81.9	4088.7	4184.8	3342.4	7887.8	3605.2	6829.8	3883.4	2480.1	1182.6	2326.0
39.2	2031.3	2052.0	1769.4	3952.7	2106.1	3489.3	2398.7	983.7	379.0	925.0
49.5	1495.5	1305.1	832.0	3655.6	1403.8	1911.0	1453.2	776.7	242.9	450.4
385.8	7266.6	6844.3	7016.5	8338.5	7137.8	7964.9	6505.9	5784.9	2941.5	5652.7
181.5	2318.9	2358.0	1829.2	5339.9	2616.6	4086.9	2109.2	1298.9	765.2	931.1
39.2	23.6	61.4	33.3	53.7	36.6	27.8	21.0	21.3	14.4	24.0
407.7	5401.2	5567.0	5695.3	8488.6	5944.5	7551.4	5181.2	4413.3	2775.5	3467.4
10366.0	5984.4	6287.5	6929.3	8535.6	6644.3	9157.4	7127.7	7868.0	7792.7	4875.8
218.3	2240.0	2512.6	2053.7	5988.8	2226.8	4820.8	2298.2	1203.4	1184.5	1500.1
91.9	2393.7	1718.2	1849.0	3490.4	2355.6	2205.3	1493.8	1812.7	1719.1	930.3
644.6	4511.0	4643.4	4249.4	7526.8	4305.7	6973.0	4145.6	2914.5	2630.5	3377.8
18194.1	7359.5	6659.4	7441.6	7011.3	7353.6	7419.8	6361.5	10732.1	8092.6	10254.5
46.1	61.3	38.4	32.7	48.7	27.6	52.7	33.6	29.9	21.4	74.2
38.8	156.1	110.4	68.2	284.0	121.8	80.1	59.4	61.6	24.2	46.0
30.7	57.0	19.4	25.4	30.2	24.7	17.0	11.6	24.1	17.7	34.4
3665.8	2889.2	2534.4	1175.3	3267.3	2708.2	3168.8	2526.3	2343.1	1177.6	2732.2
41.0	204.2	135.0	104.8	465.2	262.6	319.8	133.0	96.2	31.4	132.9
811.1	5181.5	5315.6	4359.6	7150.9	5101.7	7018.9	4431.5	3564.8	1096.8	3666.5
34.1	859.2	1006.3	1181.3	2232.5	1408.4	1380.2	1155.2	676.5	318.1	840.2
4128.1	4518.7	4231.7	4792.5	5853.3	5109.3	5994.4	4943.3	6865.9	5963.0	8097.9
16777.2	9130.4	8831.2	9356.3	8333.7	8409.1	9001.1	8784.0	10342.2	8686.1	12207.9
411.3	3466.5	3552.2	3748.6	5778.9	3840.9	5483.1	3786.0	2486.3	836.2	2834.8
1731.4	4997.5	4026.5	4152.7	5522.0	4102.9	5274.3	3917.3	6623.8	5358.8	3289.0
188.4	5329.9	5397.8	4635.1	8922.5	5544.7	7784.8	4530.5	3052.4	1103.6	2890.1
54.3	99.9	19.4	14.3	202.2	208.6	177.2	15.1	27.4	19.8	251.5
183.1	3266.0	2925.4	3239.7	4520.0	3437.0	3841.3	3281.7	1745.4	1304.8	2198.7
39.3	1471.8	1700.8	1354.8	2835.9	1646.5	2680.3	1244.4	613.0	196.7	517.1
21151.4	5021.9	4461.3	5269.7	5527.8	4532.5	4924.3	3884.7	7019.3	6316.7	6639.2
50.2	53.2	34.2	33.7	66.1	33.1	53.9	32.1	19.4	24.7	36.0
33.8	626.2	596.5	532.0	1510.7	581.0	1109.1	760.6	389.6	177.7	407.4
33.7	600.3	572.3	620.2	1789.6	553.4	1021.3	505.7	105.3	58.5	288.2
287.6	2833.0	3389.1	3798.8	5569.1	3344.2	4137.8	3915.5	1401.4	1916.8	1894.1
35.3	56.3	20.9	25.7	47.7	24.5	31.7	27.2	21.9	16.0	34.3
56.1	46.7	62.0	66.5	94.7	54.6	62.5	55.4	48.0	19.0	24.3
28.4	165.1	42.3	65.7	425.3	145.9	234.6	44.2	23.1	24.3	114.3
40.7	230.2	218.0	197.7	424.7	233.8	271.6	278.2	134.3	74.7	112.8
34.8	403.3	125.8	157.3	1357.7	398.2	730.7	380.2	78.3	50.9	185.8
35.6	335.9	264.0	264.4	899.4	464.7	438.9	229.4	289.6	149.3	110.5
123.8	4041.9	5079.6	3387.5	4814.4	3542.4	5091.1	3113.4	1776.4	1865.5	3810.5

992.1	660.5	759.2
1162.5	726.4	506.6
3394.2	3033.8	4454.5
2015.1	1530.1	2326.2
1158.0	985.2	1343.1
6033.4	6014.5	7340.8
1764.0	1521.4	1551.3
21.4	30.4	36.2
4073.0	4940.0	6667.1
6485.8	7075.7	7331.0
2365.4	1812.5	1972.3
1733.9	1539.2	1586.4
3667.0	3124.1	5196.0
6262.4	8784.6	6903.9
28.3	36.5	30.3
66.9	85.0	94.5
15.8	15.4	16.9
2345.8	2538.3	2677.8
130.5	89.4	199.3
4847.2	3758.4	5665.8
962.4	1429.3	1618.0
4844.2	5909.7	4841.3
7553.0	9516.1	9522.7
2986.2	3474.1	4830.6
4022.6	4451.3	5160.5
4618.3	3650.3	7117.4
16.1	20.7	17.2
3246.1	3247.8	5088.4
1319.5	1083.9	2546.6
4170.6	5201.1	4080.6
40.4	48.5	98.0
868.2	690.9	1657.8
386.4	517.3	1037.7
3743.4	3482.3	4997.2
22.3	30.2	31.2
50.8	89.5	72.9
57.0	69.9	130.7
145.5	248.9	275.8
194.9	209.4	386.6
294.3	191.2	631.6
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GU172180.1 gg_id:578268 Microbial Eucalyptus plantation soil clone DSM-R8 GU172
EF019126.1 gg_id:209352 aspen rhizosphere clone Amb_16S_1757 EF0191
EF516261.1 gg_id:220494 grassland soil clone FCPO467 EF5162
EF019883.1 gg_id:211980 aspen rhizosphere clone Elev_16S_1248 EF0198
GQ356142.1 gg_id:594250 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
CU919143.1 gg_id:572340 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU918228.1 gg_id:549254 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU920760.1 gg_id:571409 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EU773048.1 gg_id:331675 Banteng feces clone BG_aaa03d04.Contig1 EU773
EU471776.1 gg_id:294166 Asiatic elephant feces clone AE2_aaa01b10 EU471
EU771419.1 gg_id:339447 Asiatic elephant feces clone AE1_aaa02h11 EU771
EU463717.1 gg_id:297614 domesticated horse feces clone horsej_aai91e11 EU463
EU471538.1 gg_id:291474 Asiatic elephant feces clone AE1_aaa02e02 EU471
EU471740.1 gg_id:291133 Asiatic elephant feces clone AE2_aaa04d02 EU471
EU473570.1 gg_id:300038 Somali wild ass feces clone WA_aaa01g06 EU473
EU775815.1 gg_id:338441 Horse feces clone horsem_aai95h08 EU775
EU471942.1 gg_id:292730 Asiatic elephant feces clone AE3_aaa04e08 EU471
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AB185519.1 gg_id:99547 rumen clone F23-B04 AB185
EU470381.1 gg_id:298808 Grevy's zebra feces clone GZ_aaa02b08 EU470
EU776446.1 gg_id:326916 Red Kangaroo feces clone KO2_aai18a10 EU776
EU864491.1 gg_id:327984 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU864
AB015546.1 gg_id:203309 deep-sea sediments depths clone BD2-18 AB015
AY114334.1 gg_id:63771 anoxic marine sediment clone LD1-PB20 AY114
CU920931.1 gg_id:556915 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
GQ259319.1 gg_id:534591 Microbial activities coastal marine sediments and water column Svalbard surface se GQ259
FN396736.1 gg_id:546665 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN396
AY114328.1 gg_id:70013 anoxic marine sediment clone LD1-PA50 AY114
AY963317.1 gg_id:151682 structures and correlated ecological factors soils two evergreen broad-leaved forests AY963
EU881223.1 gg_id:333383 Karst region natural restoration land soil clone KNR200711-042 EU881
EU135433.1 gg_id:257941 tallgrass prarie soil clone FFCH3955 EU135
AM162463.1 gg_id:154318 and situ identification acidic sphagnum peat bog clone B69 AM162
EU135525.1 gg_id:236593 tallgrass prarie soil clone FFCH8458 EU135
EU135455.1 gg_id:240895 tallgrass prarie soil clone FFCH1225 EU135
EF516767.1 gg_id:220193 grassland soil clone FCPT575 EF5167
EU135479.1 gg_id:251458 tallgrass prarie soil clone FFCH10633 EU135
AF465651.1 gg_id:50325 thermal soil clone YNPRH34A AF465
EU135506.1 gg_id:249781 tallgrass prarie soil clone FFCH14037 EU135

62.5	1284.0	1233.1	1221.6	2427.0	1490.0	1915.1	1029.3	595.7	316.9	622.6
26.9	155.5	116.7	99.5	179.8	51.3	189.3	49.8	20.6	15.0	69.8
64.4	443.2	437.8	419.7	623.9	537.9	556.2	331.9	395.6	184.2	305.8
559.5	3304.3	2814.6	2660.4	4521.6	3704.9	3444.4	3553.3	3744.0	1276.2	1835.7
49.3	988.7	554.1	410.9	3067.1	1055.6	1769.3	582.5	228.6	97.4	409.7
66.8	2730.4	3541.2	2528.5	4175.6	2592.9	4123.4	2221.2	1881.6	415.6	1348.4
38.9	29.2	27.5	30.2	32.5	24.3	28.3	24.2	24.9	23.3	30.1
12586.5	11362.3	10271.0	11643.5	9873.0	9954.2	10976.9	9239.1	13021.1	11613.2	16534.2
64.8	1415.1	1364.9	1356.6	1746.3	1782.6	2325.5	1259.8	814.6	316.0	779.1
167.5	2866.6	3289.0	3289.0	3767.8	3236.0	3924.2	3074.4	1274.4	1235.5	2060.2
136.0	1711.1	1775.5	2233.2	2067.6	1747.6	2361.1	2269.0	895.0	1451.6	1384.1
1657.1	4392.1	5451.1	5563.5	6534.0	5382.4	7050.1	5674.9	4533.6	4652.0	5096.6
1524.4	3249.4	2959.2	3037.0	4501.6	3673.5	4546.9	2900.0	2959.2	2133.8	1843.2
1606.1	5513.5	5983.9	6239.9	6926.7	6061.9	7588.7	6054.3	7015.5	7148.6	5673.2
2043.4	4748.0	4462.4	3796.2	5303.0	4181.5	4449.2	4339.6	4052.9	4024.0	5361.9
530.9	2413.5	2734.4	3185.7	3462.3	2851.6	2697.5	3051.1	1869.1	767.9	2311.5
6302.2	2848.5	2712.3	3219.7	4286.9	3310.5	4174.3	3742.9	1841.2	1903.1	3541.5
109.4	3100.2	4157.7	3908.0	4915.1	3923.0	5191.3	4337.9	2978.5	2451.1	3470.8
5627.1	3181.0	3993.7	3626.1	3827.2	3814.0	3846.7	3794.5	3315.8	4399.5	3470.8
194.7	1791.5	2481.4	2699.4	2417.0	2098.0	2570.6	2243.0	1133.5	1164.5	1193.0
50.8	3123.9	4315.8	4933.2	3298.0	3931.8	5947.5	3994.7	1263.8	442.5	2826.3
642.8	1852.3	2365.9	2453.7	2142.1	2001.7	3637.8	2059.4	614.6	458.2	1181.5
696.3	8129.6	9236.6	9527.2	10869.3	9114.0	12190.9	8982.1	7408.1	3377.4	7028.6
5681.0	6050.7	6032.9	7539.3	5873.9	6375.4	7308.8	6598.6	5776.8	4680.9	6678.4
5903.9	4832.6	5650.7	6525.9	5207.1	5780.7	6602.2	5433.2	4963.6	5405.6	6096.8
2403.8	6307.1	6747.0	7372.4	6222.0	6547.4	8280.8	6892.7	4523.8	3083.9	6139.5
30.7	352.5	618.1	617.5	344.3	548.8	520.5	672.4	144.1	136.6	431.9
47.8	497.1	1456.4	1865.1	836.8	601.4	915.5	825.5	289.1	189.7	354.3
383.1	4737.4	5509.5	6180.7	5939.7	5711.4	7847.7	5269.2	2609.9	2161.2	4797.5
58.1	1933.7	2852.9	3244.5	2477.1	3097.7	4379.8	2720.1	531.5	215.1	1307.4
37.0	413.5	587.1	631.6	451.3	566.3	591.0	558.3	350.7	178.9	358.6
151.3	663.6	632.0	512.8	663.9	544.2	1179.2	575.6	319.9	189.8	337.9
45.3	1736.5	2643.0	2119.5	3720.5	2094.4	3720.0	1620.2	972.2	98.9	1130.8
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147.1	381.2	563.8	470.5	402.1	403.1	766.1	550.5	177.9	53.4	312.1
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EF516676.1 gg_id:221568 grassland soil clone FCPO598 EF5166
DQ676318.1 gg_id:221692 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AY212643.1 gg_id:107428 water 20 m upstream manure clone 190up AY2126
GQ339133.1 gg_id:514963 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
FM209351.1 gg_id:567812 Microbial Negev desert s sand soil clone 2031 FM209
AM162456.1 gg_id:155778 and situ identification acidic sphagnum peat bog clone B52 AM162
FJ625341.1 gg_id:551837 Influence lead contamination on boreal pine forest soil clone HF_NC_2 FJ6253
AM162459.1 gg_id:151165 and situ identification acidic sphagnum peat bog clone B129 AM162
FJ479471.1 gg_id:512910 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF516574.1 gg_id:221251 grassland soil clone FCPP665 EF5165
EU335294.1 gg_id:251275 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EU135503.1 gg_id:238929 tallgrass prarie soil clone FFCH13652 EU135
DQ676422.1 gg_id:220892 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
EU335227.1 gg_id:248808 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
FJ478628.1 gg_id:512539 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EU135464.1 gg_id:255118 tallgrass prarie soil clone FFCH5116 EU135
EF516222.1 gg_id:218456 grassland soil clone FCPT508 EF5162
AJ617869.1 gg_id:110756 oxic-anoxic interphase flooded paddy soil clone D142114 AJ6178
EF516552.1 gg_id:217929 grassland soil clone FCPU600 EF5165
DQ125505.1 gg_id:132722 uranium contaminated soil clone AKAU3464 DQ125
FJ479069.1 gg_id:590252 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
AJ863241.1 gg_id:126772 poplar tree microcosm bulk soil flooded clone 21BSF21 AJ8632
EF516075.1 gg_id:223550 grassland soil clone FCPT406 EF5160
DQ450782.1 gg_id:161263 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EU937949.1 gg_id:321753 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EF515942.1 gg_id:225894 grassland soil clone FCPP485 EF5159
FJ468383.1 gg_id:585431 Bioaugmentation Pseudomonas sp. strain MHP41 promotes attenuation and changes FJ4683
EU135478.1 gg_id:250253 tallgrass prarie soil clone FFCH10577 EU135
EU135518.1 gg_id:253183 tallgrass prarie soil clone FFCH17360 EU135
AF523995.1 gg_id:63232 coal effluent wetland clone FW4 AF5239
EF612425.1 gg_id:248066 historic semiarid lead-zinc mine tailings site soil clone OS-C04 EF6124
EF019315.1 gg_id:206560 aspen rhizosphere clone Elev_16S_510 EF0193
AM162462.1 gg_id:155827 and situ identification acidic sphagnum peat bog clone B64 AM162
GU444057.1 gg_id:523991 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
AM162461.1 gg_id:151640 and situ identification acidic sphagnum peat bog clone B147 AM162
DQ521482.1 gg_id:186160 Antarctic lake ice cover clone ANTLV1_D01 DQ521
EU135543.1 gg_id:248805 tallgrass prarie soil clone FFCH18403 EU135
EF516440.1 gg_id:219094 grassland soil clone FCPU636 EF5164

