46.0	2831.1	2612.4	1263.6	2036.1	2788.0	1877.3	1298.6	2361.6	1979.0	478.1
113.1	3189.2	3486.6	1587.2	2219.6	2189.1	2237.0	2499.5	3513.7	2535.1	1752.3
73.5	5802.1	4651.8	1738.2	2138.8	5203.4	1796.1	2234.8	6269.5	4550.9	1612.8
1157.2	6313.1	3302.0	1622.3	3040.1	3867.8	2477.5	1956.2	5899.5	3501.3	1019.1
5598.9	11562.7	9690.6	4248.4	6365.8	9102.8	7429.4	6312.6	14461.6	10230.9	5028.2
286.4	9819.4	7071.7	1893.6	3263.6	6361.8	3203.9	4148.1	10083.5	6673.6	2629.5
50.9	10919.4	7985.8	1983.0	3008.6	6275.7	2190.0	5089.6	11257.5	8476.6	4586.0
257.9	8875.7	7076.4	3631.7	6868.1	7447.2	7175.1	5454.4	12931.9	9052.8	4565.8
450.2	9260.1	6042.1	3421.0	4292.8	6784.5	3864.4	3345.3	10663.7	6747.7	3342.8
1773.6	13170.7	7353.3	3012.0	2701.9	5386.2	2718.7	4114.8	13396.3	10697.4	3468.7
46.9	6133.7	4894.0	1390.1	2459.8	5607.3	2081.9	1400.1	3824.4	3567.2	720.7
8138.0	9177.3	6842.6	5865.4	5570.3	6027.9	6563.7	5969.7	10116.2	4487.8	5982.5
905.2	12304.1	8999.5	4078.1	7330.7	8043.2	7365.3	6947.5	14432.2	11423.5	5262.2
103.5	10729.2	7606.7	3081.2	5351.2	6612.3	4422.1	3959.5	11687.3	8272.4	3031.5
321.6	6328.3	4993.0	2575.1	4095.5	5079.3	3808.4	2614.3	4988.9	3610.9	1415.4
223.7	3499.0	3887.5	3581.3	6053.4	4397.6	5026.0	3786.3	3962.8	3230.8	3459.5
422.2	11125.5	8416.5	2352.0	3754.5	7795.5	3546.6	3586.9	8908.3	6077.6	2337.2
408.2	7019.5	5519.5	2349.8	2833.2	4465.1	3396.4	3645.7	7610.9	5553.3	2114.5
202.9	5992.5	4552.6	2564.8	4542.5	4202.7	4268.0	4316.7	6229.1	5828.7	3239.9
38.2	13903.8	10498.9	2986.3	6362.0	9690.9	5313.7	4297.7	13366.0	11281.7	3147.4
118.4	3215.6	1988.7	805.5	1451.4	2427.2	1221.0	883.6	2847.8	1823.2	541.0
98.0	3978.0	3165.8	1774.5	4125.6	3199.5	3806.6	2494.1	3069.1	2479.3	1589.7
150.2	10380.7	8545.6	2013.1	4433.4	6796.1	5212.8	2943.5	11780.9	8725.1	2557.1
127.8	3664.9	2427.3	1147.8	2086.6	3018.4	1694.4	1781.7	4846.6	3240.4	1361.5
161.3	12039.5	9299.3	3410.5	5324.7	9965.3	4097.5	4627.8	11615.5	10447.3	3207.7
1245.5	5415.8	5564.7	5202.2	4627.0	5376.2	5009.4	5117.7	6320.9	7348.3	5639.6
12980.9	8084.8	6576.4	5624.3	7210.2	6167.8	7702.9	5052.0	5197.3	3590.7	5418.2
189.0	12826.4	8778.2	3077.3	5158.9	7627.5	5460.2	6002.2	13103.5	9357.1	4768.1
113.6	3823.3	2963.2	2598.5	3960.7	3088.6	3792.7	2228.8	2757.8	1963.4	1411.7
185.6	7329.1	5237.3	1845.6	3747.9	3952.5	3513.1	2151.1	5035.8	4182.9	1070.1
2075.9	15105.2	10635.1	7218.8	9256.0	11701.7	8434.6	7486.9	16348.6	13041.4	7250.2
127.8	6252.4	4551.1	2051.1	2462.3	3316.6	2398.2	3249.0	6416.0	6345.9	2263.1
203.4	4183.3	3500.0	2299.4	3607.7	3697.8	3547.0	3048.6	4808.9	4104.6	2135.6
3172.2	4611.4	4290.4	4071.0	5180.7	4478.1	5283.3	4186.7	5225.2	4487.8	3688.7
265.5	11142.3	8827.6	4079.7	6992.1	9158.5	7208.8	5050.2	8897.4	10212.0	3371.4
183.9	3873.1	3981.3	2589.9	3500.6	4245.3	2331.8	2572.0	2802.4	3906.0	1391.4
2631.3	9558.0	7124.2	4542.8	4993.9	6761.5	4720.6	6246.1	9923.3	8701.6	5440.1
827.0	14124.6	9931.3	2341.4	3124.2	8298.8	2880.5	6484.6	15058.1	11864.2	6040.0
320.9	7741.4	6634.3	5121.5	7125.0	7711.1	5475.6	5228.5	6977.9	7346.0	3290.3
8565.6	7256.1	5824.9	5244.8	6097.5	6538.9	6578.0	4680.9	4417.2	3080.8	4743.0
3873.5	5746.7	4930.9	3218.3	3783.9	4559.4	4436.3	3525.1	9681.0	5334.8	3962.3

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5465.2	4193.3	4870.2
7326.2	4206.3	5045.9
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5715.3	3262.4	3753.2
2786.9	2218.7	2449.1
3684.9	1575.9	2142.0
4016.4	1790.8	3015.1
6868.5	2692.8	3353.3
1291.4	587.9	1134.3
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3536.7	2013.7	2418.4
2373.1	1657.5	1888.4
6135.1	2340.9	4120.1
5478.1	6656.3	5185.3
6948.8	5106.6	6351.9
6100.1	2449.2	3023.2
3986.7	2830.8	2618.1
4115.5	1252.8	1642.4
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3919.3	2129.6	3241.3
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EF466129.1 gg_id:204293 Agrococcus sp. str. MSL 13 EF4661
AJ575538.1 gg_id:96421 freshwater clone D2 AJ5755
EU344913.1 gg_id:272176 Hepialus gonggaensis guts equalized library larval gut clone Hg5-03 EU3449
FJ865215.1 gg_id:546764 Microbacterium sp. str. CC-012309 FJ8652
AB378302.1 gg_id:340810 Glaciibacter superstes str. AHU1810 AB3783
EF459527.1 gg_id:216764 Himalayas Kafni Glacier soil EF4595
DQ525859.1 gg_id:233856 Frondicola australicus str. E1HC-02 DQ525
FM873290.1 gg_id:369423 occupant source house floor dust clone FD01B10 FM873
AJ310412.1 gg_id:25807 Agreia pratensis str. P 229/10 AJ3104
AJ565418.1 gg_id:103245 Leucobacter sp. MWH-NPG1 AJ5654
AJ575503.1 gg_id:96614 freshwater clone R7 AJ5755
AJ575541.1 gg_id:95873 freshwater clone W2 AJ5755
AJ575511.1 gg_id:96124 freshwater clone S10 AJ5755
EF466127.1 gg_id:215675 Microbacterium sp. str. MSL 15 EF4661
FN298502.1 gg_id:581286 Leifsonia sp. LAA-2009-i47 str. i47 FN2985
AY948030.1 gg_id:142159 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9480
GQ069168.1 gg_id:435928 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ069
GQ263970.1 gg_id:590071 Structure Simulated Level Waste Site simulated level waste site clone WC2_55 GQ263
GQ059362.1 gg_id:382360 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ059
EU801462.1 gg_id:331095 It's all ranking aquatic Chesapeake Bay MD clone 3C002757 EU8014
EF423344.1 gg_id:206162 Subtercola sp. str. 5004 EF4233
DQ223680.1 gg_id:161253 Cryocola antiquus zf-IIIRlt1 DQ223
EU465787.1 gg_id:302479 argali sheep feces clone AS2_aao35e03 EU4657
EU539957.1 gg_id:283537 profile human microbiota antecubital fossa (inner elbow) skin clone nbt108d11 EU5399
EF103208.1 gg_id:193635 Microbacterium sp. str. MSCB-11 EF1032
DQ521470.1 gg_id:177142 Antarctic lake ice cover clone ANTLV1_A09 DQ521
EF451633.1 gg_id:212217 Cryocola sp. str. KAR3 EF4516
EU636017.1 gg_id:278036 Antarctic str. N88 EU6360
AM935000.1 gg_id:573186 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AM494541.2 gg_id:223593 Humibacter oleicus str. SC.083 AM494
AY372075.1 gg_id:94524 Tipula abdominalis symbiont AY3720
DQ125539.1 gg_id:131209 uranium contaminated soil clone AKAU3508 DQ125
DQ347534.1 gg_id:146721 Microbacterium sp. B-2027 DQ347
DQ125561.1 gg_id:132619 uranium contaminated soil clone AKAU3545 DQ125
AB378301.1 gg_id:310647 Glaciibacter superstes str. AHU1791 AB3783
DQ125925.1 gg_id:133126 uranium contaminated soil clone AKAU4200 DQ125
DQ337564.1 gg_id:149009 Leifsonia sp. CHNTR46 DQ337
AM697495.1 gg_id:223053 sequencing libraries indoor dust clone BF0002D006 AM697
DQ125552.1 gg_id:131363 uranium contaminated soil clone AKAU3528 DQ125
EU642847.1 gg_id:278886 Salinibacterium sp. JC2487 str. JC2487; IMSNU 14141 EU6428
AF224722.1 gg_id:38522 Subtercola boreus AF2247

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1707.9	13523.3	10364.4	2229.6	5779.6	10014.0	3465.4	4498.2	15086.2	11330.0	3458.5
4454.2	7502.9	5449.7	4051.3	5163.3	6204.0	4589.5	3794.2	6529.3	4349.5	3578.1
921.6	7083.6	4978.9	3146.9	3865.1	4674.8	4438.6	2987.1	7105.0	5179.7	3307.4
42.2	11938.2	9191.3	1596.5	3380.6	8888.5	3853.7	3993.6	12238.6	10285.1	2696.6
752.0	11143.5	8161.6	2785.3	4611.3	6652.2	3394.2	4555.0	11899.4	8515.5	2943.7
147.3	5011.4	4337.6	1945.4	2905.5	3095.9	2473.4	3373.5	5404.9	4181.8	1774.4
184.3	4277.7	4225.5	3414.5	3370.1	5378.8	1822.9	2050.9	2030.1	3113.5	1234.0
42.7	2895.2	2551.8	1299.6	1856.6	1899.0	2140.8	1379.9	3739.1	3074.4	689.5
85.0	18005.2	13084.6	1930.8	3932.5	13820.6	3089.0	4160.3	19301.1	14331.5	2796.7
5126.5	6224.4	5421.4	4754.0	5754.6	5400.1	5425.8	4125.5	5522.0	4216.8	3966.0
44158.7	12745.0	10794.9	11500.8	10064.3	10613.8	11171.9	9749.9	16373.4	12464.2	14978.4
523.6	10049.5	7880.6	4668.6	4670.2	7575.7	3835.5	5185.9	12121.7	8931.8	4145.8
643.4	6563.3	5163.8	4355.3	3728.9	5504.9	2664.5	4514.4	4518.3	4835.2	2911.7
1022.6	15611.6	12169.0	2811.3	2177.5	11819.0	3477.5	5598.4	17535.8	13251.8	4719.1
9162.7	11712.4	10351.7	8250.8	8858.9	9714.3	8542.7	7651.5	9914.9	9362.3	12939.9
6976.7	6584.5	6057.9	5052.4	5968.5	6449.9	4845.9	5068.2	5456.0	4380.2	3541.7
230.7	6983.9	4759.5	2133.7	4125.5	4780.3	3892.4	3705.0	6370.0	5502.3	1604.0
722.0	13127.7	10197.2	4622.9	5785.1	10463.0	7067.7	5345.1	16971.1	12229.5	4456.1
124.3	4605.8	3085.2	724.6	1989.9	1617.0	1930.6	2033.2	3182.9	2812.4	921.0
12352.0	11279.3	8870.8	7466.6	8768.7	9324.2	8302.8	7063.6	13544.0	9300.5	11006.8
405.2	2400.3	2212.7	1336.8	2454.7	2861.8	1864.7	2297.5	3422.1	3410.4	607.1
842.8	7019.3	6058.1	3834.3	5120.7	6039.2	3573.5	3564.2	8296.6	6048.7	2973.9
1042.0	8443.4	6336.8	5264.7	5552.4	5945.8	6524.1	4750.5	6276.8	5371.8	4044.4
152.1	8779.2	6635.9	2838.7	4938.7	6190.1	4635.7	4435.4	8603.1	6828.1	2904.2
104.8	14068.9	10052.8	2004.3	3221.4	7576.3	2382.9	7268.9	16711.7	13529.2	5958.4
451.8	16054.2	12802.0	4675.4	7818.0	12460.2	8300.0	6640.7	19225.7	14815.3	6415.8
138.6	6164.7	4560.9	2391.6	3426.3	4823.4	2542.7	3975.5	6445.5	5099.2	2299.2
328.2	3061.5	2244.5	1162.3	2428.4	1946.4	1381.9	1436.1	2486.8	1797.5	629.2
836.6	7238.7	5553.4	2352.2	2263.5	5113.0	2905.1	3425.9	10442.2	7013.9	2596.1
42.0	3455.5	2778.1	1497.0	3750.1	2038.5	2130.7	1421.6	2127.1	1923.2	802.9
426.2	2538.0	1870.6	1414.6	2074.2	1965.8	1381.2	1662.8	1796.5	1728.7	756.6
223.9	11365.9	8234.8	2248.8	2680.7	6505.1	1846.8	4897.4	11250.9	8839.8	4242.3
657.5	12722.3	10072.3	4846.5	6558.4	8898.2	6568.2	6234.7	15932.9	11634.1	5695.2
295.1	6281.8	5565.0	2775.4	4825.0	5200.9	4599.5	2517.6	9859.9	7363.2	1956.7
77.1	4092.8	3102.7	1157.8	2392.9	3482.9	1512.1	1697.4	4848.5	3480.4	853.8
40.5	859.0	879.4	407.3	986.6	821.4	550.4	526.1	1333.5	1085.6	249.3
9391.2	11426.5	9742.4	5904.7	6740.9	8072.3	6110.0	8199.7	14453.7	11120.3	10318.0
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61.4	3150.8	2631.2	1034.2	2012.1	1972.0	1208.3	1587.8	2843.3	2585.2	807.8

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5885.9	3733.0	4738.8
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3074.1	4644.1	4379.6
4804.8	4792.3	3725.7
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6475.6	5304.5	4576.2
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6142.5	3830.6	4872.9
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5506.8	3424.5	3908.1
5929.7	4475.1	5037.1
5949.4	2713.0	2996.7
3511.3	1271.1	2081.5
6420.9	4161.5	5461.2
3616.8	2691.8	2926.0
2791.4	1122.8	1309.7
2508.8	2744.9	2054.3
2738.6	1158.2	835.0
1872.4	1767.7	1405.2
2822.5	1762.2	2021.1
6588.5	5176.1	4698.7
5536.7	2585.0	2710.2
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EU636014.1 gg_id:277986 Antarctic str. 3C3 EU636
FJ542898.1 gg_id:529444 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5428
EF540446.1 gg_id:220033 Leifsonia sp. 3_1K EF5404
DQ533552.1 gg_id:169000 Labedella kawkjii str. KSW2-17 DQ533
AY660689.1 gg_id:103579 Frigoribacterium sp. cryopeg_3a 3a AY660
EU636015.1 gg_id:279325 Antarctic str. 2CD EU636
EF587758.1 gg_id:230900 Curtobacterium sp. str. DCY26 EF5877
AM697358.1 gg_id:225374 sequencing libraries indoor dust clone BF0002C055 AM697
FM955871.1 gg_id:586126 Okibacterium sp. str. Asd M5-11B FM955
DQ316374.1 gg_id:152592 and seasonal dynamics Actinobacteria four lakes Northeastern Germany freshwater DQ316
DQ378178.1 gg_id:152865 oil-polluted soil clone F13_Pitesti DQ378
AY571813.1 gg_id:105783 Frigoribacterium sp. 34/19 AY5718
DQ125867.1 gg_id:133028 uranium contaminated soil clone AKAU4116 DQ125
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AM696980.1 gg_id:217423 sequencing libraries indoor dust clone BF0001B006 AM696
AB042093.1 gg_id:37441 Curtobacterium sp. Ac-2058 str. VKM ac-2058 AB042
AB362159.1 gg_id:320871 Iamella luteola str. IAM 15435 AB362
EU801874.1 gg_id:307298 It's all ranking aquatic Chesapeake Bay MD clone 3C003251 EU8018
CU919848.1 gg_id:537351 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AB464943.2 gg_id:354551 Altitudinal changes flora on Gulkana Glacier Alaska analyzed sequencing and -cycle c AB4649
AJ717386.1 gg_id:110386 Gram-positive AC30 AJ7173
DQ256087.1 gg_id:145275 Parkia alkaliphila str. KSL-113 DQ256
EF373534.1 gg_id:206096 Salinibacterium aquaticus str. CW1 EF3735
DQ521497.1 gg_id:198791 Antarctic lake ice cover clone ANTLV1_H04 DQ521
AM990459.1 gg_id:279509 Arthrobacter sp. str. V-34 AM990
AF511518.1 gg_id:65387 Arthrobacter agilis VincaOsa AF5115
AF218242.1 gg_id:71476 Arthrobacter sp AF2182
AJ577725.1 gg_id:89737 Arthrobacter agilis str. 37R AJ5777
AF197049.1 gg_id:19576 Arthrobacter sp. 'SMCC ZAT031' str. SMCC ZAT031 'SMCC AF1970
EU086819.1 gg_id:253119 Arthrobacter cumminsii str. G664 EU0868
EU086827.1 gg_id:249483 Arthrobacter cumminsii str. Z486 EU0868
EU086787.1 gg_id:238812 Arthrobacter cumminsii str. 1378 EU0867
EU086785.1 gg_id:247474 Arthrobacter cumminsii str. 1361 EU0867
AJ609629.1 gg_id:100770 Arthrobacter arilaitensis Stp101 AJ6096
AJ609626.1 gg_id:100301 Arthrobacter arilaitensis Po101 AJ6096
CP000474.1 gg_id:189233 Arthrobacter aurescens TC1 str. TC1; ATCC BAA-1386 CP0004
AJ609630.1 gg_id:104469 Arthrobacter bergerei str. CIP 108036 Ca106 AJ6096
CP001341.1 gg_id:530580 Arthrobacter chlorophenolicus str. A6 CP0013
AJ316305.1 gg_id:72222 Arthrobacter sp. str. LMG 20239 AJ3163

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248.3	4792.8	3558.7	2361.9	4073.5	4243.2	4041.2	2743.1	3502.7	2971.5	1662.9
35.4	2569.9	1927.5	1111.9	3704.8	1941.9	2776.4	1143.3	695.6	1164.5	475.7
228.3	6546.9	4648.2	2399.2	4215.8	5003.4	3945.1	2873.6	5729.9	4156.1	2005.8
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3510.1	11987.4	8471.3	7302.4	6891.8	8991.4	8390.3	7449.3	14428.5	11361.4	7425.1
32.0	13.6	14.8	22.2	19.8	13.7	20.0	15.8	19.3	15.4	12.8
483.1	5102.6	3448.9	2379.9	4002.6	3292.9	3459.4	2797.0	5226.8	3909.3	1647.1
54.1	4406.5	4796.2	5171.3	3056.7	4636.5	4840.0	2891.5	1849.9	2196.7	2376.6
1166.7	15415.9	11937.6	2449.6	3359.6	12904.5	3175.8	4978.5	15444.2	11239.1	3168.3
105.9	2247.5	2615.3	2259.5	3766.8	2319.6	3345.3	2060.5	1898.1	1387.6	1182.7
70.6	2941.7	2339.3	2742.2	3386.9	2283.5	4246.9	1981.1	1394.3	1252.2	1271.9
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172.9	1424.8	2089.9	1658.7	501.0	2329.8	768.5	912.1	1168.7	692.5	1090.6
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70.6	3377.7	1977.4	577.2	1410.4	2152.6	1331.7	779.5	793.4	965.9	274.4
1005.9	11323.4	7011.5	2029.6	2966.3	6665.7	2590.5	3950.0	10450.4	7334.7	2293.9
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237.5	1341.0	2046.7	1662.9	2494.1	1515.0	1708.4	1840.7	917.4	301.5	1061.8
98.6	6854.9	4542.7	1118.4	2611.1	3198.3	2441.4	2029.5	5851.1	3892.3	1287.5
218.8	7367.0	5240.8	2304.6	3973.1	4366.9	3471.2	4179.9	9673.0	7042.1	3611.8
617.2	8582.1	6334.5	3230.3	4946.6	5865.4	4542.6	4299.9	10901.8	8056.2	3692.1
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4727.5	2172.2	3019.8
3745.3	1694.7	2421.6
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EU362184.1 gg_id:318333 Arthrobacter sp. str. C11
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GU385852.1 gg_id:522768 Arthrobacter nitroguajacolicus str. QT6
EU729736.1 gg_id:341280 Arthrobacter aurescens str. MM10
X80743.1 gg_id:12444 Arthrobacter nicotinovorans str. DSM 420
FJ626656.1 gg_id:566378 Arthrobacter sp. str. MH144
X80742.1 gg_id:12374 Arthrobacter ramosus str. DSM 20546
AM111056.1 gg_id:140943 Arthrobacter sp. str. 7318
AJ715980.1 gg_id:99753 Arthrobacter sp. str. NJ43
AF134179.1 gg_id:12417 Arthrobacter psychrolactophilus
AY509239.1 gg_id:100636 Arthrobacter rhombi str. S189
FJ380172.1 gg_id:369524 ornithogenic Ross Sea region Antarctica AB1 soil clone 13/4/1B
NR_028925.1 gg_id:590495 Arthrobacter roseus str. CMS90; DSM 14508
DQ173007.2 gg_id:152402 Arthrobacter sp. str. TSBY-45
DQ995975.1 gg_id:190199 Arthrobacter sp. str. B5
FJ626618.1 gg_id:562938 Arthrobacter sp. str. MH135
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AF256196.1 gg_id:41769 Arthrobacter keyseri str. 12B
GU385866.1 gg_id:523131 Arthrobacter nitroguajacolicus str. QT20
AB244479.1 gg_id:240899 Arthrobacter woluwensis str. limp 2
FN397658.1 gg_id:463819 Arthrobacter sp. str. PON4
DQ108397.1 gg_id:138002 Arthrobacter sp. Tibet-IIVa3
GU377115.1 gg_id:516397 Arthrobacter sp. str. sptzw27
AF197025.1 gg_id:16350 Arthrobacter sp. 'SMCC G960' str. SMCC G960 'SMCC
EU360469.1 gg_id:266985 Arthrobacter crystallopoietes str. B6A
EF634027.1 gg_id:245133 Paenibacillus polymyxa str. ISSDS-854
EF103214.1 gg_id:197304 Arthrobacter sp. str. MSCB-17
AB017354.1 gg_id:12448 Arthrobacter sp. str. RC100
NR_029026.1 gg_id:580807 Arthrobacter gangotriensis str. Lz1Y; DSM 15796
FJ011429.1 gg_id:557194 Arthrobacter globiformis str. BGSm404
EU466258.1 gg_id:288260 bighorn sheep feces clone BH2_aao21a02
AB248530.1 gg_id:191973 Arthrobacter sp. str. LC9
AJ920001.1 gg_id:114802 Arthrobacter sp. str. strain CK22
AF197055.1 gg_id:17928 Arthrobacter sp. 'SMCC ZAT262' str. SMCC ZAT262

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327.9	5997.2	5580.8	2993.0	5048.4	5201.7	3817.2	2176.1	4966.6	3529.8	1585.8
1848.1	5372.7	4635.0	3904.9	6065.6	4102.8	5277.5	3955.2	8143.8	4783.8	2566.9
77.3	2486.2	2041.2	1070.3	4391.4	2443.2	2415.5	1037.0	2256.4	2362.0	721.5
176.6	3410.0	2497.7	1790.3	4629.0	2431.1	2964.1	1348.2	2871.0	2771.9	664.5
81.3	2982.7	2576.5	1393.7	4923.6	2781.3	2521.2	1405.2	2219.6	2180.5	691.8
54.4	2382.3	2171.5	1274.9	4266.6	2228.7	2282.8	1356.6	1659.8	1725.0	652.5
313.4	1970.1	2128.0	1680.7	3797.4	1946.7	2377.1	1425.7	2232.3	754.4	4183.3
78.4	2838.9	2446.8	1478.1	4805.7	2823.2	3050.1	1366.0	2536.6	2973.6	855.3
169.0	1951.5	1458.5	721.7	2436.9	1682.5	1462.6	918.6	2150.2	1763.0	551.8
29.2	1062.9	758.5	983.9	6235.4	1294.8	2968.7	608.2	413.4	1110.5	417.7
1420.5	5582.7	4318.4	4645.3	5838.5	5296.1	5064.4	4072.8	6834.7	5155.2	4858.9
140.8	3697.2	3809.0	2882.4	5386.7	3901.4	3645.8	2327.6	3231.1	2410.6	2306.2
12377.8	7643.5	6955.3	6076.6	5818.9	6395.6	5106.3	5099.6	7923.6	5269.7	6619.9
971.6	3244.1	2407.3	2721.2	5437.3	3798.3	5056.4	2060.4	2571.6	3550.3	2185.9
110.6	1259.6	1638.6	1640.4	4119.6	1989.5	3042.1	1252.9	933.5	1133.7	971.1
3803.2	6302.3	4796.5	3040.1	4249.7	4384.8	3326.6	3319.2	5864.8	4984.5	2467.1
147.7	1794.3	1249.4	1687.1	6692.3	2122.6	3971.1	803.7	1320.5	2457.8	527.3
55.4	2974.9	2270.2	1277.7	3942.8	2842.2	2922.4	1325.0	2829.8	3281.2	1298.4
146.7	2080.6	1683.8	893.6	3495.0	2253.2	1752.1	883.0	1894.3	1883.2	433.1
2455.3	4459.2	3663.6	2971.2	5304.7	4173.1	4288.9	2873.8	5269.4	3262.2	3201.2
55.0	1789.8	1523.6	962.4	4153.1	1851.7	1990.0	735.3	1122.6	1585.8	438.1
64.2	1890.9	1656.6	921.8	3133.6	1910.5	1692.3	1122.2	1468.5	1346.6	495.6
2077.4	3442.5	4868.0	4926.7	5381.4	4358.0	4879.9	3740.1	4115.1	7936.9	4212.6
50.3	224.7	238.7	250.8	1859.7	687.6	517.9	125.3	89.7	500.9	83.7
54.1	2404.0	2230.0	1267.1	4527.3	2185.9	2387.6	1378.5	1663.0	1794.6	650.5
487.6	4388.5	3669.7	2205.2	3751.8	4586.5	2331.4	2409.8	4688.8	2508.2	1439.3
445.6	3635.0	2342.7	2016.7	4471.4	2610.2	2584.2	1873.0	4362.9	1781.8	1454.7
949.0	7125.7	5966.1	4203.1	6938.4	5427.3	5572.2	3947.1	7210.0	7596.0	3207.4
62.4	1060.9	893.8	916.3	5310.4	1159.8	2676.5	902.7	1552.6	1240.0	309.3
263.8	2848.8	2706.9	1704.6	3550.7	2980.8	2415.5	1786.1	3695.3	2509.9	1669.3
204.0	4857.6	4157.9	2162.7	5323.2	3822.0	3569.9	2446.9	5097.6	3360.8	1472.8
1083.3	6059.0	5225.5	4474.3	6718.8	4951.0	4940.5	4430.8	6885.3	4346.1	3160.1
39.3	136.5	90.1	95.6	78.6	112.5	173.5	55.5	88.4	88.3	69.2
126.2	1616.2	893.0	725.0	3371.0	1316.6	1834.2	662.9	1835.8	1547.4	350.1
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399.6	4878.0	3328.0	2617.2	5698.0	3706.9	3828.3	2843.1	4084.5	2802.9	1867.3
231.5	4509.7	4126.1	2741.7	6662.9	4180.4	4800.1	2888.9	6117.9	4607.8	1994.8
97.5	2767.7	2640.0	1717.1	2738.2	3509.5	1928.4	1509.4	2189.2	2276.6	877.8
87.0	1779.7	1238.1	1018.8	5669.2	2185.0	3113.8	442.5	1179.6	2590.0	357.3
2387.2	3302.5	2861.6	2665.3	7945.5	3130.6	4809.4	2492.4	4418.6	3019.5	2166.0

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3604.8	2710.6	2177.0
4974.0	4081.6	4314.3
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2363.7	1076.9	1282.5
3043.0	902.2	1158.6
2906.4	870.7	1110.5
1643.7	1284.9	1197.4
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1475.4	672.1	930.5
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5176.1	6203.6	5474.1
3142.0	2126.0	2823.8
1708.4	1209.7	1262.1
4319.9	2918.1	2508.0
1871.5	887.1	1610.5
2576.2	1084.6	1116.9
1938.7	515.5	745.2
3786.2	3926.5	4223.7
2319.0	492.9	681.6
2133.7	711.1	926.1
4180.3	4997.7	4630.6
479.8	86.8	242.6
2924.4	889.5	1107.0
3028.3	1705.4	1785.1
1844.9	1864.7	2027.1
5056.3	4184.0	4077.8
1451.4	631.0	998.5
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3434.7	1557.4	2175.0
2979.9	3504.2	3438.3
117.7	57.6	81.0
1544.1	628.8	856.5
5396.8	3580.5	2883.4
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EU466711.1 gg_id:292452 argali sheep feces clone AS3_aao20c11 EU466
AJ551149.1 gg_id:93638 Arthrobacter sp. An10 AJ5511
EU465754.1 gg_id:291499 argali sheep feces clone AS2_aao34g03 EU465
FJ535486.1 gg_id:557949 Arthrobacter sp. str. B28 FJ5354
EU466301.1 gg_id:302216 bighorn sheep feces clone BH2_aao21f01 EU466
GU272378.1 gg_id:584662 Arthrobacter sp. str. TP2MF GU272
EU057865.1 gg_id:248723 Arthrobacter sp. 8J EU057
AY738758.1 gg_id:105558 Arthrobacter sp. str. NJ1 AY738
EU571135.1 gg_id:277507 Arthrobacter sp. str. 2-22 EU571
FJ894322.1 gg_id:538749 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
EU465849.1 gg_id:295787 argali sheep feces clone AS2_aao36h04 EU465
DQ223663.1 gg_id:160520 Arthrobacter sp. zf-IRlt5 DQ223
EU466751.1 gg_id:288464 argali sheep feces clone AS3_aao20h11 EU466
AY167856.1 gg_id:77502 Arthrobacter globiformis str. SAFR-004 AY167
EU571167.1 gg_id:262151 Arthrobacter sp. str. 17-10 EU571
EU466484.1 gg_id:295678 bighorn sheep feces clone BH2_aao24e04 EU466
AB002635.1 gg_id:12437 deepest sea mud Mariana Trench clone AB002
GQ280028.1 gg_id:581042 Arthrobacter sp. str. BJ-18 GQ280
AY833098.1 gg_id:110553 Arthrobacter nicotinovorans Ph13 AY833
GQ284326.1 gg_id:579223 Arthrobacter oxydans str. TSWCSN30 GQ284
DQ486130.1 gg_id:158010 Arthrobacter luteolus LNR3 DQ486
EU086806.1 gg_id:255863 Arthrobacter cumminsii str. 742 EU086
EU584503.1 gg_id:262324 Arthrobacter sp. str. Everest-gws-107 EU584
FN397671.1 gg_id:383501 Arthrobacter sp. str. AMV8 FN397
EU181231.1 gg_id:248443 Arthrobacter sp. str. 72H12-2 EU181
FJ415325.1 gg_id:356978 Micrococcus lylae str. B4 FJ4153
EU466508.1 gg_id:291788 bighorn sheep feces clone BH2_aao24g09 EU466
EU797643.1 gg_id:356341 Arthrobacter sp. str. BJQ-6 EU797
AY748914.1 gg_id:105987 Arthrobacter sp. str. NIPHL090904/B5 AY748
EU466340.1 gg_id:288477 bighorn sheep feces clone BH2_aao22c02 EU466
AY660686.1 gg_id:103149 Arthrobacter sp. cryopeg_2 2 AY660
DQ173017.2 gg_id:152534 Arthrobacter sp. str. TSBY-59 DQ173
AJ971874.1 gg_id:130586 Arthrobacter sp. Bt 25 AJ9718
X83407.1 gg_id:12451 Arthrobacter ilicis str. DSM 20138 X83407
EU466420.1 gg_id:289923 bighorn sheep feces clone BH2_aao23d06 EU466
EU221355.1 gg_id:257746 Arthrobacter globiformis str. N2P4 EU221
EU231606.1 gg_id:239892 Arthrobacter sp. str. TCCC23001 EU231
EF682999.1 gg_id:255347 Eastern Mediterranean atmosphere clone F27_9F_FL EF6829
X83410.1 gg_id:12462 Arthrobacter uratoxydans str. DSM 20647 X83410
EU221365.1 gg_id:244414 Arthrobacter globiformis str. B2S5 EU221

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385.4	8179.0	5792.7	2760.6	8547.0	6520.1	4889.0	3528.0	8334.2	8138.0	3148.9
1445.7	5719.1	5559.8	4200.5	6507.8	4658.5	5206.1	4406.4	7551.0	5600.7	4801.4
122.3	2271.0	1538.5	694.3	1325.7	2246.3	1055.1	683.2	2681.8	1672.2	426.7
1042.3	4838.2	4425.1	3108.7	6013.2	4273.6	4703.7	2962.9	6617.9	5198.1	3032.5
3912.0	3381.9	3646.9	4637.5	4961.6	3465.7	3692.0	3373.1	2244.0	1725.6	2937.2
3813.0	5682.5	6922.4	4601.7	4701.7	5632.7	4893.4	3739.2	8210.0	7995.2	4971.1
426.7	6961.3	5212.6	2907.2	7226.9	4952.2	5398.5	2792.9	6048.7	4928.8	1749.7
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27296.6	13986.7	12785.2	12403.3	13354.9	12690.7	14356.1	11406.7	18447.8	14544.3	16170.0
47.7	386.9	321.2	323.2	1659.5	411.5	758.2	136.6	265.6	328.3	106.3
79.4	1917.4	1727.7	1442.9	4551.8	2341.6	2593.9	1259.5	1555.1	2140.1	628.5
354.5	2869.2	2445.2	2209.1	4270.8	2474.4	3130.1	2026.2	2074.3	2668.8	1037.5
32.0	1013.5	835.6	996.7	6018.1	1371.8	2526.5	807.8	486.6	1228.6	363.3
1442.8	8220.5	6198.7	4784.5	5757.5	6394.5	5434.2	4787.6	9940.8	6806.6	4624.3
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42.8	679.2	825.0	661.6	2090.2	867.1	1281.4	526.6	366.7	1105.2	233.7
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3287.0	3435.2	3994.3
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3945.7	1567.0	2022.4
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4853.2	7203.0	5319.8
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2807.7	3262.1	1937.8
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310.1	204.9	193.1
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893.5	337.1	351.3
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AJ551163.2 gg_id:93370 Arthrobacter ardleyensis str. An25 AJ5511
DQ125897.1 gg_id:132985 uranium contaminated soil clone AKAU4158 DQ125
NR_025083.1 gg_id:562815 Arthrobacter methylotrophus str. TGA; ATCC BAA-111; DSM 14008 NR_02
EU465827.1 gg_id:301483 argali sheep feces clone AS2_aao36d03 EU4658
AY176765.1 gg_id:78941 Arthrobacter sp. str. HJ4 AY1767
DQ157995.1 gg_id:191438 Arthrobacter sp. str. J3.33 DQ157
AB167237.1 gg_id:107944 Arthrobacter sp. str. c106 AB1672
EU466637.1 gg_id:298124 argali sheep feces clone AS3_aao18h12 EU466
EU538378.1 gg_id:285046 profile human microbiota antecubital fossa (inner elbow) skin clone nbt88e07 EU5383
DQ223677.1 gg_id:161042 Arthrobacter sp. zf-IIRlt1 DQ223
EU402968.1 gg_id:274598 Arthrobacter nicotianae str. MCCB 104 EU402
EU086817.1 gg_id:247002 Arthrobacter cumminsii str. 99-0140 EU0868
AY572475.1 gg_id:110831 Arthrobacter sp. R33S AY5724
X83405.1 gg_id:12452 Arthrobacter aurescens str. DSM20116 X83405
AY392127.1 gg_id:98137 Arthrobacter sulfureus str. BW1010 AY3921
EF612306.1 gg_id:241160 Arthrobacter sp. str. OS-08 EF6123
AM746690.1 gg_id:256966 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A12 AM746
AM236153.1 gg_id:152113 Arthrobacter sp. str. PRH1 AM236
DQ177479.1 gg_id:140335 Arthrobacter sp. str. Tibet-IIU24 DQ177
EU834260.1 gg_id:303464 Arthrobacter arilaitensis str. DS37 EU8342
EF093128.1 gg_id:254100 Arthrobacter sp. str. VTT E-052915 EF0931
AB046358.1 gg_id:71728 Arthrobacter sulfureus str. IFO 16294 AB0463
AM422805.1 gg_id:255976 Arthrobacter protophormiae str. 041201 AM422
EU466684.1 gg_id:297910 argali sheep feces clone AS3_aao19h08 EU466
EU466675.1 gg_id:300768 argali sheep feces clone AS3_aao19f12 EU466
GQ406812.1 gg_id:549707 Arthrobacter sp. str. LI3 GQ406
DQ125642.1 gg_id:136467 uranium contaminated soil clone AKAU3686 DQ125
FM955856.1 gg_id:551025 Arthrobacter luteolus str. Asd M1L1 FM955
FJ267538.1 gg_id:324426 Arthrobacter sp. str. II_GA_K_5_2 FJ2675
EU466734.1 gg_id:300124 argali sheep feces clone AS3_aao20f06 EU466
AB299278.1 gg_id:214435 Arthrobacter flavus str. JCM 11496 AB2992
AJ315070.1 gg_id:17468 Arthrobacter monumenti str. LMG 19502 AJ3150
EU333869.1 gg_id:274037 Arthrobacter oxydans str. K22-04 EU3338
EU086803.1 gg_id:251250 Arthrobacter cumminsii str. 720 EU0868
GQ181046.1 gg_id:513250 Arthrobacter nitroguajacolicus str. BLN18 GQ181
EU584515.1 gg_id:258723 Arthrobacter sp. str. Everest-gws-39 EU5845
GQ284325.1 gg_id:573361 Arthrobacter oxydans str. TSWCSN38 GQ284
EF103210.1 gg_id:184693 Arthrobacter sp. str. MSCB-13 EF1032
FJ894182.1 gg_id:554217 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8941
EF540495.1 gg_id:217668 Arthrobacter sp. 4_C7_37 EF5404

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137.5	8865.3	6312.8	2459.5	5411.6	7141.0	4460.4	3789.9	9266.9	5538.4	2574.9
115.5	2964.7	2420.6	2220.8	4096.4	3165.5	2647.9	2230.6	2592.3	2892.8	1687.8
155.2	1950.8	1267.2	824.6	3366.7	1780.3	1739.2	634.3	2106.3	1584.0	319.0
5032.1	8959.4	6770.5	6767.5	10425.7	8069.7	9528.2	6332.2	12904.1	10877.8	7469.1
15813.3	5423.4	5277.4	5617.8	9453.3	5429.0	6758.6	4403.5	8460.7	6589.0	7325.5
128.8	2126.5	1942.5	1731.4	3839.7	2070.0	1979.1	1320.0	1360.4	1100.0	744.4
100.9	775.6	644.0	883.4	5791.0	1321.7	2949.7	480.2	302.2	1582.3	338.9
756.0	7025.8	6493.5	5471.9	8699.4	5933.4	7939.8	5130.4	8888.3	5194.7	3777.3
330.7	5279.9	3699.0	1778.1	4438.3	3748.5	3102.2	1992.0	5747.5	4585.0	1212.0
132.7	1844.2	1563.6	866.6	3135.4	1442.9	1615.4	698.2	1730.2	1310.2	457.1
438.7	5510.2	4044.5	2800.3	4948.5	4727.4	3762.8	2557.7	4793.0	4156.0	1544.9
1378.1	4030.0	3310.5	2722.6	3336.6	3022.3	2651.9	2133.0	3690.0	3729.4	2867.9
61.9	1285.7	1051.1	716.2	4438.0	1468.3	1971.4	773.6	912.9	988.3	402.3
42.3	1359.2	1337.9	1131.4	3943.6	1457.8	1846.9	937.3	576.6	1153.0	387.0
77.8	1222.0	987.5	750.2	3890.5	1318.4	1734.4	682.1	876.6	1389.8	346.3
40.3	1046.4	805.7	707.2	5389.3	1096.5	2631.4	521.1	449.4	1168.3	337.6
82.4	620.6	649.1	782.3	2401.1	608.1	1196.5	357.5	387.7	803.2	511.6
572.2	8342.0	6236.5	3968.5	5230.4	6928.0	4920.3	3852.7	8719.3	4553.4	2610.8
1644.5	9001.9	6710.1	5084.1	5876.0	7010.6	5550.9	5138.5	11199.3	8012.0	5117.8
5028.2	8320.1	6402.3	5119.0	6858.9	6635.2	6231.8	4603.3	10878.6	6909.7	4150.2
549.1	6139.6	4214.7	2426.6	4227.7	4081.8	3080.5	2640.2	6914.6	3943.5	1637.0
169.5	1941.6	2301.0	2316.3	6227.8	2754.3	4358.0	2028.7	1452.5	2070.4	1178.1
299.3	4859.0	3944.8	2751.4	4622.1	4966.8	2887.1	2674.0	3937.5	3290.4	1707.3
658.0	6898.1	5472.1	3839.2	6411.3	5408.2	5332.9	3994.4	10123.8	7351.7	3354.2
940.6	5644.3	4912.7	4701.6	8333.4	5138.2	6956.0	4290.6	6067.7	4304.1	3850.6
59.0	3006.3	3335.2	3373.1	6286.4	3218.6	6272.2	2925.9	1692.9	1483.5	2136.7
2500.0	4298.5	4297.0	2889.7	5531.3	4235.2	3810.1	3749.1	5145.5	6066.3	2204.4
1060.4	6249.6	5104.3	4019.2	6310.6	5139.8	5084.1	4300.7	7383.1	5172.7	2958.1
40.6	905.6	988.8	778.5	3375.8	912.8	1323.3	913.8	428.6	656.4	248.7
241.0	4852.3	4924.0	4771.8	4903.1	4348.5	5197.9	4151.5	3974.1	2836.1	2891.1
120.4	2657.2	2025.1	1335.6	5991.8	2204.8	3314.7	1262.2	2249.4	2011.8	724.7
381.4	3338.6	3069.3	2324.2	6397.3	3321.4	3612.0	1985.1	3683.5	2149.2	749.2
409.1	5470.3	3752.7	3303.5	4835.0	4994.7	2611.6	2594.0	4042.3	2200.2	1918.8
4552.7	4655.2	3977.4	3595.7	4553.2	3506.9	3827.2	3202.8	4138.9	4125.8	4039.5
74.1	1838.7	1515.6	930.9	2246.3	1774.0	1107.4	756.6	1630.3	1405.7	485.1
321.6	1697.6	1372.6	1475.9	4965.6	1515.7	2865.7	1130.0	1220.1	1210.4	574.5
2938.1	3032.9	3412.4	2772.6	5058.0	2511.0	3649.2	2342.4	4714.1	2623.2	2126.8
546.9	3739.0	2614.4	1894.1	4556.6	3245.2	2946.1	1919.7	4959.4	3240.5	1350.2
58.4	2197.8	2772.9	2828.2	4060.2	2376.6	3344.1	2046.3	1439.9	1540.0	1232.0
46.9	765.8	724.0	904.8	5880.4	1178.3	2600.7	717.7	692.5	837.5	300.5

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1268.9	320.5	833.5
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3598.2	1620.3	1581.7
1037.0	714.2	696.8
3237.1	2488.1	2999.1
2808.8	2693.8	2410.3
1748.2	643.7	879.8
2423.0	730.1	889.0
1356.9	689.5	787.0
1081.8	609.8	716.0
615.9	464.5	415.3
3618.5	3604.1	4065.7
5279.4	4393.0	4595.2
4823.0	4930.9	5486.9
2880.2	2379.8	2890.1
2552.8	2445.6	3147.0
3496.4	2815.4	3382.9
4397.1	3360.9	3731.6
5154.4	4441.3	5432.6
3218.1	2728.2	3760.6
4077.9	3311.0	3469.9
4925.0	3523.5	4011.2
1449.5	752.2	1081.7
4135.5	3537.1	5904.9
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3222.0	2316.3	2570.6
3693.6	3646.3	3592.7
1643.3	424.5	616.8
1991.8	1154.3	1182.6
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2428.1	2278.6	1765.4
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EU467976.1 gg_id:298128 cheetah feces clone CE2_d06_1 EU467
AJ551162.2 gg_id:132718 Arthrobacter ardleyensis str. An24 AJ5511
AY370616.1 gg_id:106963 Arthrobacter sp. str. GWS-BW-H41M AY370
FJ976577.1 gg_id:510137 Arthrobacter globiformis str. LCR68 FJ9765
AF235091.1 gg_id:27187 Arthrobacter sulfonivorans str. ALL; ATCC BAA-112; DSM 14002 AF235
EU465703.1 gg_id:298378 argali sheep feces clone AS2_aao33g09 EU465
EU466556.1 gg_id:297032 argali sheep feces clone AS3_aao17e08 EU466
X80736.1 gg_id:12427 Arthrobacter globiformis str. DSM 20124 X80736
EF127626.1 gg_id:206672 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE004I EF1276
EU086804.1 gg_id:255379 Arthrobacter albus str. 740 EU086
EF612308.1 gg_id:237512 Arthrobacter sp. str. OS-10A EF6123
EU468069.1 gg_id:296732 cheetah feces clone CE2_c05_2 EU468
DQ298268.1 gg_id:154636 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AJ616763.1 gg_id:104522 Arthrobacter psychrophenolicus str. DSM 15454 = AG31 AJ6167
DQ279380.1 gg_id:144475 Arthrobacter sp. TM15_9 DQ279
FJ894703.1 gg_id:545539 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota BME; ear p FJ8947
DQ172990.2 gg_id:151245 Arthrobacter sp. str. TSBY-20 DQ172
EU086784.1 gg_id:240058 Arthrobacter cumminsii str. 124 EU086
EU036698.1 gg_id:238876 Arthrobacter sp. str. MT16 EU036
EF103198.1 gg_id:196380 Arthrobacter sp. str. MSCB-1 EF1031
EU466298.1 gg_id:292144 bighorn sheep feces clone BH2_aao21e10 EU466
AY053487.1 gg_id:44226 gas hydrate clone AT425_EubD11 AY0534
X93354.1 gg_id:12400 Arthrobacter cumminsii str. 445 X93354
FJ950571.1 gg_id:463861 Arthrobacter protophormiae str. c37 FJ9505
EU571143.1 gg_id:262070 Arthrobacter sp. str. 3-9 EU571
AY572482.1 gg_id:110475 Arthrobacter sp. R36S AY5724
DQ125734.1 gg_id:134257 uranium contaminated soil clone AKAU3839 DQ125
EU465751.1 gg_id:290457 argali sheep feces clone AS2_aao34f10 EU465
DQ298160.1 gg_id:144051 Micrococcus sp. SWM_Isolation_2 DQ298
AM039435.1 gg_id:135870 Arthrobacter ramosus str. CCM 1646T AM039
GU434160.1 gg_id:515407 Arthrobacter sp. str. OW19 GU434
AY730708.1 gg_id:102167 Micrococcus lylae str. 120304JB10 AY730
EU466295.1 gg_id:300985 bighorn sheep feces clone BH2_aao21e07 EU466
AJ491107.1 gg_id:64361 Arthrobacter gandavensis str. R5814 AJ4911
EU466665.1 gg_id:299226 argali sheep feces clone AS3_aao19e05 EU466
DQ298373.1 gg_id:153395 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
FJ766438.1 gg_id:592518 Arthrobacter sp. str. GZK-1 FJ7664
AJ251417.1 gg_id:17863 Arthrobacter nicotianae str. DSM 20579 AJ2514
AB248532.1 gg_id:193587 Arthrobacter sp. str. LC12 AB248
EU465823.1 gg_id:302496 argali sheep feces clone AS2_aao36b11 EU465
AM113544.1 gg_id:139687 Arthrobacter ramosus str. FG1 AM113

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458.2	3890.6	2986.0	2042.0	5500.6	3988.6	3730.9	2056.0	3416.7	3735.9	1162.1
632.8	6472.5	4796.5	3176.7	5658.8	5223.9	4813.1	3197.1	6412.8	5351.2	2030.4
66.4	1591.9	1262.8	942.7	5507.1	1928.2	2388.9	826.3	1335.2	1506.4	541.1
73.3	1704.9	1117.2	672.8	2915.8	857.4	777.6	864.4	2047.4	1169.7	568.7
902.2	9123.0	7422.8	6465.9	7953.4	7913.6	7549.9	6862.8	10795.1	7687.6	5219.9
1669.1	7576.0	6597.4	5476.6	7985.9	6556.5	7500.5	5438.8	11090.1	9488.8	5390.1
50.3	940.3	950.6	983.3	6181.7	1328.7	2741.1	914.9	500.0	952.1	422.0
4801.4	9826.7	8399.2	6012.8	10234.2	7740.0	8209.2	6845.5	12532.7	7622.3	5281.6
326.7	6365.8	5876.6	4724.7	5546.5	6878.5	5095.1	5540.7	8030.5	5826.1	4942.7
171.4	4465.4	3123.5	2128.0	7538.0	3395.8	4526.8	2638.8	3825.5	3593.8	1360.7
1592.9	3598.1	3193.6	2927.1	3668.9	3337.5	2818.2	2754.3	3944.6	4493.0	2222.8
75.3	1541.4	1393.1	1791.5	5178.5	1675.0	2801.9	1434.4	1210.1	989.1	698.7
86.8	3772.8	3843.4	3789.9	6548.9	2822.2	5864.6	3022.6	2684.5	2338.7	2462.8
686.5	8153.0	6051.0	4580.9	5226.0	5607.4	4941.2	5053.1	7540.0	6250.5	4162.8
154.3	3211.1	2575.7	2141.3	5682.6	2751.8	3732.9	1597.0	2199.9	3112.5	705.7
62.9	1581.5	1336.4	1202.7	7003.2	1941.8	3507.5	745.3	801.6	2235.0	446.9
1901.2	7819.7	5869.1	4586.0	7169.4	5625.1	6143.9	5490.3	6755.6	4846.9	3999.1
72.1	1122.3	984.0	1102.6	4072.3	1274.6	2088.6	477.8	465.5	732.5	266.1
402.2	2787.4	2663.7	1560.1	3424.8	3153.1	2613.3	1988.4	4421.4	2909.5	969.3
497.4	5128.1	3702.9	4100.5	5174.2	4058.5	5432.7	3973.1	4658.5	2933.0	2926.8
646.7	9295.5	7444.3	5253.6	7138.2	6588.6	5482.6	4505.6	14093.8	8240.4	4904.5
608.2	6004.0	4747.2	3763.7	4953.9	4902.3	4583.2	4366.9	6062.7	3553.6	3187.6
484.6	4392.5	3712.6	2766.0	5702.0	4412.0	4106.8	2913.4	4314.3	3679.8	1587.1
241.1	4058.4	2853.3	1409.1	6380.8	3188.3	3109.7	1698.1	4195.3	3033.8	1183.7
76.7	109.4	313.4	476.6	1232.3	353.8	472.3	353.2	578.7	635.7	164.0
910.5	3787.2	3617.8	3235.7	5984.5	3201.2	4395.4	2621.6	2765.2	2014.6	2850.7
10509.0	9988.4	8356.1	7155.8	9023.4	8723.2	8570.0	7080.9	12831.0	11801.9	8736.9
14184.7	8955.0	7904.7	8385.2	9161.6	8091.0	8944.8	7842.8	13132.4	7427.4	9500.7
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77.2	479.3	533.5	435.5	956.1	350.5	525.6	316.8	734.0	599.2	184.2
8257.3	3405.5	3080.4	2627.7	3723.6	3009.8	2809.9	2790.5	6262.8	4233.2	4270.8
17690.7	12339.3	10890.6	8442.0	10251.2	10902.6	10735.3	8666.1	16144.9	12564.3	10766.6
1079.9	4199.3	3459.6	2749.2	3800.8	3223.2	4090.6	2661.2	4230.2	3344.7	2143.7
576.6	8507.3	6113.4	2822.9	6428.8	5469.9	4928.5	3467.7	10101.8	7277.0	2230.8
338.3	2520.6	1926.2	757.7	1305.9	1891.9	1210.7	614.4	2517.6	1605.7	342.1
76.7	2348.8	2367.6	2030.0	6006.8	2003.9	3546.4	1167.0	1825.0	1748.9	906.9
353.1	5426.2	4079.6	2946.9	5248.4	4520.1	4183.4	2597.9	4525.8	4219.0	1789.8
280.8	3297.0	2815.6	1495.8	5897.6	2911.5	2981.3	1560.1	3016.7	2714.0	1730.3
680.5	5302.9	4588.6	3632.1	5503.7	4248.8	4368.7	3972.3	7271.4	4676.6	2847.4
67.0	539.0	290.5	209.7	1889.6	328.8	853.9	159.9	313.7	541.0	164.6

7982.1	8070.7	7129.1
2504.1	2050.2	2469.0
3531.8	2931.4	3637.9
1997.1	717.4	1028.2
553.0	504.7	410.4
7424.1	6361.9	7337.4
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1797.3	1059.1	1464.4
6699.7	5820.4	6271.1
5598.6	5792.3	3907.8
3958.5	1540.5	2173.6
2812.4	3536.3	2436.7
1569.3	1128.2	1329.5
3442.6	2870.8	3527.4
4258.4	4121.2	4727.8
3384.5	1396.7	1828.7
2042.1	786.0	1218.3
5604.9	5469.4	5510.8
1411.8	578.2	344.6
2292.6	2009.0	1817.0
3865.8	3904.1	4563.6
5801.4	4804.0	4392.0
4405.8	4012.3	4049.0
3301.9	2869.0	3549.3
2558.8	1119.1	1267.4
441.7	211.6	208.7
3665.1	3137.4	3400.7
7271.5	7526.7	7519.0
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1647.1	830.3	1031.9
309.6	259.1	284.3
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9276.8	8188.3	8369.9
3256.2	2535.4	2652.4
4321.9	2400.6	2932.1
1084.6	672.4	624.2
2101.2	1679.4	1670.5
3301.1	2139.8	2640.6
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EF459528.1 gg_id:204534 Agrococcus citreus KFC-31 EF4595
FM213392.2 gg_id:346297 Arthrobacter globiformis str. MN48 FM213
EU466584.1 gg_id:289914 argali sheep feces clone AS3_aao18a03 EU4665
DQ060385.1 gg_id:133261 Arthrobacter sp. str. P27-1 DQ060
EU466568.1 gg_id:292261 argali sheep feces clone AS3_aao17g03 EU4665
FJ976527.1 gg_id:540565 Arthrobacter sp. str. LCR18 FJ9765
EU466003.1 gg_id:296002 African elephant feces clone AFEL3_aao15f06 EU4660
FJ894219.1 gg_id:536228 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8942
AY651317.1 gg_id:101701 Arthrobacter sp. AG1 str. AD1 AY6513
AB024412.1 gg_id:12398 Arthrobacter sp. str. SN16A AB0244
EU465747.1 gg_id:301915 argali sheep feces clone AS2_aao34f04 EU4657
EU466526.1 gg_id:292876 argali sheep feces clone AS3_aao17a09 EU4665
EU466534.1 gg_id:302575 argali sheep feces clone AS3_aao17b07 EU4665
DQ298159.1 gg_id:143810 Arthrobacter sp. SWM_Isolation_1 DQ298
X83409.1 gg_id:12454 Arthrobacter sulfureus str. DSM 20167 X83409
DQ177482.1 gg_id:140327 Arthrobacter sp. str. Tibet-IK23 DQ177
AB070602.1 gg_id:44124 Arthrobacter sp. JCM 1339 str. JCM1339 AB0706
EU730943.1 gg_id:323545 Arthrobacter agilis str. 234 EU7309
DQ298369.1 gg_id:151910 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
EU466415.1 gg_id:293037 bighorn sheep feces clone BH2_aao23c12 EU4664
EU466538.1 gg_id:302925 argali sheep feces clone AS3_aao17b12 EU4665
EU467968.1 gg_id:290069 cheetah feces clone CE2_c08 EU4679
EU466431.1 gg_id:293031 bighorn sheep feces clone BH2_aao23e10 EU4664
AY509238.1 gg_id:100484 Arthrobacter ramosus str. S206 AY5092
EF601820.1 gg_id:228217 Arthrobacter sp. str. WX4 EF6018
EU466332.1 gg_id:298444 bighorn sheep feces clone BH2_aao22b02 EU4663
EU019984.1 gg_id:252809 Arthrobacter sp. str. LAM 11 EU0199
AY436791.1 gg_id:104085 Arthrobacter sp. str. C4 AY4367
FJ894330.1 gg_id:571417 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
EU466580.1 gg_id:296601 argali sheep feces clone AS3_aao17h09 EU4665
DQ104992.1 gg_id:137766 Arthrobacter sp. str. P1-2 DQ104
NR_026234.1 gg_id:546700 Arthrobacter histidinolovorans str. DSM 20115 NR_02
EU466469.1 gg_id:289890 bighorn sheep feces clone BH2_aao24c02 EU4664
AJ298940.1 gg_id:48874 Micrococcus lylae str. d10 AJ2989
AM236152.1 gg_id:151804 Arthrobacter sp. str. VP3 AM236
AY370618.1 gg_id:107268 Arthrobacter sp. str. GWS-BW-H45M AY3706
EU571168.1 gg_id:269598 Arthrobacter sp. str. 18-1 EU5711
EU466304.1 gg_id:302254 bighorn sheep feces clone BH2_aao21f06 EU4663
X80739.1 gg_id:12474 Arthrobacter nicotianae str. DSM 20123 X80739
EU086794.1 gg_id:237487 Arthrobacter cumminsii str. 219 EU0867
DQ015981.1 gg_id:133345 Arthrobacter nicotianae str. BCT-1 DQ015

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68.4	2676.2	2379.5	2532.2	6664.9	2762.2	3963.0	2532.0	2288.5	1634.1	1433.1
1793.7	12380.7	11583.8	9548.6	10164.0	10086.8	11826.5	9628.7	13655.8	10553.2	11427.0
284.9	3368.3	3040.6	2543.0	4048.0	2809.6	3518.3	2721.3	3276.0	2828.0	1259.3
206.9	4243.0	4286.8	4059.6	5840.3	3910.8	4967.0	3372.1	4424.4	3051.6	2342.0
3146.5	4608.6	4795.2	5166.9	5924.4	4475.1	4766.2	3738.8	5642.5	3214.0	5409.9
449.8	4725.5	4989.7	4411.6	5107.2	4875.0	5823.3	3792.5	4545.8	5712.7	3375.2
137.8	3363.1	2832.9	2031.7	5984.3	3136.1	3872.2	1698.5	2583.0	3390.5	892.7
366.2	3956.6	3656.2	2531.0	6222.0	3686.3	3481.5	1702.9	4022.1	3031.6	1863.6
145.4	951.3	983.8	539.0	592.5	731.8	467.5	544.7	860.4	1018.4	585.4
5274.6	7516.5	6561.8	5937.4	7180.0	6346.8	7678.9	5993.6	10270.8	8709.4	6143.0
1382.5	7970.5	7282.3	5993.7	8391.6	7550.7	8028.0	5953.4	10137.9	8045.8	6832.0
552.7	5159.7	4308.0	3322.0	5541.3	4208.6	4572.1	3568.9	7313.1	5396.1	2621.0
121.1	2801.7	2221.4	1183.6	3426.5	1653.7	1401.3	1631.8	2879.3	2202.4	1603.7
2541.8	6886.2	5852.2	5277.8	7835.1	6378.6	5804.7	4523.1	6883.7	4447.1	3468.8
527.9	3109.3	2290.0	1887.2	4945.7	2919.8	2958.9	1605.8	3722.1	2656.6	1320.3
33.4	813.9	732.2	976.3	4883.3	1422.7	2485.4	878.8	662.4	890.6	394.5
1412.8	4024.8	3348.0	2551.8	2591.0	3091.1	1885.6	2684.4	4375.1	2903.5	1589.3
78.3	1794.0	1753.5	1093.4	1821.6	2017.8	1617.4	1487.0	2646.9	1703.5	970.3
95.2	5246.9	4405.5	2290.2	4099.6	4391.0	3802.7	2752.5	4886.3	3366.2	1594.9
636.0	6788.2	5918.0	4814.6	6860.8	5731.7	5765.5	4761.4	9936.5	7499.7	3937.7
217.1	2720.5	2513.1	2199.7	5881.2	3205.1	3849.1	2088.1	2281.5	2682.7	1123.1
363.7	10851.6	8549.9	6092.2	10944.0	9134.2	8390.5	6914.9	13916.8	10817.2	5842.7
68.4	471.9	402.2	360.4	918.2	459.5	463.9	293.1	342.5	341.3	166.4
62.4	1976.9	1666.2	930.9	3590.6	1975.2	1881.8	1105.3	1473.1	1432.2	521.4
3768.0	7382.8	6151.0	5606.5	8982.6	6365.7	7177.6	6263.9	9860.7	7125.8	5836.0
74.3	2350.4	1866.4	1221.9	3694.5	2266.9	1972.0	1030.6	2540.5	1912.5	797.4
1266.4	4472.5	3116.9	3135.5	5075.8	4082.5	4182.2	3224.9	7835.3	6178.4	2931.4
11879.6	6510.0	5515.5	5393.2	6557.8	5345.3	6257.9	4621.7	8612.9	6651.5	5798.0
397.6	4672.5	4104.2	3434.3	5371.4	4700.1	4631.2	3863.1	4243.5	5246.9	2425.6
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99.3	2301.7	1825.8	1326.8	4706.7	2290.7	2915.5	1053.7	2315.7	2564.0	565.6
707.8	8659.4	7320.8	6762.1	8635.8	7557.4	8703.5	6325.5	10271.2	8765.4	5657.8
405.2	6429.4	5588.0	2996.7	6852.0	6224.5	4907.6	3692.8	6308.9	5392.6	2224.6
5803.4	5683.0	5062.6	4297.0	6130.8	5281.8	5301.1	4407.5	8063.4	4688.3	5867.0
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1606.2	10402.2	8274.4	7336.1	7275.8	8088.4	8305.6	7217.6	13340.2	10064.3	8155.1
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257.5	4428.4	3386.2	2279.8	5708.9	4034.8	4196.2	1990.6	3997.4	3792.9	1016.0

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3054.5	1819.9	2641.7
8753.3	7924.8	9128.3
3133.7	2390.9	2554.5
3797.6	2664.7	4876.8
3790.6	5263.8	3202.4
4325.4	4133.6	4175.1
3702.1	1265.8	1529.2
2358.2	1273.9	2048.4
627.5	857.5	504.0
5862.7	6867.6	6090.6
6027.3	4969.3	5739.1
3821.6	2964.7	3225.1
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2379.4	1873.1	1840.1
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EU584509.1 gg_id:264151 Arthrobacter sp. str. Everest-gws-17 EU5845
AB248528.2 gg_id:194632 Arthrobacter sp. str. LC7 AB2485
DQ628958.1 gg_id:172758 Arthrobacter sp. PSA A20(6) DQ628
EU465829.1 gg_id:298221 argali sheep feces clone AS2_aao36d05 EU4658
FJ897780.1 gg_id:566120 Arthrobacter sp. str. BN090020 FJ8977
EU466604.1 gg_id:288027 argali sheep feces clone AS3_aao18c10 EU4666
GU391465.1 gg_id:553901 Arthrobacter oxydans str. Mm2 GU391
GQ280021.1 gg_id:540422 Arthrobacter sp. str. BJ-11 GQ280
EU086798.1 gg_id:239293 Arthrobacter cumminsii str. 352 EU0867
FJ894314.1 gg_id:563347 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8943
AY370617.1 gg_id:107123 Arthrobacter sp. str. GWS-BW-H53M AY3706
FJ217702.1 gg_id:337268 Arthrobacter sp. str. 20B FJ2177
AY116497.1 gg_id:63457 Arthrobacter koreensis str. CA15-9 AY1164
AB098571.1 gg_id:78055 Arthrobacter sp. str. TUT1003 AB0985
FJ894266.1 gg_id:538604 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8942
AF332384.1 gg_id:20720 Arthrobacter sp. B44 AF3323
EU326482.1 gg_id:253946 Arthrobacter globiformis str. K01-01 EU3264
EU772033.1 gg_id:322261 Argali sheep feces clone AS2_aao36d02 EU7720
EU465677.1 gg_id:302819 argali sheep feces clone AS2_aao33d03 EU4656
EU772057.1 gg_id:341415 Argali sheep feces clone AS3_aao18h04 EU7720
EU772017.1 gg_id:311160 Argali sheep feces clone AS2_aao35c06 EU7720
AM111005.1 gg_id:140822 Citricoccus sp. str. 3054 AM111
DQ923275.1 gg_id:183011 Micrococcus sp. m2-21 DQ923
EU714900.1 gg_id:316667 Micrococcus xinjiangensis str. SRDD42 EU7149
FJ674681.1 gg_id:512185 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
AB473562.1 gg_id:410406 Citricoccus sp. str. PS9 AB4735
FJ675261.1 gg_id:527385 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
FJ671267.1 gg_id:526344 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6712
FJ674626.1 gg_id:521124 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
EU379300.1 gg_id:268686 Kocuria kristinae str. 6J-5b EU3793
X80749.1 gg_id:12508 Kocuria kristinae str. DSM 20032 X80749
FJ894414.1 gg_id:537644 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8944
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AM697319.1 gg_id:226388 sequencing libraries indoor dust clone BF0002C016 AM697
EU539757.1 gg_id:283591 profile human microbiota antecubital fossa (inner elbow) skin clone nbt105g08 EU5397
EU537145.1 gg_id:282622 profile human microbiota antecubital fossa (inner elbow) skin clone nbt68d10 EU5371
EU379280.1 gg_id:271644 Kocuria marina str. 4RS-4b EU3792
EU535439.1 gg_id:286683 profile human microbiota antecubital fossa (inner elbow) skin clone nbt02h07 EU5354
EU536661.1 gg_id:287136 profile human microbiota antecubital fossa (inner elbow) skin clone nbt64f07 EU5366
FJ894258.1 gg_id:574820 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8942

71.2	1385.9	1299.5	1190.7	5994.3	1718.0	2955.9	683.9	415.2	1791.4	371.3
245.4	1272.1	1078.2	1153.2	3969.2	1226.4	2403.5	804.3	815.0	1172.7	472.5
29494.4	8227.7	7810.4	8851.6	8413.6	7373.2	7723.8	7283.7	11190.0	8825.5	14081.4
50.2	828.9	732.7	733.4	4724.1	929.6	2366.7	544.3	319.0	901.3	381.2
11900.6	10665.0	8753.4	7809.1	10244.3	9176.8	9429.6	7134.8	15516.8	12212.0	8863.2
46.8	930.8	1006.1	1000.6	5440.3	1312.9	2462.1	779.8	628.2	1310.0	326.9
4240.2	10397.8	9716.1	7212.4	10610.7	9330.8	8832.1	7431.3	13077.4	9783.2	7503.9
457.6	2917.8	2709.8	2321.5	4600.3	2330.6	2521.4	1660.9	2345.2	1423.4	1319.4
585.0	6337.1	4704.4	2860.2	6009.1	5383.6	5017.6	2959.6	6428.5	5458.2	1933.7
1625.9	7929.3	6201.1	5129.5	6524.8	6818.1	6129.3	5388.7	9262.2	6566.4	4992.1
133.6	4347.1	3349.0	2129.6	5096.4	3108.8	3584.8	2031.5	3438.8	3254.0	928.4
459.5	5070.1	4012.5	3137.7	6155.9	4193.7	5034.6	2850.8	4671.3	4347.1	1746.3
211.5	2038.0	1723.8	1623.8	4689.3	2448.2	3228.4	1512.5	1314.0	2426.2	864.9
320.0	3643.6	2770.6	1390.9	3638.9	2528.5	2624.2	1267.9	4469.4	3242.1	752.1
173.8	4050.7	3266.7	1594.9	1630.6	4884.6	1639.6	1976.7	3197.5	2128.8	1208.9
147.6	3917.4	2772.5	1867.9	5298.5	3011.3	3487.6	1572.6	3150.0	3594.5	771.5
22729.9	9533.4	7654.4	6720.1	9155.8	8254.6	8150.2	6475.5	10525.9	8269.7	7411.2
4343.1	5229.4	3920.6	4102.5	6865.2	4385.5	5280.9	3562.5	5410.9	4721.4	3308.3
509.4	5010.4	6134.8	4854.1	5296.3	5225.1	6165.0	5043.0	5360.2	4527.1	3775.3
272.5	6640.8	5787.4	3583.7	7573.5	5785.1	6090.2	4067.9	8132.8	6815.0	2664.5
3504.1	9060.2	8721.9	8200.6	10039.5	8399.2	10632.7	8766.8	9445.4	7316.1	7487.8
1395.5	4401.5	4316.9	4748.5	4150.6	3693.0	3972.5	4570.1	5534.6	3332.8	3647.7
5684.5	4138.7	3315.8	3815.3	5079.9	3654.8	4199.8	3469.6	5254.8	3583.0	4916.8
728.8	7095.3	5776.0	3606.9	6320.1	6021.1	5249.6	3786.7	6203.3	5813.7	2648.4
482.5	8516.1	5878.6	3387.4	6629.0	6597.0	5646.8	3640.9	8499.0	5792.5	2647.7
3116.7	10230.4	7724.2	5658.5	8315.3	7695.2	8909.4	6676.7	9622.0	8466.6	5356.1
525.1	7317.3	6079.8	4077.5	6324.9	6545.5	5272.6	3832.7	6231.8	4522.8	2832.1
1741.2	5056.2	4983.9	4901.7	4486.5	4451.2	6827.0	4777.9	5053.6	3720.5	4585.2
1687.5	5142.5	4677.9	4117.7	3954.2	4387.2	5953.1	3941.3	4762.3	3427.0	4255.8
5398.4	4777.2	4185.0	4072.2	3583.0	3991.2	4873.0	3960.0	4663.2	3656.1	4650.2
92.2	5331.1	3843.7	1561.4	3321.0	4317.3	2819.7	2090.4	3974.3	3590.3	1190.2
1451.9	5391.4	4168.2	2147.9	4058.8	4809.6	3349.1	2638.3	4094.8	3738.4	1528.5
3356.2	8378.1	6138.7	4580.8	5873.7	6562.5	5395.2	4958.5	8985.2	6096.0	5004.8
6881.7	8225.4	6541.3	5419.5	6657.3	6910.2	6304.1	5953.6	9416.4	7735.4	6234.3
3808.1	7815.7	6505.1	6671.6	6839.6	6548.4	8078.8	5504.5	9737.0	6391.3	6874.4
13754.9	11309.5	10015.2	10663.8	11208.4	10468.3	10530.6	10044.4	16312.2	11084.6	14202.5
5778.5	7812.8	6375.7	6315.6	6133.5	6890.8	6689.6	6267.6	10233.1	8005.1	7459.9
456.2	4108.7	2943.2	1664.4	3231.6	2575.1	2672.5	2014.8	3652.8	2809.5	1002.3
3920.0	8431.1	6962.5	5996.1	7575.8	7613.3	7416.0	6103.4	9109.4	8455.0	5512.0
1173.0	7843.5	4883.4	3028.2	5483.9	5631.5	4087.2	3424.9	7092.3	5343.3	1745.4
3942.3	6881.5	5031.2	4660.2	5519.1	5033.1	5773.9	4795.1	8616.2	6965.8	4576.2

2534.0	585.3	951.3
1623.2	965.6	887.0
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1158.0	587.3	755.8
8123.2	7398.9	7687.9
1631.3	1151.1	1334.1
8307.4	6133.4	6299.5
2023.3	2049.6	1698.0
3466.4	2721.0	3500.8
5811.1	5810.2	5530.2
3737.8	1575.8	1749.2
3384.1	2550.0	2867.8
1892.6	1341.9	1627.0
2097.0	1173.1	1335.8
2108.7	1214.4	1374.5
3428.3	1190.3	1661.7
6909.6	7116.4	7476.7
4122.5	5086.5	4976.5
4875.6	4504.4	6568.0
5389.3	2460.9	3171.0
9322.9	7316.9	9866.8
4335.3	4538.4	4402.9
2433.5	4498.3	3495.1
3460.2	3301.3	3634.2
3756.2	3084.1	3767.3
6187.3	5069.5	5425.1
4005.2	3160.7	3838.6
3848.0	4642.0	5298.8
3512.4	3539.7	4450.0
3412.8	4567.4	4804.1
3019.6	1445.2	1622.0
3436.4	2478.7	2402.4
5474.3	5310.4	4215.7
5887.9	6125.7	5078.9
5243.6	5826.2	5798.4
9616.3	9571.3	8442.8
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1997.0	1525.0	1704.3
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GQ260086.1 gg_id:513894 Kocuria marina str. ICIRC146 GQ260
EU379291.1 gg_id:271335 Kocuria palustris str. 5N-4 EU379
FJ825842.1 gg_id:567669 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea; FJ8258
GQ280092.1 gg_id:508890 Kocuria sp. str. JS-22 GQ280
AM292061.1 gg_id:250560 Kocuria palustris zf-47-II AM292
GQ026297.1 gg_id:386231 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
AF542074.1 gg_id:76966 Kocuria varians str. ATCC 15306 AF542
EF528277.1 gg_id:226190 Arthrobacter globiformis str. CICCHLJ Q57 EF5282
AF542072.1 gg_id:75116 Kocuria rhizophila str. ATCC 9341 AF542
CU914931.1 gg_id:462730 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU914
CU914991.1 gg_id:393626 and dynamics adapted microbiota during degradation Tunisian zarzatine enriched se CU914
DQ059617.1 gg_id:137077 Kocuria aegyptia str. YIM 70003 DQ059
DQ227792.1 gg_id:142110 Kocuria sp. PIC-C6 DQ227
DQ448783.1 gg_id:158234 Kocuria sp. str. CNJ928 PL04 DQ448
FJ527817.1 gg_id:561067 Kocuria sp. str. KSL5401-224 FJ5278
FJ607312.1 gg_id:588712 Kocuria sp. str. P31 FJ6073
GQ497940.1 gg_id:589054 Arthrobacter sp. str. KO_PS43 GQ497
DQ158126.1 gg_id:139352 Use Field-Based Stable Isotope Probing Identify Adapted and Track Carbon F throug DQ158
AY030341.1 gg_id:19877 Kocuria rhizophila str. KL-057 AY0303
DQ979377.1 gg_id:197836 Kocuria halotolerans str. YIM 90716 DQ979
FJ674767.1 gg_id:529839 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
NR_029297.1 gg_id:586618 Kocuria varians str. G33; DSM 20033 NR_02
FM873886.1 gg_id:363167 occupant source house mattress dust clone MB02E06 FM873
FJ595528.1 gg_id:570671 rock Black Canyon New Mexico: and Geochemistry rocks no varnish clone NV36_2f10 FJ5955
AM697266.1 gg_id:226642 sequencing libraries indoor dust clone BF0001C107 AM697
AJ639827.1 gg_id:104897 Arthrobacter pigmenti str. LMG 22284 AJ6398
NR_025285.1 gg_id:562170 Micrococcus antarcticus str. T2; JCM 11467 NR_02
GQ199615.1 gg_id:568913 Arthrobacter sp. str. BSw21447B GQ199
DQ125716.1 gg_id:130481 uranium contaminated soil clone AKAU3812 DQ125
FJ984531.1 gg_id:430699 Micrococcus luteus str. NBSL29 FJ9845
AY167858.1 gg_id:77387 Micrococcus luteus str. SAFR-002 AY1678
FN393775.1 gg_id:543578 Micrococcus luteus str. ES-2301a FN393
FJ380971.1 gg_id:540642 Micrococcus luteus str. BQN1T-03d FJ3809
EU867327.1 gg_id:564493 Micrococcus luteus str. CCGE3064 EU867
AJ971846.1 gg_id:134459 Arthrobacter sp. Am 05 AJ9718
FJ357615.1 gg_id:574142 Micrococcus luteus str. BBN4B-01d FJ3576
DQ370013.1 gg_id:151899 Micrococcus luteus str. czh-8C DQ370
FN393785.1 gg_id:557706 Micrococcus luteus str. ES-308-9d FN393
FJ816022.1 gg_id:581693 Micrococcus luteus str. G3-6-08 FJ8160
EU071592.1 gg_id:239423 Micrococcus luteus str. EHFS1_S02Hd EU071
FN393763.1 gg_id:541725 Micrococcus luteus str. ES-128S FN393

3895.0	8021.4	6012.0	4547.7	6550.4	5724.2	5396.4	4826.7	7987.8	6043.3	4172.5
421.7	7353.1	5040.8	2482.9	4287.4	4697.9	3914.0	2798.9	6092.5	4657.7	1667.1
314.5	5102.4	3620.5	3341.0	4062.6	3173.0	4211.1	2757.3	4670.7	3759.5	2952.5
5654.3	6345.4	5306.2	4488.1	5389.9	4820.9	4665.6	4084.9	5706.1	8709.5	4898.9
373.9	6532.7	4563.2	2258.6	4571.7	4355.8	3741.4	2502.9	5527.2	4577.9	1594.3
4092.4	13142.2	10419.7	10396.7	11218.1	10085.7	11941.5	7762.2	13987.3	10741.9	9127.6
16011.3	7728.0	7001.2	7180.4	7317.9	7153.8	10715.4	6264.7	9909.8	7457.2	8595.6
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473.0	4024.5	3207.9	2959.8	5478.1	2851.5	4543.6	2448.4	4290.8	2113.9	1810.5
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131.0	5580.6	4439.6	2025.2	5238.6	4928.4	4358.3	2244.0	5261.5	4274.8	1352.4
822.4	7110.1	5288.4	3652.5	6220.5	5786.7	5044.8	3770.0	8581.0	4861.1	2581.5
985.6	4272.2	3280.1	2656.8	5393.1	2847.1	3845.0	2635.4	4912.8	2906.0	2066.9
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213.6	6865.6	4676.8	2578.9	4532.5	5120.3	3965.7	3218.5	5724.7	5219.1	1950.8
170.6	937.4	956.9	1495.9	1967.7	1110.8	1231.8	780.2	857.2	457.7	523.1
6737.0	9228.1	8167.3	7290.4	9959.9	6953.0	9276.6	6945.9	8097.6	9001.5	7505.2
199.9	7566.1	5505.4	1833.5	4849.3	6322.6	3406.6	1986.3	7095.1	5249.4	1631.6
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143.7	5481.0	4571.2	3896.6	5254.2	5062.9	3852.5	3695.8	5160.7	4725.9	2841.3
193.8	3004.3	2933.2	2979.9	4426.9	2904.7	3371.7	2157.8	2029.8	1555.3	1553.9
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74.1	2140.6	2199.7	1946.7	2371.5	2715.6	2251.0	1474.3	1253.5	1421.0	804.1
138.0	2609.8	2445.2	1216.4	1487.0	3036.2	1854.3	1174.8	2108.4	1693.9	991.7
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232.2	2737.6	2756.5	2977.8	4230.0	2801.0	3260.7	2125.7	1308.9	1417.3	1511.2

4639.6	4778.7	3999.0
3463.8	2104.6	2238.6
3697.9	3000.4	3179.0
4955.0	5319.9	4469.5
3210.2	1871.6	2029.5
9257.8	9372.2	10366.3
6230.7	7478.5	7072.5
3327.9	2614.8	2216.4
3718.3	4103.4	6545.5
7144.3	5968.4	6460.1
2451.8	3186.7	3600.3
2078.1	1079.0	1233.5
4548.4	3225.7	3052.0
1532.9	1080.6	1134.8
7458.3	7007.2	6407.5
5321.3	6679.8	8035.7
2043.3	1561.3	1289.6
2443.6	2138.4	1949.5
7252.7	7398.4	5895.4
3705.0	4073.3	4204.5
3513.5	2072.6	2423.7
3047.1	1554.1	1849.5
4433.1	4073.6	4984.5
3178.9	2798.4	2433.3
1320.4	847.1	968.8
6312.9	7313.8	6439.4
3743.1	1611.8	2100.4
1642.8	1000.1	783.6
7262.8	5901.4	6853.3
2395.9	1209.2	1603.1
3437.3	3260.2	3475.2
4025.3	3772.4	3017.8
2399.9	1750.4	2109.4
1685.4	1689.6	1632.4
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959.6	857.3	667.7
3312.2	3600.1	2752.8
2306.9	1606.8	1266.2
1256.7	1148.7	914.0
705.8	539.6	311.2
2782.9	1919.4	2289.2

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g__Micrococcus
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s__Micrococcus luteus	40373
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AB247644.1 gg_id:166097 Micrococcus thailandicus str. S3-4
AJ717369.1 gg_id:109993 Micrococcus luteus CV44
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GQ856255.1 gg_id:589588 Micrococcus luteus str. ER4
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EU379295.1 gg_id:268373 Micrococcus luteus str. 6J-4a
AM237392.1 gg_id:154144 Micrococcus luteus OS-159
EU730941.1 gg_id:307330 Micrococcus luteus str. 164
FN393771.1 gg_id:537706 Micrococcus luteus str. ES-176S
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AJ536198.1 gg_id:78140 Micrococcus luteus str. DSM 20030
EU907919.1 gg_id:338075 Micrococcus sp. str. SKUK MB1004
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EU379288.1 gg_id:260431 Micrococcus luteus str. 4RS-9d
GQ401239.1 gg_id:576509 Micrococcus luteus str. VITSCA03
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FN393780.1 gg_id:555822 Micrococcus luteus str. ES-305-5
DQ869037.1 gg_id:252119 Micrococcus sp. str. DW-1
X80750.1 gg_id:12480 Micrococcus lylae str. DSM 20315
EU135634.1 gg_id:258066 Micrococcus sp. str. YIM C694
AF194538.1 gg_id:42157 Methylomicrobium sp. str. 6G
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EU931551.1 gg_id:350663 Micrococcus luteus str. ZFJ-12
GQ280053.1 gg_id:578762 Micrococcus luteus str. BJ-43
AF218240.1 gg_id:22419 Micrococcus sp
AM992194.1 gg_id:281439 Micrococcus luteus TS IW 23
FN393760.1 gg_id:560649 Micrococcus luteus str. ES-122S
EU095950.1 gg_id:248922 Micrococcus luteus PAH-8

EU071
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FJ0408
FN393
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FJ9845
EU438
GQ856
DQ855
EU379
AM237
EU730
FN393
EU071
AM237
AY8812
EU379
AJ5361
EU907
EU071
EU379
GQ401
AJ4090
FN393
FN393
DQ869
X80750
EU135
AF1945
EF1872
EU9315
GQ280
AF2182
AM992
FN393
EU095

170.7	5055.6	4410.9	4301.2	4572.3	5423.0	3602.8	4050.8	5709.5	4851.9	2697.0
101.7	3886.6	2914.6	2543.6	3203.8	3586.9	2449.7	2692.4	4456.3	4182.3	1874.3
260.9	5463.6	3164.1	1592.0	5068.2	4174.1	2912.6	2056.5	4154.9	3495.1	1541.9
637.9	3413.5	3573.3	3755.4	4679.3	3092.2	4103.4	2676.6	2347.9	2003.5	2517.7
2460.6	9128.0	6131.4	6140.8	6945.4	8436.9	5361.7	4587.2	8106.2	6174.2	6685.2
225.3	3836.6	3566.6	3172.6	3873.1	3418.0	3027.0	2133.7	2295.0	1911.6	1783.2
74.0	1553.2	1361.5	913.0	1436.8	1563.0	1394.9	755.7	890.0	1192.4	344.2
97.1	3619.6	2793.6	1076.3	2164.8	3327.1	2042.4	1445.1	3605.8	3114.4	894.2
128.6	4725.4	3562.0	3090.9	4793.1	4670.7	3260.6	2982.7	5171.2	4925.4	2076.7
220.1	2880.2	2863.7	2646.6	3764.8	2530.0	2862.8	1826.1	1757.7	1329.5	1483.8
171.1	3892.9	3309.9	1684.2	3486.6	4077.1	2676.3	1739.5	3300.8	2700.3	1281.7
197.9	3701.5	3452.3	2895.2	3766.4	3291.2	2774.5	1972.7	2185.3	1824.9	1655.6
158.6	1813.0	1755.9	1573.7	2295.5	1777.0	1676.0	964.9	919.6	658.8	639.1
948.2	7092.6	4301.0	1420.5	3284.0	6173.7	2582.0	1881.2	5526.1	4353.1	1351.7
375.9	3569.0	3192.8	2091.0	2841.2	3161.5	2344.3	1675.7	2938.4	2626.0	1447.2
351.5	3407.8	2648.8	1330.6	2712.6	3111.9	1863.7	1182.3	2888.7	2895.6	792.6
108.5	3559.9	2480.4	1755.4	2545.1	3308.5	1525.7	1589.2	3161.5	3082.9	986.2
647.6	4007.7	4040.8	4058.6	5024.5	3769.3	4214.4	2868.5	2629.5	2393.0	2634.0
160.4	3331.3	3328.8	2213.0	3737.4	3638.2	3487.5	1889.4	2509.8	2305.2	1172.1
270.2	8001.0	5601.5	3048.9	5258.6	6740.2	3197.1	3089.9	7045.6	5392.7	1969.5
216.3	3081.4	2554.4	2145.6	3631.2	2734.8	2436.4	1414.8	1984.1	1791.9	967.1
127.5	2004.7	1544.1	706.1	1795.7	1833.3	1696.6	679.5	1737.0	1686.6	423.5
164.2	5161.8	3742.8	2119.6	3527.1	4440.9	2554.7	2147.4	4828.9	4501.5	1414.3
139.5	2026.3	2006.4	1823.0	2074.4	1979.2	1417.4	1201.8	1423.3	968.8	1152.5
123.5	2659.0	2586.9	1526.6	2708.0	3093.8	2552.2	1387.6	2179.0	1900.0	950.7
176.5	4511.6	3342.0	2718.6	3447.6	4135.3	2500.2	2617.3	5002.4	4618.6	1892.8
258.3	4835.1	4046.2	1674.3	2933.7	3770.1	2184.1	2029.5	3966.8	3189.4	1803.3
258.7	9379.4	6643.5	2054.1	4770.2	7779.7	3588.4	3173.3	9452.2	8296.4	1925.6
556.6	3854.0	3939.3	3930.9	4265.8	3647.5	3786.0	2828.2	2562.5	2175.6	2583.7
598.8	3405.3	3552.4	3618.9	5236.2	3139.9	4238.9	2717.9	2268.8	2069.8	2415.8
2942.0	7840.0	6323.4	3503.0	5398.1	7718.1	4762.8	3811.9	6618.6	6481.7	3523.6
1376.3	6118.7	5089.5	2438.3	6137.5	4892.2	4383.8	3333.4	7372.7	5695.8	2364.7
195.8	6971.8	5022.4	2727.1	5271.3	6669.8	4312.5	3505.7	7405.5	6478.5	2280.6
160.7	5843.6	4473.0	2303.8	4551.6	4913.5	4593.3	2996.8	5725.6	5117.7	1963.4
17004.2	9584.6	8123.6	5873.6	6434.6	9192.8	7226.4	5461.6	12118.8	9839.3	7795.4
119.4	7176.3	4553.3	2030.5	3509.1	6342.1	2422.4	2067.1	5490.4	4506.9	1696.9
924.4	6030.8	5339.4	3683.3	5627.8	5316.6	4812.4	4746.2	6021.2	7390.9	3254.1
104.6	6178.1	4310.7	2819.9	5134.2	4968.2	3663.0	3379.9	6022.3	5581.0	2411.3
160.4	5252.7	4222.7	2899.8	3449.4	5522.4	2871.4	2784.8	5128.7	4437.3	2332.6
519.6	3271.8	2554.2	2892.0	5602.4	2771.8	3941.0	2620.0	2864.2	2402.2	1842.5
2936.2	12400.7	8836.5	6629.4	7788.8	9811.6	6771.0	6827.0	12024.2	9899.7	7147.6

3305.0	3824.1	2743.3
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2425.0	1331.3	1639.6
3228.1	2848.6	2946.5
4751.3	4796.9	4726.1
3110.6	2153.6	2289.9
1765.4	1039.0	549.0
1659.4	1493.6	848.7
3490.0	3154.5	2145.7
2399.0	1940.8	1986.9
1802.8	1079.4	1318.2
2963.8	2051.0	2124.2
1420.5	1108.0	987.8
2545.2	1817.5	1373.1
1674.7	1660.2	1606.4
1788.6	1122.9	980.4
2317.2	1889.2	1135.3
3905.3	3005.6	3208.6
2400.9	1766.7	1461.2
4066.9	2289.4	2131.1
2543.4	1445.7	1467.3
1071.7	899.7	504.9
2851.2	2268.2	1454.3
1295.5	1345.8	1285.3
1556.1	1335.5	947.6
2801.8	3346.5	1765.3
2714.9	1427.6	1262.2
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5277.2	6578.9	4809.2
3024.4	1598.2	1969.3
4444.5	3839.5	3728.9
4116.1	2270.6	2337.4
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3732.5	5199.9	2745.4
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FJ217202.1 gg_id:568886 Micrococcus luteus str. BQAPs-05d FJ2172
DQ223665.1 gg_id:159932 Micrococcus sp. zf-IRlt7 DQ223
GQ861526.1 gg_id:522152 Micrococcus luteus str. BF1-6 GQ861
AB023371.1 gg_id:12467 Micrococcus luteus str. IFO 16250 AB023
AJ409096.1 gg_id:23916 Micrococcus luteus str. Ballarat AJ409
GQ060348.1 gg_id:398784 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ060
DQ229318.1 gg_id:144367 Micrococcus luteus BCNU121 DQ229
AY702663.1 gg_id:170121 Micrococcus alkanovora str. MS8 AY702
GQ169060.1 gg_id:564586 Micrococcus sp. str. CTDB2 GQ169
AY914063.1 gg_id:112715 Nesterenkonia sp. -7A AY914
AY958876.1 gg_id:133295 Microbes on human vaginal epithelium clone rRNA103 AY958
EU432564.1 gg_id:262645 Nesterenkonia sp. str. 10004 EU432
FM179648.1 gg_id:323263 Nesterenkonia sp. AKB-K1-251 str. K1-251 FM179
AY928901.1 gg_id:113080 Nesterenkonia jeotgali str. JG-241 AY928
AY764166.1 gg_id:108017 Renibacterium salmoninarum str. GC-96-1 AY764
AJ812213.1 gg_id:107764 Acaricomes phytoseiuli str. DSM 14247 AJ8122
AB071950.1 gg_id:59471 Arthrobacter russicus str. GTC 863 AB071
EU086805.1 gg_id:252828 Arthrobacter sp. str. 741 EU086
EU293888.1 gg_id:252229 Rothia aeria str. Lan EU293
AF543284.1 gg_id:58293 Rothia dentocariosa str. ChDC OS32 AF543
GQ079137.1 gg_id:388529 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ079
GQ030912.1 gg_id:450368 Topographical and Temporal Human Skin Microbiome skin palm clone nbw884e11c1 GQ030
GQ106520.1 gg_id:417109 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ106
GQ114134.1 gg_id:459539 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ114
GQ076902.1 gg_id:404554 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw1155 GQ076
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GQ032885.1 gg_id:407390 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ114733.1 gg_id:409908 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ114
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GQ106467.1 gg_id:375018 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ106
GQ011317.1 gg_id:498348 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw742 GQ011
GQ030730.1 gg_id:466830 Topographical and Temporal Human Skin Microbiome skin palm clone nbw882a11c1 GQ030
DQ822568.1 gg_id:169191 Rothia sp. str. L-143 DQ822
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GQ066426.1 gg_id:377780 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ066

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297.0	8157.9	5682.1	2429.4	4809.2	5413.3	3610.5	4683.1	8965.6	6607.2	3579.8
2462.9	10356.9	7345.8	4424.6	7644.9	6836.8	6302.6	6153.3	9656.8	7889.3	4393.8
306.4	7292.0	6198.8	4606.8	5524.0	7224.4	4497.0	4300.7	7752.6	6513.2	3221.3
14682.0	6090.3	5325.4	4888.3	6454.8	6466.3	4745.6	4816.8	5428.7	5116.6	7740.3
124.9	2445.2	1910.1	870.6	1354.6	2388.6	1379.2	821.6	1938.2	1847.3	485.4
3041.6	9449.2	7194.4	6403.4	7350.1	7869.8	6655.9	7263.7	10430.2	8487.4	6681.9
334.9	4009.4	3558.8	2266.5	2400.1	3716.8	2026.9	1817.8	3153.0	2798.1	1509.1
250.1	7562.2	5082.9	3742.0	5325.3	6237.5	4181.3	4497.5	7863.9	6654.9	3081.7
630.5	6822.0	5274.7	1832.5	3162.9	5679.8	2132.9	2395.8	7959.8	5955.4	1580.4
49.6	55.3	43.3	70.1	220.7	83.1	114.8	21.5	22.6	91.5	29.3
121.2	385.2	403.7	658.0	635.4	398.2	675.8	356.0	151.5	119.3	163.2
407.7	3754.3	4097.5	1226.6	4346.2	3235.3	3297.0	2415.0	6103.6	3476.9	1725.2
56.7	51.5	71.4	46.9	107.5	59.3	44.9	47.3	50.7	47.2	40.5
522.2	2236.2	2439.1	2497.6	4909.1	2129.4	4593.8	2314.7	2076.2	2236.6	1285.9
307.6	3891.0	2742.7	942.9	3702.5	2991.4	1928.3	1159.1	3410.0	2446.8	724.9
249.0	3609.6	3762.5	2268.4	2499.4	3288.9	2504.6	2490.7	2951.0	1591.6	1933.1
179.6	2050.8	1530.3	872.9	3988.6	1962.6	1981.6	1123.3	1865.4	1644.0	548.5
1682.1	8283.1	6403.4	3904.3	5442.5	5858.3	6402.4	4615.2	8943.4	7101.3	5490.5
493.2	5103.7	4041.7	3324.5	5100.4	4278.2	4552.1	3243.5	4967.7	4721.4	1758.2
466.3	4875.9	3788.9	2285.3	4606.6	4483.5	2694.3	2750.0	4826.3	3012.1	2176.3
1022.8	4404.6	3939.4	3780.5	4747.4	4049.0	4476.0	3312.2	4161.5	6517.1	4427.7
260.3	4082.2	3921.3	2670.1	3385.7	3777.9	3007.7	3064.5	4763.2	5415.8	2363.1
825.1	6572.7	4771.1	2403.6	3590.7	5945.8	2137.3	2561.2	6269.2	4515.9	1548.7
277.3	2772.1	2587.7	1994.0	2561.8	2689.4	2652.1	2205.9	2346.2	4427.6	1187.7
280.2	7552.1	5321.0	2642.1	3240.0	4396.4	2735.2	2974.9	6707.0	5487.9	2428.7
665.4	1638.5	2590.0	2256.7	2065.6	1402.9	2806.9	1874.9	1088.2	832.6	1086.7
545.6	7108.9	5479.8	3878.2	5504.9	5205.4	5120.7	4446.7	6506.6	7501.8	3058.8
379.8	4044.3	3716.8	3598.0	4126.5	3447.1	4550.5	4034.4	2934.5	3692.9	2339.0
10003.2	7590.0	6863.9	6777.6	5565.5	7497.2	5550.6	6221.7	10703.2	7621.3	8956.8
284.1	6335.0	4168.7	2114.5	3174.5	3632.6	2356.7	2166.3	4261.5	3335.8	1310.1
4070.5	7530.7	6124.4	4955.6	5545.2	5281.4	5603.1	4367.9	8589.6	6669.0	7893.6
459.9	5129.0	3863.7	2027.0	4150.6	3984.5	3630.1	1725.9	6477.9	5166.2	794.9
10784.4	5771.5	5523.4	5688.3	5705.7	5324.7	5568.1	5509.6	8133.5	7273.6	7626.4
11124.5	5820.2	5241.8	5931.7	5962.1	5512.7	6063.5	5367.3	7120.6	6286.8	8768.1
8002.5	8540.8	7251.1	5797.8	6566.7	5804.5	6139.8	5672.7	9033.7	7521.6	6946.5
2623.1	4820.6	3627.5	2815.7	3204.3	3806.2	3764.6	3012.9	5935.2	4698.0	3648.1
821.4	4270.8	3167.1	2204.7	3021.5	1971.2	2428.3	1941.8	3266.1	3455.8	1622.6
905.2	4581.0	3070.6	1898.6	3868.7	4005.0	2358.2	1866.3	4331.5	3295.2	919.4
230.8	2801.2	3776.8	2440.8	3416.4	2453.9	3899.5	2332.9	1337.6	988.8	2142.8
2208.1	6518.4	4292.4	3591.4	4547.4	4791.4	4672.7	3749.7	8601.4	6086.2	3477.7

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1512.4	969.8	675.9
6494.1	7994.7	7359.2
2171.2	1730.4	1777.3
4201.3	3455.8	2910.9
2047.6	2041.6	1531.8
102.6	27.4	57.8
355.3	327.3	448.1
2542.1	1649.0	2035.8
47.3	64.7	77.4
2445.7	2038.9	3064.6
1239.8	980.3	748.2
1995.7	2164.0	2693.0
1499.7	807.8	952.6
4260.3	4382.1	4610.6
4106.1	3394.6	3641.3
2695.3	2450.5	2553.1
3806.0	3610.4	3815.1
3139.3	1510.2	2267.7
2555.4	2010.7	2131.4
2227.8	2372.2	2303.4
3977.5	2590.8	3540.5
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4629.3	2167.4	4545.7
3562.0	2708.7	5188.3
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3070.4	1830.2	2062.1
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3448.7	1779.4	1757.0
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4917.2	5543.2	5122.7
6150.7	6079.3	6787.1
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2118.0	1966.5	2732.0
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s__Actinoplanes italicus	41450
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s__Actinoplanes philippinensis	41764
s__Actinoplanes teichomyceticus	41577
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GQ066700.1 gg_id:451985 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ066
AB248533.1 gg_id:198437 Arthrobacter sp. str. LC13 AB248
X80746.1 gg_id:12490 Arthrobacter atrocyaneus str. DSM 20127 X80746
DQ490462.1 gg_id:158249 Representation heterotrophic isolates respective libraries recent Hawaiian (<300 yr DQ490
AB248531.1 gg_id:193334 Arthrobacter sp. str. LC10 AB248
GU332621.1 gg_id:555969 Arthrobacter sp. str. AG2-13 GU332
FM955860.1 gg_id:583677 Arthrobacter sulfonivorans str. Asd M3-2 FM955
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DQ177496.1 gg_id:140519 Arthrobacter sp. str. Tibet-S942 DQ177
AM933499.1 gg_id:304140 Arthrobacter oxydans FB5 AM933
AB009839.1 gg_id:235825 Arthrobacter sp. str. BA-5-17 AB009
DQ094184.1 gg_id:134679 Arthrobacter sp str. 9#2 DQ094
EF423346.1 gg_id:210926 Arthrobacter sp. str. 5010 EF4233
AJ864856.1 gg_id:133401 Arthrobacter sp. J64 AJ8648
EF522134.1 gg_id:227154 Micrococcus sp. str. CU207 EF5221
EU685813.1 gg_id:318338 Kocuria sp. str. PK-11 EU685
EF540513.1 gg_id:225019 Arthrobacter sp. 4_C16_51 EF5405
AY512631.1 gg_id:99048 Arthrobacter polychromogenes str. A1-69 AY5126
DQ298298.1 gg_id:153889 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AJ292364.1 gg_id:68681 Arthrobacter nasiphocae str. M597/99/10 AJ2923
DQ298286.1 gg_id:151297 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AF330692.1 gg_id:46937 Arthrobacter scleromae str. YH-2001 AF3306
DQ177474.1 gg_id:139857 Arthrobacter sp. str. Tibet-IIR62 DQ177
AJ535637.1 gg_id:76404 Arthrobacter sp. str. SB30 AJ5356
FM955887.1 gg_id:553286 Arthrobacter oryzae str. Asd M5-8 FM955
FJ425902.1 gg_id:569667 Zhihengliuella sp. str. JSM 071043 FJ4259
EU937749.1 gg_id:330617 Zhihengliuella sp. str. JG 05 Iti 3 EU937
AM980986.1 gg_id:564840 Actinocatenispora silicis str. CS5-AC17 AM980
AB263096.1 gg_id:166311 Intrapaticulam serus str. KV-744 AB2630
AB048215.1 gg_id:51187 Actinoplanes durhamensis str. JCM 7625T AB0482
AB468943.1 gg_id:369289 Actinoplanes sp. str. MN07-A0368 AB4689
AB037002.1 gg_id:41171 Actinoplanes ferrugineus str. IFO 15555T AB0370
AB048219.1 gg_id:52031 Actinoplanes globisporus str. JCM 3186T AB0482
AJ277576.1 gg_id:17385 Actinoplanes ianthinogenes str. IMSNU 20032 AJ2775
AB048217.1 gg_id:24733 Actinoplanes italicus str. JCM 3165T AB0482
AB047505.1 gg_id:24378 Actinoplanes sarveparensis str. IFO 13998 AB0475
NR_026018.1 gg_id:533940 Actinoplanes philippinensis str. P-15; ATCC 12427 NR_026
D85474.1 gg_id:71458 Actinoplanes philippinensis str. IFO13878 D85474
AB047513.1 gg_id:37529 Actinoplanes teichomyceticus str. IFO 13999T AB0475
AJ277584.1 gg_id:52136 Actinoplanes teichomyceticus str. IMSNU 20043 AJ2775

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208.0	874.8	865.5	626.5	711.2	802.3	738.7	491.6	960.3	498.5	530.0
278.6	2474.1	2617.4	1840.1	4070.1	2503.8	2850.4	2071.9	3612.9	2370.3	883.7
2263.0	6872.6	5698.5	5423.6	5898.2	6058.7	7048.6	6144.6	7700.2	6319.0	5357.8
4677.9	8027.6	6660.1	8159.2	8505.1	7749.4	10019.9	8782.0	9855.9	7558.1	8074.9
118.9	2212.7	2221.4	1564.4	3414.8	2333.4	2354.3	1948.0	2609.1	1708.1	970.3
251.8	6035.5	4537.4	1929.0	4886.6	5344.8	3754.2	2399.5	6534.1	4312.2	1343.8
54.0	2169.6	1699.1	1230.7	4639.4	1479.8	2387.9	1411.7	1797.0	1672.2	770.4
167.3	4241.5	3986.9	3013.5	5518.2	4081.5	4811.0	4135.8	3580.9	3532.5	2114.6
37.1	421.5	288.4	327.3	2953.9	448.1	1544.8	29.0	14.2	802.1	55.2
63.5	1298.3	1011.7	1041.3	6983.8	1706.7	3414.7	590.2	329.2	1838.8	344.8
292.8	2046.2	2080.2	1913.8	4057.6	2366.3	2931.6	1604.2	2638.5	1861.2	1275.4
146.0	3548.1	2925.2	1816.5	2635.3	2686.1	2347.8	1231.0	3414.5	2244.6	1254.4
76.0	2959.5	2373.0	1191.4	4058.8	1952.8	3039.0	2156.9	2538.6	2097.0	853.2
47.3	1642.4	1290.3	800.9	4286.0	1141.8	1478.0	967.9	1268.8	1300.8	532.4
291.3	7850.0	6439.6	2819.6	6105.9	7145.5	4732.7	4542.3	6600.9	6188.2	3403.5
119.9	1512.7	1506.5	1412.4	2384.2	1315.7	1190.5	1686.8	1720.6	1291.9	842.5
95.2	1682.0	1339.8	1393.3	6340.0	1881.5	3281.7	761.3	520.0	2042.9	465.9
103.1	2382.1	1896.0	616.8	3077.4	2157.1	1789.8	728.4	2766.5	2072.9	567.9
3376.3	1823.4	1786.8	1433.4	1490.4	1630.7	1815.7	1811.9	2380.0	2561.3	1770.9
5969.5	6213.1	5244.4	4691.4	8025.4	5646.8	5752.0	4849.7	6512.8	6675.6	4286.8
306.5	5438.7	3906.0	1930.7	3111.0	4062.6	2777.0	2567.6	5786.9	3849.8	1494.1
2820.9	4588.1	4103.7	3387.9	8794.3	4192.0	5774.7	3233.2	6131.3	4155.2	2383.5
45.8	1195.5	957.3	869.0	5618.8	1228.8	2841.7	707.4	473.4	1266.9	350.9
30.7	139.9	68.2	80.4	135.2	71.6	75.5	79.7	31.8	22.8	28.7
37.9	1270.9	1487.1	898.6	3150.1	1856.5	1584.7	1296.0	602.3	996.3	264.5
322.1	3945.7	3830.9	2682.8	6420.4	4387.2	4152.4	2358.8	4765.7	4277.1	1550.1
89.0	4522.9	2477.9	1254.7	4190.0	3633.1	2761.6	1087.4	2450.2	2731.9	554.2
971.0	4565.3	3454.3	2503.1	3702.4	3751.3	3597.6	2717.5	3416.4	2072.1	958.1
33.9	59.7	80.1	79.2	167.9	68.7	134.3	62.1	55.1	47.5	38.9
185.0	431.3	244.1	364.1	858.7	179.4	384.5	351.6	665.7	217.0	121.9
96.6	2022.6	1758.3	2401.4	5300.7	1563.5	3202.6	1553.1	375.9	312.5	975.5
86.9	2675.2	2054.2	1733.8	3801.4	1811.3	2779.4	1717.3	753.8	734.4	987.1
426.7	2651.0	2061.6	1392.3	3666.6	2199.2	2287.9	1943.4	1928.8	1413.3	860.0
32.0	657.7	616.9	548.9	1364.3	703.6	1006.0	772.8	433.4	350.9	290.2
497.6	2908.9	2557.1	3133.0	5456.1	2732.8	3857.9	3046.4	2939.4	1732.2	1188.3
554.6	4287.4	3739.3	3594.2	4823.8	3715.2	3988.8	3459.9	2920.9	3005.2	1802.4
349.1	2273.1	1855.8	1882.7	4062.8	1885.4	2550.5	2044.7	2417.6	1424.9	703.1
436.1	3090.6	2798.2	2563.3	3995.9	2780.1	2883.6	2943.1	2472.0	1834.2	1384.3
272.3	3149.8	3044.6	2212.8	5195.7	2465.9	3387.2	2074.3	2031.0	3072.7	651.7
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4830.1	5401.1	6302.1
7720.6	7707.6	8320.8
2538.3	1394.3	2554.5
2795.0	1372.7	1996.4
1511.5	1023.3	1013.0
3945.3	2308.2	3538.7
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2845.0	1182.8	1351.6
3692.9	1568.8	2390.4
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AB037010.1 gg_id:31041 Actinoplanes rectilineatus str. IFO 13941T AB037
AB036999.1 gg_id:32651 Actinoplanes derwentensis str. IFO 14935T AB036
AB047489.1 gg_id:39135 Actinoplanes arizonaensis str. IFO 14837T AB047
AJ277575.1 gg_id:37443 Actinoplanes garbadinensis str. IMSNU 20040 AJ2775
FM177520.1 gg_id:554420 Actinoplanes sp. str. RP-AC33 FM177
AB047504.1 gg_id:37247 Actinoplanes rutilosporangius str. IFO 13970T AB047
AJ277572.1 gg_id:44085 Actinoplanes missouriensis str. IMSNU 22051T AJ2775
AB037012.1 gg_id:51900 Actinoplanes utahensis str. IFO 13244T AB037
X80823.1 gg_id:12821 Actinoplanes utahensis str. ATCC 31044 X80823
AB546284.1 gg_id:523680 Actinoplanes sp. str. IR51-RC111 AB546
AJ277578.1 gg_id:39832 Actinoplanes pallidoaurantiacus str. IMSNU 22128 AJ2775
AY922006.1 gg_id:113657 farm soil clone AKYG409 AY922
X93188.1 gg_id:12820 Actinoplanes regularis str. DSM 43151 X93188
AJ277577.1 gg_id:24564 Actinoplanes kinshanensis str. IMSNU 20034 AJ2775
AB048216.1 gg_id:49449 Actinoplanes palleronii str. JCM 7626T AB048
AJ277580.1 gg_id:33156 Actinoplanes penicillatus str. IMSNU 22129 AJ2775
X93186.1 gg_id:12818 Actinoplanes cyaneus str. DSM 46137 X93186
AY921991.1 gg_id:114168 farm soil clone AKYG1815 AY9219
AB047503.1 gg_id:36605 Actinoplanes roseosporangius str. IFO 13969T AB047
EU841702.1 gg_id:313401 Actinoplanes capillaceus str. HBUM173732 EU841
AJ277566.1 gg_id:31721 Actinoplanes derwentensis str. IMSNU 20027T AJ2775
FJ478979.1 gg_id:589246 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
AM400230.1 gg_id:164505 Actinoplanes couchii str. GW8-1761 AM400
AJ865473.1 gg_id:109037 Actinoplanes garbadinensis str. DSM 44321 AJ8654
AB047514.1 gg_id:47233 Actinoplanes tuftoflagellus str. IFO 14021T AB047
EU119240.1 gg_id:250572 Actinoplanes sp. str. HBUM 87051 EU119
X93198.1 gg_id:12887 Catellatospora citrea str. DSM 44098 X93198
DQ344631.1 gg_id:145578 Catellatospora yuxiensis str. YIM 45508 DQ344
EU133208.1 gg_id:237912 tallgrass prarie soil clone FFCH839 EU133
EU193042.1 gg_id:370045 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
NR_028758.1 gg_id:574020 Catellatospora koreensis str. LM042; IMSNU 50729 NR_02
AB047491.1 gg_id:40127 Actinoplanes auranticolor str. IFO 13992 AB047
AB546276.1 gg_id:516372 Pseudosporangium ferrugineum str. IR8-RCA105 AB546
X92630.1 gg_id:12902 Dactylosporangium thailandense X92630
X93192.1 gg_id:12907 Dactylosporangium fulvum str. DSM 43917 X93192
AB546297.1 gg_id:519572 Dactylosporangium sp. str. IR30-DHHV-605 AB546
U58529.1 gg_id:12899 Dactylosporangium roseum str. IFO14352 U58529
D86941.1 gg_id:71488 Dactylosporangium roseum str. IFO14352 D86941
AB236958.1 gg_id:139794 Luedemannella helvata str. 3-21(27) AB2369
GU002095.1 gg_id:556137 Micromonospora sp. str. FXJ6.182 GU002
EF527854.1 gg_id:225681 Micromonospora sp. str. 161423 EF5278