46.2	2333.6	2953.8	2317.7	4011.9	2553.4	4339.4	2019.6	1536.0	213.1	1170.4
36.3	139.7	223.9	134.5	362.3	208.3	289.5	133.8	47.5	25.1	86.2
47.5	2219.7	2778.0	2214.2	3286.4	2341.4	3785.6	1584.4	1038.4	275.0	862.7
910.7	6209.3	6894.0	6377.4	8209.5	6383.5	9202.3	6091.6	5470.7	2862.9	4715.7
161.6	1972.6	2557.3	2094.6	3414.1	2762.2	3687.8	1835.1	828.5	494.0	1089.0
46.5	1022.8	986.3	769.4	1025.9	830.0	1296.8	690.6	228.2	77.8	317.2
4614.8	4554.3	4791.3	4568.8	4635.8	4414.8	5320.9	3553.4	4077.5	3667.4	3592.7
219.5	4090.8	5761.7	4620.7	5668.1	4637.0	6258.4	4981.8	3308.1	710.9	2706.5
36.3	196.3	445.1	253.6	562.3	344.2	1512.5	134.8	76.2	21.6	115.2
159.8	5807.0	6533.5	5943.1	8610.8	5508.7	9003.7	4853.2	3323.6	1129.3	3770.4
47.8	1218.1	1919.2	1119.1	2401.7	1170.6	2906.0	850.7	448.0	51.1	420.1
88.6	1277.4	1611.3	1691.5	2585.6	1236.6	2663.7	1660.3	712.6	289.4	969.0
40.5	209.7	282.5	207.7	272.1	177.8	301.9	76.8	91.3	36.0	78.1
9953.6	5880.7	6513.1	5826.2	8056.5	5897.3	8203.7	5644.8	5363.9	2781.1	5822.8
193.3	6771.3	7204.9	7427.6	10937.6	7118.7	9349.8	6664.5	6595.2	1889.6	6774.9
47.9	745.2	874.6	641.7	825.6	604.9	1590.1	403.6	438.8	21.8	225.1
533.0	6718.5	7082.6	6746.6	9045.3	6836.3	8806.0	6378.4	4797.8	1986.8	5235.1
5712.2	7592.2	7563.9	7467.7	10886.2	7226.6	10249.0	6017.6	7221.7	4143.0	6759.0
78.9	4524.7	4561.1	3322.6	5742.3	3359.7	6461.1	2590.0	1834.5	816.8	2567.0
39.6	1778.8	2074.1	505.4	2440.8	1970.8	2683.5	1963.1	1320.9	259.8	1365.4
35.7	756.3	1149.8	813.7	827.9	580.1	910.0	382.6	287.8	16.5	196.0
101.2	199.0	210.6	232.1	251.4	161.1	508.7	180.0	96.8	129.3	132.3
39.0	213.8	286.9	225.6	336.3	245.0	417.9	210.1	85.9	33.3	112.6
38.9	2721.7	3449.8	2848.5	4513.6	2950.2	4686.5	2347.2	1110.7	204.4	1435.2
54.6	985.8	1396.2	747.8	1486.4	703.4	1618.9	378.1	119.6	29.0	266.0
51.3	542.7	559.2	519.8	573.8	508.0	793.0	979.9	155.9	69.4	250.2
134.2	1238.1	1611.8	1495.9	1651.2	1524.2	2152.2	2024.7	468.7	76.3	723.0
343.5	4457.9	5858.1	5140.8	7064.5	5096.3	7031.3	4732.3	3436.8	1978.6	3762.0
26821.2	8627.2	8497.3	9079.6	8806.5	8534.7	9562.0	8589.5	15167.6	11083.9	14973.4
65.4	3308.8	3786.1	3222.6	4601.0	3570.6	5538.6	2881.4	1836.4	330.1	2028.3
87.8	2320.7	3294.0	2717.4	4408.8	2820.8	4019.5	2674.1	1301.9	397.6	1774.2
640.0	3979.6	4597.4	4847.2	6458.4	4454.1	5647.5	4638.3	3501.1	2868.2	3751.4
59.9	932.5	1288.9	672.2	1337.7	810.5	1414.1	723.3	593.9	34.4	343.6
44.8	1226.9	1710.9	1186.0	1870.9	1387.8	2372.0	1395.9	700.7	40.1	620.9
502.0	2175.4	2224.5	2388.2	2785.6	2183.4	2759.3	1963.4	1686.5	663.1	1650.2
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10551.6	7612.7	7284.8	7798.0	9729.4	7397.2	9380.0	6290.8	8573.9	5487.6	7179.5
4699.9	6399.1	6294.7	6884.7	7345.5	6131.5	8154.7	6218.9	5168.4	4621.2	6454.1
62.7	2173.4	2685.3	1919.3	3985.8	2002.7	4338.2	1485.6	742.9	131.0	697.8
2161.6	7216.6	8115.5	7799.2	11239.6	7369.5	11018.4	6970.4	5686.0	3499.4	5860.1
46.5	166.8	145.5	85.6	118.6	89.1	93.9	65.4	46.6	17.0	63.7

2268.6	1053.6	2822.7
64.2	81.2	257.0
1318.0	1569.3	2155.6
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1782.8	2374.8	3636.3
393.4	269.4	622.1
3301.7	3249.4	3362.2
3652.5	3701.3	5148.1
84.7	101.2	448.8
4132.0	3030.1	5606.1
714.2	293.1	1322.1
836.6	863.4	1264.0
58.2	118.3	191.0
4836.7	5043.7	6411.0
5459.6	4635.9	7460.1
178.0	235.4	1240.3
5416.8	6432.6	7625.6
6059.2	5984.6	7491.0
1871.9	1539.6	3747.9
1655.7	1295.0	2053.6
256.7	180.7	500.9
170.6	196.8	282.6
137.3	130.7	184.2
1734.4	1023.9	2849.0
208.3	175.2	669.8
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1170.9	1075.3	1452.6
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1932.3	2002.2	3214.2
2009.1	1617.3	2106.8
3227.9	4559.5	4911.8
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AY921923.1 gg_id:113303 farm soil clone AKYH1372 AY9219
EU135437.1 gg_id:256933 tallgrass prarie soil clone FFCH6314 EU1354
EU135514.1 gg_id:257782 tallgrass prarie soil clone FFCH15477 EU1355
EF020079.1 gg_id:207326 aspen rhizosphere clone Elev_16S_1488 EF0200
FJ592707.1 gg_id:543327 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5927
EU335255.1 gg_id:241999 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
EF516775.1 gg_id:218032 grassland soil clone FCPU668 EF5167
GQ348914.1 gg_id:560563 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ155059.1 gg_id:318309 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone CB FJ1550
GQ348513.1 gg_id:542753 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
GQ348797.1 gg_id:535223 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
DQ302118.1 gg_id:156301 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
FJ628330.1 gg_id:513658 transition and zone within near-shore basin: brackish water anoxic fjord Nitinat Lake FJ6283
FJ615181.1 gg_id:544538 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 125m anoxi FJ6151
FJ615159.1 gg_id:557490 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 100m anoxi FJ6151
DQ071110.1 gg_id:131960 marine surface water clone SJC1.38 DQ071
AY028219.1 gg_id:32593 marine clone Arctic97B-4 AY0282
DQ071044.1 gg_id:130139 islts and fld smplng Glf Strm Rng chlrphll mxmm cln Chl1.3 DQ071
AM176893.1 gg_id:159970 Recovery mangrove sediment clone SZB49 AM176
GU061235.1 gg_id:574533 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
GU208329.1 gg_id:570490 Study on Sediment Dongping Lake sediment clone Se2-17 GU208
EU135454.1 gg_id:237237 tallgrass prarie soil clone FFCH12732 EU1354
DQ125868.1 gg_id:131444 uranium contaminated soil clone AKAU4117 DQ125
EU135432.1 gg_id:254690 tallgrass prarie soil clone FFCH13487 EU1354
FJ479563.1 gg_id:579528 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EU135494.1 gg_id:237927 tallgrass prarie soil clone FFCH12670 EU1354
EU937926.1 gg_id:337426 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9379
AJ853567.1 gg_id:110302 landfill leachate clone GZKB73 AJ8535
CU917597.1 gg_id:546967 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9175
AF027005.1 gg_id:1572 hot spring clone OPB35 AF0270
FM994912.1 gg_id:550907 springs Velingrad region Bulgaria hot spring Mizinka clone VS-21 FM994
EU104111.1 gg_id:310462 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
DQ017913.1 gg_id:134130 upland stream clone S-Btb7_11 DQ017
DQ396294.1 gg_id:153452 deep-sea octacoral clone ctg_NISA252 DQ396
FJ905685.1 gg_id:535898 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
EF516930.1 gg_id:225632 grassland soil clone FCPN502 EF5169
EF516856.1 gg_id:224253 grassland soil clone FCPS671 EF5168
EF018903.1 gg_id:212324 aspen rhizosphere clone Amb_16S_1397 EF0189
AY395425.1 gg_id:102024 pasture soil clone EB1106 AY3954
FJ478519.1 gg_id:536090 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785

41.6	1784.2	2035.9	1802.5	6802.3	2461.8	2801.2	1721.0	1283.4	216.7	1232.0
85.0	1241.2	1487.8	1384.7	1888.9	1254.5	1991.4	1357.8	615.7	128.3	501.0
599.1	5960.7	5548.6	5521.3	7469.8	5755.4	7008.3	5144.9	4533.3	2909.3	4109.3
37.8	496.4	1339.2	982.3	730.0	815.0	1359.0	640.7	155.1	37.7	209.4
41.5	59.8	140.8	126.2	212.5	228.3	225.2	237.0	255.7	31.5	248.7
217.8	7315.5	8550.0	7785.0	12830.4	8123.4	12544.9	6725.5	5186.3	1462.1	4978.3
48.3	2022.0	2477.9	1828.0	3055.0	1705.2	4049.3	1148.9	689.8	111.9	666.5
374.3	5633.7	6443.6	5886.7	8794.0	5692.7	8273.3	4335.6	3637.2	1526.2	3437.8
1527.8	6774.9	7632.0	8322.2	9082.4	7147.9	10126.0	6911.6	4956.0	3850.4	6506.1
151.0	787.8	1080.6	835.7	1138.0	899.3	1447.1	871.4	796.8	345.7	498.5
5751.9	6764.9	7059.4	7648.7	8299.5	7026.1	9659.4	7287.2	8418.3	5190.0	8442.9
878.0	7972.1	8783.2	9161.1	10805.0	8734.1	11831.3	8347.6	7630.7	4848.9	6888.1
46.5	88.2	96.3	89.1	113.7	67.4	142.6	110.0	56.0	35.4	54.5
180.7	3893.1	3711.9	3763.1	4238.0	3496.6	4692.0	3950.4	3492.3	2103.6	3677.1
197.1	1119.0	940.0	786.1	986.6	1036.2	1008.3	851.5	1644.0	1245.9	557.7
11737.0	6128.9	5365.8	5594.5	5089.4	6099.9	6061.7	5357.4	9016.3	5584.4	6451.5
143.5	685.6	655.3	580.4	605.9	664.8	750.9	647.6	897.4	602.2	419.1
1653.6	4365.3	4921.1	5336.7	3812.4	5137.7	4275.2	4128.0	2482.8	1727.7	4448.6
40.8	158.6	293.1	212.8	403.5	318.4	412.3	294.2	90.6	34.6	71.8
35.4	438.8	484.8	363.5	405.9	237.0	389.3	139.2	90.5	31.3	77.4
1029.9	9452.3	10276.3	10571.7	14332.6	9772.5	13825.5	9544.2	8363.1	3230.3	9017.0
590.0	5901.2	6450.9	6400.8	9473.6	6079.6	9105.3	5906.5	4471.2	2907.4	4933.1
330.2	4781.1	5305.2	5235.2	6358.0	4743.6	7105.7	5489.6	3906.7	1743.9	3699.7
58.9	2315.1	2540.7	2050.3	2183.9	2146.2	3570.9	2929.4	1239.4	470.2	1864.9
2336.2	6529.9	6397.6	6130.7	7862.8	6455.9	7495.4	5715.5	5282.6	1826.0	4562.6
1087.1	8006.8	8000.1	8284.5	11393.6	8236.1	10355.3	7282.8	7252.1	4785.4	6493.4
5855.4	9441.1	8545.4	8330.5	9638.8	9517.7	9899.1	9602.8	7691.6	3653.4	8446.9
2557.4	5961.5	5838.8	5668.1	6102.5	6497.9	6422.0	6299.2	5840.2	3124.1	6044.7
161.0	6299.2	6339.7	6609.6	7420.2	7041.2	7530.3	6039.6	4603.8	1260.8	4737.6
368.3	4698.4	5335.7	6800.5	4958.8	4361.0	5703.8	5568.6	2828.8	1787.8	4554.4
98.2	686.5	989.9	1456.5	1087.5	460.8	739.0	718.7	129.0	225.7	387.5
126.0	2005.5	2874.0	2298.2	3019.5	2761.5	3825.1	1978.2	1227.7	361.4	1198.9
52.1	151.0	388.3	293.6	350.9	1006.7	334.2	1956.4	2698.6	41.4	474.4
62.5	1308.8	1484.9	1423.5	2486.7	2065.5	1948.5	1885.6	1275.6	267.5	1031.5
1586.5	4859.9	5313.9	5298.8	6449.4	4927.0	6792.8	5404.8	3143.9	5027.8	4397.7
169.5	1263.6	1417.1	1053.8	505.7	1086.7	661.6	1938.2	1182.6	252.5	913.7
39.8	1537.5	1621.4	1269.8	2762.5	1312.5	3022.5	764.8	301.9	68.9	511.6
445.2	2388.5	3309.9	2761.2	3137.3	2227.9	3216.8	2845.6	1376.2	648.9	1984.1
44.0	3395.7	3859.3	3225.9	5309.9	2746.7	4782.1	2321.4	1014.3	241.4	1165.9
7273.4	3404.5	3062.2	3064.0	3945.3	3413.8	3981.0	2586.0	3323.6	2174.1	2975.7
197.8	4592.8	5309.8	4973.6	7687.8	4282.5	7247.6	4044.3	2412.6	1064.9	2689.3

1046.1	1167.6	1914.2
874.0	515.7	1501.6
4895.7	4109.2	6431.8
204.6	226.9	1440.9
294.2	184.7	194.1
5899.1	4802.9	7593.1
1309.1	727.8	2137.8
3972.5	4341.9	6315.9
7181.7	6617.3	8862.6
664.4	1020.4	868.7
6561.5	7376.7	8002.0
7150.8	7193.9	10289.0
69.2	78.1	68.8
2981.2	4073.8	3781.7
996.5	848.8	773.4
5453.6	6173.6	5076.2
552.4	540.1	614.7
3997.4	4867.3	4540.7
306.5	226.3	422.2
67.9	102.3	310.1
9146.1	9132.4	12494.6
4743.8	5540.8	7574.3
3960.7	3637.0	5959.8
1472.6	1415.9	3217.2
5132.4	4185.0	6488.9
6095.7	6936.8	8512.0
9596.5	8350.9	11258.6
5686.2	6665.0	6806.1
4800.5	5026.1	10006.4
3981.3	5066.0	5979.4
408.3	471.1	699.0
1365.9	1859.6	2626.8
507.7	367.7	300.4
1543.1	1712.9	1965.5
4836.1	5619.7	5054.9
1114.9	1206.7	967.4
398.1	765.7	2117.8
2680.1	2573.0	3373.9
1251.8	1294.6	2769.5
2656.2	2781.7	3260.9
2889.0	3058.4	4697.4

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AB487257.1 gg_id:549692 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB487
EU135434.1 gg_id:238183 tallgrass prarie soil clone FFCH7408 EU135
GQ402552.1 gg_id:593900 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF019592.1 gg_id:212455 aspen rhizosphere clone Elev_16S_1113 EF0195
DQ404817.1 gg_id:151664 contaminated sediment clone 655945 DQ404
DQ451523.1 gg_id:156917 forest soil clone FAC84 DQ451
EU335323.1 gg_id:242989 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
EF099597.1 gg_id:184418 mouse cecum clone SWPT4_aaa01f05 EF0995
EU459611.1 gg_id:291051 ring-tailed lemur feces clone RT_aai09c04 EU459
EF099110.1 gg_id:192171 mouse cecum clone SWPT2_aaa02d09 EF0991
CP001071.1 gg_id:278234 Akkermansia muciniphila str. ATCC BAA-835 CP001
DQ807825.1 gg_id:178569 human fecal clone RL180_aah37f08 DQ807
DQ805565.1 gg_id:183323 human fecal clone RL203_aai64c10 DQ805
EF400323.1 gg_id:214443 human fecal clone SJTU_E_11_61 EF4003
DQ805338.1 gg_id:177459 human fecal clone RL203_aai61d02 DQ805
EU508722.1 gg_id:262854 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap49h09 EU508
EF099112.1 gg_id:174132 mouse cecum clone SWPT2_aaa02d11 EF0991
EF604904.1 gg_id:230139 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6049
AY982401.1 gg_id:125420 human sigmoid colon mucosal biopsy clone MK66 AY982
EU459638.1 gg_id:298839 ring-tailed lemur feces clone RT_aai09g05 EU459
EU763463.1 gg_id:345321 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EF604517.1 gg_id:234298 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
DQ793539.1 gg_id:178086 human fecal clone RL246_aai73b07 DQ793
AY977829.1 gg_id:118714 human cecum mucosal biopsy clone LF22 AY977
EU506706.1 gg_id:261175 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap54h02 EU506
DQ807201.1 gg_id:185152 human fecal clone RL244_aaj47e04 DQ807
DQ805485.1 gg_id:174822 human fecal clone RL203_aai63c06 DQ805
DQ805597.1 gg_id:177705 human fecal clone RL203_aai64g05 DQ805
EU506506.1 gg_id:274986 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa03b03 EU506
DQ805539.1 gg_id:185779 human fecal clone RL203_aai64a01 DQ805
FJ365265.1 gg_id:368894 feces adult twins and mothers; TS1 clone TS1_a04g10 FJ3652
AJ408970.1 gg_id:31006 human colonic clone HuCA18 AJ4089
EU507500.1 gg_id:258589 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa04b09 EU507
FJ364958.1 gg_id:359195 feces adult twins and mothers; TS1 clone TS1_a01c01 FJ3649
AY986145.1 gg_id:116910 human stool clone D491 AY986
EU006397.1 gg_id:255263 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
DQ805319.1 gg_id:195328 human fecal clone RL203_aai61b04 DQ805
EU763313.1 gg_id:334717 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
FJ365018.1 gg_id:365334 feces adult twins and mothers; TS1 clone TS1_a01h05 FJ3650
DQ803989.1 gg_id:181549 human fecal clone RL200_aai60g06 DQ803
DQ805473.1 gg_id:197876 human fecal clone RL203_aai63b03 DQ805

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183.3	3177.6	4182.0	3931.4	5266.4	3471.1	5372.8	4343.2	2933.8	720.1	3217.0
2013.5	6775.2	7668.6	7650.8	9509.9	6578.3	9926.5	6039.4	5102.8	2847.8	5113.9
4248.4	4298.6	4319.0	3869.6	4680.5	4103.7	4645.3	2536.9	2778.5	2104.4	3166.8
38.4	459.5	505.1	262.5	674.1	249.5	824.3	165.4	58.9	35.5	90.0
636.4	3234.0	2878.4	2569.6	3095.2	2741.1	3293.5	1477.6	1160.5	930.5	1289.3
65.1	2163.4	2179.7	1603.8	2570.2	1347.6	1880.0	608.4	233.4	95.2	583.6
26932.9	9357.8	8949.0	9529.4	8087.4	8975.9	9911.1	9065.6	19838.2	9125.4	12762.9
5642.8	9884.2	9106.8	10175.3	10049.4	9034.7	10837.3	9445.0	15274.1	9716.6	10668.5
2942.0	6130.1	5431.9	5959.9	6290.9	6287.5	6454.6	5199.4	7423.1	7888.5	7421.2
220.2	2798.3	2978.0	2709.2	3149.3	2602.4	2989.4	2116.4	2268.8	1203.9	2636.2
150.8	4112.1	3834.2	4357.5	5453.8	4141.7	5418.5	3658.8	3407.2	1853.3	3494.9
12557.1	5193.5	5385.8	5904.8	6849.1	5162.2	8640.2	5442.5	7299.2	4957.7	6860.9
2552.0	3634.7	3552.7	3550.3	4865.7	3239.7	3575.5	2533.0	2492.9	1671.2	3986.9
1025.8	3757.5	3455.0	3745.7	4673.9	3932.2	4395.9	4531.5	5339.0	3891.0	2390.0
224.2	5901.7	5664.1	5894.5	8069.7	5689.9	7058.0	4435.7	5331.1	2232.6	4350.4
201.5	5031.3	5060.2	5106.4	6747.6	4912.3	6107.8	4018.0	4853.9	1867.9	3885.9
178.5	3131.8	3666.4	3786.3	2630.6	3081.9	3274.8	5351.2	3151.2	2058.0	3167.1
181.8	4476.4	4417.1	4882.3	4960.7	4207.8	4846.0	3545.5	6088.4	2922.0	4059.0
315.2	5339.0	5473.6	5801.0	7481.9	5147.6	6715.3	4607.2	4939.7	1912.6	3810.1
1234.9	3715.9	3363.0	4114.2	4078.3	3732.8	4478.2	4257.0	6744.3	5806.1	2605.7
562.0	5249.9	6385.6	6908.7	6977.6	5662.7	8079.7	5792.7	4882.8	3006.2	5588.7
214.1	4892.7	4696.4	4920.8	6358.1	4577.5	5636.0	3624.9	4458.3	2088.5	3570.7
179.5	4162.8	4127.4	4365.1	5192.2	3788.2	4949.5	3208.4	3887.9	1821.5	3231.8
1789.3	4815.6	4403.1	5009.0	6194.4	4940.4	5854.5	4945.1	4819.5	2154.4	4808.4
265.1	4726.7	4673.0	5334.7	6706.6	4765.4	6201.7	4055.1	4517.0	2910.6	4204.1
86.3	4086.9	3917.7	4350.6	5821.0	4417.1	5356.4	3971.2	3260.1	1480.6	2628.0
64.0	3801.5	3809.9	4092.9	5200.3	3935.3	5347.0	3356.0	3314.0	1794.2	2430.1
215.0	3600.7	3549.6	3631.6	4583.0	3398.6	3968.4	2689.5	3026.8	1299.6	2485.1
77.4	4761.7	4470.4	5428.0	5815.8	4337.7	6079.3	4820.7	6029.5	5809.4	3377.0
119.3	5542.3	5587.0	6251.0	8112.9	5682.9	7459.7	5221.6	5167.4	2716.7	4086.5
81.3	3395.4	2909.4	3296.1	4099.6	2997.3	3568.5	2240.3	2619.9	1621.4	3736.3
631.1	3911.5	3464.1	3881.5	3962.3	3507.9	3575.9	2969.2	4930.6	2717.0	4295.7
208.2	4752.3	4275.0	4852.2	6181.3	4841.5	5967.3	3971.1	3803.7	2206.7	3905.9
540.5	2834.9	3056.9	3344.5	4141.7	2848.1	4268.4	3199.3	2600.4	665.4	2745.1
233.2	2853.9	2973.8	3297.8	3811.5	2634.2	3526.4	2568.6	2459.1	1804.3	2181.5
68.8	4446.9	4058.3	4642.7	6196.2	4721.4	6009.3	4164.0	3839.4	2105.5	2834.9
165.5	3599.4	3566.5	3912.4	5128.7	3962.6	4830.0	3392.4	3405.1	1952.3	2446.3
2602.3	8159.7	8084.6	9554.4	9903.5	7945.4	10422.5	7937.7	8902.9	5128.9	8453.6
285.5	5127.1	5171.0	5486.5	6783.0	4818.8	6834.5	4334.4	4254.4	1879.6	3601.3
80.5	4093.8	4057.4	4724.5	5737.1	4203.5	5284.3	3993.5	4112.9	2042.4	2721.6

2233.6	2614.1	4709.3
2639.5	3058.7	3891.1
4918.8	4881.9	7005.6
2150.5	2683.9	2789.5
109.0	124.2	196.0
1239.2	1231.5	1762.4
383.3	568.4	1747.0
8511.1	11206.5	8864.3
8332.4	11367.7	7747.4
5313.9	5825.3	6028.8
2278.0	1902.5	2667.3
3517.0	2829.2	3656.7
5057.4	5488.2	5195.8
2802.6	2358.0	3287.1
3675.6	3417.3	3540.3
4510.0	3498.0	5035.7
4285.2	3185.8	4476.1
7169.8	2242.7	3665.4
3586.9	3651.7	3149.9
4453.1	4015.9	6071.1
3549.9	4061.0	3862.8
5014.8	4949.6	7963.5
3697.3	3130.0	3936.3
3555.8	2888.7	3540.9
4653.1	3411.4	4066.2
4154.9	3611.1	4476.5
3676.2	2542.4	4584.0
3380.1	2114.0	3166.4
2822.3	2620.3	3303.2
4483.6	3168.7	3197.7
4868.3	3658.8	6076.3
2349.8	1210.6	3074.0
2666.1	2709.4	2651.6
3945.7	3508.0	5113.3
2714.7	2326.5	4461.9
2709.2	2190.5	3269.6
4234.5	2706.3	4246.2
3267.2	2313.6	2892.9
8003.7	7230.0	7891.0
4346.4	3462.5	4856.9
3668.3	2609.0	3737.1

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s__Akkermansia muciniphila	55338
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s__Akkermansia muciniphila	55808

EU509469.1 gg_id:263656 cecal contents Mus musculus strain C57BL/6J; MD9 clone MD9_aap58h05 EU509
DQ805273.1 gg_id:192919 human fecal clone RL249_aaj84b10 DQ805
EU939409.1 gg_id:335768 Fecal wild pygmy loris feces clone WF16S_131 EU939
DQ803720.1 gg_id:179163 human fecal clone RL200_aai57e09 DQ803
DQ803687.1 gg_id:177813 human fecal clone RL200_aai57b09 DQ803
EU763746.1 gg_id:346624 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EF099090.1 gg_id:180789 mouse cecum clone SWPT2_aaa02b02 EF099
EF099511.1 gg_id:185740 mouse cecum clone SWPT3_aaa04b11 EF099
DQ805333.1 gg_id:187220 human fecal clone RL203_aai61c08 DQ805
EF099126.1 gg_id:181513 mouse cecum clone SWPT2_aaa02f08 EF099
FJ371231.1 gg_id:359222 feces adult twins and mothers; TS6 clone TS6_a02e02 FJ3712
FJ364037.1 gg_id:360894 feces adult twins and mothers; TS150 clone TS150_a02c03 FJ3640
FJ365015.1 gg_id:367987 feces adult twins and mothers; TS1 clone TS1_a01h02 FJ3650
EU768083.1 gg_id:340215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ364103.1 gg_id:366847 feces adult twins and mothers; TS150 clone TS150_a03a07 FJ3641
EF098492.1 gg_id:197822 mouse cecum clone SWPT15_aaa04b09 EF0984
DQ805416.1 gg_id:197098 human fecal clone RL203_aai62d02 DQ805
FJ371195.1 gg_id:361687 feces adult twins and mothers; TS6 clone TS6_a02a08 FJ3711
FJ366647.1 gg_id:361853 feces adult twins and mothers; TS27 clone TS27_a02b07 FJ3666
FJ363943.1 gg_id:359085 feces adult twins and mothers; TS150 clone TS150_a01b10 FJ3639
DQ793729.1 gg_id:185943 human fecal clone RL246_aai76c11 DQ793
FJ369647.1 gg_id:366053 feces adult twins and mothers; TS51 clone TS51_a03b08 FJ3696
FJ369644.1 gg_id:366982 feces adult twins and mothers; TS51 clone TS51_a03b04 FJ3696
EF099031.1 gg_id:188922 mouse cecum clone SWPT2_aaa01c10 EF099
FJ369652.1 gg_id:365331 feces adult twins and mothers; TS51 clone TS51_a03c03 FJ3696
EU768211.1 gg_id:349733 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
FJ364059.1 gg_id:368699 feces adult twins and mothers; TS150 clone TS150_a02e04 FJ3640
DQ803799.1 gg_id:180056 human fecal clone RL200_aai58e09 DQ803
DQ806904.1 gg_id:187104 human fecal clone RL198_aaj75b08 DQ806
EU768169.1 gg_id:344643 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ803992.1 gg_id:185431 human fecal clone RL200_aai60g09 DQ803
FJ371678.1 gg_id:366631 feces adult twins and mothers; TS8 clone TS8_a01a06 FJ3716
FJ365028.1 gg_id:359843 feces adult twins and mothers; TS1 clone TS1_a02a04 FJ3650
EU506426.1 gg_id:277079 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa01e12 EU506
FJ371109.1 gg_id:358268 feces adult twins and mothers; TS6 clone TS6_a01a10 FJ3711
AY978065.1 gg_id:120670 human cecum mucosal biopsy clone LI24 AY978
DQ805371.1 gg_id:191984 human fecal clone RL203_aai61g09 DQ805
DQ805313.1 gg_id:185545 human fecal clone RL203_aai61a06 DQ805
FJ369694.1 gg_id:359376 feces adult twins and mothers; TS51 clone TS51_a03f11 FJ3696
FJ371129.1 gg_id:364544 feces adult twins and mothers; TS6 clone TS6_a01c08 FJ3711
EU509276.1 gg_id:263476 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap47a09 EU509