636.0	3004.1	2996.4	2633.3	5023.9	3168.3	3487.8	2849.2	1975.6	1322.7	1016.9
377.2	3785.2	3257.9	3749.9	5751.0	3322.4	4651.0	4339.0	3093.0	2138.7	1827.1
194.1	1917.8	2005.8	2809.4	4103.0	1952.5	2926.6	2759.6	1997.6	2428.0	1015.7
746.5	3296.9	2599.0	2338.1	3810.3	2581.5	2790.7	2652.6	2830.1	1951.3	869.9
239.6	1586.9	1442.1	1128.8	2914.8	1270.0	1907.8	1375.6	1408.0	1314.0	424.3
234.1	1542.3	1732.2	1591.9	2444.4	1195.8	1608.6	1958.5	1455.7	1606.3	487.4
1990.2	1937.6	1906.8	1531.1	3408.8	1800.4	2363.4	1341.8	1619.2	1574.1	1336.4
204.8	1773.7	1561.3	1823.9	3881.3	1654.0	2445.2	1974.3	1802.4	1299.2	1029.9
221.2	4790.9	4038.6	3455.1	6731.5	4620.7	4737.2	4205.8	4587.8	3080.9	1901.5
195.4	5352.7	4964.0	5688.1	9628.7	4937.9	8790.6	4421.8	2485.7	2202.4	2911.5
142.5	1672.3	1002.2	451.5	2146.9	1185.3	1187.7	763.6	785.0	301.0	215.6
179.0	2465.0	2153.7	2389.7	4058.3	2536.3	2749.7	2713.5	1926.9	1774.6	1096.1
53.8	342.2	372.5	286.3	379.1	306.4	492.8	195.1	276.2	139.5	280.1
166.2	1845.3	2420.3	1993.6	4267.2	2248.8	3026.0	1756.0	1841.2	1034.9	1008.8
376.0	2063.4	2332.2	2421.0	4811.4	2232.5	3002.9	2667.1	1342.4	902.6	1025.0
328.0	2493.2	2151.6	2424.7	4319.9	2262.1	2847.6	3248.0	2582.8	1431.8	1146.0
539.7	3022.0	1911.4	1753.4	3072.8	1766.6	1978.2	2032.7	2944.2	1250.7	743.0
163.6	2141.2	1557.3	1466.5	3791.6	1466.3	2241.0	1808.6	1038.0	993.3	721.5
392.7	2942.4	2588.2	2353.0	3955.1	2540.8	2677.8	2767.6	2488.6	1884.1	1241.3
489.3	6643.7	4314.4	3325.9	4592.7	4596.8	3806.7	3232.1	6523.4	4299.0	1818.8
123.1	1470.2	1303.0	1112.8	3475.8	1606.7	1744.4	1236.1	752.6	589.6	422.1
1103.4	5965.3	5566.9	4199.7	7042.9	4862.2	5173.4	4461.7	6446.1	3850.8	2784.9
356.5	2340.3	1780.6	2565.7	5854.3	1958.8	3498.9	2342.6	2630.4	1762.1	918.0
217.1	1545.1	1647.1	1596.8	3636.1	1995.1	2390.7	2169.4	1132.2	1189.8	484.5
727.3	5642.4	3957.4	1423.5	3892.4	3729.9	2695.7	2200.0	4003.4	3250.7	1056.7
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56.5	463.5	489.2	651.8	2814.2	538.7	873.7	761.5	214.2	391.4	120.1
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648.0	6550.8	5145.6	3121.4	5742.4	4892.9	4341.2	3413.1	4934.8	4419.6	2072.9
1240.4	8227.2	5867.0	3331.6	6145.1	5630.1	4940.8	3218.7	7212.2	4841.4	2376.2
29185.7	6154.3	4551.5	6247.1	7159.3	5831.3	7135.7	5790.3	9243.6	8633.4	9320.5
12882.6	5128.6	4594.2	5207.7	7230.4	4746.8	5864.1	5089.9	7416.4	5460.0	5963.0
283.3	3154.0	2314.9	2311.5	5866.6	2548.3	3496.9	2479.9	1278.6	1613.0	902.7
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2375.4	837.9	1671.1
2175.1	831.4	1429.7
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1008.8	821.7	1227.8
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s__Micromonospora lupini	41414
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EU437816.1 gg_id:268409 Micromonospora sp. str. 206106
X92622.1 gg_id:12859 "Micromonospora lacustris"
X92600.1 gg_id:12858 "Micromonospora globosa"
X92627.1 gg_id:12857 "Micromonospora fulvopurpureus"
AY822607.1 gg_id:144449 Micromonospora aurantiaca str. JK-1
GQ163471.1 gg_id:537978 Micromonospora coxensis str. HBUM55005
X92616.1 gg_id:12845 "Micromonospora brunnescens"
FJ999589.1 gg_id:372313 Micromonospora carbonacea str. HLSBA16
AB196716.1 gg_id:109754 Micromonospora krabiensis str. MA-2
FJ547111.1 gg_id:539118 Micromonospora coxensis str. HBUM175158
AY569009.1 gg_id:115146 Micromonospora aurantiaca str. Marseille
GQ163480.1 gg_id:583706 Micromonospora krabiensis str. HBUM49306
EU841637.1 gg_id:346249 Micromonospora chaiyaphumensis str. HBUM82707
DQ126267.1 gg_id:138639 Micromonospora echinospora str. FIM 203
FJ481615.1 gg_id:570172 Micromonospora sagamiensis str. HBUM49503
FJ938344.1 gg_id:584940 Micromonospora sp. str. FXJ1.347
FJ486500.1 gg_id:551140 Micromonospora coxensis str. HBUM80191
FJ486499.1 gg_id:512858 Micromonospora coxensis str. HBUM81174
GQ163477.1 gg_id:539295 Micromonospora coxensis str. HBUM49417
EU841639.1 gg_id:315228 Micromonospora coxensis str. HBUM174926
EU119220.1 gg_id:245500 Micromonospora sp. str. HBUM 49436
FJ481619.1 gg_id:509771 Micromonospora echinaurantiaca str. HBUM49487
GQ163462.1 gg_id:573595 Micromonospora sagamiensis str. HBUM49490
AJ783996.1 gg_id:111021 Micromonospora sp. str. lupac 14N
AY360159.1 gg_id:93360 Micromonospora sp. str. e32
AJ783987.1 gg_id:109630 Micromonospora sp. str. lupac 4B
AM260557.1 gg_id:158468 Micromonospora sp. lupac 15
AY221485.1 gg_id:82551 Micromonospora sp. str. N0073
AB196712.1 gg_id:110933 Micromonospora marina str. JSM1-1
DQ462651.1 gg_id:157326 Micromonospora sp. str. 032495
EU841642.1 gg_id:321650 Micromonospora pattaloongensis str. HBUM174917
EF527867.1 gg_id:220930 Micromonospora sp. str. 162225
X92610.1 gg_id:12867 Micromonospora inositola
FJ262995.1 gg_id:571005 Micromonospora sp. str. M1
FN298637.1 gg_id:562703 Micromonospora sp. SB1-4
FN297793.1 gg_id:551229 Micromonospora sp. MIA26
AB241454.1 gg_id:142673 Micromonospora chokoriensis str. 2-19(6)
EU274375.1 gg_id:237544 Micromonospora echinospora str. RtII200
AB196715.1 gg_id:111029 Micromonospora krabiensis str. MA-1
DQ462664.1 gg_id:158781 Micromonospora echinospora str. B266

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FJ9383
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FN2986
FN2977
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EU2743
AB1967
DQ462

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81.2	417.2	691.9	823.0	2948.5	317.7	759.5	1375.4	537.4	973.4	98.0
1832.6	5675.1	4780.0	3439.8	6225.2	4666.0	4719.2	3464.5	6506.2	3877.8	2512.9
15229.9	4977.5	4998.1	4964.3	5912.3	4633.6	5424.7	4740.9	7160.9	5912.1	6518.8
464.9	4633.2	3786.9	3335.9	5118.3	3512.5	3801.0	2723.8	2473.6	2615.7	809.5
123.1	2458.4	1997.2	2000.8	4301.4	1844.2	2339.8	2053.2	931.4	1892.6	379.7
140.1	1094.6	1144.2	1540.9	3692.6	1225.7	1778.7	1598.8	790.7	670.8	622.9
17623.1	4985.3	4253.9	4733.8	7251.2	4784.4	5322.0	4915.3	5394.9	4747.8	6635.1
59.4	519.0	555.1	948.0	3473.5	653.9	1000.0	1395.1	428.0	429.2	222.3
41.7	311.6	316.3	438.9	2002.0	331.9	404.2	825.3	254.3	326.9	104.3
73.1	935.6	991.8	1154.8	3384.8	1068.3	1231.7	1228.8	578.2	601.2	369.4
113.4	625.7	882.9	1153.7	3793.2	661.5	1332.6	1516.7	657.8	648.4	216.6
668.0	2067.2	1760.6	2456.6	3994.0	1236.2	2854.9	2546.7	1304.7	912.6	1475.6
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253.0	840.8	937.3	1477.3	3849.7	1084.2	1647.8	1765.2	1153.2	857.4	303.5
109.7	766.6	1139.6	1213.4	3568.6	1156.1	1617.7	1046.3	911.3	670.8	444.9
347.4	1987.9	1831.1	2429.1	4513.9	1647.6	2811.6	2225.2	1141.5	986.1	1126.2
572.5	2092.9	1989.6	2634.6	4611.9	1698.4	2920.7	2404.8	1318.8	1235.7	1323.0
290.7	1977.0	1802.7	2391.7	4336.9	1954.2	2715.5	1806.6	1082.1	1341.6	635.0
43.6	59.9	94.3	104.1	1843.0	85.8	140.8	195.2	70.5	128.1	29.3
288.4	1430.7	1589.3	1528.7	4568.5	1414.5	2201.0	2072.5	1712.3	1310.1	376.7
326.7	2439.6	2345.3	2710.4	5597.6	1965.3	3298.8	2618.9	1792.7	1473.9	913.9
294.3	1744.1	1962.6	2222.5	4996.3	1717.0	2689.5	2378.4	1695.0	1448.7	674.9
16786.6	5666.8	5234.3	5638.1	6145.4	5569.8	6507.7	5278.6	7692.9	5104.3	6920.0
2948.9	3863.5	3249.5	3821.5	5234.1	3129.5	3867.8	3710.9	3757.5	2288.8	2813.4
295.2	1923.9	1734.8	1664.3	3305.6	1898.8	2152.6	2193.0	2191.2	1672.0	884.3
18420.6	7738.8	6656.6	8234.4	9474.8	6695.7	8945.5	7152.3	9080.5	6462.7	9018.9
229.1	1772.5	1358.3	1101.0	4243.4	1526.4	1700.1	1649.6	1047.8	1045.7	389.3
109.3	1159.4	1308.3	1629.1	3731.4	970.3	1673.7	1755.4	834.2	1581.3	159.8
455.1	3289.3	3055.0	2527.5	5965.1	2978.5	3616.7	2879.4	4556.7	3827.0	1298.3
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233.5	1738.4	1458.7	802.5	1627.7	1465.9	808.0	1180.9	1811.8	1322.2	521.5
273.7	3403.1	3375.1	4006.2	5002.8	2840.1	4541.3	3247.1	1881.1	1015.6	1822.1
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215.5	1670.2	1352.7	1371.0	2566.6	1481.4	2220.3	1439.8	917.6	722.1	679.0
144.1	2156.3	1841.9	1600.7	3119.5	1465.3	1668.5	2045.0	998.1	1509.9	422.4
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1327.0	2242.4	1880.4	2140.6	3941.0	1829.2	2238.5	2276.5	2572.4	2503.1	2423.3
188.0	1486.3	1859.8	2003.5	3311.4	1783.8	2280.9	1704.9	1569.8	1413.0	863.4

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5042.5	5265.2	4480.0
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1795.9	926.4	1907.6
3126.1	2211.7	4169.0
3363.9	2302.7	4284.0
3371.9	2241.0	4386.6
309.2	107.3	692.0
2774.6	1196.7	3016.1
3923.6	2095.7	4345.5
3362.2	1670.6	3940.0
5120.9	5873.1	5463.4
4429.5	2361.4	4201.6
2553.9	1228.0	3235.3
7615.2	7447.6	7726.6
2125.8	820.4	2113.6
2898.2	970.8	1920.1
4209.9	2349.8	3473.6
3669.9	2439.4	4219.8
1435.0	937.0	1761.3
3375.6	3034.6	3429.6
5132.3	4622.2	5811.7
2379.5	1331.9	1403.0
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AB107231.2 gg_id:101313 Micromonospora eburnea str. LK2-10
AY862315.1 gg_id:110268 Micromonospora terrae str. MMS-DA
FJ160413.1 gg_id:584386 Micromonospora inyonensis str. TS388
X92599.1 gg_id:12879 Micromonospora chalcea
X92618.1 gg_id:12872 Micromonospora echinaurantiaca str. DSM 43904
X92601.1 gg_id:12848 Micromonospora halophytica
AF152109.1 gg_id:44843 Micromonospora matsumotoense str. IMSNU 22003T
EU214947.1 gg_id:258465 Micromonospora sp. str. CNS-729_SD06
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X92623.1 gg_id:12878 Micromonospora viridifaciens str. DSM 43909
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AY360152.1 gg_id:94058 Micromonospora sp. str. e4
GU002100.1 gg_id:589135 Micromonospora sp. str. FXJ6.217
EU274367.1 gg_id:248036 Micromonospora chersina str. RtIII8
FN298633.1 gg_id:588175 Micromonospora sp. SB2-5
FJ486510.1 gg_id:555273 Micromonospora echinospora str. HBUM80188
EU132551.1 gg_id:242784 tallgrass prarie soil clone FFCH13505
AB196711.1 gg_id:110270 Micromonospora chaiyaphumensis str. R1-1
GU002081.1 gg_id:593665 Micromonospora sp. str. FXJ6.097
X92617.1 gg_id:12850 Micromonospora citrea str. DSM 43903
X92602.1 gg_id:12844 "Micromonospora narashino"
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U58532.1 gg_id:12846 Micromonospora echinospora str. ATCC15837
X92608.1 gg_id:12877 Micromonospora echinospora
L41047.1 gg_id:135946 Actinoplanes sp str. A8232
X92611.1 gg_id:12843 Micromonospora purpureochromogenes
FJ205734.1 gg_id:563976 Micromonospora sp. str. 51
X92605.1 gg_id:12864 Micromonospora brunnea
X92595.1 gg_id:12874 Micromonospora purpurea
DQ419518.1 gg_id:153595 Micromonospora sp. L0902
U58531.1 gg_id:12863 Micromonospora chalcea str. ATCC12452
X92598.1 gg_id:12852 Micromonospora coerulea
EU119226.1 gg_id:243016 Micromonospora sp. str. HBUM 80189
X92620.1 gg_id:12854 Micromonospora fulviviridis str. DSM 43906
AB241455.1 gg_id:143263 Micromonospora coxensis str. 2-30-b(28)
X92612.1 gg_id:12866 Micromonospora rhodorangea
DQ419522.1 gg_id:151891 Micromonospora sp. L0607
X92624.1 gg_id:12871 Micromonospora sagamiensis str. DSM 43912
X92628.1 gg_id:12849 Micromonospora chersinia
AY723730.1 gg_id:101819 Micromonospora stanfordense str. MMS1

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X92601
AF1521
EU2149
EU4377
X92623
EF5387
AY3601
GU002
EU2743
FN2986
FJ4865
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AB1967
GU002
X92617
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EF5278
U58532
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FJ2057
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AB2414
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DQ419
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X92628
AY7237

519.4	2636.5	2661.3	2753.8	4124.2	2728.9	3511.7	2889.0	2490.5	1862.8	1130.9
105.7	2066.4	1521.3	1289.4	2837.4	1128.8	1896.1	1544.8	983.8	966.9	633.1
381.4	2337.5	1959.3	1348.4	3272.7	2121.8	2473.7	1680.0	1616.0	1567.4	679.8
191.9	3391.6	3015.9	3046.1	5231.7	2954.5	3769.7	2475.5	1930.5	1901.6	1274.4
200.1	1117.3	907.2	1279.5	4839.2	1013.0	1644.2	1879.9	1126.4	828.7	338.7
436.0	2970.5	2642.3	2383.2	6388.4	2275.3	3566.5	2696.4	2713.9	1708.4	814.2
124.2	1386.4	744.3	305.0	3154.6	154.3	644.2	614.8	1155.7	380.3	138.4
2138.9	2383.5	2822.6	3117.7	3346.6	2813.8	4093.3	2720.0	3164.8	2405.8	2567.9
328.2	2719.7	1619.6	1388.3	2730.4	796.8	1814.5	1450.6	1315.8	882.8	645.3
82.7	364.2	686.9	788.9	1214.6	278.0	516.8	951.3	414.1	711.3	119.0
787.7	4922.6	4012.1	3251.0	6463.5	3475.2	4630.6	3159.1	4602.6	2874.4	1795.4
212.9	1454.6	1420.3	1771.0	3592.0	1475.6	2381.7	2068.6	1155.8	893.2	971.9
267.1	2439.5	1756.9	1910.8	3378.7	1947.4	2509.6	2354.8	1119.1	1095.3	926.7
116.0	1410.0	1646.1	1788.3	3902.5	1324.4	2017.9	2248.0	1705.4	2083.7	620.8
102.2	704.1	1378.8	955.0	2076.9	1156.5	1426.1	1088.4	647.2	515.9	250.6
317.7	3215.6	2684.5	3181.9	5486.0	2515.1	3950.1	2500.0	1402.7	1436.9	1441.3
416.0	2470.9	2633.4	2619.3	3021.3	2719.2	3085.7	2753.5	2339.0	1581.6	2733.0
396.2	2971.7	2676.6	1655.2	3464.5	2475.6	2547.0	2129.2	2693.0	2093.8	761.3
77.7	1514.4	1588.9	1284.2	3572.3	1736.2	1775.2	1375.4	1058.5	1162.7	513.5
131.3	671.5	674.1	974.1	2022.4	739.1	1034.8	1368.0	460.3	392.8	346.8
375.4	2593.0	1993.6	1299.4	3149.9	2080.2	1912.5	1642.3	3191.5	1897.9	809.7
1406.0	4604.8	3717.3	3070.3	5961.5	3787.2	4033.9	3049.0	2644.3	2903.5	1458.7
110.7	51.2	61.0	62.0	341.2	60.7	45.0	161.8	74.0	45.1	53.7
155.8	1993.6	1789.2	1857.4	3435.3	1107.9	2113.5	2036.9	1035.0	1453.9	575.9
450.6	2927.0	2241.6	1692.3	4338.1	2452.9	2256.4	2390.6	3195.7	2335.3	736.0
13700.6	5544.0	4561.5	3783.2	6424.5	4439.4	4402.9	3231.1	5030.8	4525.3	3889.5
659.5	5161.9	4007.2	2954.2	5430.3	3361.3	4082.8	2965.4	4064.7	2778.6	1410.9
613.2	5173.2	4018.9	3168.2	4527.1	3897.2	3674.9	3420.5	3778.1	4212.7	3457.0
405.5	4449.1	3282.7	2388.4	4714.7	3949.1	3445.4	2948.5	4592.2	3639.2	990.0
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14761.1	7475.2	5909.8	6627.8	8217.5	5985.8	8472.2	6418.2	7057.4	5955.4	7167.1
658.0	5153.4	3864.3	3342.4	5477.0	3629.5	3906.8	3111.5	7563.3	5028.8	2428.3
1220.8	2670.8	2009.3	2117.6	3099.6	1894.9	2545.4	2716.8	3483.0	2799.5	1720.9
13561.9	3871.7	3598.7	4187.9	3688.5	3656.2	4261.3	3388.9	6568.4	4315.9	5109.0
43.2	61.4	68.3	83.9	2036.8	82.0	112.4	220.1	53.5	96.1	27.0
360.6	3220.7	2900.1	2367.6	6084.5	2655.5	3737.0	2428.2	2118.5	1811.5	1283.4
201.3	1700.4	2137.6	2149.9	4674.4	2033.3	2939.2	1991.1	1779.9	1506.8	993.4
8977.0	3484.5	3643.6	4057.5	6274.6	3414.4	4210.7	3391.4	4962.8	3815.3	4797.3
105.9	919.4	1661.4	1292.0	3722.8	1414.0	1755.4	1563.1	874.0	703.3	332.7
528.4	1088.2	692.2	1008.9	4479.3	851.5	1624.4	1349.9	663.0	519.1	429.7

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2400.4	809.1	2586.9
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1731.1	1654.6	1522.1
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4122.1	3922.9	3907.5
3631.8	2515.3	3453.5
4581.8	2637.3	3208.6
3506.9	1911.0	2409.2
2598.1	994.5	1708.0
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GQ163461.1 gg_id:567221 Micromonospora sagamiensis str. HBUM49488
AJ560635.1 gg_id:82514 Micromonospora endolithica str. AA459 = DSM 44398
X92626.1 gg_id:12881 "Micromonospora yulongensis"
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EU570342.1 gg_id:277389 Micromonospora chokoriensis str. 173803
FJ205728.1 gg_id:549288 Micromonospora chalcea str. 36
X92607.1 gg_id:12853 Micromonospora echinospora
DQ126266.1 gg_id:137540 Micromonospora floridensis str. FIM 03-1149
FJ205715.1 gg_id:558748 Micromonospora sp. str. 11
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X92609.1 gg_id:12868 Micromonospora chalcea
EU841641.1 gg_id:333629 Micromonospora endolithica str. HBUM174919
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X92631.1 gg_id:12865 Micromonospora rosaria
EU119219.1 gg_id:247564 Micromonospora sp. str. HBUM 49435
DQ126264.1 gg_id:137601 Micromonospora chalcea str. FIM 02-523
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EU563223.1 gg_id:270969 Micromonospora sp. str. 49416
FJ547133.1 gg_id:564350 Micromonospora auratinigra str. HBUM49317
AY291589.1 gg_id:87823 Micromonospora sp. str. EN43
X92615.1 gg_id:12847 "Micromonospora globosa"
X92629.1 gg_id:12873 Micromonospora inyonensis str. DSM 46123
X92625.1 gg_id:12851 Micromonospora echinofusca str. DSM 43913
AY360156.1 gg_id:93841 Micromonospora sp. str. e16
AJ626950.1 gg_id:102454 Micromonospora mirobrigensis str. WA201
X93190.1 gg_id:12808 Pilimelia terevasa str. DSM 43040
D86946.1 gg_id:72263 Pilimelia terevasa str. IFO15964
NR_026289.1 gg_id:553755 Pilimelia anulata str. DSM 43039
AB548688.2 gg_id:530434 Pilimelia subsp. columellifera str. JCM 3367
AY562202.1 gg_id:110213 Salinospora sp. M414
DQ224163.1 gg_id:167181 Salinispora arenicola str. CNH941 SC01
FJ436031.1 gg_id:364369 Salinispora sp. str. YKPC3
EU714244.1 gg_id:305908 Salinispora sp. str. AB1
DQ224161.1 gg_id:162043 Salinispora pacifica str. CNR114 GU02
NZ_AATJ01000006.1 gg_id:172932 Salinispora tropica str. CNB-440

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495.4	2770.2	2395.7	2096.7	5511.6	2386.5	3289.6	2562.4	3466.0	2296.4	772.5
123.7	4075.7	2545.1	2619.2	4750.7	3074.0	3226.2	1686.7	725.7	1648.8	602.1
1606.3	5321.6	4435.7	3481.5	5768.4	4181.7	4682.6	3386.5	5435.4	3341.2	2324.5
1554.5	1782.0	1651.6	1675.5	4649.0	1767.6	2103.9	1982.7	1916.4	1233.5	1179.9
481.9	2757.8	3128.4	2103.6	3070.4	2270.4	1966.0	2686.5	2190.0	1919.6	2826.9
365.3	2067.6	1464.7	1419.5	4111.2	1903.3	2158.9	1667.7	1871.9	1144.6	645.0
1507.5	2481.4	2360.7	2365.8	5167.0	2455.8	3147.0	2640.1	2421.0	1675.6	1448.8
113.3	1123.8	1018.8	998.2	2590.4	769.9	1077.5	1535.1	656.9	1142.5	188.9
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205.8	3903.2	3099.9	2048.4	3816.7	2905.5	3447.2	2473.0	1700.0	1714.9	1022.8
1508.0	1584.4	2051.3	1768.6	2690.1	1713.6	2376.7	2180.4	2323.5	1821.0	1410.0
72.0	340.4	328.4	500.2	1909.0	388.0	640.4	894.3	377.9	354.1	155.9
322.3	2528.9	1669.4	1583.9	4037.3	1637.9	1972.4	1836.7	2469.7	1324.8	398.3
493.2	1155.6	663.8	1123.2	3723.0	493.5	1436.1	1036.5	1846.2	607.1	275.5
401.7	3808.0	3883.9	3142.5	4768.4	3627.7	3601.4	2721.0	4772.3	4509.3	1963.0
270.5	3340.7	2767.0	1787.6	3164.0	2568.5	3221.7	2198.6	4625.8	2773.6	915.4
1669.7	4819.5	4353.5	4609.1	5035.4	4569.1	5788.2	4546.8	7065.3	7080.9	4548.6
122.2	815.8	1099.9	1245.9	5043.9	718.6	1524.8	1820.6	1492.3	1505.4	193.9
472.2	1410.8	1262.6	1174.0	3711.2	1246.9	1713.7	1918.7	1774.1	1205.9	402.5
173.1	1727.6	2074.2	1795.4	3212.2	1995.2	2103.7	2257.4	2407.5	2380.7	803.5
373.0	3428.1	3036.4	2183.0	3931.0	2880.5	2628.6	2158.4	3019.9	2984.4	1054.1
132.2	1175.2	819.1	766.0	2245.2	808.0	1051.7	1483.5	638.8	632.1	275.2
34.9	66.6	71.3	31.5	583.5	27.2	46.9	84.1	85.0	44.4	12.4
73.1	1890.8	1778.7	1719.2	2524.1	1650.7	2364.5	1661.8	1960.8	1446.7	941.8
270.8	4287.7	3046.9	2917.6	4996.4	2916.3	3621.1	2642.1	3671.4	2085.4	731.8
454.6	3196.0	2820.3	3852.4	6544.1	2205.2	4709.5	2840.5	2028.0	1623.6	1849.6
1893.6	1631.0	1841.4	2250.4	4389.5	1733.5	2660.1	1906.5	1546.9	1262.4	1896.6
104.6	1257.5	1261.3	1290.6	3455.8	930.4	1485.3	1884.1	898.0	1444.0	249.7
5017.0	5002.3	4565.5	4241.9	5435.4	4474.7	5608.2	4143.2	4213.0	4661.0	4431.6
204.6	1547.6	1949.8	1331.0	2620.7	1730.0	1985.8	1285.2	1390.0	917.0	319.2
278.9	2464.7	2725.9	1197.8	2561.0	1907.4	1660.1	1568.8	2284.4	1616.6	621.7
103.7	2529.0	2209.7	1126.6	2855.7	2147.7	1873.7	1350.6	1472.9	1507.8	506.1
271.6	7262.6	5847.1	2943.7	5343.4	5911.8	3933.5	3495.8	5810.7	4168.4	1626.9
2625.3	4249.0	3605.4	3693.9	6830.9	2914.9	5221.8	4001.6	2916.5	2530.0	1936.1
4445.5	4223.4	3803.4	4063.6	6639.9	4088.3	4732.6	3581.7	3114.0	2690.8	3623.4
7771.0	7718.4	7764.0	8618.5	9910.3	7978.1	9002.1	7565.4	11459.6	12642.2	7449.2
2619.5	3106.3	3057.9	3266.7	7018.9	2793.0	4126.9	2912.2	2077.6	1555.0	1967.9
1044.8	3499.8	2591.5	2337.1	4517.5	1746.5	3082.5	2251.8	1720.4	1456.0	1263.4
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1964.9	1523.9	2312.6
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2462.4	1067.3	2200.9
1214.5	448.0	1320.6
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2647.8	413.2	1676.0
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1679.4	600.7	2233.9
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3870.3	1688.5	2386.8
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FJ436029.1 gg_id:363926 Salinispora sp. str. YKPC1 FJ4360
AY552758.1 gg_id:100333 Solwaraspora sp. str. UMM514 AY5527
AY552768.1 gg_id:105394 Solwaraspora sp. str. UMM576 AY5527
AY552770.1 gg_id:100281 Solwaraspora sp. str. UMM480 AY5527
AY552756.1 gg_id:100024 Solwaraspora sp. str. UMM559 AY5527
AY552773.1 gg_id:100746 Solwaraspora sp. str. UMM479 AY5527
AY552762.1 gg_id:104499 Solwaraspora sp. str. UMM485 AY5527
AY552766.1 gg_id:105085 Solwaraspora sp. str. UMM481 AY5527
EU214973.1 gg_id:258927 Micromonospora sp. str. CNS-728_SD06 EU2149
AY552765.1 gg_id:104935 Solwaraspora sp. str. UMM573 AY5527
FJ830632.1 gg_id:578932 Micromonospora sp. str. SY1 FJ8306
AB236956.1 gg_id:140392 Krasilnikovia cinnamoneum str. 3-54(41) AB2369
AY922033.1 gg_id:114151 farm soil clone AKYG568 AY9220
AM232832.1 gg_id:154710 Micromonospora flavogrisea str. YIM 46034 = CCTCC AM232
AM920417.1 gg_id:359367 Penicillium chrysogenum str. Wisconsin 54-1255 AM920
AB223089.1 gg_id:156807 Polymorphospora ruber str. TT 97-42 AB2230
EF516315.1 gg_id:219743 grassland soil clone FCPS496 EF5163
EU132687.1 gg_id:251159 tallgrass prarie soil clone FFCH1111 EU1326
AB454379.1 gg_id:317027 Micromonospora sp. str. CM2-8 AB4543
EF019001.1 gg_id:211265 aspen rhizosphere clone Amb_16S_1526 EF0190
AJ865470.1 gg_id:109034 Catenuloplanes japonicus str. DSM 44102 AJ8654
GQ153845.1 gg_id:404948 Micromonospora viridifaciens str. B7-3 GQ153
AY921724.1 gg_id:113702 farm soil clone AKYH579 AY9217
FN297809.1 gg_id:535973 Micromonospora sp. MIA65 FN2978
X92613.1 gg_id:12841 Micromonospora chalcea X92613
AB036998.1 gg_id:23551 Actinoplanes deccanensis str. IFO 13994T AB0369
EF612364.1 gg_id:249182 historic semiarid lead-zinc mine tailings site soil clone OS-C07 EF6123
EU274362.1 gg_id:246282 Micromonospora eburnea str. RtII69 EU2743
EU132648.1 gg_id:238435 tallgrass prarie soil clone FFCH10740 EU1326
FJ479180.1 gg_id:580850 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
AY922104.1 gg_id:113935 farm soil clone AKYH1349 AY9221
AB546281.1 gg_id:524751 Krasilnikovia sp. str. IR27-RCA116 AB5462
NR_024800.1 gg_id:552236 Longispora albida str. K97-0003; NRRL B-24201 NR_024
EU133153.1 gg_id:248468 tallgrass prarie soil clone FFCH647 EU1331
GQ163468.1 gg_id:578248 Micromonospora pattaloongensis str. HBUM49516 GQ163
EU696752.1 gg_id:293880 Verrucosispora sp. str. FIM06019 EU6967
FJ478866.1 gg_id:564025 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
AY234686.1 gg_id:112244 soil isolate Ellin6034 AY2346

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470.4	1379.6	1108.8	763.3	3749.2	1022.9	1310.6	993.1	963.1	692.8	295.7
780.3	2511.8	2345.7	1727.7	4764.1	2034.6	2522.2	2343.9	2140.3	1623.1	626.8
24712.7	8985.3	8314.5	8462.2	9325.7	7846.8	9278.9	6981.2	12601.9	11501.5	12430.2
53.8	906.0	709.4	932.3	2094.4	790.6	1132.8	759.2	301.8	683.3	92.6
46.0	268.8	251.4	331.4	2002.8	274.9	597.4	609.9	208.6	182.5	77.9
53.1	912.2	676.4	923.1	2829.1	812.9	1250.8	656.1	278.2	622.6	87.5
1473.7	4051.7	3413.4	3148.6	4461.8	3356.8	2900.9	3157.7	4480.5	5036.0	2817.3
44.7	276.9	270.7	363.8	1496.0	326.0	591.7	608.5	242.1	243.7	79.1
51.0	913.8	765.8	1011.7	3185.1	856.0	1339.1	826.0	309.5	681.5	105.7
2253.0	5402.0	5724.0	4421.1	4773.8	4483.7	5015.9	4725.2	6029.6	5992.5	6306.2
228.4	655.4	692.8	1006.7	3040.1	842.9	1125.9	1504.6	872.9	876.2	228.4
153.2	783.2	729.1	873.8	2832.1	742.4	1296.1	1210.6	947.9	887.3	421.8
41.2	289.8	324.3	392.6	2433.5	289.5	627.9	779.3	288.4	284.5	104.0
112.4	2098.6	1967.5	2150.5	3787.4	1793.0	2956.5	2272.4	1727.0	1454.8	1440.4
108.8	2509.7	2972.3	3002.4	4355.7	2572.0	3946.0	2605.7	1604.6	970.4	1398.4
2454.4	3345.7	3429.9	4071.9	6212.6	3525.1	4527.0	3542.0	2790.0	1438.1	3088.5
5433.9	6022.5	5258.5	4697.1	7427.7	5499.3	5301.6	4451.1	5796.2	4039.5	3611.6
846.2	3077.3	2272.3	2212.9	4418.1	2034.5	2459.2	2347.5	3713.3	1637.7	821.5
4175.9	2948.0	2763.3	3725.9	7622.6	2795.4	4576.0	3207.3	1689.8	1504.4	1359.1
61.2	683.7	740.6	734.8	4027.2	1082.7	1546.4	827.5	318.3	487.0	315.0
59.9	583.8	371.8	256.4	793.7	339.2	609.1	922.0	825.2	450.4	103.0
565.5	5807.5	5687.0	4884.4	5543.7	5183.5	5238.0	4501.6	5774.8	6603.8	5993.2
1754.9	8256.0	6180.7	4365.5	6683.2	5968.9	5939.7	3938.1	6833.1	4103.0	2829.5
515.8	2388.1	2171.1	2709.0	5400.3	1872.8	3013.1	2583.6	1844.7	1558.6	1043.0
10796.4	8706.0	7947.9	8192.2	11573.4	8088.9	10638.1	7288.2	6181.4	7004.8	7895.6
39.6	546.9	695.9	768.4	3287.9	571.7	941.4	904.9	359.1	329.3	271.1
124.6	1153.6	1234.1	1257.5	5047.6	1116.6	1987.6	1473.5	1079.3	823.9	429.4
368.7	3058.7	2412.7	1031.3	4167.3	1791.5	1616.5	1923.1	2935.2	2186.4	669.6
282.6	2616.8	2591.9	1388.6	3729.1	2420.6	2009.1	2169.9	3879.2	2979.1	869.7
55.5	316.6	405.1	416.5	1368.1	353.3	658.1	622.3	262.7	133.3	207.2
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104.2	751.7	484.0	506.8	2049.8	478.9	861.6	562.6	793.6	414.3	171.4
442.7	2740.7	3764.4	3658.0	4716.3	3773.1	5791.4	3533.5	1493.5	1702.3	2462.1
465.3	5484.8	5278.4	5079.9	8454.1	4819.1	6433.2	4156.6	4173.9	5016.6	4043.1
48.7	46.9	59.5	60.7	109.3	42.5	85.3	45.1	41.0	33.9	34.9
341.7	1558.7	1823.4	1694.3	5277.6	1612.1	2420.0	2294.3	1550.5	1294.3	473.4
193.9	2432.9	1422.9	1484.1	3788.0	1376.4	2067.3	1485.4	1299.0	940.1	418.5
63.6	692.7	579.7	559.6	2511.7	512.8	987.5	693.6	476.7	558.6	164.6
611.0	1423.6	1397.4	1528.5	7012.7	1457.4	2702.2	1823.8	1264.5	1169.1	541.7
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780.8	255.2	967.8
1312.2	908.7	1559.6
3606.8	3249.4	3241.6
856.3	284.5	975.2
1528.2	960.6	1625.7
4027.4	4486.5	4032.1
1904.2	599.8	1875.1
1384.8	742.4	1645.2
1067.0	306.4	1405.9
2481.7	1731.2	2267.6
2924.1	2256.2	3975.7
3495.1	3380.6	4488.0
5340.8	4257.2	5196.0
2927.8	2041.0	2665.5
3499.0	2712.9	3460.2
1398.4	957.3	1763.3
921.7	293.5	1312.0
5044.1	4410.0	5917.5
5562.2	3989.7	3906.3
3863.9	2042.1	4284.5
7409.9	7584.1	8586.7
1327.6	719.6	1770.9
2253.1	801.5	1839.8
2742.2	1026.8	1583.9
2894.8	1375.5	1863.7
681.6	418.9	891.7
3992.1	2214.1	3871.9
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2767.5	3173.9	4071.2
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DQ129566.1 gg_id:138062 microarray level air two cities Texas urban aerosol clone AKIW609	DQ129
FJ715940.1 gg_id:537002 Catenuloplanes niger str. JCM 9533	FJ7159
AB047515.1 gg_id:51864 Actinoplanes violaceus str. IFO 14458T	AB0475
FJ155992.1 gg_id:304224 Asanoa sp. str. 210121	FJ1559
AJ277571.2 gg_id:52270 Actinoplanes humidus str. IMSNU 20031T	AJ2775
FJ715941.1 gg_id:565395 Catenuloplanes nepalensis str. JCM 9536	FJ7159
EU158334.1 gg_id:243846 Micromonospora sp. str. HBUM 49401	EU1583
EU132986.1 gg_id:250989 tallgrass prarie soil clone FFCH1761	EU1329
EF191199.1 gg_id:176901 Verrucosispora shenzhensis str. YIM 1013	EF1911
AB048214.1 gg_id:51111 Actinoplanes consettensis str. JCM 7624T	AB0482
EU427445.2 gg_id:277183 Micromonospora sp. str. RtIII47	EU4274
EF544150.1 gg_id:227123 Verrucosispora sp. str. 173201	EF5441
DQ448713.1 gg_id:158091 Micromonospora sp. str. CNS326 PL04	DQ448
EU214969.1 gg_id:259114 Micromonospora sp. str. CNS-682_SD06	EU2149
GQ264461.1 gg_id:581811 Structure Simulated Level Waste Site simulated level waste site clone WW3_161	GQ264
AB037000.1 gg_id:24528 Actinoplanes digitatis str. IFO 12512T	AB0370
EU714256.1 gg_id:309154 Solwaraspora sp. str. BC1	EU7142
GU189536.1 gg_id:585612 Micromonospora sp. str. YIM 65395	GU189
AB275607.1 gg_id:169225 Micromonospora pattaloongensis str. TJ2-2	AB2756
AJ277565.1 gg_id:44122 Actinoplanes deccanensis str. IMSNU 20026T	AJ2775
EU274361.2 gg_id:236575 Micromonospora chaiyaphumensis str. RtIII94	EU2743
FJ479351.1 gg_id:510347 species richness estimates obtained nearly and simulated pyrosequencing-generated	FJ4793
EU274359.1 gg_id:242850 Micromonospora pattaloongensis str. RtII196	EU2743
D85471.1 gg_id:160066 Actinoplanes auranticolor str. IFO12245	D85471
NR_028659.1 gg_id:563833 Micromonospora auratinigra str. TT1-11; DSM 44815	NR_028
DQ008604.1 gg_id:118254 Micromonospora sp. str. 84521	DQ008
EU119238.1 gg_id:235477 Actinoplanes sp. str. HBUM 84231	EU1192
NR_025872.1 gg_id:557564 Spirilliplanes yamanashiensis str. YU 127-1; IFO 15828	NR_025
FM873861.1 gg_id:357423 occupant source house mattress dust clone MB01H12	FM873
AB546282.1 gg_id:519160 Couchioplanes sp. str. IR27-RC105	AB5462
EU119242.1 gg_id:255077 Actinoplanes sp. str. HBUM 171148	EU1192
DQ347895.1 gg_id:200014 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi	DQ347
X93199.1 gg_id:12886 Asanoa ferruginea str. DSM 44099	X93199
X92603.1 gg_id:12842 Micromonospora peucetia str. DSM 43363	X92603
AB047516.1 gg_id:17380 Actinoplanes yunnanensis str. IFO 14459T	AB0475
EU714241.1 gg_id:347817 Verrucosispora sp. str. A1	EU7142
EU696739.1 gg_id:298196 Verrucosispora sp. str. FIM06029	EU6967
EU696741.1 gg_id:298873 Verrucosispora sp. str. FIM06053	EU6967
EU696751.1 gg_id:296339 Verrucosispora sp. str. FIM06038	EU6967
EU560725.1 gg_id:258766 Verrucosispora sp. str. 201803	EU5607

5234.3	5042.1	4223.6	3109.0	3723.2	4177.0	3751.5	2937.2	4632.8	4155.1	2662.0
312.5	2684.6	2432.2	2750.5	3698.3	2557.7	3716.1	3378.4	2102.5	679.3	1502.6
729.6	7976.3	5297.5	3776.3	6413.8	5684.0	5654.7	3553.9	4843.0	3329.3	2054.4
22236.6	11863.9	10686.1	10389.3	12211.6	10465.0	12663.7	9581.5	15705.7	12314.9	13162.3
5306.5	5613.8	5687.8	4669.6	6208.1	4551.2	4949.7	4235.8	5168.5	4315.7	4223.1
1462.1	6537.9	6288.2	5311.2	7409.0	5937.5	6623.4	6548.9	8451.7	7088.1	3386.8
89.9	2315.5	2291.1	2269.0	5324.6	2909.6	3375.8	2424.5	1853.4	1425.6	949.7
5061.9	3095.6	2600.6	2321.1	5207.8	2477.3	2759.7	2283.9	4425.3	2344.5	2284.6
5383.2	7984.7	6886.1	6081.0	8229.2	7037.7	6673.2	5351.0	9198.5	6107.4	5421.3
208.7	4401.4	3135.5	2502.1	4977.4	3687.0	3310.3	2810.2	2441.9	2595.1	930.3
538.1	4071.0	4034.8	4181.3	6448.5	3712.1	5181.2	4793.6	3757.9	2220.3	2228.1
129.0	1235.7	1324.0	1085.0	3650.3	1109.8	1618.0	1647.1	1152.6	906.1	418.3
70.5	481.6	572.4	679.0	1992.2	559.7	875.0	937.0	475.1	314.1	243.5
163.3	1948.3	1252.3	727.3	1993.8	1055.6	1066.7	1334.8	1759.4	915.8	368.5
227.3	2723.2	2583.0	2229.4	4890.5	1977.5	3165.2	2318.9	2106.7	1958.1	1423.8
963.8	4240.6	4098.2	3584.1	7834.1	4813.3	5330.4	3489.1	3234.1	2843.7	2010.5
202.2	435.8	258.9	486.6	1910.9	159.5	698.2	352.5	748.8	254.3	221.5
111.7	247.9	44.9	313.4	694.0	247.8	346.2	398.3	49.4	197.7	91.1
2326.2	3612.6	3144.1	2726.5	4718.2	2642.9	3022.2	2834.2	3018.4	1837.5	1955.2
180.8	1687.9	1366.1	1040.5	3192.4	856.8	1604.4	1379.6	1302.4	989.4	417.5
1725.0	2711.7	2096.2	2830.0	5191.9	2363.7	3413.3	2605.7	3122.9	1272.3	1823.3
527.0	1716.3	1871.1	1921.3	5739.7	1871.0	2398.3	2391.9	1474.2	956.4	956.2
278.1	4701.8	3816.9	3857.0	6446.8	3455.4	4500.0	3099.0	3421.0	2506.8	1636.4
335.9	2219.9	2233.5	1463.9	3350.4	1719.9	2036.2	1862.6	1918.5	1488.4	697.9
306.7	4951.4	4718.2	4306.2	6184.7	4415.5	5018.0	4360.3	5050.7	4459.1	3046.8
686.8	3043.2	2713.9	2404.5	4322.7	2634.4	2971.1	2774.3	3436.2	2597.0	1124.9
49.6	315.4	660.7	350.6	2587.5	243.8	683.7	903.4	183.2	382.7	90.0
315.5	2667.2	2697.1	2036.6	3517.6	2528.3	2889.6	2746.3	2726.1	1430.3	1199.9
1114.9	5834.0	4788.3	3404.1	7728.4	5036.2	4586.1	3635.6	4397.8	3546.2	1365.7
91.2	1149.0	911.7	668.6	3585.4	997.4	1372.8	811.4	635.4	505.6	229.9
735.2	4309.1	3076.7	2328.8	5459.9	2713.8	3485.1	3031.2	2921.9	2215.1	1056.9
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747.7	4707.9	3908.8	3241.9	5488.4	3550.0	4038.1	3671.8	3547.4	2723.4	1843.5
40.5	34.8	32.3	32.7	113.0	37.9	31.6	37.1	27.7	21.8	27.0
240.3	3444.2	2649.3	2005.4	5300.2	2408.4	2753.0	2465.7	2881.4	2201.1	1770.4
292.9	2430.1	1876.0	1715.1	4448.1	1984.8	2893.8	1837.0	1223.2	1062.8	584.4
60.4	778.9	956.0	1222.5	3807.7	857.3	1696.2	1274.7	483.8	345.5	374.9
2291.9	1399.4	1446.2	1703.8	2932.3	1323.4	1968.4	1621.5	1579.2	1352.0	1296.9
203.2	5207.5	2931.1	2858.9	5234.0	3530.5	3651.5	2356.0	1277.4	2308.9	712.0
46.6	431.2	521.3	636.2	1381.6	559.3	842.8	831.0	439.1	223.4	258.4

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2464.1	3433.1	3450.4
5694.8	4452.5	3107.5
10059.4	10248.9	10444.0
5549.6	4624.3	5357.3
6377.1	4860.1	6344.9
3421.2	1862.7	2753.0
2320.8	3044.0	2911.0
6665.8	6072.8	7398.0
3925.6	1733.6	2821.9
4801.4	3109.5	4409.6
2425.9	718.4	1573.1
1062.4	562.4	1100.7
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2930.8	1854.5	3394.3
4864.9	3999.5	4972.8
606.1	131.3	354.1
502.0	173.4	323.9
3442.0	2246.9	2896.6
1913.8	862.0	1592.3
3241.3	2170.1	3306.9
2522.0	1419.3	2888.4
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s__Mycobacterium frederiksbergense	38007
s__Mycobacterium gilvum	37866
s__Mycobacterium gordonae	37396
s__Mycobacterium gordonae	38035
s__Mycobacterium gordonae	38085
s__Mycobacterium gordonae	38347
s__Mycobacterium gordonae	38372
s__Mycobacterium haemophilum	37511
s__Mycobacterium haemophilum	38075
s__Mycobacterium insubricum	37749
s__Mycobacterium interjectum	38019
s__Mycobacterium intracellulare	37628
s__Mycobacterium kansasii	37669
s__Mycobacterium kansasii	37772

FJ479084.1 gg_id:564093 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
NR_024648.1 gg_id:535010 Virgisporangium aurantiacum str. YU438-5; IFO 16421 NR_02
EU132997.1 gg_id:240258 tallgrass prarie soil clone FFCH17928 EU132
AJ416940.1 gg_id:29667 Mycobacterium abscessus str. MB849 AJ4169
AJ416939.1 gg_id:37469 Mycobacterium chelonae str. MB300 AJ4169
GU143891.1 gg_id:589339 Mycobacterium massiliense str. INCQS 594 GU143
EF054881.2 gg_id:242278 Mycobacterium arosiae str. T1921 EF0548
AB239927.1 gg_id:169008 Mycobacterium arupense str. CST0506 AB2399
DQ058406.1 gg_id:128209 Mycobacterium nonchromogenicum str. ATCC 19530 DQ058
FJ538896.1 gg_id:550227 Mycobacterium arupense str. GR-1513-542 FJ5388
FJ538897.1 gg_id:567268 Mycobacterium sp. str. GR-1516-15743 FJ5388
FJ172298.1 gg_id:563407 Mycobacterium aurum str. ATCC 23366 FJ1722
X52918.1 gg_id:13133 Mycobacterium avium str. chester (DSM 43216) X52918
AF410479.1 gg_id:64868 Mycobacterium avium Myc373 AF4104
CP000479.1 gg_id:198166 Mycobacterium avium str. 104 CP0004
AB292583.1 gg_id:250504 Mycobacterium bovis str. GTC 602 AB2925
X55588.1 gg_id:13173 Mycobacterium tuberculosis str. H37/Rv X55588
AF502574.1 gg_id:66586 Mycobacterium pinnipedii AF5025
DQ303288.1 gg_id:143735 Microbial ecology macroscopic filaments extreme Tinto River acidic river clone ff4 DQ303
AF480598.1 gg_id:36821 Mycobacterium cookii str. ATCC 49103 AF4805
AJ536040.1 gg_id:77688 Mycobacterium celatum str. DSM 44243 AJ5360
AY457072.1 gg_id:108583 Mycobacterium chelonae str. CIP 104535T AY4570
AJ416941.1 gg_id:73622 Mycobacterium chelonae str. MB834 AJ4169
X79292.1 gg_id:13032 Mycobacterium chlorophenolicum X79292
AJ431371.1 gg_id:75651 Mycobacterium pyrenivorans str. DSM 44605 AJ4313
AY449729.1 gg_id:101383 Mycobacterium cosmeticum str. 2003-11-06 AY4497
GQ924944.1 gg_id:593662 Mycobacterium elephantis str. GN-12198 GQ924
AJ276274.1 gg_id:46211 Mycobacterium frederiksbergense str. DSM 44346 AJ2762
AF544636.1 gg_id:58265 Mycobacterium gilvum VM0442 AF5446
GU142930.1 gg_id:589893 Mycobacterium gordonae str. M223 GU142
FJ382617.1 gg_id:571970 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3826
FJ382289.1 gg_id:513678 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
FJ382264.1 gg_id:570748 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
FJ382711.1 gg_id:513773 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3827
L24800.1 gg_id:13227 Mycobacterium haemophilum L24800
DQ851570.1 gg_id:226531 Mycobacterium haemophilum str. SD DQ851
EU605695.1 gg_id:277862 Mycobacterium insubricum str. FI-06250 EU6056
AJ272088.1 gg_id:30291 Mycobacterium interjectum MB739 AJ2720
AJ422047.1 gg_id:38808 Mycobacterium intracellulare MB971 AJ4220
X15916.1 gg_id:13139 Mycobacterium kansasii str. DSM 43224 X15916
X52919.1 gg_id:13230 Mycobacterium gastri str. ATCC 15754 X52919

26729.7	9852.2	8659.4	8838.9	10043.5	8966.6	9197.4	7750.2	12434.6	8725.6	9689.2
3423.3	5822.7	5059.7	4669.4	8170.9	4938.0	5963.8	4173.2	4947.7	3526.1	3017.0
2486.2	7391.2	6215.9	5206.9	8147.9	6193.2	6845.6	4348.3	5969.7	3385.7	6002.6
11311.1	5845.3	5696.5	5646.3	7051.8	6733.1	6068.0	6402.0	7371.8	5879.8	7248.7
1334.5	4336.9	3797.1	4034.8	4280.5	4990.1	4626.7	4909.9	3988.0	3049.2	3266.8
945.1	5652.2	4031.9	3648.2	5263.6	4340.2	5023.4	4664.7	4958.2	2952.3	2516.4
51.2	397.2	291.2	213.6	630.7	406.4	337.5	736.8	271.7	295.2	65.7
88.3	2304.9	1827.5	1680.6	2662.8	2220.2	2227.6	2486.2	2751.4	2319.5	675.6
122.1	2799.0	2188.9	1717.4	2956.8	2111.3	2431.8	2379.8	2381.1	1933.9	651.1
130.9	3762.5	2620.4	2203.2	3503.9	3252.7	3027.4	2922.0	3026.7	2801.8	881.4
149.9	3619.7	2448.2	1814.0	3040.4	2402.1	2559.3	2563.3	2415.2	2272.1	673.2
39.4	1401.2	1209.9	1318.7	4271.1	1686.4	1577.9	2266.7	933.8	910.0	467.7
114.6	543.2	331.5	316.7	929.2	596.3	485.4	756.9	231.9	213.6	137.3
120.9	1095.5	702.4	551.6	1409.2	994.1	864.0	1185.4	691.8	676.4	205.5
48.6	909.1	562.6	419.1	987.7	669.6	670.6	952.4	515.3	524.1	152.8
3473.9	5353.1	5060.1	4471.7	4935.9	4538.4	5068.4	5203.3	5504.5	4208.0	5172.7
137.1	3542.1	3590.3	2340.2	3551.3	3237.5	3396.1	2872.0	3501.1	3204.1	1745.1
197.2	2253.3	2607.8	1995.3	2767.9	2198.1	2679.8	2221.2	1852.7	1708.6	1125.6
69.0	1529.9	1005.1	738.3	1309.6	1110.7	1008.2	1236.1	929.4	705.3	169.7
116.0	1160.6	750.0	790.4	1753.9	917.1	1171.5	1917.7	912.1	911.7	255.5
48.7	3185.6	1963.3	1286.1	2634.2	2466.7	2446.5	3470.8	2765.5	2768.4	713.8
1292.5	6813.8	4661.9	3850.8	4759.0	5140.8	5154.9	4810.7	7147.7	3957.8	2831.4
1045.1	6929.1	4776.7	3634.6	5222.4	4858.0	5399.2	4709.1	6855.0	4439.2	3031.6
216.7	3301.6	2874.2	2549.5	5583.7	3463.6	3129.8	3776.8	3456.0	3155.7	1491.7
250.5	3408.3	3261.4	2934.0	5674.2	3944.0	3977.1	3775.3	3364.5	3189.4	1714.8
30.6	1785.9	1235.7	1391.4	2755.5	1622.0	1718.4	2418.8	1168.1	1005.6	305.0
51.1	1333.7	907.0	823.9	2686.5	1426.2	1099.5	2447.5	466.7	604.8	172.2
46.1	1372.7	1048.1	1142.1	2273.9	1249.7	1445.4	1844.0	686.4	764.0	263.3
5918.4	7446.6	6384.9	5070.1	9201.9	5186.5	6771.7	5532.9	9698.1	4709.2	3698.0
2377.8	4791.4	4378.2	3700.0	3198.1	3864.4	4793.0	3960.4	4228.9	3644.8	5092.6
636.6	2966.3	2680.1	1740.4	3169.9	2787.1	2084.5	2078.8	2535.5	1330.2	1016.4
1671.4	4972.2	4777.9	3325.5	4787.9	4316.6	4380.6	3406.5	4954.8	3180.5	3427.4
275.8	2659.0	2173.2	1470.3	2265.4	2074.6	1988.2	2128.5	1936.5	1808.1	636.4
287.2	2464.6	2001.9	1957.7	2965.7	2171.2	2465.5	2973.3	1828.8	1600.0	1048.0
285.0	5687.8	3363.8	1392.3	2800.4	4089.6	2428.6	2501.7	5500.1	4144.7	759.9
128.9	746.6	766.4	656.8	1085.3	670.4	1050.3	1159.6	383.0	331.9	207.2
377.8	4743.0	4085.7	1824.4	3374.0	2777.0	2347.8	2881.4	3875.2	2387.4	875.5
128.9	1512.0	1060.0	914.1	2107.9	1133.4	1309.7	2028.9	1229.0	1183.1	236.7
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2170.5	2085.2	2056.9	1974.5	2601.7	1754.6	2607.6	2211.0	1803.8	873.7	2087.1
2171.5	2438.7	2258.6	2154.9	2858.2	1997.6	2816.8	2616.8	2226.2	1176.6	2132.2

9051.4	8578.1	8470.9
5812.5	4661.6	5335.6
5057.2	5147.1	6070.8
6574.8	6186.6	6410.4
5199.0	3751.8	5080.4
4668.9	3025.5	4286.7
643.4	177.0	826.2
3342.0	1937.1	2972.5
3382.3	1856.8	3290.9
4099.2	2304.2	3324.0
3686.3	1884.6	3125.3
2516.4	949.6	2496.4
768.9	281.5	956.9
1334.5	567.1	1431.4
872.0	485.8	1201.1
5814.9	4580.6	5152.6
3342.9	2840.1	3126.3
2662.2	2276.2	2660.7
1479.1	553.5	1522.7
2157.2	719.9	1926.9
4355.3	1359.8	2671.5
4540.6	3100.8	3942.1
4734.6	3129.3	4238.4
4075.2	3005.0	3333.0
4121.5	3956.2	4055.7
2989.0	1011.6	2422.7
3081.6	695.6	2996.1
2547.9	854.3	1759.7
5782.1	5063.9	5627.7
4813.9	3530.1	4105.1
2817.6	2540.5	2275.8
3330.5	3475.1	3445.3
2399.4	1395.1	2445.8
3448.8	1843.0	3027.2
2915.2	1179.5	1953.7
1046.1	519.1	1526.5
3461.0	2141.9	2600.8
2602.7	858.7	2007.0
609.3	169.3	811.6
2268.2	1730.3	2625.4
2642.4	1868.9	2843.3

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s__Mycobacterium kyorinense	37673
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s__Mycobacterium thermoresistibile	37961
s__Mycobacterium triviale	37899
s__Mycobacterium vaccae	37478
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s__Mycobacterium xenopi	37995
s__unclassified	37391
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s__unclassified	37408
s__unclassified	37412

AB370113.1 gg_id:248613 Mycobacterium kyorinense str. KUM 060529 AB370
AJ581477.2 gg_id:135971 Mycobacterium lentiflavum str. M6 AJ5814
X55022.1 gg_id:13163 Mycobacterium leprae X55022
FJ382231.1 gg_id:585147 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
FJ382118.1 gg_id:538954 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
AJ746071.2 gg_id:237240 Mycobacterium lazari MG14 AJ7460
FJ382335.1 gg_id:544470 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3823
FJ382121.1 gg_id:509323 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
FJ382182.1 gg_id:509206 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
FJ382225.1 gg_id:579201 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
FJ382101.1 gg_id:540899 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
FJ382207.1 gg_id:542008 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
EF551396.1 gg_id:218935 Mycobacterium mucogenicum BCMUCO_06-704 EF5513
GQ153277.1 gg_id:587686 Mycobacterium nebraskense str. ATCC BAA-837 GQ153
NR_025767.1 gg_id:548075 Mycobacterium nebraskense str. UNMC-MY1349; ATCC BAA-837 NR_02
FJ172302.1 gg_id:561179 Mycobacterium neoaurum str. ATCC 25801 FJ1723
AJ416910.1 gg_id:26463 Mycobacterium fortuitum str. MB44 AJ4169
X52921.1 gg_id:13190 Mycobacterium fortuitum str. ATCC 14472 X52921
AF448435.1 gg_id:34657 Mycobacterium sp. str. MEU-1 AF4484
AF023664.1 gg_id:13183 Mycobacterium alvei str. CIP 103464 AF0236
EF551408.1 gg_id:218031 Mycobacterium phocaicum BCMUCO_06-708 EF5514
EF551406.1 gg_id:221713 Mycobacterium phocaicum BCMUCO_07-444 EF5514
DQ866764.1 gg_id:189302 Mycobacterium salmoniphilum str. AUS DQ866
AJ419968.1 gg_id:42323 Mycobacterium chelonae str. ITG 96-0295 AJ4199
AM884325.1 gg_id:245331 Mycobacterium chelonae str. T14 AM884
DQ866768.1 gg_id:194098 Mycobacterium salmoniphilum str. ATCC 13758 DQ866
GQ153271.1 gg_id:547556 Mycobacterium scrofulaceum str. ATCC 19981 GQ153
EU877064.1 gg_id:352120 Streptomyces scabrisporus str. HBUM174716 EU877
AM884333.1 gg_id:253579 Mycobacterium barombii str. T4 AM884
DQ058407.1 gg_id:133041 Mycobacterium terrae str. ATCC 15755 DQ058
FJ236481.1 gg_id:320457 Mycobacterium thermoresistibile str. GN-6223 FJ2364
DQ058405.1 gg_id:132344 Mycobacterium triviale str. TMC 1453 DQ058
AF480591.1 gg_id:23360 Mycobacterium vaccae str. ATCC 15483 AF480
AF544639.1 gg_id:58264 Mycobacterium vaccae VM0588 AF5446
X55601.1 gg_id:13179 Mycobacterium vaccae str. ATCC 15483 X55601
AJ536033.1 gg_id:78273 Mycobacterium xenopi str. DSM 43995 AJ5360
AF107039.2 gg_id:13150 Mycobacterium monacense str. B9-21-178 AF107
FJ382254.1 gg_id:510153 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
EU132942.1 gg_id:243988 tallgrass prarie soil clone FFCH16609 EU132
NR_026286.1 gg_id:540879 Mycobacterium hodleri str. DSM 44183 NR_02
AF480600.1 gg_id:72357 Mycobacterium fallax str. ATCC 35219 AF480

4786.2	5284.7	4159.2	4417.2	6383.5	4577.4	4950.1	6147.5	5195.6	3985.5	3761.9
111.0	1279.9	884.8	999.4	2572.5	1484.4	986.6	1709.4	472.6	581.7	251.9
22503.7	10098.5	9289.1	7811.8	8000.4	9542.7	9296.5	7359.4	10866.0	9832.9	4892.4
4588.7	3220.3	2598.0	2811.5	4677.4	2857.0	3158.9	3041.2	2438.0	1563.2	1864.7
13384.3	7834.1	6566.5	6643.9	7905.7	6772.0	7090.8	6804.1	12220.2	8843.1	6697.4
116.0	1675.9	1145.2	1157.7	2391.2	1487.4	1154.6	1416.9	918.3	749.3	274.8
111.0	1799.3	1489.1	1465.0	3209.1	2047.2	1553.2	2515.5	1074.7	1088.9	348.2
343.8	2636.7	2125.3	2046.9	2977.3	2524.5	2642.8	1939.2	2033.5	1628.6	950.6
263.5	2142.6	1402.9	1627.7	3007.9	2413.1	2332.8	2082.1	1145.9	1442.8	368.4
117.8	2016.1	1545.1	1508.4	2958.0	1871.4	1864.6	1723.5	1101.1	946.0	377.8
12074.5	7221.4	6317.3	6135.1	6785.6	6488.8	6395.4	5640.7	10626.3	6970.9	7805.6
133.8	2263.8	1742.8	1670.8	3209.0	2079.2	2117.2	2069.2	1392.0	1271.2	428.6
137.5	2834.9	2273.2	2045.7	3421.0	2425.4	3291.0	3080.5	1850.8	1547.6	800.2
121.9	731.7	748.1	648.8	1016.7	683.8	1054.4	1194.1	405.1	352.0	204.3
175.6	1998.0	1403.8	1545.7	1412.4	1431.0	1856.9	1660.7	1210.8	957.3	1112.7
44.4	1504.0	1394.2	1582.5	3315.7	1818.4	1988.4	2328.7	651.3	844.3	357.6
39.5	941.1	1058.7	799.9	1214.5	946.5	1008.7	1400.1	652.3	432.2	424.4
72.9	1519.2	1202.9	973.8	1773.3	1324.8	1321.7	1747.6	669.7	710.9	373.7
74.3	1493.4	1223.5	989.5	2136.2	1368.9	1429.3	1759.3	651.4	637.3	366.9
69.6	1463.4	1155.6	960.2	1743.0	1259.4	1276.0	1755.7	604.4	670.5	358.1
131.0	2762.6	2168.9	2016.2	4065.9	2513.6	3340.5	2964.5	1518.0	1761.7	718.7
160.5	2757.8	2297.9	2192.5	4360.3	2710.2	3433.7	2915.7	1683.1	1776.7	785.2
435.8	3368.1	2492.3	2191.3	3690.7	2713.0	2904.1	3170.3	3205.8	2330.1	1112.1
782.1	4356.2	2961.2	2334.3	2647.8	3345.2	2990.0	3275.0	4430.1	2797.9	1741.9
752.1	5036.8	3388.8	2779.7	3892.6	3775.5	3624.5	3792.7	4868.6	3117.8	2072.1
3330.0	4094.2	3422.0	3204.3	3419.7	3431.9	3206.0	4213.9	4247.0	2779.6	3311.2
288.8	1063.0	1031.3	828.2	1335.4	1110.1	1066.6	1392.1	1330.8	959.8	679.0
151.4	3582.5	2686.8	2085.3	2873.7	3115.7	2413.2	2860.7	2799.0	3016.5	1283.4
145.0	2408.9	1816.5	1408.9	3476.1	2311.8	1783.0	2878.6	1972.2	1802.8	423.1
188.9	2661.6	2114.8	1825.3	3043.6	1972.4	2449.3	2847.1	2340.1	2251.4	640.7
1136.1	2336.3	1660.0	1522.7	3281.0	2174.1	2074.6	3014.9	1084.7	1079.5	542.3
59.3	4720.9	3321.2	2869.6	5303.8	4220.8	3951.6	4987.6	5078.5	3660.4	1346.9
46.7	2411.8	1864.6	1790.2	3652.2	2690.4	1917.8	3594.4	1553.1	1337.6	474.1
33.0	885.3	613.8	688.7	2002.5	871.3	569.2	1316.8	801.8	583.5	143.1
37.4	1969.9	1495.9	1423.4	3063.2	2364.9	1395.1	3081.2	1260.8	1115.3	370.1
6842.3	8408.9	7147.6	7692.6	10023.9	7825.2	8959.0	7591.4	9333.3	7715.7	7900.4
106.1	2823.7	1725.2	1433.1	3242.7	1922.4	1302.5	2213.9	1427.6	838.0	375.5
10918.6	7597.9	6574.1	6250.3	6679.8	6986.0	7279.4	6411.5	10698.8	8983.9	7659.9
95.1	1993.7	1615.8	1545.7	3123.9	1658.0	2193.9	3100.6	1181.1	1377.1	385.8
47.1	446.4	698.8	369.2	699.6	443.6	270.1	814.9	116.4	119.2	89.8
48.3	1767.1	1168.9	902.4	1372.3	1579.5	956.8	1661.2	1631.4	1094.2	389.6

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7977.9	7607.4	7717.6
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2266.1	1058.0	2450.8
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2700.5	1765.1	3529.5
3275.7	1101.8	3315.5
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1036.9	501.6	1550.1
1345.5	1534.2	2140.7
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1568.8	695.6	1376.6
2460.4	805.4	1223.0
2386.1	867.4	1332.8
2529.8	795.2	1102.5
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3894.7	2177.5	3064.4
4171.6	2547.5	3660.3
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3915.2	1559.4	2780.3
4259.5	2242.0	2971.9
4318.8	1426.6	3661.1
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4374.0	942.7	3930.8
1673.7	491.5	1534.4
3597.7	851.2	3111.5
8222.2	7589.0	9496.4
3319.7	1269.9	2629.2
5795.3	6792.7	6050.6
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525.2	139.5	647.9
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EU703149.1 gg_id:300187 Mycobacterium sp. str. 1797 EU703
GU201853.1 gg_id:522393 Mycobacterium sacrum str. Qtx-19 GU201
EU741212.1 gg_id:576049 Mycobacterium fortuitum str. 13667H EU741
DQ448781.1 gg_id:158340 Mycobacterium sp. str. CNJ881 PL04 DQ448
GU142918.1 gg_id:573674 Mycobacterium gastri str. M227 GU142
X63608.1 gg_id:13261 Mycobacterium confluentis X63608
AF133902.1 gg_id:38495 Mycobacterium kubicae str. CDC 941078 AF1339
X93030.1 gg_id:37418 Mycobacterium sp str. MCRO 19 X93030
AF480587.1 gg_id:73949 Mycobacterium petroleophilum str. ATCC 21497 AF480
X55597.1 gg_id:13056 Mycobacterium obuense str. ATCC 27023 X55597
EF018567.1 gg_id:215776 aspen rhizosphere clone Amb_16S_833 EF0185
AF544624.1 gg_id:74074 Mycobacterium austroafricanum VM0451 AF544
FJ671237.1 gg_id:511255 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6712
AF480579.1 gg_id:36933 Mycobacterium flavescens str. ATCC 23033 AF480
AY859685.1 gg_id:149619 Mycobacterium barrassii str. CIP 108545 AY859
AF541924.1 gg_id:85394 Mycobacterium sp. str. YM12 AF541
DQ069216.1 gg_id:133267 gold mine clone FW30 DQ069
AJ616230.2 gg_id:104030 Mycobacterium florentinum str. FI93171 AJ6162
GU142927.1 gg_id:553373 Mycobacterium phlei str. M226 GU142
DQ372734.1 gg_id:151905 Mycobacterium sp. K337Y1 DQ372
NR_026285.1 gg_id:556768 Mycobacterium parafortuitum str. DSM 43528 NR_02
AF014937.1 gg_id:13207 Mycobacterium interjectum patient 3 AF014
AF480599.1 gg_id:30995 Mycobacterium diernhoferi str. ATCC 19340 AF480
EU132910.1 gg_id:241763 tallgrass prarie soil clone FFCH15424 EU132
AJ833917.1 gg_id:115097 Mycobacterium ratisbonense str. FR13 AJ8339
GU142932.1 gg_id:578612 Mycobacterium intracellulare str. M220 GU142
X67847.1 gg_id:13262 Mycobacterium intermedium X67847
AF264700.1 gg_id:71298 Mycobacterium doricum str. FI-13295; DSM 44339 AF2647
NR_028759.1 gg_id:539838 Mycobacterium heckeshornense str. S369; DSM 44428 NR_02
FJ382318.1 gg_id:547338 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3823
FJ382185.1 gg_id:570848 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
AJ429045.1 gg_id:28966 Mycobacterium agri str. DSM 44515T AJ4290
GQ072691.1 gg_id:425202 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
X55600.1 gg_id:13048 Mycobacterium madagascariense X55600
AB537170.1 gg_id:572651 Mycobacterium madagascariense str. JCM 13574 AB537
AF480582.1 gg_id:28954 Mycobacterium lacticola str. ATCC 9626 AF480
X88911.1 gg_id:13123 Mycobacterium sp str. IWGMT 90160 X88911
X70961.1 gg_id:13204 Mycobacterium interjectum X70961
EF408842.1 gg_id:204863 Mycobacterium sp. str. wged16 EF4088

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4627.6	6374.8	6200.8	5217.6	8086.6	5124.5	6702.1	5183.9	9390.1	4547.5	4072.8
70.0	1405.3	1017.4	1055.9	2326.8	1474.9	1785.7	2160.6	779.9	1139.1	253.1
99.1	2451.5	1486.0	828.4	1922.5	1226.0	1075.6	1906.1	870.0	915.7	230.3
192.7	2604.2	1917.6	1184.6	2091.9	1841.1	1886.2	2666.4	1801.8	1484.7	433.0
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77.2	5370.7	3827.0	2472.5	4197.4	4664.9	2707.2	4218.5	6445.2	4642.7	1659.8
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693.8	1573.0	1515.6	1721.4	4133.0	1727.8	2239.5	3150.0	1853.3	1402.1	512.6
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653.5	2543.7	2253.9	2369.4	4470.4	2540.1	2465.9	3108.9	4101.8	3054.8	1299.5
268.1	1842.1	1611.8	1727.0	2122.3	1751.7	1814.9	1595.9	1039.1	871.7	769.0
729.7	1883.6	1715.3	1792.4	5069.8	2200.7	2322.0	2756.7	1397.4	1092.5	823.2
41.2	1129.8	660.4	776.1	1795.2	1043.9	1015.5	1895.4	370.4	507.9	207.4
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119.5	2268.8	1691.3	1247.2	3297.4	2127.2	1640.9	2705.8	1992.2	1732.8	392.6
231.3	4373.0	3186.8	2509.0	3483.2	2717.5	2994.7	3348.2	4659.2	1859.6	1400.0
45.5	750.9	686.6	790.3	3230.4	1048.5	749.8	1478.4	450.9	410.5	248.5
735.6	3354.6	2745.8	2252.9	5557.4	3254.7	2727.4	3488.5	3801.1	3002.5	1679.3
1707.8	2238.6	1637.8	1442.2	2808.8	1612.4	1923.5	2410.6	1933.5	1385.7	1142.8
33.1	1815.4	1408.2	1614.6	3496.9	2156.2	1930.9	2682.1	742.4	771.9	306.6
63.4	2248.2	2075.6	2200.1	2793.8	2238.5	1686.0	3203.1	1974.8	1145.3	1642.4
110.2	2026.5	2135.1	2336.0	4327.8	2626.5	3525.7	2873.3	1232.8	1343.5	843.1
48.4	465.3	405.7	295.6	1754.4	569.2	441.1	1010.9	345.8	306.9	81.8
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59.7	1346.0	1023.6	847.6	1808.6	1497.5	1748.1	2087.1	904.4	1262.3	256.2
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2906.3	754.4	1705.0
2920.3	917.4	1340.1
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5078.1	2784.7	4110.1
2610.9	693.9	1885.3
2968.4	1259.1	2667.9
3317.8	1244.0	2355.8
3562.5	2317.6	2848.6
1488.9	1251.1	1292.8
3231.9	1559.4	2966.7
2484.2	618.9	2671.0
4823.7	2460.8	3824.9
3133.9	637.7	2078.6
1990.2	555.7	1219.6
3244.6	2830.4	3745.9
3723.9	1356.0	2478.0
4694.2	2734.5	3589.1
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3996.9	2918.1	3132.2
3034.0	1529.2	2614.6
3461.2	1030.0	3193.7
3979.9	1767.5	2553.8
3754.6	2427.2	3227.2
944.8	275.4	1073.9
1817.8	925.7	2040.0
2617.3	869.1	1831.2
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3125.2	1563.8	2197.5
2818.8	776.8	1723.6
1604.4	829.9	1276.0
3993.3	5013.5	3849.2
2364.4	764.3	1529.9
3781.7	1903.6	3099.2
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AJ580826.1 gg_id:93004 Mycobacterium tilburgii AJ5808
EU008079.1 gg_id:328227 Mycobacterium avium complex str. 64 EU008
FJ382100.1 gg_id:594108 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
EU528255.1 gg_id:281424 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AJ010747.1 gg_id:13146 Mycobacterium elephantis AJ0107
GQ057469.1 gg_id:416745 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ057
GQ103945.1 gg_id:417165 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ103
AM749747.1 gg_id:240515 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
NR_025235.1 gg_id:536095 Mycobacterium poriferae str. ATCC 35087 NR_02
NC_009565.1 gg_id:234320 Mycobacterium tuberculosis str. F11 NC_00
NR_025529.1 gg_id:552389 Mycobacterium rhodesiae str. DSM 44223 NR_02
GQ009545.1 gg_id:500121 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
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DQ324791.1 gg_id:145603 Mycobacterium sp. G1368 DQ324
GQ390231.1 gg_id:565869 oxic-anoxic interface meromictic crater lake Lac Pavin clone Eub62A1111 GQ390
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AF544622.1 gg_id:58279 Mycobacterium austroafricanum VM0456 AF5446
GU142939.1 gg_id:544816 Mycobacterium elephantis str. 485 GU142
FJ382132.1 gg_id:583335 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
FJ382244.1 gg_id:552407 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3822
AJ416913.1 gg_id:17299 Mycobacterium sp. str. MB69 AJ4169
FJ214359.1 gg_id:354851 Mycobacterium sp. str. YIM 65220 FJ2143
AF367025.1 gg_id:66700 Mycobacterium malmoense Myc250 AF367
EU440645.1 gg_id:562384 Soil are Changed Agricultural Practices agricultural soil clone Plot17-2A09 EU440
AF406783.1 gg_id:18950 Mycobacterium lacus str. NRCM 00-255 AF406
DQ054531.1 gg_id:134554 Mycobacterium rhodesiae str. TRW-2 DQ054
U94745.1 gg_id:13145 Mycobacterium duvalii str. ATCC 43910 U94745
EF591053.1 gg_id:293579 Mycobacterium avium complex str. 4355387 EF591
X67096.1 gg_id:13047 Mycobacterium hiberniae str. ATCC 9874 X67096
FJ179485.1 gg_id:538985 Hoyosella altamirensis str. OFN S31 FJ1794
X55604.1 gg_id:13129 Mycobacterium asiaticum str. ATCC 25276 X55604
AJ416914.1 gg_id:70429 Mycobacterium celatum str. MB72 AJ4169
AJ812215.1 gg_id:99103 Mycobacterium immunogenum str. DSM 44764 AJ8122
X88909.1 gg_id:13210 Mycobacterium sp str. IWGMT 90203 X88909
DQ906054.1 gg_id:218190 nickel resistance genes metagenome Tinto River rhizosphere clone ERF-1C3 DQ906
AY457077.1 gg_id:108588 Mycobacterium porcinum str. CIP 105392T AY457
EU132556.1 gg_id:235654 tallgrass prarie soil clone FFCH17926 EU132
AY859683.1 gg_id:148114 Mycobacterium aubagnense str. CIP 108543 AY8596

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1624.6	1495.3	1277.9	1103.9	1631.4	1217.8	1268.2	1641.2	1537.0	865.4	1133.0
836.5	4350.1	3853.9	4240.5	5471.4	3999.3	4561.6	5214.8	3904.0	2713.6	2049.8
10411.9	8438.0	7724.3	8460.4	10479.0	7034.7	9641.2	6755.8	6745.0	6130.1	9995.1
83.9	1550.2	1460.4	1601.4	2806.7	1600.2	1897.8	2525.9	1592.8	1713.0	557.3
95.3	2179.6	1500.8	1536.2	2865.3	1421.6	1945.2	3076.4	2343.2	1633.0	522.9
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86.6	3127.9	2905.8	1576.9	2460.0	2690.9	2289.1	2453.7	3136.7	2749.6	1088.9
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521.1	3269.0	3391.7	3511.5	5898.2	3716.9	5289.3	4004.9	2856.9	2616.5	1761.7
34.0	962.4	797.3	772.8	2090.5	845.6	1297.4	1020.2	439.5	413.6	327.8
84.7	945.3	562.3	665.8	1161.1	929.7	723.3	1878.3	407.5	611.3	156.2
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269.7	1457.5	1303.5	1075.9	1734.4	1487.4	1327.8	1978.1	1805.2	1357.9	799.1
1431.7	4513.7	3708.6	3230.2	4234.6	4041.0	4144.0	3350.2	6156.7	4691.8	2057.8
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729.6	1442.6	1189.4	1431.0	4453.6	1804.1	1707.6	2138.1	917.4	860.9	533.6
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305.7	6330.8	4911.7	3621.2	5488.1	5137.6	4247.5	5069.1	4331.1	4309.8	2243.8
3264.5	8555.8	7583.4	7149.1	8020.4	7506.6	7525.0	6315.1	8543.5	6880.1	6240.4
69.0	858.2	614.8	506.1	1164.6	634.2	828.8	1224.4	612.3	616.3	176.7
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1717.7	1755.3	1692.5	1475.3	2016.6	1335.3	2174.8	1957.5	1332.7	848.0	1230.2
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301.1	1064.7	1097.9	877.7	2366.9	855.3	1492.0	1450.1	684.3	575.1	470.0
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223.5	3804.2	3263.6	2409.3	4163.8	3296.0	3413.7	3166.9	3684.7	2635.4	1517.3
45.9	111.7	119.9	76.3	164.4	110.3	117.5	102.7	108.0	74.9	40.3
42.8	1421.2	929.0	743.4	1630.6	1214.0	1000.5	1842.2	1030.2	1042.0	245.7
27506.6	5854.1	4718.2	2553.8	5840.4	5342.6	5597.0	5872.6	7786.2	5555.5	6574.7
4912.4	5205.6	3361.7	3366.9	6340.6	3726.9	4506.0	4496.5	3887.5	2411.6	2234.1
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1639.6	2763.8	2060.6	1996.6	3642.5	2386.5	2603.7	2932.2	1531.6	1399.8	998.9
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U65104.1 gg_id:13115 Mycobacterium sp U6510
EU180557.1 gg_id:247201 Mycobacterium sp. str. BAC86 EU180
FJ382274.1 gg_id:542828 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
NR_029298.1 gg_id:583810 Mycobacterium conspicuum str. 3895/92; DSM 44136 NR_02
EU132660.1 gg_id:241158 tallgrass prarie soil clone FFCH10818 EU132
EF591054.1 gg_id:290695 Mycobacterium avium complex str. 3256799 EF591
AF480577.1 gg_id:42140 Mycobacterium engbaekii str. ATCC 27353 AF480
GQ064270.1 gg_id:376037 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw6 GQ064
FJ380142.1 gg_id:365607 ornithogenic Ross Sea region Antarctica AB1 soil clone 1/5/6A FJ3801
AY786470.1 gg_id:113826 Mycobacterium austroafricanum str. IFP 2015 AY7864
DQ227004.1 gg_id:143188 Mycobacterium smegmatis str. mc2 155 DQ227
EU703148.1 gg_id:293029 Mycobacterium sp. str. 1791 EU703
Y15709.1 gg_id:13191 Mycobacterium anthracenicum Y15709
AF498650.1 gg_id:60765 Mycobacterium rhodesiae str. JS60 AF498
AB548662.1 gg_id:523871 Mycobacterium sp. str. NJS-1 AB548
X88914.1 gg_id:13263 Mycobacterium sp str. IWGMT 90161 X88914
FJ382311.1 gg_id:512946 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3823
AJ416909.1 gg_id:23238 Mycobacterium septicum str. MB804 AJ4169
AF330038.2 gg_id:137365 Mycobacterium montefiorense str. ATCC BAA-256 AF330
X93031.1 gg_id:49725 Mycobacterium sp str. MCRO 24 X93031
GU205284.1 gg_id:523221 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
DQ298364.1 gg_id:150891 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
FJ592815.1 gg_id:535768 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AY082001.2 gg_id:59294 Mycobacterium manitobense str. NRCM 01-154 AY082
X70960.1 gg_id:13041 Mycobacterium heidelbergense X7096
X88907.1 gg_id:13131 Mycobacterium sp str. IWGMT 90018 X88907
NR_028940.1 gg_id:582064 Mycobacterium palustre str. E846; DSM 44572 NR_02
EU132550.1 gg_id:256326 tallgrass prarie soil clone FFCH13482 EU132
NR_025233.1 gg_id:546972 Mycobacterium brumae str. ATCC 51384 NR_02
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GQ067242.1 gg_id:376563 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ067
AM884328.1 gg_id:237082 Mycobacterium angelicum str. DSM 45057 AM884
FJ382322.1 gg_id:577540 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3823
DQ473310.1 gg_id:226932 Mycobacterium gadium str. CIP 105388 DQ473
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FJ827867.1 gg_id:563608 Seasonal nutrient additions eutrophic integrated lake epilimnion clone ME002H10 FJ8278
GQ049145.1 gg_id:467145 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu469f11 GQ049
DQ973806.1 gg_id:183795 Mycobacterium fortuitum DQ973
AJ011771.1 gg_id:13116 Mycobacterium immunogenum MN 3744 AJ0117

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58.1	1047.4	668.2	724.5	1536.7	1179.9	914.1	1708.3	513.0	597.6	151.9
2156.0	4373.1	3014.8	2720.0	4287.7	3750.1	3340.5	2900.2	2262.6	1524.2	1822.7
157.2	2504.2	2141.8	2210.8	4705.8	2464.5	2669.5	2975.8	1622.2	1660.9	574.0
8259.9	5309.3	4281.5	3615.6	4811.4	4317.4	4432.4	4174.5	5585.7	3373.5	3900.4
44.3	978.5	670.8	509.7	1293.6	994.8	436.7	967.1	342.7	409.8	94.0
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142.7	4624.8	3321.0	2449.1	4110.3	3704.0	3260.8	3253.4	3373.5	2972.9	1001.2
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113.5	1046.1	659.9	673.7	1394.0	1014.1	498.8	1363.6	413.8	346.7	139.4
72.3	1336.1	865.4	569.2	1408.9	838.3	717.2	1464.8	742.6	607.9	145.7
249.1	3053.8	2433.6	1840.2	2829.8	1950.4	2096.8	2864.4	2777.3	2090.3	955.6
51.0	730.7	543.4	546.5	2465.8	720.9	684.5	1229.0	754.5	583.1	145.6
917.0	4544.7	3729.5	3805.5	5100.9	4010.9	5143.7	4365.8	3069.0	2042.2	2351.9
68.3	2385.9	1647.2	970.8	1745.2	1871.1	1214.0	2133.9	2079.3	1737.9	498.2
52.3	1193.5	716.9	741.5	1709.9	1203.9	566.4	1335.9	429.5	592.4	160.8
51.8	1347.2	646.1	544.5	1494.9	963.4	976.7	1885.3	759.2	866.7	139.4
4468.4	6444.1	6181.7	4981.5	6079.2	5683.0	5444.3	5952.7	7019.9	6480.6	4924.0
46.4	251.4	376.9	431.1	489.5	377.8	557.2	562.3	225.0	95.0	177.4
198.5	3657.3	2694.4	2282.7	3431.0	3005.8	2540.2	3856.9	2761.4	2286.9	1047.9
64.5	1990.1	1564.6	1374.3	2999.8	2107.5	1434.7	2342.9	1614.5	1579.8	489.4
142.3	1108.2	1257.1	1285.6	2811.7	1261.9	1549.9	1838.2	678.7	598.8	415.3
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85.8	1201.8	903.2	930.9	3177.3	1222.6	1185.6	1781.5	890.6	906.8	242.6
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2776.0	2543.5	1916.6	1842.2	3343.2	2399.9	2454.1	2965.6	1816.7	1462.5	1589.3
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4620.9	3871.3	4123.7
1398.5	393.8	1393.1
5771.8	4166.5	4399.0
642.5	182.1	807.3
4691.6	2730.9	3728.0
2965.2	1185.2	1592.6
7493.2	6029.2	6559.9
944.5	415.2	897.2
4721.4	2571.2	4017.4
1974.4	436.2	1539.1
2242.4	450.5	1247.8
1923.7	556.9	1448.3
3159.0	1958.8	2279.7
1310.6	430.2	1368.7
4789.5	3892.8	4377.7
2810.0	1379.7	2016.9
1994.3	473.2	2068.8
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683.6	240.4	364.5
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2017.1	972.1	2067.6
2513.1	527.8	1387.6
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NR_028998.1 gg_id:577003 Mycobacterium psychrotolerans str. WA101; DSM 44697 NR_02
FJ382192.1 gg_id:579999 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
AJ580802.1 gg_id:103169 Mycobacterium neglectum str. BN 3150 AJ5808
GQ060645.1 gg_id:428178 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03f06c GQ060
FJ382232.1 gg_id:569139 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3822
FJ382168.1 gg_id:584359 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
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DQ347851.1 gg_id:202331 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi DQ347
EU274642.1 gg_id:236733 Mycobacterium riyadhense str. NLA000201958 EU274
FJ671392.1 gg_id:517707 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6713
X55593.1 gg_id:13035 Mycobacterium diernhoferi str. ATCC 19340 X55593
EU132552.1 gg_id:254659 tallgrass prarie soil clone FFCH14174 EU132
EU203590.2 gg_id:259253 Mycobacterium lepromatosis str. FJ924 EU203
GQ023911.1 gg_id:485758 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ023
FJ382105.1 gg_id:509889 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
GU142926.1 gg_id:541382 Mycobacterium conceptionense str. M137 GU142
X82234.1 gg_id:13228 Mycobacterium sp str. H 52157 X82234
AF408993.1 gg_id:100050 Mycobacterium sp. str. Ellin151 AF408
FJ382339.1 gg_id:533900 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3823
GQ342298.1 gg_id:568360 Mycobacterium conceptionense str. CG-T5 GQ342
AJ310467.1 gg_id:27078 Mycobacterium holsaticum str. 1406 AJ3104
GQ281070.1 gg_id:581446 Mycobacterium brisbanense str. NBCS10 GQ281
EU239955.1 gg_id:250184 Mycobacterium noviomagense str. NLA000500338 EU239
GU205288.1 gg_id:514711 unusual Microbial Venezuelan Tepui (Orthoquartzite) Cave: Dominance Chloroflexal GU205
AJ005005.1 gg_id:13055 Mycobacterium shimoidei str. ATCC 27962 AJ0050
X93026.1 gg_id:13148 Mycobacterium sp str. MCRO 10 X93026
FN421546.1 gg_id:546655 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 14_B05 FN421
AF408984.1 gg_id:104109 Mycobacterium sp. str. Ellin142 AF408
AM884330.1 gg_id:239513 Mycobacterium aemonae str. DSM 45058 AM884
FJ382138.1 gg_id:541321 Potentially pathogenic and air stem cell transplant summer hospital shower water BN FJ3821
GQ056820.1 gg_id:407296 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ056
GQ072820.1 gg_id:484556 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201e11c GQ072
GU134623.1 gg_id:557044 Mycobacterium austroafricanum str. SE12 GU134
AJ422048.1 gg_id:73821 Mycobacterium heidelbergense str. ITG 7971 (MB43) AJ4220
X80768.1 gg_id:13138 Mycobacterium isoniacini INA-I X80768
EF019529.1 gg_id:214595 aspen rhizosphere clone Elev_16S_1032 EF0195
DQ249999.1 gg_id:141584 Mycobacterium sp. str. L47 DQ249
AJ277284.1 gg_id:54160 Mycobacterium bohemicum str. E743 AJ2772
X55598.1 gg_id:13174 Mycobacterium aichiense str. ATCC 27280 X55598
X55591.1 gg_id:13142 Mycobacterium komossense str. ATCC 33013 X55591

300.9	2127.6	2060.1	2019.0	2844.2	1783.7	2492.6	2315.8	2186.1	1220.7	1355.7
148.6	2636.2	2195.5	1913.3	4972.6	1641.0	2184.2	2339.6	1652.0	1678.0	518.4
185.7	3962.3	3406.5	2841.6	4205.8	3571.4	3576.7	3623.8	2725.6	2232.5	1534.7
394.3	3970.9	3308.1	3441.7	6217.3	3788.7	4140.5	4469.1	4696.8	2481.1	2098.3
114.3	1980.9	1604.0	1334.0	1411.8	1587.9	1698.2	1977.5	1765.1	1274.9	684.4
213.6	2023.2	2010.2	2096.1	3287.0	1804.8	2897.3	2607.9	1889.4	1121.7	936.0
473.3	3881.3	2580.9	1502.6	2466.0	2846.4	2284.1	2150.2	4237.9	2866.2	1036.0
1810.4	2161.9	1477.6	1611.3	2668.6	1708.9	1931.6	2852.7	1589.1	1321.9	892.7
42.1	789.9	579.4	422.8	798.1	511.0	585.8	1213.5	606.5	570.7	117.5
1559.7	1549.1	1265.6	1201.6	2717.3	1287.1	1435.7	1721.3	1306.6	908.3	1059.5
47.1	678.3	522.6	467.0	822.7	640.3	794.2	1349.7	331.3	575.3	85.1
1336.6	2246.4	1780.8	1640.6	2820.6	2302.9	1714.7	3023.0	2256.5	1849.7	1215.4
371.8	1778.9	1725.5	1863.8	2857.9	1890.5	2404.6	2466.3	1558.1	813.8	1112.7
1256.8	7182.1	5233.6	3652.4	5549.6	6018.9	5391.8	4078.4	7784.8	5264.4	2853.9
341.3	1264.4	993.3	964.4	1590.6	1448.6	1577.7	1785.8	817.1	911.3	654.9
118.5	2847.3	2229.4	1815.7	3318.1	2495.5	2343.4	3635.0	2420.1	2032.3	706.6
90.8	1399.3	968.0	672.4	1484.8	740.8	691.0	1524.5	713.7	506.7	170.3
2110.2	3767.9	2742.2	2945.9	4815.6	3117.6	3242.8	4908.7	3341.8	2791.1	1441.2
16526.5	7671.2	6674.1	6222.0	6217.6	6428.6	6032.9	6024.4	6489.8	6856.5	6830.3
1014.2	6160.6	5059.6	3903.7	4827.4	5106.2	4573.3	4448.8	5282.0	5125.4	3075.9
575.2	1413.8	1050.8	821.2	1501.4	977.5	948.9	1522.7	774.0	465.1	311.7
110.7	1364.8	1041.4	973.6	2351.3	1378.1	1315.2	2450.9	867.4	701.6	289.3
196.5	3551.0	3489.8	3405.7	5043.6	3735.3	5161.7	3389.8	2817.0	2970.0	1135.0
2156.7	4124.1	3301.2	3479.3	5197.8	3633.2	3908.4	4972.5	4220.4	3131.6	2097.6
124.5	1790.9	2000.4	1914.6	2475.7	1802.4	2206.7	2762.0	1427.3	1277.6	884.6
40.9	783.6	579.0	551.6	2335.5	765.0	771.1	1529.1	673.6	630.5	168.3
87.6	1025.2	576.6	267.7	437.0	220.2	230.3	407.0	360.4	275.4	89.4
75.4	741.5	390.5	192.7	812.1	388.4	592.1	1174.6	707.8	790.0	86.9
90.9	1305.6	1195.1	852.9	1285.4	1196.1	1238.2	984.2	911.6	1052.5	328.6
61.7	448.0	318.3	161.0	451.6	191.2	323.4	317.1	280.4	266.1	97.2
6184.7	6221.9	5452.2	4945.3	5640.5	4893.5	6066.8	4566.8	6696.1	5752.2	4668.2
142.3	2001.8	1403.4	1376.3	1983.3	1508.5	1597.1	1667.9	2071.9	859.3	693.1
949.9	4758.4	3904.8	4264.2	4865.5	4273.5	5063.0	4420.6	5195.6	4430.3	3018.4
2326.7	2380.0	2249.2	2017.3	3960.0	3288.1	3062.2	2133.3	2789.5	3936.5	2820.2
1702.8	2436.1	1761.7	1739.4	3652.3	2004.0	2196.1	2948.1	2028.0	1528.9	1168.3
153.4	1695.9	1334.9	797.1	1502.1	1354.2	1086.6	1266.9	434.1	472.3	217.7
43.0	42.8	48.6	74.0	247.5	28.9	38.5	30.5	32.5	22.3	36.8
58.3	1944.6	1655.5	1819.1	2415.9	1786.2	1815.9	2523.7	2056.4	2323.0	779.8
83.4	532.1	595.7	414.5	853.0	498.4	807.8	832.7	389.8	280.2	203.0
89.1	1701.6	1445.7	1615.3	2879.0	2039.7	1676.9	2798.5	1085.0	1309.5	393.5
229.2	2457.7	2190.3	2054.2	2474.4	2251.0	2153.7	2711.3	2297.2	1528.0	1288.7

2575.9	3202.5	2840.2
3277.3	2291.0	2575.2
4023.0	2667.3	3237.5
4946.7	3119.9	4689.7
2715.1	1396.3	1656.2
2595.4	1981.3	2077.4
2408.0	2278.2	1571.5
3446.3	1674.8	2833.9
1408.7	362.9	869.0
1727.8	1191.0	1931.5
2045.1	318.1	656.4
3361.3	1642.8	2723.6
2816.2	2046.2	2120.6
4235.4	3666.0	4159.4
3028.8	1054.3	1219.4
4471.0	1605.4	2936.3
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5600.0	2183.9	4310.9
6191.9	5729.5	5606.4
4626.5	4852.7	4155.6
2237.4	941.1	1264.6
3237.7	1155.8	2392.1
4007.1	3524.2	3472.4
5930.0	2983.2	4737.3
2462.1	1378.4	2135.3
1713.1	503.2	1221.7
689.8	309.7	429.6
1612.1	272.3	940.2
1237.0	1126.0	1115.8
470.2	302.4	364.3
4628.0	5848.1	4789.3
2207.6	1390.8	2269.9
5133.7	5350.7	4269.1
1713.4	3206.6	3075.4
3747.0	1720.3	3118.8
1313.1	649.6	965.6
65.0	38.0	26.6
3184.9	1840.6	2260.2
844.2	391.9	1009.4
2990.6	982.2	2724.5
2871.4	2059.1	2193.6

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s__Nocardia brevicatena	37659
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AF544628.1 gg_id:58273 Mycobacterium frederiksbergense VM0503 AF5446
GQ060534.1 gg_id:459926 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw03a03 GQ060
AM056053.1 gg_id:144824 Mycobacterium murale str. MA-168-96 AM056
Z13990.1 gg_id:13102 Mycobacterium ulcerans Z13990
NR_025737.1 gg_id:542205 Mycobacterium canariasense str. 502329; CCUG 47953 NR_02
X88908.1 gg_id:13043 Mycobacterium sp str. IWGMT 90174 X88908
EU379247.1 gg_id:262897 Mycobacterium mucogenicum str. 1RN-2A2 EU379
AF544626.1 gg_id:58276 Mycobacterium austroafricanum VM0452 AF5446
EF516422.1 gg_id:223583 grassland soil clone FCPU460 EF5164
AY208856.1 gg_id:105652 Mycobacterium saskatchewanense str. NRCM 00-250; ATCC BAA-544 AY2088
FJ382177.1 gg_id:577689 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
AJ002094.1 gg_id:140543 Mycobacterium sp str. E4 AJ0020
FJ382252.1 gg_id:533023 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3822
AJ429046.1 gg_id:32216 Mycobacterium pulveris str. DSM 44222T AJ4290
AM749748.1 gg_id:235579 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
FJ382174.1 gg_id:562695 Potentially pathogenic and air stem cell transplant summer hospital shower water BM FJ3821
EU038037.1 gg_id:255004 Episodic subaerial speleogenesis controlled mineralogy microbial colonization and cc EU0380
DQ370008.1 gg_id:151103 Mycobacterium sp. str. czh-8 DQ370
AB065369.1 gg_id:47244 Gordonia alkanivorans AB0653
EU636020.1 gg_id:277895 Antarctic str. 3C6 EU6360
AM778124.1 gg_id:247315 Saxeibacter cremoris str. DLS-10 AM778
FM873571.1 gg_id:359912 occupant source house mattress dust clone MA04B07 FM873
AB212947.1 gg_id:125184 Nocardia abscessus str. IFM 10568 AB2129
GQ376158.1 gg_id:564442 Nocardia alba GQ376
FJ486325.1 gg_id:544517 Nocardia arthritidis str. HBUM173647 FJ4863
AB092569.1 gg_id:77166 Nocardia asiatica str. IFM 0731 AB0925
EU841703.1 gg_id:353472 Streptomyces gardneri str. HBUM174916 EU8417
AM746989.1 gg_id:245443 Nocardia levis str. IMMIB L-100 AM746
AB094647.1 gg_id:105581 Nocardia beijingensis str. IFM 0722 AB0946
AF154129.1 gg_id:13609 Nocardia beijingensis str. AS4.1521T AF1541
AB094650.1 gg_id:100619 Nocardia beijingensis str. IFM 0841 AB0946
AB108779.1 gg_id:105983 Nocardia araoensis str. IFM 0575 AB1087
AB108780.1 gg_id:100721 Nocardia pneumoniae str. IFM 0784 AB1087
AB184754.1 gg_id:154330 Streptomyces gardneri str. NBRC 3385 AB1847
EU099366.1 gg_id:269975 Nocardia blacklockiae str. N-1087 EU0993
X80591.1 gg_id:13642 Nocardia brasiliensis str. ATCC 19296 = CIP 33 X80591
X80600.1 gg_id:13641 Nocardia brevicatena str. ATCC 15333 = CIP 17 X80600
U92800.1 gg_id:13616 Nocardia crassostreae str. OB3 U92800
AB094576.1 gg_id:105747 Nocardia cyriacigeorgica str. IFM 0875 AB0945
DQ235272.1 gg_id:142538 Nocardia gamkensis str. CZH20 DQ235
GU233955.1 gg_id:567015 Nocardia exalbida str. X0078 GU233

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2443.3	5403.0	4060.7	4260.7	5474.1	4593.1	5034.7	5131.8	5717.3	3669.1	4005.1
120.4	1445.0	1349.1	843.6	1871.9	1374.7	960.0	1567.2	1293.6	1054.0	255.4
79.9	2595.5	2000.4	1414.1	2989.0	2229.3	1909.0	2290.3	2027.2	1546.5	752.9
22.9	1543.9	1103.4	1133.5	2137.7	1402.6	1221.8	1903.1	766.1	798.4	270.0
33.0	568.0	463.7	380.1	1028.6	633.7	579.6	946.7	252.1	263.5	94.2
1292.9	9750.4	6996.1	5584.7	8641.8	8343.9	6794.2	5974.4	10178.1	5198.2	3259.0
6201.8	3511.8	3233.8	3251.3	5671.1	3320.2	3507.2	4348.4	4183.5	3135.7	3808.5
3226.4	2253.8	1883.0	1981.1	3843.6	1896.4	2173.5	2617.2	1913.0	1423.5	1014.6
129.1	1148.7	992.2	766.4	1723.5	840.4	1327.3	1516.2	866.4	708.8	253.9
173.5	2536.3	2351.8	1917.1	4161.6	2802.0	3167.4	2968.4	1716.1	1710.6	868.4
762.4	4616.3	3412.3	3207.7	5332.7	3548.8	4781.2	4692.1	4637.5	2744.3	1987.0
89.2	2449.0	2175.6	2221.3	3833.0	2350.3	3062.4	3474.1	2011.5	1525.2	725.8
91.5	1974.7	1859.6	1795.4	2593.9	1823.3	2689.8	2981.9	2179.4	2078.7	659.7
83.7	2153.4	1579.1	1329.4	3625.8	1875.6	1973.2	3200.0	1655.1	1834.3	323.8
1448.7	3964.5	3195.9	3233.0	5599.3	3380.4	4655.0	3258.4	2488.9	1631.8	1223.6
2509.7	3291.3	2727.0	3012.8	4860.3	3056.4	3848.2	4290.6	2915.2	2383.5	2015.2
509.5	4099.8	3261.8	3268.4	5782.9	4087.9	3529.1	6030.5	4084.5	3540.4	1244.8
14704.4	10854.9	10499.8	12480.6	12477.3	10785.3	12608.0	9145.3	9998.5	5807.5	12425.2
44.4	93.1	56.6	174.7	3390.9	196.1	1683.9	31.0	35.5	24.7	37.5
158.8	6066.8	5168.1	3615.6	4495.4	4950.5	4693.0	3655.9	6270.6	5324.2	2044.5
349.6	1517.7	1324.4	1461.0	2663.9	1429.3	2292.1	1602.3	1693.1	904.1	489.9
93.8	2457.1	2453.0	1635.6	3731.8	2575.5	2783.7	2481.4	1968.4	1810.4	862.3
99.4	1958.1	1821.9	921.2	3022.2	1626.4	2763.7	1133.3	1340.9	1360.4	521.9
172.5	2064.3	2032.6	1235.4	2927.9	1879.6	2310.9	1615.5	2108.5	1323.3	710.1
107.4	2486.4	2445.6	1432.3	4251.4	2462.9	2565.9	2067.4	2042.5	1427.2	1042.3
118.7	2611.4	2510.1	1765.8	3672.1	2557.4	2742.0	2482.6	2344.8	1904.3	737.9
171.2	6618.8	5594.0	4045.7	5527.4	6379.9	4591.4	4831.9	7507.5	7291.0	3154.6
127.5	3131.7	3230.6	2138.9	5059.9	3076.0	3379.0	2908.9	2971.1	2199.2	1467.4
7997.5	7115.1	6821.8	6648.9	8015.1	6308.3	7319.4	6700.1	9042.8	7492.4	7127.8
152.7	2802.0	2502.2	1845.7	4766.5	2956.2	2946.2	2762.5	2069.6	1747.9	1093.9
112.6	2513.9	2425.0	1713.1	3555.1	2468.4	2797.1	2442.8	2459.9	1899.0	840.7
187.7	4804.6	4252.2	2967.3	5878.6	4657.7	4675.5	3914.3	4448.3	3478.4	2046.1
288.0	4273.9	3878.0	3016.5	5351.8	4005.5	4720.7	3567.3	3376.2	2569.3	2440.9
184.9	2536.5	2522.0	1478.7	2898.0	2453.7	2182.5	1941.9	2900.2	2026.8	736.4
98.4	2056.1	1983.5	1546.9	3817.0	2043.9	2616.9	2007.4	1652.1	1140.3	674.2
379.2	3138.1	2646.5	2923.3	5791.3	3013.4	4156.8	3146.1	1732.0	1502.6	1880.6
44.4	1379.5	1596.4	1666.9	3794.2	2331.5	4847.4	2146.4	1395.9	551.0	617.8
38.2	377.5	358.7	262.2	1834.4	388.2	459.3	633.5	213.8	197.0	70.3
142.6	3615.8	3058.3	2016.3	4411.8	3720.3	2989.4	3218.1	3252.9	2645.1	992.6
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4745.0	2836.7	3653.2
3246.3	2330.2	2306.3
1694.3	666.6	1700.1
3822.9	2207.8	3128.8
4798.2	3645.3	4727.6
3977.3	1890.8	2997.7
4218.4	2260.0	3080.7
4106.3	1012.5	2627.0
3903.6	3450.2	4549.0
5066.3	2267.9	3604.0
7153.4	2227.5	5447.8
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79.6	70.8	41.2
3689.3	2975.0	2785.6
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3212.8	1540.8	2480.2
1768.7	1042.7	1323.9
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2739.2	1147.3	2194.5
3523.0	1623.2	2802.8
5076.8	4648.6	3919.0
3704.6	2041.0	3319.1
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3899.5	1526.6	2965.5
3510.9	1681.9	2739.1
5025.2	2962.9	4285.0
4566.9	2711.9	3885.7
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GQ376168.1 gg_id:574445 Nocardia flavorosea
AB121769.1 gg_id:104292 Nocardia testacea str. IFM 0937
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EU593589.1 gg_id:258879 Nocardia fluminea str. 173590
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EU570345.1 gg_id:268872 Nocardia salmonicida str. 173685
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AF277208.1 gg_id:49884 Nocardia sp. str. R112
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AB092561.1 gg_id:84206 Nocardia yamanashiensis str. IFM 0265
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DQ659909.1 gg_id:163931 Nocardia kruczakiae str. ATCC BAA-948
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AB092565.1 gg_id:84353 Nocardia niigatensis str. IFM 0833
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AF430042.1 gg_id:81200 Nocardia pseudobrasiliensis str. DSM 44290
EU371110.1 gg_id:275795 Nocardia puris str. 36173618/Athens/07
GQ217500.1 gg_id:577313 Nocardia puris
AB108776.1 gg_id:91450 Nocardia shimofusensis str. YZ-107
EU158361.1 gg_id:247795 Nocardia sp. str. HBUM 49423
DQ840025.1 gg_id:188084 Nocardia takedensis str. WE30
EU543223.1 gg_id:275430 Nocardia tenerifensis str. CS682
Z46752.1 gg_id:13637 Nocardia uniformis str. JCM 3224
GQ853071.1 gg_id:568053 Nocardia vaccinii str. W7669
X80597.1 gg_id:13628 Nocardia vaccinii str. ATCC 11092 = CIP 17
AF278572.1 gg_id:24358 Nocardia veterana str. M157222; DSM 44445T
AF430055.1 gg_id:82356 Nocardia veterana str. DSM 44445
DQ659919.1 gg_id:171531 Nocardia vinacea str. JCM 10988
AF421564.1 gg_id:63690 Nocardia sp. str. 99-08-244A
EU099363.1 gg_id:264854 Nocardia wallacei str. N-140
Z82229.1 gg_id:25190 Nocardia asteroides str. ATCC 49872