173.9	4988.9	4760.0	5047.2	6490.9	4656.8	5826.0	3677.9	4331.4	1843.6	3469.7
247.4	1756.1	2894.5	2737.9	875.3	1621.0	1482.1	2462.4	627.7	433.3	1780.1
58.7	1507.3	1562.7	1710.5	2152.5	1368.1	2110.0	1463.2	926.7	748.5	1204.3
301.1	5472.8	5727.7	6139.5	7503.9	5136.5	7219.8	4734.5	5185.7	2111.6	3902.7
352.4	3476.9	3997.8	4585.3	4019.2	3081.4	4212.4	3068.2	4866.0	2562.7	3415.7
121.6	3920.7	3676.9	4319.5	5724.9	4049.1	5226.1	3711.6	3362.9	1725.1	2540.7
47.4	1713.8	1618.7	1863.5	2470.4	1922.9	2755.3	2620.8	2045.8	551.7	1066.9
246.3	6344.4	6281.6	6784.6	8378.6	6212.3	8075.6	5313.4	5484.4	2275.6	5285.9
63.2	4626.0	4194.5	4770.0	6251.3	4911.7	6057.1	4412.0	3950.3	2156.4	2879.0
1503.2	3717.4	2999.8	3394.1	3106.3	3927.2	3621.0	3592.3	3511.0	3410.5	2754.0
250.0	4102.3	4389.0	5341.1	6022.0	4152.5	5809.2	4001.3	3712.8	2859.9	3427.2
262.9	3664.3	3783.5	4343.3	5099.4	3723.3	4907.6	3386.7	3342.8	1788.5	3258.9
155.3	4125.6	4089.3	4645.1	5454.6	4180.0	5417.6	3529.3	3206.0	1860.5	3528.4
2683.5	5128.7	4613.0	5143.7	6991.7	5336.1	6012.2	4558.9	4766.0	2582.7	3497.0
239.5	4808.9	4737.7	5421.2	6616.2	4784.8	6419.6	4093.2	4494.8	2800.3	4159.8
5336.2	7623.9	8005.2	9542.8	9440.1	8651.1	10495.1	10455.8	10569.4	12031.2	11498.5
11889.4	10456.3	10127.4	10954.9	13317.4	11064.4	14086.5	10223.8	13377.6	7675.6	10936.7
370.9	4643.0	4929.9	5266.6	6837.4	5168.0	6562.0	4445.7	5059.5	2289.3	3661.9
450.4	6420.5	6187.9	6808.7	8272.6	6375.2	8302.6	5721.4	5923.1	3240.5	5897.0
401.2	4412.9	4055.1	4292.5	4257.3	4107.8	4901.4	3702.4	4088.4	3249.9	5364.1
116.9	3538.4	3609.6	4278.2	4172.4	3574.6	4171.1	3045.1	4291.9	2639.3	3701.1
146.5	4185.7	4453.6	4312.3	5204.8	3922.4	4922.3	3329.8	3859.0	1489.0	3039.0
187.4	4109.4	4205.6	4347.5	5296.6	3928.0	5077.4	3350.8	3435.2	1183.9	3066.2
159.8	5033.2	4797.6	4984.7	6382.4	4767.2	6363.1	3884.0	3902.7	1742.6	3807.2
174.8	3712.3	3613.1	3758.0	4715.8	3478.0	4158.4	2742.5	2899.9	1054.7	2384.0
23560.7	6461.8	5987.2	7809.4	6404.4	6127.0	7063.2	7291.7	9424.6	6660.8	8626.4
6404.6	5349.8	4858.8	5497.2	5757.3	5598.5	6503.7	5133.0	4695.0	4045.5	7454.1
212.0	4706.8	5110.9	5729.3	6754.3	4562.5	6472.2	4182.9	4340.9	1854.2	3248.8
235.3	4588.0	4375.5	4980.6	6197.6	4622.4	6193.3	3919.9	3767.2	2672.7	3999.9
95.2	1563.4	865.9	717.7	694.6	804.1	872.0	774.8	1295.7	820.3	514.4
272.3	5141.1	5517.6	5851.0	6789.7	4857.1	6838.6	4433.0	4267.9	1885.8	3639.1
214.4	3702.3	4074.2	4802.8	5349.5	3718.3	4996.0	3586.2	3623.4	2164.5	3128.6
494.0	6397.0	5480.2	6277.3	7332.9	6558.2	7419.4	5527.8	5929.7	3794.2	6433.5
38.7	1641.4	1247.2	1240.8	1837.2	1815.4	1721.7	1152.1	1393.8	702.7	1311.7
3116.4	8202.7	8629.3	7889.7	8317.4	7337.5	9447.8	6883.4	9155.9	6398.7	8684.4
186.5	5401.5	5352.4	5636.6	7071.8	5106.9	6745.0	4286.2	4771.3	1972.7	4151.8
83.3	3075.6	3606.0	4220.3	4100.0	3223.9	4447.3	3159.8	3364.5	2689.9	2601.5
66.4	3802.6	3574.1	4092.9	5200.9	3935.7	5014.6	3593.6	3315.1	1922.3	2429.9
2126.3	1197.6	866.7	882.0	953.3	1048.0	839.6	1066.4	1692.0	1622.1	1458.3
264.5	3448.6	4029.7	4626.5	5083.8	3513.2	4902.1	3479.3	3350.6	1794.9	2893.4
316.6	2666.8	4163.7	3245.6	1613.6	2690.9	2124.3	2498.4	1668.9	634.9	4322.8

3690.0	2831.1	3988.7
1324.8	1802.3	528.8
1375.8	304.9	1448.1
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2845.7	2624.0	2711.1
3459.3	2429.4	3341.1
2050.2	1808.2	1277.8
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3278.8	3173.5	3617.4
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4598.5	3343.3	4913.1
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7570.5	12275.4	9575.3
9766.1	8464.1	10527.1
4423.6	4525.1	5595.5
5891.0	4477.1	6728.2
3656.7	3988.2	3698.6
2745.1	2533.6	2878.9
3215.4	2550.2	3498.0
3538.8	2943.7	4350.0
4304.7	2954.3	4417.7
2805.6	2321.5	3355.5
6400.5	6833.2	5817.5
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4044.4	3308.6	4253.9
479.2	804.6	701.9
4388.6	3521.3	5115.7
3441.6	3248.8	4608.8
5570.5	4498.2	4920.5
1019.6	878.2	1784.6
6933.1	6490.6	6798.5
4377.3	3453.4	4983.1
2973.1	2219.7	2288.4
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751.2	1093.8	715.4
3339.6	3361.1	4428.1
1710.0	2451.3	1262.8

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AY271254.1 gg_id:108381 Akkermansia muciniphila AY2712
EU763663.1 gg_id:329021 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7636
DQ803966.1 gg_id:175631 human fecal clone RL200_aai60e04 DQ803
FJ365471.1 gg_id:364577 feces adult twins and mothers; TS20 clone TS20_a03c08 FJ3654
FJ369765.1 gg_id:360437 feces adult twins and mothers; TS51 clone TS51_a04e09 FJ3697
FJ365053.1 gg_id:361231 feces adult twins and mothers; TS1 clone TS1_a02c08 FJ3650
EU768293.1 gg_id:335652 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7682
DQ803735.1 gg_id:174931 human fecal clone RL200_aai57g05 DQ803
EU763518.1 gg_id:324181 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7635
EF605150.1 gg_id:228461 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6051
AY977862.1 gg_id:117139 human cecum mucosal biopsy clone LF60 AY9778
DQ805536.1 gg_id:187614 human fecal clone RL203_aai63h08 DQ805
AY979545.1 gg_id:122434 human transverse colon mucosal biopsy clone M203 AY9795
AY978016.1 gg_id:116512 human cecum mucosal biopsy clone LH55 AY9780
EF099119.1 gg_id:196722 mouse cecum clone SWPT2_aaa02e11 EF0991
DQ805988.1 gg_id:193357 human fecal clone RL186_aah59f01 DQ805
DQ806880.1 gg_id:181550 human fecal clone RL198_aaj74f05 DQ806
DQ805309.1 gg_id:190845 human fecal clone RL203_aai61a01 DQ805
EU768222.1 gg_id:353694 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7682
DQ806875.1 gg_id:199020 human fecal clone RL198_aaj74e01 DQ806
FJ369500.1 gg_id:359082 feces adult twins and mothers; TS51 clone TS51_a01c11 FJ3695
FJ365276.1 gg_id:362860 feces adult twins and mothers; TS1 clone TS1_a04h10 FJ3652
EU467005.1 gg_id:289470 African elephant feces clone AFEL2_aao32f01 EU4670
FJ369724.1 gg_id:359380 feces adult twins and mothers; TS51 clone TS51_a04a08 FJ3697
DQ805402.1 gg_id:187472 human fecal clone RL203_aai62b06 DQ805
FJ363939.1 gg_id:356979 feces adult twins and mothers; TS150 clone TS150_a01b06 FJ3639
DQ806025.1 gg_id:178761 human fecal clone RL186_aah60b02 DQ806
EU763566.1 gg_id:308538 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7635
EU459757.1 gg_id:291532 ring-tailed lemur feces clone RT_aai12c06 EU4597
EU763340.1 gg_id:355331 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7633
FJ371365.1 gg_id:356771 feces adult twins and mothers; TS6 clone TS6_a04b02 FJ3713
DQ824286.1 gg_id:194232 human fecal clone RL304_aal74a01 DQ824
FJ366780.1 gg_id:361014 feces adult twins and mothers; TS27 clone TS27_a03g05 FJ3667
EU767349.1 gg_id:307006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU7673
AJ315481.1 gg_id:24442 isolate HuCC13 clone AJ3154
DQ824346.1 gg_id:187580 human fecal clone RL304_aal74g09 DQ824
EF402545.1 gg_id:216106 human fecal clone SJTU_B_09_36 EF4025
DQ805361.1 gg_id:180315 human fecal clone RL203_aai61f09 DQ805
EF098504.1 gg_id:179446 mouse cecum clone SWPT15_aaa04d10 EF0985
EU006393.1 gg_id:253279 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU0063
EU470114.1 gg_id:290245 trancaspain urial feces clone TU1_aaa01e03 EU4701

202.2	1564.3	1842.1	1395.3	1489.4	1412.8	1550.8	1204.6	1246.5	528.6	1519.0
84.0	3664.3	3440.1	3897.0	5047.0	3777.7	4709.4	3465.9	3636.5	2058.3	2499.9
248.0	2932.9	3224.8	3448.4	3906.4	2554.0	3603.0	2649.1	2575.5	1831.3	2453.3
184.6	5235.7	4817.9	5353.3	6606.0	5271.4	6684.7	4488.8	4652.0	2947.3	4527.0
199.3	3968.9	4170.7	4115.0	5140.4	3939.6	4813.7	3349.6	3496.1	1121.5	2940.6
322.1	3599.8	4054.4	4376.4	5069.2	4016.2	5098.9	3641.7	3775.8	1798.3	3541.2
1898.3	3798.2	3442.3	5081.6	5770.8	3676.2	5175.5	4457.4	4365.9	3167.9	2655.9
209.1	4540.9	5200.1	5468.3	6614.5	4372.7	6548.7	3887.4	4259.4	1851.3	3118.6
2793.0	4164.6	3906.7	4190.9	5171.9	4122.4	4306.9	3557.5	4313.4	3034.1	3587.6
348.5	2766.4	3192.7	3383.8	3665.8	2447.3	3555.8	2563.8	2416.2	1661.0	2279.9
54.9	2788.7	2597.6	2908.9	3097.4	2432.8	2587.8	2301.6	3374.7	1635.9	2521.5
23261.5	5748.8	5808.9	7426.7	6611.6	5819.9	6501.2	7089.7	7199.1	6249.3	8653.1
85.9	3307.6	3313.7	3740.2	3201.3	3219.5	4540.1	3042.2	2379.0	1293.3	3207.9
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133.2	4931.5	4430.5	4774.3	6770.5	4902.5	6301.3	3648.2	3616.5	1747.9	3355.5
106.4	4583.0	4668.7	4864.4	6248.5	4530.3	5798.9	4224.2	4079.4	1953.6	3510.7
545.8	5478.3	4420.2	5238.9	5876.3	5301.8	5708.3	4108.0	4828.0	3084.1	5638.3
112.9	3189.0	3246.4	3732.0	4442.5	3295.7	4070.4	3103.8	3368.8	1788.0	2094.4
2712.2	4445.4	4185.2	4691.9	6130.6	4537.4	5066.1	4071.5	4218.0	2488.3	3238.6
73.1	988.4	1312.9	1311.6	1192.9	1160.9	1584.6	1345.1	1057.4	324.5	1155.3
5607.4	3186.3	3567.5	3135.7	2543.8	2917.0	3575.7	2910.5	3027.1	1457.9	3376.3
292.9	4032.9	3953.1	4349.6	5515.9	4325.4	5418.5	3512.1	3504.7	1813.3	3369.3
183.3	3940.2	4804.1	4945.4	5460.3	3837.0	5933.5	3736.7	3855.9	1493.7	2835.1
4347.0	5370.5	5607.9	5676.6	5706.7	5103.1	6241.3	5088.0	5312.3	2579.5	6071.9
59.9	3755.4	3371.7	3848.6	5091.5	4026.7	4921.0	3495.4	3078.1	1479.4	2214.7
210.1	4580.7	4225.1	4817.7	5968.9	4462.4	5943.8	3774.7	3830.4	2544.2	3708.1
344.3	3897.4	3454.2	4831.1	5132.9	3642.1	4805.8	4605.6	5320.6	4018.3	2838.9
62.4	4048.8	3742.1	4264.9	5386.2	4194.8	5497.2	4023.3	3463.3	1901.1	2613.7
1738.1	8056.2	6606.8	7470.4	7889.4	7987.2	8117.0	6223.5	10170.2	6726.6	9538.9
98.2	3604.5	3588.7	3939.2	5218.3	3992.4	4952.5	3695.8	2925.0	1164.6	2369.6
280.1	4433.9	4669.7	5683.9	6685.0	4450.5	6192.1	4323.0	4515.9	3117.9	3690.7
134.2	4063.1	4424.8	4866.8	6119.3	3979.4	5980.4	3364.6	3897.3	1700.6	2820.8
159.9	5299.8	4985.3	5426.3	7485.7	5242.2	6683.2	4050.4	4547.1	1978.0	3700.1
217.1	3693.8	3844.0	4563.1	5396.6	3498.5	4866.8	3466.3	3616.5	2821.2	2688.4
4991.3	8265.7	8194.5	9067.0	8316.4	9565.6	8510.2	7904.1	11224.5	8581.6	10719.1
198.4	5261.0	5317.5	5404.2	6915.5	5118.5	6481.2	4285.0	4927.5	1875.0	4026.3
33.6	2172.1	2027.6	2069.6	2773.7	2118.3	2803.2	1587.6	1616.7	791.6	2321.7
69.6	3129.5	3159.4	3274.8	4123.3	3473.3	3998.3	3266.6	2642.9	1328.7	1985.3
5753.8	5386.2	4710.1	5287.4	4848.5	5001.8	5116.8	5568.5	5781.2	3881.0	5954.2
4342.6	2564.0	3373.3	3838.5	3979.7	3341.9	4098.5	3169.6	3872.8	1839.4	3319.1
823.5	6952.3	6371.7	6815.3	6462.8	6605.4	7229.0	5827.1	9737.2	6137.4	4205.2

1294.0	1410.7	1402.6
3329.0	2450.8	2977.2
2491.0	2302.7	3357.1
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3401.3	2872.7	4185.8
3475.0	3572.6	4399.1
3729.9	2989.4	2443.1
3795.9	3013.7	4424.1
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5971.2	5805.5	5469.9
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4081.0	2939.2	3915.8
3923.8	3860.2	4220.2
2931.4	2225.9	2672.1
3861.8	2954.6	3908.9
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1570.3	851.9	2127.2
2521.9	3273.1	2599.3
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EF099214.1 gg_id:199361 mouse cecum clone SWPT2_aaa04a08 EF0992
FJ362945.1 gg_id:363199 feces adult twins and mothers; TS148 clone TS148_a01b02 FJ3629
AY982465.1 gg_id:118488 human sigmoid colon mucosal biopsy clone MM09 AY9824
GQ491900.1 gg_id:546153 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU006398.1 gg_id:239988 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF605166.1 gg_id:230601 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6051
EF099268.1 gg_id:175690 mouse cecum clone SWPT2_aaa04g11 EF0992
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EU508159.1 gg_id:264121 cecal contents Mus musculus strain C57BL/6J; MD26 clone MD26_aaa02a06 EU508
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EU459667.1 gg_id:288635 ring-tailed lemur feces clone RT_aai10e08 EU459
DQ797676.1 gg_id:190478 human fecal clone RL206_aaj14e06 DQ797
DQ803739.1 gg_id:174281 human fecal clone RL200_aai57g10 DQ803
EU506565.1 gg_id:277003 cecal contents Mus musculus strain C57BL/6J; MD19 clone MD19_aaa04d05 EU506
GQ492737.1 gg_id:585879 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
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DQ793678.1 gg_id:173820 human fecal clone RL246_aai75e04 DQ793
GQ493064.1 gg_id:577245 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493

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93.6	3314.1	3347.5	3829.7	4472.0	3281.9	4666.9	3037.9	3903.6	1994.7	2953.6
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2437.8	4856.0	3693.3	4824.3	5104.2	4352.9	5390.4	4190.1	3656.8	1638.3	3783.9
324.5	4115.4	4171.2	4903.4	5388.4	4031.3	5019.2	3791.8	3562.3	2488.5	3000.9
106.1	2523.6	2822.1	2908.0	3484.7	2181.0	3122.1	2197.9	2331.9	1693.6	2168.6
184.6	5522.5	5447.1	5660.8	7356.1	5408.5	6788.0	4470.2	4742.8	1800.0	4359.3
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165.5	3464.3	3866.8	4242.5	4858.4	3207.8	4830.5	2860.6	3184.1	1452.3	2314.2
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461.1	3227.4	2731.6	3107.4	2952.0	3013.9	3287.0	3235.4	3930.3	2254.1	2406.6
884.4	2639.2	2531.9	2481.9	2387.9	2479.4	2566.7	3255.5	2527.4	2057.4	3785.2
3953.3	5990.2	6117.9	6561.1	8857.1	6364.6	7823.6	5583.5	6969.4	2160.5	5305.6
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97.7	4168.4	4072.2	4461.4	5632.7	4060.6	5596.7	3420.7	3106.4	1476.9	3007.9
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365.5	2364.6	2541.6	3028.3	3231.2	2143.0	3081.9	2272.1	2021.8	1620.2	1929.6
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184.0	5474.3	5184.3	5778.3	7526.0	5348.5	7152.8	4392.6	4844.3	2226.2	4128.8
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6280.5	3510.9	2979.4	2794.2	3255.5	2677.6	3246.4	3422.3	4300.8	1368.5	1610.7
240.1	6211.0	5924.5	6304.3	7991.2	6277.9	7721.7	5277.7	4606.6	1965.8	5179.9
3790.3	5010.6	5624.4	5891.3	7428.1	5492.7	7014.4	4907.0	6529.3	2073.8	4979.0

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3697.5	2658.5	4285.8
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2206.6	2109.0	2745.5
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1712.7	1794.9	1414.8
2348.8	2602.9	3201.3
2717.3	2336.0	3843.2
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EU507216.1 gg_id:270914 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa03f12 EU507
FJ367560.1 gg_id:365237 feces adult twins and mothers; TS2 clone TS2_a01a04 FJ3675
DQ823974.1 gg_id:179397 human fecal clone RL204_aaj57f06 DQ823
GQ491465.1 gg_id:537012 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU506850.1 gg_id:260295 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07c08 EU506
DQ797870.1 gg_id:196376 human fecal clone RL206_aaj16g12 DQ797
EU006464.1 gg_id:245541 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
FJ367593.1 gg_id:359766 feces adult twins and mothers; TS2 clone TS2_a01d01 FJ3675
DQ805310.1 gg_id:177858 human fecal clone RL203_aai61a03 DQ805
EF605156.1 gg_id:227800 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EF603774.1 gg_id:233386 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6037
EF099020.1 gg_id:180596 mouse cecum clone SWPT2_aaa01b09 EF099
GQ491995.1 gg_id:584653 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU006396.1 gg_id:251790 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU006177.1 gg_id:253234 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
FJ371421.1 gg_id:363508 feces adult twins and mothers; TS6 clone TS6_a04g05 FJ3714
EU507388.1 gg_id:276012 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa02e06 EU507
EU507089.1 gg_id:266625 cecal contents Mus musculus strain C57BL/6J; MD22 clone MD22_aaa01a11 EU507
AY979494.1 gg_id:123265 human transverse colon mucosal biopsy clone M135 AY979
DQ824431.1 gg_id:176638 human fecal clone RL304_aal75h11 DQ824
GQ491867.1 gg_id:579826 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ803761.1 gg_id:190136 human fecal clone RL200_aai58b01 DQ803
DQ793686.1 gg_id:182478 human fecal clone RL246_aai75f02 DQ793
DQ803743.1 gg_id:194760 human fecal clone RL200_aai57h03 DQ803
EF603613.1 gg_id:233237 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
EF602796.1 gg_id:232549 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6027
DQ803928.1 gg_id:176439 human fecal clone RL200_aai60a08 DQ803
GQ492726.1 gg_id:543645 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ492710.1 gg_id:533891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU469988.1 gg_id:289362 trancaspain urial feces clone TU1_aaa03b07 EU469
GQ491356.1 gg_id:589626 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ793673.1 gg_id:177438 human fecal clone RL246_aai75d08 DQ793
GQ493744.1 gg_id:562137 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ803674.1 gg_id:182771 human fecal clone RL200_aai57a07 DQ803
DQ824465.1 gg_id:199450 human fecal clone RL304_aal76c12 DQ824
EU451703.1 gg_id:316576 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU451
EU006404.1 gg_id:254430 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF605151.1 gg_id:234253 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EF603854.1 gg_id:230720 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6038
DQ803856.1 gg_id:179974 human fecal clone RL200_aai59b12 DQ803

210.0	3526.5	3799.5	4368.7	4857.5	3286.2	4976.6	3005.0	3379.9	1694.2	2405.6
20336.6	8708.2	7442.7	8358.2	8997.6	8339.4	8800.0	7160.8	10212.1	6633.8	13502.3
3842.1	4375.9	5316.6	5333.1	6089.8	4689.6	6157.2	4562.5	5526.5	1381.6	4275.6
35.4	26.7	32.0	31.3	44.7	21.7	42.6	23.2	20.5	22.2	24.7
4139.9	5362.9	6629.8	7227.2	8606.1	6091.4	8097.6	5378.7	7807.7	3270.6	5900.4
3960.1	7291.8	6435.3	7039.3	6438.4	7696.4	6609.1	6136.3	11161.2	7049.5	10210.4
48.6	1937.2	1670.2	1879.7	2588.9	2181.1	2640.1	1459.3	2027.1	1201.2	1217.5
644.4	3210.6	3058.6	3232.7	3610.1	3021.2	3285.2	2675.7	2413.9	1613.4	2773.6
63.7	4378.7	3827.1	4607.5	7041.0	4300.5	5352.1	3124.8	3435.2	2411.4	2907.3
202.7	1513.1	1672.9	1979.0	2190.5	1589.5	2027.1	2165.1	1155.1	489.5	993.5
203.1	3783.6	4018.7	4188.0	5061.7	3483.1	4614.8	3185.6	3359.6	2222.5	3041.8
230.3	3743.8	3843.6	4064.3	4737.3	3449.2	4320.2	3145.6	3021.9	1738.7	2844.8
1895.9	8695.4	6855.7	7234.7	8458.8	7739.6	8625.4	6388.3	12254.8	8951.2	8064.1
3917.6	3866.3	4133.0	4368.0	5750.4	4207.6	5787.2	3869.5	4638.1	1427.0	4036.6
637.8	6304.7	5783.8	6266.1	7572.1	6623.7	7076.9	5002.0	6281.3	4490.3	4860.0
10693.1	5478.4	6001.0	6911.5	6328.3	4956.7	6008.3	4811.8	5805.1	3913.2	6260.9
321.4	4188.3	4519.1	4767.2	5820.8	4019.7	5336.0	4013.4	4069.7	1424.4	2992.9
27.9	860.2	845.9	1419.0	583.5	471.1	544.4	455.7	67.9	56.0	404.3
3136.4	9383.4	9251.6	10244.8	8299.9	9637.5	8460.8	8060.0	11238.1	8585.2	12543.4
350.1	7375.2	6182.7	7168.8	7639.2	7218.5	8731.1	5606.8	5848.6	4943.4	8037.2
50.7	3287.4	2877.3	3157.8	4297.1	3564.7	4397.9	2566.3	2645.3	1279.3	2684.3
4350.1	6473.2	7202.0	7933.9	10378.0	7328.8	9119.5	6391.7	9288.3	3786.4	6688.1
41.4	3879.5	4312.4	4132.0	5477.0	4269.0	5785.9	4323.1	2897.8	1114.0	2643.3
11949.0	6295.8	5466.3	5475.9	4978.7	5211.6	5460.1	4869.2	7017.5	3560.2	8385.5
220.9	4472.4	4827.4	5407.2	6569.1	4329.1	6493.4	3815.8	4252.6	1838.4	3087.8
4128.5	7832.1	7634.8	8788.5	9942.3	7632.0	9226.8	7161.0	9154.8	9221.3	8333.0
349.9	4157.7	4386.5	4695.9	5445.5	3802.7	5053.3	3609.9	3432.6	2358.9	3314.7
1450.0	1118.6	1201.2	1110.9	832.0	997.3	1033.6	1049.0	1278.3	396.5	979.3
213.8	2184.6	1933.2	1909.8	3098.1	2090.6	2770.9	1779.8	1875.3	1033.6	1604.6
142.3	2675.4	2249.8	2096.7	3188.6	2569.7	2937.4	2478.2	1829.4	874.1	1875.0
1064.2	10183.9	10146.1	11252.5	12549.4	10268.1	13419.5	9530.2	8174.9	7284.3	12033.3
4344.2	7225.8	7152.7	7765.0	10061.0	7703.9	9407.4	6702.8	8784.6	3769.8	6964.3
133.4	5156.1	4665.5	5192.3	6435.0	5150.5	6403.6	5294.1	6420.2	2780.9	4816.3
4289.0	6788.1	6832.6	7595.8	9678.1	7037.0	8647.8	6432.2	8743.2	3616.4	6612.4
55.4	56.8	79.7	104.7	85.5	81.1	94.9	75.4	57.9	41.8	63.6
120.7	2385.7	2409.1	2787.0	2741.5	2201.6	2901.3	1827.7	3411.3	1654.0	2368.7
31469.0	9578.0	8743.7	9819.6	10106.7	8710.9	10264.0	10095.5	14054.9	9768.5	12486.9
244.3	2851.8	2967.5	3526.1	3803.7	2633.8	3520.6	2737.6	2459.7	1922.3	2182.1
331.1	2986.2	3164.2	3293.6	3801.1	2731.9	3627.2	2713.7	2573.0	1666.5	2353.3
91.0	3864.6	3591.1	3499.6	3721.6	3158.0	3577.4	3052.1	2860.5	1596.1	2801.1
463.5	11201.4	10494.1	12406.4	10299.2	11253.1	12062.3	10530.7	9255.6	4982.8	12122.0

2962.2	2601.0	3174.6
7086.3	6545.7	5179.1
4223.0	3836.1	6192.8
34.0	65.6	30.3
5431.0	4889.3	6887.3
5872.8	8410.1	5968.5
1864.9	1828.7	5517.5
2449.6	2231.7	3969.7
3887.8	2849.0	3845.9
2053.4	2019.5	2020.3
3151.5	2727.6	4401.2
2935.0	2578.5	4195.0
5781.1	5498.6	5889.7
4005.3	2884.1	5511.8
5867.3	3986.4	6487.6
4603.5	4868.9	5898.3
3578.6	3771.4	4667.0
895.3	656.6	3476.1
7670.0	9462.5	8445.1
5888.1	5050.6	6240.3
2211.6	1420.0	2782.3
6306.0	5934.3	8612.5
3237.2	3237.0	4814.0
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3446.6	3253.9	4808.7
837.9	1825.9	703.7
1770.3	2088.5	2884.1
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GQ493707.1 gg_id:588996 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU474343.1 gg_id:297296 western lowland gorilla feces clone GORSD_aaa02d12 EU4743
DQ803801.1 gg_id:175615 human fecal clone RL200_aai58e11 DQ803
EU508365.1 gg_id:262989 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa03h06 EU5083
FJ367694.1 gg_id:364483 feces adult twins and mothers; TS2 clone TS2_a02e02 FJ3676
DQ797786.1 gg_id:197591 human fecal clone RL206_aaj15g12 DQ797
DQ824257.1 gg_id:192313 human fecal clone RL304_aal73f01 DQ824
EF605153.1 gg_id:232422 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6051
EF603066.1 gg_id:230664 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF099628.1 gg_id:184620 mouse cecum clone SWPT4_aaa02b07 EF0996
EF099133.1 gg_id:198936 mouse cecum clone SWPT2_aaa02g06 EF0991
EU507293.1 gg_id:262054 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa01c03 EU5072
GQ493815.1 gg_id:568909 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU509193.1 gg_id:268293 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45f10 EU5091
GQ448638.1 gg_id:544288 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448
EU474260.1 gg_id:294287 western lowland gorilla feces clone GORSD_aaa03a03 EU4742
EF604906.1 gg_id:234335 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
EF099038.1 gg_id:178077 mouse cecum clone SWPT2_aaa01d08 EF0990
EU459692.1 gg_id:300791 ring-tailed lemur feces clone RT_aai10h12 EU4596
EF603938.1 gg_id:227678 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
GQ493480.1 gg_id:540440 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ824314.1 gg_id:194496 human fecal clone RL304_aal74d01 DQ824
GQ491874.1 gg_id:550767 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU508387.1 gg_id:270147 cecal contents Mus musculus strain C57BL/6J; MD27 clone MD27_aaa04g02 EU5083
EF604791.1 gg_id:232493 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
GQ492159.1 gg_id:561627 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU451506.1 gg_id:353432 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4515
EF604911.1 gg_id:227993 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
DQ807255.1 gg_id:187988 human fecal clone RL244_aaj48b11 DQ807
GQ493932.1 gg_id:570491 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY980944.1 gg_id:121335 human rectum mucosal biopsy clone LR95 AY9809
EU474294.1 gg_id:294378 western lowland gorilla feces clone GORSD_aaa03b05 EU4742
DQ824408.1 gg_id:199666 human fecal clone RL304_aal75f10 DQ824
EU506595.1 gg_id:269033 cecal contents Mus musculus strain C57BL/6J; MD20 clone MD20_aap53a03 EU5065
EF099070.1 gg_id:175442 mouse cecum clone SWPT2_aaa01g10 EF0990
EF099675.1 gg_id:187986 mouse cecum clone SWPT4_aaa02g06 EF0996
EF602794.1 gg_id:228401 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6027
EF099117.1 gg_id:180918 mouse cecum clone SWPT2_aaa02e08 EF0991
GQ492323.1 gg_id:588591 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ803906.1 gg_id:183355 human fecal clone RL200_aai59g07 DQ803