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EU099
Z82229

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184.2	2152.9	1707.6	1179.4	2222.7	1774.8	2246.5	1132.7	869.8	965.1	479.1
184.3	2297.0	1609.5	1201.1	2624.2	1880.0	2183.4	1244.9	885.8	980.1	488.0
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140.5	967.1	859.6	705.6	1379.3	887.4	1275.1	693.2	612.0	457.0	283.4
229.5	1470.9	1254.2	1061.6	1891.2	1216.1	1617.7	1080.4	1346.7	897.1	427.1
67.5	1097.0	1096.2	986.5	1810.2	1109.3	1448.5	1288.3	670.2	464.8	642.6
418.5	1953.2	2278.6	1613.5	2386.6	1633.5	1830.7	1882.6	2147.2	1443.0	2022.4
124.8	2276.4	1410.7	1221.4	2587.5	1664.8	1897.2	1469.0	603.9	751.3	593.2
94.8	1577.9	1440.2	1612.4	2370.0	1625.5	2062.6	1504.8	679.6	332.9	1082.0
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2017.5	3707.8	3477.0	3602.8	4626.6	3267.2	4977.6	3533.8	2938.0	1856.3	2591.9
49.5	520.8	501.4	520.7	2009.0	763.6	719.7	990.1	322.2	365.3	83.7
18881.1	8723.3	8084.7	8614.1	9123.1	8374.5	9029.0	8070.1	10695.5	10402.2	12242.3
33.3	393.2	259.2	296.5	1482.2	284.5	481.8	306.6	189.2	82.3	83.3
85.4	1487.4	1131.8	792.3	2442.4	1144.1	1486.4	967.3	541.4	453.2	197.4
43.5	354.5	323.9	265.8	743.0	310.4	288.2	639.7	219.6	179.4	175.1
46.3	431.7	392.4	317.8	1250.3	381.4	356.6	765.0	235.8	205.3	196.3
43.8	217.2	681.5	433.7	294.7	208.4	616.5	658.6	111.8	117.2	433.0
71.2	2780.6	1724.7	991.3	2873.5	2152.9	2181.4	1241.1	643.2	957.4	320.9
400.5	2425.6	2248.6	2363.9	4925.7	2352.0	3362.5	2776.4	1944.3	1537.5	1226.6
207.4	1918.9	1859.5	2007.3	4221.7	2029.7	2902.7	2310.9	1272.0	1062.2	1019.0
144.1	1473.9	1114.6	1202.0	3306.5	1401.5	1721.3	1549.7	716.3	832.9	563.6
5048.2	9762.2	7601.3	5242.6	7245.4	8366.9	6849.1	5488.9	8507.1	8555.4	6152.3
156.9	3826.5	2801.5	2028.5	4339.2	3200.3	3203.9	2416.6	1772.2	2033.5	1361.1
68.0	552.2	535.3	552.5	3350.1	616.4	1005.4	783.0	312.1	321.4	213.4
77.3	1832.3	1191.1	1330.3	4571.1	1747.5	1779.1	1847.1	726.0	604.8	793.9
110.5	3355.3	3195.5	1851.6	4194.0	3297.2	3564.2	3016.5	3112.8	2386.0	1338.5
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63.8	1504.6	1370.0	829.1	1905.2	1401.3	1250.2	1153.5	1301.1	1006.4	501.3
3481.4	5642.2	4865.7	3665.1	6556.3	4134.6	6211.6	3418.8	4289.4	3171.8	3466.3
488.0	2771.6	3116.7	3719.9	4786.3	3008.9	4202.3	3072.6	3072.5	3600.9	3405.3
70.5	1091.9	770.7	563.2	1887.1	913.7	869.7	725.1	263.9	434.9	177.1
62.0	1033.3	814.9	884.7	2370.8	1003.3	1170.4	977.9	410.1	385.0	480.0
34.7	214.9	132.0	156.0	752.5	173.6	265.9	137.9	64.1	84.3	40.2
60.5	212.7	129.2	143.4	773.1	153.9	249.4	123.5	70.0	70.7	47.7
39.1	996.0	935.1	873.7	3061.4	997.5	1253.3	1092.6	402.1	400.9	279.8
70.0	186.4	364.3	147.0	167.4	147.8	192.2	147.4	97.6	66.9	182.0
107.9	2337.5	2227.6	1191.5	2275.9	1977.8	2287.0	2234.3	2249.6	1567.7	947.6
82.0	2449.8	2203.8	1365.8	2983.8	2181.9	2650.9	2396.3	2161.9	1618.9	1084.1

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8080.7	7196.9	7591.9
1348.7	796.1	1498.2
1377.3	847.2	1616.8
3599.4	5053.6	4280.0
711.0	467.3	1037.3
1040.9	684.7	1543.6
1690.9	672.5	1036.9
1934.2	1555.4	1695.4
2166.5	879.5	1216.8
1940.7	1568.6	2236.0
6068.4	6045.3	4763.7
3555.9	2575.2	4963.1
1786.2	527.7	1221.8
8375.1	9225.7	8659.3
627.3	215.9	333.4
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576.4	269.7	537.4
714.0	301.1	711.8
428.5	204.8	557.4
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6890.6	3895.0	5519.3
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8083.1	5917.4	7279.9
1588.1	784.5	1373.2
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3296.3	3821.4	3982.3
1382.4	628.4	813.3
1583.1	737.6	1086.1
367.9	149.9	166.5
294.3	128.5	95.9
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AB086862.1 gg_id:111699 Nocardia pseudobrasiliensis str. IFM 10099
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AJ854058.1 gg_id:108814 Nocardia elegans str. IMMIB N-403
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AF277203.1 gg_id:22063 Nocardia sp. str. S24
AF277223.1 gg_id:40439 Nocardia soli str. W30
AF277212.1 gg_id:45989 Nocardia sp. str. R18
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AB084448.1 gg_id:92185 Nocardia transvalensis str. IFM 10065
DQ282122.1 gg_id:146790 Nocardia harenosa str. WS-26
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X80609.1 gg_id:13639 Nocardia transvalensis str. DSM43405
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GQ342300.1 gg_id:537110 Nocardia farcinica str. CG-T7
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AB084445.1 gg_id:92117 Nocardia transvalensis str. IFM 0505
AB192415.1 gg_id:107342 Nocardia testacea str. JCM 12235

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AB1924

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96.2	1632.1	1280.5	896.1	3691.9	1340.7	2606.0	1080.6	690.2	800.6	270.1
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160.1	4758.1	3237.5	1877.3	6524.3	2989.3	4217.1	1959.2	2387.7	2242.9	941.7
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109.0	1306.7	1658.1	1438.3	1681.6	1105.2	1565.9	1714.4	643.7	871.1	1046.0
163.9	4064.5	3180.5	2167.4	5368.6	3305.7	3249.5	3104.7	3285.9	2172.5	1546.6
232.1	1377.1	1131.2	948.0	1709.1	1081.6	1427.0	984.9	1304.2	816.6	392.4
99.5	2463.7	1605.4	1220.2	2540.8	1879.6	2257.8	1360.9	788.5	698.2	620.9
122.5	680.6	536.4	603.9	2600.6	820.0	940.4	930.9	499.3	618.5	200.0
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92.8	1752.3	1339.8	377.2	1466.2	1464.1	1415.0	1319.8	1903.8	1668.1	285.7
40.3	1023.7	1100.4	789.7	2412.3	1152.6	1132.6	1191.0	819.3	646.0	246.5
6699.7	4310.8	4006.8	2548.4	2672.1	3919.8	3713.9	2495.5	4855.9	3934.4	3523.0
39.1	321.1	417.9	366.3	872.4	369.0	394.6	436.0	142.1	161.2	223.0
80.5	1841.2	1821.3	2202.4	2665.8	1679.3	3141.7	1605.1	858.6	635.7	1262.5
78.2	719.8	874.6	749.6	1565.4	871.3	1150.9	858.3	535.2	396.6	367.7
424.7	2151.6	2216.4	1521.3	1760.2	1560.4	1876.9	1824.9	1922.8	1377.3	2011.0
180.7	6636.9	5594.0	4071.4	6045.9	6401.7	4331.3	4876.1	7532.8	7300.3	3159.3
123.5	904.7	982.7	825.6	1781.2	807.9	1874.2	557.3	403.3	322.5	207.4
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GQ853075.1 gg_id:564909 Nocardia pneumoniae str. W9813
AF430026.1 gg_id:82420 Nocardia asteroides str. DSM 43255
EU570347.1 gg_id:276772 Nocardia cummidelens str. 173638
Z36927.1 gg_id:13632 Nocardia vaccinii str. DSM 43285()
Z82228.1 gg_id:29160 Nocardia asteroides str. N488
EF418604.1 gg_id:214714 Nocardia rhamnosiphila str. 202GMO
Z36936.1 gg_id:13619 Nocardia farcinica str. M. Goodfel N898/ATCC 3318(typ
GQ376184.1 gg_id:566916 Nocardia speluncae
EF546424.1 gg_id:223911 Nocardia sp. str. 171842
GU367176.1 gg_id:545904 Nocardia sp. str. YIM 65653
FN396974.1 gg_id:388434 Nocardia asteroides str. E2
X80598.1 gg_id:13602 Nocardia transvalensis str. ATCC 6865 = CIP 175
Z82227.1 gg_id:40151 Nocardia asteroides str. N450
AB092437.1 gg_id:58653 Nocardia sp. YU011-1
Z82235.1 gg_id:43592 Nocardia transvalensis str. N1080
AY036053.1 gg_id:36906 Nocardia novocastrensa str. N1251
AY846841.1 gg_id:110249 Nocardia seriolae str. H031016
Z82240.1 gg_id:34077 Nocardia transvalensis str. N630
X91041.1 gg_id:13610 Nocardia farcinica str. GD1
AF430035.1 gg_id:81484 Nocardia carnea str. DSM 43397
AF430046.1 gg_id:82429 Nocardia pseudovaccinii str. DSM 43406
AY944254.1 gg_id:114480 Actinomycetales N28
AF430025.1 gg_id:81174 Nocardia asteroides str. DSM 43258
AF430068.1 gg_id:81683 Nocardia otitidiscaviarum str. S639
EU841601.1 gg_id:311616 Nocardia cummidelens str. HBUM174846
EF513204.1 gg_id:220410 Nocardia seriolae str. N628-1
AF430058.1 gg_id:82175 Nocardia sp. str. DSM 43399
FJ938341.1 gg_id:577298 Nocardia sp. str. FXJ1.334
DQ840028.1 gg_id:190165 Nocardia nova str. SH22a
AF302232.1 gg_id:40966 Nocardia africana str. SD880
GU391496.1 gg_id:564286 Rhodococcus baikonurensis str. Pc4T
AJ306402.1 gg_id:43835 Rhodococcus coprophilus orange NZRM 4028
EU834262.1 gg_id:349708 Rhodococcus equi str. DS41
X82052.1 gg_id:13588 Rhodococcus equi str. ATCC 7005T
DQ157910.1 gg_id:551777 Rhodococcus equi str. CUB 1196
X80613.1 gg_id:13594 Rhodococcus equi str. DSM43199
DQ150572.1 gg_id:565317 Rhodococcus equi str. ATCC 333702
X80594.1 gg_id:13591 Rhodococcus equi str. ATCC 33707 = CIP 1784.88
DQ157911.1 gg_id:552780 Rhodococcus equi str. CUB 1258

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DQ150
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DQ157

18032.1	6567.7	5919.9	6409.2	7564.3	6127.3	6955.1	5832.3	9345.7	6866.6	9347.7
10996.0	9290.8	6943.3	7767.8	9303.6	8934.2	8804.9	8354.0	8113.6	6625.7	9484.8
331.2	4890.0	4234.2	3655.9	6684.0	4708.2	5255.9	4402.3	3754.2	3081.4	2707.9
68.4	1706.8	1152.2	643.2	1416.2	1105.8	1101.3	892.2	367.3	542.9	348.6
41.8	438.6	584.0	432.3	1087.3	558.7	510.5	670.5	195.9	210.0	188.1
195.3	4123.3	2909.3	2420.0	5553.9	3415.7	3564.3	2590.6	1214.5	1516.1	1180.1
138.4	3941.4	3779.8	2825.8	6082.4	3893.3	4350.7	3460.0	2588.8	2201.9	1918.5
152.3	3495.7	2188.5	1387.2	4124.6	1824.3	2444.9	1718.0	1715.1	1346.8	487.7
12281.3	5800.6	6406.5	5933.6	6169.4	5788.4	9190.8	4824.4	7105.9	5842.4	6695.8
204.5	1996.5	1566.9	1334.2	3263.1	1555.5	2842.9	1324.5	1371.9	867.4	576.0
37.6	308.0	251.0	209.5	617.8	263.3	276.7	299.6	141.3	125.3	98.0
99.8	2291.4	1715.3	1035.8	4293.2	1794.6	3271.9	1169.0	880.2	1107.4	450.5
63.9	1117.7	868.6	617.6	1663.0	948.4	955.3	730.7	303.0	373.6	198.0
60.7	1062.5	1003.2	556.9	3484.4	1374.5	1785.7	1119.4	1169.5	628.0	422.8
97.5	2377.7	2212.7	1497.9	3464.1	2454.6	2480.6	2480.8	2042.3	1392.6	793.3
353.5	3362.5	2756.4	2081.7	3675.7	3080.6	3479.9	2042.7	3776.2	2523.5	1106.1
114.2	1804.4	1796.6	1177.8	2413.0	1885.3	2047.4	1567.3	1526.1	954.9	841.0
74.5	1663.1	1625.1	1262.0	3445.6	1723.6	2201.2	1776.3	1149.3	907.7	470.5
142.1	926.6	1098.4	1142.0	1992.4	1046.4	2063.3	1118.5	836.2	815.1	603.0
127.4	1326.4	1166.5	788.1	1831.9	1364.7	1587.6	1171.5	1446.6	1273.6	525.7
137.5	2617.1	2535.9	1518.1	3258.2	2494.9	3253.8	2058.8	2146.8	1585.4	800.6
174.0	2066.7	1591.9	1147.8	2051.8	1648.7	2051.6	1122.9	892.7	952.7	446.6
59.0	1184.8	805.1	542.2	1797.4	941.6	832.2	724.5	299.2	476.3	181.9
58.2	1296.6	1157.1	1110.9	1929.4	1341.4	1522.5	1688.7	864.2	594.2	824.8
81.0	1097.3	797.3	686.7	2053.3	944.8	918.1	1198.7	361.2	476.1	308.1
33.8	347.6	238.3	255.1	758.9	314.2	370.3	286.0	176.7	54.4	63.7
76.4	1182.0	1175.2	1092.1	2416.9	1210.3	1544.0	1487.8	708.6	496.6	653.8
311.9	2502.1	2635.8	2337.8	3401.7	2689.0	3098.2	2066.9	3588.3	2805.8	1502.9
202.4	1872.3	2295.8	2394.1	4541.6	2153.5	2990.2	2670.5	1587.1	1706.8	1019.1
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119.0	2167.4	1354.7	1268.6	2838.8	1809.9	2012.2	1470.8	587.9	744.9	579.0
700.2	4320.5	3281.6	3271.7	5075.4	3522.0	3890.1	3433.2	4232.0	2161.6	2475.0
70.8	1453.3	2209.7	1587.2	2767.9	2532.0	2142.4	2298.6	2430.4	2132.4	415.0
226.4	1805.9	1459.7	1354.7	2777.7	1440.2	2139.6	1851.0	1531.7	1205.0	559.0
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117.1	1233.1	1053.9	1369.0	1276.9	1076.0	1511.2	1341.7	793.4	493.9	748.6
161.5	2632.5	1912.6	1505.4	3241.8	2080.8	2436.5	2205.7	1514.0	1437.1	631.6
222.5	2926.8	2337.8	1876.7	3679.1	2458.1	2948.3	2554.8	1770.2	1806.4	902.9
1298.5	2719.7	2189.1	2133.4	3241.1	2314.4	3063.0	2474.9	2527.2	1752.3	1510.5
175.1	1941.0	1638.6	1395.6	2843.3	1674.1	2179.5	1981.9	1589.6	1256.3	705.9

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7327.1	8663.0	7218.6
5621.5	3440.5	4853.0
1342.8	630.6	861.6
893.0	689.4	696.2
3930.8	1829.8	2425.8
4404.4	2447.1	3841.5
2103.9	1134.7	2648.2
4838.2	5706.4	7548.8
1880.7	959.6	2037.8
524.8	211.0	521.3
1954.9	948.5	1325.8
1280.2	701.4	1100.1
1087.5	574.8	1116.5
3324.8	1334.6	2545.8
2166.9	2337.6	2091.7
2108.0	794.8	1162.5
2291.4	1309.2	2047.8
1259.7	1045.1	1151.3
1265.3	697.6	1009.9
2341.7	976.0	2757.5
1285.1	715.3	1357.3
1594.9	524.2	791.9
1885.3	837.4	1689.5
1367.2	594.7	1226.7
664.9	272.5	298.5
1973.0	741.0	1229.6
2857.9	2330.4	2321.2
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1689.7	1902.6	2722.9
3212.8	2160.2	3183.8
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4357.3	2824.5	3519.5
3388.6	1818.2	1488.8
2493.0	1132.8	1880.0
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1171.8	1806.3	1621.2
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GQ249216.1 gg_id:512720 Rhodococcus sp. str. lxb-6
AJ576249.1 gg_id:89578 Rhodococcus fascians 7Y
AY953293.1 gg_id:114528 Rhodococcus sp. D2
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AB070458.1 gg_id:65243 Rhodococcus sp. str. YK2
X81930.1 gg_id:13587 Rhodococcus fascians str. ATCC 12974T
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AB269261.1 gg_id:237018 Rhodococcus kyotonensis str. DS472
AY188941.1 gg_id:80394 Rhodococcus sp. str. P_wp0233
AY745830.1 gg_id:108610 Rhodococcus sp. str. JL-60
AM111053.1 gg_id:140872 Rhodococcus sp. str. 7315
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AM236239.1 gg_id:152649 Rhodococcus sp. AM6
DQ462183.1 gg_id:157032 Rhodococcus sp. FW72
AY745831.1 gg_id:108611 Rhodococcus sp. str. NPO-JL-61
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EU004419.1 gg_id:238571 Rhodococcus rhodochrous AK40
AB214866.1 gg_id:131121 Rhodococcus sp. str. ED7
AB271142.1 gg_id:168442 Rhodococcus rhodochrous str. SF
AB210983.1 gg_id:115223 Rhodococcus rhodochrous str. SSCT49
FJ887962.1 gg_id:559942 Rhodococcus sp. str. 3HYL
EF581125.1 gg_id:298153 Rhodococcus ruber str. R6
AY247275.1 gg_id:85556 Rhodococcus ruber str. M2
AF447392.1 gg_id:67231 Rhodococcus aetherivorans str. Bc663
AF529079.1 gg_id:60987 Rhodococcus sp
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AY566576.1 gg_id:108725 Rhodococcus erythropolis str. PG-03
GQ871747.1 gg_id:578319 Rhodococcus sp. str. SCSIO 00026
DQ279384.1 gg_id:141198 Rhodococcus sp. TM14_1
FN555393.1 gg_id:584450 Rhodococcus qingshengii 79049-3
DQ000156.1 gg_id:118995 Rhodococcus erythropolis 3C-9
AJ250927.1 gg_id:40386 Rhodococcus erythropolis str. Y2

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3658.9	1935.0	1519.0	1842.4	3495.9	2172.3	2179.2	2178.5	1102.6	1282.5	1557.1
146.7	2164.3	1852.4	1997.1	4976.8	2127.7	2545.4	2338.7	1348.7	1038.9	974.5
184.2	2055.9	2336.5	1939.4	2352.3	2405.0	1863.6	2202.4	3770.8	1545.3	1130.1
391.1	4343.4	4149.8	4921.8	5692.9	4881.7	4987.1	5027.1	4126.7	3284.1	4429.5
868.9	6182.2	6265.2	5902.3	5960.6	6698.4	5832.5	5709.1	7146.0	4813.0	6347.5
128.6	1561.4	2001.8	1613.8	1920.5	2085.5	1559.2	1718.6	3026.9	1125.4	930.6
150.1	1723.3	1242.2	1026.6	2136.4	1153.5	1157.5	1113.4	1561.7	784.2	418.3
346.2	2832.3	2730.1	2581.0	2932.1	2824.7	2654.4	2505.6	3391.8	1506.2	1446.2
130.7	465.7	355.6	433.5	1711.6	471.9	602.1	492.1	103.0	419.1	90.0
168.6	1644.7	2113.4	1671.7	2031.4	2103.8	1568.2	1795.4	3602.9	1407.0	1002.4
172.7	2120.6	1447.0	1243.6	2412.6	1421.9	1439.7	1491.4	2004.8	917.8	516.7
711.9	2065.8	2019.0	2078.1	2768.9	2084.3	2594.7	1729.4	2663.4	2125.3	1659.7
177.9	2039.3	1544.6	1348.1	2548.2	1492.0	1548.4	1575.5	1871.5	928.4	542.1
195.5	2110.6	2405.3	1978.7	2458.7	2449.6	1959.2	2240.6	4105.1	1558.4	1105.4
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329.2	2527.8	2526.4	2392.4	3438.3	2618.3	3249.9	2090.6	1931.6	1132.5	914.9
32.2	140.3	62.7	76.1	247.0	149.1	102.6	26.5	29.2	95.8	22.9
438.6	4312.3	2887.0	2655.1	3228.2	2816.7	3106.5	2519.0	4228.4	2103.9	1977.6
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107.3	1634.0	1693.4	1442.8	1657.2	1655.3	1410.4	1762.8	1773.3	1164.0	898.6
620.4	1656.5	1714.5	1863.1	3061.8	1716.3	2896.4	2888.5	2033.2	1323.8	780.7
110.1	1797.8	1947.7	1627.4	2665.7	1965.6	1950.5	1689.9	953.4	776.4	769.3
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492.1	2680.5	2541.0	2327.9	1699.0	2963.8	2373.6	1949.7	2959.8	2914.1	1546.0
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543.4	3690.4	3071.3	2878.4	2160.9	3652.7	2651.2	2858.5	4736.8	3389.7	2438.7
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418.7	1791.1	1584.3	1403.8	1968.5	1567.7	1454.9	1675.7	1179.2	921.7	831.2
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733.5	2849.4	2622.4	2114.0	3838.2	2421.7	2427.8	2907.5	2805.9	1829.6	831.9
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1060.5	2662.3	2468.7	2134.5	2986.6	2673.3	2987.9	2435.0	1955.3	1378.0	1548.7
217.3	666.2	568.0	576.7	1216.6	571.0	714.4	787.0	690.3	539.3	175.0
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2077.9	1711.3	1160.5
226.6	45.5	80.2
2325.0	3113.2	2759.3
3677.6	1559.8	1736.5
2976.4	667.7	1029.8
5812.4	6322.6	5910.9
6406.1	5765.4	5360.6
1283.9	825.3	1022.2
10075.1	8568.1	8651.4
3697.4	2385.8	3044.8
635.2	369.7	188.8
3551.9	1502.2	2118.5
3837.9	2272.7	2808.7
2121.1	891.0	1427.5
2080.8	1178.0	1610.5
3499.9	1006.1	1358.1
2194.3	797.8	1803.4
3187.2	1670.6	3200.0
3284.6	785.0	1274.9
1609.9	1761.0	2422.8
3507.7	1999.6	3516.5
1124.6	397.2	739.4
2721.4	1452.7	3015.7
4057.5	4093.7	4765.3
2535.2	1472.3	1893.7
5007.5	3525.6	4258.7
3390.0	3252.1	3742.1
2953.1	1112.9	1747.6
843.0	297.5	613.5
3783.1	955.3	1473.8
4971.2	3411.7	3420.4
3244.2	2245.7	3760.7
391.4	85.1	156.1
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s__Aeromicrobium fastidiosum	38518
s__Aeromicrobium fastidiosum	39922
s__Aeromicrobium marinum	38950
s__Aeromicrobium marinum	40018

AF191343.1 gg_id:13510 Rhodococcus zopfii str. DSM 44108 (T) AF1913
X89240.1 gg_id:13540 Rhodococcus sp str. DN-22 X89240
AY785747.1 gg_id:108234 Rhodococcus erythreus OUCZ108 AY7857
AB044557.1 gg_id:42265 Rhodococcus sp. str. PN1 AB0445
EU741153.1 gg_id:566894 Rhodococcus erythropolis str. 13648E EU7411
EU439411.1 gg_id:263816 Rhodococcus sp. str. DB-13 EU4394
DQ316785.1 gg_id:147296 Rhodococcus sp. str. P7 DQ316
EF635425.1 gg_id:238235 Rhodococcus sp. str. NJUST16 EF6354
EF690428.1 gg_id:257679 Rhodococcus erythropolis M14-4 EF6904
NR_025190.1 gg_id:567592 Rhodococcus maanshanensis str. M712; JCM 11374 NR_025
AB098592.1 gg_id:77648 Rhodococcus sp. str. TUT1024 AB0985
AJ250928.1 gg_id:30786 Rhodococcus erythropolis str. NCIMB13064 AJ2509
FJ675432.1 gg_id:530516 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
DQ985073.1 gg_id:179775 Rhodococcus sp. str. JL1088 DQ985
DQ167401.1 gg_id:138846 Rhodococcus erythropolis str. DS-3 DQ167
AJ576250.1 gg_id:88661 Rhodococcus erythropolis MR32W AJ5762
DQ864513.1 gg_id:166898 Rhodococcus erythropolis DQ864
AM403230.1 gg_id:170062 Rhodococcus sp. D11-33.1 AM403
AF409012.1 gg_id:103057 Rhodococcus sp. str. Ellin170 AF4090
AY090021.1 gg_id:55435 Rhodococcus sp. str. PNAN 5 AY0900
AJ716151.1 gg_id:129637 Rhodococcus erythropolis str. AJ300 AJ7161
AJ250925.1 gg_id:21646 Rhodococcus erythropolis str. m15-3 AJ2509
AJ490526.1 gg_id:59505 Rhodococcus erythropolis str. AJ270 AJ4905
DQ397663.1 gg_id:168347 Rhodococcus erythropolis str. Z6 DQ397
DQ855406.1 gg_id:166727 Rhodococcus erythropolis str. T7-2 DQ855
AJ250929.1 gg_id:37773 Rhodococcus erythropolis str. GJ70 AJ2509
AF227864.1 gg_id:73846 Nocardia sp. str. 86349 AF2278
FJ671924.1 gg_id:523421 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
NR_028629.1 gg_id:546404 Rhodococcus tukisamuensis str. Mb8; JCM 11308 NR_028
DQ070478.1 gg_id:132913 Skermania piniformis str. J8 DQ070
AJ416152.1 gg_id:46901 Skermania piniformis str. DSM 43998T AJ4161
GQ060459.1 gg_id:409497 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw01f08c GQ060
AB243007.1 gg_id:141953 Nocardia sp. str. Hou_blue (= MBIC06267) AB2430
DQ997045.1 gg_id:190184 Rhodococcus kunmingensis str. YIM 45607 DQ997
NR_025086.1 gg_id:538164 Actinopolymorpha singaporensis str. IM 7744; JCM 10761 NR_025
AB535715.1 gg_id:525694 Thermasporomyces composti str. JCM 16421 AB5357
EU706350.1 gg_id:340457 Actinopolymorpha sp. str. YIM 48868 EU7063
AY571805.1 gg_id:101043 Nocardioides sp. 43/14 AY5718
Z78209.1 gg_id:12756 Aeromicrobium fastidiosum str. DSM 10552T Z78209
AY166703.1 gg_id:84596 Aeromicrobium marinum str. T2 AY1667
EU834249.1 gg_id:321721 Aeromicrobium kwangyangensis str. DS23 EU8342

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1355.2	6075.5	7009.8	3172.5	3082.0	5038.6	2713.0	5289.6	8837.3	8700.3	4682.4
1670.3	6228.1	6022.7	4530.9	6953.4	5631.4	5427.2	6240.2	7282.5	5704.4	2946.0
1031.9	1872.6	2292.7	2066.5	2534.1	2023.1	2149.4	2158.3	1621.1	1917.0	1378.8
868.0	2678.7	2250.6	1919.1	3556.5	2264.6	1987.6	2569.2	2064.1	2266.4	789.2
234.5	1242.7	1158.4	1375.2	2745.9	1215.9	2049.3	2016.2	1509.1	699.5	610.7
1311.4	3222.6	3068.3	2824.8	3655.4	3062.2	3712.6	2818.6	2632.9	1640.2	1966.7
953.4	5930.7	4900.7	3731.6	4920.2	5396.5	4850.6	4637.5	7030.7	5207.5	2796.4
3459.0	7303.0	6794.1	6139.0	6616.1	6813.1	6687.1	6909.6	8706.0	6506.8	5864.5
108.0	1052.5	1054.5	728.4	1864.5	939.3	767.4	1108.5	894.0	657.7	222.1
115.2	1973.1	2200.3	1398.2	2221.9	2070.7	1860.9	1380.3	1613.3	1566.2	520.3
238.7	1414.6	1315.9	1196.2	2190.7	1441.0	1394.2	1664.1	1909.8	1107.2	601.5
19955.8	8680.3	7096.3	6704.5	6950.7	7976.3	7430.7	6086.0	12847.0	8068.1	11511.3
180.4	837.0	923.8	810.8	2158.1	964.4	1308.2	895.8	358.6	469.0	187.9
722.9	2679.6	2085.1	2787.3	4524.9	2345.0	3088.7	3021.1	2086.8	1542.8	1238.2
216.1	891.6	740.3	725.1	1300.2	673.9	754.4	874.4	776.1	604.0	251.6
403.8	1373.0	1151.1	1207.1	2173.2	1207.1	1544.0	1627.9	1261.7	828.8	627.0
96.0	1546.8	1152.1	1167.0	2727.2	2045.6	1130.3	1687.3	1565.4	1311.9	581.7
341.6	2347.8	2174.1	1895.6	3155.9	2662.5	2758.7	1926.2	3173.0	1914.4	691.4
1155.0	3580.6	3109.1	2585.0	3767.2	3308.6	3662.1	2577.3	2680.4	1833.3	1772.4
945.2	3780.5	3440.0	3269.1	5423.5	3501.0	4403.0	4285.0	4186.8	1811.8	2564.3
145.7	1679.2	1663.5	1524.9	2569.3	1802.6	1729.3	2233.4	1359.6	1176.4	617.2
10657.6	7640.3	6937.1	7884.0	10152.1	7557.6	8694.7	7692.8	11355.6	7499.9	8738.7
15916.6	7182.8	5990.7	6564.5	6460.2	6929.4	6789.5	7255.7	7529.9	7651.4	9451.3
1242.6	5049.0	4388.2	3044.1	4095.6	3748.0	4020.7	4394.3	8268.3	5253.3	2623.7
243.3	1317.0	1252.3	1115.8	1632.0	1316.4	1311.8	1631.3	1870.6	1077.3	604.5
12677.7	8824.1	7309.3	6765.9	7335.7	7190.2	7482.1	6625.7	10879.5	8329.5	9815.4
2509.8	4739.9	3814.4	3316.2	5158.4	3802.0	4273.5	3081.2	5217.4	2812.5	2729.8
5038.1	3420.0	3211.0	2992.4	3795.9	3449.0	3507.4	2974.5	897.4	1719.4	2984.0
37.0	50.5	56.9	55.8	139.0	57.7	64.6	71.3	40.9	36.9	28.6
316.6	1536.2	933.6	1118.9	1383.2	1716.9	1411.4	1632.1	1852.5	477.2	987.9
1565.9	3234.0	3295.5	3518.4	4399.5	3264.9	4281.0	3396.0	2474.2	1885.3	3721.0
46.1	65.3	60.5	41.6	107.6	53.9	60.8	45.9	18.4	30.7	38.7
97.8	1210.8	1281.6	997.0	1976.6	1227.5	1616.8	1328.4	1429.4	549.2	536.2
200.1	2250.3	1665.9	709.7	1200.2	1297.0	655.1	1055.2	2780.7	2123.5	468.3
3706.7	4448.8	4687.1	4939.6	6747.7	5172.9	6065.5	4827.0	3145.9	3806.0	2836.4
1675.8	5403.7	5630.9	5720.0	8814.3	5155.7	7583.6	5327.2	6138.6	5306.6	4406.6
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558.7	7962.7	6498.8	4784.4	6053.5	7375.6	5649.0	5006.1	8072.4	6096.6	3905.8
50.3	3032.3	1990.6	789.4	2222.6	2056.7	3376.7	1153.6	2815.5	1811.8	826.9

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6958.3	4034.4	6301.8
1986.6	2830.1	2516.8
3849.2	1958.3	2929.6
2100.8	913.1	1905.0
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2721.2	1495.5	3411.1
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6624.2	7239.3	6008.8
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1801.9	756.1	1313.8
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AY822044.1 gg_id:109040 Aeromicrobium alkaliterrae str. KSL-107 AY822
AM778683.1 gg_id:248622 Aeromicrobium ponti str. HSW-1 AM778
AB245387.1 gg_id:147176 Aeromicrobium panaciterrae str. Gsoil 161 AB245
AF005021.1 gg_id:12760 Aeromicrobium erythreum str. NRRL B-3381 AF005
AM696979.1 gg_id:221835 sequencing libraries indoor dust clone BF0001B005 AM696
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DQ532175.1 gg_id:165030 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
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Z78206.1 gg_id:12741 Friedmanniella antarctica str. DSM 11053T Z78206
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AM778578.1 gg_id:246156 Kribbella sancallistae str. BC634 AM778
AY995147.1 gg_id:126701 Kribbella swartbergensis str. HMC25 AY995
EU132912.1 gg_id:239934 tallgrass prarie soil clone FFCH15462 EU132
FN643222.1 gg_id:558911 Kribbella karoonensis str. DSM 17344 FN643
NR_029048.1 gg_id:574614 Kribbella antibiotica str. YIM 31530; DSM 15501 NR_02
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AY253862.1 gg_id:102895 Kribbella solani str. DSA1 AY2538
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DQ298376.1 gg_id:154976 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
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EU977820.1 gg_id:560678 Nocardioides oleivorans str. 1P06AC EU9778
AF005008.1 gg_id:12761 Nocardioides plantarum str. NCIMB 12834 AF005
AF498652.1 gg_id:60763 Nocardioides sp. str. JS614 AF498
EF466114.1 gg_id:207728 Nocardioides sp. str. MSL 19 EF4661

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EU289452.1 gg_id:248483 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
AM295257.1 gg_id:241942 Nocardioides hwasunensis str. HFW-18 AM295
AJ511294.1 gg_id:69420 Nocardioides sp. str. ND6 AJ5112
AM943897.1 gg_id:559607 Nocardioides maritimus str. SST-40 AM943
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GQ339904.1 gg_id:559914 Nocardioides sp. str. Gsoil BX5-10 GQ339
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DQ411542.1 gg_id:172913 Nocardioides furvisabuli str. SBS-26 DQ411
EU289500.1 gg_id:237194 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2895
CU922508.1 gg_id:533951 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9225
EU867298.1 gg_id:540142 Nocardioides sp. str. CCGE2239 EU8672
GQ921955.1 gg_id:554428 Nocardioides sp. str. C210A3 GQ921
EF633684.1 gg_id:249247 Nocardioides sp. 'TD 07' str. TD IW 07 EF6336
EU539935.1 gg_id:286030 profile human microbiota antecubital fossa (inner elbow) skin clone nbt108a11 EU5399
EU132805.1 gg_id:250656 tallgrass prarie soil clone FFCH13230 EU1328
X94145.1 gg_id:12763 Nocardioides sp X94145
DQ129311.1 gg_id:137915 microarray level air two cities Texas urban aerosol clone AKIW882 DQ129
DQ298320.1 gg_id:156466 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
FN396955.1 gg_id:563612 integrative isotopic approach study degradation mixed Mixed (US3-M) enriched grou FN3969
EU143364.1 gg_id:257075 Nocardioides sp. str. J111 EU1433
AF529063.1 gg_id:60989 Nocardioides aquiterrae str. GW-9 AF5290
AY167844.1 gg_id:77309 Nocardioides fulvus str. SAFR-045 AY1678
AB273624.1 gg_id:204879 Nocardioides exalbidus str. RC825 AB2736
AF465213.1 gg_id:21031 Nocardioides sp. str. JS884 AF4652
AY509240.1 gg_id:104329 Pimelobacter simplex str. S151 AY5092
GQ921954.1 gg_id:542377 Nocardioides sp. str. C1S GQ921
FJ666101.1 gg_id:516593 Nocardioides sp. str. GSoil 346 FJ6661
AF005024.1 gg_id:12782 Nocardioides nitrophenolicus str. NSP 41 AF0050
GQ079810.1 gg_id:433883 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw1132a GQ079
DQ786794.1 gg_id:167263 Nocardioides insulae str. DS-51 DQ786
U27856.1 gg_id:12799 picric acid degrading consortium clone FJ21-A U27856
EF466109.1 gg_id:207298 Nocardioides sp. str. MSL 21 EF4661

549.8	5873.4	5144.8	3843.7	5989.8	5064.8	5244.3	3768.9	6897.5	5235.7	2969.2
10276.3	6152.4	5310.5	5265.6	6445.5	5444.3	5762.0	5418.6	5478.8	4899.2	6817.0
773.0	4950.8	3235.4	3064.2	5570.5	3681.4	4431.4	3115.3	2193.1	1348.1	1603.3
578.5	6388.2	5776.1	4520.4	5141.4	5173.3	4606.8	4774.1	7567.9	6230.5	5025.6
49.4	2317.6	1484.0	1268.0	2693.4	1711.5	1963.7	1330.0	501.7	699.3	540.4
312.8	4118.3	3511.3	2602.4	4080.7	3525.1	3358.0	2246.5	4207.4	3428.6	1854.6
413.6	3779.8	3372.5	2972.0	4855.2	3457.0	4662.1	2724.3	3436.8	1574.6	1367.1
222.4	4678.2	3160.8	1551.8	2651.3	3224.3	2316.9	1991.7	5343.5	3829.6	1132.3
643.6	6070.6	4150.4	2843.7	5362.8	3530.7	4396.5	3032.1	3942.9	2301.8	1391.2
1300.2	5398.8	3325.7	3465.6	7191.2	3261.5	4618.4	4108.7	3099.4	1887.3	1590.8
59.1	1547.5	1424.1	1365.5	2562.8	1675.2	1748.7	1177.6	1613.8	1957.0	1144.6
1586.6	7790.7	6966.6	6895.0	8603.0	7257.1	8178.2	5854.1	6457.7	5331.3	5895.4
73.2	1339.9	986.7	622.3	1394.9	735.6	1570.6	930.1	922.4	637.5	363.0
173.9	3910.5	4177.1	4177.8	5041.3	3930.0	4948.4	3676.6	4550.3	2960.4	3043.9
135.9	930.3	1324.0	1519.7	2435.8	1216.2	2757.7	1278.0	560.2	398.8	503.7
515.2	5320.5	4745.7	4736.3	5799.7	4247.9	4384.6	4040.5	6211.8	4320.9	3184.0
426.7	3263.0	3112.9	2971.7	3958.9	2633.8	3115.6	2499.1	2891.2	2881.0	2789.5
1233.8	5656.4	5274.7	4023.6	5107.0	4155.1	4857.5	3780.2	5401.2	4352.2	3285.0
1950.5	5399.8	4745.2	4528.5	5194.4	5020.0	5362.6	4337.8	5726.5	3458.1	2940.0
330.8	4004.7	2378.7	2416.8	5874.6	2981.3	3290.3	3071.8	1693.0	1502.4	790.0
128.2	1404.0	1172.1	1182.9	2075.9	1443.8	1145.1	1354.9	1473.9	909.3	1329.2
48.1	1288.6	1132.0	1189.3	1787.7	994.8	1942.1	980.2	744.9	450.3	357.5
580.8	1567.2	1596.0	2032.8	2866.8	1611.7	2895.0	1913.4	498.5	354.5	742.3
289.8	4359.9	4237.0	3183.5	3620.6	3734.2	3044.5	3513.9	4398.6	2369.4	2357.9
668.3	5022.6	4406.7	4328.8	5356.4	4502.7	5246.8	4523.3	4934.1	4141.3	2847.5
1511.3	5422.5	3717.8	3399.6	4107.3	3724.1	4146.9	3429.4	3835.8	3408.1	2504.4
4304.0	4271.4	2858.1	2237.6	2842.8	2514.6	2397.0	2396.3	2238.4	1634.9	2434.8
95.4	2507.0	1557.2	728.7	1122.5	1289.9	786.8	543.8	1617.0	740.0	271.4
356.3	3477.5	2772.0	3302.2	3767.4	2492.7	4350.0	2640.1	3856.0	1786.4	1252.1
63.4	5271.9	3965.2	2248.7	3406.6	3730.8	3073.6	2314.5	4405.3	2851.5	1586.3
341.9	2898.7	2444.6	2721.5	5357.4	3105.3	3279.9	3509.7	3156.0	2482.7	1151.9
351.0	6574.3	5295.1	4850.5	7180.3	4813.6	5766.2	4252.5	4400.3	3555.4	3556.3
175.1	4696.9	3392.2	2408.2	3577.1	3187.2	3811.5	2458.1	2700.6	2469.4	1030.8
698.4	1003.8	2311.5	2478.5	4451.6	2345.3	3585.3	1857.7	521.8	903.9	1587.7
623.5	2446.4	3163.7	3960.5	3408.9	2075.5	3340.8	2949.0	1289.5	877.4	2680.6
395.7	2595.7	2140.7	2023.0	2653.4	2347.9	3065.1	1680.9	2074.9	1997.2	1068.7
45.2	990.6	1013.9	1230.3	4105.1	1217.6	2627.4	720.7	303.7	524.2	234.6
136.5	870.3	970.3	1079.5	1498.6	1173.3	1126.1	1236.8	1178.0	210.3	581.3
90.6	1348.9	1121.4	601.7	1208.9	926.3	1004.1	866.9	2448.1	909.2	342.5
5437.2	2161.5	1862.2	2024.9	2358.4	1991.3	2116.3	1585.6	88.7	1028.8	2174.6
43.3	214.5	468.6	416.1	709.7	452.5	700.5	346.9	208.9	129.4	121.2

5168.5	3874.5	3404.2
5340.8	6051.2	5924.0
3765.3	3265.9	4084.0
4766.2	5801.7	3572.3
1861.7	843.6	1272.7
3559.9	2986.8	2855.2
3930.5	2649.0	4209.9
2546.2	1445.3	1425.0
4387.1	3096.2	3381.3
4830.6	3234.7	4549.2
2133.1	1787.3	1178.3
6590.8	6021.8	7868.0
1295.4	586.2	468.5
4304.1	4315.9	4397.1
2139.7	1290.2	1561.3
5147.0	3494.3	3767.0
3523.3	2857.0	2139.9
4024.8	4454.2	5518.4
5037.8	4199.3	4775.0
4220.4	1492.1	2987.8
1460.8	1386.3	1218.2
1603.3	1177.5	1083.8
2399.0	986.4	1635.8
3826.4	2713.9	2879.1
4789.4	3553.6	5601.9
3606.7	3280.1	2847.8
3035.7	2329.8	2320.2
1686.8	634.3	539.0
3480.9	1906.1	3111.0
2769.0	2485.4	1830.1
3954.9	1789.8	3840.1
5144.6	4662.2	4621.0
4090.9	2525.5	1982.6
2872.0	1985.4	2567.1
3500.2	2932.4	3192.0
2426.7	1582.9	2980.9
2713.7	1059.3	1252.4
1240.6	936.0	1411.7
940.3	677.0	822.3
2126.5	1729.8	1823.8
562.4	303.3	594.2

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g__Pimelobacter
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s__unclassified	38547

GQ263609.1 gg_id:563475 Structure Simulated Level Waste Site simulated level waste site clone FW3_163C GQ263
AB245396.1 gg_id:145531 Nocardioides ginsengisoli str. Gsoil 1124 AB2453
EU104290.1 gg_id:325277 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1042
AY439194.1 gg_id:99987 soil clone MeCl 87 AY4391
EF466107.1 gg_id:214797 Nocardioides sp. str. MSL 14 EF4661
AJ549286.1 gg_id:82319 Nocardioides sp. str. NS/27 AJ5492
EF623863.1 gg_id:243943 Nocardioides sp. str. DCY24T EF6238
AJ576388.1 gg_id:104754 midgut homogenate Pachnoda ephippiata larva clone PeM19 AJ5763
AB078858.2 gg_id:47074 Propionicimonas paludicola str. Wd AB0788
AB078820.1 gg_id:19175 Propionicimonas paludicola str. K5 AB0788
AB078859.2 gg_id:49459 Propionicimonas paludicola str. Wf AB0788
FJ535513.1 gg_id:511542 Microbial digestion swine wastewater anaerobic UASB reactor clone SWADLP1-43 FJ5355
DQ176646.1 gg_id:167566 Propionicicella superfundia str. BL-10 DQ176
FM178524.1 gg_id:343580 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
EU812987.1 gg_id:329785 Microbial structure thermophilic reactors biogas reactor fed corn silage clone TUM-M EU8129
AJ009505.1 gg_id:12746 anaerobic TCB-transforming consortium clone SJA-181 AJ0095
GQ067225.1 gg_id:418791 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ067
GQ066469.1 gg_id:464430 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ066
AJ229243.1 gg_id:12753 Actinobacteria str. VeSm15 AJ2292
FM178825.1 gg_id:338708 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
FM178523.1 gg_id:319520 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
EF515377.1 gg_id:219989 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23f02 EF5153
AB012607.1 gg_id:12751 Micropruina glycogenica str. Lg2 AB0126
FM178834.1 gg_id:342081 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
AB166787.1 gg_id:99115 EBPR sludge clone UTFS-OF09-36-43 AB1667
FM178811.1 gg_id:321654 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
DQ378203.1 gg_id:154789 oil-polluted soil clone F41_Pitesti DQ378
FM178526.1 gg_id:347265 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
AB198497.1 gg_id:135409 termite gut wall fraction clone RsW01-070 AB1984
AY921964.1 gg_id:113533 farm soil clone AKYG1602 AY9219
FJ672605.1 gg_id:515746 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6726
CU920907.1 gg_id:576220 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9209
GQ060298.1 gg_id:412264 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ060
GQ065951.1 gg_id:372007 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw94g11c GQ065
AB195905.1 gg_id:109193 Anaerobic sludge clone N04 AB1959
FJ711217.1 gg_id:512378 Nocardioides sp. str. KC-EP-S1 FJ7112
EF157076.1 gg_id:249340 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1570
EF466113.1 gg_id:209543 Nocardioides sp. str. MSL 28 EF4661
GQ088428.1 gg_id:414150 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw3 GQ088
EF127612.1 gg_id:216616 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE088 EF1276
GQ339903.1 gg_id:552729 Nocardioides sp. str. Gsoil 958 GQ339

106.2	1267.1	1586.8	1776.1	2973.3	1521.6	1813.1	1656.4	1116.3	324.5	933.0
47.0	533.3	648.0	686.8	733.9	112.9	933.5	528.7	253.6	102.7	331.8
166.7	3433.8	4302.2	3925.3	5614.2	3718.2	5090.9	3526.5	2287.2	1503.2	2755.6
7851.7	2095.9	1723.8	614.6	3458.6	2237.1	2644.2	2057.8	3143.6	1898.2	2429.7
40.6	38.9	51.8	38.5	58.5	38.0	38.6	40.8	20.2	21.3	21.5
233.8	2521.2	1958.5	1112.0	1340.1	1934.8	1303.0	1049.0	2824.3	1988.3	620.3
27.8	1034.9	913.9	726.5	1328.6	987.3	880.6	570.7	521.3	439.9	151.1
1106.7	941.9	780.4	846.5	1405.4	816.6	1272.4	504.9	330.2	223.3	362.9
1419.4	5774.9	6376.8	4732.4	4936.5	5682.2	5783.2	5193.5	5940.8	6237.1	4802.1
170.3	2543.0	3005.6	3036.2	3797.0	3224.1	5129.4	2882.3	2019.2	3377.2	2201.0
108.9	1582.2	2010.7	1599.5	2292.7	2372.0	2076.4	1772.5	1419.8	777.9	1119.1
371.5	3349.3	2805.3	2355.2	3355.8	3026.6	3497.8	2784.8	2931.3	3378.9	1274.8
58.6	3210.3	1942.4	1296.7	1296.0	2548.1	1724.1	1008.6	2418.0	1143.9	477.6
394.5	6769.2	5286.5	3005.0	4261.5	5549.1	3986.5	3559.1	8098.0	5503.7	2797.6
624.2	4651.2	5166.5	3694.7	3688.2	4761.9	4518.5	4583.2	3113.4	3907.9	5076.9
12829.7	6956.9	5971.1	5261.1	6380.8	5918.1	6406.5	4787.4	8529.5	7275.2	5568.5
577.0	1773.9	1411.4	1732.5	1441.2	2122.3	1636.8	1826.3	1527.8	2583.0	635.1
3971.0	6725.5	6599.8	6512.2	6395.6	6273.8	7501.2	5421.7	11551.5	8421.8	5628.2
133.1	3191.0	1989.5	1348.4	3137.0	1327.1	4309.5	1521.5	4086.5	1264.3	646.6
1888.4	1264.2	1222.3	1122.5	1881.3	1281.2	2354.4	963.6	973.1	859.1	571.1
509.8	1846.0	1488.2	800.4	2311.4	1545.8	3474.2	885.2	340.3	467.7	284.8
4152.9	3409.0	3502.3	3605.3	4049.8	3469.9	3987.9	3385.5	4221.3	4176.8	4493.9
84.6	4134.9	3176.0	1936.2	3231.0	3187.8	2467.8	2066.7	3510.0	2279.7	883.5
220.1	2973.3	3001.6	2119.1	4075.2	2887.0	4259.9	2318.6	3151.4	1615.8	1164.5
23517.7	7488.5	8347.8	7497.7	7728.3	8070.2	9249.9	7919.2	11012.4	9640.1	13119.2
123.0	3135.8	3034.4	3067.9	4182.2	2964.6	4639.4	2613.4	2774.6	1597.2	2499.9
93.6	1364.5	1463.7	988.0	1849.2	1345.6	1389.6	1232.7	1269.6	601.4	585.7
228.9	2349.9	2151.7	1600.6	3333.7	2280.9	2058.1	1956.6	2268.0	1345.8	750.9
195.9	1339.1	1271.5	1244.4	1319.2	1349.3	2158.6	1304.9	816.3	565.1	507.6
20876.1	11190.3	9285.1	8587.1	8900.9	8464.5	10081.5	7504.7	14325.8	9677.5	8749.1
77.1	1369.9	1449.4	982.5	1882.4	1411.0	1055.3	1300.7	1228.0	1122.3	936.5
65.9	4390.7	3344.6	1827.2	2482.6	3412.6	2368.8	2700.6	3520.5	1676.9	2534.8
706.7	4481.7	3921.5	3078.3	3754.8	4049.6	3492.9	4323.0	2515.5	1589.9	2741.4
887.3	1414.4	1583.1	2044.9	1707.2	2106.6	1712.9	1972.8	782.1	2310.8	787.3
47.6	140.2	219.2	124.5	360.0	172.0	367.3	126.2	64.6	60.8	67.1
298.2	5876.1	5349.2	4617.4	6832.9	5929.1	6014.2	4956.5	7073.8	5310.2	3076.2
361.1	3017.2	2250.7	1561.9	1942.1	2046.2	1849.2	1459.7	2368.7	1581.9	1111.6
723.3	3594.3	3303.9	3084.2	5442.1	3315.7	4515.3	2757.4	2685.6	1415.7	1749.8
5765.6	8763.2	7281.0	8155.1	8569.3	8927.3	8632.6	6286.2	8756.1	6752.6	5812.5
35.2	421.7	207.9	106.5	349.5	248.2	273.3	166.8	233.6	134.5	59.4
53.4	248.5	316.2	361.7	611.7	250.6	538.5	129.3	62.9	32.4	56.8

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37.5	39.1	112.4
1374.9	1058.0	866.9
1889.4	366.4	477.7
1271.9	651.2	1073.6
5788.8	4752.6	4646.9
3154.2	2669.7	2842.9
1990.4	1976.8	1782.7
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1089.0	1168.7	1908.0
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3140.7	4165.0	4022.7
5124.3	5631.2	5188.5
1854.6	1499.4	1745.2
6174.1	6224.8	6599.3
1354.9	1762.9	5213.1
999.6	1631.8	1087.8
1469.8	908.6	984.2
3577.3	4028.4	3885.5
2295.0	2106.3	2517.0
2631.1	1845.0	1976.1
6256.3	8247.3	8319.9
2714.5	2481.9	3398.9
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2113.6	1584.5	2178.9
1374.9	1203.5	1095.3
7832.2	8172.7	10415.0
1277.3	1552.1	1301.0
2168.6	1409.3	1256.3
4718.9	2957.0	3483.8
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5598.8	4044.3	4573.3
1868.3	1554.4	1295.8
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6694.3	5420.1	8412.2
168.1	180.7	176.1
702.1	121.8	227.0

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FJ671561.1 gg_id:522198 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6715
GQ007842.1 gg_id:501824 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ007
FM873019.1 gg_id:365828 occupant source house floor dust clone FB02H10 FM873
AB361360.1 gg_id:247113 Nocardioides sp. str. S147 AB3613
EF466121.1 gg_id:217144 Nocardioides sp. str. MSL 11 EF4661
AB374375.1 gg_id:263308 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
AM935384.1 gg_id:549557 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
Z78210.1 gg_id:12785 Nocardioides jensenii str. DSM 20641T Z78210
DQ125522.1 gg_id:132361 uranium contaminated soil clone AKAU3484 DQ125
DQ129362.1 gg_id:138177 microarray level air two cities Texas urban aerosol clone AKIW459 DQ129
FJ750845.1 gg_id:541566 Nocardioides sp. str. YC6903 FJ7508
GQ339890.1 gg_id:580619 Nocardioides sp. str. MK04 GQ339
GQ097070.1 gg_id:392153 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ097
GQ043925.1 gg_id:431801 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
GQ093814.1 gg_id:376735 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
GQ116303.1 gg_id:418342 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw691b0 GQ116
AY234666.1 gg_id:111791 soil isolate Ellin6014 AY2346
EF466120.1 gg_id:208818 Nocardioides sp. str. MSL 05 EF4661
EF534291.1 gg_id:218299 Nocardioides sp. str. MSL10 EF5342
DQ448719.1 gg_id:157893 Aeromicrobium sp. str. CNJ889 PL04 DQ448
EU132501.1 gg_id:243180 tallgrass prarie soil clone FFCH943 EU1325
AM286546.1 gg_id:172332 Aeromicrobium sp. SCLB AM286
AY928902.1 gg_id:114316 Nocardioides dubius str. KSL-104 AY9289
DQ824745.1 gg_id:197085 human fecal clone RL185_aaj72f03 DQ824
EF018974.1 gg_id:210417 aspen rhizosphere clone Amb_16S_1489 EF0189
DQ298335.1 gg_id:155185 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
EF466110.1 gg_id:210408 Nocardioides sp. str. MSL 01 EF4661
AB508351.1 gg_id:455651 Nocardioides sp. str. DN36 AB5083
AY571809.1 gg_id:101707 Nocardioides sp. 35/18 AY5718
EU861822.1 gg_id:341901 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
EF466115.1 gg_id:212767 Nocardioides sp. str. MSL 09 EF4661
EF540473.1 gg_id:224809 Nocardioides sp. 2_4V EF5404
AB167244.1 gg_id:107952 Acidovorax sp. str. c116 AB1672
EU133244.1 gg_id:237339 tallgrass prarie soil clone FFCH9830 EU1332
DQ401093.1 gg_id:151383 Nocardioides sp. str. CL-DD14 DQ401
DQ298283.1 gg_id:152307 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
EU133114.1 gg_id:257538 tallgrass prarie soil clone FFCH5314 EU1331
EF466117.1 gg_id:211507 Nocardioides sp. str. MSL 22 EF4661
EU863845.1 gg_id:307611 Marmoricola sp. D13 EU8638
AY423719.1 gg_id:96649 Nocardioides aestuarii str. JC2056 AY4237
EF019383.1 gg_id:211360 aspen rhizosphere clone Elev_16S_613 EF0193

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98.7	1046.0	957.7	1185.2	2171.9	745.0	2314.8	938.6	276.1	383.3	345.9
240.4	4041.6	3281.1	3587.7	5283.2	3540.4	4852.1	3567.9	3452.6	2241.8	2349.2
107.9	2137.8	1783.9	2299.4	3040.6	1431.2	2446.8	1736.2	748.1	615.0	842.7
80.3	2212.7	1378.5	1024.5	2209.9	1939.0	1438.3	1235.1	508.1	720.5	491.5
612.3	4628.4	3039.6	2647.8	2855.7	2848.0	3162.2	2959.1	5267.3	2585.4	2135.6
665.5	10916.4	9225.3	7253.0	7344.3	8878.7	7791.9	6673.4	10116.4	8644.5	7817.3
2671.7	6815.1	5159.7	4169.8	5726.6	6034.0	5764.5	4303.1	5199.3	3579.3	3790.6
127.8	3647.3	3446.8	2166.3	2111.2	3066.2	2055.9	2191.9	3728.3	1693.2	1585.0
7369.3	3334.2	3279.1	3536.6	3903.3	3726.6	4485.4	3201.2	3187.4	3213.9	4081.9
425.2	5329.3	3903.9	2932.4	2936.1	3833.8	3371.2	2609.0	3443.9	4618.1	2586.0
62.7	3460.6	2025.1	1872.5	3575.4	1885.9	2617.2	1822.5	1132.9	918.7	769.1
1559.9	2212.4	1974.9	2048.9	2826.9	2484.4	2262.6	2064.0	1770.9	1551.5	1970.9
803.6	12001.2	8714.0	5701.7	7134.1	9372.6	7060.1	5700.5	11950.0	9473.2	4078.3
33.3	1456.5	932.9	1422.9	1673.0	1437.5	1850.4	1320.6	348.6	296.6	639.4
245.0	4183.7	3324.1	2575.1	4570.8	3903.9	3669.9	3117.9	2592.5	2681.6	853.2
101.5	1860.5	2119.7	2178.7	3447.5	2250.3	3089.8	2532.6	1849.4	1208.0	960.9
64.3	2079.8	1912.2	1489.5	2562.2	2029.8	1744.0	1681.7	1751.7	916.3	775.1
280.7	2229.6	1452.5	295.9	1191.1	1475.3	721.2	577.9	1588.2	1291.3	252.4
51.6	58.3	59.5	40.3	90.7	35.2	72.0	47.2	28.6	38.9	25.0
1053.6	7256.9	6357.8	8613.5	8627.2	5928.7	7614.7	6797.3	7950.4	5802.6	5633.8
1327.9	5812.6	4406.4	3225.0	3415.6	4375.7	4151.6	3015.9	2721.0	3218.2	1871.0
137.3	1159.9	1004.6	440.3	1193.4	1081.1	805.4	490.9	559.1	147.9	188.6
448.9	3953.4	3062.0	4133.5	5627.9	4078.4	4837.7	3504.6	3322.5	1990.7	3231.3
4738.6	4186.6	4132.7	2434.6	3050.1	4349.6	2826.0	2637.0	4384.7	2838.7	2081.9
790.1	6070.1	4517.6	3759.5	5068.5	5047.5	5276.0	3740.5	4286.5	3006.0	2561.6
49.0	170.8	210.9	176.6	506.9	117.6	406.7	332.8	129.4	132.2	58.2
57.9	800.9	857.1	967.5	993.2	714.5	1217.1	804.7	652.6	454.3	429.1
2429.6	5093.0	4471.9	6034.6	7910.7	4933.4	6841.4	4798.8	3373.3	2404.4	3976.8
2876.0	2209.6	2353.9	1176.0	2640.7	2389.5	2188.5	1181.1	1868.7	1508.9	1437.2
845.0	4874.6	4740.3	5921.4	6264.4	5219.3	6960.5	4381.5	4306.8	5781.1	3802.7
394.0	4270.3	3303.7	2170.5	4159.7	3095.0	3452.2	2324.9	4806.8	3564.9	1102.7
235.8	4296.2	3242.1	2641.3	3351.6	3031.3	3446.5	2888.0	4377.5	3819.0	1674.2
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61.3	940.2	548.7	653.0	1434.7	370.3	762.4	833.2	153.0	246.3	192.7
386.1	2739.3	1616.9	1219.2	1775.0	1581.9	1595.1	1445.6	2349.7	1907.2	834.6
433.3	3496.1	2202.6	2372.6	3758.7	2461.6	4126.9	2649.8	1762.1	1043.9	1450.4
348.5	4691.1	4146.1	3821.6	5033.6	3791.2	4891.9	3882.9	4033.8	3336.1	2778.8
377.9	5876.0	4584.8	4713.2	6023.1	4721.1	5744.0	4616.3	6909.6	3539.5	3147.5
1917.1	4593.6	3004.3	2358.5	4050.0	3546.5	3741.8	2422.4	2973.0	1796.4	1575.7
17311.0	6233.7	6003.1	6614.1	7461.8	5795.3	7807.5	5632.2	7900.7	5856.6	7560.3

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1982.3	666.1	785.8
5272.4	3576.8	3324.3
1860.1	1374.5	1901.2
2829.6	937.0	1471.3
3096.8	2477.7	2893.3
6528.8	7004.0	5392.9
4433.9	3456.8	4317.4
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3101.2	3712.2	3574.8
3755.6	3132.9	2771.3
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2011.0	1993.5	2074.9
6357.4	5154.7	7806.8
1619.0	812.7	1054.2
4099.4	2173.9	2481.0
2915.7	2142.0	3220.5
1791.2	1599.7	1529.0
857.0	239.7	300.4
80.2	71.3	37.4
7209.8	6171.6	6212.4
4066.2	3247.3	3290.7
1531.5	381.8	496.2
4018.5	2879.7	3577.1
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4300.4	3386.8	4243.5
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1511.2	1158.0	1059.7
6133.9	3916.0	5715.0
1213.6	2259.3	2698.2
5884.7	4306.2	5929.9
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3327.0	2895.3	2696.2
2920.3	1905.3	2534.7
1145.3	130.2	764.5
1789.1	1450.6	1132.9
2675.8	1904.8	2094.5
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5646.7	4838.4	5294.1
3596.9	2120.5	2830.4
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DQ298299.1 gg_id:155939 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AB271053.1 gg_id:165735 Nocardioides panacihumi str. Gsoil 616 AB271
DQ298304.1 gg_id:154113 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
EF466111.1 gg_id:210861 Nocardioides sp. str. MSL 25 EF4661
GQ088113.1 gg_id:377237 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
DQ906840.1 gg_id:246385 Oman subsurface soil clone 7B-17 DQ906
EF466116.1 gg_id:205152 Nocardioides sp. str. MSL 12 EF4661
EF451709.1 gg_id:208432 Nocardioides sp. str. KAR81 EF4517
EU464762.1 gg_id:295675 Hartmann's mountain zebra feces clone AFZEB_aaj70d01 EU464
DQ673618.1 gg_id:173111 Nocardioides sp. str. PD653 DQ673
AJ316318.1 gg_id:34725 Nocardioides sp. str. LMG 20237 AJ3163
DQ347886.1 gg_id:203408 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi DQ347
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FJ891029.1 gg_id:557413 Hypolithic structure hyperaird core Atacama Desert quartz clone AY5_18 FJ8910
GQ043415.1 gg_id:426543 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw96 GQ043
AM398438.2 gg_id:166467 Nocardioides sp. str. D287 AM398
AF360734.1 gg_id:67689 Nocardiopsis composta str. KS9 AF360
FJ486426.1 gg_id:564001 Nocardiopsis dassonvillei str. HBUM174832 FJ4864
FJ532466.1 gg_id:545814 Nocardiopsis dassonvillei str. HBUM174177 FJ5324
EU570392.1 gg_id:276924 Streptomyces flavidofuscus str. 173746 EU570
AY277558.1 gg_id:88777 Nocardiopsis dassonvillei str. F101 AY2775
AB368714.1 gg_id:246161 Nocardiopsis exhalans str. NBRC 100346 AB368
AY027776.1 gg_id:52175 Nocardiopsis alba AY027
EU570349.1 gg_id:264921 Nocardiopsis exhalans str. 173901 EU570
EU849610.1 gg_id:310696 Nocardiopsis umidischolae str. B410-71 EU849
AF251709.1 gg_id:25615 Nocardiopsis xinjiangensis AF2517
DQ387958.1 gg_id:194856 Nocardiopsis sp. str. YIM 90022 DQ387
AY030320.1 gg_id:47196 Nocardiopsis dassonvillei str. JPL-3 AY0303
AB184655.1 gg_id:152528 Streptomyces flavidofuscus str. NBRC 15404 AB184
X97884.1 gg_id:11983 Nocardiopsis alba str. DSM 43845T X97884
X87313.1 gg_id:11974 Actinomycetaceae SR 210 X87313
EU841645.1 gg_id:306580 Nocardiopsis synnemataformans str. HBUM174881 EU841
AY117435.1 gg_id:55606 Nocardiopsis viridoflava str. T64 AY1174
AF105971.1 gg_id:41607 Nocardiopsis tropica str. VKM Ac-1457 AF1059
AY336512.1 gg_id:91919 Nocardiopsis sp. str. 20037 AY3365
NR_025653.1 gg_id:541908 Nocardiopsis umidischolae str. 66/93; DSM 44362 NR_02
EU214943.1 gg_id:272266 Nocardiopsis sp. str. CNP-966_SD01 EU2149
EU741177.1 gg_id:556920 Nocardiopsis sp. str. 13651T EU741
AB491226.1 gg_id:550175 Nocardiopsis sp. str. 1183-22 AB491
AY230848.1 gg_id:83383 Nocardiopsis alkaliphila str. DSM44657T; CCTCC AA00103T AY2308
AM236238.1 gg_id:155746 Nocardiopsis sp. AM5 AM236

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233.1	5485.7	3844.5	2327.8	3876.6	3884.6	3511.0	2352.0	4407.9	2763.1	1056.5
19460.6	7090.4	5668.1	6226.0	6692.8	6469.3	6642.2	5600.6	6824.5	6749.5	8783.0
374.4	3294.6	2910.8	1613.8	2873.0	2799.8	2007.8	2427.8	3995.3	1715.2	844.9
634.0	5659.3	4448.2	3361.7	5411.7	4380.6	5158.6	3281.9	3318.8	2851.1	2179.5
224.8	1127.9	1442.3	2027.5	2219.4	1320.8	1869.9	1560.2	794.2	685.8	1108.5
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157.6	3009.2	3643.4	4142.6	4010.3	4558.2	2652.6	4198.6	4011.5	6115.2	2678.8
408.1	6790.3	4123.0	2970.1	4480.3	4438.0	4386.9	3552.3	3254.0	4340.4	2434.7
222.8	1709.5	856.1	821.7	1674.9	814.3	1530.4	930.0	1203.2	370.7	377.4
751.3	3294.3	2545.6	1869.3	1846.4	2962.2	2086.8	1940.1	2979.2	1771.1	2400.4
174.6	2816.1	1994.0	1880.2	4252.4	1940.3	3076.4	2364.6	1881.7	1441.6	1056.4
1204.6	11602.4	8300.4	5210.6	6773.5	8583.7	6036.9	5468.3	8915.8	7876.5	4354.4
577.0	10904.9	7857.4	4573.4	6063.8	8177.0	5802.9	5168.7	12378.3	9225.5	3548.1
1743.8	2513.7	2334.5	3171.4	4215.5	2271.2	3970.7	2368.3	2350.0	1413.1	2078.5
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239.0	2959.6	2451.2	2333.8	3454.4	3008.2	3503.1	2362.7	2010.9	2237.3	1688.1
212.6	2598.3	2209.8	1600.6	2256.5	2357.2	2375.5	1734.1	2274.9	2417.4	939.9
173.1	2099.6	1546.5	1527.5	2236.1	2057.0	2318.9	1477.5	1282.5	1247.3	1022.0
296.1	1392.8	1321.1	1509.6	2161.7	1600.1	2492.2	1409.7	879.2	747.5	1022.6
173.2	7950.6	6215.0	4799.8	6604.5	7853.3	5469.6	5337.2	9447.7	6778.2	3687.6
188.7	5087.2	3410.9	1269.5	2218.0	2615.7	1478.1	1449.8	3528.6	2628.1	849.0
299.3	5481.8	3802.5	1739.6	3029.5	3115.0	2008.8	1985.6	3907.2	2669.2	1033.2
231.1	5661.1	4362.6	2314.6	3941.2	4309.5	3702.7	2656.3	5515.3	4500.8	1516.4
158.7	2678.7	2367.2	1353.7	2393.0	2343.2	2087.1	1784.8	2301.1	2307.0	693.0
155.2	3662.2	2773.2	1567.8	2803.4	3032.2	2661.1	1843.4	3265.4	2604.7	972.2
418.2	5880.9	4954.6	4432.2	5652.8	5297.0	5435.7	4277.7	4794.0	5847.8	2968.4
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575.3	5066.6	3499.4	1988.0	4078.1	3653.3	2890.2	1657.0	4840.7	3540.7	1046.8
15768.7	5575.0	4723.7	5129.3	5236.6	5038.6	5247.8	4200.4	6497.4	4476.1	5676.0
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311.0	4803.2	3676.0	2236.7	3116.6	2884.9	2604.8	2191.2	2950.8	2055.2	1077.0
188.6	1865.3	1671.9	1042.9	1832.4	1869.8	1717.2	1304.1	1408.1	1501.6	664.0
6350.3	5037.2	4412.9	4197.1	4926.1	5287.1	5202.1	3726.4	4758.4	4395.2	3340.3
134.1	4364.6	3622.9	2143.2	3736.3	3853.3	3468.6	2593.1	3245.7	3391.0	1211.3
64.6	1481.3	1221.6	580.6	1170.6	1404.8	1325.1	670.0	1252.8	1586.2	319.7
230.6	3125.7	2336.9	2665.7	4163.1	3242.1	4151.5	2589.5	1255.4	1735.7	2014.8

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5524.0	4025.2	3572.6
4759.8	3013.0	3319.3
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g__Nocardiopsis
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g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Nocardiopsis
g__Prauseria
g__Streptomonospora
g__Streptomonospora
g__Thermobifida
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g__unclassified
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g__unclassified
g__Cellulosimicrobium
g__Cellulosimicrobium
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g__Cellulosimicrobium
g__Cellulosimicrobium

s__unclassified	41831
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s__unclassified	41845
s__unclassified	41959
s__unclassified	41994
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s__unclassified	42204
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s__unclassified	42429
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s__unclassified	42026
s__Thermobifida fusca	41312
s__Thermobifida fusca	41872
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s__unclassified	42419
s__unclassified	41107
s__unclassified	41112
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s__unclassified	41597
s__unclassified	41862
s__unclassified	42034
s__unclassified	42133
s__unclassified	42231
s__unclassified	42430
s__Cellulosimicrobium funkei	40233
s__unclassified	40401
s__unclassified	40458
s__unclassified	40570
s__unclassified	40667
s__unclassified	40768
s__unclassified	40784
s__unclassified	40808
s__unclassified	40938
s__unclassified	40998
s__unclassified	41063

EF216368.1 gg_id:213755 Nocardiopsis sp. TFS 806
EU805509.1 gg_id:320814 Nocardiopsis sp. str. BCEAA 7603
AF195412.1 gg_id:53459 Nocardiopsis kunsanensis str. HA-9T; KCTC 9831T
FJ973467.1 gg_id:431581 Nocardiopsis sp. str. VITSVK5
AF540000.2 gg_id:55246 Nocardiopsis tangguensis str. CCRC 16303 D3615
AY619715.2 gg_id:101126 Nocardiopsis chromogenes str. YIM 90109
AY373031.1 gg_id:94921 Nocardiopsis salina str. YIM 90010
AB368713.1 gg_id:241260 Nocardiopsis halotolerans str. NBRC 100347
AY619712.2 gg_id:100646 Nocardiopsis flavoviridis str. YIM 90087
EF597511.1 gg_id:235389 Nocardiopsis quinghaiensis str. YIM 28A4
EU570350.1 gg_id:267022 Nocardiopsis listeri str. 173794
EU428765.1 gg_id:270818 Nocardiopsis halotolerans str. PS-3
AF360735.1 gg_id:67687 Nocardiopsis alba str. KS21
EF095149.1 gg_id:173918 Nocardiopsis arabia str. S186; CGMCC 4.2057
DQ667026.1 gg_id:161123 Streptomonospora sp. str. YIM 90564
AB006171.1 gg_id:32820 Thermobifida fusca str. IFO 14071
AB211018.1 gg_id:115212 Thermobifida fusca str. SSCS23
AJ298058.1 gg_id:52732 Thermobifida cellulosilytica str. TB100
AF028247.1 gg_id:11966 Thermobifida alba str. ATCC 27644
EU250489.1 gg_id:236523 Thermobifida halotolerans str. YIM 90462
AF002265.1 gg_id:11967 Thermobifida alba str. 3169
DQ923130.1 gg_id:191592 Haloactinomyces albus str. YIM 90648
NR_024958.1 gg_id:570500 Nocardiopsis trehalosi str. VKM Ac-942
GU112453.1 gg_id:591087 Marinactinospora sp. str. CXB654
GU253338.1 gg_id:574980 new genus Nocardiopsaceae salt pond sediment
Y07678.1 gg_id:11980 Prauseria hordei SH261
EF212019.1 gg_id:214362 Nocardiopsis sp. TFS 233
EU214944.1 gg_id:265962 Nocardiopsis sp. str. CNP-957_SD01
FJ853144.1 gg_id:546433 Nocardiopsis sp. str. GW9-2
DQ448723.1 gg_id:157021 Nocardiopsis sp. str. CNR923 PL04
AY523787.1 gg_id:103317 Cellulosimicrobium funkei str. CDC#JB6123ot
AB098580.1 gg_id:77900 Cellulosimicrobium cellulans str. TUT1012
AB210980.1 gg_id:115285 Cellulosimicrobium cellulans str. SSCT54
EU545400.1 gg_id:543074 Cellulosimicrobium cellulans str. XW31
FJ811879.1 gg_id:593658 Cellulosimicrobium cellulans str. PL5-GFJ
EF076760.1 gg_id:186856 Cellulosimicrobium terreum str. DS-61
NR_029291.1 gg_id:577275 Cellulosimicrobium cellulans str. DSM 43879
AB547224.1 gg_id:527191 Cellulosimicrobium cellulans str. NCCP-43
DQ530364.1 gg_id:159270 Cellulosimicrobium cellulans str. IBL10
AB023355.1 gg_id:12303 Cellulosimicrobium cellulans str. IFO 16148
FJ811880.1 gg_id:547791 Cellulosimicrobium cellulans str. MA3A-GFJ

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EU8055
AF1954
FJ9734
AF5400
AY6197
AY3730
AB3687
AY6197
EF5975
EU5703
EU4287
AF3607
EF0951
DQ667
AB0061
AB2110
AJ2980
AF0282
EU2504
AF0022
DQ923
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GU112
GU253
Y07678
EF2120
EU2149
FJ8531
DQ448
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AB0985
AB2109
EU5454
FJ8118
EF0767
NR_029
AB5472
DQ530
AB0233
FJ8118

558.7	4302.4	3396.3	3300.0	5039.6	3653.3	4267.6	3048.2	3706.2	2287.8	1924.6
395.4	6243.5	3958.7	1759.8	3930.3	3007.5	2859.0	1683.6	2891.5	2268.2	753.6
160.2	3070.8	3014.8	2524.6	3528.0	2948.1	3143.2	2440.5	2020.2	1972.0	1215.2
230.9	6063.7	4758.1	3570.8	4813.7	5185.3	4130.7	3727.0	5263.3	4299.6	2486.2
448.7	3596.2	2775.7	2806.2	4242.5	3217.8	3812.9	2620.8	2058.9	1832.2	2118.1
2924.4	9056.4	7033.2	4006.9	6572.8	6486.0	5424.9	4524.8	8527.0	6913.5	2794.0
1052.2	6764.4	5994.7	3156.1	5328.9	5308.6	4428.1	4169.0	6395.4	5694.8	2088.7
812.8	4625.1	3828.1	3093.4	5171.5	4534.9	4424.7	3548.4	3052.7	2536.4	2314.9
5897.5	7471.3	6938.5	6112.5	7968.0	6453.3	7977.7	5945.3	6290.1	7148.8	4339.9
640.9	5429.0	4389.6	3814.4	6112.1	4865.6	5663.0	3677.4	3768.9	3533.0	2665.1
159.5	5283.5	4003.3	2527.1	3843.7	4469.2	3542.7	2851.5	4944.4	4088.8	1697.2
9926.4	2530.9	2647.9	2387.2	3434.7	3098.3	3929.9	2288.4	2874.1	3724.9	1822.6
215.4	4120.7	3184.6	2010.5	3376.4	3749.8	2625.1	2260.9	3438.0	2898.9	1330.2
2255.5	5832.2	4768.9	4830.9	6868.6	5005.4	5581.2	4117.6	3692.2	3096.8	3194.3
2014.3	1650.3	1703.7	1580.1	2552.3	1504.7	1762.1	1227.1	1650.6	1085.9	945.9
8684.8	7741.5	6786.8	5820.5	8329.6	7365.6	7621.3	5564.1	8342.5	7608.4	6488.7
2644.7	6443.1	6479.4	5505.7	7852.0	6342.6	7019.9	5401.7	5560.2	4378.2	3780.0
115.5	4023.8	3738.0	1467.7	3724.5	3367.8	2726.5	2285.0	4705.6	2493.8	464.3
4663.8	4416.5	4493.3	2716.9	3670.3	3854.1	3636.5	3309.4	6712.9	3979.0	2286.0
121.1	1664.8	1924.1	972.3	1132.6	1705.3	976.2	1334.4	3556.5	1538.3	562.3
1195.9	6794.7	5568.0	2963.2	5731.6	5355.7	4737.4	3528.0	7253.8	4428.6	1975.4
146.2	294.0	350.7	392.8	452.2	310.2	479.5	633.1	219.0	125.1	197.3
435.9	8234.8	5881.7	3176.0	5851.6	6419.5	4785.8	4494.0	6586.1	5140.1	3086.4
190.0	2740.4	2331.9	2439.3	3674.7	2409.5	3090.8	1935.3	1769.3	1446.8	1475.5
1824.5	3571.0	3149.8	3028.0	6109.3	3670.6	4115.2	2913.6	3498.4	2180.3	1781.3
213.3	4216.2	3304.5	2191.6	3561.8	3802.2	2888.7	2550.0	3603.6	2805.3	1422.4
392.5	2880.4	2436.8	1832.0	2748.8	3001.0	2615.6	1883.4	2147.8	1200.2	946.7
463.6	3666.1	3633.8	3192.4	5618.7	4126.3	4681.3	2616.2	2242.7	1867.3	1363.4
189.6	1167.7	1035.2	969.2	2519.3	1113.2	1794.8	880.4	454.7	715.0	347.3
528.3	3881.8	3123.0	3286.0	5026.5	3642.2	4468.4	2927.1	2229.8	2069.3	2283.5
99.0	2946.9	2447.4	1395.4	2802.2	2443.2	2098.8	1720.1	2201.9	1947.2	894.1
325.2	3775.2	2756.7	987.1	2551.9	2746.3	2113.2	1561.5	2983.3	2190.2	723.8
331.4	5761.3	4931.8	2173.6	4504.3	4934.5	2845.5	2989.1	5317.8	4529.2	1353.7
208.5	4112.4	3203.1	1545.7	3148.0	3328.6	2632.1	2073.4	3097.6	2361.7	1044.5
996.9	3466.7	2465.3	1374.7	2009.4	2572.4	1254.8	1764.8	2171.9	1668.9	1234.8
744.2	8298.7	7091.2	3968.4	5972.9	7205.9	5551.8	4896.2	6868.4	5023.2	3184.2
1182.5	5244.9	3925.0	2430.3	4930.0	4242.4	3973.3	2538.6	3534.5	2996.4	1629.1
1182.7	4293.2	3411.5	2577.8	3586.7	3103.3	3063.7	2670.7	5763.0	4238.9	2591.2
334.5	4279.2	3155.1	1174.8	2512.7	3287.4	1900.9	1679.8	3256.2	2483.5	816.5
7990.3	3625.0	3193.6	2805.2	4425.9	3257.9	3307.4	3184.6	3653.5	3460.3	3820.6
2147.7	7789.4	6314.3	5689.8	6484.9	6381.4	5801.5	5573.3	9011.0	7345.9	6946.2

3844.7	4118.5	4030.2
2854.1	2035.4	2606.1
2830.2	2859.4	3575.2
4232.1	3619.4	3516.2
2923.5	2297.8	3816.3
5442.3	3868.1	4416.9
4929.7	4031.0	4678.5
4039.7	3524.1	4101.1
6481.8	5349.5	6783.4
4558.1	3061.3	4650.4
3335.2	2650.1	2617.4
2137.6	3157.2	2430.7
2741.2	1970.3	2146.5
5151.8	4357.1	5131.7
1517.1	2117.3	3855.1
6407.3	6066.1	6016.8
5395.7	4277.8	5691.9
2663.3	1635.0	2478.0
2939.6	3096.5	2930.1
1069.3	888.4	1174.7
4083.2	2583.2	3526.1
425.1	893.2	126.2
4965.2	3021.0	3175.2
2381.9	1904.4	2475.2
3259.0	2977.6	4021.1
3014.8	2170.4	2316.8
1855.9	2074.6	2503.1
3298.8	2302.9	3170.2
1243.5	1005.4	2388.9
3583.1	2741.7	4304.9
2835.9	1430.8	1852.3
1945.1	1195.4	1417.8
5057.3	2069.3	2812.9
2948.9	1728.4	2268.8
2223.2	2081.9	1266.1
6304.3	3925.3	4556.3
3724.6	3217.7	3163.4
3820.8	2771.5	2574.8
2443.9	1283.1	1518.6
3824.4	3662.7	3095.6
5753.4	6979.1	6679.2

k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
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k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria

o__Actinomycetales	f__Promicromonosporaceae
o__Actinomycetales	f__Promicromonosporaceae
o__Actinomycetales	f__Promicromonosporaceae
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g__Isoptericola
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g__Xylanimicrobium
g__Aestuariimicrobium
g__Aestuariimicrobium
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g__Microlunatus
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g__Microlunatus
g__Microlunatus
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g__Propionibacterium

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s__Promicromonospora sukumoe	40180
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s__unclassified	40991
s__Xylanimicrobium pachnodae	40608
s__Aestuariimicrobium kwangyangense	40045
s__unclassified	40038
s__unclassified	38525
s__Microlunatus phosphovorus	39321
s__unclassified	38770
s__unclassified	39426
s__unclassified	39863
s__Propionibacterium acidifaciens	40693
s__Propionibacterium acidipropionici	40374
s__Propionibacterium acnes	40139
s__Propionibacterium acnes	40154
s__Propionibacterium acnes	40158

FJ152699.1 gg_id:340107 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FJ152555.1 gg_id:328803 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1525
AJ298873.1 gg_id:52667 Isoptericola variabile str. MX5 AJ2988
EU124554.1 gg_id:249326 Promicrospora sp. str. OSS 3 EU1245
DQ298321.1 gg_id:152486 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AM992980.1 gg_id:285868 Promicromonospora sp. CC0387 str. CC 0387 AM992
AB489222.1 gg_id:546947 Isoptericola halotolerans str. NBRC 104116 AB489
FJ976553.1 gg_id:580704 Promicromonospora sp. str. LCR44 FJ9765
AB023360.1 gg_id:12337 Cellulomonas sp. IFO16239 str. IFO 16239 AB0233
FJ672639.1 gg_id:517982 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6726
AB489223.1 gg_id:570027 Isoptericola hypogeus str. NBRC 104396 AB489
AB546279.1 gg_id:529445 Myceligenerans xiligouense str. IR20-RCA104 AB546
AY354285.1 gg_id:102216 Myceligenerans xiligouense str. XLG9A10.2 AY3542
EU200679.1 gg_id:241390 Promicromonospora cymbopogonis str. YIM 56864 EU200
EU863844.1 gg_id:325500 Promicromonospora sp. D8 EU8638
EU939448.1 gg_id:305873 Promicromonospora sp. str. ERI-01 EU9394
AY929250.1 gg_id:112713 Cellulomonas sp. str. CG-311 AY9292
DQ297997.1 gg_id:142567 Microbial hydrocarbon contaminated soil clone UF11 DQ297
EU677782.1 gg_id:284285 Promicromonospora sp. str. FXJ2.018 EU677
FJ214352.1 gg_id:309033 Promicromonospora sp. str. YIM 61515 FJ2143
GQ263454.1 gg_id:581821 Structure Simulated Level Waste Site simulated level waste site clone FW2_141B GQ263
X83808.1 gg_id:12310 Promicromonospora citrea str. DSM 43110T X83808
AB192130.1 gg_id:142602 termite gut homogenate clone M1NP1-26 AB192
AJ298927.1 gg_id:39735 Cellulomonas sp. str. d20 AJ2989
AB188662.1 gg_id:114038 termite gut homogenate clone Pl-P1-63 AB188
AB188225.1 gg_id:99304 Isoptericola sp. str. TUT1258 AB188
AF403541.1 gg_id:62747 Xylanimonas cellulosilytica str. XIL07 AF4035
AY273185.2 gg_id:137325 Xylanibacterium ulmi str. XIL08 AY2731
NR_024956.1 gg_id:537867 Xylanimicrobium pachnodae str. VPCX2; DSM 12657 NR_024
DQ830982.1 gg_id:165106 Aestuariimicrobium kwangyangensis str. R27 DQ830
EU535598.1 gg_id:279978 profile human microbiota antecubital fossa (inner elbow) skin clone nbt27g07 EU5355
NR_025507.1 gg_id:550057 Luteococcus sanguinis str. CCUG 33897 NR_025
NR_026537.1 gg_id:547562 Microlunatus phosphovorus str. NM-1; DSM 10555 NR_026
AB468984.1 gg_id:370035 Microlunatus sp. str. M5_21 AB4689
AB468985.1 gg_id:360365 Microlunatus sp. str. O37_6 AB4689
EU741106.1 gg_id:566533 Microlunatus aurantiacus str. 13629F EU7411
FJ746024.1 gg_id:581816 Propionibacterium acidifaciens str. C5A_34 FJ7460
AJ704570.1 gg_id:98969 Propionibacterium acidipropionici str. NCFB 570 AJ7045
GQ094638.1 gg_id:409558 Topographical and Temporal Human Skin Microbiome skin nare clone nbw373a01c1 GQ094
GQ008399.1 gg_id:501267 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ008
GQ050607.1 gg_id:418890 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu488a GQ050

196.0	2126.3	2181.4	1594.2	3803.6	2390.7	2384.0	1720.7	1917.9	1943.3	920.2
1198.9	4447.4	4766.9	3013.4	3929.8	5051.7	3661.0	3726.2	3905.3	7504.9	1907.5
68.6	2228.8	1910.4	1599.9	2077.6	1758.3	1898.8	1352.2	188.4	1546.7	1372.1
59.0	3511.4	2933.6	2016.3	3303.9	3283.5	2374.6	1755.9	204.5	2087.4	1287.5
174.0	1421.6	1388.4	1402.0	2142.3	1306.4	1904.1	1684.1	2172.2	1967.9	1401.4
360.1	3783.3	2978.9	3249.5	3817.3	3625.9	3233.6	3044.7	2899.1	1834.2	2743.0
245.1	3552.7	3234.1	2089.0	4235.9	3564.9	3180.3	2165.5	3427.9	2850.2	1781.3
163.6	2945.3	2331.8	1295.4	3065.0	2744.9	1975.0	1562.9	1482.6	1479.2	622.5
160.4	2889.8	2544.7	1487.4	3202.9	2414.4	2695.7	1662.6	2291.7	2013.9	866.9
2362.8	2359.7	1920.0	1511.8	2243.0	2184.9	1760.3	1580.4	3380.4	2998.8	1636.8
743.8	3220.3	2908.9	2417.2	4118.1	3044.1	2749.4	2233.9	3011.5	1627.7	1293.9
97.2	1570.7	1789.5	1677.3	2221.4	1987.2	2567.9	1725.6	1006.5	967.9	674.0
7547.2	1204.7	1150.7	1143.4	885.3	1312.6	1337.9	1004.6	1919.2	1910.8	1893.3
742.9	3203.4	2989.6	2789.0	3047.5	3620.6	2883.7	2736.2	3030.1	1938.0	2104.3
84.6	2413.4	2503.4	1655.0	2794.5	2662.2	2229.3	1815.9	970.2	926.1	707.5
293.0	3489.2	2519.5	2820.6	3758.5	3326.5	3123.9	2325.4	2533.7	1207.2	1437.2
1947.5	5773.5	6269.1	5182.0	6489.0	5817.8	5964.2	5704.5	4134.3	3124.2	4651.8
911.5	2282.2	2692.0	2679.8	3504.3	2728.9	3323.2	2878.8	1685.9	1313.8	1523.4
413.0	3348.3	2800.1	2628.7	3934.0	3590.5	2304.7	2000.0	3560.8	2082.2	1286.4
88.4	1783.4	1851.0	1338.9	2308.9	2278.6	1772.8	1476.0	1209.6	790.4	568.8
2766.7	2357.6	2577.8	1816.5	1635.4	1961.2	1951.9	2098.6	2441.5	1830.3	2862.1
217.0	1570.3	1522.9	1106.8	2280.7	1724.6	1551.6	1107.0	460.3	716.2	532.0
152.2	214.8	272.9	338.7	220.6	275.6	318.7	408.9	240.3	80.8	260.2
2887.5	7907.3	4936.2	2791.6	5435.4	5512.0	4255.0	3103.0	8707.1	4429.8	3406.4
66.1	2879.1	2753.9	2907.2	2256.0	3039.2	2069.8	3634.6	935.6	978.4	2530.2
82.9	1000.7	856.8	880.4	2080.6	1281.8	1632.7	684.8	587.2	501.8	277.8
46.4	492.2	511.0	629.0	1771.1	571.1	986.3	552.2	135.9	310.1	173.4
119.5	1420.0	873.0	1697.7	2551.6	1690.5	2294.9	2336.9	1063.1	917.0	2725.1
284.8	1920.8	1501.8	1395.5	2718.8	1790.5	2364.9	1521.8	1396.7	1320.5	711.7
61.5	246.3	211.1	213.4	575.8	240.8	305.8	176.4	162.4	138.7	99.5
273.9	2714.6	2430.0	2035.3	3488.2	2185.8	2156.1	2011.3	1957.0	1315.7	1304.0
1857.3	6955.1	5613.1	5271.5	4890.4	4779.6	4517.7	4446.5	6397.4	5342.0	4085.4
635.8	2154.3	2187.2	2080.5	4772.7	1597.5	4514.9	2077.3	1316.6	904.5	678.0
974.4	6406.4	5179.5	3896.9	5595.3	4870.5	5802.1	3651.8	2959.2	3125.5	2035.3
158.4	5554.7	5049.9	3962.8	6213.4	5597.2	6061.7	3657.8	4345.9	2421.9	2629.3
339.1	1214.2	1484.6	1344.3	3386.1	1294.5	4143.5	1143.0	331.6	219.3	456.8
3110.3	4331.1	3385.5	3540.6	3610.7	3120.6	3947.8	3050.4	4486.8	3532.6	3259.4
1691.6	269.3	646.6	345.3	274.6	372.9	533.3	453.4	193.5	63.4	67.3
10377.6	6324.5	4946.9	3942.5	4570.4	4394.2	4745.9	3884.5	8654.2	5750.2	4864.8
2606.0	6260.5	4492.4	3383.6	3920.4	4755.8	3400.3	2885.6	4224.2	4406.4	1536.9
23445.2	13313.9	11519.5	11725.6	11749.7	11099.6	12703.4	10330.6	16872.1	11708.3	13886.6

3073.3	1546.3	1971.6
3724.2	3120.7	2995.7
1283.8	1414.4	1334.8
3370.9	1951.8	1852.8
1472.7	1474.8	991.5
3094.6	2995.6	3676.6
2955.4	1729.9	2439.1
2116.1	1519.8	1504.2
2004.1	1300.7	1625.5
2659.4	1999.2	1548.8
2371.1	2149.2	2216.8
2111.3	2675.8	1834.6
1078.0	1638.7	1331.0
3309.0	2991.7	2516.2
2043.4	1615.7	1670.2
2530.9	2488.2	3029.7
4886.4	5409.6	4968.8
3017.4	2979.8	2701.6
3297.5	1883.5	2326.9
1652.3	1302.7	1403.1
1488.2	2111.5	1577.7
1901.9	1305.7	1645.6
214.7	341.6	540.8
3739.9	2829.9	2601.8
1893.1	4815.9	3075.8
873.1	1052.2	1410.0
690.6	260.6	575.3
1620.6	1262.1	1955.2
1462.5	1235.3	1624.4
240.3	334.9	190.9
2445.9	2069.0	2055.1
3859.5	5008.1	3822.1
2797.4	1530.0	2375.3
5078.0	3430.1	3885.1
4155.5	3100.1	5016.9
1631.8	963.8	1800.9
3344.0	2818.3	3863.8
1332.1	249.8	310.2
4838.7	3475.6	3441.6
4346.8	3619.4	3056.4
11092.0	10607.9	10821.0

k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
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o__Actinomycetales	f__Propionibacteriaceae
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s__Propionibacterium granulosum	40241
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GQ051243.1 gg_id:449196 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ051
GQ106569.1 gg_id:370772 Topographical and Temporal Human Skin Microbiome skin back clone nbw537e04c1 GQ106
GQ026553.1 gg_id:458827 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ026
GQ052941.1 gg_id:387423 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ052
GQ067374.1 gg_id:418416 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ067
GQ022070.1 gg_id:487598 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GQ112208.1 gg_id:420444 Topographical and Temporal Human Skin Microbiome skin nare clone nbw585h06c1 GQ112
GQ060511.1 gg_id:436699 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw02f06c GQ060
GQ496494.1 gg_id:567406 Identification Clinically Important Anaerobic Oligonucleotide Array Propionibacteriu GQ496
GQ092956.1 gg_id:411059 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407c03c GQ092
GQ054501.1 gg_id:437722 Topographical and Temporal Human Skin Microbiome skin back clone nbw1089g02c GQ054
GQ011586.1 gg_id:498081 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw793g11 GQ011
AB264622.1 gg_id:170705 Propionibacterium sp. S555a AB264
GQ060886.1 gg_id:384273 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw06h GQ060
GQ057389.1 gg_id:464911 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ057
GU207838.1 gg_id:532671 Propionibacterium freudenreichii str. RVS-2 ims GU207
FJ785716.1 gg_id:546238 Propionibacterium granulosum str. D-34; ATCC 25746 FJ7857
FJ670843.1 gg_id:531274 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6708
EU109728.1 gg_id:245155 Propioniferax sp. str. P7 EU109
GQ090834.1 gg_id:390034 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw338g07 GQ090
GQ091072.1 gg_id:438367 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw341g10 GQ091
GQ090846.1 gg_id:420909 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw338h07 GQ090
GQ099297.1 gg_id:397493 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
GQ091027.1 gg_id:390575 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw341c06 GQ091
GQ088463.1 gg_id:458596 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
GQ060387.1 gg_id:403866 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ060
AF234623.1 gg_id:49248 Propionibacterium microaerophilum str. M5 AF2346
GQ089244.1 gg_id:372676 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ089
GQ091275.1 gg_id:421815 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw344b06 GQ091
GQ093411.1 gg_id:412498 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ093
GQ091123.1 gg_id:425273 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw342d09 GQ091
GQ045670.1 gg_id:447050 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw9 GQ045
GQ086271.1 gg_id:456275 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
AJ704571.1 gg_id:99121 Propionibacterium jensenii str. DSM 20535 AJ7045
GQ091315.1 gg_id:437589 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw344e12 GQ091
GQ088206.1 gg_id:462314 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
GQ084644.1 gg_id:432192 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ084
AJ315953.1 gg_id:18155 Propionibacterium propionicum str. DSM 43307T AJ3159
GQ036180.1 gg_id:434076 Topographical and Temporal Human Skin Microbiome skin palm clone nbu361b09c1 GQ036
AJ003058.1 gg_id:12704 Propionibacterium propionicum str. DSM 43307 AJ0030
GQ036216.1 gg_id:391736 Topographical and Temporal Human Skin Microbiome skin palm clone nbu361e11c1 GQ036

23344.3	11376.5	9858.0	10713.2	9167.6	9572.3	10168.9	9384.4	15373.8	12421.4	14512.7
7625.6	7420.1	6008.7	5306.0	5632.6	6179.7	5678.2	4927.7	8642.5	5982.5	6092.4
21972.6	5531.1	5458.7	5867.8	4998.4	5295.2	6244.2	3909.3	8282.9	5833.9	9293.3
37579.0	12876.7	11716.7	12908.1	12708.2	11606.1	13598.5	12168.3	15138.2	13820.3	17751.8
2563.9	3320.5	4002.5	4076.3	4412.9	3300.0	4499.9	3895.8	3145.7	1764.3	3007.3
6572.5	8852.2	6433.1	5505.6	6852.9	6916.7	6479.7	5852.6	10109.9	6657.0	4548.6
3581.9	6960.9	5624.7	4786.9	5428.0	5473.2	5791.6	4681.7	7482.6	5059.3	3816.0
2417.1	7140.4	6731.5	6028.7	5054.4	6343.3	5451.0	5170.5	8043.6	7305.6	7370.8
6955.7	4076.0	3354.6	3604.0	3585.8	3860.0	3838.9	3232.6	4004.0	3657.0	3829.3
5310.7	3987.0	4057.5	4447.9	4895.4	3956.2	6090.5	4126.3	3750.5	1993.9	3514.3
26434.7	10249.2	10162.1	10113.8	9019.5	9258.9	10101.6	9257.8	14599.3	11249.3	14557.1
4118.4	5876.6	5035.0	4456.2	5144.8	4876.3	5484.7	4535.4	7881.1	5457.6	3649.5
3734.2	3241.6	2671.5	2692.8	2463.1	2934.6	2762.8	2914.8	3989.0	2482.6	2025.8
1932.9	1309.1	1144.6	1089.9	1175.5	1206.9	1182.2	1248.5	1573.0	882.5	694.2
22126.3	12559.8	11817.4	12504.7	12286.0	11220.2	13777.9	11028.0	14504.2	11741.8	15628.2
44.5	54.7	95.2	78.4	37.0	26.2	65.6	95.5	35.1	34.7	26.1
374.1	955.6	1010.5	1021.3	1094.2	995.3	1187.8	1014.6	563.8	370.0	491.6
146.7	2666.1	2535.3	2529.0	3068.3	2404.5	3167.2	2636.4	2180.5	1533.9	2024.9
96.9	564.0	606.9	426.5	613.9	322.6	585.9	433.7	201.1	170.2	124.8
1670.0	10616.9	6812.4	3664.6	4779.2	6172.2	4822.6	5205.8	11117.0	9530.5	4772.5
2561.3	5859.3	4782.6	4747.5	5023.9	5252.2	5269.6	4733.9	8130.0	7829.4	4797.1
1009.7	2386.4	3108.9	2963.9	2781.2	3056.1	3777.4	3423.0	2409.0	2975.6	2607.2
1026.2	5507.3	4526.0	4048.4	3936.2	4397.0	4354.4	4606.9	4616.3	3776.1	3792.8
4150.0	2402.6	2237.1	2562.0	2817.2	2332.9	2576.0	2002.5	3635.6	2096.7	3583.5
2867.0	4409.6	3388.7	2854.5	3272.2	3402.7	3639.9	2837.4	4957.0	4209.0	2791.8
6424.8	10731.0	8030.8	7783.2	8213.4	8041.5	7856.5	7264.5	10063.8	11562.6	9553.6
4309.1	4418.4	3641.7	3122.4	3341.4	3300.6	3886.6	2957.3	5083.2	3871.3	2568.5
6341.5	10036.2	7572.7	7316.0	6539.6	7437.5	6562.4	6706.2	9666.2	8235.6	8360.4
630.9	2590.3	2226.1	2496.5	2624.1	2124.5	2996.6	2287.8	2952.3	2152.0	2042.6
22910.3	11964.9	8843.5	8698.7	8531.2	8740.6	8927.5	7705.6	13746.1	12671.8	12530.7
23912.5	15569.8	12317.2	12087.5	11930.6	12571.5	12321.3	10808.2	17931.2	14851.5	14693.1
7852.9	11788.2	8885.0	8517.1	8341.7	8907.4	8550.1	7863.8	11905.3	11016.6	10601.5
6849.4	10956.4	8101.5	6860.7	7877.9	9338.6	7390.7	6046.6	11305.3	9890.9	7168.0
2026.1	6016.3	5003.7	4681.4	4992.3	5445.4	5605.4	4442.5	6169.4	4645.0	3423.9
6079.3	9950.1	6917.1	6636.7	7551.5	7236.1	7139.8	5941.5	9455.4	8148.5	7687.4
4449.8	11568.1	8734.3	7462.0	8256.4	8631.4	7529.7	6419.8	12280.7	10813.4	9457.4
7563.0	10257.4	7323.0	6532.7	6292.2	7567.7	6903.1	5949.3	10015.6	7293.3	10997.5
507.1	6988.4	5852.5	3907.9	6716.2	6289.4	5919.0	4438.9	6434.8	6692.8	2916.7
34393.4	15267.5	13231.7	12816.6	13694.7	15400.8	13342.6	11266.8	19855.8	15122.1	16008.2
642.4	1128.6	1477.5	1004.5	4062.7	2726.5	1592.2	877.1	350.3	276.8	395.9
1377.9	4788.5	4694.2	3639.3	3232.1	3468.0	3629.0	3806.3	4381.1	3144.6	6028.7

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4756.9	4834.5	5304.0
5632.5	6045.2	5055.4
11730.5	13568.3	13021.5
4118.3	3706.2	4557.8
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5878.8	4292.3	5249.9
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1400.0	2901.6	3615.9
5299.6	3199.8	4684.8
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3514.8	2703.2	2441.9
2635.0	942.4	1169.1
10778.4	11479.0	13365.5
62.7	119.2	95.1
923.1	1238.0	878.7
2347.0	2655.5	2745.1
467.9	399.4	264.0
6436.6	3842.7	3815.4
3949.8	4571.9	4729.3
3362.5	4914.3	3967.9
4522.9	5155.9	4909.4
2139.8	2265.2	2174.2
3845.8	2538.0	3124.5
5472.6	6527.7	8799.9
3823.1	4234.6	2979.4
5042.4	6475.2	7821.8
2262.8	2315.7	2519.5
7968.1	8281.4	8247.0
11131.6	12479.4	11314.2
6161.4	8321.9	8902.3
5270.7	6431.8	6519.3
5508.1	5060.5	5826.4
4870.5	5695.7	7090.4
7815.4	7125.9	7062.1
6169.2	5984.8	5708.1
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1545.6	722.2	602.2
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GQ043231.1 gg_id:459328 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ043
GQ091232.1 gg_id:430735 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw343f10 GQ091
GQ090863.1 gg_id:449128 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw339b0! GQ090
AF287757.1 gg_id:19216 human subgingival plaque clone BN085 AF287
GQ085552.1 gg_id:375238 Topographical and Temporal Human Skin Microbiome skin palm clone nbw277d11c: GQ085
GQ090718.1 gg_id:448658 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw337e0: GQ090
GQ090874.1 gg_id:396731 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw339c0! GQ090
GQ083160.1 gg_id:456924 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ083
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GQ103317.1 gg_id:380647 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw698h0 GQ103
GQ086181.1 gg_id:450935 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ086
FM872539.1 gg_id:365921 occupant source house floor dust clone FA01H03 FM872
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GQ115623.1 gg_id:432335 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw688e1(GQ115
GQ089320.1 gg_id:407284 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ089
AF225962.1 gg_id:23815 Propionibacterium australiense str. LCDC-98A072 AF225!
GQ098576.1 gg_id:403746 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw703h GQ098
GQ037338.1 gg_id:377401 Topographical and Temporal Human Skin Microbiome skin palm clone nbu392b04c1 GQ037
GQ021953.1 gg_id:487714 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ088169.1 gg_id:392612 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ088
GQ103682.1 gg_id:392003 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw700a0 GQ103
AJ937773.1 gg_id:115376 Propionibacterium jensenii str. NCFB 571 AJ9377
GQ034613.1 gg_id:396087 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ034
AM393882.1 gg_id:241064 Tessaracoccus flavescens str. SST-39 AM393
FM872645.1 gg_id:357208 occupant source house floor dust clone FA04E09 FM872
FJ671028.1 gg_id:516124 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6710
FM178840.1 gg_id:312491 Tessaracoccus sp. str. KSS-17Se FM178
DQ521508.1 gg_id:174732 Antarctic lake ice cover clone ANTLV2_C06 DQ521
GU111566.2 gg_id:561672 Tessaracoccus sp. str. SL014B-20A1 GU111
DQ539501.1 gg_id:168713 Tessaracoccus bendigoensis SBRD13 DQ539
AF038504.1 gg_id:12733 Tessaracoccus bendigoensis str. Ben106 (ACM 5119) AF038!
FM872874.1 gg_id:367851 occupant source house floor dust clone FB04A12 FM872
FJ478779.1 gg_id:512068 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EU289501.1 gg_id:249430 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched : EU289!
EF522316.1 gg_id:219813 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS09(EF5223
FJ595541.1 gg_id:568735 rock Black Canyon New Mexico: and Geochemistry rocks no varnish clone NV56_1c12 FJ5955
FJ479278.1 gg_id:538835 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
DQ366007.1 gg_id:156337 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone DQ366
EU289514.1 gg_id:249330 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched : EU289!
FJ478884.1 gg_id:578917 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788

1853.5	2159.6	1782.6	1944.9	2052.1	1796.7	2069.5	1808.5	2493.3	1815.7	2164.6
1687.3	5973.3	4655.6	4316.8	4244.6	4742.3	4852.9	4508.8	5395.3	4851.9	4797.9
2046.3	4203.3	4408.9	3631.6	3503.7	3753.0	4348.1	3902.3	4770.3	3197.6	5931.4
1396.7	2414.6	2384.1	1961.7	2366.9	1723.9	2266.7	2239.3	1292.6	977.5	1575.5
17302.3	5837.2	5733.7	4068.0	7258.8	6206.9	6789.1	5227.1	7641.6	6081.5	8250.5
4412.1	3852.1	3366.6	3135.1	2934.6	3330.9	3218.9	3133.8	3827.3	3356.4	4654.5
383.8	1909.2	1229.6	1193.2	1021.6	1203.8	1415.7	1080.3	1227.9	737.4	927.8
4993.3	9104.2	6826.1	5718.4	6738.7	6958.8	6734.0	5093.1	9327.2	8334.4	5932.5
1492.5	5263.1	4769.1	3842.3	3480.0	4283.0	4352.0	3943.9	5601.0	4824.4	6401.4
2353.8	6632.5	5439.1	5615.7	5655.9	5180.8	5641.6	5633.6	6966.2	7941.7	5743.4
1723.9	5964.1	4209.2	3195.2	3828.3	4213.6	3920.1	2751.0	5791.2	5289.5	3333.7
11799.4	3327.8	2778.7	2900.1	2543.4	2765.6	2815.0	2489.5	3779.9	2718.0	4830.5
618.4	2706.5	3207.5	3092.1	4192.7	2616.7	5497.4	2612.3	1869.3	2479.4	1871.0
6960.0	12277.1	8068.9	7404.8	7484.8	8155.2	7215.9	6671.0	11681.2	10830.6	9652.9
901.1	5466.1	4086.5	3744.4	3418.9	4107.6	4008.3	3784.5	3955.0	3489.5	3748.6
13807.0	9095.7	6881.7	7904.4	6673.7	6198.4	7245.8	6868.5	9404.5	6867.6	13105.7
1376.6	833.4	1059.9	920.3	1870.2	942.6	1079.5	990.0	466.0	274.9	300.2
1909.0	5999.7	5676.8	4183.6	4017.7	4332.9	4668.4	4294.2	5738.8	5048.4	7184.7
849.0	8069.5	5509.8	4028.9	4974.7	4995.0	4556.2	4709.8	8256.6	8640.9	4176.9
5707.9	8427.7	5579.3	4247.9	5935.2	5130.8	4972.5	4413.2	8776.3	8290.7	5013.5
8970.6	6361.5	5554.6	4934.1	4712.6	4926.2	4679.3	4576.6	6843.4	6389.1	5543.5
1253.4	8820.8	5612.0	4813.7	5536.6	5900.2	5154.4	4687.9	8456.6	6238.5	5541.2
3648.7	5705.3	4891.0	3931.0	4256.9	5281.1	4631.5	3735.1	7619.3	5530.8	4240.1
26797.2	9547.8	6868.4	8952.1	7910.1	7686.2	9045.1	7429.6	12474.6	11298.7	14349.5
4292.9	5659.2	5500.7	5874.8	7868.4	5741.5	7989.7	5245.0	5007.4	3875.0	4687.9
3058.3	3992.8	3319.3	2042.9	4071.2	2861.0	2975.2	3112.4	5032.6	3894.5	2492.7
19087.3	5648.0	5490.8	6313.2	5966.5	5349.0	6317.7	5480.6	5619.8	6122.7	6777.7
10791.4	8418.6	8286.4	7133.2	8097.4	7259.1	7716.2	6341.4	8803.7	8467.1	7353.4
69.4	1554.2	1633.6	1872.3	3109.9	1637.2	3174.6	1659.7	1280.1	774.7	879.5
377.2	5915.8	5047.0	4329.9	5084.6	4272.5	5964.0	4305.1	6134.8	3377.2	3409.9
46.0	176.2	376.4	197.1	455.4	208.3	1009.5	266.1	142.8	55.4	92.5
66.2	3398.9	2355.5	1934.5	2556.3	2021.9	2237.1	2601.4	2875.8	2163.8	2432.0
343.9	1983.7	2039.9	1778.9	3726.4	1725.7	4813.4	1763.3	621.7	221.9	732.3
689.9	1238.5	1539.7	1993.8	2306.8	1284.6	2234.8	1837.9	1333.0	1552.1	1076.6
154.6	2881.1	3132.7	3368.9	4457.8	2531.0	4916.1	3153.4	2021.8	1781.3	2210.2
1510.0	2916.1	2624.2	2883.7	4365.2	2578.7	3685.8	3107.6	2947.0	1588.0	2297.3
174.7	3049.3	2725.4	2189.8	3026.0	3172.4	3520.1	2126.3	2492.3	1857.6	1079.1
263.9	6351.8	5917.4	5697.8	7331.0	4866.7	7441.3	5513.0	5455.5	4534.5	3830.4
1976.0	9369.9	6825.7	4745.0	6869.6	5632.7	6623.4	4842.6	10499.8	6261.8	4402.3
709.3	2964.1	3295.5	2537.2	3012.4	2591.3	3365.3	3130.9	1461.8	1385.6	2181.1
2201.1	8424.8	7593.0	6638.2	8002.9	7341.1	7946.4	7174.5	13108.3	12804.7	6050.2

2049.2	2119.1	1855.5
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3874.1	2771.8	3635.8
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3699.7	4660.6	4530.5
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1787.1	734.8	1075.7
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5061.4	5883.3	6042.4
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EU861867.1 gg_id:315847 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU8618
AJ003056.1 gg_id:12734 Propionimicrobium lymphophilum str. DSM 4903 AJ0030
DQ196625.1 gg_id:170832 Brooklawnia cerclae str. BL-34 DQ196
EU980607.1 gg_id:326457 Propionibacterium sp. str. B2M2 EU9806
GU002063.1 gg_id:579455 Actinoalloteichus sp. str. FXJ7.260 GU002
AB184362.2 gg_id:153970 Streptomyces chromogenus str. NBRC 13374 AB1843
EU429488.1 gg_id:550861 producing pigmented colonies aerosol and soil s remote glaciated areas (Antarctica / EU4294
AY129771.1 gg_id:59961 Amycolatopsis sp. str. GY276 AY1297
AF214482.1 gg_id:49974 Amycolatopsis lactamdurans str. NRRL 3802 AF2144
AJ243301.1 gg_id:54677 Amycolatopsis lactamdurans str. LC411 AJ2433
AJ293754.1 gg_id:91736 Amycolatopsis mediterranei str. IMSNU 20056T AJ2937
AY083604.1 gg_id:67634 Amycolatopsis mediterranei str. F1/24 AY0836
AY125600.1 gg_id:63752 Amycolatopsis mediterranei str. KCTC 1739T AY1256
EU570741.1 gg_id:274446 Amycolatopsis thermoflava str. 173573 EU5707
EF017716.1 gg_id:187664 Amycolatopsis mediterranei str. SIIA 0093 EF0177
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EU551680.1 gg_id:362413 Amycolatopsis sp. str. C17 EU5516
AF223354.1 gg_id:37332 Amycolatopsis sacchari AF2233
EU593588.1 gg_id:269209 Amycolatopsis coloradensis str. 173617 EU5935
AF466100.1 gg_id:55272 Amycolatopsis sp. str. GY295 AF4661
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EF371434.1 gg_id:210721 Amycolatopsis orientalis str. 14143 EF3714
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AY129774.1 gg_id:59955 Amycolatopsis sp. str. GY088 AY1297
DQ076482.1 gg_id:145675 Amycolatopsis minnesotensis str. 32U-2 DQ076
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AB327254.1 gg_id:244000 Amycolatopsis iriomotensis str. TT 99-32 (= NBRC 103392) AB3272
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725.2	3457.1	3084.7	2466.4	3853.8	2793.6	4185.4	2275.4	2400.9	1059.2	1618.2
190.9	1404.5	1315.7	1064.9	908.8	1082.7	947.2	1019.8	940.1	557.8	824.3
55.8	85.5	124.3	133.5	140.0	110.7	152.7	153.4	115.7	97.0	69.8
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97.5	1830.2	1730.4	1729.3	2960.1	1942.2	2031.1	1931.2	1151.7	1002.6	1401.0
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37.2	496.9	444.1	149.5	2723.6	631.7	1435.7	795.9	431.5	185.9	213.1
58.4	695.6	605.2	668.4	1046.5	906.3	485.4	1141.4	578.2	380.3	180.6
64.7	199.2	198.2	177.4	752.0	305.8	319.4	266.8	84.2	188.0	85.8
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AF408986.1 gg_id:104427 Amycolatopsis sp. str. Ellin144 AF408
AY262825.1 gg_id:88192 Amycolatopsis plumensis str. SBHrStrp1 AY2628
AF222022.1 gg_id:32724 Amycolatopsis rubida str. 13.4 AF222
DQ792500.1 gg_id:164705 Amycolatopsis saalfeldensis str. HKI0457; 2406-001 DQ792
GQ381310.1 gg_id:588889 Amycolatopsis sp. str. RM287 GQ381
AB327251.1 gg_id:257675 Amycolatopsis albidoflavus str. NBRC 100337 AB327
NR_025088.1 gg_id:546057 Crossiella equi str. NRRL B-24104 NR_02
AB327258.1 gg_id:242624 Goodfellowia coeruleoviolacea str. NBRC 14988 AB327
AM422451.1 gg_id:244880 Jiangella alkaliphila str. YD8-87 = JBRI 2008 AM422
AB297964.1 gg_id:245309 Prauserella rugosa str. NBRC 14506 AB297
FJ444996.1 gg_id:554357 Prauserella sp. Ms498 str. MS498 FJ4449
GU292537.1 gg_id:549001 Prauserella sp. str. AE-4y GU292
FM956091.1 gg_id:525091 Prauserella sp. str. 05-Be-005 FM956
DQ344632.1 gg_id:145056 Pseudonocardia sp. str. YIM 45505 DQ344
Y08534.1 gg_id:12927 Pseudonocardia halophobica str. DSM 43089 Y08534
AY340622.1 gg_id:91804 Pseudonocardia dioxanivorans str. CB1190 AY340
EF589993.2 gg_id:233686 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5899
FJ478886.1 gg_id:509487 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU722521.1 gg_id:309461 Pseudonocardia yunnanensis str. YIM 11981 EU722
DQ448727.1 gg_id:159042 Pseudonocardia sp. str. CNS004 PL04 DQ448
AY921961.1 gg_id:114587 farm soil clone AKYG1573 AY9219
FJ948110.2 gg_id:566127 Pseudonocardia sp. str. P3TTW2701 FJ9481
EF216360.1 gg_id:215732 Pseudonocardia sp. TFS 1235 EF2163
AY221600.1 gg_id:88338 metal and hydrocarbon contaminated soil clone HN1-47 AY2216
AJ252833.1 gg_id:30436 Pseudonocardia kongjuensis str. LM 157 AJ2528
DQ343763.1 gg_id:147510 Pseudonocardia sp. YIM 43848 DQ343
DQ448726.1 gg_id:157755 Pseudonocardia sp. str. CNS139 PL04 DQ448
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EU722520.1 gg_id:319257 Pseudonocardia xinjiangensis str. XJ 45 EU722
AB521672.1 gg_id:590285 Pseudonocardia sp. str. MN08-A0297 AB521
AJ252828.1 gg_id:43413 Pseudonocardia petroleophila str. IMSNU 22072T AJ2528
GQ082333.1 gg_id:411845 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw11 GQ082
AB546273.1 gg_id:523314 Pseudonocardia sp. str. RI44-RCaA106 AB546
EU722523.1 gg_id:327290 Pseudonocardia sp. str. S053 EU722
AJ252829.1 gg_id:51028 Pseudonocardia saturnea str. IMSNU 20052T AJ2528
AF325727.1 gg_id:27130 Pseudonocardia aurantiaca AF3257
AJ252830.1 gg_id:44587 Pseudonocardia thermophila str. IMSNU 20112T AJ2528
GQ924573.1 gg_id:550512 Pseudonocardia sp. str. ACT-0146 GQ924
AB547126.1 gg_id:518306 Pseudonocardia spinosa str. JCM 3136 AB547

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2382.1	1849.1	1603.1	1509.5	2337.2	2034.3	1903.0	2292.0	1894.3	1639.2	1487.8
214.1	1690.2	1687.8	1986.2	584.7	1844.4	1298.7	1887.0	840.3	455.1	891.7
1980.7	1106.8	998.3	1013.0	1810.7	1072.4	1227.1	1406.3	1445.9	1036.3	703.9
18362.1	5661.0	7811.4	7014.7	7282.0	6212.0	7652.7	7161.8	10211.4	4314.1	9989.6
907.1	1970.7	1388.1	1321.7	2130.2	1522.1	1321.8	2042.5	1167.6	835.0	687.5
3170.4	7830.0	7100.7	6360.2	7124.8	7735.8	6510.2	7194.3	8022.9	7954.2	5728.7
251.7	1134.9	960.0	812.0	1674.7	739.9	1262.4	614.7	949.2	494.0	359.8
123.1	1440.9	1540.7	1340.4	1780.6	1583.5	1534.7	1240.7	953.5	690.4	430.5
683.1	1218.0	1232.8	1322.3	2979.5	1250.3	2131.2	1214.3	365.8	192.3	531.0
48.1	36.6	50.3	51.8	61.1	39.6	54.7	58.6	46.0	39.7	39.8
447.0	2840.5	2085.2	1630.3	4886.8	2421.7	2439.1	1946.6	3044.1	2009.6	655.3
47.0	2426.7	1955.9	1186.2	2429.1	1694.3	2136.3	1844.5	1417.3	1236.2	551.3
4266.5	3811.1	3943.2	3845.7	5357.2	3428.2	5608.7	3830.0	4394.5	1774.2	3615.1
55.0	597.3	763.0	814.1	2957.3	1196.2	1373.1	808.6	353.2	298.9	282.5
1192.2	3991.8	3343.8	3429.6	6574.8	4162.0	4612.4	4144.6	3296.2	3571.5	3263.3
40.7	590.3	368.1	564.4	4065.5	453.0	739.3	477.4	169.1	324.9	230.4
69.2	1860.1	1896.0	2127.7	4295.9	1638.5	3140.6	1444.4	501.6	583.7	829.6
201.0	2009.8	1239.5	1288.5	4014.8	1863.3	2149.9	1337.4	754.1	560.0	961.1
259.0	2456.4	2024.6	1112.9	3550.9	2754.2	2087.8	1089.8	2396.7	2430.7	679.5
67.3	974.5	1013.3	870.6	3128.8	1056.3	1206.7	861.6	524.1	444.6	509.2
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461.5	1239.0	1080.0	1251.6	2455.7	1189.5	1653.8	999.7	1399.0	1032.7	833.8
92.5	1219.1	985.0	643.4	2077.7	990.7	834.7	463.3	1026.4	667.9	321.3
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37.3	125.0	163.4	176.1	360.0	161.7	134.0	216.7	115.8	41.8	82.9
242.8	1937.6	1806.5	2010.3	6622.7	1935.9	2959.1	2189.6	3131.0	1246.1	795.6
2129.2	8025.6	4603.2	2628.3	6269.3	5511.6	4121.0	2455.8	6448.9	4773.7	2555.1
37.2	366.5	295.1	351.8	2544.3	414.4	649.0	231.2	160.3	206.9	104.5
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1452.8	1231.9	1936.4
49.9	75.9	29.1
1756.2	1087.9	1833.2
2063.7	1140.8	1617.5
4018.3	2929.9	3042.4
787.7	831.3	1388.9
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706.9	298.3	794.0
1809.6	1009.5	1358.6
1695.2	1453.1	1262.0
1365.0	1325.5	1904.1
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1710.3	1055.7	1785.1
1209.7	1159.9	1560.0
500.5	586.2	1059.7
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AJ249206.1 gg_id:42025 Pseudonocardia spinosispora LM 141T AJ2492
EU722519.1 gg_id:319688 Pseudonocardia alaniniphila str. YIM 16303 EU722
GQ065789.1 gg_id:440748 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw93a04c GQ065
DQ129564.1 gg_id:138207 microarray level air two cities Texas urban aerosol clone AKIW476 DQ129
NR_029323.1 gg_id:577382 Pseudonocardia asaccharolytica str. 580; DSM 44247 NR_02
NR_025213.1 gg_id:550950 Pseudonocardia chloroethenivorans str. SL-1; ATCC BAA-742 NR_02
GQ263688.1 gg_id:533011 Structure Simulated Level Waste Site simulated level waste site clone FW3_85C GQ263
AY500143.1 gg_id:104434 Pseudonocardia sp. H9 str. H9; AS 4.1877 AY500
EU921261.1 gg_id:314065 Pseudonocardia sp. str. GMKU095 EU921
FJ805426.1 gg_id:400950 Pseudonocardia sp. str. EUM 374 FJ8054
AB074634.1 gg_id:77990 actinobacterium clone:APe4_52 clone APe4_52 AB074
NR_027229.1 gg_id:533270 Saccharomonospora glauca str. K62; DSM 43769 NR_02
EU430565.1 gg_id:561390 Saccharomonospora viridis str. VTT E-062998 EU430
EU741223.1 gg_id:558024 Saccharomonospora sp. str. 13672A EU741
AF127525.1 gg_id:13020 Saccharomonospora thermoviridis str22.1 AF127
Z38018.1 gg_id:13024 Saccharomonospora cyanea str. M. Goodfel K168=NA134 (type s Z38018
AM420293.1 gg_id:214755 Saccharopolyspora erythraea str. NRRL 2338 AM420
DQ381814.1 gg_id:154705 Saccharopolyspora hirsuta str. ATCC 27875 DQ381
EU741165.1 gg_id:535215 Saccharopolyspora antimicrobica str. 13651G EU741
AF154128.1 gg_id:12942 Saccharopolyspora flava str. AS4.1520T AF154
AF002819.1 gg_id:12943 Saccharopolyspora taberi str. DSM 43856T AF0028
EU132839.1 gg_id:247530 tallgrass prarie soil clone FFCH13846 EU1328
DQ923129.1 gg_id:181203 Saccharopolyspora halophila str. YIM 90500 DQ923
EU741232.1 gg_id:510614 Saccharopolyspora sp. str. 13674Q EU741
EU421887.1 gg_id:268513 Un-culturable Indian Himalayas soil under glacier Lahaul-Spiti Valley clone KC-86 EU4218
DQ069279.1 gg_id:160968 Saccharopolyspora pogona str. NRRL 30141 DQ069
DQ438939.1 gg_id:150863 Saccharopolyspora sp. str. ASL9 DQ438
EF104116.1 gg_id:186068 Saccharopolyspora shandongensis str. 88 EF1041
EF030715.1 gg_id:214049 Saccharopolyspora cebuensis str. SPE 10-1 EF0307
EF687715.1 gg_id:257520 Saccharopolyspora salina str. YIM 91168 EF6877
AM992060.1 gg_id:297261 Saccharopolyspora sp. str. IMMIB L-1070 AM992
EU005371.1 gg_id:241577 Saccharopolyspora gloriosa str. YIM 60513 EU005
U58524.1 gg_id:11987 Thermobispora bispora str. JCM3082 U58524
AF116559.1 gg_id:12128 Thermomonospora chromogena str. ATCC43196 AF1165
U83911.1 gg_id:11990 Thermobispora bispora str. ATCC19993 U83911
EU132635.1 gg_id:239404 tallgrass prarie soil clone FFCH10565 EU1326
EF372523.1 gg_id:215682 Actinopolyspora iraqiensis str. DSM 44640 EF3725
AY921685.1 gg_id:113711 farm soil clone AKYG500 AY9216
DQ367416.2 gg_id:155544 Saccharomonospora salina str. YIM 90502 DQ367
FJ478624.1 gg_id:555033 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786

82.8	3592.7	3663.9	3860.4	9010.3	3690.2	5540.1	4245.9	1998.4	2340.6	2581.4
166.2	1894.0	2077.3	2139.7	7408.3	2226.8	3699.5	2546.4	1506.1	756.0	1239.5
90.9	1286.4	1123.7	812.2	2839.6	1169.3	1193.1	785.4	825.8	578.5	629.9
779.9	3784.9	2433.3	3019.9	5610.6	3684.9	3563.0	3394.5	2333.5	1502.1	1908.9
308.4	3715.8	2561.4	2412.5	6345.9	3512.8	3383.6	2324.7	2959.0	1931.9	1365.1
1460.3	1156.6	1004.0	838.4	1374.7	1051.3	819.4	894.3	654.4	435.8	626.4
2221.5	7712.3	5951.0	5224.0	7900.6	6602.1	6544.6	5446.9	7124.8	7594.2	4317.8
81.5	5572.9	4570.7	4571.1	9584.0	4502.3	5423.7	4318.5	5541.9	4600.6	4950.4
80.5	424.8	429.2	510.8	2525.0	556.0	614.0	452.3	290.9	211.1	198.1
185.5	1287.0	1272.9	1562.0	5121.4	1696.4	1980.2	1590.8	766.6	611.0	908.2
59.3	645.0	592.9	338.9	3124.0	552.3	1098.4	312.9	697.3	400.0	363.5
50.5	3282.8	2513.9	1945.6	9206.4	2202.6	3340.1	1928.4	3306.1	2474.0	938.8
570.4	5672.1	5448.6	4619.2	5853.2	5564.2	5605.7	3922.4	3232.0	2950.5	2579.4
12925.6	6043.6	6064.7	6100.3	5756.8	5713.0	7027.8	5410.0	6443.3	4765.0	4579.6
3098.5	2797.0	3007.1	3327.9	3592.9	2966.0	3992.8	2828.8	2836.4	2995.0	3627.6
25235.5	8152.7	9084.2	8376.8	10263.8	8052.2	9459.1	7701.1	12360.2	8249.8	11034.4
499.5	5145.0	4596.1	3093.3	5164.3	4208.9	4715.4	2968.8	5317.8	3031.7	2461.4
76.3	2999.1	2173.1	1545.0	3869.8	2171.2	1864.8	2083.8	1860.5	1625.6	728.8
106.8	3113.8	3858.7	2187.0	5136.1	2904.9	3314.7	2866.8	2530.6	1579.3	849.5
203.3	1848.1	1485.6	1254.6	2401.6	1545.0	1487.8	1408.4	1432.1	737.3	650.8
75.6	2275.4	2143.4	1503.3	2262.0	2886.4	1260.3	1334.0	1132.1	927.7	738.4
60.4	3099.2	2260.6	1731.4	5019.4	2523.6	2223.6	2394.2	2142.8	1435.8	789.1
2598.0	6562.5	6352.9	5340.1	7475.4	5921.5	6408.9	5374.0	8939.4	6502.9	6766.9
2199.3	5219.2	4011.9	4114.4	3852.8	5370.7	3793.4	3030.9	4484.1	4511.2	3461.8
74.2	732.7	778.5	725.0	2063.6	961.4	1057.0	841.1	312.6	449.0	310.3
318.2	2002.2	2593.8	2245.0	3814.6	2815.7	2111.5	3264.6	1588.0	2406.2	2536.4
1181.2	1956.2	1857.0	1908.5	4778.8	1893.5	2265.9	2181.6	1643.0	1029.2	1094.7
176.6	1766.4	1627.4	1890.7	4433.0	2352.2	2327.1	2145.2	763.0	809.4	715.5
36.0	61.7	71.6	93.0	214.0	48.4	148.9	92.3	62.2	86.9	36.8
1179.5	4337.2	3863.9	3595.2	4039.4	3882.0	3640.2	3410.0	5052.5	5099.4	3035.9
397.5	3685.4	3424.7	3001.7	4765.6	3558.4	3884.4	3464.3	2266.9	3222.0	1972.8
186.0	1095.2	1276.4	1219.1	3225.1	1178.6	1260.4	1511.9	562.4	532.0	721.0
290.5	3470.7	3024.7	2768.1	4844.2	3556.9	3675.0	3983.0	2458.8	3311.4	1578.6
56.0	704.8	1048.5	1117.9	686.0	507.7	720.4	850.4	392.5	205.4	822.6
66.7	79.3	55.4	40.9	94.1	51.2	60.7	33.1	44.6	31.7	30.0
54.0	369.0	586.2	503.0	521.7	476.5	554.6	677.9	125.8	337.7	244.7
479.7	1703.3	1782.2	2302.6	2221.1	2305.1	2411.2	2604.1	2749.7	1862.3	1331.7
430.6	2438.4	3003.3	3344.5	3627.6	2608.2	4377.3	2448.0	1648.2	1341.2	1950.3
2095.9	7862.8	6704.6	6182.3	7277.2	7166.2	6403.1	5060.0	10788.2	5916.9	4564.8
891.2	2806.3	3694.9	3185.1	4113.9	2786.6	2865.7	3027.1	2150.7	2675.4	2572.4
421.0	2781.7	3031.1	2715.7	4748.7	2932.1	3434.4	2662.6	3565.7	1999.4	1463.3

4224.2	4305.2	5725.9
3012.3	1998.0	3086.0
798.8	1463.7	1422.8
3782.6	2512.8	2901.5
2784.0	2204.1	2769.0
850.1	1126.3	610.6
5363.5	5817.6	6107.4
4977.0	4405.3	5742.4
647.0	406.7	670.6
1395.2	1532.7	1484.5
444.3	319.7	311.5
3241.6	1906.5	2855.8
5035.1	4543.4	6604.1
6178.0	5777.8	5644.4
3262.1	3926.7	2840.9
8007.7	9167.1	7770.4
3982.7	2402.9	3648.2
2285.7	1716.4	2457.2
2759.5	1971.6	3341.1
1772.5	1413.1	1658.3
1082.7	790.7	934.3
2461.8	2100.8	2644.4
4858.2	6304.3	6623.8
3062.4	3151.7	3239.0
1187.4	752.4	1054.8
2877.6	2462.4	3070.0
2247.0	1885.8	2307.5
2351.5	1993.2	2808.5
182.1	80.7	27.5
3214.4	4101.3	2460.0
3653.3	3617.3	3418.2
1500.2	982.7	1554.5
4632.3	2636.2	4350.9
613.3	1415.6	672.5
30.4	43.2	62.7
434.0	471.5	1361.3
2544.7	1712.8	1875.4
2322.7	3073.8	3615.5
5010.0	4596.8	4644.1
3086.4	2506.7	3188.2
2355.9	2093.8	1879.4

k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
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o__Actinomycetales	f__Pseudonocardiaceae
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o__Actinomycetales	f__Pseudonocardiaceae
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o__Actinomycetales	f__Rarobacteraceae
o__Actinomycetales	f__Rarobacteraceae
o__Actinomycetales	f__Sanguibacteraceae
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s__Streptacidiphilus luteoalbus	38586
s__unclassified	38762

DQ298375.1 gg_id:153720 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
X79184.1 gg_id:12701 Thermocrispum municipale str. DSM 44069 X79184
DQ298343.1 gg_id:154591 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
AJ278497.2 gg_id:19135 Saccharomonospora halophila str. DSM 44411T AJ2784
GQ263071.1 gg_id:573070 Structure Simulated Level Waste Site simulated level waste site clone F2_20X GQ263
FJ671681.1 gg_id:515526 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
FM209146.1 gg_id:550414 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr FM209
AB056127.1 gg_id:72525 Rarobacter faecitabidus str. IFO 14760 AB056
AB056128.1 gg_id:73335 Rarobacter faecitabidus str. IFO 15223 AB056
AB056129.1 gg_id:71022 Rarobacter incanus str. IFO 16558 AB056
X79452.1 gg_id:12353 Sanguibacter suarezii str. ST26 X79452
X79450.1 gg_id:12361 Sanguibacter keddieii str. ST74 X79450
EF211071.1 gg_id:240818 Sanguibacter antarcticus str. KOPRI 21702 EF2110
FJ675290.1 gg_id:525081 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
GQ064897.1 gg_id:422208 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ064
AB126692.1 gg_id:104435 Sanguibacter sp. str. SG-4 AB126
AY608920.1 gg_id:100442 Segniliparus rugosus str. CDC 945 AY6089
FJ468343.1 gg_id:544911 Segniliparus rotundus DSM 44985 str. CIP 108378 FJ4683
X72377.1 gg_id:11449 Sporichthya polymorpha X72377
EF490376.1 gg_id:225724 Speleomyces feengrottensis str. HKI 0501 EF4903
AB184625.1 gg_id:154012 Kitasatospora cystarginea str. NBRC 14836 AB1846
AB184778.2 gg_id:154942 Streptomyces sayamaensis str. NBRC 3519 AB1847
AB022879.1 gg_id:23352 Kitasatospora griseola str. OM-5023 AB0228
AB022870.1 gg_id:45323 Kitasatospora griseola str. AM-9660T (IFO14371) AB0228
AB022875.1 gg_id:51815 Kitasatospora cineracea str. SK-3255 AB0228
AB184576.2 gg_id:153892 Kitasatospora setae str. NBRC 14216 AB1845
AB249960.1 gg_id:161362 Kitasatospora niigatensis str. NBRC 16453 AB2499
AB278568.1 gg_id:258936 Kitasatospora saccharophila str. SK15 AB2785
U93316.1 gg_id:24904 Kitasatospora cochleata str. IFO 14768 U93316
U93326.1 gg_id:11797 Kitasatospora melanogena str. JCM 3337 U93326
AB022869.1 gg_id:50005 Kitasatospora phosalacinea str. KA-338T (IFO 14372) AB0228
AB022871.1 gg_id:32322 Kitasatospora cochleata str. IFO14768T AB0228
AB184593.1 gg_id:153821 Streptomyces atroaurantiacus str. NBRC 14327 AB1845
AF050493.1 gg_id:11816 Kitasatospora cheerisanensis str. YC75 AF0504
U93314.1 gg_id:11790 Kitasatospora phosalacinea str. IFO 14627 U93314
U93324.1 gg_id:11823 Kitasatospora mediocidica str. IFO 14789 U93324
U93328.1 gg_id:11795 Kitasatospora paracochleata str. 14769 U93328
EU841634.1 gg_id:317386 Kitasatospora phosalacinea str. HBUM174554 EU8416
AY999756.1 gg_id:133142 Streptomyces albolongus str. JCM 4716 CSSP414 AY9997
AY530188.1 gg_id:100103 Streptacidiphilus luteoalbus str. IS091 AY5301
AY530182.1 gg_id:99174 Streptacidiphilus griseosporeus str. IS104 AY5301

144.6	738.1	854.6	736.1	1686.7	906.1	1336.7	698.5	450.4	181.5	484.3
47.9	216.2	201.4	156.3	277.5	178.9	212.1	173.4	151.3	202.1	99.1
287.5	5138.6	3821.8	2393.7	2170.1	3731.8	2464.5	2337.7	2441.2	2138.6	1474.5
372.6	1299.1	1327.9	1524.6	2043.8	1437.3	2269.8	1113.1	922.6	918.3	824.2
918.6	4722.3	4037.5	2636.1	4454.3	4406.4	3962.5	2921.7	4358.0	3564.5	2314.2
297.1	5536.8	4852.5	2925.7	5753.9	4613.1	3688.0	3241.6	6006.8	4904.9	2407.1
94.9	5383.2	3498.0	1429.4	2829.3	3266.9	1824.4	1991.8	4985.4	2280.3	1303.2
52.0	54.5	103.9	78.7	98.2	91.2	67.5	98.6	48.9	73.9	41.7
27479.4	4265.3	3899.9	4628.6	5162.7	4253.5	5177.0	4140.5	6063.6	6257.3	8287.3
4945.7	4729.2	4631.3	3636.1	7889.3	5081.9	5956.5	3685.5	4072.0	3032.1	2793.0
5709.1	9728.4	6334.2	4479.9	5837.5	6139.4	5697.0	5206.0	11328.3	7257.8	5942.7
1221.1	10124.0	9723.1	5565.6	6962.9	8342.5	6962.2	5956.6	11171.6	9702.4	5686.6
137.8	6719.2	5403.1	3009.1	3335.4	4209.7	3188.8	3750.5	5428.1	3857.4	2985.6
15859.6	8822.0	7947.2	9332.3	9235.6	8814.0	9364.2	8640.7	10936.4	7650.2	9668.4
15971.8	13812.6	11366.1	9900.7	10610.0	12425.1	10543.4	9468.1	12656.7	10765.2	9188.2
1200.4	2860.1	2859.4	2543.3	2450.3	2806.7	3738.2	2212.3	2349.0	1969.4	2619.2
554.4	2974.6	2367.8	2722.0	2692.1	2828.5	2208.3	2676.1	2809.2	1709.3	1087.3
302.7	1093.9	983.4	1386.8	2095.9	1163.3	2318.5	1465.1	599.3	376.1	729.5
82.9	2810.4	1861.6	1391.6	3907.6	1771.7	2965.1	1551.3	4076.7	1572.3	691.2
65.9	1085.6	1175.8	1236.5	2517.2	1152.4	2263.1	1333.2	773.5	611.9	628.1
686.8	4078.9	3544.9	2999.3	4762.2	4198.8	4217.5	2957.1	2988.6	3467.5	2675.2
457.9	4092.1	3779.2	3262.7	4752.5	4014.9	4170.2	3600.4	4381.4	3314.0	2820.4
335.0	3291.4	2983.1	2515.1	3594.9	2897.2	3163.9	2297.5	3532.0	3502.3	2592.1
45.5	567.4	594.2	459.8	1162.8	500.4	905.3	553.3	360.3	248.8	229.3
5011.5	4733.6	4022.1	3852.3	4479.9	3771.0	4331.1	3843.5	4621.6	3315.2	3987.5
114.5	656.8	635.3	704.0	1070.1	489.5	675.3	554.9	282.0	201.1	218.5
1593.2	2840.5	2629.5	2672.7	3434.9	2685.1	2916.4	2347.3	2505.1	2151.5	2571.6
131.9	573.7	534.8	510.9	963.2	411.7	636.3	455.4	302.3	306.4	173.5
43.4	3270.6	1876.8	186.7	308.0	951.7	262.6	972.2	3073.8	2315.1	588.5
1903.8	3205.7	2598.2	1569.4	2580.0	2542.0	2019.7	2149.9	3767.1	2681.6	2025.1
133.0	932.4	876.3	883.9	1399.9	797.7	924.5	852.4	568.6	527.3	298.2
2989.2	5126.0	4110.1	3696.7	4547.4	4204.5	4084.9	3708.1	3893.8	3677.5	3847.5
1446.8	6349.7	5185.3	4767.4	5060.6	5039.3	4911.9	4403.1	5167.1	5657.7	4069.2
273.5	1397.5	731.7	1294.9	1696.5	1263.0	1834.4	1234.5	1202.7	1197.0	1440.0
2188.9	6209.4	5214.3	4878.5	6108.9	4905.7	5834.1	4562.5	6160.7	5259.1	4834.1
410.9	7248.7	5708.5	4237.1	5950.1	4847.1	5140.5	4688.3	6034.7	4941.3	2912.4
1361.7	6325.2	5400.0	4598.8	4737.3	4298.8	5376.5	4797.0	6665.5	5078.5	3144.6
135.9	454.2	578.9	500.5	733.6	369.7	389.6	457.2	262.9	317.6	154.5
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5157.2	1965.2	4186.8
6490.2	5247.9	6384.4
3757.1	2489.5	3022.9
8281.3	8260.1	8146.5
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2470.4	2491.9	3242.1
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1747.9	1225.9	1819.8
2103.2	1326.5	1736.1
1639.9	1300.0	1397.6
4673.6	2864.5	3415.2
3668.3	3316.1	3250.3
2983.2	2405.1	2493.8
903.4	437.6	941.1
3686.9	4126.1	5015.3
826.7	724.7	775.4
3121.4	2605.6	2883.4
754.3	534.3	640.4
280.9	383.7	256.1
2442.2	2171.1	2337.6
1110.1	913.4	993.7
4212.9	4572.4	4342.4
4923.9	4972.2	5622.0
1592.0	1011.8	1183.5
5505.1	4672.3	4979.2
5238.7	3951.0	5993.0
4566.9	4914.2	4219.9
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2615.5	2022.7	2397.7
2023.4	1482.1	1592.5

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AY314780.1 gg_id:89875 Streptacidiphilus jiangxiensis str. 33214 AY3147
AY389139.1 gg_id:98108 Streptacidiphilus jiangxiensis str. 22202 AY3891
AF074410.1 gg_id:11828 Streptacidiphilus neutrinimicus str. JL 206; DSM 41755 AF0744
DQ375791.1 gg_id:156760 'Candidatus philanthi' endosymbiotic Streptomyces antennae Philanthus digger was DQ375
DQ375781.1 gg_id:156988 'Candidatus philanthi' endosymbiotic Streptomyces antennae Philanthus digger was DQ375
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FJ262968.1 gg_id:352835 Streptomyces sp. str. 30702 FJ2629
DQ375796.1 gg_id:156975 'Candidatus philanthi' endosymbiotic Streptomyces antennae Philanthus digger was DQ375
AY297778.1 gg_id:107435 Nocardiopsis sp. str. 10035 AY2977
DQ375790.1 gg_id:156884 'Candidatus philanthi' endosymbiotic Streptomyces antennae Philanthus digger was DQ375
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DQ375798.1 gg_id:156839 'Candidatus philanthi' endosymbiotic Streptomyces antennae Philanthus digger was DQ375
AY207588.1 gg_id:104995 Streptomyces acidiscabies AY2075
AY207589.1 gg_id:105144 Streptomyces acidiscabies AY2075
AB258461.1 gg_id:157832 Streptomyces acidiscabies AB2584
AY621376.1 gg_id:103501 Streptomyces acidiscabies AY6213
DQ448786.1 gg_id:157671 Streptomyces sp. MAR4 str. CNR927 PL04 DQ448
X87316.1 gg_id:11848 Streptomycetaceae SR 257 X87316
EU214946.1 gg_id:276605 Streptomyces sp. str. CNS-776_SD06 EU2149
EU273528.1 gg_id:247332 Streptomyces ahygroscopicus XSD-122 EU2735
EU285475.1 gg_id:240031 Streptomyces ahygroscopicus str. XSD-130 EU2854
EU814698.1 gg_id:355035 Streptomyces diastatochromogenes str. TUST-2 EU8146
AY999748.1 gg_id:133201 Streptomyces albireticuli str. JCM 4116 CSSP396 AY9997
FJ377308.1 gg_id:370257 Streptomyces albireticuli str. HSX001 FJ3773
EF017719.1 gg_id:199229 Streptomyces kitasatoensis str. SIIA 0194 EF0177
AB184720.1 gg_id:156160 Streptomyces stramineus str. NBRC 16131 AB1847
AY845349.1 gg_id:109871 Streptomyces alboniger str. DSM 40043; ATCC 12461; KCTC 9014 AY8453
FJ919750.1 gg_id:440086 Streptomyces griseoruber str. cfcc3080 FJ9197
EU200685.1 gg_id:252170 Streptomyces artemisiae str. YIM 63135 EU2006
AY094363.1 gg_id:112075 Streptomyces sanglieri str. A5843 AY0943
AY094364.1 gg_id:111900 Streptomyces sanglieri str. -CR2 AY0943
AB006159.1 gg_id:11777 Streptomyces microstreptospora str. IFO14669 AB0061
EU570531.1 gg_id:265847 Streptomyces atratus str. 173450 EU5705
AY999839.1 gg_id:133090 Streptomyces misakiensis str. DSM 40222 CSSP704 AY9998
DQ462659.1 gg_id:158418 Streptomyces aureofaciens str. B197 DQ462
AB184322.1 gg_id:151583 Streptomyces aureofaciens str. NBRC 13183 AB1843
AY442263.1 gg_id:102444 Kitasatospora nipponensis str. HKI 0315 2148-13 AY4422
GU350486.1 gg_id:552019 Streptomyces avellaneus str. MJM9859 GU350
AF060792.1 gg_id:11825 Kitasatospora sp. str. C2 AF0607
EU521696.1 gg_id:264063 Streptomyces aureofaciens S38-2 EU5216

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957.5	4752.7	4140.6	3840.4	4376.1	4027.0	4219.1	3450.8	4577.4	2956.4	3160.0
65.4	873.7	942.2	1046.4	2116.0	1053.7	1705.9	974.2	352.5	397.8	436.8
266.2	1551.9	1473.1	1463.1	3060.9	1753.7	2218.5	1590.9	1373.7	1301.7	556.7
234.8	1246.2	1171.8	1236.2	2536.7	1276.4	1917.5	1225.7	1110.9	1011.8	480.7
40.0	572.0	548.5	553.0	1088.4	563.6	845.4	755.4	407.0	586.6	253.5
40.4	57.4	193.3	138.0	476.2	108.9	315.7	47.4	31.1	56.5	25.5
55.9	659.1	612.7	705.9	1468.5	630.0	1096.2	835.2	476.2	460.5	234.9
531.0	1981.2	1870.6	2322.4	2615.7	1968.7	2613.0	2065.2	1578.4	1435.8	1906.3
44.3	795.3	666.2	610.4	1206.6	687.3	904.3	861.7	704.6	539.4	270.8
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1613.4	2156.7	3756.8	3843.0	4966.0	3726.7	4965.0	3253.2	1569.4	1458.6	3531.2
35288.8	10655.7	9494.9	10736.4	10954.4	9961.6	8772.2	9123.8	13953.5	9675.4	12227.8
5611.4	8295.9	7447.1	7876.1	8143.3	7654.4	8132.0	7223.6	8028.4	7046.4	7739.3
106.1	2097.0	1921.9	1134.5	1906.9	1971.5	2501.8	940.2	1847.9	1684.1	433.5
149.8	4075.6	3967.2	4712.6	4422.1	3698.2	3517.5	3604.5	4908.1	2372.3	3177.3
223.3	5552.5	4837.3	3700.0	4593.4	4891.2	3846.8	3440.1	5073.3	3041.0	2299.4
2177.2	1836.9	1652.9	2171.6	2655.5	1906.3	2428.1	1815.1	1293.3	1197.1	1215.2
2274.8	2394.8	2094.2	2329.9	3515.1	2571.0	2989.7	2252.5	2422.6	1913.2	1364.5
2567.3	3784.4	3084.0	2698.9	3022.1	2627.8	2305.1	2786.1	4224.4	2999.3	2322.2
141.1	3434.8	2541.2	1908.6	2969.0	2878.8	2242.5	1947.2	1965.4	1605.9	650.0
160.0	2952.3	2639.9	2253.2	2440.5	2994.5	2010.4	2151.5	2438.5	1537.2	897.3
64.7	98.5	119.3	100.0	109.7	83.8	121.3	95.0	76.5	50.3	71.6
68.2	1894.5	1483.1	1055.0	1724.6	1289.0	1506.2	1308.1	771.3	967.1	607.1
1179.3	1625.9	1772.8	1852.7	2324.7	1863.9	2582.4	1940.7	1394.0	890.5	1066.9
55.3	2260.7	2670.5	1986.0	2183.4	2299.0	2418.8	2089.8	1427.8	1226.0	1235.8
783.1	4321.7	3900.2	3444.2	5003.2	4286.4	4250.1	3593.1	4252.8	4224.3	2724.0
95.4	2072.1	1521.7	559.1	1109.4	1187.0	1182.4	919.3	1956.7	1557.1	632.2
164.6	984.5	1045.4	982.5	1913.7	1150.7	2688.7	1361.2	713.2	357.8	654.7
5472.4	3938.6	2568.9	2529.3	3715.2	2767.8	3231.7	2771.1	3946.1	2946.0	4619.2
59.0	434.4	329.2	295.7	636.2	388.2	457.2	352.5	456.4	359.0	144.7
1699.4	7523.7	6587.8	6514.9	7200.9	6871.8	7028.8	5781.2	5911.2	5960.0	6347.0
183.8	2835.3	2162.9	1674.7	3032.7	2450.0	2806.9	1815.0	3348.3	2125.4	1245.9
472.3	3694.1	2929.5	2456.5	4112.8	3484.0	3723.8	2502.9	4065.0	2922.2	2370.9
1343.5	5674.0	5387.5	5063.3	5299.1	5636.2	5649.4	4956.5	4674.9	5053.4	5103.2
982.2	6652.3	5885.2	5231.9	6404.5	5744.9	6054.7	5396.8	6664.8	5080.6	4211.3
904.2	5486.7	4209.5	3778.4	4805.6	4290.9	3944.7	3756.8	5018.2	3226.1	2544.2
9898.7	12777.9	10290.1	9163.2	10167.6	10778.6	9755.0	9125.0	12704.0	11677.3	10804.7

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1794.6	1319.1	1842.3
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701.7	561.7	1058.4
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2556.1	2272.2	3205.4
3259.7	4405.4	4867.4
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1797.5	1728.4	2271.3
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2234.3	1900.2	1836.1
2545.8	1465.3	2040.3
2178.4	1355.2	2027.7
77.7	113.9	117.3
1427.6	937.1	1315.2
1809.2	1527.2	1881.9
2371.6	1550.7	1954.4
3097.0	3320.5	4039.5
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2201.4	781.7	2085.0
2936.3	2972.5	3033.5
383.7	199.6	357.6
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2863.2	2071.9	2603.4
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AY442264.1 gg_id:102601 Kitasatospora kifunensis str. HKI 0316 2122-22
EU570483.1 gg_id:276150 Streptomyces avermitilis str. 173436
DQ408296.1 gg_id:153449 Streptomyces sp. ZS1-2
EU570694.1 gg_id:258703 Streptomyces avidinii str. 173905
EU841668.1 gg_id:350854 Streptomyces avidinii str. HBUM173531
EU593747.1 gg_id:277025 Streptomyces avidinii str. 173484
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AB249910.1 gg_id:160145 Streptomyces blastmyceticus str. NBRC 12747
AY999892.1 gg_id:132775 Streptomyces griseoverticillatus str. 4.1842 CSSP434
AB184520.1 gg_id:151500 Streptomyces sp str. NBRC 13838
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EU170121.1 gg_id:248679 Streptomyces ascomycinicus str. DSM 40822
AJ391827.1 gg_id:42266 Streptomyces yogyakartensis str. (S3) C4R3
AB249963.1 gg_id:160896 Streptomyces indonesiensis str. NBRC 100776
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AY999807.1 gg_id:134383 Streptomyces griseoviridis str. KCTC 9780 CSSP672
AB184643.1 gg_id:153460 Streptomyces champavatii str. NBRC 15392
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EU570650.1 gg_id:274685 Streptomyces niveoruber str. 173557
GQ176865.1 gg_id:588304 Streptomyces argenteolus str. TH-105
EU841654.1 gg_id:327778 Streptomyces niveoruber str. HBUM173783
EU273543.1 gg_id:235781 Streptomyces krainskii XSD-107
GU350508.1 gg_id:572463 Streptomyces parvisporogenes str. MJM12043

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6144.1	7569.9	6460.0	6300.9	6280.9	5352.5	7018.4	5891.2	9017.1	8409.7	6417.3
790.7	6237.4	4948.6	2984.1	2828.8	5474.4	3982.6	3048.8	5732.0	3612.9	2405.8
252.2	10794.2	7647.7	3914.5	4550.9	8589.6	4540.9	4780.5	10573.9	5600.5	2658.2
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1102.2	7163.9	5377.7	3089.5	3247.2	6400.2	4026.8	3077.6	7078.4	4280.9	2114.6
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68.2	1302.1	1118.1	1136.5	1389.4	1194.9	1271.9	939.3	375.0	369.0	518.3
250.4	5709.3	4494.7	4160.1	4502.8	5097.8	3983.5	3707.5	3160.1	2542.0	2096.0
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211.8	5164.4	3685.3	3833.2	3800.4	3952.8	3654.4	3232.5	2786.8	1914.0	2040.1
213.7	4757.1	3902.4	3472.0	4145.2	4017.1	3911.3	4106.4	4037.1	3759.3	2665.0
768.8	6577.9	6348.7	6983.4	6298.9	7142.0	6939.5	6777.1	5528.1	10022.6	5155.3
9754.7	4520.9	4575.9	4650.4	4533.5	5655.2	4992.7	4459.7	5386.4	4203.5	6032.7
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428.9	1956.3	1374.1	954.7	1230.0	1429.4	1355.0	1174.8	2141.9	1217.2	645.3
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4647.2	3334.5	2247.3	2269.0	3004.1	2383.8	2616.2	2403.9	4785.7	2280.0	1908.9
2472.8	1017.0	766.9	934.2	1329.0	819.3	1126.8	1001.2	907.7	644.2	720.0
1958.3	946.1	1017.0	924.1	1176.0	896.0	905.6	1035.1	876.9	897.2	769.1
2346.5	2297.2	1879.5	1566.3	2238.3	1847.5	1651.1	1753.2	2573.3	2005.5	1316.6
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2251.0	4362.0	3506.6	2785.2	3435.6	3167.1	2842.9	3195.8	5566.1	3912.2	2453.4
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4175.6	3698.9	5695.7
3408.3	3019.1	6078.2
2122.9	2264.6	4821.2
2453.8	2402.0	4349.9
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1537.0	1183.5	2612.8
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1262.8	615.7	1267.1
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AJ621609.2 gg_id:104579 Streptomyces chrestomyceticus str. DSM 40545
AJ007399.1 gg_id:37438 Streptomyces somaliensis str. DSM 40760
X81573.1 gg_id:11846 Amycolatopsis lurida str. DSM43187
AB184480.1 gg_id:154743 Streptomyces lividus str. NBRC 13787
EU196762.1 gg_id:245021 Streptomyces hypolithicus str. HSM#10
EU570619.1 gg_id:265667 Streptomyces chryseus str. 173642
EU593575.1 gg_id:263280 Streptomyces chryseus str. 173624
AB184717.1 gg_id:153136 Streptomyces cinnamoneus str. NBRC 15927
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FJ442824.1 gg_id:553328 Streptomyces sp. str. PNA
FJ610322.1 gg_id:548605 Streptomyces sp. str. GT1005
DQ462661.1 gg_id:159011 Streptomyces cuspidosporus str. B200
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EU841567.1 gg_id:336972 Streptomyces cyaneofuscatus str. HBUM173522
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AB184537.1 gg_id:154669 Streptomyces abikoensis str. NBRC 13860
AB249967.1 gg_id:161573 Streptomyces abikoensis str. NBRC 12887
AB184867.1 gg_id:151882 Streptomyces ehimensis str. NBRC 13470
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EU841658.1 gg_id:318873 Streptomyces cinnamocastaneus str. HBUM173422
FJ436402.1 gg_id:553672 Streptomyces sp. str. TN119
GU350503.1 gg_id:562428 Streptomyces polychromogenes str. MJM11317
FJ532421.1 gg_id:564720 Streptomyces virginiae str. HBUM175141
FJ799186.1 gg_id:532841 Streptomyces sporoverrucosus str. MJM8425
DQ531624.1 gg_id:161059 Actinomyces sp. str. sw20
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FJ532453.1 gg_id:546498 Streptomyces virginiae str. HBUM175148
FJ532415.1 gg_id:537207 Streptomyces lavendulae str. HBUM175130
FJ799190.1 gg_id:575056 Streptomyces sporoverrucosus str. MJM8863
AB249931.1 gg_id:159980 Streptomyces flavovariabilis str. NBRC 100764
EU570674.1 gg_id:265387 Streptomyces flavoviridis str. 173309
GU434674.1 gg_id:531574 Streptomyces sp. str. AH4
FJ532419.1 gg_id:535017 Streptomyces bellus str. HBUM175137
EF585403.1 gg_id:232846 Streptomyces sp. str. 23F
EU294134.1 gg_id:245533 Streptomyces pulcher str. CRF17
FJ486431.1 gg_id:556810 Streptomyces cellulosae str. HBUM83819
FJ547110.1 gg_id:554267 Streptomyces rubrogriseus str. HBUM175156

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66.2	997.4	1038.9	1460.1	1891.1	1159.9	1668.6	1086.8	441.6	443.9	532.4
74.1	3713.9	2906.7	2287.1	2184.6	2356.4	1656.4	2484.4	4463.8	2870.7	2011.8
514.7	7708.7	5486.8	4352.6	4874.7	5842.0	4498.0	4829.8	7390.9	6146.9	3310.7
16081.9	8430.3	7821.4	8591.9	7623.4	9031.9	8780.0	7474.6	11182.8	8352.4	13230.9
39.0	420.6	565.7	600.7	378.2	611.9	467.1	590.6	361.9	623.9	328.1
88.7	409.8	412.7	193.8	565.0	339.5	544.3	413.7	173.6	127.9	93.2
85.2	1154.4	1192.4	1033.3	1800.5	1280.0	1510.0	1173.4	674.0	454.2	386.6
98.8	1288.1	1320.1	1254.4	2003.4	1488.4	1656.7	1357.5	813.5	618.7	440.9
119.4	2962.5	2395.6	1994.5	2924.2	2666.9	2518.3	1935.0	1738.3	1402.5	937.2
58.6	1047.0	989.1	854.4	1841.2	1088.5	1103.9	1096.0	569.5	953.9	323.2
419.5	3318.0	2878.7	2865.6	3958.3	3560.3	3511.5	2741.0	3368.2	3167.8	2427.1
77.7	1930.7	1747.6	1031.1	1240.0	2547.8	817.3	1050.5	1207.1	847.8	552.5
134.3	1093.3	1150.0	1274.6	2508.0	1097.6	1913.0	1262.3	739.7	839.6	521.3
57.7	1953.5	1724.3	1204.9	1093.9	2690.5	902.0	1125.4	1192.0	754.2	742.5
225.0	3398.4	2865.5	1572.9	2152.7	2301.0	2073.2	2033.6	3784.0	2610.7	1370.8
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532.8	3775.1	3162.3	1854.6	2188.7	2502.1	2612.8	2229.1	2757.0	2293.9	1559.8
2500.8	6378.5	6249.4	6647.0	6269.4	6350.3	7430.9	5648.8	7034.3	6837.2	6122.9
183.9	2520.9	2295.7	1366.8	1871.1	2582.1	1272.1	1664.5	2273.5	1844.8	826.0
89.0	2182.2	1719.7	1146.2	1700.6	1890.2	1343.7	1604.7	684.1	874.1	533.1
159.1	2456.7	2250.5	1334.8	1757.8	2333.3	1351.8	1818.4	2340.5	1724.7	886.2
68.0	1390.1	1228.0	780.2	1487.2	1196.3	1145.5	1223.0	530.8	583.0	373.2
257.7	1936.5	1914.0	1635.8	3330.0	2017.4	2536.9	1963.2	2010.9	1597.0	668.3
44.8	773.2	785.3	359.4	578.2	357.3	429.4	298.2	162.7	137.8	194.3
43.6	278.5	326.7	389.0	586.5	305.0	453.4	290.3	76.3	104.3	132.1
87.6	867.9	644.8	514.4	1280.2	765.9	862.4	603.8	707.8	490.1	205.2
606.9	2158.9	1627.6	1442.0	1323.5	1945.2	1956.7	1371.3	1312.8	1118.7	1112.0
4541.3	4519.3	3614.1	3444.3	3793.5	3555.2	4324.1	3217.6	4530.8	3331.2	3163.5
42.2	220.4	185.7	157.7	311.3	183.4	186.7	196.4	51.3	108.8	94.8
37177.1	11372.9	10507.5	11271.7	10758.0	10544.4	12065.0	9248.1	16104.0	11915.5	14684.7
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12801.3	4752.1	4640.4	4799.2	5337.8	4995.6	4834.2	4876.4	6634.6	5106.1	6122.1
365.6	1859.6	2289.3	1724.6	1325.0	1939.2	1719.0	1544.7	3404.0	78.9	4128.1
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65.2	650.4	652.5	694.2	1229.8	756.9	1053.3	508.5	470.0	497.5	318.3

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1678.4	1267.4	1340.3
4216.1	3405.7	4102.4
6161.3	9067.5	7036.4
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381.3	237.7	655.8
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2575.7	1470.9	2323.4
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206.2	198.1	395.5
746.1	561.4	973.5
1669.3	1409.4	1804.3
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182.5	133.6	464.4
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s__Streptomyces kasugaensis	38846
s__Streptomyces kunmingensis	39472
s__Streptomyces kunmingensis	39611
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AB184710.1 gg_id:153980 Streptomyces aureorectus str. NBRC 15896
AY999828.1 gg_id:132760 Streptomyces djakartensis str. KCTC 9722 CSSP693
AB184282.1 gg_id:154315 Streptomyces malachitofuscus str. NBRC 13059
EF063478.1 gg_id:198574 Streptomyces sp. str. 85Gan103
FJ481630.1 gg_id:534200 Streptomyces olivoverticillatus str. HBUM175186
FJ792574.1 gg_id:513617 Streptomyces hawaiiensis str. cfcc3162
AB184542.1 gg_id:154647 Streptomyces macrosporeus str. NBRC 13897
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EF063497.1 gg_id:189847 Streptomyces flavoviridis str. 4622
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EU570515.1 gg_id:275041 Streptomyces acrimycini str. 173529
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EU570496.1 gg_id:266317 Streptomyces fumanus str. 173498
EU240411.1 gg_id:252273 Streptomyces galbus str. B116
EU273538.1 gg_id:238147 Streptomyces galilaeus XSD-102
AY999761.1 gg_id:131745 Streptomyces coelescens str. JCM 4739 CSSP420
AY699792.2 gg_id:100485 Streptomyces pharetrae str. CZA14
GQ262799.1 gg_id:550453 Streptomyces tricolor str. vh85
FJ486296.1 gg_id:544949 Streptomyces glaucescens str. HBUM173215
AY999881.1 gg_id:130014 Streptomyces griseoaurantiacus str. 4.1837 CSSP402
AB362247.1 gg_id:261747 Streptomyces sampsonii str. JAM-AC0101
GU132473.1 gg_id:585901 Streptomyces coelicolor str. JJA-2
DQ462652.1 gg_id:157646 Streptomyces rutgersensis str. A180
GQ906357.1 gg_id:581208 Streptomyces sp. str. GQQ10
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EU593606.1 gg_id:270305 Streptomyces griseoloalbus str. 173909
EU679113.1 gg_id:288797 Streptomyces sp. 307-9
DQ907256.1 gg_id:168876 Streptomyces sp. str. USVI 211-3
EU593632.1 gg_id:274617 Streptomyces variabilis str. 173652
AY207593.1 gg_id:100343 Streptomyces ipomoeae
AY999920.1 gg_id:130648 Streptomyces kasugaensis str. NRRL B-24288 B24288
EU054382.1 gg_id:247050 Streptomyces sp. str. 9-2
DQ442513.1 gg_id:181248 Streptomyces kunmingensis str. NRRL B-16240T
AF361786.1 gg_id:32361 Streptomyces niveiscabiei str. S78
AB184482.1 gg_id:152876 Streptomyces miharaensis str. NBRC 13791
AB184126.1 gg_id:154558 Streptomyces echinatus str. NBRC 12763

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AY2075
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AB1841

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70.9	1725.4	1284.7	693.7	1835.9	1755.1	1334.3	566.9	1529.2	895.2	277.1
404.8	6182.3	4656.3	3159.0	3352.6	4573.6	2653.5	3227.3	7963.5	4511.5	2370.1
216.7	1506.3	1657.8	1796.1	2734.2	1468.0	2831.5	1533.2	1650.7	1067.8	1060.4
118.1	1003.6	807.7	895.1	1359.8	766.9	937.3	795.6	307.7	684.4	509.2
815.6	510.7	449.7	338.2	432.6	487.0	237.7	509.3	274.8	104.1	176.9
820.5	4680.4	3710.0	3183.5	4973.0	3946.6	3820.6	2973.3	3994.4	3309.7	1770.8
2097.7	1138.5	1039.6	1260.4	1441.9	1069.9	1168.8	1153.8	807.7	670.7	1004.8
86.2	1425.8	1274.4	754.3	1247.6	1120.5	762.9	809.0	1639.3	1146.3	376.9
107.0	1940.5	1536.6	955.7	1438.2	1215.5	905.4	1461.9	2040.3	1650.4	893.9
90.3	441.1	509.5	457.4	1101.6	450.3	684.6	410.1	185.8	296.8	185.6
164.9	1094.5	1204.9	1279.3	2684.6	1363.4	1733.3	874.8	1050.8	1226.9	519.8
419.1	1765.8	1352.5	968.4	1935.4	1503.1	1460.9	1043.9	1901.3	1588.0	519.7
96.6	2600.5	2095.5	1262.4	1598.1	1685.1	1048.9	1508.8	2877.1	2107.2	960.0
63.7	680.1	633.8	232.7	409.3	304.6	295.8	327.2	187.7	156.7	153.8
66.2	1642.0	1320.6	386.3	543.4	634.8	442.6	657.4	852.6	566.0	366.0
87.7	2895.9	2194.7	888.5	922.2	1270.4	672.0	1427.8	2291.3	1569.4	1023.9
69.6	308.0	305.8	322.8	866.6	312.6	507.1	272.4	99.8	177.5	102.4
70.9	796.6	583.8	691.8	1022.8	659.4	567.9	661.1	970.8	611.0	211.4
74.0	3270.8	3441.7	2368.0	2730.2	2765.1	1989.7	2090.5	2032.6	1324.8	1438.3
57.0	2445.2	2163.6	2126.7	2332.9	2417.0	1687.7	1880.5	1863.4	1283.3	1519.9
1589.5	3614.4	3281.3	3945.3	4091.8	3873.5	3818.6	3482.5	3240.8	2846.2	3096.2
17163.2	6374.1	7312.5	6856.4	7656.7	8155.7	7751.7	7268.2	8405.0	6315.0	8224.4
46.1	899.6	949.1	881.7	839.3	955.9	962.4	896.5	504.1	374.0	384.9
2558.4	4556.0	3557.4	2717.3	3099.1	3377.1	2368.0	3029.9	5006.3	3388.7	2227.1
2375.3	1722.8	1428.9	1413.7	2175.5	1667.8	1677.7	1634.7	1974.5	1263.0	1044.0
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39.9	88.6	64.5	83.8	150.8	53.4	78.9	88.8	30.9	38.1	38.1
1492.1	2914.3	2436.4	3140.9	3640.9	3201.3	3884.6	3111.8	2688.9	1739.0	2338.3
50.8	111.3	118.1	112.5	201.4	86.4	102.3	107.2	31.9	73.8	64.8
41.4	602.6	559.8	384.1	509.7	488.8	361.2	555.4	648.8	436.5	252.7
107.0	1662.4	1246.6	1089.2	1975.2	1182.1	1721.5	1149.2	1197.7	786.2	524.1
3892.1	7391.0	6170.3	5708.9	6998.2	6490.7	6537.9	5678.9	10788.8	4490.1	4349.2
45.4	217.3	393.2	361.9	217.4	183.4	163.6	315.4	211.6	107.1	217.9
53.5	1097.1	938.3	806.4	2174.8	963.6	1406.5	821.5	1150.1	678.9	244.0
142.1	1172.0	1090.5	771.0	1554.7	1233.0	1186.9	1186.2	1381.7	1127.8	531.8
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339.7	610.8	318.7	237.3	610.8	218.7	212.5	309.4	621.2	224.3	143.1

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783.1	457.8	1159.1
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1720.7	1990.9	2125.1
957.8	557.5	1183.4
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2975.2	2412.8	3166.1
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850.5	489.4	551.2
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564.4	331.1	668.8
1157.8	761.8	1342.8
2000.7	825.3	1594.3
1229.4	788.7	865.4
319.3	196.0	388.3
472.4	298.3	446.3
813.7	649.1	795.3
437.2	205.9	798.9
616.4	410.0	788.7
1448.1	1399.5	1397.7
1410.9	1154.4	1202.1
2980.7	3666.9	3445.8
6026.6	7714.6	6485.7
577.8	653.7	1227.8
2451.3	2042.9	2391.5
1585.9	1289.7	1372.1
2019.4	1519.3	1655.9
63.0	44.8	76.0
3164.2	3573.0	5003.3
110.5	86.1	185.2
238.0	238.6	227.9
1524.4	971.6	1339.5
6028.7	5541.6	5396.5
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1231.8	688.2	996.2
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s__Streptomyces morookaensis	39267

EU635725.1 gg_id:279485 Streptomyces triostinicus str. CKM7
AF361785.1 gg_id:40357 Streptomyces puniciscabiei str. S77
GU084132.1 gg_id:583367 Streptomyces sp. A7(2009b) str. A7
EU571130.1 gg_id:258962 Streptomyces sp. str. 2-9
EU216596.1 gg_id:246148 Streptomyces recifensis str. ST100
AB184845.1 gg_id:153041 Streptomyces lanatus str. NBRC 12787
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AB184344.2 gg_id:152493 Streptomyces thioluteus str. NBRC 13341
EU240414.1 gg_id:254417 Streptomyces longwoodensis str. B126
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EU413900.1 gg_id:270043 Streptomyces sp. str. 42-2
GU084129.1 gg_id:575170 Streptomyces sp. str. A4
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GU350494.1 gg_id:574398 Streptomyces malaysiensis str. MJM10645
FJ532460.1 gg_id:541057 Streptomyces malaysiensis str. HBUM80452
AF306660.2 gg_id:53467 Streptomyces sacchari str. N755
DQ442526.1 gg_id:192453 Streptomyces mashuensis str. NRRL B-8164T
EU240408.1 gg_id:256117 Streptomyces olivochromogenes str. B105
GQ867035.1 gg_id:571514 Streptomyces sp. MP2(2009) str. MP2
AB369121.1 gg_id:243715 Streptomyces olivochromogenes str. A018
EU367983.1 gg_id:266636 Streptomyces natalensis str. 20-4
AB184412.1 gg_id:151452 Streptomyces mirabilis str. NBRC 13450
AF112180.1 gg_id:51426 Streptomyces mirabilis str. ATCC27447
AY999842.1 gg_id:131815 Streptomyces morookaensis str. DSM 40503 CSSP707
AB184865.1 gg_id:153103 Streptomyces morookaensis str. NBRC 13461

EU635
AF361
GU084
EU571
EU216
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AY015
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EU413
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AB369
EU367
AB184
AF112
AY999
AB184

78.1	783.4	1639.6	1148.9	2246.8	1424.2	1307.4	1018.3	291.6	276.7	690.9
905.3	2986.7	2999.2	3538.6	5974.5	2961.6	4328.3	2834.2	3421.2	1643.3	2625.4
199.2	905.5	813.0	1166.9	2315.1	808.8	1425.6	1071.2	505.5	362.4	370.6
34.2	924.1	715.7	480.5	938.9	661.8	632.2	467.9	447.9	387.9	166.1
144.4	358.3	526.8	404.2	990.0	406.1	355.0	532.4	244.3	361.6	167.0
191.5	1144.4	937.9	637.1	1202.1	856.5	525.5	963.0	1597.6	739.6	479.8
11866.1	3640.4	3647.2	3761.1	3620.4	3599.3	3290.3	3214.7	4895.0	4014.1	4886.5
146.1	2296.2	1780.2	1645.4	2558.0	1792.4	2056.9	1810.7	1253.7	1290.6	949.0
174.3	1079.9	736.9	624.6	1479.1	633.0	606.5	677.0	1243.7	460.2	233.3
59.9	1557.8	1137.4	912.3	2614.7	1547.0	1563.7	903.0	514.9	496.2	270.8
165.7	1729.9	1350.0	1134.6	2261.5	1477.8	1274.0	1370.8	1741.3	939.2	567.9
2260.7	7182.4	6388.3	6659.8	6340.8	6460.1	6238.7	7063.8	6821.1	4623.0	5834.7
166.9	1768.1	1110.5	743.1	2307.8	1443.9	1304.1	830.6	347.5	500.4	285.6
201.4	1141.7	939.2	631.0	1222.8	854.0	517.6	965.7	1598.1	840.4	479.1
79.0	577.7	433.7	444.2	1305.2	436.9	737.9	490.2	514.6	242.5	144.8
179.0	2357.5	1738.1	616.1	1424.5	892.5	629.9	738.8	1666.7	821.3	380.7
429.5	1009.7	651.5	803.8	1624.5	617.4	945.1	779.3	1801.5	696.2	336.7
1042.0	5858.5	4482.3	2400.9	1679.5	3243.6	2968.1	2601.1	3962.2	3046.5	2484.2
42.2	242.1	188.2	121.1	155.5	179.5	110.9	107.3	118.4	114.1	84.6
580.5	1802.1	1768.7	1958.1	2158.4	2061.8	1909.9	1971.9	1528.6	1279.7	1230.8
74.2	702.2	578.6	659.8	1208.0	728.2	896.8	640.1	618.9	330.7	200.0
1302.2	2194.9	1949.4	1702.1	2683.2	2311.3	2211.2	1449.8	2537.7	1523.3	1138.8
93.8	2071.7	1893.7	1689.3	2207.1	1930.7	1619.3	1883.7	2453.3	1645.9	749.0
59.3	1811.0	1558.7	1112.7	1001.6	2743.9	872.6	985.0	1155.9	650.4	592.6
354.2	3950.2	3189.8	3478.4	3923.6	2997.1	3511.5	2897.8	2996.1	2579.4	1878.8
318.1	4167.7	3239.1	3438.4	4432.5	3087.1	3893.4	2955.4	3115.0	2716.4	1753.3
48.0	590.9	636.2	586.8	830.0	819.1	571.9	640.3	133.7	224.5	193.5
52.2	1846.4	1575.9	1487.9	2457.4	1805.8	1948.6	1355.4	763.6	809.8	654.7
80.9	2798.3	2195.8	2035.9	3151.0	2650.5	2512.6	1866.0	1105.7	1143.2	1011.0
50.5	1301.0	1377.7	1504.9	2317.5	1702.7	1701.7	1273.6	818.3	664.9	717.7
75.0	2690.6	2124.7	1922.4	3190.8	2415.2	2546.2	1784.4	1103.7	1137.4	932.2
3299.3	9417.9	7846.3	6464.9	7689.8	7715.9	8264.3	5918.8	9691.4	7371.3	5769.9
166.8	8394.3	5213.0	4143.2	5066.5	4646.4	4448.2	4127.8	6945.0	4336.4	3009.4
4367.8	4807.8	3879.6	2505.1	3351.5	4069.7	3133.0	2649.1	5144.9	2367.8	1892.0
3717.5	3008.5	2767.3	2818.4	3767.4	3062.6	3636.8	2779.7	3416.2	1989.9	1713.4
3468.1	3374.5	3044.2	3176.2	3503.4	3306.2	3903.5	3418.9	2813.8	1801.5	2139.4
4783.4	2605.2	2291.1	2573.8	2805.5	2472.5	3028.1	2522.1	2576.6	1767.2	1719.7
3479.8	5058.1	4250.8	3172.9	3507.1	3610.5	3645.4	3511.1	3271.5	2169.5	2327.5
4223.5	7613.9	5392.8	3639.0	3511.0	3888.3	3940.4	3744.7	4902.0	3374.3	3618.8
149.0	3345.6	2693.8	2373.8	3524.6	2447.9	3121.3	2250.2	2281.4	2092.5	1236.4
167.6	4670.2	3477.5	2858.3	4309.4	3501.5	3868.1	2779.2	2507.9	2525.7	1466.1

778.9	554.5	776.7
2865.3	2474.6	2977.2
1101.4	581.7	999.2
921.9	474.0	635.2
1121.4	438.3	559.9
589.5	485.8	597.5
2831.7	4179.6	3109.0
1769.2	1247.0	2059.6
553.3	474.8	744.5
1723.3	857.9	837.0
1364.5	1024.0	864.7
5456.0	5508.3	6255.9
1743.5	976.6	701.4
670.5	487.3	463.9
785.8	362.6	895.7
660.2	484.5	861.1
753.3	604.0	795.7
2323.6	2321.4	2812.5
112.1	94.9	389.9
2156.2	1961.8	1878.9
751.4	640.8	828.7
2261.7	1488.7	1763.2
1487.1	1376.3	1461.8
703.9	525.8	871.1
3512.8	2176.5	3373.8
3373.3	2286.0	3733.0
709.2	366.0	1041.4
1799.7	1442.2	1634.8
2462.0	1989.9	2220.7
1492.9	1565.2	1751.3
2440.4	1954.6	2121.6
5795.2	6078.2	8298.5
4175.2	2734.0	3084.2
2871.3	2878.0	3035.6
3033.5	2470.0	3219.1
2960.9	2965.2	2970.2
2237.5	2827.6	2711.4
3030.7	2976.6	3072.4
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2484.7	1781.6	2702.6
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EU570424.1 gg_id:268491 Streptomyces mutabilis str. 173870
EU570495.1 gg_id:264390 Streptomyces mutabilis str. 173376
EU570625.1 gg_id:275876 Streptomyces mutabilis str. 173675
EU593602.1 gg_id:266076 Streptomyces mutabilis str. 173684
EU570683.1 gg_id:263537 Streptomyces spinoverrucosus str. 173372
EU593639.1 gg_id:272633 Streptomyces mutabilis str. 173956
EU570513.1 gg_id:273981 Streptomyces mutabilis str. 173375
EU570627.1 gg_id:272986 Streptomyces mutabilis str. 173637
EF178671.1 gg_id:204130 Streptomyces netropsis str. NRRL 2886
AB249911.1 gg_id:160533 Streptomyces netropsis str. NBRC 12769
AB184612.2 gg_id:153822 Streptomycoides glaucoflavus str. NBRC 14668
DQ026629.1 gg_id:161323 Streptomyces jumonjinensis str. AF1633
EU570584.1 gg_id:260406 Streptomyces nitrosporeus str. 173694
AB184853.1 gg_id:151932 Streptomyces olivoreticuli str. NBRC 12896
EU841672.1 gg_id:326534 Streptomyces roseoviolascens str. HBUM173022
EF178697.1 gg_id:213732 Streptomyces omiyaensis str. NRRL B-1587
FJ790786.1 gg_id:540453 Streptomyces sp. str. DA07101
FJ486473.1 gg_id:510204 Streptomyces exfoliatus str. HBUM175118
EU741137.1 gg_id:510020 Streptomyces omiyaensis str. 13647G
EU841576.1 gg_id:311953 Streptomyces venezuelae str. HBUM174005
EU841673.1 gg_id:354553 Streptomyces tanashiensis str. HBUM174095
EU367972.1 gg_id:258907 Streptomyces omiyaensis str. 13-3
AB184392.1 gg_id:155032 Streptomyces ostreogriseus str. NBRC 13423
AB184349.1 gg_id:153447 Streptomyces xantholiticus str. NBRC 13354
AB184309.1 gg_id:155551 Streptomyces verne str. NBRC 13097
AJ621604.2 gg_id:103816 Streptomyces purpurogeneiscleroticus str. DSM 43156
FJ486324.1 gg_id:569562 Streptomyces radiopugnans str. HBUM174023
FJ919753.1 gg_id:395266 Streptomyces olivochromogenes str. cfcc3154
EU570706.1 gg_id:272574 Streptomyces turgidiscabies str. 173719
AY207585.1 gg_id:104553 Streptomyces reticuliscabiei
EU677790.1 gg_id:284940 Streptomyces sp. str. FXJ2.009
EU828535.1 gg_id:547963 Streptomyces turgidiscabies str. 255
EU570707.1 gg_id:275765 Streptomyces turgidiscabies str. 173712
EU714061.1 gg_id:321528 Streptomyces sp. str. E23102
GQ262797.1 gg_id:590769 Streptomyces rochei str. vh52
AY247716.1 gg_id:83402 Streptomyces maritimus
FJ532468.1 gg_id:555669 Streptomyces enissocaesilis str. HBUM174967
FJ792558.1 gg_id:574985 Streptomyces rochei str. cfcc3131
AY730619.1 gg_id:101422 Streptomyces griseodotifer str. SR-11

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FJ7925
AY7306

200.2	1341.3	1137.4	959.3	1639.8	1119.5	995.1	882.4	1308.7	1017.3	466.5
310.0	1128.1	1122.4	1407.5	2313.8	1095.7	1703.2	1098.6	932.0	1047.1	652.4
168.7	1181.4	926.2	720.9	1193.8	982.4	679.3	937.2	1221.0	820.4	533.8
453.1	1217.9	1023.6	763.8	1738.9	1087.0	1091.2	717.8	1782.1	868.1	375.0
2311.1	946.3	845.5	823.7	1636.1	744.1	1085.9	1072.9	913.2	373.7	572.4
412.4	1077.6	822.6	617.5	1257.8	795.6	865.5	635.6	1900.0	862.1	330.5
70.5	700.1	1009.9	599.7	1190.8	777.9	632.1	856.7	799.7	853.4	307.2
489.6	1076.3	821.5	613.5	1254.3	793.5	858.2	638.5	1609.7	862.5	331.4
280.5	893.1	830.0	1077.0	1959.3	814.4	1392.1	931.8	880.9	976.6	444.6
79.9	1265.7	888.5	1118.5	865.1	844.1	1216.6	829.4	776.4	469.2	739.8
100.2	4864.0	3389.6	1599.0	2163.5	2290.8	1847.6	1554.8	2748.8	2746.9	1488.6
84.6	3489.5	2759.3	1395.9	2566.9	2148.0	2093.4	1767.6	1846.1	1633.4	862.8
692.1	952.3	877.3	694.7	1797.1	870.1	1094.6	662.6	720.3	776.7	304.6
148.0	2042.7	2192.4	1788.8	2683.3	2557.1	2297.5	1967.3	1995.6	1521.9	784.0
156.0	3440.2	2922.9	2275.4	3421.9	3319.1	2765.9	2587.2	2951.4	2240.4	1016.0
95.6	6094.9	4109.2	1992.1	3161.9	3489.8	2429.6	3043.1	1663.8	1832.4	1086.7
160.6	1943.1	2279.8	1700.6	2523.4	2282.1	2121.9	1908.5	1196.6	761.8	822.4
199.3	3550.2	4096.4	2249.4	3861.2	3561.3	2732.6	2806.3	3111.7	2297.7	1596.3
5524.1	4994.4	3751.3	2402.9	3046.5	4276.6	2983.2	2553.3	6354.4	4966.9	2785.0
160.1	2412.9	3030.6	1833.9	2607.8	2419.4	1881.7	2140.8	1117.2	992.8	1191.1
111.2	924.5	1064.8	903.2	1411.0	1012.3	1249.1	955.2	716.6	713.2	580.3
2010.1	3242.2	2963.4	2643.8	3210.4	3476.9	2206.0	2797.4	2562.8	1539.1	1599.7
298.1	4200.5	3689.2	2535.5	3549.9	3451.5	3052.1	2912.5	3967.0	3117.4	1814.1
131.4	2893.4	3524.7	2008.2	3536.9	2893.8	2378.7	2458.6	2245.9	1597.1	1353.1
79.9	2987.2	2767.5	1775.1	2246.0	2116.9	1656.9	2251.1	3431.2	2251.9	912.1
43.8	2005.0	2290.6	1727.7	1791.0	1498.6	1585.4	1922.1	1321.1	1182.6	1021.1
1371.3	2928.3	2505.4	2312.6	1113.8	2180.3	2161.0	2055.2	2840.1	3018.7	2827.8
1366.9	1842.3	1754.5	1987.7	857.4	1662.4	1956.8	1483.8	1556.1	1993.4	2316.3
162.4	5219.1	4181.7	2996.6	3188.2	3744.0	2639.2	4189.5	5021.9	3305.3	2858.1
1889.3	3077.1	3357.3	2860.5	3907.1	3004.2	3408.4	2993.1	3145.7	2544.0	1498.4
3877.3	5618.5	4665.0	2413.4	4355.0	3919.2	3254.7	2844.8	5299.9	3660.8	2156.1
1133.8	6288.0	6933.6	6903.4	8259.9	6047.5	8618.1	6794.5	6604.9	5959.0	6002.8
3930.9	4705.5	4901.4	4014.4	3931.0	4119.8	3543.7	4009.3	4813.9	3459.6	2781.6
1984.3	2310.8	2558.5	2004.6	2957.5	2430.0	2522.5	2073.4	2673.4	1929.5	1346.1
728.0	3062.7	3517.8	1483.3	2113.7	1664.5	1624.1	1744.0	1688.2	1158.9	765.6
11289.8	5055.4	4722.4	5022.7	4746.5	5004.8	5740.8	4397.8	6757.4	4797.1	6040.9
3090.2	2261.5	2870.3	2335.1	2109.7	3358.1	2839.6	3583.5	2998.4	3055.5	2476.6
53.4	60.7	115.0	90.2	71.7	86.5	74.8	62.8	51.8	30.0	37.2
462.4	1092.8	940.2	654.3	1356.3	911.5	1063.6	691.2	1930.5	871.2	301.7
249.0	2134.7	1661.0	963.6	988.1	1380.7	872.5	1182.8	3486.6	1779.8	610.1
84.7	1351.6	1181.2	791.5	563.1	876.2	548.6	970.1	1725.6	960.4	578.9

693.3	464.6	740.1
1168.4	983.3	1411.7
762.6	893.9	1280.4
659.2	544.9	947.0
911.6	1056.9	1148.7
536.0	454.4	715.9
2103.7	714.9	628.2
505.3	455.5	689.6
1028.1	847.3	1252.7
842.9	1000.0	1347.1
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2137.8	1171.7	1669.3
758.2	833.0	827.1
2126.7	1404.1	2473.2
2297.3	1596.7	2728.5
2822.6	1977.0	2504.5
1691.2	1796.2	2220.4
2716.8	2029.5	2307.5
2726.3	3127.8	2394.4
1622.4	1320.0	1847.0
805.0	804.6	834.8
2388.5	2168.8	1951.8
2786.9	2111.1	2682.9
2221.4	1747.1	2004.8
1433.5	1518.4	1811.0
1371.2	1676.0	1851.6
1759.9	1744.9	1994.7
1628.1	1508.2	1755.8
2486.3	2341.3	3011.2
3049.7	2225.7	2399.5
3214.0	2458.2	2675.2
6531.5	6532.5	7265.5
3102.8	3005.6	2995.5
2112.2	1656.9	1723.2
1679.0	1348.7	1419.0
4148.4	5250.6	5404.7
2685.0	3928.9	2947.4
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AB184590.1 gg_id:155286 Streptomyces sclerogranulatus str. NBRC 14301
AB045880.1 gg_id:51375 Streptomyces albofaciens str. JCM 4342
FJ799191.1 gg_id:549317 Streptomyces cellulosae str. MJM11558
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AY277559.1 gg_id:88857 Streptomyces lateritius str. CSC113.1
EU273533.1 gg_id:253548 Streptomyces zaomyceticus XSD-118
EU570655.1 gg_id:264311 Streptomyces zaomyceticus str. 173255
EU570537.1 gg_id:260010 Streptomyces narbonensis str. 173444
EU521702.1 gg_id:274130 Streptomyces termitum S72-10
EU521703.1 gg_id:258956 Streptomyces termitum S76-1
U94488.1 gg_id:11877 Streptomyces thermocarboxydovorans str. DSM 44295
AB184679.1 gg_id:151857 Streptomyces rameus str. NBRC 15453
NR_025291.1 gg_id:538295 Streptomyces thermocoprophilus str. B19; DSM 41700
X79322.1 gg_id:11948 Streptomyces glaucescens str. DSM40716
AB249980.1 gg_id:159908 Streptomyces thermogriseus str. NBRC 100772
AY999848.1 gg_id:130649 Streptomyces thioluteus str. IFO 13341 CSSP715
AB184753.1 gg_id:151862 Streptomyces thioluteus str. NBRC 3364
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GQ262800.1 gg_id:513499 Streptomyces globosus str. vh18
GQ282616.1 gg_id:581371 Streptomyces toxytricini str. vh55
DQ442548.1 gg_id:193205 Streptomyces toxytricini str. NRRL B-5426T
AY745498.1 gg_id:104459 Streptomyces lavendulae str. CH56-4

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322.1	4863.0	4515.4	2357.2	3942.9	3596.0	2924.1	3046.2	4104.9	2720.6	1468.7
581.2	6750.8	5804.8	2893.2	4672.7	5011.2	3501.0	3483.7	6541.5	4242.9	1906.8
180.4	3684.3	4120.7	2070.1	3250.7	3127.8	2394.1	2517.0	3006.2	2252.7	1416.4
50.6	198.4	863.0	654.9	1814.3	800.8	941.7	384.9	27.4	79.8	277.0
128.9	712.1	642.3	525.8	436.0	482.8	851.4	482.7	403.9	263.4	290.7
338.3	1785.4	1784.7	1763.1	1981.7	1572.8	2013.7	1789.4	743.5	816.7	3139.3
44.1	2115.7	1785.9	1439.1	1557.3	1288.1	1235.4	1713.3	2506.4	1560.8	1225.5
105.5	1432.5	1114.1	1305.1	1898.2	1021.8	1566.1	1247.4	790.6	623.5	642.5
95.4	1709.6	1671.0	1838.0	1762.8	1954.1	1564.9	1630.2	1201.7	857.5	898.4
154.8	1487.4	1356.3	1483.2	1622.7	1666.1	1342.6	1229.3	1124.3	835.9	675.6
58.7	2682.3	2245.7	1998.1	1950.0	1710.4	1604.9	2051.3	2739.7	1900.1	1569.4
54.7	579.8	617.6	605.8	1233.7	535.0	934.0	681.9	297.8	332.1	213.0
1092.1	2936.1	3048.5	2596.0	2744.9	2786.3	2885.1	2746.9	2163.8	1714.5	3809.8
1182.0	3303.4	3525.5	2825.1	3461.2	3172.2	3587.3	2936.8	2763.3	2117.4	3801.3
1244.0	3525.8	3528.6	2610.1	3114.9	3107.2	3282.5	2733.0	3386.5	2626.5	3638.9
44.2	515.1	441.2	377.7	594.1	502.4	476.0	490.8	453.3	376.1	167.0
281.0	2731.7	1987.9	1329.6	1953.0	1979.4	1292.1	1195.4	3737.0	1631.6	670.8
108.4	1139.1	1281.4	816.2	1931.5	1196.5	1306.2	1254.0	1150.6	848.2	347.1
237.2	3875.0	3784.8	1824.1	3562.4	2726.1	2586.4	2470.5	3163.6	2262.5	1186.7
46.0	28.3	33.3	45.0	52.1	27.6	47.1	25.6	38.0	23.8	14.8
545.2	6177.8	4891.5	2202.5	3347.1	3836.7	2830.4	2726.5	5405.0	3613.1	1741.2
267.5	4134.1	3927.1	2951.1	3450.8	3608.4	3213.5	3161.2	3741.5	2936.7	2139.9
14163.7	8384.4	7275.7	7451.8	6879.4	8170.9	8686.5	7367.1	10329.7	8873.9	8176.7
142.9	2071.6	2642.3	1799.3	2642.1	1958.8	1784.6	1810.6	1530.9	1090.6	830.8
90.5	1945.8	2844.3	1473.6	2808.4	1816.6	1968.0	1776.5	1057.3	856.5	852.3
81.9	570.6	523.5	584.3	1175.3	496.9	768.4	593.6	267.3	242.7	176.3
55.5	2505.4	2846.5	2312.5	2615.3	2514.8	1666.5	2038.6	1506.9	1545.6	1527.5
46.0	1327.7	2186.9	1783.5	2486.4	1758.1	1723.4	1402.7	408.0	768.0	818.8
35.2	2147.0	2264.7	1792.0	2274.1	1941.3	1825.6	2467.8	1943.9	1448.0	1476.8
102.9	247.9	263.4	203.9	304.6	188.4	191.3	240.5	154.6	96.9	115.4
212.4	4133.5	3269.9	2739.6	3327.0	3493.8	3043.7	2657.8	3029.6	2703.2	1598.7
168.1	3716.1	2228.7	1597.6	2722.1	3303.0	2043.9	1966.5	820.7	1570.2	727.4
348.3	7073.8	4473.3	3308.4	4406.6	5448.1	4226.6	3774.4	3833.9	2826.5	1938.3
397.6	7160.2	5576.4	3908.5	5761.0	6150.1	4948.2	3735.3	5533.5	4207.3	1991.2
117.7	2062.0	1304.9	1146.1	2826.2	1833.7	2041.3	1177.0	645.3	969.4	366.6
186.9	4673.1	3364.3	2649.7	3845.2	3372.2	3506.4	2677.4	2595.2	2489.4	1439.8
158.5	999.6	1168.5	1080.9	2099.1	1244.2	2458.9	1715.4	725.1	417.2	557.1
126.2	1313.6	1089.8	514.0	1057.4	1034.6	828.4	638.2	1307.3	1098.2	353.5
78.3	3661.1	2749.0	1886.6	1754.0	2286.8	1559.8	2077.2	2476.1	1912.9	1315.9
79.3	1095.0	759.5	547.0	1018.8	845.5	863.7	612.6	212.6	386.0	216.5

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2636.6	2001.8	2475.2
3281.0	2243.4	2749.0
2430.6	1526.9	1992.9
321.4	190.3	205.0
375.0	461.0	374.2
1569.5	2015.2	1781.4
1132.7	902.1	1147.9
1191.8	1023.9	1949.9
1160.5	1092.7	1529.2
1012.8	907.0	1268.3
1317.1	1296.7	1305.4
734.9	450.0	921.9
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2624.7	2932.9	2616.3
563.3	324.9	474.7
1089.0	996.9	1384.1
1345.5	611.3	995.0
2480.6	1718.1	2155.8
25.7	31.4	30.2
2492.8	1713.0	2419.6
2738.2	2030.9	2681.7
6987.7	9549.9	7929.2
1738.0	1017.4	2419.1
1825.8	1177.5	1606.4
697.0	362.0	882.6
2289.5	1328.5	1439.0
1633.6	922.4	1101.5
1596.4	1319.9	1692.1
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2652.3	2126.5	2709.9
2498.7	1344.6	1816.1
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4237.5	2724.4	3396.9
1945.8	806.5	1429.9
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s__Streptomyces xantholiticus	40118
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AF346480.1 gg_id:67676 Streptomyces tumescens str. Cu-2-1
AB184636.1 gg_id:151187 Streptomyces olivoverticillatus str. NBRC 15273
DQ442545.1 gg_id:179099 Streptomyces subrutilus str. NRRL B-12377T
EU841687.1 gg_id:337216 Streptomyces xantholiticus str. HBUM174044
AY876940.1 gg_id:112120 Streptomyces sp. str. 1307
AY882020.1 gg_id:111817 Streptomyces sp. str. 913
AY897205.1 gg_id:112036 Streptomyces sp. str. 157
AB249943.1 gg_id:161667 Streptomyces yeochonensis str. NBRC 100782
AB546301.1 gg_id:532263 Streptomyces xanthochromogenes str. RI51-SDHV15
EU570403.1 gg_id:272321 Streptomyces goshikiensis str. 173297
AB184629.1 gg_id:150763 Streptomyces armentosus str. NBRC 14890
EF012127.1 gg_id:183291 Streptomyces sp. str. 1A01655
EF178680.1 gg_id:213158 Streptomyces nitrosporeus str. NRRL B-1316
EU477215.1 gg_id:262721 Streptomyces sp. str. Bd 095
EU301835.1 gg_id:254535 Streptomyces macrosporeus str. SCF25
EF418611.1 gg_id:203956 Streptomyces viridogenes str. ATCC 39387
AF345862.1 gg_id:46451 Streptomyces sp. str. KACC 20159
EU593645.1 gg_id:268665 Streptomyces coelicoflavus str. 173942
EF550509.1 gg_id:219126 Streptomyces sp. 172624b
AB441718.1 gg_id:323469 Streptomyces sp. str. NBRC 104276 (= BTCC B607)
DQ448732.1 gg_id:158910 Streptomyces sp. str. CNR924 PL04
DQ442539.1 gg_id:175700 Streptomyces phaeofaciens str. NRRL B-1516T
AY999824.1 gg_id:130934 Streptomyces ederensis str. KCTC 9726 CSSP688
AY876942.1 gg_id:112252 Streptomyces sp. str. 701
AB184559.2 gg_id:151918 Streptomyces sviceus str. NBRC 13980
GU722514.1 gg_id:519338 Streptomyces seoulensis str. IFB-A01
EF371421.1 gg_id:210969 Streptomyces vinaceus str. 2255
AB249970.1 gg_id:160943 Streptomyces seoulensis str. NBRC 16668
GQ268016.1 gg_id:593856 Streptomyces macrosporeus str. NBE12
FJ883743.1 gg_id:511211 Streptomyces tendae str. cfcc3130
EU570632.1 gg_id:276984 Streptomyces albogriseolus str. 173254
FJ792549.1 gg_id:565198 Streptomyces lavendulae str. cfcc3099
FJ486408.1 gg_id:576182 Streptomyces badius str. HBUM175013
EU521697.1 gg_id:262538 Streptomyces aureoversilis S49-1
EU118769.1 gg_id:253467 Streptomyces sp. str. L196
FJ217218.1 gg_id:313035 Streptomyces sp. str. SK126
AB184623.1 gg_id:154799 Streptomyces vellosus str. NBRC 14823
AJ971885.1 gg_id:134277 Streptomyces sp. Bt 50
FJ792546.1 gg_id:552021 Streptomyces mediolani str. cfcc3057
AB294147.1 gg_id:214283 Streptomyces sp. str. BC43
DQ085812.1 gg_id:132052 Streptomyces sp. str. C35

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FJ7925
AB2941
DQ085

61.7	339.7	399.7	290.4	369.3	393.3	243.8	267.5	315.9	177.2	127.4
85.7	1719.3	1511.4	1158.7	2118.4	1534.6	1503.2	1433.8	593.3	641.0	510.9
805.4	1030.3	1135.3	1177.5	1779.1	1037.9	1267.8	1379.0	715.1	476.6	709.8
44.9	1950.5	2198.6	1702.9	1696.8	1574.0	1681.6	1588.8	1282.3	1201.4	907.3
2728.8	2324.1	1853.9	2048.7	2825.7	2621.6	2098.9	1890.1	1938.4	1602.4	1189.6
1209.5	3638.2	3273.6	3653.8	4730.7	4122.5	4068.5	3052.1	3291.6	3364.2	3819.6
1277.4	3423.7	3102.7	3523.7	5388.2	4185.7	4301.3	3551.7	2561.5	2995.3	5212.3
188.9	3556.1	3417.4	2991.8	4586.2	4127.6	3996.4	2831.8	4399.9	3654.6	2610.9
108.5	1557.8	1738.3	1529.2	2508.6	1622.8	1632.9	1493.7	1551.3	715.9	509.9
3145.6	11744.8	9071.4	7525.9	5781.6	9097.4	7642.1	7072.2	13136.2	10211.5	8180.5
57.9	881.9	752.4	639.8	731.6	572.0	830.4	716.8	441.4	318.6	262.7
2642.6	2787.0	2649.0	2611.4	2934.0	3496.6	2761.3	2837.8	2184.5	2502.7	2389.7
230.9	3831.8	3500.6	2778.1	3678.3	3095.2	3571.5	3047.9	3681.0	2665.4	1640.0
236.5	1728.3	1433.0	1772.2	1738.2	1528.5	2176.8	1584.0	1661.6	1118.5	1594.0
330.2	2078.7	1850.0	1893.2	2571.4	1605.4	2432.6	1677.8	1096.8	960.3	1054.7
49.6	604.9	704.0	750.6	1256.6	632.1	994.8	870.6	360.4	320.2	400.1
158.4	2576.2	3319.4	2531.4	3120.0	2720.4	2976.5	2852.1	3180.7	1498.0	1945.3
68.7	3839.4	2756.3	1077.7	2095.5	2802.6	1766.2	1257.3	2609.8	1533.5	726.3
51.1	816.5	657.1	333.5	336.9	628.7	243.1	738.0	1429.4	594.2	369.6
4794.3	7651.4	6625.6	7074.9	7647.0	6711.5	6986.9	6065.9	8697.2	6887.5	5739.7
2356.1	2893.6	2612.9	2194.0	2895.9	2222.4	2837.3	2525.2	2562.2	1815.4	1505.6
127.2	2408.9	1989.9	1683.9	2315.7	2002.1	2209.7	1917.5	1876.2	1251.6	925.3
136.8	2326.5	2383.6	2202.8	3893.6	2178.3	4066.7	1759.5	2480.9	1738.2	1616.4
160.3	1020.1	851.7	1017.7	1727.4	1057.7	899.0	1112.7	485.6	449.3	420.5
1491.8	1212.9	1326.2	1332.4	1957.4	1289.7	2231.9	1330.7	669.3	486.3	748.9
23801.8	10184.5	10261.2	10391.1	10614.5	9568.0	11386.1	9774.9	13522.2	12423.5	13337.6
4140.4	4335.6	3617.6	3749.3	3359.4	3975.8	4028.8	3546.6	4350.0	3142.5	3355.7
1931.3	1467.6	1615.9	1749.0	2834.7	1462.5	2281.5	1862.6	1141.4	597.3	945.7
78.7	81.9	66.4	39.3	56.0	56.6	39.1	28.4	47.5	49.2	33.1
5238.3	3052.9	2455.7	1999.0	1727.7	2546.7	1880.4	2930.2	4449.5	3511.9	2003.7
6286.7	3326.4	2899.9	2273.8	3266.0	3182.9	2713.9	2207.2	3136.0	1643.7	1703.8
17996.5	6177.8	5190.0	5451.2	5980.3	6066.0	5926.7	5583.6	7125.1	5720.5	7785.9
73.2	240.1	215.9	193.6	600.3	250.0	330.1	320.0	154.6	255.3	97.1
16540.9	12906.1	10648.2	10659.0	11597.4	11467.0	11904.1	8934.0	13407.9	10359.7	13137.3
39344.0	9825.1	9148.6	10514.3	10585.3	9505.1	10994.1	10185.1	15578.1	10738.6	14049.7
136.8	3502.1	2657.6	2268.3	3350.4	2754.6	2738.4	2092.8	1495.9	1525.5	1031.5
61.0	773.9	689.1	620.5	718.9	617.4	431.4	800.8	351.8	380.5	172.8
6925.5	3616.1	3651.9	3745.4	4671.5	3794.7	4521.4	1770.4	4031.3	2647.3	3880.3
4471.7	2241.3	1616.3	1670.1	1880.2	1996.7	1759.3	1857.3	3151.5	2216.2	1662.7
9665.8	7239.2	6028.5	6107.5	5550.0	5526.8	5193.8	5768.3	10116.8	5227.1	6089.5
607.5	2872.4	2273.1	1213.8	1793.0	2238.9	1428.2	1232.5	4084.7	2665.7	754.2

175.5	233.2	386.2
1623.7	1174.6	1627.0
1011.2	1548.7	1510.3
1217.2	1436.1	1790.2
2544.9	1756.9	2133.8
4516.6	2764.6	4971.4
4729.1	2945.5	4831.2
3791.1	2229.3	3192.5
1277.4	829.5	1615.8
6279.7	6811.7	10158.8
470.1	617.7	1363.2
2317.1	2275.0	2367.2
3023.7	2340.1	3785.0
1306.7	1588.2	2169.0
1752.3	1530.1	2664.3
643.5	637.9	882.6
2429.7	2918.9	5605.1
974.4	882.0	1926.7
268.3	245.1	60.8
6540.8	6557.4	8539.9
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1246.4	1343.5	2114.4
2352.7	2461.8	2429.5
1520.3	661.8	1292.6
1386.9	1196.0	1602.6
10193.7	10035.3	9063.2
3207.7	3204.6	4017.0
1618.8	1679.7	1719.9
40.7	43.0	51.2
1680.9	2740.8	2096.4
2381.2	3120.0	2840.8
5763.3	5690.3	5481.2
278.2	146.8	305.5
10212.8	9656.6	9590.8
8770.2	10720.0	9562.9
2510.3	1679.1	2497.4
485.5	300.7	758.8
2913.0	3909.7	4711.6
1432.0	2549.5	1821.6
4783.2	5864.0	5211.3
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GQ258685.1 gg_id:555742 Streptomyces griseus str. cfcc3167 GQ258
DQ026650.1 gg_id:160404 Streptomyces flavoviridis str. NRRL ISP-5153 DQ026
AY921652.1 gg_id:114388 Streptomyces griseus str. A540 AY9216
FJ486362.1 gg_id:561720 Streptomyces lienomycini str. HBUM174506 FJ4863
EU570701.1 gg_id:259017 Streptomyces microflavus str. 173328 EU5707
EU570629.1 gg_id:265853 Streptomyces griseorubens str. 173471 EU5706
EU828539.1 gg_id:559823 Streptomyces turgidiscabies str. 304 EU8285
EU048542.1 gg_id:241003 Streptomyces galilaeus str. CGMCC 4.1320 EU0485
EU570637.1 gg_id:271467 Streptomyces niveoruber str. 173346 EU5706
NR_025623.1 gg_id:553869 Streptomyces tubercidicus str. DSM 40261 NR_025
AJ781343.1 gg_id:132535 Streptomyces heliomycini str. LMG 19960 AJ7813
EU214914.1 gg_id:260908 Streptomyces sp. str. CNP-942_SD01 EU2149
AY999929.1 gg_id:132086 Streptomyces vinaceusdrappus str. NRRL 2363 AY9999
EF063481.1 gg_id:174180 Streptomyces nojiriensis str. B-33 EF0634
AB245390.1 gg_id:146174 Streptomyces panaciterrae str. Gsoil 1538 AB2453
EU593743.1 gg_id:267727 Streptomyces aureus str. 173034 EU5937
AY566561.1 gg_id:104473 Streptomyces sp. str. RJ12 AY5665
DQ231567.1 gg_id:144433 Streptomyces sp. str. AcH 505 DQ231
AY999737.1 gg_id:131451 Streptomyces violascens str. ISP 5183 CSSP183 AY9997
EU294138.1 gg_id:236860 Streptomyces malachitofuscus str. CTF9 EU2941
AM913901.1 gg_id:402998 Streptomyces sp. LM78a AM913
FJ883740.1 gg_id:587406 Streptomyces canus str. cfcc3059 FJ8837
AB184382.1 gg_id:153832 Streptomyces lavenduligriseus str. NBRC 13405 AB1843
FJ486350.1 gg_id:546333 Streptomyces atrovirens str. HBUM174170 FJ4863
AF492845.1 gg_id:67228 Streptomyces sp. str. NK528 AF4928
EU593611.1 gg_id:263274 Streptomyces griseorubens str. 173928 EU5936
AB184547.1 gg_id:152438 Streptomyces purpureus str. NBRC 13927 AB1845
EU008821.1 gg_id:244680 Streptomyces sp. str. WBF11 EU0088
DQ442500.1 gg_id:174258 Streptomyces gardneri str. NRRL B-5615T DQ442
AB184436.1 gg_id:154957 Streptomyces olivaceiscleroticus str. NBRC 13484 AB1844
AB184103.1 gg_id:155510 Streptomyces poonensis str. NBRC 12556 AB1841
AB249909.1 gg_id:160081 Streptomyces thermoalcalitolerans str. NBRC 16322 AB2499
AB184393.1 gg_id:150718 Streptomyces spectabilis str. NBRC 13424 AB1843
EF620359.1 gg_id:245268 Streptomyces bikiniensis str. HD-087 EF6203
EU430264.1 gg_id:272895 Streptomyces sp. str. -29 EU4302
EU379273.1 gg_id:274693 Streptomyces mutomycini str. 3L-10G EU3792
AY999849.1 gg_id:134351 Streptomyces aureoversilis str. IFO 13021 CSSP716 AY9998
EF017717.1 gg_id:198756 Streptomyces noursei str. SIIA 0113 EF0177
EF620358.1 gg_id:240373 Streptomyces melanogenes str. HD-010 EF6203
AB184104.1 gg_id:151020 Streptomyces violens str. NBRC 12557 AB1841
GQ263434.1 gg_id:549818 Structure Simulated Level Waste Site simulated level waste site clone FW2_120B GQ263

49.1	208.5	145.6	141.6	509.6	119.6	373.2	188.0	68.1	85.0	34.6
429.8	3697.8	3303.8	2116.2	2934.0	2870.9	2391.6	2035.4	5249.8	4776.2	2164.4
77.5	548.5	555.6	654.8	1128.5	775.4	640.6	622.5	639.3	274.6	253.2
161.2	4380.2	3028.3	1692.0	2383.1	3515.5	2104.8	1897.2	4279.3	2486.9	1176.2
231.7	2431.2	2069.4	1027.1	1991.2	2383.8	1339.1	1129.8	2636.4	1669.1	583.7
52.6	873.4	740.2	293.3	666.1	616.8	303.0	405.8	695.4	493.8	197.8
2135.7	2540.7	2675.9	2321.1	3417.5	2422.6	3012.7	2513.9	2995.2	2147.8	1411.3
164.1	1534.4	1537.8	1252.4	2166.0	1570.8	1740.5	951.1	1394.9	1031.3	550.6
4186.2	6097.9	4821.1	3649.8	3264.1	4422.4	3006.0	4316.1	7216.3	6388.6	4125.5
190.8	3260.7	2823.6	2523.2	3086.7	2885.5	2378.9	2392.7	3782.8	2600.7	1865.0
66.7	966.5	830.1	882.5	1214.9	920.5	1050.1	711.8	794.2	623.0	463.2
118.9	3301.5	3964.1	3749.9	2557.1	3747.6	3431.8	3129.0	1548.5	954.5	3226.6
226.8	2114.6	1645.4	951.4	961.1	1379.1	861.3	1181.0	3216.9	1781.5	602.8
876.1	2761.7	2861.5	2799.1	2716.5	2757.3	3357.1	2574.9	2740.5	1831.6	1919.5
335.3	3992.0	3088.6	3325.9	3685.1	3160.4	3174.8	2945.1	3304.9	2784.3	1914.7
1932.5	2563.3	2641.3	2270.8	3529.6	2531.5	3399.4	2921.9	1880.0	1884.6	2430.5
28.4	285.4	418.9	200.3	722.4	320.1	254.6	333.1	255.7	320.7	84.0
100.1	1929.8	1839.2	1241.6	1559.2	2220.4	1315.2	1468.9	2071.9	1667.4	807.3
44.5	716.2	770.5	744.5	1357.6	735.7	1185.0	603.8	525.3	736.3	388.9
42.2	64.8	72.5	39.0	53.8	51.8	35.8	23.3	27.7	44.3	22.4
4815.0	4231.5	2917.5	2834.7	2795.3	3813.9	2402.8	2755.2	3915.7	3415.4	4816.4
78.2	1398.9	1164.3	956.4	1622.3	1048.9	1175.3	1145.9	1746.3	933.1	433.8
62.2	2994.3	2918.7	2127.0	2473.9	2287.4	1592.8	2078.7	3465.0	2048.8	1667.4
81.9	2419.0	1890.5	1333.8	1518.8	1615.1	1171.6	1476.3	2474.8	1778.8	1016.0
1684.9	5925.8	4503.5	3289.1	3436.9	4121.3	3871.7	3600.6	5905.6	4921.3	3626.7
73.4	4109.4	2879.4	1399.6	1781.8	3091.6	1695.6	1751.3	4254.1	2197.6	1133.3
91.1	4747.6	4348.1	3150.4	3203.6	3181.2	2430.8	3312.0	4480.1	3030.2	2464.9
1235.6	5070.2	4219.0	3839.7	5251.5	3929.6	4845.0	3529.2	3939.4	3253.1	2602.1
604.8	5047.3	4207.6	2668.6	4244.2	4001.1	3560.0	3108.5	5407.0	3914.5	1806.8
515.3	3662.6	2912.4	2377.9	1909.1	3492.9	1985.7	2170.4	2802.9	1680.8	1501.1
1029.6	2795.8	2587.3	2843.8	3570.0	2921.0	2876.3	3141.9	1356.8	2360.7	1684.2
144.9	1024.5	1182.2	936.0	1665.2	1171.8	938.8	1335.5	659.5	489.4	331.6
201.2	2462.5	2394.1	2403.5	2215.5	2501.3	1884.1	2118.8	1658.4	1171.1	1205.2
8898.5	6977.1	6957.2	4627.6	3478.1	6223.9	3766.3	4950.6	8859.2	7830.5	6232.3
1719.0	2444.9	2653.3	2302.2	2839.3	2272.3	3022.3	2444.4	1530.4	1344.2	3504.2
108.4	1737.8	1421.9	660.9	1126.6	665.3	839.1	683.9	776.6	447.7	384.9
197.6	4867.7	3765.5	3091.9	3860.3	4227.2	3752.1	2969.0	3024.4	2389.3	1501.4
74.2	873.6	808.7	709.1	885.6	1277.7	507.4	940.8	778.3	824.3	164.4
172.1	2631.8	3575.0	2680.9	2138.7	3105.4	2245.5	2735.8	1967.3	1462.8	1468.7
172.8	872.9	1171.9	1223.9	839.9	1302.9	1010.2	1212.6	620.7	1712.9	651.5
594.8	1070.9	1269.0	1666.2	1793.4	1286.2	1520.3	1308.0	852.7	393.2	1175.9

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1110.0	1256.3	1107.0
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2531.5	1816.6	1911.8
1423.3	808.7	1111.8
3179.5	3644.4	4562.7
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590.2	579.8	473.6
2157.6	3218.6	3180.1
2929.1	2403.7	2755.3
2418.5	3218.6	2630.3
667.8	271.5	293.0
1411.4	1284.7	991.0
982.6	487.1	681.6
35.5	43.7	32.5
2347.5	3013.8	2230.2
1365.1	767.2	833.2
1334.8	1189.0	1020.6
930.2	745.2	1000.7
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1105.2	979.6	1828.4
2157.1	1981.3	2027.7
3829.4	3019.1	3956.6
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1835.2	2444.4	1915.9
2731.1	2387.8	3310.7
1781.5	436.4	1548.2
1463.1	1224.1	1852.0
4066.0	5484.1	3776.4
2315.6	2831.3	2520.6
685.1	518.1	837.2
3056.3	2036.0	3199.0
784.5	320.2	596.4
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967.1	765.1	879.1
1528.6	1019.4	1590.4

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AB184578.1 gg_id:155211 Streptomyces spinoverrucosus str. NBRC 14228 AB1845
AJ870981.1 gg_id:110622 Streptomyces danangensis str. XKDN19 AJ8709
FJ538595.1 gg_id:570435 Streptomyces griseus str. CGMCC 1370 FJ5385
EU559729.1 gg_id:270996 Streptomyces scabiei str. T2 EU5597
AB184538.1 gg_id:156283 Streptomyces jumonjinensis str. NBRC 13869 AB1845
DQ442551.1 gg_id:181296 Streptomyces variabilis str. NRRL B-3984T DQ442
DQ442555.1 gg_id:184694 Streptomyces viridochromogenes str. NRRL B-1511T DQ442
EU841590.1 gg_id:336557 Streptomyces longwoodensis str. HBUM174899 EU8415
EU570714.1 gg_id:258192 Streptomyces coeruleofuscus str. 174514 EU5707
EU570516.1 gg_id:267874 Streptomyces griseoloalbus str. 173214 EU5705
GQ263690.1 gg_id:577146 Structure Simulated Level Waste Site simulated level waste site clone FW3_91C GQ263
EU841632.1 gg_id:311222 Streptomyces bingchengensis str. HBUM174849 EU8416
EU544237.1 gg_id:272393 Streptomyces sp. str. SD 576 EU5442
AB184370.1 gg_id:155273 Streptomyces nobilis str. NBRC 13386 AB1843
EU828544.1 gg_id:562973 Streptomyces scabiei str. 14 EU8285
AY999820.1 gg_id:132465 Streptomyces pulveraceus str. KCTC 9766 CSSP684 AY9998
AB184794.1 gg_id:154752 Streptomyces roseoverticillatus str. NBRC 3726 AB1847
AY207580.1 gg_id:103792 Streptomyces cf. griseus AY2075
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EU570702.1 gg_id:267632 Streptomyces microflavus str. 173334 EU5707
GU263884.1 gg_id:536996 Streptomyces sp. str. 195024 GU263
EU570635.1 gg_id:263925 Streptomyces olivaceus str. 173303 EU5706
AB184149.1 gg_id:152854 Streptomyces litmocidini str. NBRC 12792 AB1841
AY999852.1 gg_id:130274 Streptomyces viridodiastaticus str. IFO 13106 CSSP719 AY9998
DQ026668.1 gg_id:160133 Streptomyces coeruleofuscus str. NRRL B-5417 DQ026
EU828547.1 gg_id:584092 Streptomyces sp. str. 286 EU8285
EF056494.1 gg_id:187328 Streptomyces sp. str. 1A01547 EF0564
GU479439.1 gg_id:517524 Streptomyces diastatochromogenes str. A11 GU479
EU570597.1 gg_id:259225 Streptomyces tendae str. 173676 EU5705
AB184490.1 gg_id:154999 Streptomyces triangulatus str. NBRC 13799 AB1844
EU570658.1 gg_id:269256 Streptomyces phaeochromogenes str. 173575 EU5706
GU084180.1 gg_id:593675 Streptomyces flaveus str. T111 GU084
AF117304.1 gg_id:11847 Streptomyces malaysiensis str. ATB-11 AF1173
DQ026637.1 gg_id:161276 Streptomyces anulatus str. NRRL B-2000 DQ026
EU285476.1 gg_id:244839 Streptomyces finlayi str. XSD-131 EU2854
EU570465.1 gg_id:263145 Streptomyces spororaveus str. 173695 EU5704
EU273531.1 gg_id:240527 Streptomyces verne XSD-125 EU2735
X76702.1 gg_id:11920 Streptomyces sp str. D921 X76702
AJ399492.1 gg_id:31407 Streptomyces pallidus str. ISP 5531 AJ3994
Y00484.1 gg_id:11928 Streptomyces lividans str. TK21 Y00484
EU593737.1 gg_id:273587 Streptomyces violaceorectus str. 174495 EU5937