3662.1	3861.7	3954.1	4498.9	5831.5	3977.7	5315.8	3619.4	4916.2	2028.5	3843.6
4231.6	6036.2	7273.2	7915.8	9893.5	6979.3	8636.1	5941.2	9213.1	3639.3	6425.0
104.5	5997.5	5230.8	6025.2	7119.9	5987.2	7036.7	5956.8	7164.4	3637.4	6239.2
360.8	6153.4	6822.6	7453.2	8643.8	6010.5	8177.7	5557.8	5856.9	2409.7	4836.7
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363.4	7154.9	5241.9	5846.7	7900.1	6123.9	7139.5	5368.6	6816.5	3785.3	4783.8
115.4	1557.5	1269.6	1412.6	2092.1	1324.6	1625.0	1031.4	1047.8	494.7	964.8
186.3	3905.8	4388.3	4707.2	5118.8	4166.9	4829.4	3531.7	4514.6	3673.2	3885.1
250.4	2851.0	3189.0	3479.0	3840.9	2451.3	3706.8	2539.7	2715.6	2191.1	2444.4
445.2	4968.0	4867.9	5308.2	6248.9	4602.8	6012.4	4268.1	4632.0	2734.3	4046.1
7804.3	5777.7	4993.4	4647.5	4285.4	4707.0	4841.2	3916.1	5460.9	3297.0	7208.8
686.4	1822.3	1837.2	2075.4	1720.9	1911.6	2379.2	2246.7	1336.2	536.0	2550.9
313.0	4666.0	4127.1	4658.2	4689.5	4173.4	4715.4	3572.5	7081.2	3720.6	4188.3
1194.5	4098.7	4209.2	4301.1	4960.0	4139.3	5113.5	3830.2	4115.6	1455.2	3380.0
41.7	6155.2	5204.0	5838.5	5992.1	5676.7	6574.8	4464.1	7645.6	4813.5	7540.0
278.5	6052.3	4972.4	4666.3	5055.6	4654.2	5318.2	5492.4	5466.5	3436.5	4961.3
124.7	4566.8	4703.6	5189.7	6314.0	4452.7	6390.0	3632.6	3970.8	1708.8	3362.4
230.4	1645.2	1713.3	2052.2	2121.4	1429.3	2052.0	1753.0	1356.1	1182.3	1269.7
673.3	2054.6	2245.3	2538.7	2317.8	2101.9	2300.4	1897.5	3664.4	2072.7	2068.5
3510.8	3223.7	3318.4	3754.7	2402.8	3122.3	3622.2	3453.8	3308.6	2295.2	3902.6
196.2	3786.8	4022.2	4191.8	5066.5	3484.7	4620.0	3186.4	3360.4	2224.4	3041.6
68.0	3334.8	3179.8	3609.1	4544.7	3049.0	3566.4	2252.3	2574.4	1559.2	1987.1
7212.2	5977.1	5328.7	5980.1	6466.4	5515.3	6121.0	4335.4	8075.9	4253.8	7305.8
3927.8	5114.7	5874.8	6152.2	7435.3	5634.4	7325.2	5165.7	6493.7	1769.6	4899.5
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223.6	2918.9	3194.4	3412.6	3887.8	2544.8	3591.6	2634.0	2569.5	1831.2	2295.5
1951.6	3143.3	2517.7	2660.2	3126.6	3090.2	3125.1	3033.8	2408.7	853.7	3959.3
223.0	2156.9	2112.4	2033.5	2770.6	1976.4	2370.3	1923.5	1762.9	841.4	1514.6
284.5	2856.9	3086.8	3228.3	3819.6	3129.1	3771.4	2339.8	2486.8	1615.2	2764.4
380.5	2807.7	2537.1	2995.2	3017.4	2890.4	2985.6	2572.5	3179.1	1791.7	2908.8
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365.4	5856.4	6401.9	6891.9	8717.5	5939.5	8238.4	5391.0	5663.7	2919.0	4596.1

3599.9	2617.5	4827.1
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EU474311.1 gg_id:295992 western lowland gorilla feces clone GORSD_aaa04a06 EU474
EF099272.1 gg_id:196113 mouse cecum clone SWPT2_aaa04h05 EF0992
GQ493776.1 gg_id:555563 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU509172.1 gg_id:269922 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap45d02 EU509
GQ491371.1 gg_id:546571 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF602896.1 gg_id:234636 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EF603614.1 gg_id:231947 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6036
EF602832.1 gg_id:227688 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EF605159.1 gg_id:232648 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6051
EU507757.1 gg_id:262819 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa04c08 EU507
EU453217.1 gg_id:340374 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
DQ793746.1 gg_id:183820 human fecal clone RL246_aai76f06 DQ793
GQ493424.1 gg_id:594106 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU506859.1 gg_id:275140 cecal contents Mus musculus strain C57BL/6J; MD21 clone MD21_aar07d09 EU506
DQ302110.1 gg_id:153007 Rubromonas marinus gen. sp. nov. first marine representative subdivision one Verru DQ302
AF513965.1 gg_id:62479 Verrucomicrobia clone LA1-B30N AF513
EF632724.1 gg_id:239291 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
AB252090.1 gg_id:155636 entrapped Puruogangri ice core clone PIC-D19 AB252
DQ015833.1 gg_id:140683 Antarctic lake water clone ELB19-212 DQ015
AJ318188.1 gg_id:46876 Waste-gas biofilter clone BItii14 AJ3181
GU208316.1 gg_id:546058 Study on Sediment Dongping Lake sediment clone Ser1-21 GU208
AB154319.1 gg_id:105709 freshwater clone S9JA-40 AB1543
FJ437947.1 gg_id:509859 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
DQ396121.1 gg_id:154817 deep-sea octacoral clone ctg_NISA122 DQ396
AY770729.1 gg_id:111348 Verrucomicrobia sea urchin Paracentrotus lividus clone PlS48 AY770
FJ715972.1 gg_id:558186 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7159
FJ437966.1 gg_id:511993 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
FJ825946.1 gg_id:556103 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea; FJ8259
GQ850550.1 gg_id:586112 surface water northern Bering Sea clone u82 GQ850
EU682496.1 gg_id:517793 Four Primer Sets Detecting Anammox s estuary sediment Mai Po Nature Reserve clo EU682
GU061933.1 gg_id:570181 and function microbial mesoscale eddy perturbations South China Sea clone S-5m-9 GU061
NR_026024.1 gg_id:564314 Prosthecobacter fusiformis str. FC4; ATCC 25309 NR_02
U60012.1 gg_id:1588 Prosthecobacter dejongeii U6001
U60013.1 gg_id:1593 Prosthecobacter vanneervenii str. FC2 U6001
EU104166.1 gg_id:319751 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
FJ612153.1 gg_id:585360 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.2.74 FJ6121
EU580493.1 gg_id:556878 Benthic diatoms Constance: functional interactions regarding growth and EPS-secret EU580
AY922120.1 gg_id:113378 farm soil clone AKYH1486 AY922
AB305640.1 gg_id:248402 Prosthecobacter sp. str. HAQ-1 AB305
EF516716.1 gg_id:225469 grassland soil clone FCPT546 EF5167
AB297805.1 gg_id:246659 Rubritalea spongiae str. YM21-132 AB297

103.6	3274.7	3493.0	3201.6	3945.3	3738.7	4575.7	3205.0	1595.8	731.5	2987.0
201.0	561.5	444.1	488.3	495.5	699.9	610.5	453.1	293.0	184.4	481.8
186.0	1658.2	1741.6	1734.8	2603.2	1795.9	2521.9	1529.6	1584.4	655.3	1266.5
453.2	8265.1	7005.9	7964.1	6581.0	8560.6	9341.3	6789.6	5502.8	2803.8	10104.5
115.4	2504.7	1839.6	1802.5	2793.6	1932.6	2147.6	1723.6	1319.1	1007.3	1600.4
54.4	5274.7	4734.2	5213.6	5913.5	5626.7	5525.6	4196.2	6119.7	4078.7	6251.1
686.8	3423.1	3870.3	4216.7	3891.6	3491.4	3921.6	3513.0	3557.8	2889.0	3798.8
252.4	2960.9	3254.1	3469.0	3919.4	2735.4	3625.8	2657.5	2579.7	1834.6	2456.1
4789.7	4762.2	5470.4	5960.2	6522.4	5085.4	6560.3	4804.4	6213.5	3007.2	6008.8
216.0	5051.0	4260.8	5047.8	6321.8	5156.3	6095.9	5169.7	4844.3	2498.5	4408.7
180.7	3021.9	2181.8	1700.5	2372.5	1828.7	2179.1	1344.7	3329.8	1883.6	1394.1
474.5	5457.4	5290.6	5273.6	6563.4	5182.7	6621.0	4323.9	4198.5	2274.9	4905.6
4796.2	5756.5	6193.5	6515.6	7121.7	6030.2	7035.0	5653.1	7335.4	3151.6	5960.1
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25.9	1020.5	1198.9	1269.4	1153.2	478.1	1382.4	514.6	1132.8	504.3	457.9
42.0	1492.3	1504.2	1522.1	2132.1	987.4	1727.5	833.2	691.6	377.6	650.3
42.3	718.5	1255.0	677.6	671.9	375.1	818.5	575.3	280.9	95.1	680.7
249.1	1950.4	2303.5	2880.0	4229.8	1994.5	4627.1	2122.7	2173.6	592.3	1354.6
274.2	4908.9	4382.5	4849.9	7613.2	4222.9	8099.5	3306.4	3939.1	1518.9	3400.8
78.2	122.0	145.4	205.2	344.7	138.8	297.3	152.3	161.7	111.7	85.1
127.4	4787.4	4423.7	4867.1	5294.3	4365.2	4975.5	3023.4	4165.9	2137.0	3074.7
63.1	5463.2	5037.1	4854.5	8196.7	5280.2	7005.8	3464.5	4179.9	2245.5	3529.5
2089.4	9297.7	8326.0	9707.8	12713.4	8288.7	11217.4	7438.5	10285.0	5899.4	8760.3
1949.8	3493.8	3946.7	4626.4	3816.9	3681.4	5059.9	3539.0	2824.6	1727.7	3054.0
109.6	2079.7	2468.0	2428.9	2694.7	2243.8	2944.7	2448.8	1783.6	932.2	1687.8
8271.7	6060.2	5749.2	6703.9	7564.4	5902.0	8174.0	6266.4	5642.2	4577.8	6178.8
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3299.6	8926.5	8219.1	8573.8	11566.4	9673.9	11153.2	7961.5	7887.4	3747.7	7485.3
44.6	656.3	509.4	603.2	902.0	1253.4	1002.3	531.7	989.3	114.1	192.6
247.9	2692.0	2514.7	2196.3	4136.5	3643.0	4829.4	2226.2	2321.9	706.0	1180.7
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757.1	5282.4	4928.0	5220.2	6799.7	5356.4	7164.3	5157.2	4158.0	1533.2	4615.4
390.8	4545.3	4405.7	4270.8	6107.2	5477.1	5721.0	3937.2	3495.0	1271.9	2862.1
41.6	539.4	489.9	375.4	450.7	1381.4	508.6	475.8	599.3	82.2	172.9
447.3	3128.8	2671.7	3180.2	3714.2	2786.1	3293.2	2306.7	2537.6	1500.3	3164.9

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1453.5	1806.9	2812.9
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4963.6	4064.3	5626.4
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8302.6	7671.1	10310.9
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2650.4	2079.6	3183.4
4374.9	2733.8	5793.2
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3916.1	4041.4	6358.5
4724.5	4577.8	5167.8
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471.3	686.6	667.2
2304.1	1837.1	3131.2

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FJ203294.1 gg_id:311682 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
FJ202109.1 gg_id:344975 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
AF454310.2 gg_id:63827 Mono lake clone ML316M-1 AF4543
AM040118.1 gg_id:149984 sandy sediments clone Sylt 22 AM040
AJ401121.1 gg_id:39097 Elbe river clone DEV055 AJ4011
EU491625.1 gg_id:258236 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
EU050932.1 gg_id:238891 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_02_56 EU0509
FJ437955.1 gg_id:549407 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
FJ543052.1 gg_id:523568 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
FJ437954.1 gg_id:565073 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
DQ300578.1 gg_id:146066 microbial ocean's interior amplicon single fosmid library pool 10m depth HOT statior DQ300
AY344427.1 gg_id:91270 Lake Kauhako 30 m clone K2-30-31 AY3444
EU236414.1 gg_id:290527 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F4 EU2364
DQ071119.1 gg_id:134657 marine surface water clone SJC3.21 DQ071
FJ205365.1 gg_id:549372 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
DQ395400.1 gg_id:155518 deep-sea octacoral clone ctg_BRRAA57 DQ395
GQ350683.1 gg_id:562414 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU491679.1 gg_id:269422 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
FJ542863.1 gg_id:522575 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
AM997555.1 gg_id:562351 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AJ441222.1 gg_id:55975 hydrothermal vent polychaete mucous clone P. palm C 85 AJ4412
DQ499289.1 gg_id:159582 acidic cave snottite biofilm clone CV35 DQ499
X90515.1 gg_id:1596 Verrucomicrobium spinosum X90515
FJ872374.1 gg_id:591617 and metagenomic Verrucomicrobia former agricultural grassland soil rhizosphere clor FJ8723
AJ441243.1 gg_id:57441 hydrothermal vent polychaete mucous clone P. palm A 54 AJ4412
GQ167324.1 gg_id:585845 Microbial Life -13C Brine Ice-Sealed Antarctic ice-entrained brine 16.5 m Lake Vida c GQ167
FJ623333.1 gg_id:510359 Efficient polyhydroxyalkanoates production waste-activated submitted process seque FJ6233
FJ543001.1 gg_id:526403 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
AB240273.1 gg_id:142471 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clor AB240
GQ259220.1 gg_id:552165 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
EU135492.1 gg_id:255112 tallgrass prarie soil clone FFCH1244 EU1354
FJ543027.1 gg_id:525506 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5430
AF234714.1 gg_id:23971 sludge clone A38 AF2347
GQ452903.1 gg_id:544574 Biodiversity planktonic bottom water Northern Bering Sea clone b31 GQ452
EU050940.1 gg_id:240964 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_25 EU0509
EU236322.1 gg_id:293293 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg5a1A9 EU2363
GQ259291.1 gg_id:560235 Microbial activities coastal marine sediments and water column Svalbard deep sedir GQ259
AJ401116.1 gg_id:48886 Elbe river clone DEV035 AJ4011
EU245399.1 gg_id:253042 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-B1: EU2453
AM259830.1 gg_id:211686 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-2-28 AM259
DQ513026.1 gg_id:161217 Microbial life fluids ridge flank crustal fluid clone FS142-18B-02 DQ513