101.2	2353.7	1901.2	1317.5	1211.1	1543.2	968.7	1664.3	2562.1	1684.0	1171.7
148.1	645.1	537.9	285.3	601.6	540.5	387.3	348.0	443.5	212.7	426.4
16183.3	6850.4	5372.3	6066.6	6311.7	5793.3	5787.9	5806.5	6437.1	5146.2	9954.0
1325.2	2873.2	2631.5	2604.2	2784.1	2129.4	2960.3	2976.6	2413.7	1695.2	1430.1
97.5	3681.0	3750.4	2163.3	2210.7	2865.2	1944.0	2819.9	3392.1	2047.9	1481.3
693.2	1547.2	1284.9	1083.7	1910.1	941.2	1352.1	1010.7	1824.7	1092.4	468.0
347.4	5423.3	3989.2	2740.9	2713.9	3533.9	2144.1	3106.2	6818.9	3927.5	2270.5
123.2	1638.1	1227.4	925.9	1002.9	1027.3	982.4	1222.9	2352.4	1192.4	603.8
43.2	1254.1	1142.3	1056.6	2042.9	1107.8	1352.6	1202.0	1548.3	763.3	495.0
49.4	521.0	462.4	299.0	373.9	436.7	224.1	471.2	598.8	406.3	225.3
1457.6	4358.2	4427.5	4379.4	4611.2	3856.2	4510.3	4058.3	3751.5	2430.9	3696.1
89.2	3243.1	2567.3	1172.1	1476.5	1619.9	1157.9	2194.8	2832.2	1861.7	1117.0
83.1	4555.8	3101.6	1621.9	2430.8	2447.9	2395.8	2364.6	3563.8	3061.7	1232.0
234.1	1415.6	1429.3	1663.5	1575.2	1376.8	1717.5	1414.3	676.7	426.8	1806.3
9071.4	6907.3	7788.4	7229.3	7845.3	6475.1	7570.9	7002.2	9277.7	7075.0	6821.1
51.0	384.3	445.7	422.7	880.6	514.5	613.0	477.3	194.6	237.5	166.1
124.4	3147.4	2352.1	1580.4	2713.8	2584.0	2272.3	1871.5	1857.4	1792.0	744.3
78.2	397.0	401.1	413.9	495.6	511.7	288.4	449.3	571.7	212.5	188.9
89.8	1375.4	1157.6	729.0	775.6	967.9	414.7	819.2	1691.9	1198.1	632.9
335.7	3251.5	2738.0	2609.6	3573.6	2862.3	2436.7	2469.6	2839.5	2525.6	1660.2
1993.4	5782.4	4402.8	2862.1	3688.6	4421.4	3674.2	3244.7	5045.7	3142.4	2050.0
64.8	4303.8	3324.0	1357.7	1558.3	2509.5	1277.8	1905.1	3722.0	2893.2	1056.5
78.7	2204.8	2890.9	1639.6	3247.0	2095.1	2014.3	1907.5	1034.1	999.7	1043.2
158.3	957.4	1528.0	812.9	1072.8	896.8	1051.1	946.8	1180.3	1194.7	146.6
128.6	3544.3	2901.7	1927.6	1820.1	2416.2	1400.8	2166.1	3981.7	2511.5	1393.3
395.0	2106.6	1835.7	1951.1	3072.1	1805.8	2776.4	1858.5	1680.1	1879.0	1310.8
195.3	1248.3	1204.6	1112.5	1412.5	1237.4	1086.7	1055.9	894.5	620.3	516.3
326.5	2940.1	3985.0	3195.3	3671.2	3391.6	3176.9	3566.8	3358.1	2014.7	1837.3
66.0	2605.6	1778.8	807.6	1126.9	2120.2	1188.4	950.8	2915.2	1294.2	656.0
325.7	4815.6	4458.2	4083.6	4420.9	4328.7	3582.9	3408.5	3769.1	3223.4	2954.3
2263.7	2382.2	2037.8	2132.5	2442.3	2261.1	2192.7	2244.6	2173.0	1467.2	1546.6
58.8	2355.6	1613.0	914.2	1999.8	1521.6	1559.6	1125.6	1439.2	1170.0	455.1
74.9	3027.8	2393.7	2062.5	3612.9	2635.1	2895.7	2012.5	1418.3	1501.4	997.6
563.7	5628.1	4207.1	2667.0	3948.7	4140.5	3831.8	3072.8	5996.0	4489.3	1793.3
101.6	2635.9	2020.4	799.6	1479.8	1018.2	1186.7	1025.4	1631.3	1090.1	561.8
1241.7	3264.0	2603.9	2533.9	1281.6	2916.4	2924.6	2005.7	3504.3	2538.3	2721.9
129.4	3145.8	2444.1	1607.5	3312.3	2260.7	2428.9	1785.9	2604.6	1740.4	711.0
51.3	197.4	360.7	404.1	171.7	229.2	260.9	226.3	59.2	43.4	145.8
204.0	2344.6	1876.0	1462.6	2207.8	2021.9	1467.1	1366.2	2526.0	1562.3	809.6
861.7	5994.3	3759.1	1944.7	2628.7	2400.5	2249.4	1892.6	3939.4	2855.3	3169.5
247.6	3075.7	3200.2	2089.3	3172.9	2935.1	2312.1	2267.5	2910.5	2536.2	1350.9

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893.8	707.8	959.4
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882.0	586.0	578.0
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981.9	981.3	1277.2
2211.4	1392.1	1885.5
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2318.9	1280.6	2042.9
230.7	335.1	348.1
588.8	488.4	763.3
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1800.2	1350.5	1698.5
1520.8	1123.4	1576.4
1225.4	1104.1	1338.3
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2620.9	2273.7	2326.4
647.2	592.1	1455.2
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EU624140.1 gg_id:583196 Streptomyces hawaiiensis str. NRRL 15010
DQ442499.1 gg_id:197166 Streptomyces fumigatiscleroticus str. NRRL B-3856T
EU834286.1 gg_id:326902 Streptomyces xanthophaeus str. DS74
DQ459019.1 gg_id:158656 Streptomyces lavendulae str. ZGO429
EU080955.1 gg_id:244007 Streptomyces sp. MI02-7b
EF063458.1 gg_id:180793 Streptomyces olivochromogenes str. 2491
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GQ357947.1 gg_id:576909 Streptomyces sp. str. HaNXJ7
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GU166433.1 gg_id:540306 Streptomyces piomogenus str. O27
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AY999832.1 gg_id:130448 Streptomyces atroolivaceus str. KCTC 9017 CSSP697
AB184430.1 gg_id:151747 Streptomyces mobaraensis str. NBRC 13476
AY207609.1 gg_id:111720 Streptomyces scabiei str. KACC 20194
AB184600.1 gg_id:150751 Streptomyces coeruleoaurantiacus str. NBRC 14526
AB184747.1 gg_id:154399 Streptomyces diastatochromogenes str. NBRC 3337
EU595361.1 gg_id:298968 Streptomyces malaysiensis str. Da08002
EU098025.1 gg_id:247459 Streptomyces sp. str. SOK5/2-05
EU570618.1 gg_id:268096 Streptomyces goshikiensis str. 173298
EU593631.1 gg_id:272172 Streptomyces griseocarneus str. 173931
AJ781352.1 gg_id:134240 Streptomyces lomondensis str. LMG 20088
AB249920.1 gg_id:159961 Streptomyces olivaceus str. NBRC 12805
EU560974.1 gg_id:267696 Streptomyces bikiniensis str. WANG-1
DQ448737.1 gg_id:157262 Streptomyces sp. MAR2 str. CNJ962 PL04
EU570439.1 gg_id:260045 Streptomyces microflavus str. 173525
EU570730.1 gg_id:263778 Streptomyces aureus str. 173010
AJ315072.1 gg_id:46425 Streptomyces sp. LMG 19504
AY459531.2 gg_id:111957 Streptomyces sp. str. M7
DQ141528.1 gg_id:200817 Streptoallomorpha polyantibiotica str. SPR; DSM 44925
DQ442542.2 gg_id:192410 Streptomyces puniceus str. NRRL B-2895T
FJ547116.1 gg_id:546466 Streptomyces polychromogenes str. HBUM175164
AY999827.1 gg_id:131609 Streptomyces noursei str. KCTC 1083 CSSP692
EF178684.1 gg_id:205186 Streptomyces yerevanensis str. NRRL B-16943
EF550511.1 gg_id:219208 Streptomyces sp. 172633c
AY207579.1 gg_id:100085 Streptomyces cf. griseus
AJ399487.1 gg_id:27863 Streptomyces cinnabarinus str. ISP 5467
EF550487.1 gg_id:220285 Streptomyces sp. 172101y
FJ547115.1 gg_id:546256 Streptomyces argenteolus str. HBUM175163
AY040614.1 gg_id:23521 Streptomyces sp. str. F50970
EF626596.1 gg_id:241691 Streptomyces matensis str. NRRL B-2576

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231.5	2571.4	2019.2	1394.7	1561.8	1884.4	1150.8	1756.0	3338.5	1953.6	854.0
1023.6	4058.7	3417.1	2921.8	2722.9	2946.2	2393.2	3272.6	3172.9	3190.2	2520.7
4516.7	4378.4	3530.2	3387.7	3567.0	3465.3	4177.9	3316.2	4376.7	3310.5	3144.7
70.9	2324.6	1506.1	900.5	2024.7	1433.2	1454.2	1124.1	1370.2	1110.9	489.3
253.0	1574.9	915.4	1809.7	3014.1	1549.0	2309.0	1633.5	1061.7	848.2	1397.4
140.4	2281.2	2463.4	2498.3	1846.9	2961.8	1836.2	2286.6	2091.2	1014.6	1057.4
9947.0	5889.2	5230.8	4769.5	5330.3	5239.8	5975.3	4144.1	7233.1	4724.1	1391.4
1623.8	3462.2	3822.8	3120.4	4129.3	3233.7	4076.4	3167.9	3177.9	1736.7	2256.8
65.2	279.8	721.2	445.4	969.4	498.1	548.7	551.2	207.8	528.0	129.1
89.0	767.6	632.7	830.9	1100.3	653.5	1094.5	628.0	357.0	245.2	329.1
279.4	2254.5	2293.7	1816.1	2765.9	2580.5	2474.0	1876.6	3140.0	1779.9	1329.9
236.2	1422.7	1431.9	1773.0	1858.0	1288.4	1650.8	1410.6	2041.4	553.6	623.8
103.0	1755.1	1395.5	1052.5	2133.0	1600.3	1618.5	1169.6	1149.5	769.5	519.4
282.0	4567.5	5099.8	2219.2	3410.6	3876.7	2917.4	4379.9	4999.9	4207.8	4518.5
83.0	6265.4	4908.8	2013.6	2049.3	3120.4	1711.9	3301.2	5003.2	4058.7	2045.1
924.2	4787.0	4399.2	3940.6	3973.1	3634.0	3612.6	4488.0	4214.6	3742.9	2578.8
85.9	3169.2	2499.3	2064.2	3618.0	2680.0	2860.7	2086.5	1677.9	1527.4	1107.6
48.2	1375.5	1326.6	1563.8	1843.1	1280.3	2051.1	1358.9	759.3	509.6	944.1
1525.0	3772.5	3232.0	2927.0	1758.8	3355.2	3121.0	2390.4	3789.7	2820.9	2397.3
73.1	2203.5	2994.1	2598.2	2503.1	2992.1	1846.5	1806.7	326.1	1243.0	1441.9
104.1	1043.0	1181.6	1036.1	1144.2	996.4	742.7	938.9	1068.7	875.8	654.7
323.2	6826.0	5109.8	3156.9	4683.6	5547.6	3729.6	3508.2	7176.8	4550.0	2093.8
4711.8	2587.1	2748.8	2942.4	4091.9	3012.5	3394.3	2539.8	2131.2	1890.6	2517.2
813.1	3752.6	3223.0	3576.8	3792.0	3405.1	3461.2	4125.6	3276.0	3245.3	3699.5
427.8	3426.6	3167.1	3690.3	5320.9	3098.9	5207.5	2467.6	3534.4	3072.2	1954.2
1214.9	2988.7	3396.6	2763.6	3032.8	3075.8	3181.9	3442.0	2279.4	1912.3	3248.4
63.0	1870.6	1586.5	692.5	917.0	1570.4	857.0	824.3	1243.8	667.4	398.4
254.8	5224.7	4184.9	3160.1	3228.5	3538.2	2527.4	3208.2	6097.8	3655.6	2378.2
22606.0	6940.8	7462.3	8268.3	8420.6	6293.3	8913.9	6704.0	7993.9	2673.7	7350.3
81.3	2328.7	2938.2	2831.6	3487.7	2608.6	3410.4	2657.8	1518.2	1020.4	1304.1
130.3	3108.8	2363.0	1552.6	3231.3	2219.5	2339.8	1731.2	2578.6	1708.5	693.4
288.6	5047.3	3904.2	2677.3	3206.9	3761.3	3336.4	2556.0	4707.3	2401.8	1651.6
478.1	3535.9	3426.8	3614.8	4562.5	3679.2	4420.6	3689.2	3223.2	2113.8	2453.1
128.2	313.5	335.0	380.1	872.5	113.4	517.9	330.5	276.4	202.2	160.1
708.1	2251.7	2214.7	1500.4	1117.4	2166.1	796.0	1426.8	1869.1	1170.2	1579.9
1827.5	4601.2	4165.4	3933.5	3942.9	2822.0	4186.8	3341.3	5373.7	3969.0	3359.4
111.8	3217.4	3383.9	1933.2	2064.9	2965.4	2318.7	1913.6	1589.5	1258.5	1199.5
224.6	5324.8	3662.2	1456.8	2284.1	2710.9	2215.7	1927.5	4148.0	3023.2	1601.8
7099.7	4171.3	3497.9	3213.3	3883.8	3441.6	3646.9	3788.6	4216.4	5312.3	5333.6
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2664.6	2408.7	3588.2
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591.6	618.4	1557.9
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EU285472.1 gg_id:238125 Streptomyces lavendulae str. XSD-127
EU124774.1 gg_id:246679 Streptomyces caelestis str. JS-6
AJ781361.1 gg_id:137014 Streptomyces roseoverticillatus str. LMG 20255
GQ867024.1 gg_id:572852 Streptomyces sp. str. HP4
FJ883753.1 gg_id:580508 Streptomyces humidus str. cfcc3166
AF060793.1 gg_id:11874 Streptomyces sp. str. X13
AY999829.1 gg_id:131004 Streptomyces celluloflavus str. KCTC 9702 CSSP694
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AB249917.1 gg_id:159689 Streptomyces glomeratus str. NBRC 15898
EU214931.1 gg_id:264680 Streptomyces sp. str. CNQ-138_SD01
EU502867.1 gg_id:573817 Streptomyces platensis str. F160280
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AY999903.1 gg_id:129552 Streptomyces avellaneus str. NRRL B-3447 B3447
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AY999867.1 gg_id:136310 Streptomyces violaceochromogenes str. IFO 13100 CSSP734
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EF582614.1 gg_id:233249 Streptomyces sp. NWAFU309
EU841569.1 gg_id:327910 Streptomyces setonensis str. HBUM174858
AJ271887.1 gg_id:46620 Streptomyces melanosporofaciens str. NRRL B-12234T
DQ026648.1 gg_id:159918 Streptomyces flavofuscus str. NRRL B-8036
DQ026662.1 gg_id:161264 Streptomyces ramulosus str. NRRL B-2714
EU570421.1 gg_id:275033 Streptomyces mutabilis str. 173341
AB045889.1 gg_id:51020 Streptomyces steffisburgensis str. JCM 4833
EF063459.1 gg_id:188035 Streptomyces aureofaciens str. 3001(1)
EF612313.1 gg_id:257961 Streptomyces sp. str. OS-14
EU124779.1 gg_id:253765 Streptomyces venezuelae str. JS-11
AB473555.1 gg_id:411101 Streptomyces sp. str. Sp080513SC-30 (= NBRC 105048)
EU621880.2 gg_id:278711 Streptomyces sp. str. 594
EF154278.1 gg_id:183260 Streptomyces griseus str. 38
AB184487.1 gg_id:155513 Streptomyces ribosidificus str. NBRC 13796
AB045885.1 gg_id:21602 Streptomyces argillaceus str. JCM 4975
FJ919749.1 gg_id:389028 Streptomyces griseoruber str. xsd08167
EU100401.1 gg_id:235897 Kitasatospora arboriphila str. CG5
AB184802.1 gg_id:152623 Streptomyces hiroshimensis str. NBRC 3839

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AB0458
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218.0	3388.8	2519.2	1563.2	2087.4	2404.0	1932.7	1915.5	3161.0	2270.0	1011.6
19650.8	5738.0	5619.9	5531.3	5543.9	5463.1	5804.7	5004.5	10351.5	6689.7	10361.2
197.3	4106.3	3040.9	2124.5	3104.5	3486.5	2605.9	2403.8	2682.4	2273.6	1060.9
230.5	4424.7	4737.6	3635.4	4386.7	3749.9	3675.5	2917.7	2892.8	2434.9	2174.3
178.9	4701.7	4698.2	4142.6	5744.7	4185.9	5297.0	4276.3	3113.5	2729.6	2314.8
144.8	836.5	871.3	860.1	982.8	808.7	832.1	1359.2	748.7	639.5	452.1
477.3	3816.5	3954.0	3510.4	3186.9	4179.1	4059.3	3105.3	2385.9	1120.0	3190.9
71.7	545.0	299.7	274.8	714.4	345.8	285.9	287.9	238.2	205.8	103.5
174.6	1199.8	1428.5	1464.3	2140.6	1387.0	1276.9	1326.5	468.0	382.3	894.9
67.0	1415.6	1043.4	947.3	1487.0	1124.1	1046.5	1057.4	950.8	1035.8	589.2
49.3	434.7	429.1	460.2	569.2	385.0	588.2	522.2	159.1	157.0	163.7
17629.4	11385.3	9545.0	10113.5	8840.3	10392.5	10056.6	8527.0	12735.1	9261.8	10891.8
102.9	2082.6	1866.3	1672.8	2894.5	2183.5	2791.4	1623.8	1938.5	1845.1	2119.9
167.5	3827.9	2546.2	1237.7	1846.2	2240.3	1423.1	1279.5	2618.2	1854.1	950.6
46.5	101.8	91.8	71.6	122.2	80.5	75.5	53.1	37.3	70.1	41.4
85.0	1532.2	1301.4	1193.7	1150.2	1383.1	708.3	1469.8	2198.9	1004.6	602.2
2271.8	968.2	881.5	1057.2	937.0	963.7	1027.8	883.2	816.8	508.1	855.1
63.5	1700.5	2251.5	1536.6	2155.9	1460.7	1764.3	1547.0	936.0	1005.7	627.6
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327.2	4748.0	3641.0	2506.3	3051.1	3842.8	2299.2	2401.6	6632.5	3587.7	1681.2
6156.0	8309.4	5965.8	3330.3	4024.3	5812.2	3523.2	4385.5	7801.4	5912.2	3573.5
96.2	733.2	802.7	717.7	1688.4	722.0	957.0	755.0	491.9	457.7	269.1
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169.1	2091.2	1554.7	1543.2	1525.2	2104.3	1518.3	1391.4	2330.8	896.4	881.7
72.5	1605.1	1331.6	815.0	687.9	2475.6	535.0	655.4	1089.2	579.4	531.9
455.6	1147.1	825.4	656.9	1256.1	795.6	861.3	640.5	1497.2	864.1	314.7
219.7	3732.5	3106.0	2441.9	2534.4	2771.4	2109.1	2186.6	4994.2	2692.4	1666.2
2219.1	2544.4	3113.2	3319.8	3962.7	2704.9	3480.0	3219.3	2589.9	2169.6	3629.9
1944.0	3459.7	2771.7	3255.9	4785.3	2952.4	4186.7	2353.6	2104.5	1489.1	1723.8
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832.5	4065.0	3543.1	1580.2	3693.7	3274.1	3053.7	2623.7	5415.4	3719.0	1473.7
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2768.1	1583.1	2324.9
2949.3	3129.5	4254.1
4326.2	3278.2	4292.6
825.7	1002.1	1068.1
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446.9	303.4	630.4
982.9	736.9	977.7
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2002.1	1414.7	1705.7
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2601.6	3204.0	1726.0
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EU214918.1 gg_id:259444 Streptomyces sp. str. CNQ-259_SD01
GU166430.1 gg_id:584490 Streptomyces mauvecolor str. SB15
DQ026664.1 gg_id:160477 Streptomyces carpinensis str. NRRL B-16921
EU570603.1 gg_id:270634 Streptomyces acrimycini str. 173763
FJ883747.1 gg_id:513580 Streptomyces cinnamonensis str. cfcc3138
FJ170075.1 gg_id:323597 Streptomyces tubercidicus str. 1UA-1
EU589442.1 gg_id:272813 Streptomyces olivochromogenes str. DA07408
EF178674.1 gg_id:207705 Streptomyces azureus str. NRRL B-2655
AB184073.1 gg_id:151505 Streptomyces olivochromogenes str. NBRC 12336
EU502862.1 gg_id:554289 Streptomyces platensis str. F155245
EU273552.1 gg_id:241206 Streptomyces collinus XSD-117
EU589334.1 gg_id:263474 Streptomyces sp. str. SCSIO 01066
AB184154.2 gg_id:154473 Streptomyces minoensis str. NBRC 12798
AB184531.1 gg_id:156068 Streptomyces kasugaspinus str. NBRC 13852
AB184589.1 gg_id:151510 Streptomyces vitaminophilus str. NBRC 14294
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EU714286.1 gg_id:356308 Streptomyces sp. str. PM342
EU570410.1 gg_id:273121 Streptomyces microflavus str. 173429
AY533137.1 gg_id:105617 Streptomyces xinjiangensis str. AH030069
AB184464.2 gg_id:150879 Streptomyces violorubens str. NBRC 13684
AJ399475.1 gg_id:50889 Streptomyces longisporus str. ISP 5166
FJ406048.1 gg_id:559640 Streptomyces albidoflavus str. DSM 40455
AY999822.1 gg_id:129399 Streptomyces violaceolatus str. KCTC 9772 CSSP686
AY999808.1 gg_id:132139 Streptomyces althioticus str. KCTC 9752 CSSP673
DQ994688.1 gg_id:179276 Streptomyces sp. SB-25
EF469608.1 gg_id:224277 Streptomyces lavendulae str. gCLA4
DQ442496.1 gg_id:196678 Streptomyces coelicolor str. NRRL B-2812T
EU301831.1 gg_id:255355 Streptomyces griseoincarnatus str. CTF15
AB045871.1 gg_id:30701 Streptomyces cattleya str. JCM 4925
AJ781332.1 gg_id:130955 Streptomyces glaucus str. LMG 19902
EU144078.1 gg_id:238468 Streptomyces canus str. ST36
FJ222809.1 gg_id:349109 Streptomyces sp. str. HV3
FJ486374.1 gg_id:509753 Streptomyces pulveraceus str. HBUM174547
EU367978.1 gg_id:272987 Streptomyces hygroscopicus str. 38-3
AM412549.1 gg_id:184425 Streptomyces sp. str. 35zhy
EF654092.1 gg_id:240958 Streptomyces katrae str. NRRL B-3093
DQ449953.1 gg_id:156571 Streptomyces bingchengensis str. 226541
AY999720.1 gg_id:129905 Streptomyces coerulescens str. ISP 5146 CSSP046
AB184535.1 gg_id:152624 Streptomyces spinicoumarensis str. NBRC 13857

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720.2	4364.6	2775.9	1332.7	2442.3	1785.1	2037.5	1244.0	2572.0	1668.2	751.6
577.8	4405.7	3624.0	4247.6	4386.9	3464.5	2657.5	4099.5	3579.3	1713.4	1854.8
51.0	654.1	765.8	492.9	934.6	729.7	697.5	764.2	361.9	209.3	334.0
69.0	243.6	205.2	324.4	1040.1	304.9	850.5	196.7	101.5	207.5	68.0
639.5	2825.9	2525.0	2443.5	3978.6	2591.2	3262.7	2030.7	1939.6	1787.5	1473.1
223.9	2261.0	1617.7	1401.6	2267.4	1875.2	1871.4	1642.6	2096.8	1602.1	949.8
71.9	4210.2	3486.6	2748.9	2485.3	2933.2	2289.9	3054.5	5727.2	3343.9	2357.6
4506.0	2386.7	2091.6	2286.8	2558.3	2415.6	2025.7	2215.3	2697.4	1447.9	1604.8
395.2	4275.4	3663.0	3071.7	4053.5	3351.5	3195.1	2796.6	4649.1	3284.3	1744.4
79.7	3752.6	2661.5	1412.5	2602.6	2264.5	2385.4	2717.2	1757.2	1733.1	1002.2
49.3	383.4	423.9	473.3	822.7	345.8	483.7	342.8	198.4	258.8	293.5
2823.0	3394.7	2574.5	1549.0	2253.7	2913.9	2044.7	1702.7	4423.8	2685.4	1429.4
82.9	320.7	232.2	191.3	437.0	278.3	268.7	445.5	325.7	186.8	102.5
3931.1	4766.8	3924.5	2993.2	3202.2	3390.1	3351.9	2928.5	3067.7	2094.8	1960.7
72.8	2690.0	2500.8	1294.1	2360.1	1906.8	1794.4	1629.1	1971.7	1667.1	779.5
352.5	2575.4	2961.9	2698.5	3591.7	2692.8	3590.2	2475.9	2721.6	3133.6	1756.7
57.5	327.9	670.6	494.9	987.6	500.8	531.5	516.5	194.7	437.6	171.4
127.7	1591.7	2221.6	1688.2	1377.6	1846.5	1426.1	1811.3	1693.9	856.8	1718.7
40.5	275.8	493.1	530.6	847.7	450.2	771.4	357.0	80.0	106.2	191.6
140.1	3473.3	3037.5	2183.5	3207.5	2721.9	3143.0	2582.2	2443.5	2735.2	1227.9
369.1	6248.7	4726.6	3229.1	3571.2	4380.8	2718.0	3448.8	7449.8	4497.6	2399.4
1952.0	3962.7	3728.4	4018.1	4934.3	3718.3	4693.1	3526.0	3010.4	3626.5	3373.0
2263.2	964.2	708.6	894.6	1091.1	800.1	915.2	922.1	749.8	565.2	702.3
919.7	8858.0	6796.4	5794.2	4352.0	5434.4	4183.4	4342.3	8051.6	5584.0	7205.7
145.4	1651.4	1389.0	1029.8	1806.9	1290.0	1367.2	1011.4	1800.5	1218.6	471.8
242.6	3024.7	2282.7	603.9	1238.2	988.3	462.5	1114.9	1848.9	1084.6	604.2
23062.0	6540.3	5052.5	5541.5	6210.9	6529.1	5271.2	5758.6	5560.0	3472.0	4883.5
2388.5	2698.7	2144.2	1725.7	2166.0	2123.4	1786.9	2164.5	3937.6	2295.1	1588.0
69.0	277.8	329.6	338.6	302.2	237.0	143.7	186.2	148.4	125.7	211.6
75.0	858.9	811.2	353.9	728.5	567.0	507.1	350.5	412.4	373.6	182.3
84.4	3477.4	2753.6	2058.5	1712.1	1911.4	1327.6	2406.9	3664.6	2483.2	1856.1
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4571.2	3275.9	2562.9	3025.9	2434.4	2757.3	2979.9	3120.8	2638.7	1590.6	2414.1
73.3	1754.2	1473.9	862.5	1718.6	1472.8	1427.5	1153.0	1630.8	1281.3	482.2
198.9	2141.7	1508.9	1228.4	3089.8	1430.3	1232.1	1448.1	3739.3	1710.1	820.4
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728.0	3169.9	2427.0	2116.4	1711.0	2986.0	2379.1	1854.0	2181.5	1608.9	1472.6
80.4	1324.6	1126.0	1101.9	1920.1	1312.4	1507.5	1283.5	777.2	773.6	369.9
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1943.8	1862.4	1808.8
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1992.1	2105.4	2289.9
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2011.2	1742.2	2260.1
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194.0	253.1	953.3
2874.1	2527.0	3535.2
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638.6	506.1	776.6
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AY999919.1 gg_id:135936 Streptomyces gancidicus str. NRRL B-1872 B1872
EU841671.1 gg_id:350654 Streptomyces polychromogenes str. HBUM174757
EF178677.1 gg_id:203616 Streptomyces hiroshimensis str. NRRL B-1823
AF454764.1 gg_id:37181 Streptomyces lateritius str. AS4.1427; JCM4389T
DQ442498.1 gg_id:185268 Streptomyces flocculus str. NRRL B-2465T
GQ925802.1 gg_id:584745 Streptomyces albogriseolus str. ABRIINW EA1145
AJ002088.1 gg_id:139928 Streptomyces sp str. NT381(11)
EU119190.1 gg_id:251282 Streptomyces sp. str. HBUM 79042
GQ924494.1 gg_id:570516 Streptomyces sp. str. PENDO-1791
X62884.2 gg_id:11845 Streptomyces rimosus str. R6-554
AY029353.1 gg_id:16961 Streptomyces thermoviolaceus str. AB106
AB449812.1 gg_id:343365 Streptomyces sp. str. TP-A0874
AB184488.1 gg_id:152681 Streptomyces setonensis str. NBRC 13797
EF512276.1 gg_id:217379 Streptomyces shandonggensis str. NWUAF 227
EU301686.1 gg_id:238492 Streptomyces sp. str. Y6D
GQ302676.1 gg_id:588474 Streptomyces sp. str. NJWGY3665
FJ792557.1 gg_id:588663 Streptomyces virginiae str. cfcc3129
DQ223679.1 gg_id:160394 Streptomyces erumpens zf-IIRlt12
FJ481065.1 gg_id:559783 Streptomyces zaomyceticus str. xsd08149
DQ026651.1 gg_id:160790 Streptomyces roseogriseus str. NRRL B-3229
FJ486467.1 gg_id:538410 Streptomyces drozdowiczii str. HBUM175063
AB184459.2 gg_id:155799 Streptomyces microsporus str. NBRC 13678
EF683014.1 gg_id:248309 Eastern Mediterranean atmosphere clone F11_6D_FL
GQ262798.1 gg_id:585281 Streptomyces avidinii str. vh32
GU132497.1 gg_id:586423 Streptomyces sp. str. JJB-6
AY232255.1 gg_id:89621 Streptomyces tendae str. SN77
FJ490532.1 gg_id:563236 Streptomyces sp. str. Av25_1
EU864309.1 gg_id:353728 Streptomyces sp. str. 2296
DQ448740.1 gg_id:157248 Streptomyces sp. MAR3 str. CNR877 PL04
AY508512.1 gg_id:99850 Streptomyces ciscaucasicus str. DSM 40275
EU841551.1 gg_id:332101 Streptomyces tendae str. HBUM82583
AB105068.1 gg_id:81060 Streptomyces aureofaciens str. CMUAc130
DQ442507.1 gg_id:186079 Streptomyces humidus subsp. antitumoris str. NRRL 3885T
AY999825.1 gg_id:136255 Streptomyces erumpens str. KCTC 9729 CSSP689
NR_026535.1 gg_id:552279 Streptomyces odorifer str. DSM 40347
FJ406047.1 gg_id:588596 Streptomyces coelicolor str. DSM 40233
GQ263455.1 gg_id:582261 Structure Simulated Level Waste Site simulated level waste site clone FW2_142B
FJ792563.1 gg_id:512336 Streptomyces misionensis str. cfcc3147
EF371441.1 gg_id:210352 Streptomyces roseogriseolus str. CH20-471
EU364839.1 gg_id:330781 Streptomyces lavendulae str. Y7

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131.8	1896.6	2121.1	1847.7	2412.9	2064.1	2231.3	1554.7	1185.3	593.9	858.5
646.0	2566.6	2120.9	1627.8	773.8	2259.8	1682.1	1733.4	2189.9	1462.9	1619.2
89.1	2529.5	1883.8	1514.9	1886.0	2394.2	1673.9	1610.5	1661.9	1234.7	1050.4
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29.3	687.8	873.6	427.3	1465.7	746.9	713.5	566.9	601.9	476.4	203.9
155.8	1196.2	869.0	486.4	1305.0	875.8	944.3	591.8	1410.6	752.8	219.1
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46.6	796.1	801.0	767.6	1295.3	975.6	834.8	902.8	390.8	271.0	258.0
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41.7	899.6	637.6	427.9	1289.1	844.4	716.0	545.4	184.3	366.0	172.5
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686.3	4287.4	4368.4	2985.4	3337.8	3836.5	3160.4	3177.7	2985.5	2267.5	2333.1
437.4	2972.0	3340.2	3287.8	5014.6	3355.6	4289.6	3518.0	2142.3	2706.3	1667.3
68.3	524.3	527.7	439.4	772.8	457.5	451.5	365.5	253.5	129.0	183.8
46.2	608.5	591.4	894.6	1291.1	798.2	1210.3	755.9	336.4	252.7	278.7
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AB184408.1 gg_id:154613 Streptomyces nogalater str. NBRC 13445
GQ258686.1 gg_id:514048 Streptomyces lincolnensis str. cfcc3132
AJ781335.1 gg_id:133230 Streptomyces gobitricini str. LMG 19910
AJ399463.1 gg_id:17946 Streptomyces fumanus str. ISP 5154
FJ492837.1 gg_id:559795 Streptomyces sp. str. SIIA 17201
FJ200397.1 gg_id:351736 Streptomyces albiaxialis str. 3182BRRJ
AY222320.1 gg_id:82727 Streptomyces nanningensis str. YIM 33098
EU570700.1 gg_id:272831 Streptomyces praecox str. 173258
EF371426.1 gg_id:209594 Streptomyces lavendulae str. 3075
DQ442543.1 gg_id:177045 Streptomyces roseoviridis str. NRRL B-2730T
AB249945.1 gg_id:159947 Streptomyces sanglieri str. NBRC 100784
DQ129584.1 gg_id:137956 microarray level air two cities Texas urban aerosol clone AKIW536
EU477227.1 gg_id:269440 Streptomyces sp. str. Lt 006
EU273536.1 gg_id:255250 Streptomyces vinaceus XSD-121
EU367984.1 gg_id:263148 Streptomyces prunicolor str. 22-1
AB184798.1 gg_id:155893 Streptomyces rameus str. NBRC 3782
AY999922.1 gg_id:133679 Streptomyces plicatus str. NRRL 2428
AB249950.1 gg_id:160801 Streptomyces cangkringensis str. NBRC 100775
EU124570.1 gg_id:256930 Streptomyces ghanaensis str. OSS 47
AB184712.1 gg_id:154844 Streptomyces heliomycini str. NBRC 15899
EF017713.1 gg_id:179150 Streptomyces verticillus str. SIIA 0357
GU184336.1 gg_id:590331 Streptomyces macrosporeus str. L1nov
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AB184445.1 gg_id:150791 Streptomyces inusitatus str. NBRC 13601
EU559728.1 gg_id:276045 Streptomyces scabiei str. T1
U22973.1 gg_id:11804 Streptomyces sp str. GP 773 E. Atalan strain no. A81319
AB184660.1 gg_id:152945 Streptomyces gancidicus str. NBRC 15412
EF178681.1 gg_id:214410 Streptomyces olivaceus str. NRRL B-1224
AY207604.1 gg_id:105615 Streptomyces griseus str. KACC 20084
EU100404.1 gg_id:238320 Kitasatospora arboriphila str. CAD
EU132985.1 gg_id:246667 tallgrass prarie soil clone FFCH17594
AB045877.1 gg_id:40019 Streptomyces capoamus str. JCM 4734
EF540458.1 gg_id:223172 Streptomyces sp. 1_C7_48
GQ985456.1 gg_id:553563 Streptomyces flavotricini str. ZG739
AB184515.1 gg_id:156015 Streptomyces owasiensis str. NBRC 13832
EU570413.1 gg_id:258752 Streptomyces variabilis str. 173500
AB217601.1 gg_id:134731 Streptomyces sp. str. ATCC 55098
AB184301.1 gg_id:155127 Streptomyces sparsogenes str. NBRC 13086
GQ284460.1 gg_id:569341 Streptomyces sp. str. TSWCW14

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165.9	1234.4	1208.9	1024.6	1729.3	1009.2	1332.9	1121.5	756.7	954.5	448.8
120.0	1987.5	1862.6	659.7	1189.5	1149.3	700.4	1311.5	1879.8	1440.2	522.0
57.0	774.3	741.7	457.0	812.3	600.7	494.9	502.0	693.0	499.6	242.2
22711.1	5509.6	5400.3	5588.7	5815.6	5219.9	5800.8	4812.1	8591.9	6090.0	7683.4
139.8	5021.0	4599.9	2694.2	2259.6	3706.1	2196.2	3679.0	4478.4	4878.7	2975.7
75.3	1195.9	1308.6	959.5	2193.6	1416.8	1140.3	882.4	723.7	568.6	456.0
356.8	3603.4	2811.6	1792.1	2295.6	3170.3	1769.2	2044.9	4159.8	2392.7	1331.5
57.9	2262.0	1468.7	860.3	1958.9	1372.4	1413.0	1146.5	1350.9	1107.9	479.8
318.3	5709.2	4907.3	2314.6	3696.9	3555.4	2800.8	2461.0	4490.4	2892.9	1349.5
52.5	1045.7	726.3	235.9	476.9	454.6	490.6	477.2	829.7	663.0	271.6
42.6	35.5	33.8	43.8	64.4	38.6	41.7	35.0	22.7	27.3	23.4
144.0	993.4	1060.5	1241.2	1487.0	1180.6	1517.3	1236.5	913.1	394.4	535.5
5171.2	5466.0	4344.1	4098.1	4105.3	4465.7	4685.7	3763.7	5390.4	3914.2	3639.9
91.4	2062.7	1892.3	1686.3	2224.1	1924.0	1615.6	1880.4	2446.8	1909.0	746.6
155.7	2449.4	1466.3	892.4	980.4	982.3	868.1	1235.5	3853.7	1396.8	530.4
1105.9	3612.4	3606.7	1314.2	1948.1	3144.1	1034.3	3331.1	5680.8	2970.0	2291.9
238.9	4408.5	2862.4	1996.2	2299.8	3353.1	2365.5	2211.9	2404.9	1765.3	1158.0
209.2	1989.4	1542.4	893.2	967.1	1296.1	814.8	1107.3	2974.6	1669.5	643.2
71.9	954.9	824.5	877.4	1211.0	906.3	1111.3	714.3	788.5	617.9	458.1
50.7	3912.2	2430.7	1694.6	2140.5	2685.7	1955.7	1939.5	2029.8	1611.6	945.4
94.8	315.5	338.4	272.6	461.3	325.5	293.1	186.5	325.5	220.2	91.1
33.4	13.4	11.4	12.6	18.9	14.2	14.0	12.9	15.5	8.8	13.3
1039.7	7978.6	7275.8	5132.0	7468.3	6913.0	6921.2	5967.9	9003.7	7318.1	4713.3
110.6	4467.4	4235.2	2027.5	2845.9	2901.0	1851.9	3058.2	3473.6	2634.6	1774.2
665.5	5099.2	4304.6	3380.7	4862.8	3916.7	4184.8	3638.7	6081.7	3776.3	1818.4
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963.2	10565.4	8767.9	6060.8	8501.7	9506.5	7730.8	6259.2	11858.3	7861.1	4546.3
165.4	1566.4	1301.3	1231.9	1783.4	1595.0	1302.3	1326.8	1924.1	785.5	586.1
108.1	3405.8	3466.9	3028.1	3861.5	3067.4	3752.9	3384.0	3650.9	3190.5	2179.9
1841.0	3631.6	3798.7	4383.6	5734.9	3527.7	5106.7	4145.5	2509.4	1840.7	2574.7
117.8	1864.8	1584.0	1056.0	1440.6	1488.3	1098.4	1425.9	2380.1	1207.8	782.6
43.8	885.4	806.5	814.3	913.2	774.3	769.6	745.3	696.3	456.3	514.9
53.2	1288.3	955.5	804.2	1554.2	1257.3	1020.6	876.0	649.6	482.0	256.5
157.8	2281.7	2479.1	2102.3	1223.1	2621.0	1055.3	1877.1	1912.0	987.3	1279.0
92.9	2003.9	1702.4	1275.2	1472.6	1232.1	1163.7	1515.7	2073.4	1539.2	1198.6
2805.0	2935.3	2505.4	2516.6	2147.7	2553.0	2323.2	2224.3	3264.3	2249.6	2404.9
62.9	1942.5	1745.1	1278.6	964.8	2766.8	931.0	1040.0	1103.3	697.7	728.4
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593.1	587.4	545.1
677.1	413.5	725.2
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2189.6	1769.1	2030.3
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1093.8	1203.8	1227.5
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426.2	397.0	523.1
1084.0	749.1	971.1
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650.9	570.1	1105.9
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AY897203.1 gg_id:112004 Streptomyces sp. str. 134
AB184072.1 gg_id:151217 Streptomyces cinereus str. NBRC 12247
DQ663161.1 gg_id:170490 Streptomyces sp. str. 3485
AJ399462.1 gg_id:25920 Streptomyces coerulescens str. ISP 5146
EF408736.1 gg_id:210759 Streptomyces hygroscopicus str. ATCC 53653
FJ486382.1 gg_id:537636 Streptomyces ramulosus str. HBUM174769
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AY999916.1 gg_id:134550 Streptomyces floridae str. NRRL 2423
AJ399470.1 gg_id:25540 Streptomyces cyaneus str. ISP 5106
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EU273532.1 gg_id:243342 Streptomyces diastatochromogenes XSD-126
FJ546727.1 gg_id:508774 Streptomyces stelliscabiei str. WI04-09A
AB184151.1 gg_id:155555 Streptomyces macrosporeus str. NBRC 12794
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AF336800.1 gg_id:17895 Streptomyces yatensis str. DSM 41771T
FJ887908.1 gg_id:555338 Streptomyces sp. str. swa-lh12
EU570610.1 gg_id:259119 Streptomyces microflavus str. 173550
EF501980.1 gg_id:226478 Streptomyces sp. str. HA01184
DQ223783.1 gg_id:140767 Streptomyces sp. str. pp2
AY999879.1 gg_id:133629 Streptomyces roseolilacinus str. 4.1865 CSSP400
AJ310927.1 gg_id:50437 Streptomyces cyaneus str. DSM 40108
FJ486314.1 gg_id:550968 Streptomyces ambofaciens str. HBUM173596
DQ442529.1 gg_id:186751 Streptomyces naganishii str. NRRL B-1816T
AB184586.1 gg_id:151684 Streptomyces thermoatroviridis str. NBRC 14276
FJ842611.1 gg_id:557675 Streptomyces sp. str. 020101
EU723880.1 gg_id:322132 Streptomyces sp. str. XF18
U93322.1 gg_id:11802 Kitasatospora kifunensis str. JCM 9081
AY999810.1 gg_id:133305 Streptomyces rubiginosus str. KCTC 9042 CSSP675
EU570677.1 gg_id:267382 Streptomyces griseorubens str. 173457
FJ532413.1 gg_id:558995 Streptomyces tauricus str. HBUM175127
AJ391817.1 gg_id:46555 Streptomyces sparsogenes str. NRRL 2940T
EU170122.1 gg_id:238912 Streptomyces huangiae str. NRRL 8180
EU477230.1 gg_id:263644 Streptomyces sp. str. Bd 059
FJ481062.1 gg_id:553624 Streptomyces phaeochromogenes str. xsd08146
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EU570678.1 gg_id:275918 Streptomyces ambofaciens str. 173399
AB249932.1 gg_id:160625 Streptomyces rectiviolaceus str. NBRC 100765

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5602.5	2418.7	2297.0	3030.0	3641.6	3211.3	3419.4	3049.6	1734.7	1382.6	3456.5
52.7	558.9	1310.0	532.9	731.6	497.3	609.9	882.1	112.5	566.3	596.1
189.0	5233.3	4805.2	3063.6	4031.3	4690.7	3863.7	3434.2	3723.6	2532.1	1872.3
2104.9	1870.1	1851.9	1994.3	3821.2	2308.1	2500.2	2040.8	1660.2	1345.3	2064.2
478.0	2751.5	2335.0	1699.1	2839.5	2361.6	1957.7	1524.0	3217.7	1739.4	831.7
131.4	2333.6	2143.0	1590.5	1688.2	1998.2	1741.7	2068.7	1624.3	899.4	1424.9
57.8	2810.9	2105.2	1944.8	2144.5	1900.2	1744.4	1837.5	2572.6	1695.1	1274.3
131.5	522.1	475.3	441.7	650.6	420.1	526.5	592.8	344.9	504.7	255.9
68.0	1826.0	1443.4	982.6	1205.3	1320.3	843.3	1176.9	2224.6	1496.7	782.2
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216.5	1870.7	1731.3	1410.9	2115.2	1449.1	1561.3	1133.5	2024.4	1133.4	672.3
64.5	1533.5	1472.7	1017.6	1053.0	1166.3	700.4	1682.9	1517.6	962.2	821.0
2591.2	5119.7	4059.8	3502.5	3435.2	3443.3	2708.1	3592.1	6107.1	4541.9	3216.0
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171.2	2121.6	1917.4	1768.2	2241.2	2377.1	2246.9	1516.3	1360.1	929.9	1211.4
67.5	2754.8	1767.3	816.2	1059.9	2231.9	1067.1	906.3	2502.1	1354.3	559.6
70.2	1047.6	1072.5	1078.3	2322.6	1143.5	1708.9	953.0	883.9	734.0	298.0
1571.0	8946.6	6810.1	5186.4	3872.9	8511.6	5965.2	4860.0	7763.6	4704.2	4215.6
233.4	3522.8	2863.8	1871.0	2543.7	2506.0	2706.7	2222.3	3673.3	2752.2	1466.0
3221.9	4267.3	2907.2	1792.9	2428.6	2575.1	2656.1	2300.7	4269.0	2838.6	2652.6
8464.5	3303.9	4492.4	4429.6	3980.1	7159.4	3867.1	4778.7	4955.4	14816.2	5357.0
91.2	2135.1	2234.3	1734.5	2244.6	1716.5	1799.0	1724.5	1862.6	1376.4	827.0
438.8	2677.4	3131.4	2322.5	3254.1	2269.6	2951.5	2496.3	2849.2	1956.8	1763.8
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368.0	3252.1	2665.4	2296.0	2990.3	2282.2	2404.6	2339.5	4393.0	2886.3	1658.4
99.2	131.7	104.1	93.0	388.3	71.1	101.3	126.2	89.1	75.8	74.9
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255.0	6656.3	5135.8	2715.3	3574.5	5617.8	3737.9	3188.3	5749.3	4912.0	2520.0
68.2	1397.6	1557.2	2125.2	1866.3	1719.0	2044.9	1649.4	544.0	405.9	966.6
120.1	2641.5	2093.8	1742.1	2129.3	1624.9	2040.3	1650.8	997.3	745.7	829.7
179.6	2237.4	1386.1	1436.3	1593.2	1722.7	1518.1	1261.7	1652.2	909.4	781.7
696.8	4297.0	4423.2	3124.6	3431.3	3913.9	3289.5	3333.6	3000.3	2182.4	2395.2
217.3	3298.5	2560.4	1217.6	1985.6	2080.1	1986.7	1656.0	3225.8	2614.0	1485.6
58.2	83.6	75.8	63.3	75.6	69.4	71.5	52.8	45.7	55.2	42.4
184.4	3249.5	3095.0	2411.2	2483.1	3020.6	2451.3	1858.5	2655.0	1785.5	2887.1

1199.6	1299.0	1286.9
2925.8	3223.3	3399.8
449.2	1353.6	1058.6
2350.5	2664.5	6336.7
2188.3	1926.5	2083.3
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1499.8	1549.3	2784.1
1706.9	1234.8	1778.1
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830.9	623.8	883.3
1557.3	1919.0	2799.9
1144.3	842.9	1460.0
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2683.7	2466.1	2064.2
2632.9	2353.7	2832.1
763.0	394.8	793.2
1332.3	1514.8	1688.8
612.9	563.5	1511.4
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4172.4	4127.2	6638.7
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2161.6	3269.1	2713.9
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2244.0	2349.4	2263.5
2745.1	2729.5	3954.9
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114.5	112.2	139.0
3160.0	3052.1	3352.9
3122.6	2504.0	3359.2
4782.7	2373.5	4197.6
2750.4	2288.0	3004.8
391.2	426.4	467.4
2258.7	2798.8	4375.6
1143.0	1132.3	2294.1
1348.2	1188.9	2597.5
958.9	1198.7	1562.3
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EU570428.1 gg_id:267737 Streptomyces pseudogriseolus str. 173735
AY999813.1 gg_id:133301 Streptomyces olivaceiscleroticus str. DSM 40595 CSSP709
DQ487015.1 gg_id:158693 Streptomyces sp. str. 4728
DQ026632.1 gg_id:161625 Streptomyces filamentosus str. NRRL B-2114
EF654091.1 gg_id:253200 Streptomyces subsp. achromogenes str. NRRL B-2120
DQ826593.1 gg_id:164623 Streptomyces albidoflavus
AB245388.1 gg_id:146148 Streptomyces panacagri str. Gsoil 519
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EU570722.1 gg_id:277556 Streptomyces californicus str. -J15-2-4
EF501981.1 gg_id:226041 Streptomyces sp. str. HA01041
EF491602.1 gg_id:218444 Streptomyces sp. str. AR3
AJ781382.1 gg_id:133762 Streptomyces purpurascens str. LMG 20526
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EU841557.1 gg_id:318555 Streptomyces albogriseolus str. HBUM83454
AB184550.1 gg_id:151420 Streptomyces sp str. NBRC 13931
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AB184085.1 gg_id:153301 Streptomyces hachijoensis str. NBRC 12363
AY999089.1 gg_id:115287 Streptomyces sp. str. 4017
AB184277.1 gg_id:153721 Streptomyces intermedius str. NBRC 13049
EU521701.1 gg_id:262208 Streptomyces mycarofaciens S71-1
DQ442560.1 gg_id:195410 Streptomyces xanthophaeus str. NRRL B-5414T
AB184380.1 gg_id:151669 Streptomyces coriofaciens str. NBRC 13403
AY999804.1 gg_id:136248 Streptomyces corchorusii str. KCTC 9715 CSSP669
FJ591130.1 gg_id:584778 Streptomyces albidoflavus str. UST040711-291
AB249965.1 gg_id:161589 Streptomyces sulphureus str. NBRC 13345
EU841554.1 gg_id:350466 Streptomyces lienomycini str. HBUM82567
GQ258688.1 gg_id:565685 Streptomyces fimbriatus str. cfcc3155
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AY526525.1 gg_id:100675 Streptomyces sp. str. 28a-33-3
Z76687.1 gg_id:11923 Streptomyces gougerotii str. DSM 40324T
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AY999775.1 gg_id:133535 Streptomyces canus str. NRRL B-1989 CSSP527
EU593654.1 gg_id:270846 Streptomyces aurantiacus str. 173966
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EU864339.1 gg_id:544370 Streptomyces sp. str. XVII
AY999811.1 gg_id:130861 Streptomyces microflavus str. KCTC 9079 CSSP676
EU593621.1 gg_id:267583 Streptomyces microflavus str. 173936
AB045876.1 gg_id:41535 Streptomyces bobili str. JCM 4624

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191.2	2378.9	2629.4	2093.2	2302.0	1851.8	2415.8	2006.3	3088.5	1652.6	1630.5
71.4	781.3	640.9	469.6	826.6	647.9	537.7	582.1	757.8	632.7	323.2
307.0	2839.6	2770.8	1913.9	1708.7	3176.6	1667.4	1940.3	1589.0	1888.1	1384.9
70.2	1919.8	2750.9	1760.3	2786.8	2129.8	2065.1	1983.0	1125.8	810.3	1050.3
302.5	4784.0	4380.8	2913.2	4124.6	3861.5	3429.6	3081.1	4440.5	3453.3	2015.2
134.3	1347.7	860.3	884.7	966.3	905.7	906.4	804.3	1784.4	617.5	275.6
5231.5	8256.0	7019.1	6979.7	6698.4	7697.2	6929.4	6100.6	8245.1	6035.9	6610.7
212.7	4255.8	3929.5	3303.7	4945.8	4111.8	5011.0	3947.0	3607.6	3095.7	2001.8
2074.5	2419.8	1809.2	1995.7	4121.6	1876.8	2442.7	1802.4	3169.9	1539.9	1791.0
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72.9	704.2	704.5	722.7	735.0	780.6	755.5	635.0	727.3	286.7	293.8
104.5	1374.7	1731.3	1603.4	1293.0	1758.7	988.6	1375.1	1062.7	896.8	900.8
1037.5	4372.5	3746.4	3305.0	4706.3	3872.4	3906.6	3423.2	4034.2	3486.3	2221.1
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67.1	2727.2	2471.6	1336.4	2081.2	1901.0	1510.8	1380.9	1943.1	1642.6	572.5
4140.4	5285.7	4117.1	3826.8	3651.5	4215.5	4314.7	3723.9	5257.0	3876.7	3557.4
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267.1	1538.4	1675.3	1855.9	1922.9	1608.3	2382.3	2048.6	1491.2	843.7	1266.0
45.4	139.6	129.2	160.8	224.6	134.1	242.5	101.4	46.5	45.1	63.8
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529.8	1343.6	1333.9	1298.3	1729.1	1304.6	1544.9	1337.3	1461.7	645.4	620.4
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1428.2	1502.1	1837.8
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940.6	671.8	946.6
5805.4	6855.7	7375.1
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2171.1	1802.4	2171.8
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610.0	555.6	914.2
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1807.3	1526.9	2061.2
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3357.6	3380.5	4191.7
931.8	1174.2	1237.4
3476.5	3791.0	3863.6
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AJ781368.1 gg_id:138038 Streptomyces sporocinereus str. LMG 20311
EF012137.1 gg_id:196520 Streptomyces sp. str. s6-201
EU841616.1 gg_id:345199 Streptomyces drozdowiczii str. HBUM174905
DQ442534.1 gg_id:197620 Streptomyces olivoverticillatus str. NRRL B-1994T
AB184489.1 gg_id:151956 Streptomyces tosaensis str. NBRC 13798
EU841651.1 gg_id:340972 Streptomyces piloviolofuscus str. HBUM173602
DQ334782.1 gg_id:153738 Streptomyces violaceusniger str. NRRL B-1478
AY741364.2 gg_id:205768 Streptomyces sp. str. AB3
EF501758.1 gg_id:223673 Streptomyces sp. str. ZhDa04010
AB184376.1 gg_id:154518 Streptomyces albaduncus str. NBRC 13397
EU841716.1 gg_id:330768 Streptomyces aurantiacus str. HBUM174626
AB249961.1 gg_id:160196 Streptomyces speibonae str. NBRC 100916
AF333113.1 gg_id:36096 Streptomyces thermospinosisporus str. AT10
EU216728.1 gg_id:235815 Streptomyces sp. str. 16II
EF017710.1 gg_id:182822 Streptomyces roseus str. SIIA 0664
EU367975.1 gg_id:270042 Streptomyces kanamyceticus str. 22-5
EU367980.1 gg_id:277567 Streptomyces setonensis str. 17-1
AB184447.2 gg_id:154252 Streptomyces agglomeratus str. NBRC 13663
AY370772.1 gg_id:94180 Streptomyces himgiriensis str. RMV-A16
AB249934.1 gg_id:159991 Streptomyces sporoclivatus str. NBRC 100767
AF184081.2 gg_id:11934 Streptomyces scopiformis str. A25
EU240413.1 gg_id:235920 Streptomyces sporoclivatus str. B125
AB184483.1 gg_id:152563 Streptomyces mycarofaciens str. NBRC 13792
EU570448.1 gg_id:261119 Streptomyces aureus str. 173862
AJ399481.1 gg_id:25321 Streptomyces pseudovenezuelae str. ISP 5212
X92614.1 gg_id:11769 "Micromonospora megalomicea"
AB184127.1 gg_id:153986 Streptomyces eurythermus str. NBRC 12764
EU521693.1 gg_id:265817 Streptomyces hygroscopicus S1-2
EU841715.1 gg_id:327234 Streptomyces ciscaucasicus str. HBUM174631
AB184715.1 gg_id:155734 Streptomyces roseoverticillatus str. NBRC 15920
AY232256.1 gg_id:90237 Streptomyces caelestis str. SN83
AB249981.1 gg_id:161572 Streptomyces brasiliensis str. NBRC 101283
EF178689.1 gg_id:214132 Streptomyces roseoverticillatus str. NRRL B-3500
EF219459.1 gg_id:215473 Streptomyces deccanensis
EU841719.1 gg_id:303875 Streptomyces speibonae str. HBUM174625
AY854956.1 gg_id:114019 symbiont
FJ486427.1 gg_id:510213 Streptomyces ambofaciens str. HBUM174855
EU124772.1 gg_id:254911 Streptomyces caelestis str. JS-4
AY999723.1 gg_id:132917 Streptomyces griseoruber str. NRRL B-1818 CSSP068
AY999719.1 gg_id:131144 Streptomyces coeruleorubidus str. ISP 5145 CSSP045

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AY9997

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61.8	592.2	561.9	617.4	845.5	712.0	570.4	572.0	138.8	213.4	156.5
468.5	3632.8	2852.0	1769.4	2187.1	2338.4	2216.3	2573.3	3825.2	2575.1	1519.8
64.2	444.0	553.0	436.9	762.9	475.6	393.9	344.6	118.9	108.1	209.1
219.4	2329.0	1994.2	1349.7	1725.3	1875.7	1248.2	1407.7	3010.8	1776.3	897.6
78.1	582.9	876.2	512.4	1891.6	1025.6	1181.7	450.4	156.3	514.5	389.9
57.2	535.7	630.6	772.0	1816.2	746.5	1255.7	399.8	123.7	216.3	229.0
64.3	1323.6	977.5	904.9	1438.8	1295.2	1141.7	852.1	339.6	448.4	278.6
77.0	730.2	576.8	569.5	619.0	509.2	360.7	508.5	716.1	463.5	386.3
410.4	1543.4	1604.1	1254.4	1127.9	1318.6	1307.9	1072.3	1699.1	1020.7	814.4
65.0	1826.2	1351.0	808.8	997.9	1075.3	612.8	1203.4	1977.1	1647.2	759.3
1839.0	3810.1	2889.3	1972.1	1971.3	2791.6	1944.7	2227.3	3891.5	2592.7	1586.3
193.6	1888.2	1353.8	1088.8	1460.8	1543.7	1355.4	850.1	2474.7	918.3	607.2
62.2	653.9	612.8	938.3	1578.9	686.4	1105.4	605.0	196.6	227.5	184.2
476.6	3264.4	4327.2	4496.4	4871.5	4526.2	5181.7	4024.0	2923.0	2322.5	3164.9
7459.8	5209.2	4918.7	4798.2	5628.5	4713.8	4982.4	4765.7	6000.5	3677.8	5922.8
11791.1	4925.0	4090.3	3987.3	3264.0	4235.2	3730.9	3148.6	5418.2	4745.2	5945.4
107.0	3795.4	3206.4	1678.0	3015.3	2436.4	2488.4	1879.7	2228.4	2021.1	811.4
93.4	1110.0	1154.0	841.4	1819.6	1164.5	1371.4	1247.6	860.7	633.0	354.3
1822.5	5769.9	4846.6	4747.9	4587.7	4926.2	4311.4	4365.1	5955.4	4206.5	3922.2
47.9	759.3	863.8	854.0	1302.2	1049.8	1030.7	1094.1	392.5	268.2	314.7
44.5	1586.5	865.6	478.4	1096.4	1029.1	742.4	679.4	1297.4	813.6	447.4
9403.5	4626.6	3949.0	4563.0	5377.8	4706.9	5172.9	4449.9	6163.2	4376.9	6184.5
40.4	2798.9	2186.8	832.5	766.1	1418.8	436.3	672.2	644.8	550.2	285.1
321.3	1039.8	1184.5	964.2	1997.2	1079.0	1874.0	1121.9	759.1	537.0	537.1
1071.8	1537.4	1400.5	1276.5	1993.2	1255.2	2206.8	1365.2	1159.6	611.6	703.3
3457.2	10672.4	6103.6	3695.1	6225.1	5250.1	5092.4	4129.0	9147.4	5657.0	3179.9
63.6	2589.4	2158.9	775.3	1687.1	1493.3	972.2	914.3	1001.8	1011.8	451.4
1323.8	1298.8	1249.0	1316.9	1767.3	1373.0	1384.6	1421.5	714.6	395.2	560.8
1797.7	2701.2	2442.2	2012.1	2833.8	2040.8	2614.1	2342.2	2650.0	1892.4	1416.6
178.9	3283.4	2432.3	2147.6	2420.8	2759.2	2198.7	2304.4	1690.9	1288.5	993.9
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56.2	1191.9	1180.9	1056.5	2050.4	1376.0	1602.5	1190.3	981.1	1022.2	348.2
3865.6	4617.8	3350.3	2267.0	2472.4	4360.3	2581.3	2412.2	4935.8	2677.7	1832.1
163.2	642.5	604.8	668.2	1360.4	604.4	876.2	589.8	490.7	301.6	282.3
1809.1	2217.1	2399.6	2369.8	2994.6	2218.2	3079.0	2219.8	1654.3	1394.9	1098.6
56.8	444.4	814.9	426.6	737.5	503.7	429.8	585.0	292.2	497.0	243.8

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1837.1	1382.3	2285.5
207.0	340.9	504.3
867.6	703.6	1022.8
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527.9	360.7	655.1
1077.5	554.7	1255.8
306.1	348.1	265.6
1243.7	1554.1	1414.1
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1584.8	1743.2	2317.6
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752.9	400.9	718.7
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2043.5	1868.8	3125.3
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2259.5	1834.0	2173.9
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2738.3	1931.3	2182.9
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AB184882.1 gg_id:151326 Streptomyces cyanoalbus str. NBRC 12857 AB1848
AJ399482.1 gg_id:44263 Streptomyces thermotolerans str. ISP 5227 AJ3994
EF408190.1 gg_id:209695 Streptomyces griseoruber str. MTCC8121_CKM5 EF4081
AB045881.1 gg_id:27121 Streptomyces aureofaciens str. JCM 4624 AB0458
AB249974.1 gg_id:159909 Streptomyces sulfonofaciens str. NBRC 14260 AB2499
AM167521.1 gg_id:141215 Streptomyces qinlingensis str. 24 AM167
AJ781374.1 gg_id:131043 Streptomyces violaceorubidus str. LMG 20319 AJ7813
AF385185.1 gg_id:30608 Streptomyces scabiei str. SBH-3 AF3851
EU841578.1 gg_id:348592 Streptomyces tauricus str. HBUM174860 EU8415
DQ442552.1 gg_id:185820 Streptomyces vastus str. NRRL B-12232T DQ442
FJ481077.1 gg_id:553271 Streptomyces coelicolor str. xsd08161 FJ4810
GQ263371.1 gg_id:591669 Structure Simulated Level Waste Site simulated level waste site clone FW1_b48 GQ263
AB184232.1 gg_id:155514 Streptomyces pseudogriseolus str. NBRC 12902 AB1842
EU502861.1 gg_id:544701 Streptomyces platensis str. F155186 EU5028
FJ007428.1 gg_id:550916 Streptomyces bottropensis str. LE-3A FJ0074
FJ196597.1 gg_id:331034 Streptomyces gilvosporeus str. ATCC 13326 FJ1965
AY999874.1 gg_id:132175 Streptomyces griseostramineus str. 4.1841 CSSP394 AY9998
EF657884.1 gg_id:251896 Streptomyces sp. str. RB72 EF6578
EU360165.1 gg_id:263356 Streptomyces sp. str. 1 EU3601
FJ792570.1 gg_id:552154 Streptomyces diastatochromogenes str. cfcc3158 FJ7925
AB546300.1 gg_id:523316 Streptomyces sp. str. RI18-DHHV3 AB5463
FJ546725.1 gg_id:585289 Streptomyces europaeiscabiei str. ID06-18B FJ5467
EU294140.1 gg_id:247986 Streptomyces griseoincarnatus str. SCF18 EU2941
AB231805.1 gg_id:156081 Streptomyces nogalater str. TT2-9 AB2318
GQ867023.1 gg_id:586648 Streptomyces sp. str. HP3 GQ867
AJ621605.2 gg_id:103965 Streptomyces violens str. DSM 40597 AJ6216
EU603357.1 gg_id:275261 Streptomyces sp. str. MJM6929 EU6033
AB184777.2 gg_id:155193 Streptomyces roseochromogenus str. NBRC 3442 AB1847
AJ007429.1 gg_id:11738 Streptomyces stelliscabiei CFBP4521 AJ0074
GQ268018.1 gg_id:581380 Streptomyces sp. str. NBE7 GQ268
AY999833.1 gg_id:130557 Streptomyces anthocyanicus str. KCTC 9755 CSSP698 AY9998
AY613990.1 gg_id:99663 Kitasatospora viridis str. 52108a AY6139
EF012136.1 gg_id:196486 Streptomyces sp. str. s6-212 EF0121
DQ442523.1 gg_id:179995 Streptomyces luridus str. NRRL B-5409T DQ442
FJ025786.1 gg_id:320338 Streptomyces sp. str. PA101 FJ0257
EU570449.1 gg_id:258981 Streptomyces spororaveus str. 173692 EU5704
AY950450.1 gg_id:114622 Streptomyces vayuensis str. N2 AY9504
AB045864.1 gg_id:30101 Streptomyces subsp. hygroscopicus str. IFO 13598 subsp. AB0458
AB184688.1 gg_id:155914 Streptomyces variegatus str. NBRC 15462 AB1846
AY876941.1 gg_id:111649 Streptomyces sp. 13c15 str. 13C15 AY8769
EU841699.1 gg_id:308014 Streptomyces radiopugnans str. HBUM174024 EU8416

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1801.2	2209.9	2437.2	2293.2	3671.8	2257.2	3483.4	2108.9	1532.2	1362.4	1046.2
479.2	3237.2	2635.8	2327.8	3657.9	3122.6	3498.0	2327.7	3516.2	2651.8	2445.9
40.9	21.1	27.5	29.3	24.8	20.6	24.6	24.2	26.0	21.3	23.6
535.0	4528.8	5650.5	4167.3	3490.5	4310.7	4921.8	4473.2	6370.8	2589.0	8711.2
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2169.2	6573.8	5300.7	3891.0	4548.4	5704.6	4521.1	4368.2	5978.2	3696.0	2419.8
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128.0	1970.6	2203.7	1545.4	2208.4	1637.5	1567.7	2157.7	2188.8	1544.0	814.2
155.8	1210.7	1168.7	1010.1	1517.0	808.7	1538.7	1040.0	1275.0	382.1	812.3
81.2	2066.6	1606.3	1067.4	1490.6	1299.8	1063.8	1458.8	2389.0	1558.2	862.7
996.1	3334.5	3731.4	3468.5	4568.7	3277.4	4413.4	3516.2	2792.2	1995.5	1781.6
106.1	1826.5	1675.6	1492.6	1480.9	1393.3	1307.0	1584.7	1530.4	1774.5	1420.3
2267.5	965.3	888.6	1096.8	982.4	986.3	1152.5	925.7	810.7	533.3	913.6
117.8	1213.3	1024.6	784.5	865.4	807.3	861.3	824.6	1180.3	1052.5	606.6
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133.2	1593.4	1593.6	1676.2	1697.9	1884.8	1239.6	1425.4	954.7	726.8	834.6
39.8	87.8	71.8	52.2	108.5	87.8	80.3	69.2	59.2	65.7	53.6
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64.9	205.4	130.1	61.1	278.2	99.7	115.2	166.7	66.8	71.1	24.7
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2720.5	3883.2	3543.9	3947.8	5012.2	4400.5	4197.2	3316.9	4005.7	3553.4	3399.5
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4593.6	4575.4	8377.8
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3216.1	1881.6	2574.7
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3071.2	5085.0	4291.9
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1304.1	1082.8	1014.9
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1061.5	824.4	1013.4
3128.0	2490.3	3336.7
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999.0	1225.7	991.2
921.0	911.9	1005.7
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4255.4	4912.4	6471.5
1017.1	814.5	839.9
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EU170124.1 gg_id:243122 Streptomyces wellingtoniae str. DSM 40632
AY299619.1 gg_id:87210 Streptomyces sp. YIM 80250
EU593655.1 gg_id:261025 Streptomyces zaomyceticus str. 174455
DQ513503.1 gg_id:161315 Streptomyces sp. str. 37
AF005019.1 gg_id:47276 Nocardioides thermolilacinus str. IFO 14336
EF397939.1 gg_id:205898 Streptomyces xanthochromogenes str. Z
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AB184841.1 gg_id:155839 Streptomyces coeruleorubidus str. NBRC 12761
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AB184416.1 gg_id:153718 Streptomyces graminofaciens str. NBRC 13455
AY999880.1 gg_id:136121 Streptomyces tricolor str. 4.1867 CSSP401
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EF654095.1 gg_id:250546 Streptomyces pactum str. NRRL ISP-5530
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EU273539.1 gg_id:247430 Streptomyces sampsonii XSD-103
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EU214942.1 gg_id:274977 Streptomyces sp. str. CNQ-147_SD01
DQ026663.1 gg_id:161518 Streptomyces candidus str. NRRL ISP-5141
EU741139.1 gg_id:540486 Streptomyces zaomyceticus str. 13647I
AY999755.1 gg_id:136130 Streptomyces aurantiacus str. JCM 3383 CSSP413
AB184188.2 gg_id:152673 Streptomyces aurantiogriseus str. NBRC 12842
FJ405904.1 gg_id:557015 Streptomyces clavifer str. 4.1604
AB184068.2 gg_id:153141 Streptomyces fradiae str. NBRC 12214
AF114033.1 gg_id:11941 Streptomyces nodosus str. ATCC14899
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FJ262971.1 gg_id:315876 Streptomyces sp. str. 40209
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EU570605.1 gg_id:272232 Streptomyces niveoruber str. 173722
AY277529.1 gg_id:85361 Streptomyces hebeiensis str. YIM 001
EU570644.1 gg_id:269610 Streptomyces albogriseolus str. 173770
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AY222323.1 gg_id:82694 Streptomyces plemorphus str. YIM 32065
FJ547124.1 gg_id:573139 Streptomyces pactum str. HBUM175174

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AY999
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FJ5471

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4908.1	5633.3	5179.3	3765.6	4710.7	5192.5	4429.0	3813.1	7130.6	5891.9	4342.3
189.3	1139.7	1182.6	1210.3	2249.3	1164.5	1892.8	1038.9	924.4	1111.3	639.1
67.1	163.2	229.8	154.4	367.9	148.2	301.0	115.5	120.5	128.1	94.6
64.9	1692.2	2510.1	1879.2	2432.9	2092.3	1898.2	1877.7	1207.1	807.4	878.2
98.2	2246.1	2453.0	2259.9	2968.1	2150.1	2720.7	1768.3	1028.1	986.6	1236.0
66.3	1488.2	1357.1	1115.4	1564.3	1386.4	1164.7	1311.2	2277.0	989.8	537.7
235.2	3246.3	3490.7	2209.6	2636.0	2976.0	2198.3	2353.6	3041.9	1966.8	1688.6
147.5	2245.2	1445.2	615.7	982.2	1497.7	1023.3	788.3	2353.9	1939.0	704.6
4184.1	3123.1	2406.7	3032.2	3588.7	2993.1	3846.4	2799.6	3115.0	2482.4	3779.3
81.7	2694.6	2841.7	2226.7	2013.8	2312.6	2194.8	2657.5	2534.4	1425.2	1622.8
65.9	4655.7	4387.1	3835.6	3547.5	3736.5	2646.5	3280.4	3694.1	2789.3	2490.8
188.9	1790.5	2551.6	1945.6	2574.8	2017.6	1993.3	2005.1	1473.1	1361.6	1132.3
18880.5	11392.9	10129.3	10156.2	9872.9	8960.4	10034.8	8749.2	14083.8	10361.1	12649.9
149.7	2133.1	1939.7	1631.8	2480.5	1545.3	2208.2	1426.9	795.4	608.0	688.7
100.5	3150.5	2569.0	754.3	1121.5	1989.9	721.9	1789.9	2712.7	1877.4	1197.4
71.0	1409.9	857.8	694.2	736.6	813.3	582.2	865.4	1809.4	707.1	388.2
10681.3	9522.0	7412.9	6704.6	9323.9	7267.8	8916.8	6398.7	11865.5	5531.4	4574.8
198.8	2887.9	2726.0	2336.2	3054.8	2854.6	2466.6	3226.1	2424.8	3037.1	1706.2
3897.0	3408.7	3996.5	3899.9	3109.4	3374.7	3573.9	3295.7	2141.0	1409.5	2547.3
7051.1	5810.5	5016.0	5050.7	5859.9	6301.2	5954.2	4335.3	6147.7	4735.3	7133.4
62.9	512.2	689.1	523.9	1056.5	693.3	706.5	594.5	261.6	601.7	318.3
187.0	2931.7	2361.2	1964.5	2912.8	2507.1	1909.7	1868.8	2160.1	1847.8	886.6
61.5	2475.8	3066.3	2387.5	3258.4	2761.7	2405.6	2060.6	1116.0	1071.1	1150.0
398.5	2701.1	2093.7	1535.2	2746.8	1961.3	925.1	1554.0	2926.2	2152.0	1275.7
60.6	2784.1	1967.0	802.2	1164.1	2312.4	1303.2	917.6	2371.4	1302.5	567.7
120.4	1017.0	960.8	733.5	1244.6	1090.2	811.9	941.3	1423.1	936.0	452.7
1315.2	2806.9	2163.7	1282.5	1019.3	1617.6	825.9	1988.3	2831.7	1976.0	1283.8
71.4	572.8	528.7	595.4	820.5	697.6	540.9	561.0	123.0	202.9	137.4
14550.6	6688.7	5772.8	5290.3	4610.8	5596.4	4944.3	5259.8	8033.7	5835.1	6915.9
2070.3	1953.7	1676.1	1667.4	2966.8	2000.8	2228.9	1690.3	2405.2	1771.2	1133.7
1430.7	2392.5	2337.9	2528.8	4720.7	3339.1	3537.8	3473.8	1352.2	4123.6	1361.6
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63.5	1038.8	908.9	581.2	849.6	778.9	538.5	583.6	261.7	276.1	219.0
2345.1	2647.0	2837.7	2983.7	3027.5	3090.9	3426.1	2943.5	3126.6	2403.3	1979.5
69.8	3010.9	2091.1	1146.3	2474.3	2682.4	1745.9	1154.2	2434.0	1438.2	564.0
73.0	2225.0	2792.9	2137.5	2779.4	2435.0	1795.6	1889.7	1171.1	1195.6	1029.7
46.4	459.5	549.8	605.7	1408.0	511.5	787.5	553.3	145.3	194.5	203.8
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1001.0	353.3	738.2
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2991.0	2933.6	3802.6
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958.1	554.1	854.0
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588.9	308.8	999.8
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AB184689.1 gg_id:152137 Streptomyces violaceorubidus str. NBRC 15463
AB184292.1 gg_id:156063 Streptomyces polychromogenes str. NBRC 13072
DQ462662.1 gg_id:157922 Streptomyces pseudovenezuelae str. B201
AB184637.1 gg_id:155573 Streptomyces aurantiacus str. NBRC 15386
DQ442556.1 gg_id:178243 Streptomyces viridosporus str. NRRL 2414T
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AB184421.1 gg_id:155143 Streptomyces bluensis str. NBRC 13460
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AJ616217.1 gg_id:103933 Kitasatospora recifensis str. Recife
DQ026639.1 gg_id:159765 Streptomyces anulatus str. NRRL B-2873
AB184521.1 gg_id:152917 Streptomyces piomogenus str. NBRC 13839
AY999927.1 gg_id:134670 Streptomyces roseoverticillatus str. NRRL B-24285 B24285
EU570478.1 gg_id:277234 Streptomyces pulveraceus str. 173717
EU593556.1 gg_id:260418 Streptomyces cinereospinus str. 173285
AB184190.1 gg_id:151731 Streptomyces candidus str. NBRC 12846
AY999739.1 gg_id:129590 Streptomyces venezuelae str. ISP 5230 CSSP185
EU214953.1 gg_id:274700 Streptomyces sp. str. CNS-730_SD06_MAR2
DQ442494.1 gg_id:195077 Streptomyces carpaticus str. NRRL B-16359T
AB249956.1 gg_id:161080 Streptomyces hebeiensis str. NBRC 101006
AB184245.2 gg_id:156427 Streptomyces tanashiensis str. NBRC 12919
EF527813.1 gg_id:224571 Streptomyces sp. str. AB5E
AB184863.1 gg_id:153957 Streptomyces griseocarneus str. NBRC 13428
EU570602.1 gg_id:273015 Streptomyces atrovirens str. 173608
AF361782.1 gg_id:26679 Streptomyces turgidiscabies str. S27
EU124775.1 gg_id:245293 Streptomyces caelestis str. JS-7
EF408733.1 gg_id:211549 Streptomyces hygroscopicus str. NRRL B-5491
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EU714277.1 gg_id:354205 Streptomyces sp. str. PM87
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AY999816.1 gg_id:133607 Streptomyces capillispiralis str. KCTC 1719 CSSP680
GU166435.1 gg_id:550267 Streptomyces flavogriseus str. O30

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201.3	1859.0	1251.8	977.3	918.2	1265.0	1086.9	867.1	1880.6	1028.0	697.7
667.4	3157.0	2424.2	2115.1	1687.8	2975.4	2369.6	1980.4	2180.2	1616.1	1468.1
55.1	364.6	325.4	186.5	353.1	188.2	197.8	242.9	337.2	127.0	90.8
170.9	6439.2	4543.9	2019.0	2710.2	4421.8	2533.1	2473.1	5471.7	3437.6	1745.2
1917.7	5421.7	5235.5	4732.6	7354.7	5201.3	6711.2	4743.3	5872.0	4032.8	3439.7
82.8	1246.1	1340.4	1300.0	2022.1	1495.3	1553.7	1224.1	761.2	735.2	412.1
218.9	3774.4	4842.0	4334.5	3689.8	4195.0	4270.0	3946.5	2233.5	2925.5	3791.8
6712.4	4375.1	3653.8	4092.2	4008.8	4820.0	3737.6	3214.9	4217.8	2243.2	2921.5
258.1	733.0	853.4	787.2	1439.8	749.0	1134.3	873.6	562.3	396.8	511.1
40.7	282.2	154.4	117.9	325.8	203.8	167.4	174.5	103.7	101.1	27.7
31188.7	12185.0	10478.3	11420.5	10744.0	10629.1	12309.5	9408.0	14856.4	11998.3	14056.6
116.3	1295.8	951.1	730.3	977.4	815.3	425.5	651.1	1731.8	526.7	319.6
637.7	4260.2	4737.0	3290.8	4086.6	3788.5	3685.3	3326.8	2752.1	2343.3	2550.1
224.8	1212.1	1148.8	1500.7	1616.5	1299.8	1104.7	1423.7	1628.7	727.8	614.3
5387.9	3934.6	3031.0	2753.4	2798.3	2842.0	2654.3	3146.3	4685.1	2873.0	1793.2
1418.2	4174.0	4968.0	4736.1	4528.6	4692.5	3956.6	4160.3	6628.3	3348.4	5556.8
962.2	6046.7	4335.2	2894.2	4881.3	4562.5	4324.7	3171.3	6509.9	5671.0	3534.3
76.2	812.0	836.3	1007.5	1247.4	1159.6	901.2	843.8	404.7	339.1	288.1
83.1	4338.0	3257.4	1986.4	2890.1	2905.8	2599.6	2441.5	1884.0	1860.2	956.1
120.0	2438.5	1892.1	877.6	1653.9	1834.2	1575.7	1266.5	2334.2	1899.0	640.4
68.1	1333.0	1505.5	893.9	1352.9	1171.5	845.9	1240.4	1910.7	1397.4	613.1
92.2	1180.5	1268.0	1331.0	1975.2	1428.9	1592.6	1366.2	671.3	595.4	434.1
284.4	4748.0	4701.6	2625.3	3819.2	3743.9	3093.6	3206.0	3855.2	2554.3	1564.5
3002.8	10024.8	9153.5	9558.0	11938.3	9122.7	10870.6	8710.9	9965.0	9116.5	8666.6
54.6	147.6	136.6	191.7	294.2	150.9	210.1	201.1	60.2	128.4	95.4
83.2	360.6	322.2	217.6	527.0	343.0	265.1	360.9	165.3	186.0	73.8
2256.1	1766.2	1278.2	1529.6	2271.1	1461.4	2054.6	1532.1	1358.5	766.2	2113.6
60.5	1939.1	1458.0	685.2	863.2	958.5	577.4	839.0	1198.7	924.7	465.1
262.6	3963.3	3303.6	2656.9	3619.1	3788.7	3264.3	2719.6	2765.5	2141.2	1328.3
131.7	3575.8	2616.2	2080.9	2241.0	2388.9	1774.8	2209.3	2914.3	2328.6	1707.6
1755.5	2436.3	2636.2	3163.8	3053.4	2285.2	2669.3	2870.9	1175.3	1184.6	1224.0
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123.3	2186.8	2190.7	2390.4	1767.8	1860.4	1514.2	1873.3	1757.1	2424.3	2355.1
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52.8	2369.7	1640.5	947.0	2029.3	1534.3	1582.8	1201.2	1438.9	1166.9	473.4
1994.7	4665.4	3895.7	3942.6	4100.2	4492.8	4952.7	3307.5	4271.1	3376.5	4349.9
71.1	2008.2	1728.4	1221.1	1491.1	1584.4	1021.4	1342.1	2173.2	1613.5	987.6
81.0	542.1	350.2	594.3	1174.4	386.4	1054.8	367.8	329.6	213.4	130.1

1084.3	713.8	818.6
3216.8	3242.4	3113.3
829.5	820.4	879.2
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175.1	155.0	503.3
1710.7	1660.0	2798.4
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3535.6	3338.8	3825.9
3136.2	3499.4	4239.5
992.7	844.0	1074.8
293.1	119.1	333.4
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521.3	609.8	994.8
3554.5	3099.5	3320.2
1375.6	1065.9	1199.6
2501.0	2699.1	2929.9
3898.3	3906.3	5629.5
3174.1	2581.1	3160.7
812.2	585.9	1202.3
2621.2	1604.2	2398.9
1207.4	756.0	1171.9
2172.8	829.8	804.0
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2597.8	1928.9	2487.0
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158.7	124.9	303.4
394.6	163.6	807.9
1670.3	1630.6	1640.6
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2859.5	1995.5	2663.0
1579.7	1194.5	1783.1
2590.5	1962.9	2936.4
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956.1	641.3	390.8
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2645.0	1975.3	2482.0
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815.4	675.0	1014.2
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AB473557.1 gg_id:373493 Streptomyces sp. str. Sp080513KE-34 (= NBRC 105046) AB4735
AB373970.1 gg_id:271489 Streptomyces sp. str. KS16 AB3739
FJ792578.1 gg_id:537379 Streptomyces corchorusii str. cfcc3168 FJ7925
D85119.1 gg_id:11757 Streptomyces virginiae str. IFO 3729 D85119
EU301836.1 gg_id:248501 Streptomyces matensis str. BG5 EU3018
EF063499.1 gg_id:188869 Streptomyces venezuelae str. 3495 EF0634
AB231807.1 gg_id:151878 Kitasatospora pitsanulaokmensis str. FLM-2 AB2318
GQ263352.1 gg_id:511203 Structure Simulated Level Waste Site simulated level waste site clone FW1_b28 GQ263
AB045858.1 gg_id:27887 Streptomyces viridochromogenes str. JCM 5013 AB0458
EU124566.1 gg_id:247428 Streptomyces heteromorphus str. OSS 34 EU1245
EF157833.2 gg_id:177854 Streptomyces sp. str. IH32-1 EF1578
EF178676.1 gg_id:211539 Streptomyces globisporus subsp. caucasicus str. NRRL B-2593 EF1786
AB184496.1 gg_id:152479 Streptomyces kagawaensis str. NBRC 13805 AB1844
EU593563.1 gg_id:277103 Streptomyces bungoensis str. 173014 EU5935
DQ462656.1 gg_id:158204 Streptomyces resistomycificus str. 6792 DQ462
AY999717.1 gg_id:136273 Streptomyces caesius str. NRRL B-12346 CSSP029 AY9997
AY207599.1 gg_id:101288 Streptomyces scabiei str. KACC 20222 AY2075
AY876943.1 gg_id:112178 Streptomyces sp. str. 1413 AY8769
EU570373.1 gg_id:266818 Streptomyces tendae str. 173511 EU5703
GQ985446.1 gg_id:539576 Streptomyces virginiae str. PW003 GQ985
AY999817.1 gg_id:132491 Streptomyces bacillaris str. KCTC 9018 CSSP681 AY9998
EF501759.1 gg_id:224037 Streptomyces sp. str. ZhDa03047 EF5017
AB184319.1 gg_id:151257 Streptomyces yokosukanensis str. NBRC 13108 AB1843
AY207596.1 gg_id:100808 Streptomyces europaeiscabiei AY2075
FJ486443.1 gg_id:567757 Streptomyces aurantiacus str. HBUM174703 FJ4864
AB184850.1 gg_id:155912 Streptomyces cinnamoneus str. NBRC 12852 AB1848
EU723881.1 gg_id:340050 Streptomyces sp. str. XF9 EU7238
EF012099.1 gg_id:197255 Streptomyces sp. str. 1A01550 EF0120
GQ263634.1 gg_id:511172 Structure Simulated Level Waste Site simulated level waste site clone FW3_19C GQ263
AY556418.1 gg_id:100643 Streptomyces sp. str. MG3 AY5564
AB184456.2 gg_id:152487 Streptomyces lavendularectus str. NBRC 13675 AB1844
EF608476.1 gg_id:254889 Streptomyces sp. str. HBUM 171361 EF6084
AB249954.1 gg_id:161344 Streptomyces malachitospinus str. NBRC 101004 AB2499
EU273535.1 gg_id:252272 Streptomyces nodosus XSD-120 EU2735
FJ792568.1 gg_id:541270 Streptomyces violaceus str. cfcc3156 FJ7925
DQ462653.1 gg_id:158512 Streptomyces cyaneus str. B188 DQ462
EU124781.1 gg_id:241638 Streptomyces showdoensis str. JS-13 EU1247
AB249927.1 gg_id:160669 Streptomyces scopiformis str. NBRC 100244 AB2499
AB184468.2 gg_id:152554 Streptomyces plumbeus str. NBRC 13708 AB1844
EF178683.1 gg_id:212242 Streptomyces spiralis str. NRRL B-16922 EF1786

808.3	7618.4	5535.4	2763.5	4488.9	4849.9	4012.0	3326.2	7839.2	5824.5	2285.3
87.8	3372.9	2932.3	1843.7	2870.6	3534.7	2573.5	1829.7	2770.3	2040.9	1100.3
2372.4	1702.3	1328.7	1536.5	2401.2	1251.5	1965.7	1332.8	1819.2	642.3	647.7
1887.5	2734.6	2740.0	1821.8	2811.1	1968.5	2865.6	1922.5	1478.9	1191.5	1119.3
75.2	2028.1	1523.4	946.2	2087.9	1335.6	1510.3	1092.2	1499.7	1177.5	418.4
85.2	209.0	233.6	188.0	136.7	148.1	97.2	143.7	126.4	91.4	141.1
141.8	4151.3	4424.5	2396.3	3874.4	3155.4	2819.6	2931.0	2791.4	2232.1	1618.9
7827.0	8031.5	6389.9	4477.8	5342.9	6916.3	5682.6	4407.1	7839.5	6565.6	4127.5
101.6	1850.4	1317.5	1108.8	2502.2	1460.0	1704.1	1073.3	459.7	684.4	340.0
1736.0	1986.7	1911.4	1682.4	2294.5	1752.0	2116.7	1914.9	1782.8	1138.7	1090.8
937.4	2692.1	2574.6	2304.9	4311.8	2572.7	3233.3	2210.8	2950.6	2535.5	1155.1
50.1	3505.5	2753.3	1441.8	1593.3	1700.1	1677.3	1767.9	2827.3	2013.1	1184.9
91.9	2406.0	2333.3	1177.2	2102.6	1796.1	1352.8	1849.8	1069.1	1059.5	581.4
110.4	1027.2	884.7	1113.6	1659.7	962.5	1280.0	1023.1	1481.9	547.1	345.7
111.3	1162.1	909.5	834.4	1443.1	912.8	1232.9	938.2	959.9	822.0	332.3
1141.7	1955.6	1827.7	1719.8	2057.4	1723.2	2296.8	1927.1	1643.5	1076.1	1136.7
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98.1	2623.6	1816.1	1688.2	2752.5	2054.8	2627.4	1648.0	1238.0	766.3	535.6
192.6	2053.8	1577.3	1871.8	1713.3	2076.4	1427.8	1817.0	2617.7	1271.5	763.1
283.2	4036.2	4671.1	3917.7	5580.6	3596.8	5270.8	4171.6	4339.3	3145.2	2288.9
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23470.1	4967.8	5214.1	4592.0	7049.1	5789.4	6673.5	5691.9	5931.1	3637.2	5581.5
2008.8	3634.9	3966.7	4424.4	5383.2	3966.6	4917.1	3928.2	3787.9	4621.7	3749.6
4953.6	6150.8	5816.3	6235.3	6827.4	6069.2	7002.9	5697.8	6402.7	4976.6	5602.4
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36.8	371.1	254.0	269.1	922.6	402.2	520.6	203.9	85.7	167.8	73.6
69.9	2164.3	2616.9	1769.6	2392.7	2155.9	1491.9	1401.0	1478.6	885.7	964.4
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14846.1	5243.9	4813.8	5370.1	4689.8	4776.7	4866.9	4540.4	4756.4	7204.9	5721.7
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79.9	106.4	120.2
2625.7	2249.3	2645.0
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1617.2	1422.9	1853.7
2455.2	1721.0	2120.7
863.1	1077.8	1580.4
1807.7	1285.8	1900.3
992.2	788.4	1110.2
1021.4	675.1	1146.5
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EU570657.1 gg_id:269910 Streptomyces vinaceus str. 173321
EU841581.1 gg_id:336639 Streptomyces aureus str. HBUM174596
AB249936.1 gg_id:161596 Streptomyces monomycini str. NBRC 100769
AB184422.1 gg_id:155585 Streptomyces pulcher str. NBRC 13462
AB184563.1 gg_id:152926 Streptomyces endus str. NBRC 14006
EU570631.1 gg_id:260117 Streptomyces variabilis str. 173806
GU350509.1 gg_id:563766 Streptomyces hygroscopicus str. MJM12143
EU714257.1 gg_id:313761 Streptomyces sp. C5(2008b) str. C5
DQ442516.1 gg_id:197785 Streptomyces lavendulocolor str. NRRL B-3367T
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EU360152.1 gg_id:265376 Streptomyces sp. str. 1x
AB249913.1 gg_id:160238 Streptomyces abikoensis str. NBRC 13907
AJ310924.1 gg_id:69890 Streptomyces peruviensis str. DSM 40592
AJ781353.1 gg_id:129764 Streptomyces lienomycini str. LMG 20091
FJ792554.1 gg_id:586969 Streptomyces filamentosus str. cfcc3117
EU841629.1 gg_id:310319 Streptomyces sampsonii str. HBUM70359
EU841580.1 gg_id:327134 Streptomyces aureus str. HBUM174850
AY999854.1 gg_id:136258 Streptomyces viridiviolaceus str. IFO 13359 CSSP721
AY289116.1 gg_id:86869 Streptomyces aureofaciens str. IMET 43577
AF170913.1 gg_id:11952 Streptomyces goraiensis str. MTCC 3154
AJ391820.1 gg_id:49805 Streptomyces hygroscopicus str. NRRL 2387T
EF550508.1 gg_id:222736 Streptomyces sp. 172624
GU143806.1 gg_id:543668 Streptomyces rameus str. L2001
EU258679.1 gg_id:243422 Streptomyces daejeonensis str. KNF 2047
GU434672.1 gg_id:520742 Streptomyces rochei str. AB1
GU136378.1 gg_id:561613 Streptomyces sp. str. Z-3-4
GU434673.1 gg_id:517030 Streptomyces sp. str. AM2
EU570464.1 gg_id:276621 Streptomyces goshikiensis str. 173817
DQ462654.1 gg_id:157028 Streptomyces lincolnensis str. B91
AB184555.1 gg_id:155222 Streptomyces mucoflavus str. NBRC 13973
GU132502.1 gg_id:543230 Streptomyces sp. str. JJG-5
AB208713.1 gg_id:140521 Streptomyces bikiniensis str. BA5
GQ268024.1 gg_id:577272 Streptomyces albogriseolus str. NBE40
AY382292.2 gg_id:96357 Streptomyces chungwhensis str. AA-98
DQ304115.1 gg_id:143008 Streptomyces sp. str. DA01013
AY533138.1 gg_id:105772 Streptomyces sp. str. AH030061
AB006154.1 gg_id:11807 Trichotomospora caesia str. IFO14562
U22974.1 gg_id:11800 Streptomyces sp str. GP 770 E. Atalan strain no. A46R51
EU119195.1 gg_id:247189 Streptomyces sp. str. HBUM 171191
AY999768.1 gg_id:131145 Streptomyces coeruleofuscus str. JCM 4358 CSSP429

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AY999

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1331.5	2741.5	2372.9	2207.4	1477.6	2323.9	2687.4	1825.4	2772.9	2242.2	1967.1
4769.9	2049.5	1676.9	2270.6	2168.3	2019.5	2584.1	1893.7	1703.9	1377.8	1754.7
298.5	1746.7	2223.7	2319.3	1585.3	1648.9	1518.9	2092.0	598.2	873.1	1313.4
59.2	1145.2	977.6	884.1	1607.8	1017.4	1145.7	879.4	1692.0	753.6	365.4
55.9	704.6	585.3	177.5	253.3	238.7	213.3	262.1	162.4	202.8	156.7
56.1	1529.0	1429.1	1362.2	1832.2	1338.5	1512.6	1162.6	1485.2	1052.1	843.3
60.5	268.2	203.1	221.1	453.5	241.8	201.9	141.1	89.7	85.6	83.6
3478.6	4813.6	5085.8	4640.6	4792.4	4229.5	4319.6	4282.2	3716.2	3393.6	4372.1
302.4	3731.0	2642.1	1697.1	1875.4	2681.5	1467.5	1913.3	5777.3	2948.0	1354.6
71.7	3125.0	2316.4	1336.9	2208.6	2901.2	2180.2	1520.9	3030.9	1927.3	881.3
592.3	2978.6	2780.1	2238.2	2986.7	2201.1	2716.0	2458.6	2376.6	1327.2	1696.0
104.2	2075.7	1248.7	844.2	1540.8	1436.2	1223.2	1128.1	718.5	671.1	409.7
40.9	147.1	494.1	171.3	477.9	268.1	233.4	246.0	133.1	346.7	52.1
67.0	3951.3	2718.3	1258.2	1405.9	2732.5	1361.1	1601.6	4227.8	2267.6	1056.0
617.2	6539.8	5263.8	2685.3	4325.4	4271.6	3597.6	2995.8	5832.8	4265.5	1957.6
437.9	2755.3	2375.2	2423.0	3177.9	2586.2	3252.6	1988.8	2748.6	2478.7	1243.2
41.7	889.9	806.5	736.8	921.3	821.6	1105.2	684.1	486.3	228.3	788.0
287.0	1906.4	1873.8	1824.5	3054.3	1775.9	2298.7	1423.7	2175.1	1593.2	793.5
244.3	1179.1	1191.0	1108.8	1144.0	977.3	1407.9	1026.6	1011.0	699.0	769.7
81.3	586.0	419.1	291.6	221.5	327.0	170.4	381.8	746.0	432.9	292.3
95.7	1767.7	1787.3	1687.6	2402.5	2104.8	2267.9	1390.9	947.7	847.1	652.5
11116.9	6494.1	6163.1	6792.7	7376.6	6409.2	7406.6	5627.0	7701.9	6500.0	8340.7
529.1	2333.0	1742.7	1467.2	3374.7	1659.3	2414.9	1599.0	4086.7	1601.8	666.2
88.6	918.7	795.7	839.8	755.6	651.4	1220.4	797.0	708.5	311.7	393.9
9758.2	8012.9	6855.4	6311.8	4931.9	6271.4	5854.1	5433.0	9913.8	7763.0	7800.4
6464.2	4114.2	3316.5	3100.6	4080.0	3554.9	4047.2	2969.8	4712.9	2808.3	1826.4
297.0	798.5	1018.1	764.6	959.9	700.4	753.9	809.7	671.6	414.6	446.4
1175.3	2397.8	2109.1	2122.1	981.6	2177.8	2846.7	1523.0	2727.9	2111.0	2183.0
159.3	1140.0	1562.9	1088.4	1863.1	1065.3	1830.7	1150.9	1060.9	1495.8	176.4
70.7	930.8	1500.1	829.0	1229.6	984.0	1384.1	734.4	474.1	250.2	510.3
145.6	4301.9	3160.9	1372.3	2240.4	2292.7	1770.2	1507.6	3193.7	1981.8	959.7
70.3	961.9	1541.4	1065.5	1933.8	1063.9	1219.2	1049.2	421.1	490.0	476.1
313.3	1719.0	1517.6	1107.4	1696.4	1466.4	1138.5	837.9	2290.0	1215.3	379.3
52.2	405.0	399.8	194.2	793.6	438.3	568.7	553.9	396.6	233.3	198.3
212.5	1152.8	917.4	1066.2	1153.0	1891.6	959.0	1640.6	1039.8	806.2	793.7
69.7	1088.0	882.6	362.8	986.1	938.8	474.5	532.9	756.5	651.9	200.6
104.3	1683.7	1488.8	684.2	1402.4	1329.3	1202.8	669.2	1701.7	1746.1	648.5
148.9	2898.6	2083.7	989.9	1178.3	1929.2	1202.7	1244.4	2947.0	2002.7	948.8
143.0	3052.5	2157.0	1973.5	2835.2	2370.7	2410.4	2118.5	1266.9	1217.1	903.3
396.9	6261.1	4729.0	3224.6	3576.7	4375.1	2717.7	3445.5	7978.0	4498.2	2402.1

2130.2	1807.4	2180.9
1682.9	1863.9	4035.1
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1632.1	2973.0	1619.4
857.7	431.1	479.3
258.1	157.8	636.2
986.6	707.0	901.0
200.1	121.6	416.0
5470.3	4248.5	4127.1
1408.7	1104.2	1227.5
1130.4	1059.1	2008.4
2157.2	1987.7	2855.3
1411.1	775.3	1501.1
970.2	366.9	484.0
1008.1	873.2	1680.5
3083.9	2202.4	2841.4
2203.9	1872.0	2216.9
477.9	977.7	955.1
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813.3	685.0	1239.0
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756.9	1264.9	917.2
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727.1	740.1	856.8
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897.1	650.6	1031.0
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1377.7	794.2	771.3
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EF063483.1 gg_id:173845 Streptomyces mycarofaciens str. E39
EF063491.1 gg_id:187825 Streptomyces hygroscopicus str. N32-80
AF455813.1 gg_id:51561 Streptomyces padanus str. PMS-702; ATCC 25646
X99942.1 gg_id:11962 Streptomyces vellosus str. NRRL8037
AY999837.1 gg_id:130216 Streptomyces californicus str. IFO 12750 CSSP702
NR_026177.1 gg_id:557107 Streptomyces bikiniensis str. DSM 40581
EU216727.1 gg_id:237060 Streptomyces sp. str. 6I
EU834278.1 gg_id:304084 Streptomyces scabiei str. DS63
EU273529.1 gg_id:251051 Streptomyces ahygroscopicus XSD-123
AB184330.1 gg_id:154052 Streptomyces finlayi str. NBRC 13201
EU181244.1 gg_id:257001 Streptomyces sp. str. 2H51-1
GQ357976.1 gg_id:584331 Streptomyces sp. str. SHLJ2
FJ792572.1 gg_id:594089 Streptomyces flavovariabilis str. cfcc3160
AB184390.1 gg_id:152986 Streptomyces prasinosporus str. NBRC 13419
AB184517.1 gg_id:152655 Streptomyces ryensis str. NBRC 13834
AB249928.1 gg_id:161599 Streptomyces thermodiastaticus str. NBRC 100020
EU683612.1 gg_id:327590 Streptomyces sp. str. Pol001
GU195048.1 gg_id:555358 Streptomyces lydicus str. BDUS 45
GQ268015.1 gg_id:584196 Streptomyces thermocarboxydus str. NBE34
AB184690.1 gg_id:154060 Streptomyces tuirus str. NBRC 15617
AB184588.1 gg_id:152710 Streptomyces cinnamocastaneus str. NBRC 14278
GU433228.1 gg_id:527568 Streptomyces sp. str. ABRIINW 111
EU593694.1 gg_id:267802 Streptomyces aurantiacus str. 174485
AB546287.1 gg_id:529029 Streptomyces sp. str. RI30-DHHV-601
AY999795.1 gg_id:130160 Streptomyces chrestomyceticus str. NRRL B-3310 CSSP548
FJ222807.1 gg_id:349554 Streptomyces lydicus str. WYEC 108
AB249983.1 gg_id:161628 Streptomyces glomeroaurantiacus str. NBRC 15418
EF178692.1 gg_id:215950 Streptomyces glomeroaurantiacus str. NRRL B-3375
DQ442517.1 gg_id:176433 Streptomyces levis str. NRRL B-16370T
EU570617.1 gg_id:263720 Streptomyces avidinii str. 173241
AF184082.2 gg_id:11833 Streptomyces sp. str. A36
AJ508062.1 gg_id:95093 Streptomyces caelestis str. US24
EU593710.1 gg_id:264633 Streptomyces rochei str. 174515
EU559727.1 gg_id:272268 Streptomyces scabiei str. D1
EU570414.1 gg_id:258807 Streptomyces variabilis str. 173634
AB184825.1 gg_id:155205 Streptomyces sp str. NBRC 13933
AJ781322.1 gg_id:136889 Streptomyces griseoflavus str. LMG 19344
FJ883746.1 gg_id:589519 Streptomyces coralus str. cfcc3136
EU214940.1 gg_id:268852 Streptomyces sp. str. CNQ-090_SD01
AB184442.1 gg_id:154651 Streptomyces alanosinicus str. NBRC 13493
EU521699.1 gg_id:260990 Streptomyces albospinus S75-3

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EU5216

99.9	4200.7	3414.1	2482.6	2223.5	2903.0	1851.7	2556.0	4643.7	3199.0	1942.2
2886.0	4544.4	3751.3	3269.7	3401.7	3552.5	3314.5	3760.1	6170.2	4070.2	3576.1
229.0	253.6	248.9	160.3	601.1	182.6	167.6	207.3	188.1	105.7	112.3
238.4	1216.8	1084.3	1365.9	1770.1	1244.0	1550.5	1808.7	1319.8	801.5	1537.3
139.7	2267.0	1958.5	2216.2	2462.0	2457.6	2427.0	2085.6	2317.0	1386.8	758.4
83.1	1065.6	1584.2	1079.2	2089.8	1117.1	1321.3	1125.2	564.7	491.4	477.7
325.5	1234.0	1341.6	987.5	1451.2	1159.2	1243.3	801.3	3575.3	803.3	1128.0
227.3	2000.6	1552.6	976.8	1574.9	1595.8	1171.1	830.6	2543.1	1363.9	393.3
2279.7	2561.1	2348.1	2634.4	3662.0	2798.4	3209.7	2414.2	2462.9	1911.8	1531.8
92.5	547.0	535.2	623.8	956.6	572.9	671.5	498.7	785.4	315.3	190.3
164.1	2330.0	2155.7	1631.2	1016.2	1585.9	1043.9	1681.3	2754.2	2766.4	1734.9
1445.4	2391.1	3299.4	3071.5	4048.0	3057.1	3781.6	2921.9	1678.4	1275.1	1787.8
80.9	3848.1	2967.4	1341.4	1751.3	1987.5	1168.0	1789.6	2893.1	2205.2	1122.3
124.3	3288.4	2626.3	1831.4	1974.7	1996.9	1481.5	2165.0	3550.2	2195.3	1453.5
341.6	6579.1	6304.3	5129.0	6653.9	5320.9	5599.3	5236.5	5031.0	4455.6	3654.2
65.9	1283.2	1477.6	1232.2	2674.7	1477.8	1902.7	1220.9	1007.8	1580.4	618.6
208.5	3663.1	2871.4	2274.7	3152.1	2909.8	3583.7	2643.8	3333.0	1989.7	1690.9
55.0	881.3	850.3	815.4	1356.4	851.9	1080.0	953.6	699.2	525.4	419.5
479.5	2433.0	2007.3	1524.1	3170.3	2174.3	2311.4	1400.7	2717.9	1745.2	583.7
217.3	2332.3	1867.6	1333.4	1645.7	1738.3	1195.4	1405.4	3257.7	1766.0	901.0
56.3	1726.6	1299.4	511.9	758.4	636.1	490.7	697.0	850.0	617.0	406.4
441.5	2626.7	2345.6	2758.2	3824.7	2796.4	2861.1	2107.7	2265.9	1005.6	1895.0
1963.9	2991.1	2516.6	1995.3	2415.9	2715.4	2437.3	2173.9	2889.4	1867.5	1586.8
242.2	3877.3	3264.6	1905.5	3568.1	3696.6	2337.8	1590.3	5019.8	2958.0	848.4
112.5	1779.4	1300.9	1137.3	1419.2	1330.6	987.8	1463.6	3100.9	1280.7	647.3
4502.0	6691.8	5735.2	5443.7	5389.9	5252.4	4857.6	5155.1	8268.9	5882.9	5164.6
1982.7	5015.9	4023.7	2774.3	3583.7	4364.5	3603.2	3149.0	4994.9	3096.6	2009.0
75.8	882.8	710.3	629.1	769.5	618.2	677.1	767.5	1331.8	473.5	223.3
29.5	809.4	711.9	395.6	342.4	546.6	238.2	629.4	1399.5	665.7	415.6
1670.4	4785.9	3929.9	3048.4	2711.3	4047.9	4000.3	2602.3	5460.8	4020.8	2340.7
249.2	2245.2	1938.9	1394.1	2887.0	1767.5	2211.0	2085.4	1803.0	1432.3	964.7
358.4	3415.8	2792.0	2164.3	1723.2	1432.1	1343.1	2179.1	3606.7	2655.8	2010.4
434.3	2167.2	1643.4	1317.4	1382.8	1707.4	1990.8	1272.1	2607.4	1307.1	680.4
922.4	3228.3	3238.0	2547.3	4193.2	2858.7	3712.1	3364.6	2845.3	2347.7	1491.1
9710.9	7059.9	6334.0	5966.2	6637.3	5713.7	6324.7	6193.7	7688.0	6803.5	5762.9
76.9	2955.8	2266.8	1592.5	1795.6	3717.0	1509.0	1343.2	1428.4	1020.2	808.7
63.4	259.8	240.7	243.5	863.8	399.9	394.6	94.4	77.7	157.2	102.6
2198.6	2423.9	2168.6	2054.0	3197.7	1963.1	2820.9	2685.8	2096.0	1100.3	1341.0
92.9	1261.4	1509.6	1355.3	3238.6	1360.0	2191.2	1531.1	880.4	1032.9	591.9
5488.0	6382.8	4548.5	4707.6	7851.3	5051.0	5130.7	4683.5	7934.8	4277.6	3232.1
211.2	2274.0	2178.8	1636.7	3156.2	2546.0	2392.4	2171.3	2799.3	1982.3	875.7

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187.2	155.6	290.1
1428.1	1390.7	1515.3
1782.4	1627.0	2508.9
1020.0	775.3	1041.1
832.4	729.0	634.7
846.5	567.1	942.2
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430.6	384.8	481.2
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2874.5	2996.0	2922.7
1405.8	972.4	1172.9
1192.4	987.9	1364.2
5205.1	4026.3	5022.2
1870.7	831.9	1241.5
2994.6	2339.6	4403.3
733.5	587.4	1077.3
1535.9	975.0	1417.8
827.7	687.0	969.6
441.3	335.3	605.2
1997.6	2857.4	3392.0
1777.1	2089.4	2601.9
2530.6	977.1	1684.6
871.1	707.5	821.2
4005.1	5415.5	4538.3
2590.5	2638.4	3669.0
494.6	544.4	967.8
270.4	234.4	426.0
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1790.5	1574.9	2056.3
1557.1	1615.6	1250.4
1057.5	930.0	1698.1
3551.0	2437.8	2444.8
4869.3	4779.7	6585.2
1257.8	876.8	1212.4
211.2	186.9	296.7
2524.9	2666.3	2474.9
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DQ513513.1 gg_id:161038 Streptomyces sp. str. a16
FJ792582.1 gg_id:553402 Streptomyces virginiae str. cfcc3174
AJ781336.1 gg_id:131005 Streptomyces lavendofoliae str. LMG 19935
EF063501.1 gg_id:175405 Streptomyces fradiae str. 5406Tu
AY999850.1 gg_id:133524 Streptomyces ciscaucasicus str. IFO 12872 CSSP717
EU594471.1 gg_id:264739 Streptomyces phaeochromogenes str. NRRL B-1131
EU570669.1 gg_id:259810 Streptomyces mutabilis str. 173506
AY154478.1 gg_id:75046 Streptomyces sp. str. A3
AY526527.1 gg_id:100996 Streptomyces sp. str. 28a-33-6
EF371433.1 gg_id:208087 Streptomyces globosus str. 12620-1
AY326621.1 gg_id:136565 Amazon soil clone 37-1
U94490.1 gg_id:11925 Streptomyces thermocarboxydus str. DSM 44293
EF491607.1 gg_id:221815 Streptomyces sp. str. AS29
FJ481057.1 gg_id:554989 Streptomyces virginiae str. xsd08100
EF540900.1 gg_id:226253 Streptomyces sudanensis str. SD509
FJ764793.1 gg_id:567040 Streptomyces sp. str. E-070
AB184424.1 gg_id:154236 Streptomyces lusitanus str. NBRC 13464
EU285474.1 gg_id:256929 Streptomyces xanthophaeus str. XSD-129
DQ462657.1 gg_id:158526 Streptomyces cinnamonensis str. B195
DQ442535.1 gg_id:181616 Streptomyces olivoviridis str. NRRL B-3374T
AB249922.1 gg_id:161385 Streptomyces hiroshimensis str. NBRC 12845
AY999917.1 gg_id:137163 Streptomyces fragilis str. NRRL 2424
AY785161.1 gg_id:108129 Streptomyces daliensis str. YIM 31724
AB184452.2 gg_id:151641 Streptomyces castaneoglobisporus str. NBRC 13669
AY999907.1 gg_id:134161 Streptomyces stramineus str. NRRL 12279
DQ026649.1 gg_id:159673 Streptomyces regensis str. NRRL B-11479
AB184440.1 gg_id:153942 Streptomyces longispororuber str. NBRC 13488
EU841570.1 gg_id:328854 Streptomyces setonensis str. HBUM82838
FJ799164.1 gg_id:550668 Streptomyces aburaviensis str. MJM311
AF503501.1 gg_id:93952 Streptomyces rubrogriseus str. DSM 41477
FJ442821.1 gg_id:538020 Streptomyces sp. str. A43
X80827.1 gg_id:11949 Streptomyces pseudogriseolus str. NRRL 3985
DQ462663.1 gg_id:157352 Streptomyces californicus str. B202
AY207608.1 gg_id:106229 Streptomyces aureofaciens str. KACC 20180
GQ268017.1 gg_id:556387 Streptomyces glaucescens str. NBC18
AB184437.1 gg_id:150826 Streptomyces poonensis str. NBRC 13485
AF441168.1 gg_id:44142 Streptomyces mexicanus str. CH-M-1035
AY247715.1 gg_id:85226 Streptomyces tendae
X95969.1 gg_id:11939 Streptomyces lividans str. TK21
EU570521.1 gg_id:269948 Streptomyces flavotricini str. 173963

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AY2477
X95969
EU5705

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223.1	4358.6	3303.3	1315.0	1950.1	2355.6	1838.0	1610.5	3347.2	2611.8	1503.8
5179.2	2431.0	2069.1	1937.0	2643.8	2446.9	2621.4	2445.1	2633.1	2257.9	1291.3
89.2	5259.0	4238.6	1928.0	2066.5	2772.4	1724.3	2796.0	4210.1	3204.9	1741.1
75.4	840.3	853.5	841.8	848.7	711.4	1180.0	711.8	316.9	253.9	1699.3
318.2	787.9	812.4	670.1	1128.1	695.8	1075.5	726.1	555.7	396.6	401.5
2285.9	1255.8	1070.7	1317.4	1530.6	1122.7	1239.4	1179.6	929.1	637.1	979.5
274.7	1424.1	705.0	612.7	799.6	1035.6	609.1	691.0	1555.2	851.0	556.8
579.7	6285.8	4597.0	2638.5	2869.1	4501.6	2683.9	2874.2	6453.2	3498.5	2133.4
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261.9	3146.1	2498.7	1317.6	1927.2	2023.0	1918.6	1715.0	3479.6	2631.8	1290.4
63.4	193.4	193.9	98.2	170.7	155.6	122.0	103.3	159.0	133.6	64.2
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753.8	3162.5	3100.4	3718.6	4636.3	3400.4	4685.6	3077.2	3174.1	1262.3	2287.8
93.1	3062.8	2279.8	1283.6	2781.2	1893.6	2073.9	1703.9	2455.4	1931.8	771.5
56.6	1900.2	2020.9	1127.4	1067.9	1786.5	817.9	1254.7	785.3	1009.6	703.2
55.7	2783.2	2335.6	1660.5	2269.8	2122.1	1766.7	2163.4	2509.3	2584.8	1114.9
86.7	597.5	818.9	418.2	852.3	651.0	468.6	683.9	711.8	843.0	248.0
2125.5	2768.7	2186.1	1949.5	3561.5	1986.2	2891.3	2137.2	2299.4	1742.1	1401.5
27.5	888.8	901.3	738.3	1452.8	871.9	1241.7	1588.0	701.3	588.4	343.8
208.2	2453.3	1866.0	1319.3	1423.1	2158.2	1191.7	1474.3	2964.4	1885.2	782.4
216.4	4002.1	3449.2	2944.6	2625.5	3822.8	2640.0	2942.9	3442.3	2337.4	1673.8
65.2	3284.2	2738.2	1106.8	1017.0	1448.2	919.8	1189.9	1650.6	1069.6	859.2
2745.2	5617.7	4884.5	4296.9	3877.2	4560.3	4369.8	4140.7	7045.1	6671.9	6886.3
46.5	1946.8	2401.5	1620.2	2079.0	1866.8	1195.1	1418.1	1214.0	907.8	1085.4
79.3	1096.4	1055.4	1005.5	1793.0	1113.0	1086.6	884.4	952.1	765.3	573.2
121.7	1817.5	1573.1	1062.0	1441.5	1476.4	1265.5	1585.1	2704.2	1365.5	777.7
88.0	303.6	444.9	334.8	1123.4	512.0	501.3	271.2	155.9	343.2	118.5
151.0	3796.6	4401.5	2888.4	4260.1	3507.4	2981.7	3089.3	2350.5	1916.2	1739.0
1887.2	4108.1	3512.1	3825.2	3449.8	3977.2	3437.8	3080.2	5126.0	3144.7	3713.9
187.7	4672.7	3033.4	1697.6	2384.8	3519.7	2108.2	1783.6	4013.7	2666.5	1181.3
376.1	4161.9	3201.7	1963.3	2454.1	3725.3	2126.7	2342.9	4884.9	4823.8	2826.2
123.7	1703.6	1580.0	1376.4	1457.9	1370.7	1418.4	1489.6	1517.3	1191.0	1124.4
231.7	2662.4	2777.5	2911.3	3604.2	2446.7	3939.0	2828.0	2291.8	1804.2	1632.1
617.6	5879.5	5270.7	4372.6	5992.6	5336.5	5300.7	4585.9	5558.4	4629.4	3722.6
67.3	799.9	869.7	840.2	1302.4	941.8	1068.0	1134.0	526.7	446.7	337.5
74.1	2117.7	1951.3	1641.5	1812.3	2118.2	1496.2	2030.4	1738.3	1511.6	840.0
37.1	2422.9	2099.9	1432.0	1710.5	1946.3	1479.3	1835.5	4269.6	2075.6	1212.6
43.6	384.9	337.0	470.8	348.8	296.8	572.7	296.0	83.4	117.4	363.7
224.7	6295.8	4654.9	3253.3	3787.0	4147.6	4003.9	3624.0	6131.5	3543.7	2369.7
138.2	3175.4	2466.0	1633.3	3341.5	2287.4	2447.2	1692.8	2608.7	1745.6	713.8

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1689.8	1522.4	1885.2
701.3	928.4	1034.6
843.1	733.7	1016.0
861.9	999.8	1276.7
571.8	994.7	673.9
1874.6	2062.2	2908.4
3281.3	4480.9	3278.5
1303.0	1273.3	1899.1
214.0	162.8	188.4
2331.0	850.3	1007.1
3321.4	2887.2	4096.3
1902.0	1345.1	1859.4
772.2	747.6	1233.7
1558.1	1473.2	2714.6
1723.5	607.2	644.0
2065.8	2006.2	2584.6
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1216.3	903.2	1503.3
2710.5	1626.6	2694.5
824.1	566.2	780.9
3946.5	6628.5	4120.4
993.8	885.3	820.4
745.4	630.8	1078.6
879.3	799.5	788.5
815.4	385.8	638.5
2819.0	2579.4	2943.4
3337.8	3636.9	4265.5
1359.4	1384.2	2536.8
2470.2	3345.6	3324.0
1314.5	909.4	1256.5
2450.3	2341.8	4118.3
5497.6	4793.3	4680.0
816.5	733.8	1183.7
1339.0	992.4	1720.2
1298.7	941.2	749.1
232.4	409.6	1532.6
2781.5	2564.0	3777.1
2226.8	1665.1	2331.7

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EU214923.1 gg_id:269083 Streptomyces sp. str. CNQ-299_SD01 EU2149
DQ513501.1 gg_id:160673 Streptomyces sp. str. 34 DQ513
EF063492.1 gg_id:191381 Streptomyces vinaceus str. N5-96 EF0634
EU570588.1 gg_id:272228 Streptomyces tubercidicus str. 173720 EU5705
EF620360.1 gg_id:254527 Streptomyces albidoflavus str. HD-103 EF6203
AB218615.1 gg_id:130748 Streptomyces parvulus SU22 AB2186
EU240415.1 gg_id:241302 Streptomyces libani str. B131 EU2404
EF017715.1 gg_id:179977 Streptomyces griseus str. SIIA 0059 EF0177
FJ492840.1 gg_id:561377 Streptomyces sp. str. SIIA 2049 FJ4928
EF012126.1 gg_id:198694 Streptomyces sp. str. 1A01653 EF0121
AB184664.1 gg_id:152610 Streptomyces glaucosporus str. NBRC 15416 AB1846
AJ781329.1 gg_id:133304 Streptomyces graminofaciens str. LMG 19892 AJ7813
AB184572.1 gg_id:150886 Streptomyces wedmorensis str. NBRC 14062 AB1845
EF371427.1 gg_id:212692 Streptomyces vinaceus str. 3078 EF3714
EU273537.1 gg_id:248870 Streptomyces albogriseolus XSD-101 EU2735
AY999888.1 gg_id:130607 Streptomyces griseobrunneus str. 4.1838 CSSP424 AY9998
U22972.1 gg_id:11762 Streptomyces sp str. GP 772 E. Atalan strain no. A46R47 U22972
FJ799165.1 gg_id:544753 Streptomyces verne str. MJM559 FJ7991
EU367977.1 gg_id:264465 Streptomyces lavendulae str. 20-2 EU3679
GU263847.1 gg_id:582591 Streptomyces sp. str. 32013 GU263
EU570529.1 gg_id:262962 Streptomyces argenteolus str. 173212 EU5705
EF371443.1 gg_id:210636 Streptomyces hygroscopicus str. N41-24-1 EF3714
AJ781357.1 gg_id:133766 Streptomyces mutomycini str. LMG 20098 AJ7813
AJ621613.2 gg_id:99737 Streptomyces catenulae str. DSM 40258 AJ6216
DQ347907.1 gg_id:203213 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi DQ347
AB184569.1 gg_id:152766 Streptomyces vinaceus str. NBRC 14035 AB1845
DQ028984.1 gg_id:139933 Streptomyces cyaneus str. NRS4 DQ028
EU098033.1 gg_id:254976 Streptomyces sp. str. SOK6/16-05 EU0980
DQ442532.1 gg_id:181545 Streptomyces caeruleus str. NRRL 2466T DQ442
AY260167.2 gg_id:136932 Kitasatospora sampliensis str. VT-36 AY2601
AB184194.1 gg_id:151935 Streptomyces chromofuscus str. NBRC 12851 AB1841
EF371442.1 gg_id:208603 Streptomyces albulus str. KT372-940 EF3714
EF564804.1 gg_id:219236 Streptomyces sp. str. VTT E-042677 EF5648
EU547520.1 gg_id:274551 Streptomyces sp. str. YIM 56142 EU5475
EU116310.1 gg_id:256002 Streptomyces sp. str. CNQ-418 EU1163
AB184500.1 gg_id:155531 Streptomyces adephospholyticus str. NBRC 13811 AB1845
GU132495.1 gg_id:547011 Streptomyces sp. str. JJA-7 GU132
FJ919811.1 gg_id:589769 Streptomyces sp. str. NCL 716 FJ9198
AY999727.1 gg_id:130740 Streptomyces lazureus str. DSM 40433 CSSP090 AY9997
DQ442525.1 gg_id:182376 Streptomyces luteosporeus str. NRRL 2401T DQ442

47.1	144.2	205.7	252.0	205.2	156.6	312.6	175.6	45.4	43.6	102.1
1142.7	5439.3	3963.4	2470.2	3780.4	4802.4	3495.7	2577.5	4672.7	3322.5	1975.0
222.6	5261.0	3860.2	1421.0	2210.4	2667.1	2173.2	1905.8	4140.1	3226.3	1710.5
2133.0	6404.9	5996.3	5006.2	5609.4	5582.7	5910.4	4760.0	7612.0	5035.3	5273.2
109.2	4913.2	3873.9	3077.1	2826.7	3095.3	2138.6	3249.4	5786.6	3910.7	2817.1
2317.1	1826.5	1551.0	1425.5	2073.4	1679.8	1504.4	1370.4	1851.4	1208.6	903.6
32.9	33.4	39.9	35.4	36.8	24.2	22.8	22.8	46.0	24.4	26.4
136.0	1320.7	1263.8	1272.5	2191.3	1653.8	1839.1	1289.2	1630.5	1022.6	600.0
1194.4	964.9	869.2	1137.3	1469.6	991.4	1334.9	1084.0	599.1	300.7	578.7
3038.2	2029.4	1694.8	1645.6	2633.6	1837.3	1852.4	1630.4	2187.5	1276.7	941.0
350.6	5586.4	4920.0	2748.8	2626.6	3750.7	2661.7	3648.7	6101.8	6364.1	4370.7
61.2	1156.0	1448.4	1253.1	1879.4	1394.3	1875.5	1356.7	750.5	1272.4	649.2
72.7	3118.6	3319.9	2462.5	2745.7	2411.0	2290.7	2556.4	1703.2	1701.7	1524.7
69.0	2217.4	2838.3	1543.2	3284.1	2145.2	2008.7	1904.3	1338.2	1163.3	1050.3
179.2	2374.8	1716.1	1323.0	1767.9	1502.0	1089.0	1514.4	2837.3	1949.2	1217.8
428.7	3502.5	2825.4	2002.4	2411.1	2835.9	1819.5	1634.3	4443.4	2676.3	974.5
78.2	2690.2	2276.0	1285.8	976.7	3585.9	793.9	1201.9	2240.5	1215.9	852.4
6255.9	4499.3	3196.7	3191.9	2625.5	3248.9	2949.4	2788.6	4576.4	2875.4	5389.2
24703.3	6453.6	5672.7	5701.4	4897.4	5720.1	5850.4	4800.0	8314.4	6478.6	7052.9
3802.7	3802.5	3304.2	3580.8	4196.2	3517.9	4458.0	3433.7	3986.5	3255.2	3109.5
965.4	2763.5	3048.5	3550.6	5017.2	3139.5	3790.1	3195.2	2096.0	2021.5	2126.5
76.4	392.0	442.0	377.9	400.8	482.5	286.8	493.5	217.9	153.1	233.2
32.2	676.0	844.5	858.4	1665.3	975.5	1234.5	932.7	383.7	252.3	254.9
103.6	2633.2	1897.8	793.4	1477.5	1015.3	1183.2	1027.5	1630.9	1088.9	561.7
115.3	4330.0	3500.6	2511.2	2505.9	3055.4	1936.1	2939.8	5138.3	3344.3	2181.3
454.4	1687.9	1738.0	1829.6	3249.3	2001.9	2403.3	1747.8	1194.6	862.3	730.8
247.9	2769.8	2121.2	1811.4	2566.2	1867.3	1863.2	2004.3	3337.5	2663.6	1456.4
237.7	1749.6	1415.7	1313.3	2281.6	1362.1	1625.2	1376.6	1921.4	1751.1	816.4
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500.3	3783.5	3760.1	3503.9	1844.9	4397.1	2505.9	3190.5	2623.7	1341.1	2857.5
188.2	1988.3	1717.6	1405.1	2597.3	1861.0	2376.9	1723.0	2141.9	1099.0	726.8
64.8	1098.9	850.9	738.1	1026.1	898.1	817.1	863.3	1679.2	950.8	364.4
145.4	1275.9	1192.2	980.4	1833.6	1354.7	1423.2	1326.8	1498.8	1030.0	528.6
116.7	1069.9	1068.5	1074.1	1413.1	1062.8	1101.1	1062.7	985.1	381.6	553.6
45.5	550.7	551.4	534.4	491.1	553.3	646.5	554.8	245.9	126.4	691.0
1104.0	3296.1	3168.7	3587.7	4178.1	3196.3	3840.6	3875.1	2789.2	2922.0	3352.7
106.7	3021.9	3511.9	2544.1	3457.3	2938.2	2606.2	2546.0	2349.2	1229.0	1361.9
407.0	6149.9	4299.1	3970.2	6259.7	4978.3	6256.6	3318.5	6568.2	4702.7	1636.6
1746.1	7222.5	6969.1	4474.4	4675.6	6913.9	4736.8	5004.9	7597.5	8121.7	5167.4
3240.2	5093.0	3705.1	2296.3	1734.9	2389.1	1810.2	2059.6	2943.4	2239.5	2348.6
170.2	8485.4	5964.4	5131.2	6511.5	4800.7	5776.6	5076.3	8357.5	5362.8	3742.6

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2301.8	2104.4	3948.9
1627.3	1446.7	2042.3
4796.6	4869.6	6026.1
2006.8	1633.3	2547.4
1445.5	1114.3	1189.4
26.9	31.7	38.6
1426.2	941.0	2799.4
1050.8	904.3	917.1
1458.0	1334.9	1624.2
3372.9	2640.0	2940.7
1611.7	1190.8	1620.3
1825.4	2346.2	2972.1
1782.0	1326.9	1626.4
1085.4	976.1	1289.8
1982.6	1126.1	1138.9
688.8	684.5	901.7
2606.5	3689.7	2359.7
4583.5	5870.5	4902.6
3418.9	3355.4	3957.4
2856.5	2625.4	2287.0
243.0	317.6	517.7
1073.9	582.9	1026.5
794.5	741.0	1093.8
1883.3	1533.8	1534.8
1997.8	1898.1	2408.1
1720.9	1442.8	1680.5
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1966.0	1626.3	1379.8
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317.3	612.0	663.5
4191.3	3707.2	4844.5
2023.7	2036.5	2550.3
2889.1	2860.7	4524.1
3787.1	4967.7	3276.0
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GU132485.1 gg_id:571692 Streptomyces sp. str. JJE-3
DQ460470.1 gg_id:157857 Streptomyces sp. str. D65
EU423876.1 gg_id:265275 soil clone Z851024
AB184460.2 gg_id:151015 Streptomyces nigrogriseolus str. NBRC 13679
AJ781364.1 gg_id:134638 Streptomyces purpeofuscus str. LMG 20283
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AY571804.1 gg_id:100881 Streptomyces sp. 35/02
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AY999766.1 gg_id:132602 Streptomyces alboverticillatus str. JCM 5010 CSSP427
AY445640.1 gg_id:101747 Microbispora sp. str. LM 164
AY445645.1 gg_id:102522 Microbispora sp. str. S21
FJ199993.1 gg_id:319018 Microbispora sp. str. DMKUA 245
U48988.1 gg_id:12150 Microbispora subsp. rosea str. JCM 3021
FJ261976.1 gg_id:347996 Microbispora sp. str. 212018
AF002266.1 gg_id:12151 Microbispora mesophila str. JCM 3151
AF492842.1 gg_id:67226 Microbispora sp. str. V2
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AB018787.1 gg_id:12117 Nonomuraea longicatena str. NRRL 15532

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1700.9	8421.2	7162.2	6457.0	7518.5	7259.2	7179.2	5863.3	7263.5	6731.8	6168.9
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142.4	2405.9	2285.5	1409.7	2304.1	1991.8	1939.5	1529.8	2526.1	1306.3	730.1
364.1	5075.4	4511.3	3598.4	4918.8	4380.6	4356.4	3943.9	4831.6	3842.8	2598.3
56.9	1760.1	1440.4	615.1	1261.2	1753.6	830.6	702.3	1398.2	770.1	337.7
55.9	563.1	609.5	613.0	1573.0	517.3	1105.3	607.2	496.9	394.7	165.0
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72.3	824.7	627.2	518.0	1028.3	634.0	896.8	601.3	780.3	399.7	293.3
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68.0	1119.0	1057.9	794.6	2035.5	1040.6	1009.0	873.3	675.9	964.9	372.3
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101.2	1224.1	1034.1	1143.2	1943.6	1103.4	1572.0	1031.8	473.8	323.7	664.0
112.9	1561.2	1157.4	1603.5	2176.1	1420.0	2027.5	1268.7	828.3	403.7	746.1
3622.0	4189.3	3418.2	4106.1	4722.1	3674.7	4826.4	3640.3	2426.6	1731.4	3785.1
115.7	1661.8	1159.2	1605.6	2175.6	1421.8	2016.4	1273.3	774.5	403.3	794.7
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2103.6	2269.1	1818.8	2194.1	2923.6	2100.6	2998.9	2462.2	2482.3	1938.8	1978.1
271.4	2429.8	1872.8	2266.4	3262.4	1652.9	3060.6	1887.1	1603.7	1048.1	1215.1
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GQ924523.1 gg_id:591226 Planotetraspora sp. str. PENDO-2174
NR_024821.1 gg_id:541414 Planotetraspora silvatica str. TT 00-51; NBRC 100141
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GQ924500.1 gg_id:590529 Sphaerisporangium sp. str. PENDO-1806
GQ924502.1 gg_id:555766 Sphaerisporangium sp. str. PENDO-1808
AB208718.1 gg_id:114928 Sphaerosporangium rubeus str. 3D-72(35)
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D85469.1 gg_id:12077 Streptosporangium album str. IFO13900
EU499345.1 gg_id:265713 Streptosporangium sp. str. YIM 48783
X89937.1 gg_id:12087 Streptosporangium brasiliense str. DSM44109

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204.4	3806.4	4195.6	3995.5	5227.1	3773.3	4539.4	3356.7	2980.0	1975.2	1902.9
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228.6	1100.7	899.8	954.1	1592.8	974.6	1452.0	1364.2	272.2	145.1	635.2
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140.3	1759.6	1305.9	1636.3	2087.3	1092.0	2037.0	1323.5	1163.5	730.7	968.8
10814.7	6802.0	7102.2	7058.4	7796.8	6758.2	7930.9	6500.1	7466.7	6574.0	7765.4
104.1	2715.5	2146.6	1255.1	2699.7	1623.0	2355.5	1608.1	1830.4	1536.5	633.3
264.3	1692.4	1067.1	1371.0	3436.0	749.3	2627.3	1074.2	516.1	737.2	705.8
16685.1	7813.6	6119.7	6322.4	8273.1	6810.2	8132.2	6788.9	8184.1	7802.8	11505.9
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139.9	1192.6	967.2	898.1	1997.9	887.1	1214.5	782.0	702.5	552.4	311.7
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AF191736.1 gg_id:12101 Streptosporangium sp. str. 5866
AB028655.1 gg_id:12104 Planomonospora venezuelensis str. JCM 3167
AF191734.1 gg_id:12080 Streptosporangium subroseum str. 7113
X89938.1 gg_id:12100 Streptosporangium carneum str. DSM44125T
X89958.1 gg_id:12073 Streptosporangium sp str. DSM43137
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NR_024778.1 gg_id:553910 Planomonospora alba str. JCM 9373
AB028654.1 gg_id:12109 Planobispora rosea str. JCM 3166
AF191735.1 gg_id:12096 Streptosporangium sp. str. 15110
X89950.1 gg_id:12084 Streptosporangium rubrum str. DSM44095
U48999.1 gg_id:12093 Streptosporangium vulgare str. IFO 13985
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AJ269555.1 gg_id:29802 Nonomuraea africana str. DSM 43748
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EU841591.1 gg_id:356049 Nonomuraea roseola str. HBUM174540
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X89939.1 gg_id:12107 Streptosporangium cinnabarium str. DSM44094
U48991.1 gg_id:12134 Acrocarpospora corrugata str. IFO 13972
DQ831042.1 gg_id:164372 Nonomuraea sp. str. NM94
U48842.1 gg_id:12122 Nonomuraea africana str. IFO 14745
AM932264.1 gg_id:260552 Thermomonospora sp. str. S22-23
AJ278220.1 gg_id:74555 Nonomuraea dietziae str. DSM 44320
AB364586.1 gg_id:247510 Actinomadura sp. str. TT 02-47 (=NBRC 103685)
EU420071.2 gg_id:540939 Actinoallomurus sp. str. GMKU370
AB364581.1 gg_id:254144 Actinomadura spadix str. NBRC 14099
AF163120.1 gg_id:22484 Actinomadura spadix str. JCM3146T
AB364585.1 gg_id:237220 Actinomadura sp. str. TT 02-15 (=NBRC 103683)
AJ293712.1 gg_id:100915 Actinomadura spadix str. IMSNU 20015T
AB364588.1 gg_id:241724 Actinomadura sp. str. TT N02-30 (=NBRC 103687)
FJ150688.1 gg_id:334906 Actinomadura sp. str. Y218
AB364592.1 gg_id:246769 Actinocorallia libanotica str. NBRC 14095
AF163117.1 gg_id:51620 Actinocorallia longicatena str. JCM9377T
AB364590.1 gg_id:253863 Actinocorallia longicatena str. NBRC 15961
AB364591.1 gg_id:251814 Actinocorallia glomerata str. NBRC 15960

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AF1631
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AB3645

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695.8	1905.4	1759.5	1592.8	2650.0	1625.8	2424.3	1362.9	1082.2	816.6	655.2
3853.0	1454.0	1123.3	1582.5	1321.5	1141.6	1712.4	1267.2	1513.1	944.1	1297.1
744.5	10195.0	7467.7	4014.1	5628.5	7126.1	6595.7	4337.7	10515.1	8021.7	3399.8
729.4	2679.6	2463.3	2691.5	3874.9	2498.7	3779.3	1944.0	1040.0	1374.3	882.7
356.1	1335.5	1082.6	877.0	1839.6	1185.2	1568.8	837.0	768.6	985.3	337.2
14798.7	10303.8	9126.2	8071.6	9497.1	8842.7	9482.9	7029.2	12979.4	9811.0	9089.6
4547.2	2878.8	2520.3	2785.3	3381.1	2329.3	3261.2	2707.6	2055.6	1431.4	1837.7
5872.7	4204.6	3999.4	3428.0	4442.8	4093.1	5442.2	4233.6	4686.3	3853.8	5918.5
713.9	6381.3	4944.9	3943.4	5645.2	4325.4	6049.9	3425.6	4857.3	3657.3	2274.0
892.3	4621.7	4285.6	1773.4	2966.2	3733.4	2863.3	2466.8	4761.4	3531.8	1685.2
562.4	2618.5	2235.3	1720.2	2834.1	2059.9	2670.7	1547.1	2042.1	1866.4	831.6
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527.0	3401.2	2564.1	3589.9	4443.3	2907.3	4266.4	2627.1	1249.9	1173.3	1400.8
145.0	1804.6	1308.9	1679.6	2257.2	1520.4	2540.7	1728.7	1152.5	542.0	749.3
528.7	3647.1	3793.4	4085.4	5653.2	3818.7	5249.8	4007.1	2665.9	2143.5	2226.5
1754.7	4772.0	3805.4	4141.2	5683.9	4026.0	5534.7	4033.0	3446.8	3021.6	3132.3
356.9	3789.3	3117.0	3308.0	4417.8	3257.1	4760.7	2868.4	2634.9	616.7	1573.3
10475.9	4378.1	3625.1	3517.8	5283.5	4168.6	4677.8	3864.2	3922.6	3720.4	5041.4
194.9	892.6	624.9	672.2	1824.2	784.7	1176.2	548.8	499.4	563.8	269.4
50.2	652.7	468.4	549.9	1596.1	545.6	1711.1	652.9	105.5	232.2	333.3
255.6	1218.0	964.2	1108.9	3173.8	1180.4	1937.2	881.6	736.9	907.3	441.3
320.0	3074.3	2554.0	2645.6	3916.2	2588.3	3498.2	1821.4	1592.4	1306.2	940.0
467.7	2511.7	2072.4	2177.8	3448.9	2204.8	3222.1	2032.3	2001.4	1313.4	1051.6
531.9	1537.4	1633.3	1698.1	3753.4	1939.5	3228.8	2066.3	1086.9	756.5	863.5
509.5	1700.2	1494.8	1372.1	2680.0	1352.9	2343.6	1285.4	1223.3	702.9	483.4
1016.2	7997.1	6785.7	5855.1	7227.0	6985.6	7337.4	5728.8	10485.1	7653.0	4573.4
336.6	733.0	533.3	560.3	3315.3	826.5	2195.7	258.4	148.7	632.3	193.8
587.4	4261.9	3910.6	3623.2	5169.5	3711.4	4879.7	3099.8	3707.9	1892.8	2158.5
721.8	4163.9	3914.8	3682.2	5522.0	3692.1	5131.3	3193.1	3189.4	1841.6	2039.4
983.5	5781.5	4944.0	4755.9	6661.2	5116.0	5762.1	4179.2	4747.9	2715.1	3045.9
696.6	4437.2	4011.7	3887.5	5167.2	3707.6	4875.3	3075.0	3580.5	1956.0	2149.6
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550.1	5176.7	4861.8	3786.9	6149.1	4332.0	5504.5	3488.4	5352.5	3674.5	2417.7
34.2	326.2	460.8	524.1	530.9	360.9	818.1	594.1	166.4	100.0	200.2
214.0	2777.2	2093.4	1815.9	3749.1	1721.9	3156.2	1956.5	2040.6	1036.6	875.4
5666.0	5272.0	3997.8	3327.6	4964.2	4609.2	4702.8	3851.6	3931.7	2858.6	2706.7
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2784.9	2445.4	3262.4
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7940.2	7780.3	7302.2
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3711.0	4470.7	4863.3
4131.2	2986.9	3562.9
2768.9	1542.0	2300.4
2029.0	1339.2	1905.3
4678.8	4838.7	4582.4
1130.3	602.7	1011.7
1981.5	1875.9	3128.3
3045.8	3182.4	4670.5
1345.5	1498.3	2655.6
3964.6	3995.4	6464.0
4986.4	4109.5	3804.3
3043.3	2862.2	5163.1
4319.6	3985.6	4052.9
875.2	500.7	776.5
591.0	555.5	1020.3
1348.8	917.2	1238.0
2412.1	2231.0	3468.9
2348.0	1944.3	2983.8
2151.8	1735.9	3825.6
1689.0	917.8	1794.1
6361.9	5933.5	6472.2
918.5	301.7	680.6
3364.7	2976.3	4562.1
3544.8	2934.3	4710.3
4630.8	3843.2	5262.5
3578.2	3117.6	4838.2
2019.0	1119.1	1511.0
4948.7	2890.5	4325.3
331.0	330.3	779.7
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AJ293704.1 gg_id:105102 Actinocorallia glomerata str. IMSNU 22179T AJ2937
AJ293703.1 gg_id:104948 Actinomadura formosensis str. IMSNU 22194T AJ2937
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U49011.1 gg_id:12036 Actinomadura verrucosospora str. IFO 14100 U4901
U49009.1 gg_id:12028 Actinomadura macra str. IFO 14102 U4900
U58527.1 gg_id:12032 Actinomadura madurae str. JCM7436 U5852
AJ420139.1 gg_id:45056 Actinomadura citrea str. DSM 43461T AJ4201
NR_026004.1 gg_id:566173 Actinomadura coerulea str. IFO 14679 NR_02
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U49001.1 gg_id:12035 Actinomadura citrea str. IFO 14678 U4900
AY035999.1 gg_id:51435 Actinomadura nitritigenes str. DSM 44137 AY0359
AM749789.1 gg_id:255670 Isolation ing candidate division soils New Zealand steam-affected geothermal soil AM749
AJ293706.1 gg_id:105412 Actinomadura livida str. IMSNU 22191T AJ2937
DQ076484.1 gg_id:150663 Actinomadura hallensis str. H647-1; KCTC 9992 DQ076
EF550498.1 gg_id:227192 Actinomadura sp. 172315 EF5504
FJ711204.1 gg_id:576085 Actinomadura sp. str. KC-IT-H5 FJ7112
AY545544.1 gg_id:104342 Actinomadura sp. str. 28a-77-2 AY5455
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AJ293714.1 gg_id:101239 Actinomadura yumaensis str. IMSNU 22167T AJ2937
EU841643.1 gg_id:317107 Actinomadura bangladeshensis str. HBUM174800 EU8416
AF134070.1 gg_id:26732 Actinomadura vinacea str. JCM 3325T AF1340
AB006157.1 gg_id:12045 Parvopolyspora pallida str. IFO14788 AB0061
EF612366.1 gg_id:248495 historic semiarid lead-zinc mine tailings site soil clone OS-C82 EF6123
FJ462361.1 gg_id:554990 Actinomadura sp. str. AV1 FJ4623
AF002262.1 gg_id:11998 Thermomonospora curvata str. JCM 3096 AF0022
EU637009.1 gg_id:341581 Actinomadura keratinilytica str. WCC-2265 EU6370
U49003.1 gg_id:12030 Actinomadura cremea subsp. rifamycini str. IFO 14183 U4900
EU214941.1 gg_id:261248 Actinomadura sp. str. CNQ-052_SD01 EU2149
DQ285420.1 gg_id:141124 Actinomadura rudentiformis str. HMC1 DQ285
AY568292.1 gg_id:107753 Actinomadura napierensis str. B60 AY5682
AB264086.1 gg_id:168232 Actinomadura chibensis str. IFM 10266 AB2640
AF223348.1 gg_id:28823 Pseudonocardiaceae str. PA123 AF2233
AF163118.1 gg_id:26839 Actinomadura oligospora str. ATCC 43269 AF1631
U49004.1 gg_id:11991 Actinomadura echinospora str. IFO 14042 U4900
AJ420137.1 gg_id:18352 Actinomadura fulvescens str. DSM 43923T AJ4201
AJ293710.1 gg_id:100606 Actinomadura pelletieri str. IMSNU 22169T AJ2937
AB331652.1 gg_id:236449 Actinomadura bangladeshensis str. 3-46-b(3) AB3316

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243.1	5713.3	3965.0	2659.4	4158.5	4279.2	3821.3	2551.0	5609.5	2924.7	1129.1
129.9	4964.8	3211.5	2025.4	4310.7	3347.8	3236.1	2218.0	5027.2	2489.7	943.8
1779.5	2753.8	2709.0	2542.8	3384.7	2337.7	3610.2	2333.0	3143.9	2177.8	2497.6
363.3	4359.2	3382.1	3534.3	4170.4	3384.8	4498.7	3870.6	3699.4	2518.6	2846.0
228.9	1156.4	1242.1	1185.3	3132.2	1299.7	1734.8	1528.4	667.7	701.2	708.0
114.3	1611.4	1576.2	1288.2	3262.1	1748.4	2191.7	1301.8	1492.2	1566.9	404.1
1914.2	4329.2	3742.2	3054.2	4471.0	3482.9	4464.7	3198.6	4416.8	3324.3	2752.6
4092.9	4653.1	4274.0	3504.2	4815.0	4182.7	4899.7	4208.5	5196.3	4424.6	3099.3
224.7	3869.8	3843.8	3172.8	4924.5	4105.2	4827.8	3755.4	4190.2	3387.8	2197.6
101.3	1750.8	1811.7	1710.5	3340.4	1576.7	2631.1	1744.9	1460.9	1545.1	986.8
517.4	5099.8	3239.3	2869.2	3566.7	3126.0	3620.0	2390.1	5521.6	2913.9	1622.3
750.9	3123.9	3056.6	3327.7	5293.8	3470.8	4836.9	3056.9	2072.7	1685.2	2368.6
937.8	8411.6	6933.7	4106.9	5931.0	6627.2	5570.7	5380.5	9493.8	7602.1	4497.1
120.0	2279.4	1895.6	1623.8	3877.9	2269.1	2335.6	1867.4	1944.0	1876.7	1168.7
41.3	751.5	917.3	1157.5	2827.0	1355.5	1735.5	964.4	386.1	617.0	346.5
40.3	24.1	20.5	25.8	56.3	20.0	36.3	23.7	24.4	20.9	16.7
1874.3	6096.6	5505.9	4078.7	7866.4	5789.7	5765.0	4179.3	5607.9	4644.0	2704.7
4599.1	2825.4	2578.2	2018.8	3643.0	2733.3	1944.1	2054.0	2250.0	2015.6	2077.8
3261.1	2888.5	2915.4	3221.9	4684.2	2980.1	4488.7	3780.6	3398.1	3014.9	2985.8
315.9	5612.1	4260.6	1794.2	4051.0	4994.9	2973.1	1986.9	4786.5	3420.1	1248.3
3279.4	3411.4	3179.5	3366.1	5148.0	3285.7	4941.7	3643.9	3598.1	3333.7	3040.8
50.2	499.3	522.2	590.0	1796.3	613.7	905.5	529.2	165.8	549.2	132.2
3124.2	4338.0	3239.1	2837.1	5685.6	3105.6	4702.9	2945.7	6624.0	4097.8	3936.1
2007.0	4976.8	4904.2	4630.0	6076.2	4317.2	6526.8	4622.9	5930.0	4573.4	5237.2
180.0	2860.7	2037.1	1159.2	2921.9	1867.6	2002.0	1227.5	3240.3	2324.5	819.0
440.2	5338.3	3506.1	2405.3	4080.1	3736.7	3621.9	2513.6	3889.8	2753.4	1123.8
889.2	3100.3	2098.9	1846.2	2567.0	2421.0	1950.9	1991.0	1954.8	1204.2	870.8
106.0	3464.0	1948.7	1037.9	1672.3	1808.9	1164.6	2304.3	3064.4	2711.3	1329.6
42.9	62.0	71.7	67.9	121.2	53.9	58.4	91.0	39.6	35.1	49.0
506.1	5592.2	4881.1	3627.7	5573.0	5113.1	4436.5	4404.1	7199.7	4696.3	2276.9
4051.9	5432.0	4634.6	4438.9	6745.2	5148.1	5418.5	4757.0	6081.4	5472.7	3857.0
2168.6	4138.6	3968.3	3446.6	5914.7	3859.6	4564.4	3704.7	3040.4	3315.2	3201.9
3662.7	4844.1	4301.9	3623.3	5545.0	4221.5	4259.8	3922.5	6131.9	4713.8	4697.5
189.2	1737.2	1189.3	994.1	1999.3	1257.0	1361.6	1037.1	1637.3	867.4	611.5
1549.2	3604.8	3638.3	2832.2	4579.1	4180.0	3795.7	2941.6	4179.2	3208.9	2722.9
489.9	6224.5	4725.0	4157.2	5943.7	3848.7	5264.0	4175.1	4768.0	2864.6	1920.2
253.2	4367.8	3484.8	3000.7	5438.8	3715.8	4174.5	2702.4	3579.5	2684.9	1345.2
278.0	1493.5	1075.9	1062.5	3026.5	1245.9	1767.8	1191.0	1392.5	1079.6	355.9
188.0	2537.1	2324.1	1990.2	4823.4	2473.0	2943.0	1962.0	1584.6	1516.8	887.1
3108.2	4119.3	3629.1	2667.6	4524.0	3818.6	3570.9	2927.1	4119.4	3467.0	2680.0

2772.4	2476.4	3017.0
2484.0	1925.5	2678.9
2377.1	1719.7	3487.9
2324.8	2311.2	2977.7
3630.4	3335.0	3935.8
1727.4	1386.4	1662.9
1452.1	1120.0	1497.7
3268.1	2617.6	3166.7
4113.8	3462.4	3851.9
3652.0	2560.4	3378.3
1751.0	1525.0	2065.5
3494.0	2453.6	2856.8
2758.2	2969.3	4921.5
5219.0	4447.3	5615.3
1879.4	1717.1	1799.1
1753.7	1172.5	1196.6
29.0	25.6	35.5
4777.8	3354.9	4677.1
1921.3	2889.9	1819.0
3269.9	2494.6	3421.5
2344.6	1532.6	2545.7
3721.4	2788.4	3645.9
942.9	445.5	800.4
3341.2	2436.1	2777.2
4598.3	4868.7	5933.7
1972.0	1225.4	1938.8
3138.0	2747.5	4478.0
2552.3	2174.5	2019.0
1601.4	1296.3	784.2
75.0	81.6	181.6
4624.9	3329.6	3934.1
4962.1	4231.9	4292.5
3713.1	3813.3	3163.7
3937.7	3521.3	3091.9
1113.9	1066.0	1419.1
3500.1	2770.8	3039.0
4306.6	2981.1	3653.5
3125.9	2752.6	5020.9
1410.6	893.8	1349.0
2608.8	2071.8	2927.7
2815.6	2636.1	2385.8

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s__Alloscardovia omnicolens	42256
s__Bifidobacterium adolescentis	41360

AF163123.1 gg_id:18830 Spirillospora rubra str. JCM6875T AF163
GQ179654.1 gg_id:512338 Actinomadura glauciflava str. S4215 GQ179
AJ293717.1 gg_id:101749 Actinomadura cremea str. IMSNU 22168 AJ2937
AB006155.1 gg_id:12038 Streptomycoides glaucoflavus str. IFO14668 AB006
DQ239428.1 gg_id:144933 Actinomadura sp. str. AC104 DQ239
AY035998.1 gg_id:51116 Actinomadura latina str. DSM 43382 AY0359
U49005.1 gg_id:12058 Actinomadura fulvescens str. IFO 14347 U49005
AF153881.1 gg_id:12040 Actinomadura glauciflava str. AS 4.1202 AF1538
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AF277195.1 gg_id:37666 Actinomadura mexicana str. A290 AF2771
AB364594.1 gg_id:256462 Actinomadura macra str. NBRC 14102 AB3645
EU399546.1 gg_id:271158 Spirillospora albida str. CMU-PNK470 EU3995
AF163114.1 gg_id:22138 Actinomadura fibrosa str. ATCC 49459 AF163
AF163119.1 gg_id:37892 Actinomadura pelletieri str. JCM3388T AF163
AB331731.1 gg_id:263027 Actinomadura maheshkhaliensis str. 13-12-(50) AB3317
EF546425.1 gg_id:218621 Actinomadura sp. str. 171848 EF5464
AJ293702.1 gg_id:104810 Actinomadura fibrosa str. IMSNU 22177T AJ2937
AF002261.1 gg_id:12126 Thermomonospora chromogena str. JCM 6244 AF0022
X85955.1 gg_id:13267 Tsukamurella inchonensis str. IMMIB D-771T = DSM X85955
AF283281.1 gg_id:20974 Tsukamurella inchonensis str. ATCC700082 AF2832
X80628.1 gg_id:13270 Tsukamurella paurometabola str. DSM20162 X80628
EU086530.1 gg_id:242076 Tsukamurella pulmonis str. BC5473 EU0865
AF272835.1 gg_id:69803 Tsukamurella columbiensis AF2728
AY254698.1 gg_id:86558 Tsukamurella pulmonis str. M67570 AY2546
AB478949.1 gg_id:569603 Tsukamurella pulmonis str. IFM 0949 AB4789
GU318217.1 gg_id:563156 Tsukamurella tyrosinosolvens str. E105 GU318
AF283283.1 gg_id:42701 Tsukamurella strandjordii str. ATCCBAA-173 AF2832
FJ917743.2 gg_id:571264 Tsukamurella sp. str. JS18-1 FJ9177
AM883151.1 gg_id:236778 Gordonia sp. str. NP8-5 AM883
AF512840.1 gg_id:65225 Rhodococcus rhodnii AF5128
AJ920291.1 gg_id:115193 Williamsia deligens str. IMMIB RIV-956Fl AJ9202
NR_024671.1 gg_id:534222 Williamsia maris str. SJS0289-JS1; DSM 44693 JoyO NR_02
EU341275.1 gg_id:241605 Evaluation Rapid Technologies Estimate Microbial Burden and Commercial Airline Ca EU3412
GQ036316.1 gg_id:435354 Topographical and Temporal Human Skin Microbiome skin palm clone nbu362g01c1 GQ036
GQ010474.1 gg_id:499191 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
AM409316.1 gg_id:193754 Williamsia muralis str. 9571414 AM409
DQ223667.1 gg_id:159776 Williamsia muralis zf-IIPht2 DQ223
AM283464.1 gg_id:161314 Williamsia serinedens str. IMMIB RS-4 AM283
FJ871122.1 gg_id:538876 Yaniella sp. str. G5 FJ8711
AJ278695.1 gg_id:63869 Bifidobacterium urinalis AJ2786
FJ369613.1 gg_id:369770 feces adult twins and mothers; TS51 clone TS51_a02f08 FJ3696

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733.5	1146.9	1111.2	918.8	2021.3	1009.2	1321.3	1024.2	824.1	1000.9	441.5
2092.6	4453.9	4597.0	4958.1	5116.4	4667.9	5725.1	4737.8	4138.9	2830.3	4821.5
4802.0	3452.3	2522.3	2367.9	3824.3	2710.0	3446.6	2588.1	3976.9	3568.5	2878.6
262.5	1534.5	1607.7	1758.6	2991.8	1691.9	2536.4	1979.6	1323.8	1316.3	607.0
1232.0	3787.9	3460.9	3605.2	4680.6	3311.3	4377.0	3441.5	3155.1	2448.5	2634.7
1903.1	4243.4	3430.4	3427.3	5058.2	3412.6	3768.1	3997.4	4373.8	3090.8	2123.3
30257.3	8715.5	8027.0	8745.3	7955.1	7925.1	10167.0	7477.4	14834.0	11957.7	12105.6
77.1	734.9	704.2	537.2	2985.0	670.3	1104.5	680.1	612.3	444.9	249.3
1512.2	2745.1	1927.0	1718.1	3570.1	1828.0	2136.4	2042.5	2452.2	1879.6	908.4
3559.8	3416.1	3562.2	3308.6	5332.5	3308.3	4601.0	3332.8	3531.4	3332.1	2966.0
895.6	7959.9	8659.4	5742.9	9290.9	7030.2	7864.5	6125.2	10981.1	7966.9	5576.1
109.9	1475.6	1343.9	1360.4	2880.8	684.1	1949.1	1140.3	606.4	840.1	540.4
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70.7	1460.3	1279.3	846.6	2113.6	1479.5	1622.1	977.1	1128.3	1055.6	609.2
308.0	3255.3	2623.7	2190.6	3154.4	1998.6	3132.4	2244.1	4127.0	1698.9	1265.5
47.9	42.9	36.5	41.3	58.1	31.2	54.6	41.0	33.6	29.7	29.7
99.2	1627.5	1103.9	604.8	1191.1	982.5	899.7	820.8	1970.5	1075.5	187.9
175.6	2723.4	1947.5	1234.8	2107.5	1554.6	1692.1	1362.1	2389.6	1630.1	586.5
64.9	2806.6	1843.5	1325.3	2359.4	2477.6	1475.2	2720.3	2217.2	1438.8	493.6
177.9	1722.5	1276.1	916.3	1581.4	1508.9	1202.2	1123.1	2606.2	1544.4	336.7
183.0	3859.8	2981.5	2070.0	2675.5	3270.2	2600.3	2607.5	5957.1	3472.0	1415.5
160.4	4852.7	3720.3	2917.9	3880.5	4031.6	3783.0	3274.0	6320.2	3998.9	2126.0
153.8	2448.6	1786.2	1407.0	1678.2	2026.3	1711.4	1543.6	3961.2	1856.8	753.8
136.1	3697.8	2679.4	1824.0	2815.4	2660.8	2475.4	1908.9	3688.4	2584.3	1195.9
462.0	3441.7	2588.0	1842.9	2570.7	2972.0	2203.7	2299.4	5210.2	3193.1	1166.1
220.5	2388.3	1779.4	1577.9	3195.1	1792.1	2135.6	2031.4	894.0	1034.7	1082.0
561.9	3698.0	2616.8	2450.1	4758.6	3993.5	2948.4	3141.4	2143.7	3741.3	1390.7
100.1	1363.6	1042.3	944.8	2211.9	1241.5	1336.8	1184.8	581.3	824.8	311.8
104.4	1381.0	1242.4	933.1	1820.5	1186.7	1539.5	1128.4	550.4	849.8	336.1
50.5	1490.4	1101.5	1033.1	3048.7	1416.1	1006.5	1477.4	1519.9	1573.6	464.7
1719.6	1228.3	1010.3	767.9	1535.3	1175.2	1068.0	1122.0	1228.6	776.8	671.4
57.3	704.4	590.0	632.2	1917.4	814.2	855.6	939.3	231.6	310.7	173.9
13784.7	8360.5	7603.6	8250.2	8038.1	7866.5	9668.3	7655.4	11602.2	7614.1	10774.8
272.4	2994.7	2773.1	2924.8	3333.1	2762.0	2363.5	2708.8	1950.7	1053.4	1710.1
295.7	1517.7	1741.6	1957.4	3539.6	1755.3	3420.2	1870.0	962.4	1155.7	661.2
87.2	1339.8	1004.4	912.3	2306.9	1199.0	1281.3	1222.7	611.4	826.7	328.4
2948.3	5756.0	5273.0	4645.1	4800.4	5420.9	4906.9	4774.5	5293.1	4551.2	2934.8
60.0	84.4	102.7	148.1	105.9	90.0	84.3	120.6	42.6	37.0	45.2
1448.6	2404.0	2482.3	2558.1	2148.2	2740.0	2691.7	2126.7	3531.9	3466.0	1907.3

2051.7	2018.8	1574.9
1032.5	1080.1	1051.7
4049.1	4495.5	4924.6
2745.0	2928.8	2992.8
2073.0	1436.4	2358.7
3729.3	3645.6	3338.8
3535.1	3433.6	3305.1
7686.4	9096.9	8105.4
962.9	569.7	776.1
2038.4	1863.8	1894.8
3454.5	3347.3	3275.6
6776.7	6200.9	6166.3
1575.8	1009.5	1391.4
2257.0	1869.0	2296.7
1259.7	1044.5	1831.4
1325.4	1242.6	911.1
2024.1	2238.2	3151.7
40.0	48.0	55.7
1027.1	650.1	838.3
1571.1	1519.9	1747.1
2994.0	1922.6	1723.0
1316.0	1077.5	970.2
2762.8	2342.2	2126.3
3226.1	3405.1	3162.9
1724.4	1664.5	1436.8
1989.9	1878.4	2266.9
2340.3	2518.5	1977.7
2652.1	2338.3	1759.0
3351.5	3519.3	3433.8
1677.3	919.7	1270.0
1598.5	1111.3	1061.0
1781.8	1936.2	1183.4
1443.9	953.6	2005.1
1330.5	724.3	1335.5
7662.5	8576.0	7856.1
3572.2	2161.4	2946.9
2407.4	1634.6	2689.1
1706.8	903.8	1524.6
4258.7	4869.6	4627.3
65.5	95.5	143.7
1970.0	2821.7	1205.7

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s__Bifidobacterium pseudocatenulatum	41330
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EU764013.1 gg_id:322549 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
NZ_AAXD02000018.1 gg_id:469849 Bifidobacterium adolescentis str. L2-32 NZ_AA
FJ368859.1 gg_id:360521 feces adult twins and mothers; TS4 clone TS4_a01d10 FJ3688
EU761819.1 gg_id:303601 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU766917.1 gg_id:338807 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ366679.1 gg_id:366831 feces adult twins and mothers; TS27 clone TS27_a02e08 FJ3666
AJ311604.1 gg_id:51788 Bifidobacterium longum bv. Infantis str. Y1 bv. AJ3116
AY694148.1 gg_id:102411 Bifidobacterium bifidum str. BF2 AY694
AY267190.1 gg_id:82861 Bifidobacterium breve str. KB76 AY267
NZ_ACCG02000012.1 gg_id:484303 Bifidobacterium breve str. DSM 20213 NZ_AC
AJ311606.1 gg_id:37229 Bifidobacterium longum biovar Longum str. Y10 biovar AJ3116
CP001750.1 gg_id:514324 Bifidobacterium dentium str. Bd1 CP001
NZ_ABXB01000044.1 gg_id:469858 Bifidobacterium gallicum str. DSM 20093 NZ_AB
GQ491152.1 gg_id:591285 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU768419.1 gg_id:331681 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ367371.1 gg_id:361008 feces adult twins and mothers; TS29 clone TS29_a02f11 FJ3673
GQ491359.1 gg_id:594044 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
ABXX01000002.1 gg_id:366993 Bifidobacterium pseudocatenulatum str. DSM 20438 ABXX0
FJ672962.1 gg_id:519290 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ677794.1 gg_id:522801 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ681952.1 gg_id:529729 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
FJ674164.1 gg_id:524845 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ673454.1 gg_id:525725 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ677405.1 gg_id:523432 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
GU361829.1 gg_id:542747 Bifidobacterium subsp. pseudolongum str. KCTC 3224 GU361
NR_029137.1 gg_id:540399 Bifidobacterium saeculare str. RA161; DSM 6531 NR_02
D89378.1 gg_id:12622 Bifidobacterium subtile str. DSM20096 D89378
GU361821.1 gg_id:561860 Bifidobacterium gallinarum str. KCTC 3235 GU361
AF357558.1 gg_id:35146 mpn-isolate group 10 AF3575
EF187235.1 gg_id:352163 Bifidobacterium asteroides str. CCUG 24607 EF1872
EF187233.1 gg_id:313828 Bifidobacterium sp. str. Bisn6 EF1872
FN600542.1 gg_id:567846 Bifidobacterium catenulatum FN600
NZ_ABXY01000019.1 gg_id:356843 Bifidobacterium catenulatum str. DSM 16992 NZ_AB
AY174108.1 gg_id:78797 Bifidobacterium psychraerophilum str. T16 AY174
AB438223.1 gg_id:295384 Bifidobacterium cuniculi str. YIT 4093 AB438
EU728759.1 gg_id:353078 Bifidobacterium sp. str. DJF_RP64k1 EU728
NZ_ABYS02000004.1 gg_id:471180 Bifidobacterium angulatum str. DSM 20098 NZ_AB
AB425276.2 gg_id:568235 Bifidobacterium sp. str. HM2 AB425
AB437350.1 gg_id:339532 Bifidobacterium minimum str. YIT 4097 AB437
AY174104.1 gg_id:78555 Aeriscardovia aeriphila str. T4 AY174
AY172657.1 gg_id:77771 Bifidobacterium breve str. KB 72 AY172

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64.3	1249.3	1267.6	1215.8	787.5	948.3	1156.2	627.3	811.1	589.3	341.2
555.7	3432.7	2149.6	1073.4	1670.4	2524.2	2257.1	1385.3	2924.4	1512.1	669.2
5395.4	5510.6	3988.4	3493.9	3804.2	3934.5	4398.4	3418.3	5502.2	4510.2	3097.3
163.4	2833.6	1984.5	1923.1	1683.9	1792.0	2402.4	1420.8	1795.0	1079.0	818.7
11666.2	6546.9	5006.1	5575.8	5068.9	5349.1	6602.5	5221.8	8052.3	7334.4	6821.4
80.7	932.6	794.0	394.6	155.0	643.9	576.3	563.0	708.4	487.2	214.9
46.7	49.2	45.4	43.5	59.0	34.9	48.3	52.4	34.4	30.1	31.4
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91.0	295.5	146.2	126.7	210.0	123.2	174.2	123.3	454.0	163.2	83.9
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3887.6	5449.0	6245.4	6801.5	6454.3	5521.6	6943.8	6105.5	6074.5	3539.1	7096.9
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658.7	3544.0	3776.7	3444.6	3025.1	2899.6	3772.1	2896.2	3744.7	3654.5	4473.7
44.4	84.4	71.6	102.8	122.6	76.1	99.0	342.7	68.0	28.8	63.1
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312.0	243.8	251.5	200.1	159.3	222.4	179.8	223.4	524.6	232.8	218.6
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44.5	350.6	363.5	487.3	606.6	337.6	574.9	350.4	387.2	179.1	78.3
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497.1	772.7	550.5
4309.0	4738.4	5341.1
3841.2	4539.5	5110.0
1281.1	1748.5	3262.2
960.1	1363.9	1901.1
1101.4	1892.8	1452.4
135.6	97.9	131.6
3815.7	5203.8	4369.4
1498.6	2231.1	2200.0
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5564.9	6358.2	7364.7
5191.7	5887.8	6741.3
3787.7	4965.4	5188.2
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3393.7	4252.4	4617.1
146.2	112.4	102.9
2631.8	3620.6	3127.6
79.2	144.2	332.2
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185.0	484.9	358.8
61.0	78.5	137.6
3610.4	3693.8	4466.5
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GU361825.1 gg_id:561020 Bifidobacterium merycicum str. KCTC 3369 GU361
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GU361817.1 gg_id:533785 Bifidobacterium choerinum str. KCTC 3275 GU361
GU361830.1 gg_id:557786 Bifidobacterium pullorum str. KCTC 3274 GU361
AB433856.1 gg_id:339819 Bifidobacterium sp. str. YIT 10443 AB4338
AJ307005.1 gg_id:63018 Bifidobacterium scardovii str. CCUG 13008 AJ3070
EU127550.1 gg_id:243420 Scardovia coagulans str. BLAPIII/AGV EU1275
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AB241106.1 gg_id:142067 Metascardovia tsurumii str. MOB115 AB2411
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AJ420965.1 gg_id:102049 Bifidobacterium simiae str. CCUG 30289T AJ4209
AM696904.1 gg_id:221821 sequencing libraries indoor dust clone BF0002A089 AM696
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EU778128.1 gg_id:347376 feces clone RL116_aaf01b09 EU7781
AB306662.1 gg_id:245388 Adlercreutzia equolifaciens str. FJC-B20 AB3066
AB306660.1 gg_id:252801 Adlercreutzia equolifaciens str. FJC-A10 AB3066
EU465013.1 gg_id:292719 African elephant feces clone AFYEL_aaj66f10 EU4650
DQ795573.1 gg_id:198774 human fecal clone RL178_aan66d08 DQ795
EF099706.1 gg_id:199590 mouse cecum clone SWPT4_aaa03c02 EF0997
EF099861.1 gg_id:180194 mouse cecum clone SWPT5_aaa01d12 EF0998
EU504902.1 gg_id:272555 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04a02 EU5049
AB379693.1 gg_id:263695 Eggerthella sp. str. YY7918 AB3796
EU511889.1 gg_id:267123 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aaf10f06 EU5118
EU456429.1 gg_id:332547 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4564
EU459919.1 gg_id:302545 Prevost's squirrel feces clone SQ_aah81c04 EU4599
DQ824677.1 gg_id:189434 human fecal clone RL185_aaj71e08 DQ824
DQ014636.1 gg_id:134778 mouse cecum clone M1_h09 DQ014
AM406030.2 gg_id:560141 percent G+C fraction libraries number Actinobacteria human faecal clone AP15K.65 AM406
DQ804406.1 gg_id:182894 human fecal clone RL187_aan79d03 DQ804
EU775387.1 gg_id:339040 Western lowland gorilla feces clone GORSD_aaa01b06 EU7753
EU791209.1 gg_id:426866 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology MMP7++ mou EU7912
EU457376.1 gg_id:338553 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4573
DQ015532.1 gg_id:133595 mouse cecum clone M3_c05_2 DQ015
EU464966.1 gg_id:295186 African elephant feces clone AFYEL_aaj65h10 EU4649
EU773468.1 gg_id:351639 Black lemur feces clone BKLE_h12 EU7734
EU507558.1 gg_id:262587 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa01a11 EU5075
EU507458.1 gg_id:263534 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_2aaa03e07 EU5074
DQ353924.1 gg_id:146867 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z58 DQ353

832.6	6458.3	3828.7	3567.8	3561.4	3383.1	3644.1	3234.5	5526.4	4758.5	2960.8
5249.7	5993.0	5580.0	4853.3	6189.1	5579.4	6505.5	4834.7	3956.1	5137.1	5101.8
4116.1	2470.8	1945.6	1925.2	2007.6	2168.4	1912.3	1831.5	3001.2	1707.5	4467.5
104.0	1670.6	2205.4	2012.4	2626.7	2585.2	2461.2	2407.1	1150.0	2780.7	1509.1
325.0	1612.2	1861.7	1724.0	1845.3	1351.5	1870.0	2075.1	1071.5	657.7	1742.5
94.2	958.1	1706.8	1845.4	1337.2	534.8	1392.2	1196.3	357.7	196.1	660.0
418.5	1596.6	1290.1	1042.9	1436.1	1603.0	1626.7	1322.4	1002.2	529.0	800.0
348.4	4245.3	4804.0	5557.3	6819.5	4612.8	6154.3	4536.5	3099.8	5158.4	3708.0
47.9	75.4	52.9	77.2	93.5	67.0	98.6	173.3	35.0	42.2	47.0
52.9	24.8	33.9	33.0	39.7	27.5	41.8	32.7	23.9	24.7	22.7
64.0	1849.6	1733.3	1427.5	2084.7	1219.9	2171.7	1459.6	1995.5	1275.0	759.8
157.9	1454.7	327.8	601.0	1087.4	1327.3	697.5	995.5	1367.8	1053.9	360.9
30.1	17.9	20.0	19.3	19.9	14.0	16.7	18.7	21.3	18.9	16.6
1126.8	4741.5	4007.0	2595.6	3891.3	4598.7	3854.2	2007.5	4779.3	3624.6	2325.7
49.4	26.6	23.2	25.1	26.7	21.2	26.7	20.2	19.8	18.3	21.6
1660.4	8283.3	5883.1	3810.1	4943.9	5918.8	5072.8	3724.3	12157.6	5534.3	2892.6
53.9	1165.9	1524.0	1379.6	801.7	1054.4	1004.5	842.3	646.4	514.6	373.1
188.4	2225.6	2283.5	2236.7	2712.8	2916.6	3343.0	2348.0	1057.5	1220.7	2301.7
361.8	2889.5	2984.7	3058.4	3646.7	3172.6	4578.7	2756.4	1483.1	1662.4	2741.9
248.8	1332.1	1325.4	1598.7	1913.4	1468.5	1674.5	1431.9	634.2	822.2	722.2
107.7	1001.4	1539.6	1523.3	1250.8	1208.4	1381.0	1497.9	964.6	240.2	930.9
5140.4	7370.7	6480.1	6568.3	5869.4	6815.0	6692.9	6132.6	7836.5	8366.6	6925.3
84.9	63.2	89.5	88.7	125.8	63.9	117.3	41.5	38.2	33.6	38.6
7474.7	2713.2	2785.1	3599.1	4136.8	2806.5	4404.3	4464.5	1982.8	1348.7	2442.0
149.2	1919.8	2166.1	2173.2	3150.9	2142.2	3689.7	2371.4	1225.1	1006.0	2029.6
241.8	2020.6	2878.5	2426.5	2987.0	2312.7	3406.5	2370.9	1045.1	842.9	1735.4
162.6	1527.4	1307.2	1117.0	1430.2	1350.3	1792.1	1054.7	1080.9	289.0	761.8
644.8	5014.4	4977.1	4655.7	6391.0	4743.5	6393.3	3981.1	4928.8	2487.5	2974.0
53.2	112.1	114.1	150.1	275.8	135.4	147.8	79.6	45.9	28.3	49.9
187.2	1763.0	2235.8	1657.7	1562.5	1782.8	3849.7	1523.3	1906.2	1170.9	1488.5
49.9	392.1	517.8	421.6	519.3	402.8	602.1	533.7	710.3	463.2	230.6
63.4	384.3	547.8	486.2	830.1	523.8	1060.4	394.4	138.0	101.7	235.9
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252.8	4879.1	6077.1	5457.5	6080.4	5332.4	6736.7	5175.3	3158.5	2916.4	5128.5
1365.6	5489.2	5790.9	6455.0	7647.1	5991.7	7889.5	6976.9	4916.8	4362.9	6009.0
52.0	55.8	58.4	48.8	75.0	60.9	79.7	33.2	27.5	29.0	32.5
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157.3	1682.4	2112.4	2012.6	2432.3	1891.5	8260.6	2112.5	2266.5	579.1	973.8
82.4	190.4	379.0	306.6	248.6	270.9	317.2	264.8	194.4	196.2	803.8
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5101.6	4107.8	5410.5
1870.3	2209.9	1150.7
1712.7	2520.5	2630.6
1471.0	1997.2	3337.2
835.9	1357.1	2748.7
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4780.7	4820.5	6684.4
62.6	124.5	215.9
34.7	43.7	35.7
1563.5	1518.4	1410.4
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16.2	22.8	64.2
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1277.3	1098.5	2053.6
4678.4	5079.8	8580.2
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51.0	66.2	58.4
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s__Collinsella aerofaciens	50507
s__Collinsella aerofaciens	50537

DQ794763.1 gg_id:173965 human fecal clone RL240_aaj32a11 DQ794
GQ038497.1 gg_id:465769 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
AY288517.2 gg_id:130587 Eggerthella hongkongensis str. HKU10 1 AY288
FJ676592.1 gg_id:512048 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
AM277970.2 gg_id:232823 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM277
DQ014875.1 gg_id:129970 mouse cecum clone M1_g04_3 DQ014
FJ880734.1 gg_id:419024 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EF099432.1 gg_id:188581 mouse cecum clone SWPT3_aaa03b05.Contig2 EF0994
EU509230.1 gg_id:274856 cecal contents Mus musculus strain C57BL/6J; MD8 clone MD8_aap46b12 EU509
EF099352.1 gg_id:190487 mouse cecum clone SWPT3_aaa02b06 EF0993
DQ015493.1 gg_id:132749 mouse cecum clone M3_g02_1 DQ015
DQ799106.1 gg_id:195061 human fecal clone RL205_aaj17f08 DQ799
EU766266.1 gg_id:336863 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
S44206.1 gg_id:11382 Atopobium parvulum S44206
S44205.1 gg_id:11381 Atopobium rimae S44205
NR_029349.1 gg_id:585058 Atopobium vaginae str. 961*00022/98; CCUG 38953 NR_02
FJ833382.1 gg_id:577349 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_16H02 FJ8333
AY278623.1 gg_id:87668 Olsenella genomosp. C1 AY278
GU303148.1 gg_id:566154 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
AF287760.1 gg_id:25658 human subgingival plaque clone C019 AF287
X67148.1 gg_id:11380 Atopobium minutum str. NCFB 2751 X67148
GU304476.1 gg_id:582069 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU304
AB270088.1 gg_id:173195 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
DQ793412.1 gg_id:196712 human fecal clone RL199_aaj43d09 DQ793
DQ798056.1 gg_id:194244 human fecal clone RL302_aal95a07 DQ798
FJ370884.1 gg_id:366874 feces adult twins and mothers; TS5 clone TS5_a02d04 FJ3708
DQ797662.1 gg_id:182774 human fecal clone RL206_aaj14d03 DQ797
DQ802697.1 gg_id:176814 human fecal clone RL188_aan95d04 DQ802
DQ799950.1 gg_id:196639 human fecal clone RL247_aaj22c03 DQ799
DQ798566.1 gg_id:178750 human fecal clone RL181_aan98d04 DQ798
DQ797345.1 gg_id:183310 human fecal clone RL248_aai98b10 DQ797
DQ794703.1 gg_id:194613 human fecal clone RL240_aaj31d03 DQ794
EU763926.1 gg_id:344582 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
DQ795339.1 gg_id:186254 human fecal clone RL178_aah53b07 DQ795
DQ795524.1 gg_id:195737 human fecal clone RL178_aan65f09 DQ795
DQ823720.1 gg_id:180558 human fecal clone RL250_aaj78b06 DQ823
DQ798532.1 gg_id:184171 human fecal clone RL181_aan97h06 DQ798
FJ371155.1 gg_id:359277 feces adult twins and mothers; TS6 clone TS6_a01e12 FJ3711
DQ794737.1 gg_id:198377 human fecal clone RL240_aaj31g03 DQ794
FJ362732.1 gg_id:365444 feces adult twins and mothers; TS13 clone TS13_a02e02 FJ3627
FJ366710.1 gg_id:369629 feces adult twins and mothers; TS27 clone TS27_a02h08 FJ3667

3776.5	1620.5	1550.5	1613.9	1315.9	1539.0	1437.9	1777.1	1766.6	1454.0	1739.8
70.0	56.5	77.0	130.6	86.8	57.5	270.5	55.2	296.6	40.0	91.0
29.9	129.9	331.0	196.8	210.1	135.9	295.1	134.8	78.2	28.0	67.0
6756.1	5755.3	5752.7	6455.6	6583.0	5806.6	8493.4	5854.4	5438.9	3431.5	4782.0
2505.0	9195.0	10039.5	10150.8	9093.0	8825.3	11819.6	9669.1	12669.6	11714.6	10429.0
60.9	56.1	70.8	77.1	120.5	46.6	96.9	50.1	34.3	23.0	40.2
4304.6	5060.6	5418.3	5508.2	6499.1	5099.3	7235.0	5517.8	4962.6	3170.4	4578.9
85.8	1081.9	828.3	1144.2	956.1	820.2	1237.5	1284.4	834.1	415.7	701.4
5604.5	5437.0	6185.7	7268.7	6751.0	5731.3	8906.2	6849.0	6325.2	4388.2	6491.6
1831.9	3006.7	2789.2	3202.1	3508.4	3206.7	5041.9	2966.8	3214.2	3217.1	2678.9
2546.3	5089.8	4334.7	3377.3	4159.4	4487.1	2269.0	3107.1	4920.1	4719.1	4247.5
149.8	845.7	802.6	781.1	1044.9	690.0	1350.4	641.2	651.9	591.3	401.0
2726.3	8237.9	9137.5	9485.5	9451.4	8170.6	11306.2	8714.0	9507.5	8044.2	8276.6
293.1	3419.1	3435.4	3610.5	2886.7	3106.3	3835.8	3178.0	2211.9	1895.9	2197.7
1640.3	3629.7	4078.0	4369.5	3957.1	3503.9	4922.6	3259.5	4295.1	1790.3	2884.2
46.7	40.8	44.1	67.0	46.5	25.1	69.5	47.8	38.3	34.1	36.7
831.1	2635.5	3558.7	3190.7	2736.0	2781.6	2908.4	3713.6	3139.9	3211.4	2445.5
39.6	135.5	200.9	189.5	116.6	148.4	199.6	146.7	36.4	44.9	79.0
4173.7	2098.6	3570.9	2287.7	2358.0	2331.0	2016.1	2845.3	1787.6	2106.2	2026.0
851.0	4175.5	3817.9	3134.1	3100.9	2886.6	3173.9	3837.9	3033.5	3457.3	2514.3
44.1	67.7	102.6	102.7	111.6	70.8	140.3	92.5	40.9	31.0	50.0
976.6	4092.1	4740.1	4900.0	4965.8	4251.8	5641.6	4831.0	4481.5	5639.2	4936.7
59.8	266.2	383.7	420.7	275.4	260.8	246.4	418.8	133.2	42.0	192.2
866.9	3670.0	5275.9	4138.2	4178.9	5335.0	4598.5	4664.2	2931.6	3904.9	3652.9
4998.8	3643.2	4025.3	4149.6	4703.5	3969.2	4600.2	3869.6	2902.5	2207.1	3194.3
180.0	519.7	639.7	694.7	599.6	431.3	431.1	452.8	240.3	93.8	226.1
360.0	2310.4	2237.1	2183.5	2111.1	1698.6	2360.9	2051.2	1819.4	973.8	1265.5
579.1	1171.5	1602.2	1459.1	1509.6	1090.5	1136.3	1848.9	1071.7	697.8	749.8
7006.5	3781.9	3466.2	3712.1	3687.7	3932.4	3602.6	2990.2	3148.5	2907.5	2946.5
8366.4	4450.4	4210.1	4418.4	4855.1	4721.3	5271.2	4004.0	3426.8	3124.3	3807.9
1248.9	1686.9	2084.2	1875.9	1853.2	1825.9	2267.8	2172.5	1201.6	824.1	1328.8
4185.1	2299.5	2894.9	2596.6	2648.1	2311.7	3192.8	2777.1	2187.5	1202.9	2244.3
473.4	1498.8	2399.3	1989.9	1861.1	1496.0	1784.5	2117.5	1805.6	1058.4	1377.7
495.3	1334.6	2084.3	2146.4	2200.6	1848.8	2695.5	2067.1	734.9	361.8	1232.4
3262.0	4887.9	4791.8	4923.9	6283.7	4832.9	6878.0	4823.1	4282.8	2491.5	4307.7
4852.5	3809.2	3860.8	3538.9	4720.6	3959.6	4740.1	4176.8	2999.4	1747.1	3117.3
1463.8	3636.9	3020.5	2418.1	2864.8	3121.2	2938.0	2820.3	3881.1	2568.9	1850.3
16409.0	5725.7	5853.6	5531.9	5705.3	5814.2	6210.2	5002.8	6571.0	5187.9	7246.1
3494.1	3981.5	3889.0	4142.9	5004.1	3997.5	5396.3	3517.3	3216.9	2040.1	3604.8
4613.2	2663.5	3131.2	2904.3	3306.5	2559.4	3556.2	2609.9	2238.8	1183.4	2192.6
937.9	1699.3	1882.9	1369.5	2055.5	1658.0	2385.0	1832.6	1670.8	1110.0	1311.5

1217.1	2116.7	1203.2
48.2	528.4	148.4
165.3	132.4	209.0
5540.6	5763.9	8635.3
8803.9	9950.4	10547.9
48.1	83.0	78.6
5261.3	5618.6	6962.6
823.9	1058.5	1278.1
6613.4	5704.0	6960.1
3403.8	2551.4	3375.6
3212.7	2964.2	3754.1
769.7	1197.7	1826.2
7881.6	8309.8	10602.7
2572.0	2676.1	3843.3
2831.8	3262.4	5074.2
43.9	47.7	74.8
3056.6	3449.6	3832.0
133.1	235.6	202.9
2531.1	2966.3	3134.6
2973.6	2322.8	3171.9
86.9	128.2	126.5
4695.5	4542.6	5494.9
282.5	335.5	373.4
5035.3	5091.3	5640.1
4103.1	4240.2	5459.1
506.4	775.1	801.5
1815.1	2375.3	2768.7
1711.6	1806.6	1413.0
2942.0	3713.3	3553.1
4203.6	5838.8	5616.9
1581.4	2531.0	2328.4
1974.5	2928.1	3312.5
1648.7	2528.1	2784.7
1586.6	2226.9	2598.9
4087.1	6092.7	5945.1
3294.4	3827.7	4375.9
2213.5	2801.9	2563.0
4899.9	6988.2	5799.6
3411.5	4266.2	5814.7
2346.1	2969.9	4539.1
1208.4	2025.7	2806.6

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k__Bacteria	k__Bacteria	p__Actinobacteria	c__Actinobacteria
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o__Coriobacteriales	f__Coriobacteriaceae
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g__Collinsella
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s__Collinsella aerofaciens	50583
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s__Collinsella aerofaciens	50803
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s__unclassified	50597
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s__unclassified	50619

FJ369185.1 gg_id:360763 feces adult twins and mothers; TS50 clone TS50_a01c07 FJ3691
FJ366663.1 gg_id:364843 feces adult twins and mothers; TS27 clone TS27_a02d02 FJ3666
DQ824087.1 gg_id:192721 human fecal clone RL204_aaj59b09 DQ824
EU763676.1 gg_id:305286 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
DQ798437.1 gg_id:175023 human fecal clone RL181_aah42f05 DQ798
DQ798523.1 gg_id:190099 human fecal clone RL181_aan97g07 DQ798
DQ800629.1 gg_id:186029 human fecal clone RL183_aao01c08 DQ800
EU777633.1 gg_id:323005 Sumatran orangutan feces clone orang2_aai66d04 EU777
FJ369759.1 gg_id:361945 feces adult twins and mothers; TS51 clone TS51_a04e03 FJ3697
EU462936.1 gg_id:301044 southern three-banded armadillo feces clone arma_aaj55c05 EU462
AB037384.1 gg_id:37392 Collinsella stercoris str. RCA55-49 AB037
NZ_ABXJ01000150.1 gg_id:361012 Collinsella stercoris str. DSM 13279 NZ_AB
EU462813.1 gg_id:302618 southern three-banded armadillo feces clone arma_aaj53e01 EU462
EU463374.1 gg_id:303197 bush dog feces clone bdog1_aai80d11 EU463
AB037381.1 gg_id:44613 Collinsella stercoris str. RCA55-5 AB037
AB031060.1 gg_id:38088 Collinsella stercoris str. RCA55-34 AB031
EU462966.1 gg_id:293536 southern three-banded armadillo feces clone arma_aaj55g11 EU462
AB031063.1 gg_id:46935 Collinsella intestinalis str. RCA56-68 AB031
AB037385.1 gg_id:23706 Collinsella stercoris str. RCA55-58 AB037
AB031062.1 gg_id:24647 Collinsella stercoris str. RCA55-56 AB031
EU463017.1 gg_id:302187 southern three-banded armadillo feces clone arma_aaj56e11 EU463
EU458534.1 gg_id:302088 spotted hyena feces clone HY2_e07_1 EU458
EU465454.1 gg_id:289322 lion feces clone LI3_aah77f02 EU465
EU462839.1 gg_id:289137 southern three-banded armadillo feces clone arma_aaj53g11 EU462
EU458483.1 gg_id:302951 spotted hyena feces clone HY2_g04 EU458
EU463042.1 gg_id:300347 southern three-banded armadillo feces clone arma_aaj56h06 EU463
EU458540.1 gg_id:293459 spotted hyena feces clone HY2_g01_1 EU458
EU468104.1 gg_id:296129 bush dog feces clone bdog3_aad67c06 EU468
EU468389.1 gg_id:297874 lion feces clone LI2_aae49c07 EU468
EU462871.1 gg_id:295720 southern three-banded armadillo feces clone arma_aaj54c06 EU462
FJ978629.1 gg_id:392696 feces clone CL_F_300 FJ9786
NZ_ABXH02000037.1 gg_id:470150 Collinsella intestinalis str. DSM 13280 NZ_AB
EU467593.1 gg_id:297912 southern three-banded armadillo feces clone arma_g05 EU467
FJ978646.1 gg_id:403535 feces clone CL_F_318 FJ9786
EU772855.1 gg_id:347709 Bush dog feces clone bdog1_c06_1 EU772
EU768091.1 gg_id:329684 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU462937.1 gg_id:301850 southern three-banded armadillo feces clone arma_aaj55c06 EU462
EU465473.1 gg_id:290360 lion feces clone LI3_aah78a06 EU465
EU463013.1 gg_id:302647 southern three-banded armadillo feces clone arma_aaj56e06 EU463
EU463040.1 gg_id:300489 southern three-banded armadillo feces clone arma_aaj56h04 EU463
EU458526.1 gg_id:290335 spotted hyena feces clone HY2_c10_1 EU458

11397.9	5515.5	5384.8	5557.0	5641.2	5657.6	6050.2	4950.5	5880.2	4504.8	6552.1
1433.7	2806.1	3682.5	3548.6	3001.4	3038.4	3017.5	3385.0	2099.7	2400.9	2567.7
4112.7	1550.6	1872.8	1764.5	2596.4	1742.3	2158.5	1528.6	1335.0	774.7	1263.7
16539.9	5738.0	6249.4	6388.8	7291.1	6332.3	7323.5	5692.2	4771.7	4649.8	5426.5
4078.4	2673.4	2892.0	2520.0	3455.4	2593.2	3385.3	2626.2	2564.9	2491.6	2745.0
5933.3	3387.7	3010.2	3651.1	3334.5	3116.9	3548.3	3764.2	2734.8	1571.8	5075.4
3672.3	2591.8	2940.9	3030.8	3477.7	2622.3	3836.0	2683.3	2315.4	1663.6	2589.1
4971.3	3562.5	3939.5	3686.4	4261.1	3614.8	4576.8	3701.5	2922.1	2314.2	3434.7
5883.6	3434.7	3845.0	3472.1	4375.6	3612.6	4414.9	3500.9	3441.3	2770.8	3233.7
73.8	886.1	1129.0	973.9	1330.3	745.0	1451.6	1275.4	745.5	505.5	797.9
12865.9	4361.7	3960.7	5979.5	6165.5	4572.1	5585.7	4840.0	5635.4	4467.6	8796.8
10120.4	5041.0	5729.5	6528.4	5905.4	5803.0	6683.1	5498.4	7603.4	4512.2	6779.2
13583.6	5060.8	4698.3	5872.3	6088.5	5380.1	5574.8	5309.6	5261.6	5712.9	6514.9
9903.3	4161.2	5106.1	5989.1	5458.4	5166.3	6316.1	4888.1	5304.1	3312.2	6044.8
176.1	1526.3	1737.4	1752.3	4066.7	1630.6	2137.8	1520.4	1089.5	2521.3	1536.8
10061.7	4765.1	5384.6	6005.7	5430.5	5544.8	6420.7	5216.2	7551.0	4565.2	6686.5
7801.7	3146.0	4079.5	5118.7	4365.8	4182.3	5335.4	4182.1	6187.2	2844.4	4880.7
9956.5	4456.6	5188.8	6267.7	5336.5	5308.9	6552.1	5099.4	7802.8	4368.0	6851.7
5709.1	4717.6	3593.0	5141.6	4179.4	3899.7	5063.4	4332.6	4553.8	2744.6	4830.9
12885.6	4550.3	4071.1	5327.6	6479.1	4661.3	5263.0	4859.1	5707.5	4520.2	7614.5
294.0	2499.3	2910.3	3258.9	4964.4	2597.0	3351.1	2557.5	1824.6	2721.2	2038.5
9289.7	4180.4	5126.8	6003.1	5473.4	4858.0	6331.8	4902.6	5717.2	3095.0	6050.6
9888.3	4158.6	5111.5	5591.7	5459.1	5162.0	6301.1	4866.6	5712.0	3299.6	6037.7
3431.3	2704.1	3457.9	3588.2	3336.0	3163.0	4446.5	3114.1	3846.3	2102.4	3317.7
6463.3	3271.7	4098.9	4834.3	4301.5	4084.4	5039.3	3912.5	4325.3	2013.9	4979.2
9776.9	3552.0	4535.6	5313.6	4805.8	4527.7	5485.9	4215.1	5112.4	3158.0	5518.0
8570.6	4645.6	4678.5	5385.0	5165.2	4810.8	5104.5	4435.8	4581.2	3889.8	5144.9
3999.5	1618.1	2731.9	3210.0	2953.5	2602.0	3664.9	2762.5	3078.6	542.2	2938.5
3921.8	5709.1	6312.3	6941.8	6611.0	5370.8	8359.5	5451.1	4566.5	3484.2	5525.8
9896.3	4181.5	5123.8	6001.1	5466.3	5174.9	6311.3	4898.2	5716.6	3314.1	6044.6
14101.4	2749.5	3832.3	3993.7	3766.3	4033.8	4259.5	3250.3	5725.6	5134.1	7352.9
10102.2	5075.2	5813.7	6590.8	6082.0	5858.4	7250.8	5609.2	8195.3	4500.4	7225.7
543.6	1228.7	1384.4	1734.7	1929.4	1181.7	1572.5	1289.1	700.8	315.9	925.2
190.1	1269.2	1299.4	1164.1	1289.8	1378.9	1854.1	1128.5	627.3	494.6	724.7
10695.2	4278.4	4451.7	4930.6	5000.7	4838.3	5943.6	4494.6	3134.9	3034.2	3563.8
4603.5	3054.8	3350.3	3467.2	4242.6	3053.0	4388.4	3091.3	2580.3	2107.2	3177.8
465.1	1931.0	2150.4	2184.3	2601.0	1993.8	3018.7	1961.7	1471.2	721.1	1479.6
16515.2	10356.6	9955.4	9987.6	11607.0	9751.2	10844.1	9592.9	10035.3	9287.9	14288.6
21276.7	8155.3	7855.2	8575.8	9533.5	8000.1	8922.6	7786.9	13009.8	8115.8	13613.9
4972.8	2841.6	3093.6	4048.5	3125.6	2544.2	3536.0	2836.6	2730.9	1748.1	2997.4
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2375.5	2888.1	3687.4
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2193.4	3106.0	4518.3
3188.5	4007.7	5133.2
3108.1	4183.8	4883.1
754.3	1313.3	1506.4
4257.7	5766.3	5536.1
5131.4	5210.0	6802.0
5660.8	5663.8	6932.1
4672.9	4434.5	6095.9
1747.7	1505.2	3191.2
4740.5	4843.7	6228.8
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4665.5	4627.8	6067.3
3674.1	4359.4	4774.8
4333.7	5786.5	6031.1
2841.2	2640.7	4034.4
4684.7	4463.5	6123.0
4666.8	4438.1	6096.0
4002.4	3445.9	4284.1
3617.5	3295.2	4714.8
4318.8	3760.9	5362.4
4099.0	4896.4	5722.5
2276.0	1879.0	3601.4
6500.3	6484.6	7655.5
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3219.9	4425.6	3374.1
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1270.8	1500.7	2525.5
944.9	1649.2	2489.9
4114.4	4776.4	6203.5
2857.6	3311.7	4845.2
1458.9	2045.0	2807.5
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EU467581.1 gg_id:288978 southern three-banded armadillo feces clone arma_b09_2 EU467
EU463038.1 gg_id:301713 southern three-banded armadillo feces clone arma_aaj56h02 EU463
EU458449.1 gg_id:299641 spotted hyena feces clone HY1_f02_3 EU458
EU465368.1 gg_id:303310 lion feces clone LI3_aah76b06 EU465
EU462795.1 gg_id:290060 southern three-banded armadillo feces clone arma_aaj53c04 EU462
EU467594.1 gg_id:297680 southern three-banded armadillo feces clone arma_g06 EU467
FJ369496.1 gg_id:368705 feces adult twins and mothers; TS51 clone TS51_a01c06 FJ3694
EU465475.1 gg_id:291808 lion feces clone LI3_aah78a09 EU465
EU468367.1 gg_id:298806 lion feces clone LI2_aae48e02 EU468
EU462873.1 gg_id:301874 southern three-banded armadillo feces clone arma_aaj54c09 EU462
EU468133.1 gg_id:301499 bush dog feces clone bdog3_aad70b08 EU468
EU458538.1 gg_id:297687 spotted hyena feces clone HY2_f07_1 EU458
FJ554834.1 gg_id:554988 Coriobacterium glomerans str. KP20W4 FJ5548
FJ554836.1 gg_id:585313 Coriobacterium sp. str. Dys2 FJ5548
X79048.1 gg_id:11367 Coriobacterium glomerans X79048
AF227849.1 gg_id:72748 str. 82345 AF227
AB011817.1 gg_id:11372 Eggerthella lenta str. JCM9979 AB011
AY321958.1 gg_id:89460 Eggerthella sinensis str. HKU14 AY321
FN178466.2 gg_id:515726 Olsenella profusa str. CCUG 45371 FN178
FN178464.2 gg_id:517887 Olsenella uli str. DSM 7084 FN178
EU592965.1 gg_id:262803 Olsenella sp. str. F0206 EU592
AF371712.1 gg_id:27160 swine intestine clone p-3423-SwA2 AF371
EU592964.1 gg_id:266446 Olsenella sp. str. F0004 EU592
GU395300.1 gg_id:514331 Slackia exigua str. 07-1951 GU395
NZ_ACUX02000006.1 gg_id:484407 Slackia exigua str. ATCC 700122 NZ_AC
AF101241.1 gg_id:11364 Slackia heliotrinireducens str. ATCC 29202 AF101
FJ368484.1 gg_id:359299 feces adult twins and mothers; TS3 clone TS3_a04h09 FJ3684
DQ808704.1 gg_id:188520 human fecal clone RL239_aaj12b03 DQ808
AM276076.2 gg_id:231940 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM276
FJ366775.1 gg_id:361191 feces adult twins and mothers; TS27 clone TS27_a03f12 FJ3667
EU776114.1 gg_id:320999 Spotted hyena feces clone HY2_g04_1 EU776
AJ608686.1 gg_id:125665 Slackia sp. str. CCUG 48399 AJ6086
FJ368806.1 gg_id:359418 feces adult twins and mothers; TS49 clone TS49_a04g09 FJ3688
EU776099.1 gg_id:350120 Spotted hyena feces clone HY2_g11_1 EU776
EU776136.1 gg_id:333194 Spotted hyena feces clone HY2_e02_3 EU776
EU776230.1 gg_id:343195 Spotted hyena feces clone HY2_b06_2 EU776
AJ583196.1 gg_id:94574 radioactive site ground water clone S15B-MN49 AJ5831
AX003092.1 gg_id:51091 Enterococcus casseliflavus AX003
DQ353921.1 gg_id:147031 Fecal Wild Gorilla (Gorilla beringei) wild gorilla feces clone Z43 DQ353
AF371713.1 gg_id:32126 swine intestine clone p-275-o5 AF371

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6456.3	3293.5	4116.6	4846.3	4309.4	4093.0	5034.5	3922.5	4662.6	2016.0	4979.0
9906.6	4124.4	5027.3	5529.4	5282.5	5106.6	5792.7	4755.8	5297.5	3311.3	5665.5
6465.1	3062.4	4123.2	4851.8	4323.5	4101.1	5061.9	3932.7	4665.0	2016.9	4987.1
16877.4	5972.9	5982.4	7555.6	5062.9	5955.2	6830.2	5652.1	7045.8	5083.1	7408.2
9300.6	4466.3	5101.8	6079.3	5412.4	4864.0	6313.2	4981.1	5335.1	3024.7	6081.7
7587.9	2273.6	3377.3	4048.3	3742.9	3485.8	4385.6	3439.4	3704.0	1643.5	3692.7
6246.4	3945.8	4246.3	3900.9	4569.8	4027.9	5008.6	4051.2	3532.1	3058.3	3922.7
16072.8	4787.6	6164.7	6492.0	6434.5	6151.1	7917.1	6054.1	7890.6	4197.9	6723.9
112.6	1284.5	1045.7	1053.1	1108.1	1133.7	1418.3	895.5	1059.9	686.8	712.6
25653.8	6702.8	6560.9	7605.9	7722.5	6735.3	7359.8	6144.4	8892.8	7421.5	10260.4
4147.9	1238.9	2370.1	2893.5	2586.0	2404.0	3108.8	2463.8	2649.9	345.1	2627.1
6336.9	2682.5	3528.4	4158.8	3649.0	3445.9	4209.1	3239.4	4133.6	1859.7	4452.4
62.6	321.6	335.2	250.6	192.5	513.4	143.5	303.9	283.0	35.6	192.7
420.8	2409.0	3443.6	3167.5	2916.4	2567.7	3037.8	2794.4	2233.2	1656.2	3036.4
533.5	698.1	711.2	684.2	770.0	828.5	900.8	578.9	818.9	576.3	396.6
53.3	231.0	242.9	266.2	375.1	226.5	433.0	212.8	149.2	133.1	116.1
13773.9	5329.4	4942.8	6965.0	6085.9	5511.7	6201.2	5204.6	5594.4	5541.8	5492.4
50.6	638.0	620.1	885.9	752.5	1026.2	1237.7	911.2	82.1	229.7	357.3
204.9	2727.5	3336.8	2492.2	3092.3	2780.0	3573.8	2278.1	2477.8	2785.7	1594.0
176.5	2745.2	2759.4	2679.7	3784.1	3358.2	4599.6	3268.9	2462.6	1760.9	1827.7
248.1	2468.8	3409.6	2620.8	3533.8	3240.1	3582.5	2805.5	1877.2	1457.8	1909.7
920.4	1905.0	3605.8	2949.1	3509.3	1923.2	3485.3	3575.3	1638.5	795.0	2795.1
286.5	3638.8	3415.6	2688.5	3870.1	3621.5	3955.8	2897.6	4052.3	1840.6	2144.4
7047.1	6188.1	5909.8	6240.3	6689.7	6844.1	6987.9	5752.8	6140.7	4859.9	5677.7
1193.7	5793.4	5170.8	5182.6	7141.0	6583.0	6113.9	4959.7	4419.2	4289.0	4181.7
2757.7	5852.2	5371.4	6443.2	8532.1	6006.8	8370.1	5820.8	4357.3	4961.1	4714.3
6182.6	3089.3	3367.4	3628.4	2780.1	2979.7	3174.5	2458.7	3607.2	3231.9	3122.1
10668.4	5534.1	4779.7	5933.7	5284.9	5259.3	5113.5	5144.6	6308.1	4437.0	6070.9
48.7	291.3	314.9	318.3	318.9	270.2	205.3	342.3	114.0	58.4	209.4
314.3	3041.1	2156.6	2490.1	2160.1	1892.0	2588.8	2198.3	3098.3	1429.9	1366.4
17295.5	8184.1	9304.1	9688.0	8686.9	8220.2	10548.4	7326.7	10843.7	8134.3	12421.1
111.5	1923.8	2978.4	2501.9	1180.1	2007.9	2467.9	2325.3	1552.9	876.7	2349.5
49.8	30.5	27.4	36.2	38.9	31.6	41.7	29.0	28.2	28.4	50.1
791.3	532.5	641.6	760.8	495.8	521.0	711.2	485.5	685.6	492.3	477.5
517.6	1086.9	1063.2	1147.3	1207.9	1086.2	1527.4	885.5	959.5	886.1	663.8
3474.7	2183.9	2807.3	2994.2	2156.9	1957.4	2844.8	1757.6	2594.3	1417.2	3399.9
50.5	368.1	77.6	548.2	474.2	312.1	827.3	370.9	149.9	94.9	133.8
758.8	4262.1	4356.8	4269.0	4078.7	3988.2	4904.1	3559.9	2784.0	2260.0	4135.0
194.9	1387.8	2129.2	2285.3	1102.6	1486.2	1565.4	1538.1	684.3	296.5	1538.1
38.5	169.6	244.4	254.9	321.8	174.3	420.5	237.9	139.5	161.4	103.6

1617.9	2112.6	3131.7
3626.6	3324.9	4737.2
4578.7	4393.1	5971.4
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4872.7	6613.7	6129.2
4696.1	4441.3	6161.6
3120.2	2673.6	4313.8
3545.0	4308.4	5430.4
6051.4	5305.8	8595.3
949.4	1206.1	1582.4
6241.7	7482.4	7885.1
2064.9	1534.3	2932.7
3263.5	2621.6	3981.3
137.5	351.0	1035.9
1425.2	2459.1	4149.8
790.3	1294.6	1686.3
227.6	225.0	381.6
6106.3	5766.9	6030.4
1005.3	1199.5	2302.1
1812.5	2154.4	4387.6
2668.1	2718.5	5015.9
1956.1	2354.4	5352.0
1883.2	2472.1	5139.9
1796.3	2908.1	4841.2
5108.5	6209.9	7998.4
4961.8	4857.4	7193.7
5762.4	6025.0	9121.6
2611.5	3653.0	3119.1
4651.2	6107.8	5909.2
388.6	251.8	304.6
1892.8	2742.4	2944.6
7877.8	8069.6	8370.6
1945.2	1946.0	4559.3
29.4	40.2	45.6
485.8	804.8	972.3
796.3	1397.9	1730.1
2216.9	2093.0	2417.4
214.5	272.4	628.8
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1917.2	2007.3	1820.2
194.0	286.1	391.2

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AJ518870.1 gg_id:136127 Denitrobacterium sp. str. CCUG 45665 AJ5188
AB269995.1 gg_id:172895 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2699
FJ368467.1 gg_id:370166 feces adult twins and mothers; TS3 clone TS3_a04g03 FJ3684
EU592966.1 gg_id:269678 Atopobium sp. str. F0209 EU5929
DQ794471.1 gg_id:175508 human fecal clone RL197_aah88c11 DQ794
AB089077.1 gg_id:78283 termite gut homogenate clone Rs-J59 bacterium AB0890
DQ824215.1 gg_id:185472 human fecal clone RL304_aal73a03 DQ824
EU748234.1 gg_id:349532 neotropical folivorous flying bird adult hoatzin crop clone hoa32_07G01.F EU7482
AM405723.2 gg_id:563304 percent G+C fraction libraries number Actinobacteria human faecal clone AP14K.90 AM405
AY160874.1 gg_id:128261 termite intestinal tract clone COB P3-21 AY1608
GQ502467.1 gg_id:580258 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf1- GQ502
FJ363677.1 gg_id:362064 feces adult twins and mothers; TS14 clone TS14_a02a06 FJ3636
DQ800788.1 gg_id:192875 human fecal clone RL183_aao03e01 DQ800
FJ880340.1 gg_id:398239 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
FJ982998.1 gg_id:410239 Aspects Oral Microbiome root canal clone OPEN_ROOT_34 FJ9829
EU773489.1 gg_id:337884 Bonobo feces clone BNO_aaa02g12 EU7734
AB189698.1 gg_id:135349 alkaline segment among various species er termites termite gut homogenate clone 1 AB1896
FJ363734.1 gg_id:358914 feces adult twins and mothers; TS14 clone TS14_a02f07 FJ3637
AB269993.1 gg_id:163566 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2699
AB269994.1 gg_id:166474 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2699
EU009849.1 gg_id:241290 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_U34 EU0098
EF097195.1 gg_id:189082 mouse cecum clone SWPT18_aaa02h08 EF0971
EU773494.1 gg_id:351744 Bonobo feces clone BNO_aaa03d11 EU7734
FJ879101.1 gg_id:410423 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
AM278923.2 gg_id:227819 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM278
EU761755.1 gg_id:315006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU7617
AB288919.1 gg_id:200827 termite gut homogenate clone BOf8-15 AB2889
AJ534681.1 gg_id:75442 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
DQ168842.1 gg_id:139221 Fermentative biohydrogen production heated anaerobic sludge clone J26 DQ168
AB192289.1 gg_id:143031 termite gut homogenate clone RPK-25 AB1922
AF079505.1 gg_id:11374 Denitrobacterium detoxificans str. NPOH2 AF0795
EU475540.1 gg_id:301038 springbok feces clone SBSD_aaa02a10 EU4755
EU475037.1 gg_id:292011 visayam warty pig feces clone VWP_aaa04h12 EU4750
AJ534678.1 gg_id:76995 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
AM275775.2 gg_id:232800 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
AB034096.1 gg_id:42186 rumen clone 4C3d-3 AB0340
AB234517.1 gg_id:149443 termite gut homogenate clone MgMjR-011 AB2345
AY053479.1 gg_id:48363 gas hydrate clone AT425_EubY10 AY0534
FJ152635.1 gg_id:354168 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
AB478418.1 gg_id:464059 marine actinobacterium F10 AB4784
GQ263040.1 gg_id:585361 Structure Simulated Level Waste Site simulated level waste site clone F2_162X GQ263

60.2	840.5	1060.8	976.8	804.8	634.0	733.8	807.5	321.0	282.4	561.1
38.3	32.5	47.9	50.2	43.5	38.1	40.0	41.9	17.9	15.0	19.2
36.3	1683.1	2455.2	2394.3	3173.3	1051.1	4743.4	1265.1	928.3	623.8	674.4
5423.9	1269.5	1334.1	1732.6	2580.1	1904.0	2018.9	2061.3	740.2	1559.5	736.1
81.2	1133.0	1108.5	1126.5	1455.7	937.5	1075.0	2990.2	780.3	472.3	2704.5
36.6	79.3	195.1	153.1	184.3	110.6	143.9	68.7	37.1	21.3	53.2
123.1	1032.5	606.7	1036.3	1251.3	1046.8	1298.4	958.2	787.7	718.6	662.7
2913.0	5518.5	5236.5	5919.2	5727.4	4955.9	7485.1	3932.1	8159.5	2477.4	4440.9
3101.7	2613.3	1365.7	3471.8	3451.9	2604.2	3486.6	2827.5	2171.2	1693.7	2521.5
1056.9	1583.7	2610.8	2431.6	1986.9	1880.0	3958.1	2559.0	665.7	515.2	1089.3
829.8	4120.7	4656.1	4832.7	4626.3	4565.9	5225.5	3972.6	3251.0	1641.0	4216.3
495.7	4345.5	3500.2	4593.1	5984.7	4105.8	6187.5	3871.2	3716.2	2687.6	3387.3
117.3	544.8	683.2	764.1	867.4	617.6	873.3	599.5	442.4	212.7	499.5
100.1	569.7	734.3	864.6	1076.7	802.5	1311.4	761.1	257.3	251.4	364.6
6090.7	9035.0	9668.7	8854.4	8754.9	8726.8	8758.3	7143.5	10488.1	9481.5	10893.9
7009.4	9304.2	9652.5	10427.3	9435.7	9328.1	9472.6	9270.6	8783.9	8532.2	10338.2
62.8	826.0	1639.3	1930.9	523.9	710.9	897.8	1494.9	1961.0	116.6	845.0
468.3	4262.3	4210.9	4467.0	3886.2	4235.8	4805.0	3568.7	3894.6	2161.1	4185.7
290.3	2675.1	3732.7	3595.9	3039.1	3303.7	3544.3	3576.1	2666.7	2122.3	2273.3
1940.3	5740.3	5703.3	5912.4	6623.1	5433.7	6958.2	5300.5	5264.7	4020.9	4394.6
173.5	3264.4	3987.5	3312.6	3612.2	3523.0	4393.6	3811.3	2809.8	2574.7	2872.6
36.0	289.0	409.0	354.4	621.8	282.2	418.2	449.9	163.0	243.4	537.3
694.4	2792.0	2402.3	2475.3	2288.5	1461.2	2232.0	1606.2	2536.1	1749.7	1292.4
10003.6	3323.6	3242.8	3460.0	2927.7	1894.4	3380.5	2754.6	4186.2	3576.6	4820.5
41.5	69.6	150.0	122.7	47.7	29.9	51.6	55.3	29.4	28.5	26.7
707.5	5268.8	6063.0	5934.2	5763.2	5294.8	6246.7	5807.8	6680.7	2780.5	5022.1
30.5	445.0	571.0	435.9	711.8	411.5	1050.5	554.0	88.5	79.0	275.2
213.4	4411.7	5106.6	4771.7	5445.6	5329.6	5077.4	5380.3	3354.1	8091.4	4003.4
56.0	221.8	315.8	285.8	315.7	217.4	373.2	513.3	79.4	44.8	194.0
221.3	1437.2	1634.6	1978.4	1304.3	1260.0	1631.5	1564.6	1062.0	429.7	1611.8
43.9	257.0	237.7	184.4	262.7	179.9	299.8	235.0	176.0	64.6	89.2
45.9	639.2	688.5	739.9	846.5	653.4	963.3	704.6	451.4	209.8	460.4
2113.6	5836.0	6431.2	7662.2	6427.8	5714.0	7630.1	5171.3	4961.2	4454.9	6604.5
1065.3	3187.1	4164.5	3771.7	4374.0	2989.5	5321.4	3378.5	2598.8	3087.3	2647.8
50.7	77.5	142.6	144.7	74.2	69.9	67.9	96.3	44.0	50.3	67.3
58.2	468.1	1180.8	651.3	390.7	615.2	335.0	678.2	498.5	151.8	382.7
1952.1	4002.5	3745.5	4014.5	3382.0	4247.1	3855.5	4106.6	4002.7	2911.3	5013.8
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185.4	1057.6	1119.5	971.2	1658.2	1156.6	1517.8	1009.9	485.9	989.6	543.2
3879.5	9548.6	8314.2	7373.6	8539.8	9353.9	9199.7	7104.6	12281.3	7769.0	5324.5

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559.1	670.9	795.0
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1123.2	1595.8	1476.5
77.7	195.5	487.2
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3333.9	4387.8	5467.7
3950.5	5269.1	4600.3
592.6	815.7	1256.9
523.8	1018.8	1481.0
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146.6	295.4	370.0
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FJ152924.1 gg_id:338718 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
DQ432396.1 gg_id:156755 prokaryotic alkaline hypersaline lakes Wadi Natrun Egypt Lake Hamra water clone W DQ432
FJ152964.1 gg_id:328890 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
FJ152905.1 gg_id:312275 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
AF448192.1 gg_id:80775 actinobacterium clone ML615J-2 AF448
AB038407.1 gg_id:41242 Chibacore 1500 AB038
EF573094.1 gg_id:227879 Coco's Island site 23 marine clone S23_1193 EF573
EU268121.1 gg_id:247055 summer Dalian and Liaodong bay determined sea water clone ZL1711 EU268
EU802784.1 gg_id:320796 It's all ranking aquatic Northeast Colon Panama clone 4C230159 EU802
EU237434.1 gg_id:257745 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
FJ745217.1 gg_id:549390 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7452
EU268081.1 gg_id:241376 summer Dalian and Liaodong bay determined sea water clone L1541 EU268
EF572551.1 gg_id:231650 Coco's Island site 23 marine clone S23_650 EF5725
GU061846.1 gg_id:593293 and function microbial mesoscale eddy perturbations South China Sea clone CEP-DC GU061
EU805049.1 gg_id:309339 It's all ranking aquatic 250 miles Panama City clone 6C233031 EU805
GQ347801.1 gg_id:550051 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU804962.1 gg_id:339859 It's all ranking aquatic 250 miles Panama City clone 6C232942 EU804
AY033302.1 gg_id:54456 marine bacterioplankton clone MB11C06 AY0333
GU061412.1 gg_id:591871 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m GU061
GU061420.1 gg_id:568523 and function microbial mesoscale eddy perturbations South China Sea clone CE1-5m GU061
EU237340.1 gg_id:241082 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
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EU804538.1 gg_id:335721 It's all ranking aquatic 250 miles Panama City clone 6C232484 EU804
AY907794.1 gg_id:136985 identification picoplankton contrasting waters Arabian Sea water clone A713807 AY907
GU119457.1 gg_id:587280 Threatened Corals Provide Microbial Habitats reef water clone Reef_A17 GU119
GU119401.1 gg_id:589405 Threatened Corals Provide Microbial Habitats reef water clone Reef_J24 GU119
GQ347951.1 gg_id:593286 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU805386.1 gg_id:324898 It's all ranking aquatic 250 miles Panama City clone 6C233394 EU805
EU801503.1 gg_id:332548 It's all ranking aquatic Chesapeake Bay MD clone 3C002811 EU801
EU268088.1 gg_id:254966 summer Dalian and Liaodong bay determined sea water clone L2513 EU268
EU802902.1 gg_id:342436 It's all ranking aquatic Northeast Colon Panama clone 4C230294 EU802
GU061499.1 gg_id:591657 and function microbial mesoscale eddy perturbations South China Sea clone CE1-DC GU061
EU237446.1 gg_id:240327 Genes transcripts Eastern and Western Equatorial North Atlantic Ocean microbial as EU237
EU804365.1 gg_id:350248 It's all ranking aquatic 250 miles Panama City clone 6C232275 EU804
GQ348362.1 gg_id:590344 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
AJ224541.1 gg_id:12752 trickling filter biofilm clone koll13 AJ2245
FJ205356.1 gg_id:570905 Prokaryotic deep-sea hydrothermal region East Lau Spreading Centre deep marine se FJ2053
EU491057.1 gg_id:261391 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X EU491
FN396746.1 gg_id:557965 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_8_II FN396
EU374108.1 gg_id:268245 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374

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551.0	4410.7	4813.6	5183.9	5389.1	4515.0	6091.9	4246.3	3821.7	3300.2	4501.0
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1903.0	4494.1	3762.0	3265.3	3849.4	3438.6	3327.2	2933.8	5368.6	5547.9	3458.1
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22952.0	8257.2	7698.5	8597.8	8623.6	8041.7	8822.4	7804.9	9330.9	9252.4	13453.6
24103.7	8303.1	6617.5	6773.9	7616.2	7477.1	7407.3	7039.7	8404.8	7296.8	9270.3
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14321.9	5943.3	5765.5	6765.0	5654.9	5514.6	5813.6	4840.7	6225.3	4640.4	7296.6
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7780.1	3490.6	4148.7	4562.4	3424.6	3834.7	3783.4	3678.1	4392.9	4836.1	5467.9
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6938.6	8069.0	8707.2
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EU491343.1 gg_id:276799 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X3 clone EU491
AF154093.1 gg_id:11881 hydrocarbon seep clone BPC063 AF154
EU491246.1 gg_id:266087 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
FJ712450.1 gg_id:530060 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
AB015267.1 gg_id:12003 deepest cold-seep area Japan Trench clone JTB31 AB015
GU118752.1 gg_id:536016 Threatened Corals Provide Microbial Habitats clone Mfra_A07 GU118
AM259898.1 gg_id:210533 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-01 AM259
EU491180.1 gg_id:266970 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
AY225655.1 gg_id:98009 Mid-Atlantic Ridge hydrothermal sediment clone AT-s2-33 AY225
EU328054.1 gg_id:277684 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
AM997746.1 gg_id:566820 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AY592138.1 gg_id:101549 marine ANAMMOX sediment clone AY592138 AY592
GQ263100.1 gg_id:551448 Structure Simulated Level Waste Site simulated level waste site clone F2_51X GQ263
GQ263243.1 gg_id:533342 Structure Simulated Level Waste Site simulated level waste site clone F3_62X GQ263
GU056091.1 gg_id:587273 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
GQ866098.1 gg_id:571157 Seasonal changes Norway lobster (Nephrops norvegicus) gut clone F1-26 GQ866
EU374095.1 gg_id:260834 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
GQ262901.1 gg_id:559440 Structure Simulated Level Waste Site simulated level waste site clone F1_58X GQ262
FJ229926.1 gg_id:509146 Microbes marine sponges Indonesia: Manado clone XA2G07F FJ2299
FJ229962.1 gg_id:564142 Microbes marine sponges USA: Key Largo Florida clone XE1E03 FJ2299
FJ229942.1 gg_id:549301 Microbes marine sponges USA: Key Largo Florida clone XB2G09F FJ2299
EF076145.1 gg_id:255203 Sponge- microorganisms: ecology and biotechnological potential Bahamas: Little San EF0761
EU491602.1 gg_id:262676 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
EU491785.1 gg_id:273839 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ229955.1 gg_id:510651 Microbes marine sponges USA: Key Largo Florida clone XB3H12F FJ2299
GQ406192.1 gg_id:575324 Benthic submerged sinkhole ecosystems sediment clone BK-45-9 GQ406
DQ811922.1 gg_id:169682 mangrove soil clone MSB-3D10 DQ811
EF632945.1 gg_id:250138 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
EU542491.1 gg_id:271885 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
EF540423.1 gg_id:222313 Impact phytoremediation on structure solid waste oil-shale chemical industry semi-c EF5404
GQ214120.1 gg_id:584943 China loess clone P936 GQ214
GQ246337.1 gg_id:583854 Temporal and spatial China North Yel Sea sediments clone Sd1-56 GQ246
DQ395394.1 gg_id:153946 deep-sea octacoral clone ctg_BRRAA49 DQ395
EU132592.1 gg_id:239247 tallgrass prarie soil clone FFCH10091 EU132
EU132610.1 gg_id:252086 tallgrass prarie soil clone FFCH10263 EU132
EU132640.1 gg_id:235667 tallgrass prarie soil clone FFCH10667 EU132
EU132562.1 gg_id:254092 tallgrass prarie soil clone FFCH5337 EU132
EU133242.1 gg_id:239952 tallgrass prarie soil clone FFCH9801 EU133
EU193087.1 gg_id:368831 -DGGE and Approach Analyze Effect Agricultural Practices on Soil agricultural soil clo EU193
GQ263211.1 gg_id:547544 Structure Simulated Level Waste Site simulated level waste site clone F3_18X GQ263
FJ478846.1 gg_id:579019 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788