466.4	1897.1	1838.9	2050.8	2653.4	2000.5	2829.9	2096.6	1688.5	936.8	1927.0
36.3	99.7	203.4	181.5	184.1	140.0	185.9	166.4	44.8	37.6	79.1
41.3	508.7	495.8	563.1	367.4	551.5	586.3	448.5	165.8	153.6	324.9
43.5	132.2	153.7	186.7	174.1	135.2	255.5	347.9	54.7	46.1	64.9
419.3	585.9	620.6	550.6	550.7	554.2	564.8	725.8	309.8	400.2	434.1
5443.9	9601.2	9766.8	11012.6	12457.9	9722.0	13135.5	9534.6	7622.3	6601.1	10408.5
1812.4	5716.7	6164.4	7673.6	7204.2	5826.4	8603.7	7087.0	3357.1	5351.1	5844.1
1214.6	4741.0	5305.3	5399.0	5902.9	5299.3	6409.1	5397.4	4624.3	3826.9	4281.5
66.7	3385.7	3195.1	2601.7	6363.2	4770.2	5379.3	3027.0	2602.1	1019.2	1564.9
424.3	2164.1	2164.6	2293.6	2363.2	2021.3	2797.1	1893.9	2496.6	580.1	1138.5
46.9	262.9	277.9	345.7	481.3	261.2	436.5	273.1	177.7	76.2	152.6
710.5	5322.8	4975.3	4810.4	7054.5	5599.0	6651.7	4483.0	5083.3	1926.7	3186.4
1474.7	11360.2	10665.5	10875.2	12068.0	10758.2	11280.1	9942.0	10313.5	8301.3	12222.9
83.2	1107.5	1318.6	1197.6	1230.5	1103.8	1036.1	1395.8	889.0	434.7	919.1
48.0	1734.5	2027.5	1582.0	2884.9	1898.7	3026.9	1661.7	1116.9	361.4	861.3
378.5	1828.8	1591.4	1307.2	1345.9	1746.9	1181.6	1457.7	2133.7	996.8	881.8
40.1	218.2	252.0	301.0	272.0	235.7	317.7	175.2	182.0	141.8	179.6
19537.7	6784.1	7829.3	8929.2	7858.6	7828.1	8193.6	8029.2	10194.0	7991.9	9723.7
566.1	4761.1	4556.3	5037.8	6151.4	5161.0	6175.6	4779.6	5150.4	1965.8	4261.0
681.5	6677.0	6508.4	6149.9	7560.5	6142.9	7461.0	6014.1	6727.3	3209.3	4655.4
61.5	656.9	736.4	718.5	663.6	646.4	685.0	1091.3	259.6	502.9	3585.7
51.8	25.1	25.4	26.7	28.8	25.4	32.3	23.2	22.2	20.6	32.9
49.8	141.9	247.9	92.7	224.4	432.4	393.6	945.8	36.8	321.9	191.1
11186.4	14009.1	12567.4	13701.2	13880.5	12835.7	14389.4	12252.8	14863.5	10400.4	15453.2
81.1	850.9	1095.6	1006.4	1758.4	949.1	1506.0	679.9	633.6	211.7	591.7
1241.0	8128.0	6845.2	7519.1	8738.7	7851.1	9263.7	6761.2	9832.4	4928.1	9081.3
996.0	11410.1	10952.5	12104.6	13783.8	11047.1	13997.7	10615.1	11652.0	5757.1	10948.3
680.2	5728.1	5685.4	6702.1	7891.4	5835.1	7699.1	6051.0	8033.5	1889.6	4516.8
239.6	3106.6	2584.8	2948.0	5234.1	3256.4	4883.2	2503.6	3065.4	886.6	1451.6
398.6	4562.6	3980.9	4924.8	4266.4	4251.6	5411.0	5011.3	2295.9	2418.8	4470.0
140.1	3553.0	3121.8	3294.9	3281.7	2354.7	4107.0	2105.0	2142.1	1304.4	2289.7
19795.2	10091.1	9495.6	10554.4	11217.5	10361.0	10936.7	9332.7	15537.3	8829.7	12992.0
44.8	282.4	342.6	263.5	255.5	300.3	227.9	217.5	226.1	88.8	313.0
549.1	5645.8	5878.5	5330.3	6828.9	6074.8	5732.4	4801.1	4880.9	4639.3	5574.3
1595.9	4891.4	5783.1	5377.5	6125.0	4804.8	6009.6	5025.8	6634.7	2620.2	6235.5
258.0	3486.1	3286.7	2359.7	2804.8	3046.8	2758.3	2390.6	3061.1	1723.2	1516.1
809.7	10490.2	9387.1	9180.6	11636.6	9445.6	11681.5	8695.1	14727.1	7479.2	7421.4
60.3	930.8	1437.9	1385.6	1874.2	1111.2	1140.3	613.1	343.9	357.9	266.2
42.8	1239.9	1289.9	1186.2	2644.7	1445.7	2233.0	998.6	514.7	140.2	463.3
103.1	4259.8	4192.8	4227.9	4030.4	4117.8	4151.6	4295.4	2684.6	2417.0	2821.3
697.2	3419.3	3397.4	3508.6	3965.3	3729.1	4216.5	3147.7	2751.1	2332.4	4302.8

1833.3	1769.4	2597.8
112.1	188.5	218.5
265.4	495.1	534.6
383.6	188.5	221.7
525.0	984.1	739.1
9966.3	9570.1	12234.3
6226.6	5523.2	7354.3
3829.7	5493.1	5889.8
3214.9	2621.0	3831.3
1290.0	1722.5	1995.6
210.6	241.7	180.2
4228.0	4277.9	5201.4
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1176.4	1828.0	1588.6
1455.1	1275.4	2467.6
1222.3	1577.5	1274.7
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11773.8	12397.2	12943.4
648.8	628.4	576.0
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5604.1	6309.5	6669.0
2188.8	2253.1	3246.2
3427.0	4296.5	5550.1
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1451.8	3161.0	3694.2

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FJ623345.1 gg_id:537149 Efficient polyhydroxyalkanoates production waste-activated submitted process seque FJ6233
EU662468.1 gg_id:564160 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat s EU6624
AB179534.1 gg_id:102039 sedimentary rock clone MIZ43 AB1795
GU454934.1 gg_id:519950 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
AB353310.1 gg_id:235366 Rubritalea sp. str. YM29-052 AB3533
DQ395559.1 gg_id:154124 deep-sea octacoral clone ctg_CGOCA10 DQ395
EU617884.1 gg_id:338616 Seasonal variation microbial Yel Sea sediment clone D13S-71 EU6178
EU369140.1 gg_id:329673 libraries oyster shell clone MBIOS-24 EU3691
FM242339.1 gg_id:308686 sequences sediment clone 6 T9d-oil FM242
EU491715.1 gg_id:264509 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4917
GQ472830.1 gg_id:580739 Biodiversity planktonic Northern surface water northern Bering Sea clone d39 GQ472
AJ401117.1 gg_id:40791 Elbe river clone DEV019 AJ4011
AY028220.1 gg_id:45741 marine clone Arctic95D-9 AY0282
AM889150.1 gg_id:587060 structure superficial sediments Bizerte (Tunisia) southern Mediterranean coastal an AM889
FJ203597.1 gg_id:346553 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
DQ329657.1 gg_id:159169 Guerrero Negro hypersaline microbial mat clone 02D2Z31 DQ329
EF683078.1 gg_id:256408 Eastern Mediterranean atmosphere clone F13_3F_FL EF6830
AB300129.1 gg_id:223836 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone k AB3001
EU385928.1 gg_id:261272 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3859
AY592662.1 gg_id:100607 deep-sea mud volcano clone Napoli-2B-40; BC07-2B-40 AY5926
FJ228319.1 gg_id:352371 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg FJ2283
DQ660867.1 gg_id:256422 DongChuan copper pyrites PRC determined acid mine drainage (AMD) clone DC-II-1 DQ660
GU205283.1 gg_id:518048 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
GQ402706.1 gg_id:575107 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AY326529.1 gg_id:136276 Amazon soil clone 271-2 AY3265
GQ402661.1 gg_id:574876 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
FJ625369.1 gg_id:509179 Influence lead contamination on boreal pine forest soil clone HF_NC_30 FJ6253
AY963380.1 gg_id:155824 structures and correlated ecological factors soils two evergreen broad-leaved forests AY9633
FJ228289.1 gg_id:318438 sulfate-reducing enriched during bioremediation experiment sediments (Brandenburg FJ2282
AY425789.1 gg_id:101372 volcanic deposit 1959 clone 1959-5 AY4257
FJ466032.1 gg_id:535993 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4660
FJ202176.1 gg_id:329801 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2021
AY328768.1 gg_id:90217 drinking water system simulator clone DSSD70 AY3287
FJ230920.1 gg_id:308650 under Level Antibiotic Selection Pressures river water clone F46 FJ2309
GQ009527.1 gg_id:500138 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
FJ437978.1 gg_id:513669 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
GU444060.1 gg_id:517876 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
EU475339.1 gg_id:299049 rock hyrax feces clone RHSD_aaa03d09 EU4753
GU174155.1 gg_id:594307 Microbial Bactrian camel estimated rumen clone XJC95 GU174
EU475271.1 gg_id:295252 rock hyrax feces clone RHSD_aaa02g09 EU4752
EU385881.1 gg_id:269023 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3858

2905.6	13980.3	13695.3	15242.4	16764.1	13353.2	17298.1	13206.4	16187.2	9426.8	14882.3
37.3	1084.8	856.6	995.5	940.8	755.6	1054.4	692.5	580.1	198.1	373.6
42.9	120.6	63.8	134.5	299.4	154.5	139.3	32.1	76.5	23.2	26.0
152.7	4542.2	4302.3	4308.9	5513.4	4248.5	5024.4	4181.5	6820.1	4353.8	3319.5
64.0	6599.3	6417.7	6873.0	6914.7	6714.0	7283.6	6157.7	4394.9	2332.9	4855.1
48.9	2638.5	2253.8	1496.3	2134.4	1880.5	1834.1	1773.6	1514.4	1393.8	959.7
893.6	2924.3	3284.0	2561.6	3433.4	3725.4	3133.8	2760.4	3441.8	2432.7	2351.3
71.8	2715.5	2668.6	2731.5	3285.5	3444.6	2630.9	2753.8	2472.8	1116.0	2096.2
488.6	7318.4	7720.2	7789.4	7642.2	6666.8	8442.6	6157.0	6657.4	3951.5	7108.3
105.4	2466.6	3513.3	3404.0	3193.0	3057.0	3983.6	2809.2	1420.4	905.1	2124.5
694.8	4462.6	4662.0	4894.6	5397.8	5030.1	5032.2	5028.6	5065.1	3013.8	3792.7
36.0	400.1	544.4	510.0	595.0	337.3	1092.5	363.2	232.7	118.0	271.2
53.5	268.2	290.7	281.4	444.5	233.6	414.2	310.8	301.5	149.5	135.7
2343.9	5605.6	6637.3	6027.8	6959.6	5160.6	6328.6	5711.0	6614.8	4961.2	6082.0
3193.2	2560.4	2721.4	2775.5	2831.5	2764.0	3303.2	2596.7	2139.4	1054.2	1140.7
84.6	1388.5	1298.0	1037.8	1005.7	807.2	1314.7	1247.0	1459.4	688.1	507.9
924.0	3231.3	4280.7	4028.3	4653.4	4413.0	4501.0	3959.0	4635.5	2736.6	4212.1
4222.2	6687.2	5953.1	6512.5	6837.7	5820.4	8982.5	5621.1	7762.9	6143.6	5487.7
9036.8	6046.6	6308.7	6705.0	6639.0	4986.2	9171.1	7765.3	8358.5	4643.7	6410.3
81.8	45.9	49.9	48.1	54.9	44.6	47.6	37.9	35.4	43.1	42.6
1265.0	4464.6	6040.9	4648.1	5524.3	3750.4	6021.0	4990.2	4321.2	7102.8	5625.7
1711.4	5321.9	5841.4	5644.7	6220.5	5260.8	6589.0	5399.1	5389.8	5297.7	5557.9
561.3	4191.9	5652.8	5330.4	4957.8	4684.7	5677.6	6038.7	6413.3	1797.5	4355.6
40.6	96.7	86.7	79.7	45.7	53.7	91.8	82.8	59.0	23.8	55.4
176.4	1184.3	1199.1	1051.9	770.6	1175.2	1095.6	1170.3	415.7	436.5	908.1
4971.3	3896.3	3701.6	5261.9	4923.8	3899.6	4523.3	3895.9	2776.2	1148.0	3148.0
1033.3	4861.1	5088.4	4763.9	5025.7	5575.8	5145.4	4929.8	6084.9	4097.5	6245.8
729.1	1776.7	1878.5	1961.6	2522.0	1966.8	2394.2	1769.0	922.7	598.1	1284.7
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406.9	2720.8	2695.4	3287.2	3451.9	2952.1	4004.5	2601.5	2258.6	1398.4	2360.3
14989.2	6298.4	6493.4	6690.3	6481.4	6236.6	7202.7	6529.1	5889.1	6444.1	6649.9
34.4	199.1	258.4	279.7	167.1	211.1	671.3	374.4	91.2	41.2	221.6
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EU245570.1 gg_id:241183 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-B0 EU245
EU386111.1 gg_id:275107 Biogeographical and microbes sediments on subseafloor sediment South China Sea c EU386
AJ009463.1 gg_id:12396 chlorobenzene-degrading consortium clone SJA-43 AJ0094
EF515388.1 gg_id:224753 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g04 EF5153
EU385810.1 gg_id:276009 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
EU385957.1 gg_id:261806 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
EU491440.1 gg_id:267092 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
EU491860.1 gg_id:264692 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU734965.1 gg_id:332707 assemblages sediment station DBSE Northern Bering Sea clone 059D21 EU734
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DQ499326.1 gg_id:159595 acidic cave snottite biofilm clone CV106 DQ499
FJ497306.1 gg_id:543036 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
GQ850584.1 gg_id:565629 bottom water northern Bering Sea clone d148 GQ850
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AF286036.1 gg_id:33594 mercury and PCB contaminated saltmarsh sediment clone LCP-67 AF286
GQ433939.1 gg_id:567951 Subseafloor ocean crust microbial observatories: (F-through Osmo Colonization Syst GQ433
FJ905749.1 gg_id:511928 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F127b FJ9057
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EU925882.1 gg_id:348335 sediments sediment station DBS1 northern Bering Sea clone 088G2 EU925
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EF602490.1 gg_id:229278 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
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AY114311.1 gg_id:63800 anoxic marine sediment clone LD1-PA13 AY1143
AM086134.1 gg_id:148962 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
DQ067002.1 gg_id:130730 Lake Washington sediment clone pLW-100 DQ067
DQ811950.1 gg_id:170215 mangrove soil clone MSB-4E2 DQ811
EU592418.1 gg_id:572696 Seasonal changes Salton Sea hypersaline sediment clone SSS7N EU592
FJ712411.1 gg_id:529621 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
DQ811955.1 gg_id:164821 mangrove soil clone MSB-5B4 DQ811
EU385788.1 gg_id:259376 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
GQ246450.1 gg_id:586441 Temporal and spatial China North Yel Sea sediments clone Ld1-55 GQ246
EU385764.1 gg_id:266329 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
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AB177136.1 gg_id:131965 seafloor methane hydrate clone ODP1230B10.05 AB177
DQ330720.1 gg_id:159127 Guerrero Negro hypersaline microbial mat clone 08D2Z74 DQ330
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EU245573.1 gg_id:255262 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-B1 EU245