2562.7	4802.2	5316.8	6142.9	6871.5	5760.3	7054.2	5881.0	3880.3	3234.2	5813.1
8444.0	2945.9	2000.9	3236.2	3072.7	2820.4	3308.5	2771.4	3366.7	2689.0	3918.8
3789.5	4160.2	3516.2	3996.9	4725.2	4181.6	6354.8	4705.9	3925.9	2058.7	2406.9
9182.5	5328.5	4391.0	4275.5	5098.7	4565.7	6368.6	4632.7	6231.2	5351.3	4024.3
648.6	4613.9	5496.5	5101.2	4353.5	4732.8	5128.8	5116.2	3383.2	3445.1	4977.4
275.2	3271.7	3346.4	3257.4	3989.2	3541.7	4427.1	2823.1	4644.2	3072.7	3524.3
90.9	52.7	50.0	46.0	55.6	52.3	72.7	52.7	52.2	34.7	53.9
9074.9	5403.1	5334.4	4645.7	4794.4	4528.8	5421.6	3972.1	4392.7	4745.1	5424.1
356.9	5045.4	4087.2	3273.5	4515.3	4106.3	3938.9	3299.7	4600.8	4140.6	2535.7
537.9	4279.3	4536.3	5056.6	5231.3	4151.5	5987.8	4751.3	2588.0	1644.7	3562.9
573.7	2972.9	2550.5	2927.2	3202.0	2771.5	3448.8	3385.8	3272.2	1208.3	2763.2
2417.6	2042.2	1985.0	2715.2	2148.5	1729.6	2061.5	2526.2	2686.4	815.6	1923.4
279.4	3688.4	3392.0	2633.5	3532.2	3335.8	3104.0	3286.1	3284.3	2279.4	2204.4
403.7	3472.3	4281.7	4200.9	1981.3	3407.8	2709.6	3465.9	1326.6	665.1	3972.8
17439.1	6451.0	6276.8	7009.9	9018.1	7583.6	7946.6	6530.0	10513.5	6820.2	9155.7
2217.4	3497.2	3570.9	4003.5	4580.3	3827.2	4568.6	4258.0	4378.5	3309.9	3897.5
16327.1	6045.3	6173.9	6408.2	5934.1	5221.5	4819.2	5321.4	7585.7	4958.1	7944.5
199.3	4945.3	3575.4	2368.3	2402.8	3802.2	2105.1	2651.6	5597.6	2768.8	2094.4
1942.7	9029.4	7677.1	7873.5	7510.4	7691.0	9217.4	8825.3	9917.1	8073.0	9248.9
815.6	11671.0	9115.1	9991.3	9163.4	9620.9	10384.0	9045.0	9210.6	6461.5	9616.3
739.7	7110.6	5821.6	5912.1	7162.0	6176.1	6787.8	5992.2	6180.8	6166.6	4946.0
4271.4	10811.9	11132.2	10445.5	9143.2	9789.7	10366.0	9721.1	11368.2	10130.1	13029.9
2360.1	10545.7	9044.1	9206.0	9909.0	9192.5	10287.7	8860.9	9942.5	6626.8	8935.0
4373.1	8012.1	6642.6	6258.2	8385.4	6487.9	8712.7	6942.5	9684.7	6169.8	5126.8
3923.9	6172.1	5751.7	5806.1	6036.5	5250.3	6233.8	4850.8	7562.2	5458.8	5607.1
40.9	402.8	463.9	385.3	207.2	474.5	492.6	511.1	67.9	36.6	383.2
125.4	528.4	887.8	1093.8	1198.5	507.2	3181.0	253.7	107.2	189.4	400.6
639.8	5342.9	5356.2	5786.2	7732.5	6608.4	7480.0	6131.2	4325.9	3808.3	5088.8
1252.2	7768.7	6966.6	7469.5	7543.1	7144.6	8387.6	7476.3	8638.8	7498.1	8740.8
146.9	1628.4	1334.1	881.3	1228.8	1167.3	1647.2	778.1	1416.3	961.6	443.1
6661.9	11706.1	8447.2	8430.4	8915.5	6924.8	9115.8	7592.9	7757.7	6854.2	4501.4
113.2	2065.0	2126.7	2376.0	2588.7	1896.0	2947.4	2041.2	1731.3	1315.3	3197.7
56.2	57.8	61.7	52.2	67.3	46.7	60.4	53.9	48.0	47.7	58.3
1120.7	7832.2	6252.0	6218.1	8631.8	6002.6	8697.5	5503.2	6339.7	4552.3	5198.4
319.0	2215.0	2043.5	2508.1	3822.0	1963.9	3314.6	2085.6	1711.6	260.6	961.4
13049.5	7368.6	7250.1	7518.5	8087.8	6751.7	7964.0	6336.3	6204.6	6035.6	6590.7
3990.9	5102.9	4651.9	5418.8	7156.9	4953.8	6672.2	4888.7	4324.4	3431.6	3749.9
261.8	3236.7	3555.9	3411.6	5273.9	3278.0	5137.5	4320.0	1893.8	1299.8	3665.5
9101.3	5404.8	4985.9	4469.1	5378.9	5554.6	6573.0	4144.2	3799.5	3465.6	3101.9
60.7	404.9	289.0	254.9	305.5	170.8	909.1	246.3	116.9	46.5	132.5
3355.5	3725.2	3832.6	3927.1	4609.8	3766.1	5454.8	3361.8	3772.3	1871.0	3323.6

6123.5	6180.2	6371.3
2683.0	4219.4	2833.5
4077.0	4384.7	3544.3
4559.5	6157.6	4603.9
3468.3	5218.8	5096.3
2695.2	3113.5	4182.7
49.1	68.9	62.7
3833.3	4858.1	4276.4
3232.2	3387.3	5807.4
3878.9	4510.3	5756.5
2847.1	3397.5	3095.2
757.1	3140.4	1681.2
3170.6	2702.8	3258.3
2573.4	3578.0	2948.6
5642.0	8619.9	7545.6
3559.5	5210.9	3972.3
4697.4	6341.4	5817.5
2106.2	2536.9	2437.9
7971.4	8224.9	8399.9
8629.4	8707.2	10275.9
6084.3	5371.3	6590.9
8997.1	9804.8	9415.5
7972.1	10168.2	9378.5
6353.3	7317.1	6526.1
5581.5	6648.5	5305.2
155.9	80.1	401.8
382.2	339.3	544.2
6309.1	5729.0	6601.5
6697.7	8095.3	7850.7
832.8	571.8	712.5
7243.4	7119.4	7896.9
2261.9	1816.2	2367.1
45.6	51.6	38.9
5259.8	5507.8	7948.4
1998.9	1662.9	3844.6
6452.6	6363.7	7917.2
4910.4	5287.0	6978.4
2980.3	3507.4	6005.9
3641.7	5046.8	6094.7
194.6	211.1	653.6
2893.5	4831.8	5080.6

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EF516284.1 gg_id:219818 grassland soil clone FCPS415 EF5162
EF019300.1 gg_id:207037 aspen rhizosphere clone Elev_16S_491 EF0193
FJ478947.1 gg_id:580973 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
EF516264.1 gg_id:217980 grassland soil clone FCPU621 EF5162
EU132678.1 gg_id:250652 tallgrass prarie soil clone FFCH11021 EU132
GQ396935.1 gg_id:541701 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GQ396927.1 gg_id:593718 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
EU132553.1 gg_id:253490 tallgrass prarie soil clone FFCH16258 EU132
DQ129581.1 gg_id:137600 urban aerosol clone AKIW543 DQ129
EU132699.1 gg_id:254009 tallgrass prarie soil clone FFCH11256 EU132
EU881117.1 gg_id:303466 Karst region primary forest soil clone KPF200711-035 EU881
EF492926.1 gg_id:236252 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
FJ415661.1 gg_id:356779 black loam soil soybean field pH 8.0-9.1 elevation approximately 142.7 m clone SOY4 FJ4156
GQ263223.1 gg_id:589383 Structure Simulated Level Waste Site simulated level waste site clone F3_30X GQ263
DQ347883.1 gg_id:200046 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding termi DQ347
FJ479080.1 gg_id:584453 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
EU490277.1 gg_id:562566 Microbial biodiversity thermophilic mineral soils Tramway Ridge Mount Erebus Anta EU490
EU132758.1 gg_id:239095 tallgrass prarie soil clone FFCH12203 EU132
EF516257.1 gg_id:227361 grassland soil clone FCPN401 EF5162
AJ536866.1 gg_id:78720 uranium mining waste pile soil sample clone JG30-KF-A23 AJ5368
EU861970.1 gg_id:305385 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
EU133228.1 gg_id:253774 tallgrass prarie soil clone FFCH9064 EU133
FJ479208.1 gg_id:590667 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EU132506.1 gg_id:247552 tallgrass prarie soil clone FFCH9080 EU132
FJ478504.1 gg_id:584366 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EF612368.1 gg_id:244063 historic semiarid lead-zinc mine tailings site soil clone OS-C108 EF6123
DQ906785.1 gg_id:242006 Oman subsurface soil clone 2B-7 DQ906
EU132960.1 gg_id:250840 tallgrass prarie soil clone FFCH17064 EU132
EU132861.1 gg_id:240169 tallgrass prarie soil clone FFCH14388 EU132
EU132554.1 gg_id:251112 tallgrass prarie soil clone FFCH16505 EU132
FJ479287.1 gg_id:572125 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
FJ152732.1 gg_id:318193 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AJ863234.1 gg_id:121120 poplar tree microcosm bulk soil flooded clone 21BSF48 AJ8632
FJ478941.1 gg_id:539978 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
EU132930.1 gg_id:240349 tallgrass prarie soil clone FFCH16272 EU132
EU644096.1 gg_id:282759 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
EU132703.1 gg_id:248033 tallgrass prarie soil clone FFCH11295 EU132
DQ125846.1 gg_id:134038 uranium contaminated soil clone AKAU4075 DQ125
EU881145.1 gg_id:322589 Karst region primary forest soil clone KPF200711-126 EU881
FJ478898.1 gg_id:563350 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
AY326618.1 gg_id:136785 Amazon soil clone 15-1 AY3266

5264.7	7336.8	6619.7	7094.3	7450.7	7218.6	8106.0	9634.5	9189.9	6758.4	7133.6
795.7	3770.9	3442.5	3952.2	6726.6	3092.3	5330.8	3402.7	1772.0	1696.5	2738.6
1685.5	5605.2	6210.0	6100.0	6237.5	5613.9	6836.2	5784.9	3890.9	2729.1	5574.7
2842.2	5348.8	5775.3	6519.5	6517.9	5292.2	6917.2	5322.7	4304.2	3339.1	6114.9
1941.9	10784.4	8311.6	7670.9	8162.1	6935.6	7943.1	7767.2	9509.4	7545.7	6415.5
8737.5	9278.7	8273.2	8543.4	9393.7	8224.1	9761.9	8074.3	7746.1	8181.0	6892.4
7449.8	4696.3	4656.6	5892.0	6838.6	4246.6	7016.8	5056.2	4408.9	1440.7	3844.3
73.3	2705.2	3131.6	2851.5	3551.3	2838.8	3916.4	3387.3	1834.8	1256.6	2070.2
151.8	1269.4	1571.3	1788.0	2050.4	1456.8	2564.1	1480.1	594.9	482.3	915.5
6025.3	10404.6	8957.1	9303.5	11496.6	8959.1	11739.1	8162.7	8699.5	6255.5	9391.6
158.4	3015.4	3698.5	3469.9	5364.7	3135.4	6004.1	3276.9	1785.8	3527.8	2523.9
3417.3	3628.7	3815.5	4452.4	4966.0	3312.0	5346.6	3695.0	2338.9	1307.8	2787.0
4186.5	7922.7	7738.5	7756.6	8178.0	7453.0	7674.5	7250.9	7275.9	4715.0	7920.5
2570.5	6117.4	5542.4	6340.9	8711.9	5098.2	9487.0	4653.6	3225.0	2424.4	4453.1
876.2	3247.9	2817.2	2924.8	3853.9	2897.6	4245.9	2628.1	4189.1	2098.5	1997.1
1548.1	4775.5	4149.3	4932.3	6995.8	4111.8	7195.4	4237.5	3415.0	1933.0	3588.7
2277.9	4450.5	4516.1	4730.3	6438.4	4441.0	7306.5	4938.1	1954.0	1437.1	4304.9
6855.9	5733.1	5913.7	5908.6	7387.2	6450.2	7053.4	5236.7	5809.3	4736.9	3724.0
1751.0	1760.4	1820.3	2022.1	2639.4	1771.0	2279.2	2432.1	1353.3	1855.2	1262.3
49.9	442.6	336.1	535.6	652.0	790.2	663.6	551.1	118.4	59.8	276.0
1566.1	3487.8	4516.6	4271.2	5920.2	3476.3	5604.1	4668.1	3894.5	2056.0	3180.2
1600.7	5031.9	4371.0	3162.4	6572.1	4327.3	4714.2	3407.7	4600.5	3707.2	2428.4
1181.7	2380.4	2601.1	1808.5	2772.1	1977.5	2860.3	1547.3	2585.8	2113.4	1163.0
6512.9	7804.3	7160.4	6653.3	7095.8	6731.3	7286.2	6761.5	8939.4	8657.4	8122.5
677.7	4869.9	4666.7	5211.0	6392.1	4301.4	6098.1	4533.4	3819.9	4499.1	4147.2
8261.9	4632.1	4443.2	5105.5	5589.9	4110.1	5407.1	4240.7	3868.1	4032.4	4013.1
2739.6	4625.4	4822.7	5067.7	6502.4	4491.2	6591.6	4735.2	3331.0	1387.6	3362.3
5535.6	6103.8	5144.3	5071.9	7678.7	5569.5	6701.1	4901.1	6914.0	5153.9	4193.3
6319.3	4605.3	4638.6	5408.2	7173.1	4690.9	6822.5	4979.6	4379.9	2262.5	3942.8
766.0	2849.5	2568.5	2759.8	3721.1	2793.6	4511.1	2359.1	1351.9	1073.5	1843.9
141.2	4760.3	5478.0	4985.5	6296.9	4166.7	6932.7	3952.1	2173.5	2770.9	3839.2
82.7	1766.3	1008.4	1124.7	1853.6	1255.3	2163.2	650.6	287.8	128.8	496.1
258.1	1333.6	1271.5	1577.4	1880.3	1407.5	2202.1	1517.8	857.6	243.5	797.8
7243.1	9039.0	7982.0	8738.6	9435.2	7718.9	8925.5	7258.1	7529.5	4271.1	6008.6
4017.4	4800.2	4563.3	5597.4	6628.9	4589.6	6737.8	4772.8	4506.0	2757.1	4066.1
234.3	4263.3	5166.0	4753.0	5282.7	4758.2	6040.8	3825.2	2936.9	2421.5	3051.9
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79.0	3247.1	3148.1	2925.6	4310.9	3025.6	3859.9	2372.6	1007.3	2473.3	2084.1
464.8	3754.2	3665.5	4165.2	4171.6	3699.3	5027.9	3042.9	2186.7	1273.0	2655.1
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34.3	24.6	19.3	28.8	28.0	24.9	25.1	24.4	21.2	19.6	21.8

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2241.9	2676.8	3423.2
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4967.4	6780.8	7288.9
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4878.9	4548.0	6137.4
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5174.3	5579.2	6668.9
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GQ495408.1 gg_id:573529 terrestrial volcanic rocks Iceland Hnausahraun lava f clone Bas-7-50 GQ495
AJ582059.1 gg_id:93368 soil near uranium mill tailings clone KCM-C-117 AJ582
FJ478916.1 gg_id:544444 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
EU132608.1 gg_id:255406 tallgrass prarie soil clone FFCH10233 EU132
EU133156.1 gg_id:253677 tallgrass prarie soil clone FFCH692 EU133
EF019542.1 gg_id:216189 aspen rhizosphere clone Elev_16S_1047 EF0195
FJ479570.1 gg_id:513760 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EU132487.1 gg_id:240713 tallgrass prarie soil clone FFCH427 EU132
GQ262954.1 gg_id:582187 Structure Simulated Level Waste Site simulated level waste site clone F1_89X2 GQ262
GQ111304.1 gg_id:410155 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
GQ111265.1 gg_id:396271 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
EU132545.1 gg_id:238107 tallgrass prarie soil clone FFCH11560 EU132
FJ479015.1 gg_id:572569 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
FJ478770.1 gg_id:591906 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
EU491469.1 gg_id:258935 Abundance and microbial life ocean crust seafloor lavas Hawai'i South Point X4 clone EU491
GQ014787.1 gg_id:494879 Topographical and Temporal Human Skin Microbiome skin palm clone nbw764c01c1 GQ014
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DQ129290.1 gg_id:138194 microarray level air two cities Texas urban aerosol clone AKIW700 DQ129
FJ479592.1 gg_id:593325 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
GU208243.1 gg_id:584642 Study on Sediment Dongping Lake sediment clone 4S2-3 GU208
GQ263175.1 gg_id:578741 Structure Simulated Level Waste Site simulated level waste site clone F3_131X GQ263
GQ263082.1 gg_id:534856 Structure Simulated Level Waste Site simulated level waste site clone F2_31X GQ263
EU132905.1 gg_id:243586 tallgrass prarie soil clone FFCH1535 EU132
DQ906908.1 gg_id:240172 Oman subsurface soil clone 12B-8 DQ906
EU335260.1 gg_id:247772 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
AY395356.1 gg_id:102490 pasture soil clone EB1037 AY395
GQ263259.1 gg_id:583767 Structure Simulated Level Waste Site simulated level waste site clone F3_87X GQ263
AY395379.1 gg_id:104049 pasture soil clone EB1060 AY395
FJ478603.1 gg_id:591747 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
EU132557.1 gg_id:235807 tallgrass prarie soil clone FFCH17938 EU132
DQ450796.1 gg_id:160311 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
AJ243870.1 gg_id:11354 Rubrobacter radiotolerans str. RALC-4 AJ2438
AF479791.1 gg_id:32106 Rubrobacter taiwanensis str. LS-286 AF479
CP000386.1 gg_id:160994 Rubrobacter xylanophilus str. DSM 9941 CP000
FJ595575.1 gg_id:536634 rock Black Canyon New Mexico: and Geochemistry rocks no varnish clone NV64_10b FJ5955
DQ129336.1 gg_id:138573 microarray level air two cities Texas urban aerosol clone AKIW774 DQ129
DQ532248.1 gg_id:168709 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
AM746686.1 gg_id:247678 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A8 AM746

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3393.0	5743.8	6139.0	6834.9	8005.5	6060.7	8960.8	6575.3	5589.2	3121.1	4719.8
69.4	503.3	478.8	693.4	1277.8	403.7	1284.0	638.6	252.5	148.5	217.4
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38.6	65.6	45.3	90.6	263.1	57.2	224.0	57.7	28.1	41.9	25.8
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247.0	2656.1	2532.1	2859.0	3837.4	2813.8	4381.2	2495.0	1699.9	871.3	1684.3
85.5	2099.8	1751.0	1883.3	3242.7	1948.5	3326.3	1886.2	1379.0	378.8	1133.5
33302.2	11080.0	9571.7	11021.1	11925.4	9751.0	12306.3	9596.8	13116.2	12729.3	15899.7
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19128.4	10667.1	10178.5	10782.3	12034.8	10781.8	12528.3	9395.4	10562.9	10619.2	11211.9
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4474.4	5155.7	4503.5	4961.1	6044.7	4147.3	6329.5	4265.6	4753.9	4687.6	3669.6
6632.2	8775.0	8349.8	8924.5	9890.2	8660.0	9665.4	7886.6	9992.6	9226.1	7316.2
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1095.4	3816.3	2825.4	2814.4	3685.7	2860.6	3365.3	3353.3	3346.4	2964.3	2823.9
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DQ532226.1 gg_id:166076 Geographical Variation Microbial Burden and Spacecraft Assembly Johnson Space C DQ532
AM746685.1 gg_id:250631 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A7 AM746
EU132476.1 gg_id:251161 tallgrass prarie soil clone FFCH12333 EU132
FJ790551.1 gg_id:510654 Chasmolithic microbial niches -altitude arid tuff Tibet desert clone VB3 FJ7905
FJ479008.1 gg_id:511185 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
DQ366004.1 gg_id:155707 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone DQ366
AM746679.1 gg_id:241104 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A1 AM746
FJ479277.1 gg_id:509763 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
EU132752.1 gg_id:242600 tallgrass prarie soil clone FFCH12170 EU132
FJ167502.1 gg_id:308664 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1675
AM176851.1 gg_id:160960 Recovery mangrove sediment clone SZB15 AM176
EF688239.1 gg_id:337942 Detection microbial sludge anaerobic wastewater treatment system clone 6A7_cons EF6882
EU407208.1 gg_id:275285 household biogas digester clone GW-24 EU407
FJ748796.1 gg_id:543722 Vertical and sulfate-reducing prokaryotes estuarine Southern China Pearl River Estua FJ7487
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NR_028979.1 gg_id:582337 Conexibacter woesei str. ID131577; DSM 14684; JCM 11494 NR_02
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AF423245.1 gg_id:19731 soil clone 288-2 AF423
AF443586.1 gg_id:89763 semiarid soil clone C-F-15 AF443
FJ592862.1 gg_id:576320 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AF443578.1 gg_id:90198 semiarid soil clone C-F-12 AF443
EU133035.1 gg_id:253089 tallgrass prarie soil clone FFCH2053 EU133
GQ264250.1 gg_id:509881 Structure Simulated Level Waste Site simulated level waste site clone WW1_b52 GQ264
EF516186.1 gg_id:222920 grassland soil clone FCPP755 EF5161
DQ129240.1 gg_id:138529 microarray level air two cities Texas urban aerosol clone AKIW806 DQ129
X92707.1 gg_id:11358 peat bog clone TM220 X92707
AF443581.1 gg_id:88335 semiarid soil clone C-F-1 AF443
EU132547.1 gg_id:255859 tallgrass prarie soil clone FFCH11914 EU132
GQ263435.1 gg_id:578041 Structure Simulated Level Waste Site simulated level waste site clone FW2_121B GQ263
DQ413118.1 gg_id:151564 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
FJ479267.1 gg_id:580173 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
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GQ015147.1 gg_id:494519 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765a05c1 GQ015
AM935542.1 gg_id:538368 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU132753.1 gg_id:235293 tallgrass prarie soil clone FFCH12178 EU132
EU335168.1 gg_id:236596 Changes microbial metabolic and along hydrogeochemically variable profile saturate EU335
EF516896.1 gg_id:217448 grassland soil clone FCPU744 EF5168
EU132567.1 gg_id:236583 tallgrass prarie soil clone FFCH8929 EU132
X92694.1 gg_id:11359 peat bog clone TM36 X92694

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926.5	3394.3	2959.2	3060.8	3211.1	3084.2	3627.1	3412.7	3352.5	2514.9	3069.4
2792.0	4863.7	4903.2	4665.4	4623.2	5033.6	5092.9	5013.1	5864.7	5000.2	4910.1
284.9	2844.7	3449.1	3161.4	4485.0	3083.6	3297.9	3252.6	1823.0	1541.3	2731.2
2286.2	4895.6	6222.7	4742.6	4486.6	4536.1	5141.2	4391.0	3286.1	1819.7	5581.6
29844.5	7100.3	6847.2	7442.3	7225.0	7926.1	7564.1	6263.5	11083.7	8630.1	9963.5
1500.1	6099.4	5926.1	5940.5	7535.9	4748.9	6689.9	6543.4	4462.1	3511.8	5085.3
41.6	39.0	65.1	49.1	128.8	40.2	111.7	33.4	26.8	20.7	20.1
1671.8	5354.7	4913.4	4512.1	4562.7	5378.9	4916.3	4991.7	4558.0	2576.5	5583.7
2342.8	3337.0	2858.2	2378.5	3031.9	2410.2	2575.8	4100.1	3431.4	2161.6	5348.6
852.2	3253.7	3632.4	4031.5	3469.4	3814.4	4106.1	4550.1	2828.6	1315.7	3033.0
1978.6	2081.5	2817.7	4291.7	2161.0	3061.1	3727.7	2993.5	1766.2	3152.1	2783.8
66.9	317.4	581.6	663.7	779.1	562.6	1068.8	356.7	130.6	50.6	196.9
1572.7	5840.9	5751.5	6485.6	7386.1	5765.5	8201.9	5669.5	5818.0	5446.0	4926.3
1735.6	4872.9	5840.6	6046.9	6223.9	5333.3	7735.5	5764.0	3152.9	3222.8	5461.3
3086.2	4048.6	3480.4	3796.1	4453.2	3604.5	4053.6	3746.6	5232.7	2495.0	2831.8
674.7	3697.3	3314.6	3295.4	4203.1	3382.3	5083.8	3452.9	3307.8	2616.8	2825.0
48.3	26.3	24.1	25.1	32.1	23.1	32.0	18.3	23.3	22.3	20.5
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218.3	2503.1	1728.5	1990.7	3163.8	2727.6	3501.1	1936.6	465.8	456.9	891.2
189.4	4732.9	4440.5	4316.9	3705.7	3951.8	3292.6	4064.5	3527.3	850.4	4240.2
615.6	5675.5	5909.4	6787.3	6548.4	5991.8	7454.9	5691.1	4793.0	3597.3	4866.4
951.2	6071.8	5581.1	5302.6	5890.2	5255.2	5382.3	5011.3	5280.6	2736.2	6430.9
9242.8	9998.8	8770.9	9360.0	10356.1	9108.1	11339.7	9066.6	8580.3	7236.6	10483.9
1164.8	6698.6	4874.8	5468.5	6421.9	5942.1	6305.6	4730.4	4649.0	3385.0	4133.0
1986.0	5513.8	5946.3	6462.5	6264.5	5556.9	6833.3	5332.2	5724.4	3499.0	5222.2
252.5	5545.6	5501.1	5195.2	5398.9	5230.1	6545.8	4699.1	3733.4	4527.5	3804.4
555.9	3654.4	5069.5	3808.7	4458.0	4284.9	5197.7	5154.1	3885.7	3875.0	2921.3
56.8	1105.4	455.1	544.4	1130.3	834.2	998.6	442.4	82.7	89.4	164.8
1117.1	8489.9	8523.9	8034.1	9309.3	7683.6	10892.6	7586.8	5861.4	4120.4	8810.3
283.1	3831.4	3442.2	3030.5	3569.3	3809.0	3775.0	2996.2	2474.1	1540.7	1748.5
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1507.5	7917.7	7330.7	7261.6	8967.1	7580.2	8900.1	6484.6	7211.2	4031.2	8062.0
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2494.1	2659.5	3407.8
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EU223949.1 gg_id:248718 -RFLP microbes Qinghai-Tin rail soil clone 79 EU223
FJ478910.1 gg_id:593430 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4789
FJ466414.1 gg_id:561981 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4664
EF516543.1 gg_id:223672 grassland soil clone FCPO657 EF5165
EU132885.1 gg_id:256705 tallgrass prarie soil clone FFCH14925 EU1328
EF516330.1 gg_id:217548 grassland soil clone FCPU559 EF5163
EU861899.1 gg_id:349634 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8618
EU289502.1 gg_id:236024 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched EU2895
EU289494.1 gg_id:244375 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched EU2894
EF019484.1 gg_id:212237 aspen rhizosphere clone Elev_16S_750 EF0194
EF516364.1 gg_id:217392 grassland soil clone FCPN720 EF5163
FJ380134.1 gg_id:361249 ornithogenic Ross Sea region Antarctica AB1 soil clone 1/2/2A FJ3801
FJ542906.1 gg_id:521099 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone A FJ5429
AJ871306.1 gg_id:110999 Conexibacter woesei CP177-2 AJ8713
EU132539.1 gg_id:239281 tallgrass prarie soil clone FFCH14556 EU1325
AJ863193.1 gg_id:125555 poplar tree microcosm bulk soil unflooded clone 20BSU41 AJ8631
AM746696.1 gg_id:248034 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A18 AM746
EU132576.1 gg_id:249699 tallgrass prarie soil clone FFCH10890 EU1325
EU093079.1 gg_id:251712 Phytoplasma sp. RYL-GD EU0930
EU223946.1 gg_id:250637 -RFLP microbes Qinghai-Tin rail soil clone 69 EU223
AM936412.1 gg_id:561181 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EU104342.1 gg_id:314357 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1043
EU132917.1 gg_id:239059 tallgrass prarie soil clone FFCH15597 EU1329
FJ592848.1 gg_id:556756 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
GQ094365.1 gg_id:452924 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ094
FJ592851.1 gg_id:533434 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
EF516426.1 gg_id:223287 grassland soil clone FCPO543 EF5164
EF516706.1 gg_id:219427 grassland soil clone FCPP507 EF5167
AB374386.1 gg_id:267851 sequences Weissenstein (white rock) / few millimeters be surface rock called 'Weiss AB3743
EF019414.1 gg_id:216330 aspen rhizosphere clone Elev_16S_658 EF0194
EU024345.1 gg_id:247938 intestinal microflora Hepialus gonggaensis larvae RFLP larval gut clone Hg22 EU0243
AB245334.1 gg_id:148846 Solirubrobacter sp. str. Gsoil 355 AB2453
GQ009353.1 gg_id:500312 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ009
GQ093851.1 gg_id:445667 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
FJ479288.1 gg_id:570893 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4792
DQ129587.1 gg_id:190707 microarray level air two cities Texas urban aerosol clone AKIW658 DQ129
EU289433.1 gg_id:254049 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched EU2894
DQ347845.1 gg_id:203420 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding term DQ347
EU289446.1 gg_id:239050 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched EU2894
DQ347867.1 gg_id:203418 Specificity Soil-Feeding Termite Mounds and Putative Origin these soil-feeding term DQ347
AY234610.1 gg_id:112045 soil isolate Ellin5259 AY2346

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607.0	5925.3	5507.0	4956.9	5636.7	5727.1	7425.6	4818.7	5161.9	3629.5	4020.2
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68.2	3957.9	3622.0	3315.8	3040.9	3311.0	3699.7	3662.1	1203.5	781.6	2630.6
256.2	2163.5	2824.7	2857.9	2927.0	2098.4	3119.0	2731.3	1923.2	1475.9	1381.3
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137.2	284.7	854.1	446.6	389.0	480.4	497.1	676.1	168.6	790.0	322.6
6492.6	4480.9	4288.8	3809.8	5765.3	4220.5	5202.2	3481.3	4902.6	3745.3	3262.1
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92.2	404.9	450.3	506.5	731.1	445.7	645.5	440.5	146.1	182.7	302.6
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7748.7	4274.4	3723.9	4275.5	3851.5	4595.3	4533.3	4311.0	5161.6	3861.3	6047.3
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9911.0	5846.4	5278.9	4968.0	5243.0	5598.4	5460.1	5272.0	7276.0	4816.5	6249.2
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4860.9	5152.9	7114.9
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2448.4	2864.1	3651.2
6251.9	6952.1	6901.5
518.0	898.8	871.7
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3981.2	4853.8	3987.1
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114.7	108.4	163.4
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5173.2	5963.2	6313.6
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4402.4	5172.3	6335.6
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FJ479580.1 gg_id:588032 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4795
EU132527.1 gg_id:240137 tallgrass prarie soil clone FFCH9481 EU1325
EU132708.1 gg_id:235417 tallgrass prarie soil clone FFCH11367 EU1327
GQ396905.1 gg_id:589372 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
EU289476.1 gg_id:252979 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
GQ016522.1 gg_id:493145 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
GQ009325.1 gg_id:500340 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ009
FJ478614.1 gg_id:566193 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
AB245336.1 gg_id:149649 Solirubrobacter sp. str. Gsoil 921 AB2453
GU359107.1 gg_id:529086 rhizosphere soil peanut clone 2G54 GU359
FJ891034.1 gg_id:568938 Hypolithic structure hyperaird core Atacama Desert quartz clone AY6_4 FJ8910
EU289455.1 gg_id:252840 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
GQ340075.1 gg_id:568363 Prokaryotic Marathonas Reservoir Greece water column clone A07-25-BAC GQ340
GU305737.1 gg_id:541327 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
FM200857.1 gg_id:533016 and distinct induced biofilm fouling operated under conditions laboratory-scale men FM200
AJ863189.1 gg_id:123528 poplar tree microcosm bulk soil unflooded clone 20BSU39 AJ8631
GQ010603.1 gg_id:499063 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
AM935655.1 gg_id:565972 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
EU132850.1 gg_id:253296 tallgrass prarie soil clone FFCH14115 EU1328
DQ067018.1 gg_id:131479 Lake Washington sediment clone pLW-74 DQ067
AM490647.1 gg_id:577551 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
DQ676371.1 gg_id:221340 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
AJ458463.1 gg_id:66766 Thermoleophilum album str. ATCC 35266 AJ4584
AJ458464.1 gg_id:66765 Thermoleiphilum minutum str. ATCC 35268 AJ4584
FJ905750.1 gg_id:535482 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F128b FJ9057
AM167960.1 gg_id:144186 flora waters upstreaming fluids deep igneous rock aquifers mineral spring clone BB8 AM167
GQ249482.1 gg_id:583433 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 0-2 cm layer clor GQ249
EU276544.1 gg_id:365355 -DGGE and Approaches Analyze Effect Agricultural Practices on Soil agricultural soil c EU2765
AF361216.1 gg_id:51617 hot spring clone SUBT-5 AF3612
AF027014.1 gg_id:11591 hot spring clone OPB41 AF0270
EF019109.1 gg_id:214806 aspen rhizosphere clone Amb_16S_1733 EF0191
EF520360.1 gg_id:235064 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-15 EF5203
EU290722.1 gg_id:246054 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2907
EU488303.1 gg_id:545186 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4883
DQ394972.1 gg_id:154687 harbor sediment clone VHS-B3-91 DQ394
AJ853543.1 gg_id:110776 landfill leachate clone GZKB49 AJ8535
DQ394962.1 gg_id:156539 harbor sediment clone VHS-B3-77 DQ394
EU644115.1 gg_id:286244 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU6441
AJ536836.1 gg_id:97060 chemocline clone 122 AJ5368
AB300103.1 gg_id:226025 Wide ancient microbial DNAs Quaternary sediments holocene mud sediment clone K AB3001

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1448.0	4532.6	5154.9	4680.4	5359.7	4398.5	6125.3	4796.3	3590.9	5877.8	4564.9
2553.5	4149.8	3883.6	3802.5	3975.6	3505.8	3813.1	3676.9	3464.6	2501.1	2532.6
174.0	3431.4	3110.1	3464.6	4684.6	3430.6	4632.1	3598.6	1560.8	2099.9	2364.4
419.7	4701.8	4612.6	4898.8	5376.0	4457.3	5656.4	4295.1	4189.8	1903.0	3034.1
10965.2	10152.3	9969.7	9583.6	8627.0	8432.7	9286.3	8229.6	9953.3	6841.0	10796.0
539.7	1805.9	1865.7	1933.1	2534.7	2038.4	3092.4	2050.4	499.1	704.9	1153.6
284.5	1723.8	1829.1	1796.2	2240.7	1674.4	2384.1	1321.1	1104.1	1024.4	974.3
2035.8	5435.9	6212.0	6368.7	6332.0	5918.1	7632.2	6282.0	4321.9	7354.2	5744.2
49.1	3009.4	3161.3	3132.9	3550.1	3478.8	4169.6	2928.4	1771.7	3311.1	1634.9
189.1	1488.3	1438.2	1501.4	1568.0	1281.6	1548.1	1348.4	1259.2	603.0	590.0
483.1	1604.9	1686.5	1501.6	2102.1	2310.8	1625.9	1973.7	1096.7	885.0	848.4
6511.1	5585.8	7503.9	9022.4	7201.5	5987.9	8090.5	7799.0	4370.5	3032.0	8988.3
9552.2	8441.9	7083.1	8453.1	8564.2	7676.4	8928.1	7232.5	7899.4	7092.6	7995.7
48.2	502.6	426.3	177.4	528.0	436.3	564.5	352.5	226.9	111.7	161.0
2315.6	1695.2	3987.4	4576.8	2017.6	1902.6	2129.9	5785.8	3501.5	1275.8	3341.7
56.6	568.2	663.2	788.4	1736.3	646.8	1511.1	878.1	148.4	130.3	313.3
126.8	4653.5	5358.8	4229.3	5510.0	4167.2	4657.5	3704.4	2569.8	1947.0	3148.2
289.0	6872.6	7146.8	7707.4	8505.6	7386.8	10632.7	7027.1	4594.6	8231.9	6021.6
1280.6	9182.7	8877.8	9485.2	10114.8	8605.9	12201.8	8900.2	7996.5	7059.8	7210.6
50.8	1152.7	1565.6	2603.1	2577.0	902.3	4935.5	1127.5	274.5	189.0	430.1
15269.2	5622.7	4197.3	5213.5	5540.2	4614.0	6287.4	4842.7	5810.6	4278.4	4631.2
215.3	1236.9	1419.9	1999.9	1622.3	1056.6	2539.3	1423.2	508.1	302.8	978.1
509.6	4962.0	4176.4	4251.3	5660.7	4230.6	5842.3	3528.4	5266.2	2373.5	2911.0
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1862.7	6407.1	5734.5	5795.8	6391.4	5763.3	6456.5	5551.7	7388.9	6213.6	4743.6
46.1	247.9	384.4	292.7	247.0	179.6	285.1	204.5	118.4	45.5	84.5
4343.9	9067.1	8512.8	6420.8	7108.3	7898.7	7292.6	6219.1	9857.6	7249.8	6256.5
51.1	162.2	229.2	262.4	359.4	235.2	265.6	225.5	64.6	41.7	107.4
34.8	71.6	138.0	135.8	115.3	188.2	112.9	208.7	48.1	33.6	59.1
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AY592368.1 gg_id:101745 deep-sea mud volcano clone Amsterdam-2B-08; BC20-2B-08 AY5923
CU922408.1 gg_id:566723 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
DQ465405.1 gg_id:223296 Bacillus decisifrondis str. E5HC-32 DQ465
EU373414.1 gg_id:276582 Bacillus pumilus str. TPR11 EU3734
EF492969.1 gg_id:238291 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EF018773.1 gg_id:216644 aspen rhizosphere clone Amb_16S_1235 EF0187
EF018972.1 gg_id:211351 aspen rhizosphere clone Amb_16S_1487 EF0189
AM749753.1 gg_id:255961 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
EU044415.1 gg_id:236245 uences structure fosters richness subtropical Altamaha Ohopee River Valley inland d EU044
DQ450732.1 gg_id:159666 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
DQ450735.1 gg_id:161224 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
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EF516192.1 gg_id:220984 grassland soil clone FCPT584 EF5161
EF018709.1 gg_id:210808 aspen rhizosphere clone Amb_16S_1160 EF0187
AJ536865.1 gg_id:79090 uranium mining waste pile soil sample clone JG30-KF-A11 AJ5368
EF515891.1 gg_id:220148 grassland soil clone FCPU527 EF5158
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AE000657.1 gg_id:153906 Aquifex aeolicus str. VF5 AE000
NR_029172.1 gg_id:564601 Aquifex pyrophilus str. Kol5a; DSM 6858 NR_02
AF393377.1 gg_id:30117 Aquifex-like str. CIR3017H090 AF3933
NR_024824.1 gg_id:538490 Hydrogenivirga caldilitoris str. IBSK3; JCM 12173 NR_02
GU233444.1 gg_id:516400 Thermothrix azorensis str. TM GU233
DQ834168.1 gg_id:166655 Geochemical Controls on Microbial and Joseph's Coat Springs Yellowstone National DQ834
EF156524.1 gg_id:193663 Microbial Norris Geyser Basin Yellowstone National Park Beowulf Yel Mat clone BY15 EF1565
DQ831993.1 gg_id:172491 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ831
DQ924743.1 gg_id:174834 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
EF156555.1 gg_id:195693 Microbial Norris Geyser Basin Yellowstone National Park Koz Spring clone KOZ114 EF1565
EF156470.1 gg_id:186739 Microbial Norris Geyser Basin Yellowstone National Park Beowulf Yel Mat clone BY10 EF1564
DQ924773.1 gg_id:179368 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
DQ834158.1 gg_id:164825 Geochemical Controls on Microbial and Joseph's Coat Springs Yellowstone National DQ834
DQ924744.1 gg_id:181623 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
DQ924720.1 gg_id:183451 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
EF156505.1 gg_id:175945 Microbial Norris Geyser Basin Yellowstone National Park Beowulf Yel Mat clone BY14 EF1565
DQ924812.1 gg_id:176562 Microbial Norris Geyser Basin Yellowstone National Park Whirligig Hot Spring clone DQ924
DQ924737.1 gg_id:177890 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
EF156516.1 gg_id:187128 Microbial Norris Geyser Basin Yellowstone National Park Beowulf Yel Mat clone BY15 EF1565
DQ831994.1 gg_id:170438 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ831
DQ834087.1 gg_id:171779 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ834
DQ924729.1 gg_id:179684 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
EU545990.1 gg_id:330531 Hydrogenobaculum acidophilum str. 2778 EU545
EF156548.1 gg_id:180187 Microbial Norris Geyser Basin Yellowstone National Park Koz Spring clone KOZ107 EF1565

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139.9	3875.1	8988.4	4127.7	3067.7	3863.5	3106.0	3989.7	2029.2	4065.8	4101.0
85.2	2100.6	1936.1	761.2	2135.4	2362.1	868.9	3152.9	675.6	3358.6	977.9
223.9	6280.6	5658.0	5882.0	7261.0	5688.6	8392.2	5291.8	3029.6	4777.0	5295.6
63.0	3443.6	3857.9	3169.7	5305.6	3566.1	6200.3	3179.0	1914.1	2147.0	2991.3
151.7	982.6	895.5	813.7	832.2	674.0	803.0	710.4	558.8	355.5	660.2
851.3	6201.5	5848.9	6260.2	4746.4	5710.4	6085.2	6307.0	4079.2	3888.7	5548.9
2856.5	9912.0	10427.8	10602.4	14388.3	10330.6	16453.3	9299.7	6400.5	6710.6	8854.2
2132.3	3475.3	4481.9	4607.3	4570.9	3560.2	6325.6	4439.9	4514.6	2169.2	3814.2
639.1	1436.3	1382.1	1661.1	1823.6	2029.1	2419.9	2314.1	546.4	868.8	935.8
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2084.7	2852.6	3534.1	3534.0	4235.0	3533.7	4157.5	3264.9	3277.4	3589.2	3991.2
178.1	152.0	257.6	399.8	240.3	331.8	625.4	284.2	106.5	20.8	142.6
501.4	1992.2	2926.3	2858.1	2437.3	2324.2	4098.5	2614.6	1740.2	1942.5	1908.3
1637.9	1681.2	1782.6	2238.4	2555.4	1290.3	3586.4	1898.6	562.3	620.0	788.8
339.2	1387.4	1819.8	1889.6	2247.7	1501.4	2468.4	1959.2	1381.4	1260.7	1657.2
461.7	315.0	454.0	396.1	357.4	319.8	423.3	336.3	407.1	172.0	339.0
154.6	449.8	795.5	484.9	468.5	540.4	389.0	739.7	331.5	434.0	448.2
91.0	161.4	197.9	174.6	171.7	127.5	212.3	142.1	127.9	77.5	111.2
86.5	95.5	221.6	209.2	260.6	226.9	214.2	250.9	115.1	65.5	128.3
33.5	50.6	58.7	67.1	83.6	61.6	83.1	53.1	54.5	22.2	39.3
868.2	1716.9	1782.3	2029.7	2520.8	1993.1	2491.0	3027.8	1372.4	1043.8	2837.5
29.3	18.3	16.5	19.5	16.2	15.4	19.1	18.2	16.2	13.4	20.4
9618.5	5571.2	4959.6	5467.2	4356.7	6467.8	5392.0	4831.9	6472.4	5104.7	6741.2
3776.8	1839.1	2248.7	2114.4	3628.4	2038.4	3450.6	2810.4	2698.6	3517.6	2668.5
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22868.9	8782.4	7975.5	8681.0	8442.1	8492.4	9146.2	7359.4	12828.9	9034.8	12477.9
5733.1	3550.3	3369.3	3193.4	3589.3	3327.5	1942.0	3606.9	2030.0	1689.6	4187.8
8313.6	4803.1	4462.8	5123.6	5118.4	4865.0	5474.8	5013.9	6361.9	4170.7	5735.0
36.3	1870.3	1887.6	1745.2	934.1	2088.6	1379.5	1480.1	670.5	401.0	1587.0
3058.9	3023.8	2615.7	3191.4	4089.7	3996.0	4097.7	3824.8	3682.8	3414.1	4587.3
136.6	596.5	471.6	684.8	508.0	676.6	791.6	813.8	301.3	182.2	526.7
340.4	768.4	836.8	1297.8	1315.1	1025.7	1664.1	1318.2	318.1	485.5	348.9
22818.5	5829.9	6530.2	6948.6	7183.4	6544.4	7397.5	8749.4	7346.1	7008.6	10080.6
5145.0	2941.8	3158.7	3094.0	2289.0	3495.4	2677.0	4409.2	3186.9	3045.3	3708.0
54.3	45.5	44.9	44.0	148.1	68.2	72.0	35.6	34.2	22.3	43.6
7799.2	2564.0	4846.1	3446.2	3180.4	3400.6	3045.1	4337.1	10100.1	3000.6	3670.4
2799.6	1490.7	1396.8	2007.5	1487.3	1676.2	1604.7	1736.1	1560.3	1017.1	1798.8
16746.3	7446.9	7544.1	8219.0	7670.9	7822.1	8132.4	8444.5	11701.2	8069.4	10326.3
3466.7	1704.3	1444.2	1687.2	1842.5	1423.2	1314.4	1321.1	1362.4	877.3	1619.4

644.7	1185.7	826.0
1838.4	3483.3	3486.7
4429.9	3762.6	6027.0
3419.2	2386.2	5333.9
5895.3	5331.0	9943.9
2770.0	3490.0	7821.0
481.7	1124.0	1049.3
4989.9	5843.5	7408.4
8893.1	8449.5	13862.6
2958.8	4477.5	5008.7
1787.1	3276.5	2469.8
1480.2	2117.8	2561.9
3184.0	4306.7	3884.3
186.1	378.3	393.1
2021.8	2777.5	4050.0
1578.4	960.8	1157.8
1739.4	2028.7	2342.4
301.8	530.0	340.3
499.2	639.3	870.8
118.0	196.9	143.0
137.8	270.3	411.2
42.6	125.6	152.3
2027.5	3455.0	3184.9
12.6	19.8	14.7
4266.6	5328.8	4124.2
2693.2	3113.4	2774.0
3840.1	5114.1	4001.5
8261.5	10008.7	7922.3
3155.3	3435.5	3948.7
4394.6	6895.2	5313.0
959.2	1358.4	1426.7
2594.7	4659.4	4965.1
261.0	560.5	640.1
1061.0	1169.7	1089.3
6902.3	8622.5	4906.3
3461.2	4549.9	2998.3
41.7	61.0	59.8
3628.1	3353.8	2760.4
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8301.3	8771.1	7589.0
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AY882803.2 gg_id:112203 hot spring clone SK254 AY8828
EF156603.1 gg_id:189504 Microbial Norris Geyser Basin Yellowstone National Park Koz Spring clone KOZ163 EF1566
DQ924760.1 gg_id:192474 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
DQ832031.1 gg_id:169346 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
EF156597.1 gg_id:197163 Microbial Norris Geyser Basin Yellowstone National Park Koz Spring clone KOZ157 EF1565
EU156144.1 gg_id:242317 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU156
DQ924730.1 gg_id:194755 Microbial Norris Geyser Basin Yellowstone National Park Echinus Hot Spring clone B DQ924
DQ834135.1 gg_id:170785 Geochemical Controls on Microbial and Joseph's Coat Springs Yellowstone National DQ834
AY882810.2 gg_id:111556 hot spring clone SK261 AY8828
DQ834121.1 gg_id:161939 Geochemical Controls on Microbial and Joseph's Coat Springs Yellowstone National DQ834
DQ832030.1 gg_id:166090 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ832
EF156465.1 gg_id:176781 Microbial Norris Geyser Basin Yellowstone National Park Beowulf Yel Mat clone BY10 EF1564
AF255599.1 gg_id:38815 Thermocrinis-like str. SRI-48 AF2555
DQ833788.1 gg_id:161844 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ833
DQ924688.1 gg_id:196562 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
AY862041.1 gg_id:112459 Washburn Spring 1 community clone WB1B011 AY8620
EU924258.1 gg_id:348543 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8 EU9242
EU635954.1 gg_id:277901 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU6359
DQ490016.1 gg_id:158831 Microbial Great Boiling Spring sediment hot spring; temperature 80 C clone GBS_L1_ DQ490
EU924254.1 gg_id:346758 Microbiology and geochemistry Little Hot Creek hot spring sediment temperature 8 EU9242
DQ924678.1 gg_id:198052 Microbial Norris Geyser Basin Yellowstone National Park Cistern Hot Spring clone BV DQ924
EF100635.1 gg_id:194035 Prokaryotic Heated Arsenic-Rich Sediments Shal Submarine Hydrothermal System An EF1006
AB462553.1 gg_id:326675 Microbial production and energy source hyperthermophilic prokaryotes geothermal AB4625
AF301908.1 gg_id:25858 Hydrogenobacter-like str. SS5H1 AF3019
AB199564.1 gg_id:110416 hot spring Japan clone NHS-03 AB1995
AB105049.1 gg_id:98942 Balnearium lithotrophicum str. 17S AB1050
AJ001049.1 gg_id:1260 Desulfurobacterium thermolithotrophum AJ0010
AJ507320.2 gg_id:85051 Desulfurobacterium crinifex str. NE1206 FK10 AJ5073
AJ316619.2 gg_id:104045 Thermovibrio ruber str. DSM 14644 AJ3166
AF068811.2 gg_id:13779 hydrothermal vent clone VC2.1Bac48 AF0688
AY268937.1 gg_id:104688 Desulfurobacterium sp. str. SL19 AY2689
AB278143.1 gg_id:191103 hydrothermal vent prokaryotes trapped 0.2- and 0.1-micro-m-filtrates obtained Mar AB2781
AY268936.1 gg_id:104531 Desulfurobacterium sp. str. SL17 AY2689
AJ969464.1 gg_id:157331 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
AY263403.1 gg_id:83837 Thermovibrio ammoniificans str. HB-1 AY2634
AY268938.1 gg_id:104841 Desulfurobacterium sp. str. SL20 AY2689
AY861839.1 gg_id:112695 Obsidian Pool prime community clone OPPB113 AY8618
AY861769.1 gg_id:112508 Obsidian Pool prime community clone OPPB026 AY8617
AY861802.1 gg_id:112563 Obsidian Pool prime community clone OPPB069 AY8618

419.4	1017.6	1219.2	1299.8	1306.9	1326.1	793.0	1231.7	773.8	319.1	1048.0
386.4	2452.8	3031.5	2095.6	2552.6	2648.1	1766.3	2372.7	2398.9	1116.5	2277.7
15481.7	2446.0	2344.1	2287.5	2627.2	2134.5	2942.5	1990.4	4327.1	2743.0	3415.2
11606.9	2969.9	2851.8	2926.3	2965.3	2512.7	3479.4	2947.8	3622.9	2661.5	3892.0
17576.7	4509.5	3694.3	4319.3	3364.6	4240.6	4229.1	4040.4	6586.1	3447.1	5493.9
309.9	1675.7	2035.7	2165.4	2411.8	2073.4	2799.8	2333.3	1275.7	798.5	1386.0
49.1	222.5	233.4	193.6	170.3	257.6	247.1	333.4	158.4	64.7	168.8
45.1	38.5	37.6	72.0	55.8	42.8	116.1	55.4	56.8	16.6	53.4
837.3	1993.9	2276.1	2515.7	1707.9	2222.2	2486.3	2368.8	1860.4	900.0	2322.7
255.8	724.8	833.8	971.4	1005.5	897.8	1319.3	824.2	241.8	186.1	731.5
4126.2	4326.3	3841.9	3927.8	3844.8	3827.0	4238.6	3585.3	5158.9	3439.3	5886.5
67.4	88.8	96.8	95.8	112.2	101.3	106.3	107.1	64.3	29.4	62.9
4038.3	1391.3	1189.5	1193.6	1263.4	1437.4	805.0	1988.7	750.5	212.2	651.9
53.4	58.6	59.2	56.3	56.7	48.0	70.6	56.8	40.0	28.0	46.4
137.9	232.4	218.6	188.3	341.3	153.2	159.8	176.3	73.4	103.5	197.5
13944.2	6998.2	5950.1	5411.6	5367.2	4982.5	6248.7	5088.8	7486.6	5948.4	7480.5
56.3	25.2	25.3	30.2	30.0	28.0	29.1	34.6	91.7	20.0	23.5
41.6	53.5	66.5	104.1	137.1	167.7	95.3	96.6	48.6	29.8	69.5
4683.3	2665.1	3134.8	3266.3	4072.0	3368.5	4337.3	3106.0	1662.2	1819.2	2245.4
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168.9	1547.2	36.7	430.4	781.1	1125.6	515.5	544.9	1319.0	880.2	340.7
5000.3	7528.8	6722.5	6697.9	6265.0	6157.1	6806.1	6098.9	9144.5	5620.2	6546.6
551.1	2071.5	2322.4	2110.7	2967.5	1957.7	2689.7	2997.9	621.9	1298.8	2850.8
63.3	611.5	701.3	804.4	1323.7	754.5	1215.3	945.2	384.7	171.7	504.5
67.5	212.2	163.2	128.4	131.3	122.4	150.4	116.0	129.2	68.3	89.2
68.1	694.3	565.0	414.9	290.7	574.5	409.1	359.2	263.4	188.8	193.8
484.5	1598.5	1754.8	1777.7	1790.4	1597.7	1935.5	1792.1	2663.0	2117.1	1885.8
3082.4	7300.4	5459.8	5483.3	6735.9	6836.2	6434.3	5497.3	7787.9	4672.7	4965.7
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AY861825.1 gg_id:112517 Obsidian Pool prime community clone OPPB097 AY8618
AY861755.1 gg_id:112659 Obsidian Pool prime community clone OPPB012 AY8617
AY861818.1 gg_id:112664 Obsidian Pool prime community clone OPPB088 AY8618
AY861819.1 gg_id:112470 Obsidian Pool prime community clone OPPB089 AY8618
NC_012438.1 gg_id:471184 Sulfurihydrogenibium azorense str. Az-Fu1 NC_01
AM259494.1 gg_id:171445 Sulfurihydrogenibium sp. str. GV2-1C1 AM259
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DQ906008.1 gg_id:164636 Calderas delineate biogeographical provinces among Yellowstone thermophiles Ang DQ906
AB071324.1 gg_id:34570 Sulfurihydrogenibium subterraneum str. HGMK-1 AB0713
AM778960.1 gg_id:249144 Sulfurihydrogenibium kristjanssoni str. I6628 AM778
FJ638563.1 gg_id:537415 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
DQ243783.1 gg_id:142593 Archaeal and Geochemically Hot Springs Yellowstone National Park USA Sylvan Sprir DQ243
DQ645250.1 gg_id:173214 Microbial and oxidation activity biofilms within Alvord Desert Basin Southeastern Or DQ645
AY882746.2 gg_id:111873 hot spring clone SK191 AY8827
AF385630.1 gg_id:63452 Persephonella guaymasensis str. H2 AF3856
AY686713.1 gg_id:138074 Sulfurihydrogenibium yellowstonense str. SS-5 AY6867
AY861820.1 gg_id:112610 Obsidian Pool prime community clone OPPB090 AY8618
DQ989208.1 gg_id:189417 Venenivibrio stagnispumantis str. CP.B2 DQ989
EU156153.1 gg_id:255003 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
AM888290.1 gg_id:250213 Persephonella sp. str. NV1 AM888
AY862061.1 gg_id:112469 Washburn Spring 3 community clone WB3B034 AY8620
DQ645258.1 gg_id:166258 Microbial and oxidation activity biofilms within Alvord Desert Basin Southeastern Or DQ645
AY862077.1 gg_id:112589 Washburn Spring 3 community clone WB3B088 AY8620
AY862064.1 gg_id:112598 Washburn Spring 3 community clone WB3B038 AY8620
AY862074.1 gg_id:112609 Washburn Spring 3 community clone WB3B070 AY8620
AY862070.1 gg_id:112521 Washburn Spring 3 community clone WB3B058 AY8620
AY862053.1 gg_id:112485 Washburn Spring 3 community clone WB3B018 AY8620
EU156150.1 gg_id:236881 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
DQ833894.1 gg_id:164976 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park . DQ833
AB302405.2 gg_id:217812 Persephonella sp. str. OY AB3024
EU134979.1 gg_id:239599 tallgrass prarie soil clone FFCH5249 EU1349
EU135015.1 gg_id:255679 tallgrass prarie soil clone FFCH3880 EU1350
EU134982.1 gg_id:243552 tallgrass prarie soil clone FFCH5572 EU1349
EU335337.1 gg_id:241653 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3353
EU335449.1 gg_id:235803 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3354
EU135016.1 gg_id:254133 tallgrass prarie soil clone FFCH10651 EU1350
EU135011.1 gg_id:246743 tallgrass prarie soil clone FFCH17123 EU1350
EU135014.1 gg_id:249907 tallgrass prarie soil clone FFCH2868 EU1350
FJ479425.1 gg_id:551234 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794

1189.7	1807.3	1449.4	1783.7	1816.1	1837.1	1953.0	1410.9	1078.9	723.8	1591.3
8875.0	4186.0	3558.1	4060.5	3938.2	3910.4	4434.5	3405.6	4097.3	3757.0	5668.6
5770.6	2276.8	1925.2	2254.6	1936.5	2127.6	2292.2	1795.8	2051.2	1587.5	2832.6
9553.2	3922.4	3561.0	4325.5	3892.1	4177.4	4408.1	3403.8	4676.9	3508.1	5672.5
11413.7	3357.8	3056.8	3157.6	3084.8	2765.4	3478.3	2869.1	3723.9	2992.9	4445.9
8876.7	4184.1	3562.9	4061.0	3904.9	3910.5	4409.6	3410.0	4096.0	3509.3	5670.2
1214.8	1739.5	1314.7	1996.0	1939.0	1881.0	2097.6	2376.0	781.1	414.3	1394.5
224.2	2560.6	2178.2	2405.6	3509.2	2427.1	3522.8	2183.1	2000.7	1539.5	1327.2
2474.3	3097.5	2532.6	3475.1	3224.5	3349.3	3136.9	2769.2	2432.1	1759.6	3824.3
2676.7	2570.8	2165.2	2940.4	2874.8	2776.7	2812.5	2409.5	2337.3	1659.9	3358.5
7352.7	7807.0	7549.6	9056.8	8681.0	7942.5	9306.0	9014.6	7796.8	6264.2	10700.1
1846.5	2417.1	2223.0	2484.4	2444.8	2501.2	3220.7	3256.8	2126.9	1204.1	3605.8
258.4	2411.9	2098.3	3273.7	3081.2	2525.3	3261.4	3360.0	1267.0	865.7	3414.1
1563.7	2422.0	1649.8	2237.9	2575.6	2004.0	2702.6	1787.5	2563.4	878.0	1563.9
2453.1	1801.7	1629.1	1841.8	1842.0	1684.1	1733.4	1647.7	1916.7	921.3	1698.9
226.6	774.7	821.6	867.6	949.1	960.2	979.1	945.2	676.8	439.2	799.5
123.3	1360.8	1416.0	1287.4	1589.6	1236.3	1839.9	1650.9	639.2	318.2	1088.0
8916.7	9136.7	7032.1	8586.8	8844.7	7996.8	8394.8	7854.9	7021.2	5550.6	10891.4
9511.4	3409.3	2891.6	3516.5	3286.1	3319.2	3560.5	2801.5	4443.5	3533.8	4655.6
66.4	77.2	91.8	85.9	92.9	81.9	112.8	64.9	44.9	36.7	72.2
1381.9	1388.8	1156.5	1593.1	1883.4	1488.8	1312.1	1595.1	458.6	226.7	1117.0
10149.8	3468.3	2131.9	2307.9	2528.3	2399.5	3089.9	2949.7	1964.2	1223.7	3661.2
1614.2	2457.6	1701.4	2288.1	2604.9	2074.0	2754.4	1830.9	2573.5	900.4	1681.5
6147.5	1988.6	1704.4	1870.3	1810.0	1636.3	1771.8	1597.7	3041.1	2017.8	2487.0
255.2	987.7	675.7	863.3	861.1	672.3	1060.8	1115.6	920.3	277.8	503.9
248.3	894.9	666.1	855.5	834.9	632.1	1049.7	1091.4	982.9	269.3	485.7
322.5	421.6	355.6	360.2	392.4	372.6	333.3	343.3	181.0	169.0	326.2
1349.0	1053.1	874.0	1024.5	1246.1	917.4	1073.0	1272.8	940.6	458.9	906.2
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12316.8	7244.7	5775.4	6446.3	5945.5	5601.2	6704.3	5573.2	8652.0	6480.5	8325.5
12159.1	7909.6	5531.9	5847.2	5496.9	5517.2	5485.2	5165.8	6187.4	3597.3	7965.6
37.0	40.7	38.7	26.8	27.7	24.4	23.7	23.5	23.2	29.6	20.5
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8905.9	7247.6	7532.6	8201.9	7644.0	7961.3	9736.0	6488.9	9077.5	8687.5	8183.5
38258.2	11659.8	10868.5	13517.1	11516.5	12349.2	13846.5	9840.5	15543.0	14559.2	17490.4
6956.0	5892.5	5634.1	6866.7	6608.2	6882.6	7768.3	5079.7	6026.7	7463.9	6446.0
13739.5	7263.8	6347.9	8061.9	7338.6	7433.7	8733.6	6033.9	8690.7	7100.8	9537.6
15071.6	6014.8	6587.5	6875.2	5801.0	6799.9	7702.0	5802.1	9011.7	9677.2	8629.7
3976.8	6312.1	6161.0	6750.6	7685.6	7095.2	8410.7	5944.9	6982.9	5555.1	6760.6
1752.0	4714.9	4334.8	4361.1	5100.0	4454.5	5003.4	4792.1	3668.3	2881.8	4301.8
681.9	5483.4	4668.4	6033.4	7138.1	5984.1	6726.2	5321.5	5522.2	2993.6	4960.3

1240.3	1521.3	1765.8
3349.6	3742.9	4055.0
1497.5	2027.9	2028.6
3140.2	3740.7	3793.3
2782.7	3222.1	3145.5
3139.3	3745.5	4054.6
2131.0	2262.4	2259.8
2469.2	2175.9	3495.2
2721.3	3036.3	3746.1
2488.8	2643.9	3224.8
8080.4	8418.3	8605.0
2234.9	3094.8	3083.8
1435.3	2791.5	3017.1
1730.0	1752.5	2974.0
1682.4	1672.6	2095.4
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1316.8	1455.5	1918.7
7430.3	8848.2	9799.8
2960.0	3144.0	3327.5
66.7	153.2	155.7
1557.2	1802.0	2048.0
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1749.0	1803.3	2998.3
1320.7	2733.8	1997.4
531.7	567.2	1060.5
508.8	562.8	1026.0
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820.9	947.9	930.9
6506.9	7469.4	7490.6
5318.2	6579.1	6510.7
4579.0	5280.3	5517.0
27.9	22.0	20.4
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6131.0	8602.1	8539.5
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5322.0	9044.5	6846.1
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AJ867895.1 gg_id:141847 Fluctuations Significantly Influence Microbial Present Nival Lakes lake water clone A2 AJ8678
AY212563.1 gg_id:112133 manure-contaminated water clone 111ds10 AY2125
EU676408.1 gg_id:296956 rhizosphere pioneer plants (Bahia xylopoda and Viguiera linearis) growing on metals· EU6764
EF683077.1 gg_id:247439 Eastern Mediterranean atmosphere clone F14_4H_FL EF6830
AY948040.1 gg_id:143151 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9480
EF516651.1 gg_id:224566 grassland soil clone FCPT595 EF5166
EU861928.1 gg_id:321601 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
GQ402731.1 gg_id:550111 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
AJ292686.1 gg_id:32254 PCB-polluted soil clone WD294 AJ2926
EU861934.1 gg_id:348576 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
EU861949.1 gg_id:319724 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619
EF516213.1 gg_id:217700 grassland soil clone FCPP590 EF5162
AB434255.1 gg_id:304101 Effect concentration on treatment non-woven biomass carrier sludge taken anamm AB4342
GQ263883.1 gg_id:544359 Structure Simulated Level Waste Site simulated level waste site clone WC2_131 GQ263
EU332819.1 gg_id:369522 FACS assist identification TFO present aerobic enhanced biological phosphorus remo EU3328
EF516982.1 gg_id:225301 grassland soil clone FCPS481 EF5169
GQ264378.1 gg_id:584471 Structure Simulated Level Waste Site simulated level waste site clone WW2_58 GQ264
EF515998.1 gg_id:221811 grassland soil clone FCPT516 EF5159
DQ975217.1 gg_id:249601 Iron sulfide and pyrite potential electron donors microbial nitrate reduction fresh w DQ975
AM749746.1 gg_id:247969 Isolation ing candidate division soils New Zealand steam-affected geothermal soil cl AM749
AJ009456.1 gg_id:1435 chlorobenzene-degrading consortium clone SJA-22 AJ0094
EU134994.1 gg_id:238881 tallgrass prarie soil clone FFCH4697 EU1349
FM866305.1 gg_id:362406 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-22 FM866
GU198500.1 gg_id:569984 Acid-tolerant microaerophilic enhance Fe(III) accumulation Fe(II) oxidizing enrichme GU198
AJ306784.1 gg_id:66917 DCP-dechlorinating consortium clone SHA-37 AJ3067
DQ330652.1 gg_id:159278 Guerrero Negro hypersaline microbial mat clone 04D2Z29 DQ330
DQ833816.1 gg_id:171283 Geochemical Controls on Microbial Rainbow and Springs Yellowstone National Park DQ833
FM164957.3 gg_id:450088 two Bulgarian geothermal springs hot spring clone S1-133 FM164
DQ645248.1 gg_id:169378 Microbial and oxidation activity biofilms within Alvord Desert Basin Southeastern Or DQ645
DQ324867.1 gg_id:146321 Geochemical and bioenergetic variability across systems Yellowstone National Park DQ324
GQ022437.1 gg_id:487233 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu31 GQ022
GQ264442.1 gg_id:568015 Structure Simulated Level Waste Site simulated level waste site clone WW3_141 GQ264
AY289459.1 gg_id:88820 soil clone ABS-629 AY2894
CU923234.1 gg_id:537151 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
AJ009490.1 gg_id:1430 chlorobenzene-degrading consortium clone SJA-121 AJ0094
FJ793161.1 gg_id:519788 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB22 FJ7931
EU887975.1 gg_id:314492 Microbial structure hydrolytic stage two-stage anaerobic digestion grass silage leach EU8879
EU246197.1 gg_id:250645 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P5-B02 EU2461
EU843463.1 gg_id:352273 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8434
DQ404796.1 gg_id:153870 contaminated sediment clone 661250 DQ404
AM490693.1 gg_id:576477 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490

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278.7	4725.3	5204.3	2959.7	4354.7	4646.0	3608.6	3016.3	3810.5	2322.8	2830.1
2118.1	6102.9	5898.6	6338.8	9164.6	6051.5	8588.1	6223.7	7347.2	5638.1	5414.4
8041.9	4689.6	3871.8	4220.9	4403.5	4145.8	4765.3	4053.9	5601.0	3375.1	4786.6
53.0	561.2	148.8	148.8	305.3	220.7	126.8	139.1	73.8	50.0	185.0
64.3	134.2	157.9	133.5	257.3	224.9	213.9	133.5	48.1	17.2	70.6
415.9	3256.8	3484.6	3494.9	4613.3	3496.1	4599.8	3815.3	1760.8	2537.0	2516.2
3899.6	8062.0	7680.6	8232.5	7197.8	7946.3	7210.9	7324.0	7785.8	5293.5	7224.4
313.3	4500.7	4383.7	5127.3	3916.6	3914.9	4466.1	3998.6	3065.1	3042.6	3811.3
2983.6	5620.0	6070.8	6293.3	6845.1	5973.6	7448.7	6234.1	3994.5	7249.0	5161.5
1303.8	5876.6	5222.2	6600.1	6923.1	5369.0	6491.8	5612.9	7558.1	3635.2	4848.0
49.5	452.6	685.5	694.2	764.1	533.4	1050.3	607.7	239.5	112.9	342.9
1806.2	1676.2	1895.1	2080.5	2139.1	1551.0	2681.3	1715.1	1309.7	1364.5	2123.3
849.1	4201.3	3949.6	4733.7	9447.1	4748.8	8903.8	5163.2	3360.7	2114.2	2985.6
552.5	1928.7	1971.0	1635.3	2055.4	1665.4	2055.6	1551.6	1300.6	516.1	1292.7
40.6	82.6	66.9	63.7	239.8	114.7	101.2	38.8	37.1	31.5	32.9
2401.4	3992.3	3817.9	3755.1	4638.8	3848.7	3821.6	3980.1	3400.4	4752.4	4360.6
49.2	334.3	329.1	314.6	525.1	239.3	326.4	245.6	65.4	77.1	89.2
1557.5	2457.2	3820.9	4219.1	6282.5	3856.7	6348.8	4019.9	1114.7	1114.9	2653.3
3759.1	8151.3	7657.2	7697.8	8106.9	7270.4	8048.9	7147.3	7932.1	4742.0	8330.2
70.8	1553.3	1618.0	1191.3	1240.7	1687.1	1448.0	1066.0	1221.1	796.5	645.7
152.8	2331.0	2796.7	3194.5	3373.5	2420.7	3663.3	2310.8	1493.1	1186.6	1713.5
321.0	1451.7	1581.3	1682.2	1791.8	1535.4	2219.6	1401.1	601.7	286.2	930.9
695.6	4485.2	4353.6	4643.8	4585.4	4578.1	4032.5	3408.7	3605.8	2466.9	4624.2
155.8	2394.3	2267.7	2456.5	1843.4	2241.3	2539.0	2501.8	1457.2	355.8	2198.9
82.7	226.2	207.9	204.2	252.2	200.1	260.9	231.9	133.4	73.8	130.1
7589.6	4853.4	5004.5	4948.3	5518.2	4763.7	6002.4	4591.9	6532.8	6022.1	6891.2
13569.5	8913.5	9155.6	10005.9	13854.1	9551.0	14121.3	7570.3	11338.5	10119.9	10066.7
50.9	121.0	251.7	251.3	115.0	115.3	177.9	203.3	58.9	38.0	85.0
62.5	42.8	43.7	46.9	59.7	52.4	40.3	30.7	46.3	37.6	50.3
407.5	5349.4	4750.2	5090.7	5346.8	4268.1	5621.4	5039.3	4985.0	2285.2	4143.3
1711.3	7960.8	7604.1	9468.0	8986.3	8856.0	9843.0	7293.8	8449.1	10240.9	9607.1
175.8	653.9	775.5	646.2	1614.4	950.2	1290.3	490.2	166.2	147.8	487.2
420.2	3286.7	3147.4	3126.5	4694.7	3732.4	4953.3	3172.9	2294.9	2606.3	2238.1
1756.3	2325.2	2255.7	2337.4	2390.4	2354.8	2720.5	2211.0	2693.9	1704.4	2810.3
391.9	4340.1	3645.9	4243.2	4127.6	4038.1	4370.7	4835.2	1762.5	2369.8	3718.0
14621.4	7362.1	6891.9	7522.2	7355.4	7098.0	8439.0	6471.0	8158.4	7502.4	8566.3
46.7	32.1	31.1	37.5	28.2	32.6	27.5	31.6	31.9	24.5	31.0
9630.9	5540.6	6187.6	6377.8	7049.2	6040.6	6264.4	6440.2	7002.1	7559.7	6881.4
2785.2	5743.2	5145.1	5763.5	5314.5	5608.4	6612.3	5428.2	4940.3	4412.7	5414.5
7243.2	7118.4	5693.6	7209.1	7218.3	6682.1	8135.3	6742.4	7550.7	5163.2	6721.1

4205.2	4298.0	6262.1
4056.2	2860.9	4260.7
7438.3	6581.7	7809.4
3975.3	5251.5	4170.8
281.6	333.7	209.9
236.7	237.5	303.5
4202.5	3775.5	5067.8
6652.5	8269.0	8111.5
3711.3	3990.2	6477.4
5497.5	7172.3	9284.8
5318.2	5831.0	8872.8
445.9	414.2	770.8
1621.2	2451.0	2424.1
6146.1	4623.0	7905.3
1600.6	1787.6	1876.8
46.8	121.3	487.9
3864.0	4079.1	4688.1
256.4	240.8	323.9
4073.5	3994.0	5063.1
6390.8	6728.7	7879.0
834.2	1083.6	2269.9
2151.7	2036.2	4305.1
1005.6	1472.5	3672.7
2886.7	3283.2	3038.0
2072.8	2118.3	3271.1
188.7	391.6	230.4
4397.0	5856.7	6210.1
7910.3	10901.9	12891.7
121.0	223.2	190.4
36.3	60.5	46.1
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7074.7	7761.9	8238.8
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4066.6	3245.9	3966.1
6110.8	8159.7	7803.3
31.0	33.8	36.9
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4927.3	5316.7	6980.5
5614.0	7388.1	7050.8

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g__sfA
g__sfB
g__sfC
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s__unclassified	52723
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s__Bacteroides dorei	69124
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AB240295.1 gg_id:143747 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
DQ787723.1 gg_id:163720 holocene lake sediment clone SLB629 DQ787
EF205585.1 gg_id:208525 among geographically regions central Tibet geothermal spring mat clone TP122 EF2055
FJ484560.1 gg_id:537376 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4845
EU456707.1 gg_id:318215 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU456
EU457210.1 gg_id:354314 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU457
EU136694.1 gg_id:256779 Bacteroides acidifaciens str. JCM10556 EU136
EU455470.1 gg_id:356164 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU455
EU457766.1 gg_id:352481 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU457
DQ456078.1 gg_id:158009 pre-adolescent turkey cecum clone CFT114B8 DQ456
AB510697.1 gg_id:541942 Bacteroides caccae str. JCM 9498 AB510
EU765625.1 gg_id:352289 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU136688.1 gg_id:246247 Bacteroides coprocola str. JCM12979 EU136
FJ363034.1 gg_id:356763 feces adult twins and mothers; TS148 clone TS148_a02b09 FJ3630
AB200225.1 gg_id:130849 Bacteroides coprocola str. M158 AB200
AY985803.1 gg_id:126815 human stool clone D057 AY9858
AB260026.1 gg_id:207799 Bacteroides coprophilus str. CB42 (= JCM 13818 = DSM 18228) AB260
AB510699.1 gg_id:536389 Bacteroides coprosuis str. JCM 13475 AB510
EU766723.1 gg_id:356621 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EU764957.1 gg_id:322715 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU764442.1 gg_id:314192 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766509.1 gg_id:332311 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
AB222700.1 gg_id:144954 Bacteroides finegoldii str. JCM 13346 176 AB222
DQ057444.1 gg_id:130819 str. ic1252 DQ057
EU761788.1 gg_id:327995 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
DQ904917.1 gg_id:169444 human fecal clone 002-a12 DQ904
EU767635.1 gg_id:322531 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
DQ057448.1 gg_id:136629 str. ic1259 DQ057
EU767843.1 gg_id:350743 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
EU136692.1 gg_id:256830 Bacteroides helcogenes str. JCM6297 EU136
EU765602.1 gg_id:341503 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
AB214329.1 gg_id:139247 Bacteroides intestinalis str. JCM 13266 mat-342 AB214
FJ366007.1 gg_id:366035 feces adult twins and mothers; TS25 clone TS25_a01f07 FJ3660
EU136691.1 gg_id:243642 Bacteroides intestinalis str. JCM13266 EU136
FJ372297.1 gg_id:357023 feces adult twins and mothers; TS9 clone TS9_a04a03 FJ3722
EU766174.1 gg_id:340970 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765141.1 gg_id:309517 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
AB510703.1 gg_id:536606 Bacteroides massiliensis str. JCM 13223 AB510
EU765962.1 gg_id:305072 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU764452.1 gg_id:342305 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766455.1 gg_id:332300 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766

93.1	305.7	510.4	314.9	222.5	340.4	503.4	431.4	78.7	36.7	157.9
143.2	1106.6	1068.3	1146.1	1212.3	1217.6	1423.4	961.1	642.7	312.6	343.8
3148.5	6060.9	6321.7	6398.9	6230.4	5713.0	6466.9	5206.5	4356.6	3940.6	5351.3
514.3	4393.8	3991.8	4605.6	5063.9	4144.8	8222.3	3829.1	3506.3	1121.8	3234.6
982.8	4389.2	3892.9	2705.1	3475.1	4214.1	4506.4	4112.0	7109.8	4968.9	4810.5
162.5	3349.0	2220.8	2594.6	1394.6	2390.7	1595.2	3019.7	2156.0	1208.2	2199.4
125.4	1555.4	849.5	887.3	198.5	930.3	362.9	1265.8	352.3	259.8	693.5
130.1	2527.2	2089.8	2488.4	1744.1	2126.1	1965.7	2574.3	2026.1	1719.4	2411.6
70.1	1136.2	995.1	940.0	261.6	846.1	514.7	1387.2	334.1	224.8	1364.1
54.2	76.2	99.0	130.3	82.9	112.6	83.4	943.5	45.4	81.1	95.8
109.2	1354.0	782.6	968.8	267.6	906.5	381.8	1176.4	455.2	184.1	769.7
44.1	617.2	450.9	447.7	593.9	499.0	643.8	448.4	279.4	181.9	218.9
179.3	2935.7	2288.1	2670.1	3073.4	2395.1	3441.9	2224.0	2706.2	738.3	2009.7
109.1	1883.7	1939.0	2701.4	1876.7	1854.7	2349.9	2206.8	1536.3	453.8	1461.6
95.0	2677.4	2350.7	2651.8	1794.3	2604.0	1757.8	2529.1	1708.1	970.5	2093.8
121.7	1678.2	1559.8	2052.6	1680.5	1561.1	1877.2	1716.1	1455.1	412.7	1150.1
45.6	115.1	217.1	253.3	177.2	109.9	421.9	506.4	244.2	45.6	150.7
37.0	372.4	412.5	515.8	296.1	333.7	561.5	513.5	161.3	102.7	286.0
195.3	3099.0	2993.3	4267.8	1971.5	2522.0	2415.0	3388.6	1015.6	776.1	2455.3
1563.7	1858.0	1872.7	1798.5	1733.9	1612.6	1615.7	1872.3	1865.8	811.1	1328.0
196.6	1214.3	1711.5	1869.4	774.4	1245.8	1278.6	1993.6	769.9	770.9	1793.4
74.8	2039.8	2497.3	2118.1	1863.1	1896.4	2002.1	2203.5	1127.1	578.5	1770.7
33.5	732.1	1001.2	1278.5	802.1	857.3	928.9	1079.0	353.2	129.2	629.3
112.5	2540.6	2842.3	3332.0	684.5	2390.9	1410.5	2999.9	1075.9	522.0	2771.7
151.4	3448.6	4248.8	5117.3	2239.7	3882.9	3733.4	4152.1	1696.9	789.8	3910.0
65.3	2197.8	2652.8	2776.2	906.8	1947.2	1181.2	2973.4	682.1	475.4	1996.2
65.1	577.2	683.9	1044.1	503.7	610.8	604.0	1121.9	210.7	96.9	443.2
100.6	4512.5	4177.7	5114.9	3859.9	5292.6	4104.8	4045.9	5247.2	3028.8	3564.1
236.0	5030.0	4656.1	5255.5	5742.9	5356.9	5460.8	4431.0	5975.1	4360.8	4119.2
30.8	1140.9	754.1	704.4	263.0	697.2	251.2	976.8	286.3	1179.8	345.6
315.2	1762.3	1858.5	2020.7	1453.8	1663.6	1948.3	1915.1	1847.4	1600.9	1368.7
128.7	3243.0	2523.7	2725.1	1250.4	2461.3	1710.7	2900.0	1236.6	1362.9	2649.4
57.9	1194.4	721.4	697.7	435.4	898.2	471.5	1004.4	350.4	2128.9	540.5
70.7	563.6	474.7	494.4	392.9	530.5	423.2	533.0	241.9	481.9	363.1
90.2	714.2	495.7	572.3	634.7	895.8	524.9	687.6	1025.5	649.5	462.9
174.9	2184.5	2680.4	3014.4	2464.8	2643.4	2958.8	2569.2	1100.2	800.8	2342.6
228.4	3326.5	3480.7	4284.7	3528.9	2709.4	3889.2	3331.9	1222.9	1141.3	3214.9
1117.9	6415.5	5960.7	7070.4	6994.6	6594.7	7234.8	6370.1	3932.1	4769.7	6357.6
88.1	2736.7	3819.8	4678.5	3032.8	2274.2	4177.9	2953.9	1054.4	840.1	3041.2
181.1	2142.1	2695.8	3043.8	2072.7	2491.8	2439.3	2414.7	986.9	791.3	2030.0
193.7	2196.9	2597.4	3295.6	2268.2	1935.7	2490.0	2538.4	1035.6	534.5	1977.7

245.5	308.7	521.3
1199.5	1106.5	2011.3
5122.5	6247.2	6618.9
3336.2	4775.4	5956.6
3760.9	4612.4	4503.7
2479.8	2268.9	1263.5
1030.4	801.2	337.2
1977.8	1584.9	1833.0
1082.0	599.2	542.0
141.9	241.0	343.2
887.3	576.5	575.8
492.9	435.4	398.3
2517.6	2111.3	2400.4
2280.8	1594.1	1630.8
2976.3	1414.6	1764.6
1532.0	1372.6	1325.3
136.5	187.7	264.1
485.9	427.1	382.0
4620.9	1948.8	1624.1
2066.3	2851.9	2150.7
1743.8	1273.9	1182.3
2203.6	2296.5	2827.6
853.0	659.1	993.2
2586.9	1544.9	1973.4
3941.1	3407.6	4027.5
1533.3	1069.9	2296.2
557.0	567.6	698.8
4615.0	3669.6	4258.0
4145.1	4656.4	4383.8
791.5	824.0	887.2
1962.7	2734.1	2333.8
2675.0	1754.9	3510.3
786.9	628.5	776.0
499.6	548.8	781.0
687.0	839.0	587.8
2504.0	2165.2	2569.1
3407.8	2513.7	2256.8
6704.3	5645.8	8916.6
3331.8	2771.9	3598.0
2663.8	1981.6	2277.5
2655.8	2122.2	2174.4

k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
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s__Bacteroides massiliensis	68583
s__Bacteroides massiliensis	68597
s__Bacteroides massiliensis	68613
s__Bacteroides massiliensis	68635
s__Bacteroides massiliensis	68659
s__Bacteroides massiliensis	68665
s__Bacteroides massiliensis	68690
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s__Bacteroides massiliensis	69097
s__Bacteroides massiliensis	69111
s__Bacteroides massiliensis	69138
s__Bacteroides massiliensis	69192
s__Bacteroides massiliensis	69228
s__Bacteroides ovatus	68506
s__Bacteroides ovatus	68520
s__Bacteroides ovatus	68533
s__Bacteroides ovatus	68566
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s__Bacteroides ovatus	69104
s__Bacteroides ovatus	69153
s__Bacteroides plebeius	68535
s__Bacteroides plebeius	68539

EU764317.1 gg_id:352365 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU764401.1 gg_id:345289 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766538.1 gg_id:340694 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU764456.1 gg_id:342150 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU765095.1 gg_id:304136 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU765852.1 gg_id:348178 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU765803.1 gg_id:340562 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU766386.1 gg_id:355400 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765932.1 gg_id:353539 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU765043.1 gg_id:309304 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU766317.1 gg_id:313020 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU764392.1 gg_id:306362 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766114.1 gg_id:322222 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
AB200226.1 gg_id:136630 Bacteroides massiliensis str. EG4-8-2 AB200
EU764425.1 gg_id:346002 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU766314.1 gg_id:351455 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765977.1 gg_id:310598 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU763365.1 gg_id:319923 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
EU766331.1 gg_id:317897 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU763920.1 gg_id:339965 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU763
DQ799335.1 gg_id:179763 human fecal clone RL305aal85a10 DQ799
EU766112.1 gg_id:322303 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ798822.1 gg_id:176388 human fecal clone RL242_aaj97g08 DQ798
FJ369010.1 gg_id:363625 feces adult twins and mothers; TS4 clone TS4_a03c03 FJ3690
DQ805617.1 gg_id:176185 human fecal clone RL306aal89a05 DQ805
AB050108.1 gg_id:37022 Bacteroides ovatus str. JCM 5824T AB050
GQ492617.1 gg_id:539888 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ491656.1 gg_id:577651 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU768716.1 gg_id:303636 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU768196.1 gg_id:318509 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
FJ365436.1 gg_id:362940 feces adult twins and mothers; TS20 clone TS20_a02h02 FJ3654
EU762338.1 gg_id:345835 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU762
EU763065.1 gg_id:356294 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU763
GQ079152.1 gg_id:377892 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1229b GQ079
DQ100446.1 gg_id:141994 Bacteroides ovatus str. SDG-Mt85-3Cy DQ100
FJ368826.1 gg_id:367134 feces adult twins and mothers; TS4 clone TS4_a01a11 FJ3688
FJ363281.1 gg_id:365909 feces adult twins and mothers; TS149 clone TS149_a01d07 FJ3632
AY982129.1 gg_id:119221 human sigmoid colon mucosal biopsy clone P716 AY982
DQ799104.1 gg_id:186140 human fecal clone RL205_aaj17f06 DQ799
DQ824367.1 gg_id:187751 human fecal clone RL304_aal75b05 DQ824
DQ823862.1 gg_id:174475 human fecal clone RL250_aaj80a12 DQ823

180.7	2398.3	3021.2	3522.0	2483.9	2632.1	2989.8	2630.7	1106.3	803.3	2369.6
229.0	3100.7	3215.8	3962.6	3232.6	2568.8	3599.1	3313.5	1112.2	1071.9	2996.4
715.2	1364.8	1852.8	1918.2	1486.0	1421.2	1890.8	1635.9	1079.9	1160.5	1491.9
185.4	2041.2	2478.4	3043.1	2148.4	2183.8	2475.8	2101.5	958.5	492.0	1805.2
194.6	2223.6	2609.1	3183.9	2075.3	2134.8	2119.5	2785.1	1112.9	660.8	2145.8
186.6	1960.0	1920.9	2239.5	1424.2	1598.0	1738.5	1530.5	790.2	495.2	1264.9
177.4	1953.6	2354.3	2846.1	1979.0	2099.0	2313.9	2030.6	925.5	465.6	1798.3
2278.9	4077.1	3873.9	4585.6	4247.9	3952.4	4444.0	3975.1	4393.3	4256.9	5070.9
225.4	3086.4	3153.0	3817.9	3105.7	2627.1	3329.2	3331.3	1084.4	1135.9	2882.4
2613.3	2950.1	3163.7	3745.6	2264.6	2293.7	2945.4	3289.4	1191.3	1146.8	2610.9
227.0	3337.1	3485.0	4283.4	3298.9	2773.1	3660.4	3564.3	1216.0	1138.1	3214.5
173.0	2310.2	2959.3	3477.1	2487.3	2542.4	2969.7	2546.4	1073.5	794.5	2219.0
182.3	2377.1	3007.7	3509.3	2318.3	2640.0	2805.3	2618.6	1110.3	793.4	2362.1
234.1	4080.2	3492.3	3698.0	3200.6	3747.2	3628.2	3826.3	1399.5	1638.9	3254.9
229.4	3353.2	3492.4	4173.1	3335.9	2908.6	3518.7	3562.1	1300.2	1267.6	3383.1
219.2	3131.7	3136.6	3788.6	3525.9	2778.8	3885.9	3507.8	1205.2	1146.1	3195.1
184.8	2170.5	2520.4	3039.0	1917.9	1721.8	2304.2	2322.1	900.3	817.7	1828.8
100.7	2879.9	2112.7	2608.9	1861.6	2827.0	1735.4	2522.1	3585.5	2516.2	1604.5
94.1	1369.6	1206.4	1416.3	298.8	1229.4	436.5	1531.8	369.4	235.2	712.7
67.0	321.6	671.9	744.2	267.1	471.7	303.0	725.5	234.9	114.6	667.8
312.1	5320.1	4563.2	5450.5	4291.7	5536.4	3939.2	5313.3	8731.3	5840.2	5593.1
103.4	752.6	708.0	760.1	490.4	847.8	546.6	826.1	343.2	178.1	561.8
39.1	972.6	1138.9	1648.6	707.5	1089.9	1001.5	1174.0	513.2	191.8	904.8
903.1	4411.4	4468.9	6759.7	3444.9	4480.8	5199.8	4891.5	4226.4	3062.4	5024.5
239.8	3489.0	3934.0	5147.4	1401.0	3073.8	3567.3	4519.4	1665.5	986.3	4933.6
304.8	2564.4	3685.5	3350.2	3254.6	3266.8	3636.2	3132.3	4734.5	4063.2	2768.4
50.9	132.2	176.3	178.5	158.7	314.4	127.3	115.0	104.4	43.9	78.5
57.9	262.8	446.7	606.1	232.2	432.0	301.9	313.8	129.7	69.4	196.0
50.1	142.6	216.3	34.1	144.7	316.0	41.1	231.7	64.3	21.7	139.4
189.1	2768.8	1819.6	2400.0	1028.1	2059.6	1534.6	2097.3	1119.2	505.8	1904.5
211.2	2443.0	2821.3	2967.0	1940.0	3237.7	2295.9	2826.6	2347.9	1594.8	1943.1
1674.2	1854.8	1800.6	2426.1	1660.1	222.4	2108.0	1582.7	2564.7	1448.3	2004.3
66.8	328.6	319.0	336.5	166.5	461.4	185.9	297.3	123.4	82.6	222.8
1944.7	1861.8	1825.3	3617.6	1369.2	1901.2	1648.7	2510.1	1285.1	750.1	1516.3
203.6	4476.0	4691.3	4418.4	4153.4	4111.4	4722.8	3495.9	3327.6	3203.8	4099.7
305.6	1243.5	1279.7	2128.8	968.1	1223.0	1664.2	1879.0	1212.8	163.1	1533.4
115.1	1231.6	1402.4	1640.4	906.7	1239.7	1363.1	1257.3	812.9	442.0	984.8
40.6	861.1	715.2	803.2	392.9	820.4	608.0	812.2	306.3	52.3	477.3
74.7	537.8	912.3	1157.5	335.1	418.6	393.0	845.5	207.4	109.7	286.7
47.4	672.4	781.5	845.4	337.4	628.8	876.4	738.6	236.9	287.2	526.8
52.8	1335.5	2066.2	2400.7	1657.7	1288.2	1857.6	1179.0	447.7	228.7	677.6

2830.9	2273.2	2584.2
3212.5	2305.7	2078.9
1549.2	1799.6	1611.1
2376.2	1850.9	2144.6
2771.2	2083.5	2175.1
2278.3	1439.1	1410.2
2258.8	1751.0	1993.9
3388.8	5020.7	3804.9
3283.4	2225.4	1958.7
2971.5	2995.8	2282.5
3450.1	2512.2	2278.0
2761.4	2239.7	2552.8
2820.1	2250.4	2576.8
3901.0	2715.8	3748.6
3523.1	2475.0	2257.6
3112.9	2421.2	2269.8
2434.8	2072.5	1921.7
2695.7	1655.7	1462.0
2171.7	1051.2	1102.5
661.4	385.6	299.7
5621.0	4547.7	4055.8
760.4	554.9	377.3
1057.0	1400.6	1263.4
4663.9	4723.0	6580.8
4680.8	3504.4	7053.5
2823.0	3374.3	2929.4
134.1	147.3	89.9
429.4	261.6	160.9
257.4	298.5	39.8
1915.4	1310.1	1505.7
2917.4	3030.1	2804.3
1353.7	1426.2	1549.4
361.4	217.8	160.8
2824.1	2520.4	3001.0
4176.1	3578.5	3787.8
1281.6	1829.7	1587.5
1704.7	1508.2	1292.3
786.3	491.9	731.3
1743.6	213.8	139.8
601.2	550.9	1337.3
1018.7	1089.8	1383.2

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s__Bacteroides plebeius	68669
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EF403466.1 gg_id:215166 human fecal clone SJTU_A2_01_56 EF4034
AB200217.1 gg_id:131236 Bacteroides plebeius str. M12 AB200
AB200219.1 gg_id:134286 Bacteroides plebeius str. M35 AB200
EU766635.1 gg_id:318833 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EF400653.1 gg_id:216960 human fecal clone SJTU_E_16_63 EF4006
EU767622.1 gg_id:315932 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
EF403124.1 gg_id:210025 human fecal clone SJTU_A1_1_22 EF4031
EU136690.1 gg_id:236480 Bacteroides salyersiae str. JCM12988 EU136
DQ905050.1 gg_id:162723 human fecal clone 2-002-d8 DQ905
DQ905008.1 gg_id:164088 human fecal clone 2-002-a10 DQ905
ABFZ02000010.1 gg_id:266138 Bacteroides stercoris str. ATCC 43183 ABFZ0
EU136684.1 gg_id:245615 Chromaphyosemion bivittatum str. JCM9496 EU136
FJ371227.1 gg_id:365084 feces adult twins and mothers; TS6 clone TS6_a02d09 FJ3712
DQ905097.1 gg_id:164178 human fecal clone 2-002-h9 DQ905
FJ370549.1 gg_id:359417 feces adult twins and mothers; TS57 clone TS57_a02d05 FJ3705
NZ_ABFZ02000011.1 gg_id:469826 Bacteroides stercoris str. ATCC 43183 NZ_AB
DQ905028.1 gg_id:165847 human fecal clone 2-002-c10 DQ905
X83953.1 gg_id:2030 Bacteroides stercoris str. ATCC 43183T X83953
DQ805722.1 gg_id:184209 human fecal clone RL306aal90c06 DQ805
GQ491307.1 gg_id:544341 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU765106.1 gg_id:354895 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU765
EU766220.1 gg_id:347407 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765541.1 gg_id:337684 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU765881.1 gg_id:355109 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
AB117563.1 gg_id:112035 Bacteroides uniformis str. NB-13 AB117
AB021157.1 gg_id:2045 Bacteroides acidofaciens str. AB021
EU766171.1 gg_id:331754 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
EU765282.1 gg_id:308188 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
DQ456111.1 gg_id:158663 pre-adolescent turkey cecum clone CFT114E8 DQ456
EU511533.1 gg_id:271150 cecal contents Mus musculus strain C57BL/6J; WD9 clone WD9_aak06b03 EU511
EU763339.1 gg_id:315474 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
FJ371809.1 gg_id:362127 feces adult twins and mothers; TS8 clone TS8_a02d10 FJ3718
AY978878.1 gg_id:124255 human transverse colon mucosal biopsy clone NE82 AY978
DQ798203.1 gg_id:191479 human fecal clone RL302_aal96g09 DQ798
DQ824385.1 gg_id:197052 human fecal clone RL304_aal75d09 DQ824
AY895194.1 gg_id:111383 Bacteroides sp. str. 4072 AY895
EU681979.1 gg_id:301746 microflora imbalances intestine dogs inflammatory bowel disease duodenum dog IBI EU681
EU136689.1 gg_id:246004 Bacteroides tectus str. JCM10003 EU136
AY981662.1 gg_id:115480 human sigmoid colon mucosal biopsy clone L940 AY981
DQ456025.1 gg_id:158651 pre-adolescent turkey cecum clone CFT112D6 DQ456
EU764615.1 gg_id:320837 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764

188.3	1460.1	1860.2	2331.7	2205.1	1569.3	2597.9	1887.3	2130.9	1930.8	1970.3
233.6	3912.3	3212.4	2465.1	2390.3	3183.5	2312.8	2593.5	3290.3	3289.8	2006.4
81.5	1828.3	1307.3	1235.6	1838.4	1097.6	1694.6	1052.4	589.2	239.7	937.7
49.4	1002.1	1372.1	1656.1	840.7	904.9	807.0	1155.3	467.5	155.7	503.5
30.4	1262.8	2076.6	2253.3	2065.9	1251.9	2279.7	1188.2	453.6	298.2	507.1
3125.0	3626.1	3562.2	3456.7	3227.8	3648.1	3256.6	3456.4	4981.0	4144.4	4057.8
1111.3	10915.1	8322.6	12114.0	8419.1	9527.0	8988.1	10362.9	14426.3	11209.4	10609.3
69.1	1033.7	551.5	587.7	290.9	537.5	301.7	787.9	244.9	1271.6	296.5
7800.5	6485.1	7147.4	8720.5	6628.9	7010.9	6816.0	5999.8	9640.0	7376.8	7953.2
78.5	280.3	230.7	386.1	61.3	276.0	150.0	410.8	100.1	54.4	214.8
37.5	310.2	401.1	416.3	285.7	267.0	317.3	410.2	152.7	332.0	399.6
58.9	1813.8	1783.5	1688.0	515.1	1622.3	1174.8	2184.4	530.1	718.3	1952.0
6258.0	9428.3	8208.9	10077.3	8165.2	8619.7	9838.4	7083.8	12647.8	10840.4	10843.9
93.9	2370.5	1957.2	2105.4	768.2	1983.3	1317.8	2709.4	952.8	1126.1	3247.0
46.6	720.0	688.6	806.0	395.5	689.8	444.8	955.9	318.2	345.4	599.2
32.7	544.4	597.9	642.6	438.0	676.3	1057.3	710.8	290.6	310.0	404.3
86.1	1669.0	1503.0	1654.0	484.5	1920.9	1194.0	1848.9	579.5	629.2	1675.1
45.1	1279.0	1155.8	1407.9	289.2	1277.2	748.7	1660.0	514.6	569.9	1911.9
44.7	92.3	46.1	70.0	40.8	35.9	40.0	89.9	29.0	27.7	48.8
94.0	1394.6	1202.8	1402.3	1412.3	1230.7	1411.2	1725.5	762.3	293.6	952.9
56.9	2034.0	1745.6	2130.5	1428.4	1806.5	1201.5	1839.0	1637.3	1233.1	1048.6
717.5	2101.3	1945.7	1815.7	1545.6	2382.9	1592.9	1975.8	1444.7	914.6	1499.9
1096.6	3204.1	4465.1	3966.1	3077.1	2807.7	4484.0	3072.9	3140.0	1977.6	5168.7
228.1	1077.3	1121.8	930.2	575.0	802.2	649.4	721.2	308.0	289.7	987.4
2799.4	1792.0	1651.2	1833.1	1658.6	1771.9	1810.8	1987.5	1592.6	1676.7	3149.3
40.6	735.3	921.9	1119.5	167.5	851.3	307.1	976.0	210.5	117.7	320.1
65.8	1603.3	2020.0	1572.5	1398.1	1456.3	1572.7	1652.9	375.6	1074.5	988.0
64.6	340.7	496.1	659.8	280.9	403.7	256.0	286.7	150.5	63.5	146.0
52.4	593.9	870.4	909.8	986.2	627.8	1506.3	619.5	440.7	182.9	491.8
55.9	1374.8	1892.4	1820.6	1372.6	1563.5	1586.6	2184.1	566.2	422.7	1231.8
49.6	534.7	527.9	663.9	229.7	223.3	309.6	385.9	146.2	183.4	272.1
58.2	1361.3	1275.7	1372.9	1103.1	1264.8	1183.3	1286.4	554.7	365.8	869.1
57.6	1060.3	1150.7	1086.8	685.6	790.9	851.1	982.0	469.6	227.9	558.7
44.8	820.5	1024.2	1139.4	840.0	948.2	1228.6	912.0	481.5	358.9	664.8
80.5	197.7	281.1	282.5	130.1	178.2	217.9	190.2	106.9	100.3	190.1
119.7	1016.9	757.5	1034.7	428.5	675.8	575.0	963.5	321.8	168.9	579.3
39.0	745.0	454.8	288.9	70.6	501.6	159.5	1065.2	181.3	79.3	355.6
70.8	500.6	456.0	501.6	178.6	351.0	224.0	565.2	111.1	71.6	244.1
163.2	1552.4	1528.5	1705.3	1301.1	1276.8	1245.4	1752.3	659.6	429.6	1280.4
42.3	1810.2	2453.2	3073.6	687.7	915.6	1368.7	1822.5	361.8	168.8	963.1
106.1	2499.0	2863.1	3280.7	3844.0	2947.4	4095.2	3474.0	1644.6	1961.5	2473.5

1024.4	2710.9	2862.4
2913.6	2906.1	2707.8
730.4	1105.5	1145.5
887.6	1100.4	770.2
717.5	1074.7	1440.9
2861.5	4471.8	3116.4
9479.3	10848.9	9612.2
603.8	403.0	262.7
5339.2	7406.4	7143.7
352.8	175.4	193.8
315.5	601.6	595.3
1506.4	1319.9	1646.5
6992.5	8985.0	12056.7
2023.8	1871.8	3091.4
665.0	539.7	1375.4
545.2	546.6	876.6
1474.5	1109.3	1548.6
935.6	766.6	1234.1
46.6	61.2	57.7
1548.6	1443.7	2285.4
1557.8	1494.2	971.0
2350.1	3062.1	2725.3
2962.0	3436.1	4737.4
719.1	904.8	442.6
1696.9	1836.1	1865.4
1342.2	706.6	757.7
1376.9	1682.2	1341.9
455.9	489.9	400.1
536.8	721.6	513.5
1797.3	1786.4	1262.9
508.7	410.9	347.5
1306.3	1063.2	1030.5
865.6	574.8	531.3
828.2	809.2	1089.0
267.9	198.8	226.1
1096.9	789.7	349.3
546.0	208.1	266.9
552.9	197.1	238.6
1986.8	1206.6	1865.8
2596.9	1337.9	866.1
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EU761963.1 gg_id:355873 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
AF227834.1 gg_id:48647 str. 31285 AF227
GQ867554.1 gg_id:564616 and prevalence blaTEM genes Arctic seals colon content clone CSH59 GQ867
FJ362922.1 gg_id:361680 feces adult twins and mothers; TS13 clone TS13_a04g09 FJ3629
FJ371985.1 gg_id:365192 feces adult twins and mothers; TS8 clone TS8_a04d11 FJ3719
EU767678.1 gg_id:332031 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
EU764074.1 gg_id:305008 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
EU766032.1 gg_id:336559 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU766
EU766963.1 gg_id:319413 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ793958.1 gg_id:174194 human fecal clone RL176_aah45g09 DQ793
EU767532.1 gg_id:345989 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
FJ681103.1 gg_id:526303 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6811
AM275521.2 gg_id:234488 fecal microbiota irritable bowel syndrome patients significantly that healthy subject AM275
GQ492318.1 gg_id:562721 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ867293.1 gg_id:551593 and prevalence blaTEM genes Arctic seals colon content clone WSp23 GQ867
AB437413.1 gg_id:358550 Bacteroides intestinalis str. AM-1 AB437
FJ683108.1 gg_id:523989 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU505150.1 gg_id:276484 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa03e12 EU505
EF434324.1 gg_id:205290 gastrointestinal tract microbiota microarray reference pool created pooling products EF4343
FJ372367.1 gg_id:370102 feces adult twins and mothers; TS9 clone TS9_a04g08 FJ3723
EU768090.1 gg_id:332404 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU768640.1 gg_id:348832 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY986070.1 gg_id:125534 human stool clone D394 AY986
FJ366443.1 gg_id:366374 feces adult twins and mothers; TS26 clone TS26_a03c11 FJ3664
EU767318.1 gg_id:329732 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
AM420078.1 gg_id:242308 Noma subgingival plaque clone 301H11(oral) AM420
AY977553.1 gg_id:119557 human cecum mucosal biopsy clone W359 AY977
AY975360.1 gg_id:117724 human ascending colon mucosal biopsy clone N653 AY975
AY975485.1 gg_id:125748 human ascending colon mucosal biopsy clone N919 AY975
GQ492611.1 gg_id:588825 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ807063.1 gg_id:189614 human fecal clone RL244_aaj45g04 DQ807
EU761916.1 gg_id:340637 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
FJ440088.1 gg_id:512957 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
EU531945.1 gg_id:271214 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
AY977810.1 gg_id:124192 human cecum mucosal biopsy clone LF01 AY977
EU762766.1 gg_id:311251 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU762
FJ363423.1 gg_id:366083 feces adult twins and mothers; TS149 clone TS149_a03b02 FJ3634
AY985214.1 gg_id:127000 human stool clone C078 AY985
EU766954.1 gg_id:320670 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ672191.1 gg_id:516365 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6721
EU768032.1 gg_id:306991 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768

83.4	1551.4	1923.3	2376.9	984.7	1157.1	1390.6	1571.7	423.1	228.4	1276.3
222.7	1430.5	2435.4	2471.3	1208.4	1833.8	1298.1	2428.1	932.8	464.7	1822.4
164.1	2591.5	2846.0	3365.1	1815.0	2802.2	2415.6	2516.1	1290.4	719.3	1770.0
110.0	2374.1	2572.8	3081.9	2031.4	1806.4	2471.8	2473.3	760.9	567.6	2022.4
82.6	646.4	723.5	416.2	247.5	861.9	750.5	569.2	184.5	164.1	406.7
179.5	2840.8	2540.0	2727.5	2196.1	2416.7	2555.9	2820.6	828.9	840.7	2293.7
89.8	5111.5	4889.8	5932.0	3693.4	3277.0	5575.3	4288.8	2176.3	2923.2	4499.3
164.7	4924.2	4685.7	4707.9	4019.8	4643.0	4575.8	4494.5	6059.4	5410.7	4612.7
45.5	363.5	271.6	234.3	276.9	406.1	424.6	301.5	146.0	71.7	123.2
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174.0	2658.0	2356.6	3251.6	1850.6	2157.7	2203.4	2723.0	768.5	589.7	2184.0
93.8	3063.6	1956.8	2406.2	2365.4	4125.5	1988.0	2285.4	2789.2	2105.8	1451.7
53.4	116.6	137.1	132.2	114.7	163.0	160.4	208.9	76.8	91.0	85.6
147.2	1971.6	1579.2	1710.9	477.7	1836.0	909.4	1946.2	569.7	307.9	1129.0
203.3	4446.6	4362.2	4132.9	2452.3	4136.1	3192.4	4333.5	2501.7	1785.3	4145.2
70.5	685.2	553.3	533.6	289.0	753.1	335.3	662.7	308.8	149.6	374.6
111.0	1883.1	1938.0	2518.5	1874.8	1856.2	2341.2	2222.0	1535.4	453.9	1462.3
167.1	2568.3	3231.9	4221.1	2765.6	2238.3	4242.3	3383.1	1088.1	821.8	3227.5
97.1	842.4	738.9	616.9	684.3	697.3	980.2	729.5	365.8	263.8	388.7
67.0	237.5	361.0	298.9	109.0	280.8	233.3	395.2	211.6	53.2	525.1
11969.2	7621.9	8188.4	8775.3	8896.4	7173.7	9248.4	7430.7	12077.6	9481.4	9424.1
179.6	3242.5	3039.6	3348.3	2286.4	2427.0	2670.8	2946.3	820.6	850.7	2352.8
41.8	249.2	147.2	153.3	141.5	194.0	208.6	217.6	83.5	20.2	108.8
172.4	1582.8	2385.1	2627.3	1015.3	2415.9	1832.1	3791.8	1058.9	365.1	2008.5
86.6	3669.0	3485.4	3880.3	3194.7	3762.2	3899.7	3699.9	4490.9	2752.3	2365.5
48.9	1680.5	1366.5	1483.1	264.3	1071.8	803.2	1846.7	528.9	117.1	847.3
386.7	3165.3	2297.2	2757.7	831.4	1975.8	1400.1	3602.4	1154.6	862.3	1498.1
67.4	2042.1	2136.4	2658.8	1737.8	1678.9	1733.5	2462.5	903.0	379.1	1778.1
3522.8	1656.4	1879.8	2379.1	1631.1	544.4	2357.2	2072.4	3106.6	3612.8	3535.6
204.1	2660.2	2130.4	2416.6	1629.2	2136.2	1851.6	2748.6	939.3	759.9	2088.2
251.0	2312.9	2358.1	2064.3	1634.1	1785.6	2431.5	1782.4	2266.7	1998.3	1920.0
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80.6	811.8	883.8	1050.2	171.1	302.1	193.1	463.2	123.2	70.3	159.2
75.3	494.8	750.0	1010.5	741.6	748.6	889.5	850.2	453.6	74.2	730.3
75.3	1762.6	2576.2	3249.4	532.8	1982.2	2185.9	1878.2	941.3	486.7	3327.8
61.5	870.0	1307.7	1523.7	429.9	432.7	779.6	824.7	221.2	158.9	574.7
84.1	770.6	1032.0	1446.6	719.6	743.8	1105.4	902.1	378.5	110.1	587.4
86.4	1599.5	2102.9	2406.0	947.1	1163.9	1492.9	1588.5	412.6	223.3	1323.4
150.9	1693.2	2075.3	2053.8	1489.9	1250.7	1542.9	1546.0	1157.7	404.6	1195.4
150.8	1566.0	1462.8	1700.8	1224.8	1677.5	1361.6	1983.1	2088.4	955.3	1201.4
68.7	982.5	1014.9	1236.8	584.3	621.3	620.8	790.9	265.7	227.4	789.3