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FJ716267.1 gg_id:563562 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
FJ712501.1 gg_id:526723 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7125
AM745159.1 gg_id:290797 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
DQ067003.1 gg_id:131050 Lake Washington sediment clone pLW-69 DQ067
GQ500696.1 gg_id:556217 Surveys Biofilms and Sediments Mammoth Cave Karst Aquifers Charon's Cascade sa GQ500
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AJ854267.1 gg_id:211083 Impact flooding on (Populus sp.) trees poplar tree microcosm bulk soil unflooded clor AJ8542
AJ582051.1 gg_id:94268 soil near uranium mill tailings clone JG36-GS-103 AJ5820
AJ390482.1 gg_id:22777 soil clone PRR-12 AJ3904
FJ479218.1 gg_id:570966 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EU135569.1 gg_id:240877 tallgrass prarie soil clone FFCH3040 EU135
FJ479480.1 gg_id:540938 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
EF032778.1 gg_id:185827 cyanobacterial mat in lava cave clone HAVOmat06 EF0327
FJ478598.1 gg_id:553028 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
AM991194.1 gg_id:277712 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
AJ863228.1 gg_id:125819 poplar tree microcosm bulk soil flooded clone 21BSF64 AJ8632
AJ390458.1 gg_id:28793 soil clone PBS-III-30 AJ3904
EU135567.1 gg_id:242108 tallgrass prarie soil clone FFCH1818 EU135
EU135572.1 gg_id:243244 tallgrass prarie soil clone FFCH12488 EU135
AY921903.1 gg_id:113334 farm soil clone AKYG868 AY921
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EU135568.1 gg_id:254604 tallgrass prarie soil clone FFCH18316 EU135
AF280852.1 gg_id:45661 bioreactor clone mle1-16 AF280
FJ712468.1 gg_id:525404 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) K FJ7124
FN396645.1 gg_id:541341 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_I FN396
FJ484438.1 gg_id:567353 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
EF999394.1 gg_id:247500 Vertical and Methanotrophs Estuarine Sediments Pearl River Estuary sediments 50cn EF9993
EF602491.1 gg_id:228206 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
DQ521801.1 gg_id:161669 Anaerobic Methane Oxidizing ANME-1b Archaea Hypersaline Sediments Gulf Mexic DQ521
AY114325.1 gg_id:63782 anoxic marine sediment clone LD1-PA39 AY1143
FJ485054.1 gg_id:555839 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
EU491142.1 gg_id:260737 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
DQ289929.2 gg_id:172911 Microbial Carbon and Nitrogen Cycling Sediments South Atlantic Bight Permeable S DQ289
FJ485078.1 gg_id:562684 microbial autonomous rover world's deepest phreatic sinkhole biomat El Zacaton 114 FJ4850
FJ902124.1 gg_id:552555 phreatic limestone sinkholes northeastern Mexico orange biomat 8m deep cenote Ca FJ9021
EF602497.1 gg_id:231901 metabolic phylum Planctomycetes anaerobic sulfide and sulfur-rich spring (Zodletone EF6024
EU135574.1 gg_id:248536 tallgrass prarie soil clone FFCH4663 EU135
AF317770.1 gg_id:136806 Nullarbor cave clone wb1_H11 AF3177

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41.3	87.4	90.1	85.9	119.6	90.3	93.3	54.1	70.6	30.3	49.7
763.8	6287.2	5517.1	5162.0	4964.2	5011.7	4665.8	5192.3	4115.5	3215.6	4479.5
11471.8	10505.7	10524.8	11513.7	13536.0	11247.0	13128.4	9680.7	9415.3	4893.3	9486.2
1313.4	6135.4	4898.4	4734.9	5407.5	5841.8	5533.7	3805.4	3361.1	1767.1	3727.0
516.5	989.2	912.5	1105.9	1809.6	864.8	3136.1	715.6	287.9	139.8	454.4
1379.9	2257.4	2761.3	2673.5	3194.8	2546.4	4826.9	2774.7	2369.5	1128.6	2262.9
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35.4	146.3	229.8	251.1	305.5	279.6	616.6	409.9	242.8	23.9	149.5
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779.5	2734.6	3089.2	4015.1	4585.7	2879.0	4762.2	3687.1	1286.5	276.1	1944.9
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156.0	3756.2	2215.9	2647.7	3711.3	3163.8	3791.0	2708.9	2609.0	1812.0	1703.1
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93.8	1101.9	1083.5	1132.5	1322.6	734.2	1110.0	888.1	648.5	276.8	601.9
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98.1	589.8	792.5	786.7	1318.5	501.9	1104.9	1084.1	218.3	92.5	368.2
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GU208350.1 gg_id:580844 Study on Sediment Dongping Lake sediment clone Td3-9	GU208
GQ347695.1 gg_id:534156 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ347
EU721779.1 gg_id:550488 microbial production water Alaskan mesothermic petroleum reservoir two methods	EU721
GU112185.1 gg_id:590013 library biogas slurry anaerobic fermentation pig manure clone 180	GU112
DQ329651.1 gg_id:200370 Guerrero Negro hypersaline microbial mat clone 062DZ75	DQ329
DQ329650.1 gg_id:201943 Guerrero Negro hypersaline microbial mat clone 062DZ40	DQ329
FJ719034.1 gg_id:529088 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_A0	FJ7190
EF516850.1 gg_id:218322 grassland soil clone FCPS649	EF5168
AY532578.1 gg_id:106562 uranium-contaminated aquifer clone 1013-28-CG38	AY5325
EF516449.1 gg_id:225148 grassland soil clone FCPT678	EF5164
AY850299.1 gg_id:135358 depending on what microbial treatment present soil clone c1	AY8502
AB089068.1 gg_id:78071 termite gut homogenate clone Rs-J96	AB089
EF454817.2 gg_id:218493 termite hindgut clone 290cost002-P3L-449	EF4548
EF454921.2 gg_id:225715 termite hindgut clone 290cost002-P3L-678	EF4549
AB192117.1 gg_id:141608 termite gut homogenate clone M2PT2-63	AB192
EF454187.2 gg_id:217932 termite hindgut clone 290cost002-P3L-1771	EF4541
AB188635.1 gg_id:113660 termite gut homogenate clone Pl-P1-21	AB188
GQ340261.1 gg_id:572828 Prokaryotic Marathonas Reservoir Greece water column clone A08-131-BAC	GQ340
DQ520188.1 gg_id:161631 shal China sequences hypertrophic freshwater lake clone ML-9-34.2	DQ520
DQ300591.1 gg_id:146168 microbial ocean's interior amplicon single fosmid library pool 130m depth HOT static	DQ300
GQ350069.1 gg_id:588419 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich	GQ350

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776.5	6701.2	5732.5	5574.4	7170.3	5861.9	8041.4	5148.7	2754.2	2049.6	5590.2
108.8	2031.6	1850.3	1350.0	1429.3	1552.1	3137.8	1276.2	731.9	622.7	917.1
75.2	1860.1	1218.6	1051.5	1206.5	831.9	2981.2	1043.5	61.3	188.7	966.8
9793.5	5873.9	5869.9	6452.7	5404.4	5786.8	6070.4	5897.4	6163.5	5123.5	8395.7
4403.6	5370.5	5121.2	5717.0	5013.3	5486.5	6523.9	5609.3	3586.2	2080.9	5451.6
199.3	6824.4	6743.8	7782.1	6482.3	7480.0	6556.4	6171.6	5515.3	2934.2	6481.1
109.7	6594.7	5380.4	5817.1	3378.9	5558.7	4690.3	5714.1	1947.7	1479.3	5802.0
268.1	4848.2	4314.7	4774.3	3482.5	4173.0	4612.0	4847.4	2514.4	1623.0	4162.7
632.1	4548.5	3928.2	3921.8	3014.7	3782.4	3524.9	3936.4	2351.0	1794.6	3465.8
87.2	3189.4	2594.2	2517.0	1383.8	3088.7	2244.3	2740.6	1129.0	421.3	2956.7
164.6	3110.2	4069.9	3603.4	3328.3	3960.5	3687.6	3859.8	3828.8	2807.7	3543.5
2953.5	6063.6	7033.8	7762.5	7327.7	6432.0	7233.4	5726.5	7604.7	4136.2	7473.3
14117.0	6327.1	5728.3	6029.7	6140.8	5497.9	6266.3	5627.8	7534.8	6863.9	7215.7
81.7	1535.8	1820.6	2125.4	1757.1	1434.2	2489.6	1538.8	913.1	976.4	1792.9
1410.6	6940.8	7355.1	8474.0	7439.5	6801.0	8216.0	6854.0	8223.5	3531.5	6089.5
1661.5	8276.8	7435.5	6624.9	5674.9	8341.1	6231.3	5334.4	12144.2	8743.4	8223.2
6699.7	4500.9	5518.5	5338.9	6479.3	4732.0	7224.6	5532.9	5071.5	3449.1	5132.3
153.2	706.9	795.9	1121.1	697.6	716.9	979.7	958.4	314.8	93.1	513.0
544.4	1320.1	1888.7	2364.6	1589.6	1731.8	1846.0	2217.5	1199.3	929.2	1224.8
295.5	3027.3	4000.3	3848.9	3072.5	3569.1	3772.3	3004.6	2046.2	1172.3	3803.9

8775.7	8881.9	11733.1
5431.1	6057.6	8182.4
3656.7	4753.3	5330.6
736.2	1711.8	2368.7
430.1	173.6	1309.2
5375.6	6126.7	5175.9
4052.1	5790.6	6471.3
5478.9	6267.8	8373.8
3106.2	5025.0	6381.0
3944.7	4127.6	5520.1
3135.6	4499.4	3827.3
1741.4	2346.8	3353.5
3525.8	4134.7	4422.6
5170.8	5578.2	7214.1
5115.7	6720.1	5768.0
1199.1	1500.1	2209.2
6508.7	5698.6	7482.5
7669.2	7644.4	8174.8
4665.6	7804.8	5973.1
630.8	585.2	1618.9
1983.2	2690.2	3356.9
2571.3	3176.7	4039.3

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ENVIRONMENTAL PROTECTION AGENCY
Office of Enforcement

#1

CHAIN OF CUSTODY RECORD

PROJ. NO.	PROJECT NAME
DIDS 2017	Region 5 Windy Ridge 2017 Phylochip

SAMPLERS: (Print Name and Sign)
Andi Hodaj

STA. NO.	DATE	TIME	COMP.	GRAB	STATION LOCATION	NO. OF CONTAINERS	Analyze: Phylochip						TAG NUM
RS B01	7-26-17	10:20		X	Iroquois River	1	X						
RS501		10:30		X	Iroquois River	1	X						
RS502		10:55		X	Thompson DS	1	X						
RS503		11:05		X	Thompson US	1	X						
RS504		11:20		X	AB	1	X						
RS505		11:30		X	Reach B	1	X						
RS506		11:50		X	Reach C US	1	X						
~~RS507~~	CB	12:00		X									
RS508		13:10		X	RB CUR 120040	1	X						
RS509		13:30		X	Curtis Creek US	1	X						
RS510	↓	14:00		X	Curtis Creek DS	1	X						
RS511	7-26-17	13:40		X	2 CC	1	X						
~~RS512~~	~~7-27-17~~	~~1000~~		X	~~TOO CB~~	1	X						
~~RS513~~	~~7-27-17~~	~~1055~~		X	~~TOO CB~~	1	X						
~~RS514~~	~~7-27-17~~	~~1110~~		X	~~FPJ CB~~	1	X						

Relinquished by: (Signature)	Date / Time	Received by: (Signature)	Ship To:
[signature]	7/27/17 1122	[signature] 7/27/17 1:23 PM	

REGION 5
7 West Jackson Boulevard
Chicago, Illinois 60604

Activity Code:

MBERS

Relinquished by: (Signature)	Date / Time	Received by: (Signature)		ATTN:
Relinquished by: (Signature)	Date / Time	Received for Laboratory by: (Signature)	Date / Time	Airbill Number
				Chain of Custody Seal Numbers

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ENVIRONMENTAL PROTECTION AGENCY
Office of Enforcement

#2

7

CHAIN OF CUSTODY RECORD

PROJ. NO.: CDS2017
PROJECT NAME: Region 5 Windy Ridge 2017 Phylochip
SAMPLERS: (Print Name and Sign): Andi Hodai

	STA. NO.	DATE	TIME	COMP.	GRAB	STATION LOCATION	NO. OF CONTAINERS	Analyze: Phylochip						TAG NUM
R5	S14	7/20/18	0930		X	FPG	1	X						
R5	S17	7/20/18	1045		X	FDE	1	X						
R5	B18	7/20/18	1055		X	TOD	1	X						
R5	B01	7/20/18	1020			Iroquois River	1	X						

Relinquished by: (Signature)	Date / Time	Received by: (Signature)	Ship To:

REGION 5
7 West Jackson Boulevard
Chicago, Illinois 60604

Activity Code:

MBERS

Relinquished by: (Signature)	Date / Time	Received by: (Signature)		ATTN:
	8/15/17 10:40			
Relinquished by: (Signature)	Date / Time	Received for Laboratory by: (Signature)	Date / Time	Airbill Number
				Chain of Custody Seal Numbers

Received on Ice

8/17/17

Tam

Sample ID	Name	Date	Time	Latitude	Longitude
B01	Iroquois River	7/26/2017	10:20 AM		
R5 S01	Iroquois River	7/26/2017	10:30 AM		
R5 S02	Thompson DS	7/26/2017	10:55 AM		
R5 S03	Thompson US	7/26/2017	11:05 AM		
R5 S04	AB	7/26/2017	11:20 AM		
R5 S05	Reach B	7/26/2017	11:30 AM		
R5 S06	Reach C US	7/26/2017	11:50 AM		
R5 S08	CLR 1200W	7/26/2017	1:10 PM		
R5 S09	Curtis Creek US	7/26/2017	1:30 PM		
R5 S10	Curtis Creek DS	7/26/2017	2:00 PM		
R5 S11	2 CC	7/26/2017	1:40 PM		
R5 S14	FPG	7/27/2017	9:30 AM		
R5 S17	FDE	7/27/2017	10:45 AM		
R5 S18	TOD	7/27/2017	10:55 AM		