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2490.3	2094.6	2172.0
2415.1	1753.6	1252.0
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2760.9	1471.1	1414.0
4412.1	3590.0	5969.6
4002.2	5494.4	4332.1
408.7	263.8	205.1
1712.6	2190.9	1781.3
3249.3	1595.9	1117.3
2346.6	2403.8	2156.3
181.9	174.6	145.7
1768.3	1030.0	1678.5
4720.5	2916.5	4878.9
595.7	492.6	512.5
2280.2	1575.3	1454.4
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594.9	635.4	1222.4
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3275.9	1694.7	1454.8
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2276.6	2187.5	1609.8
3374.9	3674.8	4518.2
1564.0	862.5	2107.8
4874.0	1743.5	2200.9
1967.6	1494.1	1630.6
1676.9	2923.8	2177.2
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1654.4	2283.9	2502.4
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1286.9	482.5	315.0
757.7	862.7	973.2
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1323.9	753.9	593.4
1222.6	739.4	1076.6
2606.4	1281.9	1166.5
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FJ370710.1 gg_id:369276 feces adult twins and mothers; TS57 clone TS57_a04c09 FJ3707
EU768154.1 gg_id:356616 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU655886.1 gg_id:283641 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU766456.1 gg_id:333475 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU766
DQ905076.1 gg_id:172060 human fecal clone 2-002-g11 DQ905
EU761699.1 gg_id:327096 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU765443.1 gg_id:345104 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B3 EU765
EU768406.1 gg_id:344420 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
EU531963.1 gg_id:261878 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
EU472048.1 gg_id:299461 francois langur feces clone FL_1aaa04f05 EU472
EU767197.1 gg_id:315993 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
DQ807484.1 gg_id:195157 human fecal clone RL307_aam07b09 DQ807
EU763736.1 gg_id:323812 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU763
GQ867518.1 gg_id:536429 and prevalence blaTEM genes Arctic seals colon content clone CSH15 GQ867
FJ371434.1 gg_id:360815 feces adult twins and mothers; TS6 clone TS6_a04h08 FJ3714
EU764091.1 gg_id:329028 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A5 EU764
AB490801.1 gg_id:570110 Bacteroides clarus str. YIT 12056 AB490
DQ905928.1 gg_id:172994 human fecal clone 29c-h5 DQ905
GQ448371.1 gg_id:550814 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
DQ805840.1 gg_id:196926 human fecal clone RL306aal91g04 DQ805
AB499846.1 gg_id:556126 Bacteroides sp. str. TP-5 AB499
FJ366345.1 gg_id:366626 feces adult twins and mothers; TS26 clone TS26_a01f09 FJ3663
EU772744.1 gg_id:356052 Bush dog feces clone bdog1_aai78e02 EU772
EU768028.1 gg_id:353215 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU767916.1 gg_id:313565 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C3 EU767
GQ043048.1 gg_id:407354 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012e GQ043
GQ492204.1 gg_id:591783 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AY981521.1 gg_id:124731 human sigmoid colon mucosal biopsy clone L650 AY981
EU136696.1 gg_id:244304 Bacteroides massiliensis str. JCM12982 EU136
EU763175.1 gg_id:342782 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A3 EU763
FJ363523.1 gg_id:358503 feces adult twins and mothers; TS149 clone TS149_a04c02 FJ3635
EU768386.1 gg_id:310386 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
FJ978549.1 gg_id:375393 feces clone CL_F_093 FJ9785
DQ441261.1 gg_id:192907 human intestinal biopsy clone CD10 DQ441
EU761595.1 gg_id:311500 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU764768.1 gg_id:316580 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
GQ492338.1 gg_id:591967 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AY980883.1 gg_id:119266 human rectum mucosal biopsy clone LQ19 AY980
EU767175.1 gg_id:306006 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
EU764895.1 gg_id:335758 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU761967.1 gg_id:313373 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761

49.5	689.3	631.5	557.1	286.9	494.1	462.6	806.6	297.2	119.4	315.3
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363.1	1480.7	1587.6	1632.1	1338.9	1978.1	1716.8	1373.1	965.8	961.1	1394.0
2142.2	3582.9	4361.8	5133.2	4232.8	4102.0	4883.8	4196.6	3285.3	1617.2	3650.6
72.9	299.3	193.7	239.6	83.5	154.1	115.4	136.8	118.2	72.6	118.1
391.7	6631.7	4959.2	5188.6	3595.2	4559.4	4641.7	5470.2	2675.3	3386.1	5165.4
48.4	1021.0	827.8	570.0	155.5	490.5	656.7	936.7	401.7	69.3	689.6
411.4	2462.9	2759.9	3863.6	430.8	898.9	732.7	1694.6	337.2	149.4	601.4
93.6	1099.0	1305.7	1522.2	361.3	926.0	738.1	1257.6	538.4	191.7	614.9
414.7	2385.1	1987.4	1814.6	1393.1	1449.5	1629.4	2129.0	2213.0	1131.7	1356.0
82.7	2436.7	1748.5	1722.1	1248.3	1728.9	1409.9	2046.4	934.5	1342.5	1928.4
73.4	1419.1	1922.6	2480.3	1937.7	1451.3	2093.6	1653.4	762.5	341.3	1256.0
132.9	1532.1	1304.1	1673.7	444.3	812.1	756.5	1313.0	481.5	566.6	653.8
194.7	1407.0	1352.2	1480.5	825.2	1336.2	1293.3	1791.6	919.1	249.9	902.9
79.2	667.5	549.5	986.2	748.1	672.0	956.7	654.6	503.4	140.6	467.8
206.4	4988.2	3425.5	3711.8	2147.0	3190.1	2683.9	4760.3	1533.6	1568.8	3399.3
40.7	549.1	564.9	564.3	212.8	709.2	281.7	853.6	150.6	51.0	509.5
62.1	1152.8	1727.0	2489.2	989.6	1211.2	1501.7	936.2	457.1	138.1	798.8
54.7	698.6	903.3	953.7	474.8	773.8	752.3	978.0	342.0	188.9	861.1
44.0	1104.7	900.5	1065.1	481.4	741.7	1064.6	734.7	228.3	91.0	483.0
131.9	2499.1	1593.0	1815.9	2014.7	2347.9	2128.2	2751.3	720.3	1040.2	1917.7
48.6	796.1	680.2	591.7	529.8	697.8	984.5	780.8	230.3	158.4	401.5
55.0	1033.3	1172.8	1618.2	385.3	282.1	705.7	565.7	204.9	90.6	406.2
48.2	1307.5	1791.9	1678.7	1448.0	1357.3	1664.2	1721.5	557.8	1718.8	1468.2
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44.2	91.1	32.9	42.5	36.6	41.6	49.1	95.4	30.9	33.7	65.0
206.4	3052.9	2473.7	2674.9	1807.3	2299.2	2252.2	3978.0	1303.0	1144.2	2453.0
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133.9	1522.5	1655.9	1935.9	676.1	1048.3	1287.5	1887.4	1714.1	389.4	877.8
93.4	2050.6	2361.4	2902.2	2362.7	1895.0	3087.8	2753.8	994.7	1056.3	1602.7
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48.3	213.4	223.8	179.6	156.8	294.0	229.4	280.9	127.7	65.8	114.0
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51.9	1943.2	1495.5	1898.8	1411.0	1485.0	1177.1	1634.7	2741.1	1477.8	1144.0
237.0	3819.7	3444.5	3827.8	2529.1	2799.0	3029.5	3649.1	1117.1	1149.2	2674.6
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1936.7	1561.0	2163.9
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397.5	247.7	117.3
5957.2	3451.2	4087.5
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1454.0	2738.7	2468.1
2017.0	1141.6	936.5
1516.5	1398.1	1013.9
1858.0	997.7	1395.4
1545.5	1362.4	4262.6
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1412.2	902.6	789.8
1487.2	530.6	669.3
307.1	224.9	197.2
2073.4	1083.5	1013.6
998.2	1761.0	1621.7
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EU767437.1 gg_id:314562 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C2 EU767
EU458543.1 gg_id:292388 spotted hyena feces clone HY2_h02_1 EU458
GQ492812.1 gg_id:574579 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU768519.1 gg_id:320344 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY082451.1 gg_id:73751 Bacteroides sp. str. 265d AY082
EU459616.1 gg_id:298021 ring-tailed lemur feces clone RT_aai09c10 EU459
EU761599.1 gg_id:318214 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A1 EU761
EU768407.1 gg_id:315901 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY976899.1 gg_id:123455 human cecum mucosal biopsy clone K545 AY976
DQ803835.1 gg_id:196080 human fecal clone RL200_aai58h11 DQ803
DQ456053.1 gg_id:158706 pre-adolescent turkey cecum clone CFT112H3 DQ456
FJ978637.1 gg_id:466274 feces clone CL_F_309 FJ9786
FJ372099.1 gg_id:369529 feces adult twins and mothers; TS9 clone TS9_a01g04 FJ3720
EU768092.1 gg_id:308644 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
X89217.1 gg_id:1988 Bacteroides sp str. BV-1 X89217
EU768194.1 gg_id:350389 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
EU722740.1 gg_id:334393 Bacteroides finegoldii str. B16 EU722
EU767054.1 gg_id:355760 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU767
GQ492136.1 gg_id:583117 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU766982.1 gg_id:307849 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
DQ456041.1 gg_id:158667 pre-adolescent turkey cecum clone CFT112F11 DQ456
EU530393.1 gg_id:268332 mucosa adherent and invasive microbes adenoma colorectal cancer profile non-ader EU530
AY979572.1 gg_id:121549 human transverse colon mucosal biopsy clone M241 AY979
FJ363227.1 gg_id:359702 feces adult twins and mothers; TS148 clone TS148_a04g03 FJ3632
EU768143.1 gg_id:355581 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
FJ370558.1 gg_id:363236 feces adult twins and mothers; TS57 clone TS57_a02e03 FJ3705
DQ806375.1 gg_id:197731 human fecal clone RL186_aan91d07 DQ806
AY549431.1 gg_id:113854 Bacteroides denticanoris str. B78 AY549
EU768015.1 gg_id:314364 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU768
AY895191.1 gg_id:111421 Bacteroides thetaiotaomicron str. 3731 AY895
FJ363131.1 gg_id:358493 feces adult twins and mothers; TS148 clone TS148_a03e01 FJ3631
EU764778.1 gg_id:322273 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EU763101.1 gg_id:319092 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A9 EU763
EF604959.1 gg_id:228420 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6049
EU764460.1 gg_id:345223 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
AB253731.1 gg_id:172821 Bacteroides salanitronis str. JCM 13657 BL78 AB253
DQ799526.1 gg_id:192839 human fecal clone RL305aal87c11 DQ799
EU772839.1 gg_id:333981 Bush dog feces clone bdog1_aai77e11 EU772
FJ978508.1 gg_id:433947 feces clone CL_F_038 FJ9785
EU766840.1 gg_id:347808 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
EU764666.1 gg_id:307730 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764

10793.1	5286.7	4666.4	6090.9	4509.7	4671.8	5280.4	4748.1	9686.3	4391.6	5321.3
92.1	2264.4	2719.1	3366.7	1456.3	1620.6	1471.2	1940.1	1148.8	570.4	1097.0
209.3	4437.1	3669.0	4096.4	2019.2	3144.3	2807.2	4234.2	2015.6	1511.7	2984.2
122.8	3852.4	3954.4	4609.8	2700.9	2747.2	3876.3	3421.0	1689.2	1077.9	3899.9
66.2	127.4	168.6	119.3	46.2	330.1	31.0	419.3	81.1	118.1	174.1
157.9	2168.6	2571.6	2234.3	1587.1	1779.3	2911.5	2370.1	1442.4	266.3	1886.4
2990.9	1519.2	1585.5	1736.2	1183.3	1438.1	1437.7	1897.7	1343.4	888.9	1204.2
194.4	2733.3	2799.0	3030.8	1709.7	1993.7	2167.3	2854.4	927.4	969.9	1906.9
39.0	53.9	32.1	28.6	28.3	21.6	21.3	44.7	18.8	17.7	20.7
34.2	30.1	54.9	58.8	31.5	44.9	34.3	31.3	24.2	28.0	33.2
42.7	22.0	21.9	26.0	23.3	21.7	20.0	17.3	25.3	22.8	29.1
49.6	61.1	109.8	74.1	134.2	86.1	153.4	43.1	22.9	18.9	54.5
115.9	825.9	1318.1	970.9	539.2	1234.4	1117.2	1270.9	1051.2	440.4	1144.7
239.8	3843.3	3500.1	3899.4	2546.8	2739.1	3022.9	3700.2	1102.0	1151.7	2558.6
59.6	2290.3	1826.6	1808.0	1443.2	1708.8	1674.1	2522.9	864.1	1705.1	1553.1
32.8	107.1	89.9	60.8	162.6	124.3	194.3	354.9	19.0	48.2	187.1
92.4	850.7	740.7	927.9	392.7	750.5	624.3	919.0	329.4	206.7	456.8
63.0	321.7	115.8	129.3	52.9	118.9	90.3	152.6	33.3	29.0	93.6
123.3	1899.0	1945.8	2929.2	1051.1	1471.2	1038.6	2562.0	720.5	243.0	1672.9
240.0	4492.9	4155.1	4456.1	3295.3	3349.3	3853.7	4255.4	1510.6	1610.7	3625.4
119.0	2324.3	2955.5	4347.5	2503.8	2751.8	2843.9	3467.6	2699.2	1353.2	4077.0
80.2	470.5	645.9	644.0	420.5	576.8	750.1	698.9	249.2	87.7	1022.7
2467.8	2022.8	2021.4	2393.9	1520.5	2099.8	2036.0	2440.9	2467.1	1445.7	1865.2
50.0	860.7	621.2	580.8	355.9	643.4	283.5	984.3	189.7	50.1	966.5
217.4	1006.2	1024.6	1185.2	925.5	940.1	1198.8	850.4	656.7	195.1	936.0
118.6	1609.1	1849.8	1493.6	797.8	1185.4	874.6	1801.6	1393.9	731.2	1114.7
59.1	578.2	434.6	420.6	444.1	450.3	705.6	386.3	200.1	155.2	184.0
61.2	272.0	356.8	366.2	158.9	276.0	189.3	346.3	66.9	46.2	158.4
135.7	3198.6	2642.3	2689.8	1636.0	2567.4	2605.8	3079.0	723.6	318.2	2407.2
229.7	7418.1	6270.1	7249.7	5470.6	5065.5	7431.9	5784.6	4797.2	6813.0	6309.1
286.2	6019.8	5892.9	6182.9	5388.0	5281.0	6365.8	6348.2	8259.2	4854.2	5599.9
189.1	2267.1	2633.7	3127.6	1943.8	1906.7	2296.6	2601.8	1012.1	892.8	2166.3
77.0	1142.7	1237.3	1548.8	598.6	632.2	740.0	858.1	275.3	249.2	779.2
76.9	642.4	569.9	759.3	227.4	208.0	470.6	384.8	310.9	132.6	163.5
125.1	2643.3	3579.1	4072.0	2389.9	2095.6	3346.8	2573.3	1195.0	1307.3	2498.1
25.8	27.5	52.9	66.9	36.4	24.8	46.8	27.2	24.9	22.0	24.9
526.0	2394.2	2304.2	2112.0	2217.7	2397.5	1558.5	2592.9	1074.4	657.0	1501.8
67.7	1429.0	1750.3	2598.3	1600.9	1726.9	1736.2	1451.5	1103.0	663.9	1140.5
109.7	3029.7	2851.8	2783.2	2144.4	2895.4	2470.4	2419.2	4195.9	3354.7	2870.6
204.7	3360.0	2758.8	3194.0	1578.3	2770.5	2092.2	3750.1	1165.2	1165.1	2567.5
398.0	2944.3	3234.9	3706.4	2676.7	2527.9	3301.9	2864.6	1937.6	1133.3	2506.7

5046.0	5695.9	5207.9
2638.2	1617.5	998.4
6025.5	2707.2	2113.2
3243.8	4027.2	4256.7
318.2	131.5	55.2
2665.6	1170.3	3170.7
2749.9	2685.3	3136.0
3571.3	1609.5	1706.7
20.6	20.3	36.8
47.3	67.8	49.2
20.1	24.6	15.4
60.7	68.4	85.2
895.3	903.4	840.7
4498.9	1973.7	1917.5
2050.9	1564.6	1368.2
162.7	111.7	116.3
1222.9	688.3	1206.7
167.9	160.8	86.1
2301.8	1334.4	541.1
4858.8	2446.9	2694.8
2605.6	3204.3	2746.6
423.4	608.2	353.4
3429.9	3372.2	4125.9
856.8	485.2	343.7
1188.8	680.2	817.1
1487.2	1474.0	780.5
598.9	388.5	276.6
284.3	238.3	130.3
2684.5	1539.5	782.3
5167.0	4546.9	6131.2
5252.9	5229.6	5108.8
2525.0	2126.1	2045.0
1158.9	658.1	433.0
986.6	356.2	161.0
3201.2	2541.8	2786.6
31.9	49.7	66.3
3296.3	2484.2	2442.1
1417.5	1213.4	1693.7
2587.4	2249.6	3271.5
5116.1	1920.4	2035.7
3828.8	3240.5	3387.1

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EU763007.1 gg_id:315093 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU763
GQ867528.1 gg_id:568757 and prevalence blaTEM genes Arctic seals colon content clone CSH32 GQ867
EU764580.1 gg_id:341721 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EF071154.1 gg_id:187179 library survey and quantitative measurement major mucosa- IBD human colonic muc EF0711
AJ811981.1 gg_id:186113 human biopsies Human ulcerative colitis biopsy clone UC9-44 AJ8119
EU762570.1 gg_id:321669 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762
GQ492505.1 gg_id:582063 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ797137.1 gg_id:195781 human fecal clone RL386_aao87d11 DQ797
AY981632.1 gg_id:126962 human sigmoid colon mucosal biopsy clone L880 AY9816
AB253733.1 gg_id:169036 Bacteroides gallinarum str. JCM 13659 C43 AB253
EU763053.1 gg_id:310481 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU763
EU764049.1 gg_id:312952 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU764
EU764629.1 gg_id:340796 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU763817.1 gg_id:315105 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A EU763
EU766989.1 gg_id:331197 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ879857.1 gg_id:466785 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
GQ079282.1 gg_id:430193 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230g(GQ079
EU768441.1 gg_id:336580 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
DQ456092.1 gg_id:158906 pre-adolescent turkey cecum clone CFT114C11 DQ456
FJ978643.1 gg_id:418340 feces clone CL_F_315 FJ9786
DQ456331.1 gg_id:158660 pre-adolescent turkey cecum clone CFT212B1 DQ456
EU767474.1 gg_id:355274 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
EU767881.1 gg_id:315203 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
FJ363181.1 gg_id:358119 feces adult twins and mothers; TS148 clone TS148_a04b04 FJ3631
DQ824075.1 gg_id:187574 human fecal clone RL204_aaj59a07 DQ824
AY895200.1 gg_id:112005 Bacteroides thetaiotaomicron str. 8669 AY895
EU768687.1 gg_id:354209 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU768
EU762810.1 gg_id:339814 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762
FJ978484.1 gg_id:451077 feces clone CL_F_007 FJ9784
EU764663.1 gg_id:347381 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B1 EU764
EU765769.1 gg_id:331820 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EU767849.1 gg_id:307633 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C EU767
EU766915.1 gg_id:336052 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C1 EU766
FJ368848.1 gg_id:365266 feces adult twins and mothers; TS4 clone TS4_a01c10 FJ3688
EU762885.1 gg_id:342841 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A› EU762
EU009790.1 gg_id:258109 intestinal microbiota domestic and wild turkeys turkey cecum clone DTB_X30 EU009
GQ079223.1 gg_id:456662 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1230a(GQ079
FJ681664.1 gg_id:530494 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816
DQ456114.1 gg_id:158839 pre-adolescent turkey cecum clone CFT114E11 DQ456
EU622718.1 gg_id:279192 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
GQ897967.1 gg_id:563880 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897

91.8	1599.4	2112.1	2562.1	937.6	1154.3	1355.1	1628.1	413.0	240.0	1325.5
200.0	3035.9	3544.2	3916.5	1975.0	3278.6	3048.4	3507.6	1405.3	882.8	2705.0
134.4	3180.6	3885.6	4347.9	2117.0	3036.1	2749.9	3964.4	1224.0	1296.7	2698.3
46.8	1052.0	1282.3	1217.7	1013.8	838.8	1411.2	1582.7	413.7	91.9	1198.9
104.2	1691.2	2056.6	2638.5	888.9	1189.2	1345.0	1729.5	468.9	248.8	1294.9
123.2	2083.8	2229.5	3092.5	1070.8	1455.6	1600.5	2092.8	659.7	415.1	1534.5
7030.6	9117.9	8558.2	8620.0	6485.2	7376.6	7900.1	6811.9	12372.0	9182.9	8377.4
68.4	448.8	326.4	220.4	112.5	363.1	186.8	490.0	83.5	73.2	124.6
780.1	1696.4	1735.9	2607.0	1380.7	1674.9	1660.5	2169.3	2466.3	1513.1	2337.7
99.7	2949.5	4086.7	3841.5	2188.3	3262.3	2719.8	3358.0	1083.2	1013.3	1848.0
220.8	3560.8	3227.7	3824.4	2706.5	2791.5	3024.9	3616.6	1117.4	1146.2	2668.8
62.9	186.0	190.9	174.7	173.0	366.0	261.5	307.7	123.5	58.4	126.0
89.6	2102.3	2441.0	2857.3	1303.9	1362.0	1834.7	1754.8	557.2	184.7	1575.3
8651.9	6576.1	5873.8	7385.5	6631.7	6166.1	6395.8	5486.2	14564.3	7848.0	7438.6
58.5	872.0	1313.7	1554.7	528.6	445.6	906.5	781.9	213.7	118.8	503.4
79.4	3127.8	3125.4	2767.3	2012.5	1949.1	3238.5	2591.2	1550.2	312.5	2007.5
64.9	1036.4	1364.7	1776.9	574.6	644.3	1042.9	953.8	252.3	150.7	664.5
226.7	3463.3	3142.4	3521.9	2361.0	2556.1	2819.1	3337.1	1032.3	992.8	2484.8
114.3	339.8	406.1	450.2	411.9	908.8	457.6	440.9	169.0	342.8	470.3
179.3	4380.4	3638.3	4036.4	2158.8	3502.4	2326.1	3192.4	2038.4	1702.0	2660.1
248.4	1194.3	1127.5	1555.5	819.1	1185.7	1042.6	1295.1	322.1	145.1	1207.6
86.5	1591.6	2072.0	2509.7	869.5	1134.9	1330.1	1595.1	434.7	236.3	1312.5
155.0	2233.9	2159.9	2443.8	1014.3	1480.2	1251.0	2217.0	795.2	662.9	1521.8
114.2	1881.7	2065.6	2695.2	1872.7	1855.3	2332.5	2222.0	1535.0	454.6	1458.4
49.1	80.8	51.1	129.8	24.6	16.3	25.5	59.7	13.5	12.8	18.6
48.3	18.1	18.2	15.6	13.9	12.8	14.9	14.0	17.9	20.6	13.9
174.8	4011.9	2376.2	2498.0	1480.3	2231.7	1892.6	3267.1	1494.9	1662.2	2351.3
335.1	2326.5	2524.3	3221.6	2048.7	1618.3	2992.3	1972.3	1152.1	1743.6	2168.3
315.9	5826.7	5889.7	6200.8	5066.8	6257.5	5294.9	5961.5	3234.7	2154.3	5925.2
185.8	2197.2	2532.1	2927.3	1724.9	1920.9	1933.8	2568.8	977.6	944.0	1996.9
94.9	2740.8	2175.3	2241.1	1503.6	1999.1	1781.3	2630.9	2727.0	1690.1	1913.7
707.5	5737.6	4397.5	4773.7	3705.1	4162.8	4625.2	5381.7	2269.4	1961.3	4595.1
154.8	1676.6	1304.8	1395.4	708.9	1199.5	1073.0	1746.2	854.1	1062.4	1033.6
61.7	1335.1	1282.2	1404.5	1282.6	1458.6	1345.8	493.8	805.4	1515.6	1136.8
64.5	1641.3	1847.2	2225.5	573.7	672.4	997.3	1111.9	403.7	846.4	571.7
30.4	42.5	47.5	50.0	33.2	43.4	41.2	134.3	97.6	20.2	33.0
58.8	772.8	1213.0	1453.3	475.8	416.7	825.7	613.4	206.1	121.7	423.4
90.9	2765.7	2205.0	3053.2	1779.8	4026.2	2101.1	3048.7	910.4	822.9	2360.4
45.9	413.8	298.3	210.0	190.5	284.8	216.7	582.4	172.6	101.0	150.0
171.0	1075.2	848.5	684.2	319.9	1242.2	538.3	1049.7	401.5	145.2	629.4
195.0	2510.2	2171.3	2713.3	1186.7	2294.6	1902.8	3334.4	1177.8	497.7	1812.1

2495.9	1334.9	950.6
3441.4	2821.7	6477.1
2850.3	2522.6	3144.0
936.0	1261.8	1464.7
2523.0	1378.0	1058.5
3314.7	1531.0	1270.0
6985.9	8303.4	7327.1
710.2	266.9	116.0
1354.7	2488.6	2424.8
3963.7	2125.7	2798.9
4454.9	1816.1	1758.0
256.6	191.8	183.3
2019.0	1627.2	1313.8
6804.1	6496.0	7798.5
1451.5	793.9	838.3
2233.5	1836.9	1446.5
1940.3	895.9	995.0
3949.3	1631.7	1434.2
855.9	499.8	566.6
3959.7	2212.3	2827.0
1198.4	897.7	1993.8
2409.6	1233.3	931.2
3013.7	1202.2	1249.5
2278.4	1677.5	1455.3
30.7	80.5	22.5
17.4	15.0	11.9
3969.1	1369.6	1216.0
2439.8	1761.1	2861.6
5626.1	3685.7	4883.0
2550.1	2033.8	1922.5
1920.3	1884.0	884.7
6383.6	3203.5	3461.5
1813.6	1016.2	1371.2
1295.6	855.8	897.7
1887.6	1182.1	1541.7
51.4	41.5	30.3
1332.7	685.6	734.9
2492.6	1504.1	2348.4
379.7	391.6	219.4
781.5	631.3	330.8
3632.9	1573.5	5938.9

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FJ363125.1 gg_id:367489 feces adult twins and mothers; TS148 clone TS148_a03d07 FJ3631
GQ448989.1 gg_id:577170 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
ABJL02000007.1 gg_id:350694 Bacteroides intestinalis str. DSM 17393 ABJL02
FJ363537.1 gg_id:361984 feces adult twins and mothers; TS149 clone TS149_a04d05 FJ3635
EU768677.1 gg_id:321309 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU768
AY975458.1 gg_id:122208 human ascending colon mucosal biopsy clone N861 AY9754
EU762666.1 gg_id:329247 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
AB264079.1 gg_id:196778 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-156 AB2640
EU468119.1 gg_id:303158 bush dog feces clone bdog3_aad68e04 EU4681
EU763236.1 gg_id:349090 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7632
EU762605.1 gg_id:341587 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU762
AY895199.1 gg_id:111709 Bacteroides thetaiotaomicron str. 7330 AY8951
EU763549.1 gg_id:308453 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7635
FJ372113.1 gg_id:363282 feces adult twins and mothers; TS9 clone TS9_a01h06 FJ3721
AF132263.1 gg_id:71331 adult human fecal matter clone adhufec355 AF1322
FJ683852.1 gg_id:531412 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6838
GQ898079.1 gg_id:583769 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ898
DQ807525.1 gg_id:174868 human fecal clone RL307_aam07f12 DQ807
FJ371831.1 gg_id:365819 feces adult twins and mothers; TS8 clone TS8_a02f10 FJ3718
GQ496623.1 gg_id:561253 Bacteroides faecis str. MAJ26 GQ496
AB050109.1 gg_id:46476 Bacteroides thetaiotaomicron str. JCM 5827T AB0501
FJ366386.1 gg_id:361304 feces adult twins and mothers; TS26 clone TS26_a02d07 FJ3663
EU009829.1 gg_id:240992 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_M48 EU0098
EU768350.1 gg_id:353533 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7683
EU767940.1 gg_id:342174 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C4 EU7679
AB490802.1 gg_id:563616 Bacteroides fluxus str. YIT 12057 AB4908
AJ608232.1 gg_id:145315 human biopsies ulcerative colitis biopsy clone UC7-16 AJ6082
EU766579.1 gg_id:341436 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
FJ366424.1 gg_id:366744 feces adult twins and mothers; TS26 clone TS26_a03a05 FJ3664
EU768600.1 gg_id:333709 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone C5 EU7686
EU766592.1 gg_id:319657 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B5 EU7665
DQ806938.1 gg_id:187639 human fecal clone RL198_aaj75g03 DQ806
EU763003.1 gg_id:346904 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7630
DQ793722.1 gg_id:182419 human fecal clone RL246_aai76b11 DQ793
GQ493546.1 gg_id:551340 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU762582.1 gg_id:343759 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A> EU7625
EU763718.1 gg_id:349576 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone A4 EU7637
EU290711.1 gg_id:240737 microbial structure biogeochemical contrasting shelf sediments Namibian upwelling EU2907
DQ647061.1 gg_id:238065 Anaerophaga sp. str. TC371 DQ647
FJ231145.1 gg_id:342042 Microbial Laguna Lejia Salar de Aguas Calientes and summit Simba volcano three altit FJ2311
FJ202953.1 gg_id:349548 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029

982.5	2027.8	2155.6	2659.5	2255.5	2205.0	2518.6	2732.3	1208.5	1300.9	2463.0
36.0	302.4	201.7	172.4	142.7	330.6	323.8	267.7	75.1	44.6	83.5
322.5	5968.0	4295.4	4159.5	4175.1	5423.2	3741.6	4951.8	8395.9	5778.9	5253.1
49.2	1158.9	1297.7	1808.2	1180.8	1154.1	1368.3	1603.4	908.9	198.4	864.1
275.9	3529.1	3442.7	3826.4	2708.8	2798.3	3030.7	3648.6	1115.9	1147.6	2672.9
136.5	1283.6	1401.4	1807.8	275.9	1111.6	592.4	1559.6	439.6	212.6	1087.8
104.2	1604.0	1614.4	1598.2	1143.6	1593.5	1121.5	1570.2	438.3	912.4	1651.0
50.9	172.5	161.9	199.5	97.2	117.6	141.1	129.9	71.4	29.2	58.9
285.5	1275.1	1480.3	2274.4	644.7	1294.1	1000.8	1621.4	605.7	136.6	672.4
149.1	4386.9	4668.2	5418.1	3332.5	3321.3	5350.1	4645.9	3224.7	3775.0	5166.1
287.1	4834.0	3961.0	4652.3	3522.7	3689.7	4799.5	5027.1	2209.5	1860.6	3731.7
851.3	8146.4	6850.6	7130.4	5159.2	6508.1	6420.0	6514.2	8476.4	5945.9	7217.4
143.0	2875.0	3142.0	3991.2	884.0	1714.6	1193.3	1907.0	750.1	1452.0	1042.0
253.1	3572.6	3842.6	3636.7	2587.4	3350.0	3628.9	3078.6	2746.3	2668.8	3135.4
653.2	1486.5	1280.2	1782.7	328.6	1198.5	680.2	1380.1	515.7	314.6	976.0
467.4	2102.5	2047.1	2212.4	1808.7	1651.5	2586.3	1581.7	2008.4	1805.1	1823.3
51.7	477.3	1193.0	939.7	424.9	344.1	488.1	621.6	376.5	81.5	195.7
153.8	2002.5	1800.4	2124.6	1712.7	1716.8	1529.7	1960.5	1312.0	924.3	1501.1
47.3	586.0	357.0	355.5	264.4	337.3	174.0	474.1	173.2	53.3	306.1
54.9	28.7	25.4	24.1	22.9	23.9	22.0	18.3	29.8	28.0	26.8
76.5	264.0	394.2	503.2	64.7	337.0	115.1	350.7	167.5	50.9	190.2
621.4	2187.5	2245.2	2790.8	2199.4	2268.3	2697.7	2429.0	1597.5	942.2	1922.1
126.6	2442.5	2593.6	3041.3	769.6	2545.7	1119.9	3050.8	857.9	603.8	1565.2
148.1	2090.7	1549.5	2095.5	772.7	1152.7	984.6	1649.8	531.1	484.9	1011.4
88.7	1185.7	1479.1	1655.1	779.4	792.6	1037.3	1094.7	347.9	193.6	986.5
73.8	544.4	623.7	637.9	205.2	600.0	228.0	541.2	136.2	266.5	177.2
168.0	1928.9	2282.0	2589.5	1652.0	1885.1	2140.5	1841.4	798.7	729.9	1649.4
221.7	2885.4	2788.7	3620.3	3005.3	2234.4	3194.9	2892.4	1018.9	786.8	2650.7
55.5	730.0	493.7	515.8	498.6	519.9	669.0	603.1	249.1	90.2	355.4
249.2	4332.0	3966.0	4324.9	2928.1	3145.5	3657.3	3960.8	1345.1	1576.2	3304.3
95.8	2738.3	3967.4	4825.7	1727.6	2493.7	2880.3	3015.7	828.1	640.2	2067.2
66.5	1064.0	1190.3	1306.1	1029.1	1012.7	1503.3	1038.1	621.2	265.9	1191.1
82.7	1656.6	2169.7	2485.6	1135.0	1254.0	1450.7	1788.7	472.0	318.1	1362.1
136.8	3256.2	2581.6	3272.3	1398.0	1787.7	2201.5	3538.4	824.3	1052.2	3173.8
55.4	532.1	826.3	823.6	843.0	841.8	819.2	782.4	277.1	109.9	468.7
96.9	4815.1	3186.6	3656.7	2744.1	3474.0	2798.3	3999.7	2507.0	1881.7	3402.8
80.3	1565.8	2024.9	2507.2	959.6	1132.5	1428.2	1551.5	401.8	216.8	1254.4
112.6	4043.6	4109.4	5043.6	5284.8	4441.4	6164.9	5261.5	2530.3	2115.7	4805.5
244.0	4369.6	6099.4	5180.4	5388.9	5039.5	6774.1	4837.8	3417.0	3573.9	5117.5
182.9	3282.5	3784.7	4088.4	4616.4	3245.2	4960.4	3441.3	2572.0	2342.6	2507.6
1719.5	3821.3	3505.5	4159.3	3449.0	4461.4	4207.9	3508.9	4198.4	3987.5	4180.2

2099.0	2896.9	3095.1
425.4	149.7	83.4
5155.9	4247.2	3601.4
1585.2	975.9	964.8
4469.7	1831.4	1783.0
1472.7	855.2	1162.4
1387.6	872.7	728.3
150.1	158.9	183.0
2022.3	1530.4	1398.9
5209.2	3892.3	6215.8
5901.1	2784.8	3367.1
6043.3	5522.0	7047.5
3555.3	2518.5	7945.4
3469.4	2784.9	2757.3
1701.4	1560.9	1773.7
1426.7	2510.1	2904.0
267.4	349.2	284.8
2816.3	1408.5	1425.5
485.8	433.0	266.4
16.9	18.7	18.5
714.9	306.1	252.6
2212.5	2561.3	3309.2
3956.3	1703.7	3160.8
2209.5	1031.9	1000.5
1566.4	896.2	825.0
665.2	483.5	474.5
2051.6	1704.4	1757.0
2851.4	1979.4	1656.2
614.2	577.5	847.1
4635.8	2211.4	2684.3
4716.5	2970.4	2318.9
1127.3	898.4	1623.7
2707.6	1325.8	1020.6
2483.0	2308.6	3617.6
693.6	691.6	570.3
3954.7	2768.1	1691.6
2592.1	1192.8	1097.8
3066.4	2675.1	4273.6
4682.7	4355.5	5238.7
2971.2	3273.2	3770.3
3293.4	3841.6	3935.0

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FJ202774.1 gg_id:315129 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
DQ336982.1 gg_id:146313 subsurface water clone EV818CFSSAHH27 DQ336
AJ784993.1 gg_id:108748 Alkaliflexus imshenetskii str. Z-7010 AJ7849
FJ675203.1 gg_id:522481 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
AF449260.1 gg_id:61849 Riftia pachyptila's tube clone R76-B58 AF4492
EF559098.1 gg_id:226425 mesophilic anaerobic digester clone C35_D7_L_B_F05 EF5590
AB237697.1 gg_id:139833 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB2376
FJ716917.1 gg_id:540416 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7169
FJ202485.1 gg_id:350582 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
EU052266.1 gg_id:251381 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
FJ516921.1 gg_id:509721 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
AJ441218.1 gg_id:57462 hydrothermal vent polychaete mucous clone P. palm C/A 221 AJ4412
DQ517535.1 gg_id:161206 Anaerophaga sp. str. HS1 DQ517
GQ261777.1 gg_id:549338 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
FJ716947.1 gg_id:542702 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7169
AJ418048.1 gg_id:51657 Anaerophaga thermohalophila str. Fru22 AJ4180
EF590038.2 gg_id:228045 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5900
DQ141183.1 gg_id:138582 Ruminofilibacter xylanolyticum str. S1 DQ141
DQ676403.1 gg_id:224027 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
FJ024713.1 gg_id:310419 Copper affects reduction and genetic enriched sulfate reducing coastal sediments exp FJ0247
NC_011565.1 gg_id:363475 Candidatus Azobacteroides pseudotrichonymphae genomovar. CFP2 NC_01
AB231289.1 gg_id:149530 Bacteroidales symbiotic Oxymonas sp. gut termite Neotermes kosunensis flagellatec AB2312
AB231016.1 gg_id:148689 termite gut wall clone HsW01-025 AB2310
AB231023.1 gg_id:148038 termite gut wall clone HsW01-044 AB2310
AB462742.1 gg_id:540265 Complex coevolutionary history symbiotic Bacteroidales various protists termites fla AB4627
AY571449.1 gg_id:114426 termite gut clone RsaHf397 AY5714
AB088922.1 gg_id:78150 termite gut homogenate clone Rs-B92 bacterium AB0889
AB192159.1 gg_id:144700 termite gut homogenate clone RsTz-18 AB1921
AB299533.1 gg_id:243363 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB2995
AB088936.2 gg_id:77941 termite gut homogenate clone Rs-B48 bacterium AB0889
AB231049.1 gg_id:148392 termite gut wall clone NkW01-005 AB2310
AB198444.1 gg_id:135574 termite gut wall fraction clone RsW01-002 AB1984
AB192208.1 gg_id:143532 termite gut homogenate clone RsTu1-13 AB1922
AB062838.1 gg_id:39177 termite gut homogenate clone BCf7-17 AB0628
DQ009684.2 gg_id:143053 termite gut homogenate clone R38A14 DQ009
AB192204.1 gg_id:141732 termite gut homogenate clone RsTu1-35 AB1922
AB088932.1 gg_id:77928 termite gut homogenate clone Rs-J02 bacterium AB0889
AB194938.1 gg_id:142402 Identification ectosymbionts distinct lineages Bacteroidales attached protists termit AB1949
AB062835.1 gg_id:38316 termite gut homogenate clone BCf7-02 AB0628
GQ502506.1 gg_id:535826 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
AB194939.1 gg_id:143775 Identification ectosymbionts distinct lineages Bacteroidales attached protists termit AB1949

48.4	741.3	1310.0	1202.1	1174.5	1113.8	1580.5	1073.9	846.5	1419.6	632.7
2411.6	2742.0	3328.6	3557.2	2998.5	3652.2	3423.0	3015.0	2086.4	7695.5	2949.9
733.5	5367.5	4167.3	4884.8	5548.4	4646.4	5842.6	4402.9	3256.6	3094.3	3869.4
8509.6	5047.0	5242.4	5788.1	4954.0	5476.3	5446.3	4372.7	7989.0	6142.3	6934.7
84.2	84.7	132.0	123.3	103.7	132.7	109.2	150.0	104.7	38.5	86.3
135.9	4494.6	3755.2	3248.7	4198.0	3387.5	4489.9	2944.1	4241.7	2275.2	2866.5
240.2	2698.6	3467.8	3641.3	2465.2	2376.1	3751.5	3207.8	2492.0	1345.4	3414.3
144.0	3580.2	4387.0	4572.0	4308.3	3763.6	4640.0	4257.1	3154.7	1561.3	3599.4
237.6	1883.9	2673.5	2870.1	2222.5	2424.4	2647.9	2931.1	2090.4	2476.5	2429.9
3882.5	5281.4	5011.4	5234.7	4389.7	4381.1	5289.9	4967.4	5889.2	7151.0	5036.1
537.2	8305.9	7961.8	8621.3	8558.8	9977.2	8283.7	8604.8	10136.9	8041.5	11755.9
41.5	55.3	55.6	58.2	54.0	63.9	46.4	98.6	42.4	37.6	67.5
56.5	44.3	43.0	49.3	58.2	46.4	39.3	46.8	44.5	29.3	28.4
1091.8	6179.2	5763.3	6255.4	7696.2	6457.1	8148.5	6661.8	5690.5	5840.3	5661.6
292.5	4044.5	4480.9	4510.1	4852.7	3796.5	4768.3	4060.0	3872.2	3773.1	3642.1
1197.1	4877.4	6153.5	5827.3	5187.7	4720.4	6011.6	4947.8	2937.8	2326.3	5702.3
71.4	1600.2	2033.8	1493.5	1496.2	1754.2	2198.1	1557.1	1415.9	872.8	1405.4
1002.3	5215.5	6856.8	5980.3	6153.3	5454.2	8438.0	6081.1	3625.0	2459.2	6206.7
33.3	166.6	277.7	609.4	298.0	267.9	286.0	320.4	117.6	81.2	378.9
587.9	3186.1	4107.4	3700.9	3445.3	3610.0	3281.8	3801.7	3201.5	4319.4	3191.4
63.1	537.8	1017.5	1141.3	332.7	643.3	744.9	1133.4	787.5	39.8	938.6
288.0	662.2	426.9	317.6	638.7	496.2	3020.2	410.7	772.1	225.1	191.2
43.3	81.9	141.2	65.7	60.7	97.0	105.3	101.1	70.6	19.4	30.8
47.6	93.4	154.4	105.8	134.8	77.8	89.0	88.3	36.7	60.8	66.1
56.6	316.4	396.9	496.9	201.0	292.2	260.0	421.4	240.1	127.6	233.5
39.7	20.2	22.1	24.4	25.8	21.5	26.5	20.5	7.1	10.7	19.5
46.3	441.4	802.1	743.8	596.1	447.6	710.5	640.5	370.9	407.0	580.7
50.8	419.2	278.5	246.3	230.8	225.8	321.9	347.2	298.2	220.2	192.6
101.0	2916.9	2902.1	3578.6	3804.2	3058.9	3975.9	2955.5	4002.1	2774.5	2510.6
35.6	296.8	215.8	315.3	142.6	193.4	238.7	260.9	106.2	52.3	151.6
45.4	377.7	534.6	576.8	986.0	416.6	475.9	411.2	149.6	73.4	263.1
93.9	2914.3	5825.3	5050.7	4011.2	3921.1	6097.7	4301.9	1341.4	678.3	4532.6
55.2	109.7	102.1	96.5	79.1	125.6	157.5	135.9	71.7	39.0	65.4
180.6	1711.5	1719.3	2036.4	1394.5	1929.5	2049.1	1892.1	1845.7	1686.2	1297.3
46.5	223.6	405.1	375.1	162.4	221.9	208.4	561.1	152.6	153.7	320.5
48.9	1030.0	1119.2	855.4	603.9	1220.4	930.2	1793.3	852.9	97.4	717.7
42.8	128.5	243.1	201.0	317.7	201.7	215.5	260.8	84.4	161.3	21.5
45.1	44.1	57.9	96.7	72.6	84.8	56.7	61.1	45.6	24.6	60.0
47.3	442.1	1172.2	1251.1	552.0	627.8	935.2	1015.5	318.7	125.7	592.2
38.1	755.8	922.1	1252.4	1089.5	738.2	1962.4	1095.6	238.7	254.8	488.3
127.4	2650.7	2806.0	3303.1	2739.4	2764.9	3409.0	3271.8	4485.9	2356.7	2309.1

558.3	903.8	592.1
3103.2	3380.6	4115.8
4752.3	4567.1	5544.9
3840.9	5747.8	4778.7
91.7	141.6	59.6
3082.3	2784.6	3075.0
2180.2	2990.4	2333.3
3530.9	3827.1	3683.3
2542.6	2948.0	2671.6
4043.8	5633.7	5561.2
8181.8	6606.3	6049.5
35.7	61.9	53.5
42.2	67.9	120.2
5240.8	5231.7	5905.0
3172.3	3014.9	3997.2
4118.5	4923.6	6438.3
1975.3	1479.4	1630.9
5397.8	5471.6	7149.0
183.3	150.8	64.5
3616.2	4012.3	3111.3
653.1	1108.5	276.0
305.9	546.0	446.0
60.4	103.6	78.1
84.3	225.8	211.6
242.8	428.4	480.0
23.3	14.2	18.1
356.5	747.7	631.5
174.1	357.7	364.7
2943.3	3586.0	2609.6
249.3	189.6	108.2
465.0	421.7	531.2
2966.7	3016.0	6072.0
86.3	215.8	355.0
1423.2	2278.2	1780.7
332.3	646.9	221.8
1440.6	1537.3	1074.3
197.5	236.7	130.9
56.3	79.5	83.0
475.6	1291.9	3739.8
594.5	601.5	1504.3
2730.1	2871.8	3147.9

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g__Dysgonomonas
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g__Parabacteroides
g__Parabacteroides

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s__unclassified	69199
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s__unclassified	69369
s__unclassified	69573
s__unclassified	69604
s__Dysgonomonas gadei	68916
s__Dysgonomonas mossii	68972
s__unclassified	68517
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s__unclassified	68574
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s__unclassified	68666
s__unclassified	68825
s__unclassified	68956
s__unclassified	69094
s__unclassified	69171
s__unclassified	69196
s__Parabacteroides distasonis	69646
s__Parabacteroides distasonis	69796

AB231017.1 gg_id:146610 termite gut wall clone HsW01-007 AB2310
AB088923.2 gg_id:77598 termite gut homogenate clone Rs-D66 bacterium AB0889
AB231290.1 gg_id:150115 Bacteroidales symbiotic Oxymonas sp. Neotermes kosunensis flagellated protist gut AB2312
AB192206.1 gg_id:141613 termite gut homogenate clone RsTu1-23 AB1922
AB088943.1 gg_id:78288 termite gut homogenate clone Rs-D29 bacterium AB0889
AB088935.1 gg_id:78052 termite gut homogenate clone Rs-M16 bacterium AB0889
AB262559.1 gg_id:186572 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB262557.1 gg_id:186877 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB262558.1 gg_id:191537 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB262556.1 gg_id:193546 Cospeciation triplex symbiosis protists (Pseudotrichonympha spp.) hosts and their er AB2625
AB548675.1 gg_id:524197 Dysgonomonas gadei str. JCM 16698 AB5486
NR_025484.1 gg_id:570833 Dysgonomonas mossii str. CCUG 43457 NR_025
GQ502485.1 gg_id:593371 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
AY643492.1 gg_id:107721 Dysgonomonas wimpennyi str. ANFA2 AY6434
FJ823922.1 gg_id:524743 Controlling accumulation fermentation inhibitors biorefinery recycle water microbial FJ8239
AB234423.1 gg_id:147708 termite gut homogenate clone MgMjD-090 AB2344
AB199571.1 gg_id:110974 river water Japan clone RVW-04 AB1995
EF608552.1 gg_id:227900 predatory Poecilus chalcites their response lab rearing and antibiotic treatment diges EF6085
GQ502504.1 gg_id:535685 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
AB288912.1 gg_id:202454 termite gut homogenate clone BOf7-08 AB2889
DQ856517.1 gg_id:239708 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1O DQ856
AB234397.1 gg_id:148589 termite gut homogenate clone MgMjD-025 AB2343
AB288875.1 gg_id:203234 termite gut homogenate clone BOf1-02 AB2888
AY953156.1 gg_id:114705 anaerobic swine lagoon clone B-1AL AY9531
AJ576373.1 gg_id:98890 hindgut homogenate Pachnoda ephippiata larva clone PeH10 AJ5763
AB548674.1 gg_id:530785 Dysgonomonas capnocytophagoides str. JCM 16697 AB5486
EF602792.1 gg_id:233332 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6027
AY916310.1 gg_id:112884 human sigmoid colon biopsy clone NX93 AY9163
AY916145.1 gg_id:113167 human transverse colon biopsy clone M048 AY9161
DQ815520.1 gg_id:164344 mouse cecum clone aab42b08 DQ815
EU728709.1 gg_id:347862 Odoribacter splanchnicus str. DJF_B089 EU7287
GQ402138.1 gg_id:544305 alpacas and sheep forestomach clone SH12 GQ402
AF001749.1 gg_id:1923 rumen clone RF17 AF0017
AB009214.1 gg_id:1943 rumen clone RFN67 bacterium AB0092
EU794157.1 gg_id:341926 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_P8 EU7941
AB009202.1 gg_id:2037 rumen clone RFN46 bacterium AB0092
EU469046.1 gg_id:288192 Speke's gazelle feces clone SP2_d12_3 EU4690
AB009197.1 gg_id:1969 rumen clone RFN41 bacterium AB0091
EU794092.1 gg_id:330762 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O3 EU7940
EF403021.1 gg_id:210264 human fecal clone SJTU_B_15_68 EF4030
GQ016637.1 gg_id:493030 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ016

47.4	151.3	158.5	190.6	167.0	116.6	196.5	124.0	40.4	50.6	77.2
82.5	1182.8	1326.1	1708.0	700.1	1188.2	1017.6	1659.1	658.8	279.9	1253.4
41.8	142.6	111.9	116.8	130.3	90.6	187.6	203.1	60.6	25.4	47.5
93.8	1052.1	790.3	1028.0	865.5	755.9	234.2	827.6	460.7	451.7	447.4
49.1	100.7	239.5	167.0	172.2	187.9	162.3	124.0	56.0	90.8	98.0
54.6	223.4	115.0	170.4	86.9	179.1	248.9	144.0	50.5	35.9	80.1
42.4	816.4	1043.1	1660.7	82.2	902.2	680.4	1472.0	469.4	22.6	1198.4
60.1	1846.5	1373.8	1750.8	1209.6	1338.3	975.3	1449.3	1334.6	668.8	932.4
250.5	4864.6	5199.7	7455.3	4801.0	5086.4	5396.5	5641.5	2976.8	1727.9	5653.1
91.9	3482.7	3284.2	3901.7	3626.5	3503.0	3598.0	3717.4	3270.5	2056.6	3531.7
35.6	561.9	930.4	913.4	1388.9	842.7	1920.8	651.6	222.9	132.5	419.4
154.5	1887.2	1864.1	2126.4	1070.8	1924.0	2174.5	2494.0	822.2	710.4	1405.7
235.3	1864.5	1483.8	2539.8	2183.7	2099.1	2875.4	2107.0	1634.8	925.3	2207.8
241.5	4341.4	3680.0	3846.8	1690.5	5008.2	3437.8	4248.5	1887.7	2451.4	4302.1
1841.0	5085.3	6122.2	6243.6	5904.2	5291.1	6392.1	5223.2	5736.8	3904.5	5890.5
232.1	3033.4	4037.6	4600.2	2419.9	4291.4	3650.4	5850.1	3110.4	1524.3	5358.8
63.6	1000.0	1102.1	1215.9	332.6	1001.3	911.6	1236.6	330.3	275.6	1165.2
100.5	1409.9	2507.7	2555.8	1736.5	1836.5	2160.0	3111.4	1508.4	538.3	1499.4
57.6	1189.6	2639.0	2104.8	1611.6	1873.3	2273.4	2043.7	830.4	535.6	863.8
331.3	2094.4	2768.9	2921.4	1636.9	2148.9	2310.3	3438.4	2572.2	1573.3	3483.3
187.7	8113.1	6904.6	6269.1	3715.5	5595.1	6349.5	6653.9	6406.5	4026.3	6867.8
52.0	489.9	562.9	603.7	722.2	367.6	524.6	625.3	282.5	802.7	468.0
456.2	4639.7	3787.5	4218.3	3158.7	3003.2	4688.2	3720.1	3444.0	1568.8	3654.0
239.0	2226.9	2578.9	2562.4	3228.0	2133.6	4043.0	2436.9	1145.0	268.2	1637.5
55.5	303.9	553.6	378.6	185.5	372.9	484.6	421.6	358.9	94.7	244.9
67.3	2260.3	1488.9	1340.4	510.9	1862.7	1177.8	1971.1	1489.6	453.5	1406.0
61.3	35.9	38.5	31.5	47.9	42.9	43.6	32.6	32.0	23.4	38.9
53.0	276.1	346.4	306.1	483.0	312.4	479.4	217.1	96.0	73.6	163.9
72.4	1428.3	1138.0	1235.8	817.3	1293.9	1639.8	821.8	824.4	302.0	478.3
32.9	42.9	80.8	89.5	71.1	53.3	76.9	82.9	57.1	50.3	24.0
73.0	23.5	25.2	29.7	38.9	21.5	28.3	19.7	29.5	20.2	29.2
237.4	4150.5	4040.1	4734.2	3260.1	3448.2	3633.4	4241.2	2669.9	2194.2	3889.8
1002.2	4635.1	4207.4	4253.5	2791.6	4503.3	4189.2	4566.5	3147.7	2762.0	3938.2
481.3	1182.9	1142.7	1278.1	943.1	1064.3	1216.6	1747.7	790.1	641.0	1050.8
2040.2	5264.6	5274.2	5458.2	4573.9	4817.5	6051.2	6497.0	6145.1	4831.5	6839.2
37.4	2740.7	2003.2	1768.7	2914.0	2211.7	2617.5	2071.5	3733.8	2090.8	2127.5
379.8	4803.0	5485.4	5719.2	2814.3	4727.6	3506.7	5489.8	4426.3	5156.7	4828.1
136.0	3323.5	3812.0	4212.8	1681.7	3552.5	2789.7	4484.0	2168.2	2125.9	4349.8
183.6	3003.9	3436.8	3078.5	2214.8	3083.0	2713.5	3138.0	2428.7	3659.0	2270.4
66.4	149.9	160.7	153.7	265.9	136.0	219.9	128.3	63.5	46.2	68.4
59.9	576.9	851.7	838.9	676.3	1189.0	908.1	904.2	501.3	95.2	545.9

202.1	217.6	275.3
926.4	778.3	1734.6
75.1	129.3	123.1
624.3	898.3	1318.4
242.6	298.8	155.3
53.6	141.7	130.8
830.0	690.8	67.7
1195.1	1355.5	854.1
4790.2	3579.9	4902.1
2938.2	3398.5	2266.6
833.5	973.2	745.3
2626.4	1569.3	1587.9
2209.4	2656.5	3379.2
4926.4	2391.1	3054.7
5325.9	6081.0	5754.7
4105.5	3331.5	4954.7
1629.2	1025.8	2287.0
2267.5	1905.9	1852.8
4413.5	2105.0	7887.3
2169.3	2715.3	2942.6
5416.8	5325.2	7278.4
409.5	550.8	352.5
6347.6	2860.4	2494.8
3461.9	2492.5	2804.0
312.4	309.0	93.6
1510.2	1128.7	2207.5
54.5	44.0	35.7
312.5	298.4	439.0
1229.9	993.6	399.6
108.4	141.7	67.5
22.7	28.4	24.2
3934.3	3776.8	3689.3
4126.1	4202.2	4330.3
1146.6	1502.6	1731.6
5441.8	7374.0	6136.1
1667.4	2551.6	2107.3
5570.6	4220.2	6267.1
4142.4	3259.4	4813.9
2706.4	2324.5	2744.5
77.9	209.3	84.1
1456.6	1048.4	1521.3

k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
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o__Bacteroidales	f__Porphyromonadaceae
o__Bacteroidales	f__Porphyromonadaceae
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s__Porphyromonas endodontalis	69625
s__Porphyromonas endodontalis	69783
s__Porphyromonas gingivalis	69619
s__Porphyromonas levii	69724
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s__unclassified	69313
s__unclassified	69341
s__unclassified	69382

EU939404.1 gg_id:308165 Fecal wild pygmy loris feces clone WF16S_117 EU939
DQ799651.1 gg_id:194286 human fecal clone RL305aal88f12 DQ799
AB470345.1 gg_id:570230 Parabacteroides gordonii str. JCM 15726 MS-3 AB470
NZ_ABYH01000014.1 gg_id:470761 Parabacteroides johnsonii str. DSM 18315 NZ_AB
FJ681504.1 gg_id:529639 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ673756.1 gg_id:520075 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
AF371918.1 gg_id:28974 swine intestine clone p-1862-c3 AF371
FJ366812.1 gg_id:357610 feces adult twins and mothers; TS27 clone TS27_a04b09 FJ3668
FJ684517.1 gg_id:515739 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
AF371917.1 gg_id:35721 swine intestine clone p-816-a5 AF371
EU774994.1 gg_id:347974 Francois Langur feces clone FL_2aaa01d07 EU774
FJ677705.1 gg_id:531069 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ674079.1 gg_id:528653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU771909.1 gg_id:306330 Southern three-banded armadillo feces clone arma_aaj53e03 EU771
FJ680516.1 gg_id:514875 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
FJ681022.1 gg_id:529102 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FJ677437.1 gg_id:514220 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
DQ071528.1 gg_id:230553 microbial cecum captive and free-living capercaillies (Tetrao urogallus) clone TuCw7 DQ071
FJ680728.1 gg_id:532407 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ677309.1 gg_id:532192 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
FJ681057.1 gg_id:523933 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FJ677094.1 gg_id:522582 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
DQ801512.1 gg_id:199622 human fecal clone RL388_aao96e03 DQ801
EU136685.1 gg_id:245932 Parabacteroides merdae str. JCM9497 EU136
DQ456138.1 gg_id:157481 pre-adolescent turkey cecum clone CFT114H3 DQ456
FJ677490.1 gg_id:529708 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ671638.1 gg_id:526025 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6716
AY975949.1 gg_id:122815 human ascending colon mucosal biopsy clone LS60 AY975
GQ448451.1 gg_id:592097 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_10wks_g GQ448
FJ683073.1 gg_id:531353 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ676802.1 gg_id:516933 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
AB430829.1 gg_id:263317 Porphyromonas crevioricanis str. ATCC 55563 AB430
NZ_ACNN01000021.1 gg_id:470807 Porphyromonas endodontalis str. ATCC 35406 NZ_AC
GU233445.1 gg_id:524704 Porphyromonas gingivicanis str. NUM 301 GU233
EU845219.1 gg_id:340509 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
AP009380.1 gg_id:294930 Porphyromonas gingivalis str. ATCC 33277 AP009
FJ792536.1 gg_id:560360 Porphyromonas levii str. ATCC 29147 FJ7925
GU454798.1 gg_id:522507 Porphyromonas levii str. Israel GU454
GQ112407.1 gg_id:423451 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
GQ074579.1 gg_id:407491 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
X76259.1 gg_id:1941 Porphyromonas cangingivalis str. VPB 4874 X76259

41.0	216.4	128.2	98.9	127.7	44.0	186.4	59.5	41.2	24.6	42.9
738.3	2530.8	2344.9	2541.4	2619.7	1892.2	2859.2	2252.2	1700.3	637.1	2077.2
418.6	2197.5	2751.4	3198.8	2394.4	2369.3	3429.0	2567.7	1620.9	1982.5	2206.2
572.0	753.9	776.0	802.8	1047.6	982.3	709.8	775.0	947.2	175.7	776.1
398.1	2275.7	2425.4	3048.9	1473.4	1932.3	1977.5	2312.0	1261.0	851.2	1379.4
66.5	347.5	491.1	528.5	256.4	467.9	434.8	491.7	237.7	337.4	288.0
44.3	192.6	228.3	244.8	465.5	263.3	244.6	252.9	230.1	145.0	144.7
558.4	3862.7	4053.5	4241.8	3208.7	3965.3	4060.0	4613.7	3125.5	3956.8	4534.8
130.9	3252.4	3913.3	5086.0	1858.4	2646.2	3158.0	3487.5	1196.8	557.3	3705.7
64.4	75.0	102.1	98.8	70.9	71.1	94.1	76.1	59.8	35.4	54.9
574.4	1681.2	1587.9	2069.8	920.1	1679.3	1154.1	1522.9	1396.7	899.6	905.9
609.6	3556.5	3943.0	5098.8	1682.4	2707.6	2337.8	3535.4	2021.9	1007.4	2565.6
262.1	3977.9	3830.8	4450.9	4000.4	3996.0	4752.9	5340.0	5526.1	3492.7	4009.3
112.6	1282.3	1064.3	1213.3	973.9	940.5	1287.4	1283.4	765.2	502.2	879.7
208.5	1631.5	1800.7	2229.9	938.4	1485.4	1101.7	1956.7	1403.7	962.6	1770.8
843.6	4051.5	4080.7	4455.5	3892.6	4807.0	5646.0	4284.2	4429.8	3884.6	3552.5
870.3	3189.8	2845.9	3043.0	2771.2	2464.9	3678.4	2846.4	3395.2	3280.9	3063.9
54.3	501.8	376.2	332.0	236.9	477.9	147.5	424.5	897.6	536.7	383.2
78.7	1517.4	1741.9	2199.9	670.1	1079.3	1246.8	1665.6	551.1	697.6	1208.0
507.0	3308.1	3486.9	4274.2	2961.8	3336.0	4153.1	3650.4	4004.0	3200.9	4134.6
66.8	2327.3	2627.6	2873.7	1534.9	1489.7	2416.2	1993.8	706.3	489.2	1365.1
897.4	1450.5	1472.2	1389.8	849.3	1260.4	1098.7	1375.6	1811.9	1557.2	1457.6
3014.2	893.8	885.6	975.0	733.2	978.0	879.1	949.8	951.0	331.4	616.3
24.3	71.0	35.3	53.6	38.0	94.7	32.5	41.7	39.6	29.6	28.6
77.9	438.8	678.4	864.7	463.9	423.7	463.2	663.1	399.2	135.0	367.1
2087.1	8129.7	6779.4	8749.6	6291.8	7468.5	7718.5	7761.8	11705.4	6723.6	11417.9
174.1	1393.8	1622.8	2068.9	914.7	1594.1	1379.3	1954.7	1166.6	792.6	1732.0
49.0	182.2	342.2	223.7	76.5	221.3	80.8	599.5	368.1	43.5	150.9
154.6	2325.5	3043.8	3633.0	2292.9	3371.7	3451.5	4359.8	1794.9	513.7	2812.8
1009.2	3189.5	3232.3	3529.1	2466.9	3741.1	3061.4	3849.9	4454.2	3771.6	3338.9
270.6	1912.6	2500.2	3270.0	2678.6	2346.9	3359.9	3126.0	1342.1	1103.4	2199.4
105.4	3078.6	2958.4	3823.5	967.8	2480.8	2089.1	3680.0	918.8	565.5	3958.9
54.1	360.9	893.3	1043.8	463.9	407.8	751.1	545.7	194.4	26.7	331.5
56.3	2215.7	3362.7	3468.3	3076.9	2886.0	4568.1	2831.7	1179.4	478.2	2510.8
90.0	3682.0	4668.2	4786.2	3323.2	4120.3	6456.2	5096.2	2465.1	1677.1	5691.4
49.7	155.4	170.8	344.6	138.0	146.0	105.7	286.8	65.4	30.5	202.3
404.9	4940.6	6236.5	7332.4	5130.4	4502.3	6293.8	6335.6	4005.4	2653.7	5042.4
106.2	2586.4	4755.4	5392.7	2689.7	2789.7	4097.5	4076.5	1811.5	1089.1	4069.8
55.4	852.8	895.6	1140.6	633.1	1176.5	596.5	895.7	624.3	706.8	510.8
34.9	80.4	74.6	93.3	48.6	56.3	77.8	70.6	40.7	22.3	42.6
54.4	1705.6	2220.0	2499.7	2269.7	1508.5	2469.5	2381.9	590.4	144.3	1930.9

39.2	65.2	76.9
2406.4	2122.4	2132.2
3452.9	2104.5	1851.8
954.9	1125.1	230.9
2774.3	2603.5	2715.9
485.8	496.2	337.4
248.0	298.6	1244.9
4429.1	3978.3	4299.1
4435.0	4351.3	4973.0
75.8	107.9	101.5
2048.2	1884.1	1125.2
3668.6	3260.5	3599.8
4482.3	4902.1	5342.6
1436.3	1393.2	954.1
1765.5	1641.3	1428.5
4420.8	4225.4	5643.0
2772.9	3640.8	4532.7
252.5	294.1	146.5
1454.8	1287.2	1484.1
3237.8	3436.6	5619.5
2754.8	1767.3	3750.0
1095.8	2026.2	898.4
999.0	1328.3	673.6
48.6	67.3	37.2
422.3	681.9	350.2
6512.7	7332.9	8805.1
1868.7	1797.0	1720.6
533.2	298.2	191.4
3278.2	3518.4	4396.1
3316.6	3640.8	2987.2
2515.7	3199.7	4950.8
3432.0	2400.2	5435.7
215.2	344.4	944.3
2310.9	3053.4	2854.8
3886.4	3029.5	4892.4
193.2	258.4	491.1
4813.0	4875.9	6290.7
2935.7	2786.4	4524.4
853.9	1070.0	1337.6
20.6	61.8	59.4
1341.0	1778.4	2360.1

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AY968205.1 gg_id:115278 Porphyromonas somerae str. WAL 6690 AY968
FJ848556.1 gg_id:542665 Porphyromonas sp. str. 2014 FJ8485
EU289097.1 gg_id:254483 microbiome cloacal openings urogenital and anal tracts tammar wallaby Macropus e EU289
GQ081345.1 gg_id:462094 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ081
EF511866.1 gg_id:221666 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5118
EU557014.1 gg_id:308956 Detection microorganisms involved infectious endocarditis cultivation techniques inf EU557
FJ848566.1 gg_id:564437 Porphyromonas sp. str. 2121 FJ8485
X76261.1 gg_id:1951 Porphyromonas canoris str. VPB 4882 X76261
FJ976295.1 gg_id:591163 Interindividual healthy human oral microbiota mouth clone 10B051 FJ9762
GQ075596.1 gg_id:387445 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
CU923280.1 gg_id:543028 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
AY570514.1 gg_id:108520 Porphyromonas uenonis str. WAL 9902; ATCC BAA-906; CCUG 48615 AY5705
EU414673.1 gg_id:268540 Porphyromonas sp. str. WAL 1926C EU414
GQ115447.1 gg_id:397693 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw685g04 GQ115
AF287986.1 gg_id:42871 Porphyromonas gulae str. coyote 1.5.1 AF2879
AB053945.1 gg_id:46214 Tannerella forsythensis str. L7 AB0539
DQ344915.1 gg_id:161737 Tannerella forsythensis str. RMA 8286 DQ344
AB053939.1 gg_id:40709 Tannerella forsythensis str. G9 AB0539
AB053942.1 gg_id:34893 Tannerella forsythensis str. KM3 AB0539
AB191996.1 gg_id:143551 termite gut homogenate clone M2PB4-84 AB1919
AF385565.1 gg_id:43915 crevicular epithelial cells clone BU045 AF3855
AB191987.1 gg_id:142913 termite gut homogenate clone M1PL1-34 AB1919
FJ374177.1 gg_id:360716 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
AB088937.1 gg_id:78297 termite gut homogenate clone Rs-E83 bacterium AB0889
AY160850.1 gg_id:97947 termite intestinal tract clone COB P5-27 AY1608
AB189687.1 gg_id:113389 termite gut homogenate clone Tc-42 AB1896
AB243256.1 gg_id:149284 acetone-preserved termite gut clone M2PB4a-054 AB2432
FJ374176.1 gg_id:368029 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
AJ576344.1 gg_id:101861 hindgut homogenate Pachnoda ephippiata larva clone PeH27 AJ5763
AJ576330.1 gg_id:105053 hindgut homogenate Pachnoda ephippiata larva clone PeH12 AJ5763
AB062826.1 gg_id:19082 termite gut homogenate clone BCf5-08 AB0628
AM420141.1 gg_id:247976 Noma subgingival plaque clone 402C09(oral) AM420
AB189685.1 gg_id:113096 termite gut homogenate clone Tc-38 AB1896
AB255914.1 gg_id:166153 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
EU470470.1 gg_id:292037 Grevy's zebra feces clone GZ_aaa04f04 EU4704
FJ671888.1 gg_id:511761 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
DQ988275.1 gg_id:198436 Microbial lab-scale A1-A2-O fixed biofilm system coking wastewater treatment with DQ988
FJ672767.1 gg_id:532401 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6727
FJ672819.1 gg_id:510506 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
EF559223.1 gg_id:221775 mesophilic anaerobic digester clone A35_D28_L_B_D06 EF5592
FJ672904.1 gg_id:521556 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6729

79.1	3894.9	5157.4	4973.7	3589.3	3114.9	4041.2	4588.4	3093.8	1600.0	3621.2
193.0	4750.6	5209.2	5776.6	3898.4	4308.3	4603.0	5021.3	3891.1	2122.1	3591.7
3559.1	4552.1	6052.1	6174.0	5373.0	5083.3	6997.6	5809.7	4754.4	4010.9	5367.9
48.4	1318.9	1862.0	2364.2	811.2	853.2	2158.2	1360.4	814.6	477.0	1274.8
55.9	398.5	596.6	773.9	247.0	562.0	145.6	513.3	170.8	141.0	143.2
300.9	2077.9	2756.9	2907.8	1251.6	1502.9	1430.4	2131.5	1587.5	449.5	1058.0
1248.8	6699.6	6790.1	8472.4	6071.8	6516.4	7463.1	6329.2	5944.6	3615.2	7024.1
90.4	1028.6	1385.5	1694.6	1463.6	1589.9	1690.8	1329.8	1243.1	647.9	793.8
68.2	1340.6	1488.2	1808.5	502.3	1074.3	517.0	802.7	380.6	291.1	434.3
82.2	433.3	347.9	446.6	469.6	300.2	491.4	444.9	167.2	608.4	255.9
124.0	555.4	1206.1	1225.1	435.7	758.4	282.4	1023.7	273.5	133.7	368.2
52.3	28.5	41.6	25.2	25.7	24.0	23.9	24.1	22.8	18.7	39.4
59.8	284.0	345.4	464.9	355.0	181.8	462.8	175.5	138.0	53.1	117.3
514.2	1547.3	1927.2	2388.5	1274.9	2087.4	1807.1	2148.9	1051.6	1205.1	2750.5
47.5	353.0	376.1	421.0	285.2	331.1	490.4	377.9	466.6	245.1	542.4
99.0	1430.0	1617.5	2117.1	1305.7	1400.4	1362.1	1886.5	805.5	397.2	1383.9
61.2	1078.4	1978.5	2412.1	1690.0	1662.3	2877.9	2001.7	1251.5	219.6	1081.0
48.6	1098.9	1627.9	1981.6	1541.0	948.6	2370.6	1196.9	548.1	471.0	1003.6
71.9	846.5	1243.7	1412.0	746.1	991.0	1009.4	1515.8	525.7	221.8	1138.7
25.1	36.2	97.3	119.3	22.9	89.1	44.5	163.4	57.5	17.1	114.7
39.9	133.3	107.9	93.3	48.1	578.5	160.2	129.0	46.5	32.9	87.6
41.4	86.2	87.0	62.7	58.2	43.5	46.7	70.2	111.4	35.8	55.4
60.9	1776.4	2248.5	2802.7	2039.2	1977.4	3205.7	2193.3	922.9	806.9	2203.8
31.5	49.8	93.6	97.1	52.8	63.6	78.5	110.1	48.6	27.2	96.5
55.0	482.5	349.5	414.6	565.7	373.8	591.9	293.0	127.4	80.5	231.8
36.9	51.0	104.3	132.6	73.1	134.7	57.4	57.9	72.1	40.7	63.4
74.6	1714.5	1713.5	1340.6	1614.0	1583.3	1254.5	1553.3	610.9	780.7	1104.2
25.4	598.4	910.6	1084.2	454.3	707.2	784.0	865.4	590.0	389.9	712.6
225.8	2884.1	2993.7	3536.7	2622.8	2952.4	3892.5	3460.4	1865.9	1716.8	2699.4
37.3	70.1	133.9	139.0	136.2	113.5	192.7	74.1	63.8	33.9	85.7
250.4	519.0	706.3	311.7	518.6	455.2	645.6	788.5	368.9	284.4	599.4
133.1	2275.3	2386.6	2630.8	2166.2	2145.4	3365.3	2409.6	1840.6	2033.2	2344.6
38.8	361.9	346.6	400.3	284.9	291.9	656.6	117.9	102.2	99.8	132.3
23.9	38.8	109.2	125.6	125.9	79.3	104.6	75.7	42.1	19.2	48.1
189.2	1821.3	2309.9	2524.6	1303.2	1828.3	2165.8	2389.8	1767.5	1689.8	2950.5
182.6	4124.5	5098.3	5869.2	4332.8	5506.7	5197.5	5607.3	4452.7	2124.4	3925.7
543.0	2378.0	2898.9	3169.8	2035.0	2437.4	3248.3	3062.7	1542.0	1447.9	2983.9
121.4	1864.6	1928.4	1675.2	1466.9	2340.2	2031.8	2274.9	1139.8	1954.8	1432.4
1203.4	7164.1	7232.0	6795.7	5612.7	6676.3	6284.8	5557.1	11399.1	9551.0	7825.9
89.9	2218.2	3251.9	2692.3	1612.2	2632.6	2718.7	3765.7	1557.3	603.3	3161.7
4392.1	6088.3	5416.1	6633.0	4866.3	6371.4	6606.7	6207.5	6731.5	8589.1	6087.4

2948.8	2981.9	3047.7
4352.1	4310.3	4597.1
4883.7	6098.4	7472.5
730.0	1811.9	2873.7
626.2	707.5	617.1
2035.5	1870.2	1809.0
6162.2	6174.3	7347.2
1485.3	1615.7	1350.4
2022.2	1239.8	791.7
316.4	502.7	414.2
941.7	1180.1	2672.7
23.8	32.6	19.0
270.9	154.9	174.7
2240.7	2283.7	3067.8
268.4	340.8	343.3
1685.5	1550.2	2092.9
1583.1	1555.5	1367.1
960.3	2074.2	2748.4
1136.2	1210.3	1074.2
71.0	38.0	38.9
104.3	151.2	1569.4
97.2	79.2	50.4
1631.8	1991.5	2209.3
66.9	75.0	102.7
280.3	280.8	150.5
121.6	133.7	66.8
2154.2	1482.1	1521.3
1051.4	786.3	819.1
2130.5	3075.3	3513.2
86.3	86.3	68.1
519.0	796.6	83.3
2265.9	2294.1	3035.0
143.3	121.2	195.9
85.7	79.5	77.3
1639.7	1979.5	2471.2
5786.2	4967.6	10635.6
3355.6	2436.3	2532.1
2591.4	2149.4	7425.7
6292.4	7359.2	7750.5
2466.3	2883.4	7434.0
5754.1	6289.1	9455.8

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EF586021.1 gg_id:254796 Methanol-assimilating anaerobic solid waste digester fed methanol clone M35_D20_ EF586
AB195878.1 gg_id:109165 Anaerobic sludge clone N17 AB195
FJ675621.1 gg_id:513577 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6756
AJ853526.1 gg_id:111183 landfill leachate clone GZKB32 AJ8535
FN563309.1 gg_id:565774 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
FJ675576.1 gg_id:521274 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
FJ205819.1 gg_id:347868 microbial integrating library sequences and metagenome data obtained 454-pyroseq FJ2058
EF559172.1 gg_id:218156 mesophilic anaerobic digester clone G35_D8_H_B_A04 EF5591
FJ664781.1 gg_id:552684 Quantitative dynamics cells plankton-fed microbial fuel cell clone PFC_3_peak_D10 FJ6647
FJ202203.1 gg_id:354185 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
GQ052695.1 gg_id:460594 Topographical and Temporal Human Skin Microbiome skin back clone nbu539g04c1 GQ052
EU469149.1 gg_id:298915 Speke's gazelle feces clone SP3_c06 EU469
GQ052715.1 gg_id:404267 Topographical and Temporal Human Skin Microbiome skin back clone nbu540a05c1 GQ052
AJ318147.1 gg_id:45562 Waste-gas biofilter clone BIhiii38 AJ3181
FJ675463.1 gg_id:530837 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6754
EU794304.1 gg_id:339564 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_R22 EU794
AB100456.1 gg_id:81498 termite gut clone Rs-003 AB100
EU052241.1 gg_id:242269 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
CR933297.1 gg_id:109632 Evry municipal wastewater treatment plant clone 060H11_B_SD_P93 CR933
FJ664818.1 gg_id:512016 Quantitative dynamics cells plankton-fed microbial fuel cell clone PFC_3_peak_A10 FJ6648
AY977440.1 gg_id:115908 human cecum mucosal biopsy clone W144 AY977
CT574073.1 gg_id:155288 Evry municipal wastewater treatment plant clone 053H07_B_DI_P58 CT574
CU926729.1 gg_id:569056 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
FJ672406.1 gg_id:524949 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
FJ716926.1 gg_id:563763 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7169
CT573875.1 gg_id:151413 Evry municipal wastewater treatment plant clone 013B08_B_SD_P15 CT5738
AY976380.1 gg_id:122025 human ascending colon mucosal biopsy clone LY65 AY9763
AM420225.1 gg_id:254175 Noma subgingival plaque clone 601G07(oral) AM420
AY983350.1 gg_id:121452 human descending colon mucosal biopsy clone A451 AY9833
EF559178.1 gg_id:220350 mesophilic anaerobic digester clone G35_D8_H_B_A02 EF5591
AY005072.1 gg_id:46885 subgingival dental plaque clone AU126 AY005
EF559129.1 gg_id:222811 mesophilic anaerobic digester clone C35_D63_H_B_H09 EF5591
EU470429.1 gg_id:290027 Grevy's zebra feces clone GZ_aaa01c12 EU470
FJ497484.1 gg_id:571407 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
EU052252.1 gg_id:251724 degradation kinetics and current efficiency cells supplied anode microbial fuel cell fe EU052
EU461317.1 gg_id:287569 red kangaroo feces clone KO2_aai17a01 EU461
EF157125.1 gg_id:237787 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AM420248.1 gg_id:237717 Noma subgingival plaque clone 701B08(oral) AM420
FJ672462.1 gg_id:511079 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
FJ674493.1 gg_id:526084 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ439854.1 gg_id:536271 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M3 FJ4398

75.4	1040.4	1096.4	1524.2	944.2	1158.4	1407.6	2001.8	342.2	130.0	1881.0
51.5	186.7	212.0	157.7	198.4	275.6	218.3	177.6	153.9	70.4	160.1
113.3	1398.7	2103.0	1819.5	1227.4	1332.3	1742.1	1459.0	524.4	323.2	1217.9
259.5	1905.4	2660.3	2809.5	3001.0	1882.8	4752.6	2163.8	899.2	944.4	1605.1
119.4	3333.9	2689.3	2773.6	1254.3	2202.6	1859.6	2980.1	1364.1	667.1	3210.1
190.4	4756.7	4807.9	5903.8	5648.3	4359.8	6583.2	5171.2	4588.0	3858.2	5385.9
1714.9	5417.6	5943.4	6652.3	4775.3	5545.9	6869.2	6003.7	6375.6	3298.7	7039.8
43.4	930.1	1711.7	1802.1	1855.6	1097.9	3205.1	1291.7	305.3	138.5	1071.4
260.2	7529.4	8702.0	8711.8	7233.3	7160.0	10772.6	7556.8	6972.2	4455.6	8233.8
63.2	2696.4	3596.9	3444.4	3883.9	3303.7	3796.4	2962.9	2183.5	2994.7	2295.5
34.9	2255.0	5534.1	6912.0	1149.2	3424.0	3793.2	8223.1	1683.8	1140.3	10165.3
1319.9	10570.7	10604.9	12470.2	11376.3	9546.9	13452.1	9677.9	9509.1	9780.8	12027.3
206.4	2725.3	3335.7	3957.4	1268.4	3333.5	2062.4	3662.6	2066.2	1403.8	3043.9
165.6	3865.4	4679.4	4845.2	4576.6	4448.6	4826.4	5044.2	3353.7	3315.6	5375.8
975.6	4578.5	4273.8	4382.1	2942.2	4161.1	3752.0	4431.0	4586.0	5186.3	4341.6
8457.2	4602.6	4405.5	4745.8	4359.3	4141.0	5018.7	4640.2	5373.7	2588.7	4891.6
207.6	3373.9	2725.4	2805.8	2729.5	2267.8	3327.0	3411.2	2665.1	2167.6	2109.3
10241.2	7574.0	6573.4	6938.0	6700.8	7457.7	7535.0	7132.9	8501.4	8210.2	7172.0
357.2	5350.7	4397.0	4509.9	3041.1	4461.3	4498.1	4544.6	4580.7	3111.8	5418.8
7845.4	6719.8	6852.6	6890.5	6046.1	6303.4	8275.4	6513.9	6607.1	7634.8	6980.7
326.2	8070.9	6961.6	7847.6	9067.9	6773.9	8834.1	7139.5	6938.6	5358.1	7207.3
47.0	234.4	276.0	273.4	188.4	299.7	384.8	237.5	86.5	79.8	147.6
28.5	64.5	73.2	88.4	127.4	114.9	131.0	91.9	33.0	26.9	42.2
473.7	7270.4	6805.5	7520.8	6806.5	7425.1	8089.2	6936.0	5281.1	7897.1	5188.4
81.8	3124.7	2657.5	2080.4	3479.9	2718.6	3501.9	2311.7	2518.2	1413.4	2225.0
54.6	129.5	220.1	221.0	306.4	228.2	206.1	168.7	60.4	105.8	89.0
2241.6	11355.0	8734.7	9515.2	9477.2	8830.7	9574.2	8080.9	8914.9	7484.3	9869.7
193.4	1998.7	2757.9	3478.0	3562.5	2802.6	3676.6	3565.4	3648.6	1238.8	2475.5
4126.4	5280.1	5972.3	6336.5	5217.2	5512.6	5911.7	4986.3	7751.2	5839.0	5556.6
48.0	67.2	108.3	90.1	71.6	134.3	117.4	124.5	41.1	30.1	56.9
345.2	837.6	1256.7	1465.0	1234.4	1260.5	1279.8	1512.8	1668.3	320.4	1317.1
4821.9	6159.3	4942.8	4655.0	4177.4	4863.2	4574.0	4583.4	10181.3	5256.4	4624.1
222.7	1498.7	1878.8	1849.4	1550.1	1855.2	1608.2	1948.1	1627.8	711.7	1089.4
80.5	4306.2	4222.7	4029.8	3578.5	3850.3	3991.5	4189.8	5216.4	3927.5	4950.3
470.0	2058.9	3188.1	1960.4	1810.7	2011.0	3329.3	1773.5	1674.6	649.0	1546.6
647.2	6196.9	6577.7	7202.6	6824.5	5410.9	8167.4	6926.1	3446.6	3536.2	7799.6
185.9	2922.3	3090.9	3843.8	1831.1	2793.0	2596.5	4588.1	1143.7	730.1	3643.9
913.4	1746.0	1824.3	1870.7	1334.0	1708.9	1767.9	1562.2	2593.0	3486.3	2266.5
783.7	1435.2	1988.4	1984.7	1380.1	1728.9	1689.0	2394.3	1772.0	967.9	2569.6
1331.7	3643.2	3558.1	3407.2	3571.9	4193.6	4037.5	3500.0	4667.1	3165.5	4202.6
230.7	7373.3	7806.1	9337.2	3686.4	6858.7	8370.5	8986.6	4247.7	2418.7	12544.9

1009.1	1299.4	7480.6
166.6	283.3	772.7
1461.6	2139.0	6732.9
1495.3	2441.4	8907.3
2247.5	1877.4	3057.7
4644.4	4835.5	5573.1
4749.7	4716.0	8974.5
595.0	1670.8	4729.6
6994.8	6002.0	7966.5
2995.4	3716.9	4495.8
3227.2	2107.6	913.8
10448.5	9630.4	9849.5
2681.3	1903.4	1519.0
3913.9	4242.5	6177.3
4588.2	5018.1	7687.6
3857.1	4795.9	3869.3
2646.2	2650.9	3173.3
6611.3	7401.2	7358.5
4826.8	4580.7	5909.6
5745.0	7302.4	7403.9
6779.8	6941.2	6962.7
285.6	228.6	1091.3
63.7	122.2	138.7
7551.1	7606.8	12492.1
2013.4	2463.1	1740.2
202.0	249.3	261.9
7345.7	9176.1	11229.0
2827.3	3034.6	4136.7
4513.4	6394.5	5183.9
103.9	325.8	2220.4
1184.9	1291.5	1352.1
4242.7	5460.0	5785.9
2236.4	1642.1	2121.5
3397.1	4099.9	3181.0
1308.7	2011.2	1884.0
5789.7	6087.6	6372.8
3643.5	3196.4	6993.4
1413.9	2381.3	1832.7
1967.7	2103.6	3207.3
3367.8	5220.3	9281.8
7086.0	5123.9	6274.3

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EF559201.1 gg_id:224801 mesophilic anaerobic digester clone A35_D28_L_B_B10 EF5592
AB015260.1 gg_id:1913 deepest cold-seep area Japan Trench clone JTB132 AB0152
U81722.2 gg_id:1975 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHA54 U8172
FJ374186.1 gg_id:368153 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
FJ672447.1 gg_id:516031 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU721787.1 gg_id:567204 microbial production water Alaskan mesothermic petroleum reservoir two methods EU7217
EU794159.1 gg_id:355683 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AF37 EU7941
AF371914.1 gg_id:102513 swine intestine clone p-238-o5 AF3719
FJ672854.1 gg_id:514271 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
AY977274.1 gg_id:123530 human cecum mucosal biopsy clone MU42 AY9772
AY571432.1 gg_id:114637 termite gut clone RsaP168 AY5714
AB088927.2 gg_id:77707 termite gut homogenate clone Rs-N56 bacterium AB0889
AJ441221.1 gg_id:57463 hydrothermal vent polychaete mucous clone P. palm C/A 33 AJ4412
AY991899.1 gg_id:129618 mouse cecum clone C20_j24 AY9918
FJ674472.1 gg_id:515586 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ674433.1 gg_id:531739 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ675106.1 gg_id:528401 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
FJ674589.1 gg_id:519671 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6745
AY991901.1 gg_id:135556 mouse cecum clone C20_k02 AY9919
AJ853536.1 gg_id:110885 landfill leachate clone GZKB42 AJ8535
CU923895.1 gg_id:573538 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9238
EU463148.1 gg_id:287576 naked mole-rat feces clone molerat_aai70f08 EU4631
AB186895.1 gg_id:101957 polychlorinated dioxin dechlorinating microcosm clone TSAI15 AB1868
FJ672467.1 gg_id:522834 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU459469.1 gg_id:300752 capybara feces clone CAP_aah97g01 EU4594
FJ374185.1 gg_id:361949 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
EU465580.1 gg_id:297581 argali sheep feces clone AS1_aao38f01.Contig1 EU4655
EF559156.1 gg_id:219368 mesophilic anaerobic digester clone G35_D8_L_B_E07 EF5591
FJ671936.1 gg_id:529973 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6719
EU358697.1 gg_id:323312 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3586
AY953229.1 gg_id:114483 anaerobic swine lagoon clone A-2X AY9532
DQ860019.1 gg_id:240669 anchovy intestinal microflora clone F1P DQ860
AF349759.2 gg_id:49573 reductive TCE-dehalogenating enrichment clone TCE5 AF3497
AB355049.1 gg_id:235348 Monitoring and archaeal two heavy polluted areas lake Egypt based on surface wate AB3550
DQ003623.1 gg_id:119392 human mouth clone MB3_P19 DQ003
FJ202527.1 gg_id:314487 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
DQ205192.1 gg_id:150369 acid-tolerant H2/CO2-utilizing methanogenic s New York State enrichment acidic pe DQ205
AJ582209.1 gg_id:93925 soil near uranium mill tailings clone Gitt-GS-109 AJ5822
AY991817.1 gg_id:131239 mouse cecum clone C20_f23 AY9918
AB237700.1 gg_id:140394 microorganisms deep subsurface groundwater sedimentary rock milieu clone HDBW AB2377
AY134906.1 gg_id:59562 oral periodontitis clone FX069 AY1349

62.0	304.1	542.2	517.3	134.8	532.4	268.8	797.8	194.3	42.8	758.9
680.9	1230.6	1498.1	1391.3	859.0	1159.6	1556.5	1601.3	1410.8	1312.1	1609.4
47.0	859.1	1278.4	1153.9	414.8	828.4	1394.9	1987.2	465.5	692.1	1866.3
192.0	3605.1	3748.3	4011.4	2440.6	3324.3	3447.7	3504.2	2929.8	2429.3	3067.2
77.2	4339.4	5378.2	5692.8	3670.6	4365.7	4965.9	5297.5	3184.7	2891.1	4986.5
91.3	681.4	923.8	968.7	599.1	794.8	1111.5	1016.2	838.9	690.1	824.5
921.0	6659.8	6456.5	8945.8	7442.3	5925.7	8818.8	7069.5	5387.1	3753.1	6142.1
427.2	4857.8	4978.0	4771.8	6096.9	4433.9	5737.3	4348.6	3951.9	2862.0	4822.9
97.7	3120.4	2365.6	2465.7	1694.9	3118.4	1858.5	2499.1	4702.1	1933.6	2056.7
33.8	468.8	718.6	488.7	537.7	518.7	425.6	536.0	442.8	570.9	336.0
56.9	269.6	235.5	273.9	297.9	220.6	329.1	140.9	171.3	69.0	92.3
48.5	720.1	802.6	877.7	368.8	689.3	608.3	953.4	301.4	109.9	533.7
1191.7	6144.6	7826.9	7144.6	7874.0	6284.1	8763.7	6940.4	6492.9	4920.8	6980.0
12759.4	6588.2	5761.0	6814.5	7299.1	6982.2	6585.8	5994.8	9330.1	10395.9	9861.3
44.5	401.2	656.1	639.5	417.1	696.8	519.9	595.1	239.3	403.5	307.8
102.9	1636.0	1880.9	2219.5	1187.1	2392.5	1383.7	2160.7	707.0	261.5	1983.8
51.2	3140.8	3170.0	3109.5	2809.9	2630.6	3077.5	3819.7	4094.4	2650.3	3172.4
106.9	2582.0	2881.2	3009.0	1595.3	2693.7	2223.3	3430.2	1725.0	818.1	2305.0
51.2	752.7	330.4	809.3	142.6	142.5	128.7	184.7	68.8	48.7	109.5
26.2	69.5	171.6	178.9	113.5	80.6	138.0	156.5	75.4	26.5	73.2
3238.3	1627.4	1811.8	1797.6	1207.4	1483.1	1512.1	1606.9	1736.0	1657.9	2854.8
8933.4	6371.2	6475.9	6679.5	6474.0	6049.6	6195.5	6040.4	10449.6	7843.1	6727.9
40.3	1419.3	1344.9	1600.5	384.5	868.4	822.8	2023.7	363.3	127.4	1437.6
205.8	1000.7	831.5	881.0	833.4	797.0	911.4	716.2	844.7	639.3	994.0
5228.1	7031.6	8605.1	8172.1	4827.8	6874.2	8988.1	8291.4	8676.3	4553.1	10710.7
347.7	4175.6	4019.8	4184.7	6563.3	5103.1	5286.6	4343.5	6423.8	2119.4	3931.7
11568.1	10746.3	9528.2	11708.3	10532.3	9697.4	12505.5	10729.4	12802.9	14868.2	15389.6
46.9	52.0	42.3	46.3	30.2	58.7	41.0	58.5	29.5	19.5	40.7
2540.4	3181.4	4607.6	4939.6	3492.0	4702.9	5167.4	4397.3	3977.4	3077.5	5052.9
117.7	1585.2	1562.7	1771.9	2219.9	1468.1	2159.4	2006.4	532.2	498.1	1778.4
42.2	90.4	185.8	128.4	71.4	129.0	92.2	151.8	51.1	52.3	147.0
108.4	2073.0	3456.4	2267.6	1572.4	2166.8	3341.9	2331.0	1246.6	1184.4	1749.9
80.1	300.9	485.2	599.1	282.5	295.4	444.1	553.3	145.6	143.0	530.1
51.2	4985.9	6121.7	6351.9	5375.8	4290.3	7991.4	4783.7	3333.8	2994.1	5201.2
1068.5	3816.3	3653.5	4115.2	3642.6	3506.7	4215.2	3840.0	3735.3	6200.5	4674.2
36.2	1038.9	2019.9	1950.7	2313.3	1862.2	2676.7	2478.6	994.0	600.2	1265.7
46.5	1631.6	2519.5	3025.2	1620.6	2137.3	3055.7	3208.5	872.1	203.5	3718.1
159.8	1214.4	440.4	1147.8	808.1	1094.5	1016.5	1622.8	2454.9	3155.4	1541.7
4052.1	2801.7	2217.4	2685.9	2553.0	2421.2	2421.8	2577.3	3628.5	3103.3	2714.3
37.7	406.1	694.9	704.2	130.2	556.7	285.4	1041.6	212.1	39.7	683.7
70.8	423.8	702.0	945.3	326.1	546.4	621.5	667.7	323.2	274.2	958.4

364.6	613.7	5305.6
1128.8	1273.8	1695.9
887.0	591.7	668.1
3292.7	3602.6	8590.0
4846.8	3810.9	8605.0
690.2	1186.7	3711.7
6649.5	6303.1	7672.8
4269.3	4201.3	4238.0
2822.9	2194.9	3457.1
556.2	545.2	352.1
155.4	337.5	179.9
756.5	1196.5	1283.8
5136.5	5422.0	7093.9
5683.9	7670.5	5711.0
949.8	1124.9	5911.3
2117.9	2850.3	8476.1
3011.6	2987.3	4462.2
2869.8	2893.6	6530.2
225.5	223.9	187.6
69.4	212.3	392.7
1370.9	2118.6	1231.9
6204.6	6706.4	5745.8
831.7	1363.4	724.0
750.4	1286.6	2203.2
6626.1	6596.1	6970.5
3518.2	5248.1	6351.0
9624.4	10668.9	10962.1
55.0	106.7	731.0
4847.8	3940.5	9972.5
1415.9	1741.0	1387.8
120.5	123.2	375.5
1757.7	2970.9	2582.8
263.0	391.2	368.3
4252.9	3309.8	5147.6
3371.5	4065.9	4263.5
1522.6	1294.8	2206.7
1784.1	1811.0	744.5
1107.3	1864.0	5066.6
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392.6	436.2	337.2
320.7	452.0	1444.1

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GQ111229.1 gg_id:385574 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ111
AB088941.1 gg_id:78217 termite gut homogenate clone Rs-P01 bacterium AB088
FJ672436.1 gg_id:516239 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6724
EU467655.1 gg_id:298534 naked mole-rat feces clone molerat_2b05_1 EU467
FJ167452.1 gg_id:315404 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
AF132281.1 gg_id:70461 adult human fecal matter clone adhufec84 AF132
FJ167475.1 gg_id:355592 microbiology granular sludge under autotrophic mixotrophic and heterotrophic denit FJ1674
AF550591.1 gg_id:75791 Bacteroidetes Ko710 AF550
EU472295.1 gg_id:288734 francois langur feces clone FL_2aaa01a02 EU472
CU923533.1 gg_id:565061 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
DQ178248.1 gg_id:139320 Ruminobacillus xylanolyticum str. G1 DQ178
FJ202599.1 gg_id:342484 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
EU573101.1 gg_id:279304 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c EU573
CU920278.1 gg_id:551524 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
CU919616.1 gg_id:551763 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
DQ447167.1 gg_id:156592 Microbial long-term performance full-scale synthesis gas fed bioreactor treating sulf DQ447
AY571436.1 gg_id:114716 termite gut clone RsaHw540 AY571
AB288898.1 gg_id:201673 termite gut homogenate clone BOf3-21 AB288
CU926773.1 gg_id:573887 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
AY949860.1 gg_id:114497 Bacteroides sp. strain str. Z4 AY9498
AB234434.1 gg_id:149277 termite gut homogenate clone MgMjR-061 AB2344
CU925579.1 gg_id:545453 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EF559149.1 gg_id:222737 mesophilic anaerobic digester clone G35_D8_L_B_D04 EF5591
AB198454.1 gg_id:135866 termite gut wall fraction clone RsW01-016 AB1984
AB194940.1 gg_id:144765 Identification ectosymbionts distinct lineages Bacteroidales attached protists termit AB1949
FJ940882.1 gg_id:590552 Prevotella baroniae str. DSM 16972 FJ9408
AJ006457.1 gg_id:2048 Prevotella bryantii str. B14 (DSM 11371 species) AJ0064
EU469476.1 gg_id:300636 black lemur feces clone BKLE_e08_2 EU469
FJ677429.1 gg_id:512581 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
EU475181.1 gg_id:298789 bonobo feces clone BNO_aaa03f04 EU475
EU461975.1 gg_id:301191 white-faced saki feces clone Saki_aaj64f07 EU461
EU461664.1 gg_id:287914 mongoose lemur feces clone ML_aaj26f03 EU461
DQ795990.1 gg_id:188367 human fecal clone RL202_aai49h10 DQ795
FJ677392.1 gg_id:524100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6773
ACBX02000017.1 gg_id:563962 Prevotella copri str. DSM 18205 ACBX0
AY979496.1 gg_id:126721 human transverse colon mucosal biopsy clone M138 AY9794
FJ678036.1 gg_id:518418 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6780
AY983808.1 gg_id:127263 human descending colon mucosal biopsy clone M868 AY9838
EU728712.1 gg_id:338913 Prevotella sp. str. DJF_B112 EU728
EU774935.1 gg_id:320044 Flying Fox feces clone FF_a09 EU774
EU462001.1 gg_id:298154 black-handed spider monkey feces clone SPIM_aaj33b06 EU462

266.9	1259.8	2050.1	2233.0	2421.1	2001.5	1750.9	1890.4	1552.7	914.2	1362.6
37.4	92.4	67.6	93.2	57.1	62.5	40.7	54.1	53.6	21.6	48.8
610.2	3757.0	2781.5	2755.2	2544.5	3476.9	2547.9	3067.2	4714.8	1937.4	2526.6
135.2	5303.9	6183.1	5114.4	4343.2	7621.7	5019.7	4962.2	2814.6	3051.3	4413.3
75.0	954.5	1368.8	1462.6	863.3	920.0	1591.6	1863.7	463.4	373.1	1234.6
17165.7	10492.3	8670.1	9603.0	10144.6	8687.5	10270.2	8991.4	12368.0	10891.5	9892.4
187.1	1381.7	1205.0	1257.1	1365.5	1006.1	1490.2	1121.0	454.9	150.6	719.1
69.4	1008.9	408.2	410.3	420.4	391.2	475.9	239.6	494.1	165.3	189.9
667.6	2309.5	2778.7	2913.6	2744.8	2626.9	2550.9	2611.1	2564.9	2763.5	1913.7
255.0	3021.1	2484.3	3109.0	2501.5	2024.8	2722.6	2878.9	1682.8	1176.8	2289.1
39.6	67.2	161.9	69.7	79.9	63.5	165.6	36.0	32.5	21.4	29.6
34.8	803.6	1786.9	1443.4	1340.9	1523.4	1737.9	2067.7	531.2	680.4	885.3
73.7	2017.2	1826.8	1554.0	2544.5	1831.1	2971.2	1798.9	1420.9	450.1	929.7
38.0	43.8	119.4	90.5	86.3	87.7	61.3	87.3	56.0	30.2	148.3
1406.1	1975.9	2293.0	2674.8	2069.9	2371.0	2896.9	2086.1	1713.7	1905.7	2348.7
33.0	29.7	30.1	31.0	44.3	33.3	24.5	20.6	23.9	21.9	23.6
49.0	640.3	851.1	1034.3	628.7	602.1	765.2	642.4	313.7	146.3	330.8
2996.6	6966.3	6709.8	7822.1	5973.3	6768.6	6295.1	7443.5	7036.3	4128.1	6329.8
44.3	2959.0	2804.1	2667.2	1772.5	2366.3	2496.9	2415.1	1334.6	657.9	1743.8
44.2	2743.7	1678.0	1280.9	1664.1	1605.1	1459.0	1116.7	1000.5	430.1	960.8
894.3	3107.1	3446.8	3787.4	3173.1	3018.0	4282.8	3335.6	1611.8	1278.9	3888.5
122.6	5854.6	5996.9	6531.4	2684.2	5146.6	4794.8	6311.5	3273.9	1771.4	5898.0
57.5	102.4	186.1	146.6	87.1	70.5	324.7	117.8	58.8	40.1	120.3
47.5	402.4	1167.3	1544.4	739.4	556.8	1688.5	1027.1	843.7	166.6	678.4
40.7	135.9	260.8	284.4	237.0	103.7	142.2	278.3	161.1	67.4	173.6
78.0	132.9	282.8	178.1	152.7	194.0	254.9	188.8	92.2	93.4	399.8
49.9	50.1	47.6	30.6	39.6	24.1	28.6	112.4	29.4	37.0	46.1
399.4	3294.9	3381.7	4300.3	3286.8	3029.5	4754.7	3197.2	1694.1	881.3	2158.2
909.6	4395.9	5351.8	6494.0	2669.1	4180.5	4727.8	4146.4	2056.1	1225.8	3211.3
141.9	2351.2	2021.8	2509.1	1677.4	1786.4	1724.8	2249.0	721.4	562.2	1546.8
39.6	1718.2	2078.4	2206.4	1197.6	1864.8	1592.1	1898.6	489.1	652.8	1071.6
1591.2	5443.1	5999.0	6925.1	4193.9	4743.0	6756.4	4897.6	2058.0	1128.2	3641.4
3787.5	6224.0	7286.2	8594.0	3161.4	5773.8	6463.7	5824.4	3404.1	1441.8	4229.8
1217.6	3097.9	4133.4	4451.5	2469.9	3387.4	3425.3	3333.0	1728.7	1414.5	2106.3
127.4	2979.8	3779.6	4614.5	950.2	2799.2	2922.2	2834.9	939.8	278.9	1979.0
1378.6	5647.5	6563.2	7822.1	4160.8	4999.7	6271.5	5254.7	2368.4	1004.8	3742.8
1300.9	3992.7	4743.2	6278.7	2539.5	4222.5	4187.9	4032.6	1226.6	670.5	2474.2
1404.4	5713.7	6578.9	7940.0	3769.0	5066.6	5969.6	5257.4	2040.8	958.9	3700.3
4737.4	3724.9	4033.5	4431.0	4169.3	3738.1	4214.5	3646.2	3360.5	1511.9	2892.4
2517.3	2187.1	2122.4	2497.5	1483.7	2028.3	2848.7	2317.7	1322.6	976.3	1409.4
1907.9	4414.7	5323.8	5955.1	1463.8	4094.8	5042.7	4221.4	1067.8	470.4	2580.2

1777.3	2427.5	3974.5
49.8	117.4	94.4
3423.4	3405.7	4999.9
6205.6	4919.2	6090.0
551.9	1443.3	3545.4
8573.4	9785.3	8933.0
1394.3	1399.0	6298.0
487.3	387.8	498.9
2794.0	3098.1	2734.2
2584.6	3013.4	1802.2
24.9	314.2	2747.7
1796.5	1523.1	2015.8
1165.2	1577.2	1911.2
34.1	113.0	563.7
1973.3	2662.0	9029.8
27.2	29.7	44.2
982.6	618.1	711.8
6284.8	7246.1	5317.7
3891.3	1859.9	2986.7
1242.2	1061.2	1261.9
3658.2	3440.7	3170.8
6094.8	4496.1	7875.4
94.9	118.0	530.2
322.9	766.1	806.9
89.8	233.3	68.5
163.8	229.3	130.5
46.9	48.5	26.8
3098.1	2783.7	2895.1
6894.1	3962.6	3801.6
2265.5	1867.3	1444.0
2158.4	1870.9	1549.0
6615.1	4764.4	3890.0
9180.3	5679.3	2831.8
4489.7	4300.9	2808.8
5174.3	2627.1	1416.4
7852.4	5336.8	4796.2
6436.3	3747.0	2889.6
8001.0	5175.5	4456.2
4118.7	4164.2	2903.8
2382.4	2688.2	3606.3
5637.3	4253.5	2145.8

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s__Prevotella tannerae	67179
s__Prevotella veroralis	68037
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AY980722.1 gg_id:125862 human rectum mucosal biopsy clone LM60 AY980
EU776839.1 gg_id:348750 Mongoose lemur feces clone ML_aaj27h07 EU776
FJ674146.1 gg_id:531121 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU461720.1 gg_id:289257 mongoose lemur feces clone ML_aaj27f09 EU461
NZ_ACBX02000014.1 gg_id:484333 Prevotella copri str. DSM 18205 NZ_AC
DQ796037.1 gg_id:195851 human fecal clone RL202_aai50e11 DQ796
AY984075.1 gg_id:120238 human descending colon mucosal biopsy clone ME85 AY984
EU775444.1 gg_id:351341 Western lowland gorilla feces clone GOR_aad33f07 EU775
AB429508.1 gg_id:292064 Prevotella falsenii str. 04161(= JCM 15128) AB429
X73965.1 gg_id:2197 Prevotella intermedia X73965
AF414831.1 gg_id:70556 Prevotella intermedia str. 23-PIN AF414
NZ_ACSI01000003.1 gg_id:471122 Prevotella melaninogenica str. ATCC 25845 NZ_AC
NZ_ACSI01000031.1 gg_id:471123 Prevotella melaninogenica str. ATCC 25845 NZ_AC
AB182485.1 gg_id:108139 Prevotella multiformis str. PPPA28 AB182
EF405530.1 gg_id:216693 Prevotella nanceiensis str. LBN 298 EF405
AY689228.1 gg_id:107476 Prevotella nigrescens str. ChDC KB6 AY689
ACUZ02000034.1 gg_id:557672 Prevotella oris str. F0302 ACUZ0
L16472.2 gg_id:2185 Prevotella oulorum str. ATCC43324 L16472
Y13106.1 gg_id:72060 Prevotella pallens str. 9423 Y13106
GU302599.1 gg_id:550622 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
AB003385.1 gg_id:2085 Prevotella sp. str. sp34 AB003
AF183402.1 gg_id:30384 Prevotella tannerae str. 131-9-1 AF183
AY836507.1 gg_id:111357 Prevotella veroralis str. ATCC 33779 AY836
EU850489.1 gg_id:308966 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF255 EU850
AY980990.1 gg_id:123369 human rectum mucosal biopsy clone V110 AY980
FJ683706.1 gg_id:526349 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
FJ679759.1 gg_id:528783 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ680505.1 gg_id:526641 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
FJ677502.1 gg_id:528859 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6775
FJ676728.1 gg_id:525468 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6767
AJ581354.1 gg_id:151386 Prevotella sp. str. BI-42 AJ5813
FJ681718.1 gg_id:519244 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ675763.1 gg_id:515100 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6757
EU467352.1 gg_id:294044 chimpanzee feces clone CHIMP12_a12 EU467
FJ364596.1 gg_id:368761 feces adult twins and mothers; TS15 clone TS15_a04h02 FJ3645
FJ682151.1 gg_id:530650 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
GQ492287.1 gg_id:554830 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AY978047.1 gg_id:127644 human cecum mucosal biopsy clone LH92 AY978
FJ682990.1 gg_id:531754 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ674177.1 gg_id:523578 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
AF018455.1 gg_id:2191 rumen clone 12-7 AF018

2171.0	4614.2	4890.7	4970.1	4542.0	4469.2	5050.6	4605.7	3902.2	2383.0	3917.7
1506.4	6217.3	6262.6	7533.7	9030.2	6020.3	9965.9	5311.4	2829.2	1739.7	4233.3
121.4	2488.3	3250.9	4403.5	1847.2	2536.9	3512.5	3541.5	1795.1	1924.1	4272.5
58.8	26.4	20.7	31.7	11.4	26.9	25.9	24.2	22.0	15.7	21.1
4851.8	5960.6	6282.5	6848.6	4887.4	5426.0	5876.1	5734.5	3662.1	1941.8	4236.9
1135.5	1650.4	1746.3	2078.3	2011.8	1863.2	2346.3	1746.9	1087.4	434.3	1203.9
506.9	5139.7	4586.4	6323.5	7202.7	4261.8	6293.9	4191.4	2125.6	1312.4	3133.9
955.6	2146.9	2379.2	2619.6	2614.2	2072.1	2459.1	2002.3	1583.5	1021.8	1682.4
40.9	1408.4	845.9	829.7	1404.2	882.5	818.6	814.9	991.9	475.9	515.1
38.2	347.1	519.0	664.7	219.5	321.6	305.7	302.2	124.6	48.4	146.7
47.4	2097.8	3125.4	3500.2	1036.3	1993.6	2708.2	2206.8	873.0	674.7	1404.5
110.4	727.8	1085.0	1489.9	389.5	728.4	1119.1	919.5	338.8	100.5	464.3
115.9	728.1	1086.2	1492.1	391.2	731.2	949.2	922.2	319.9	103.9	434.1
33.3	105.2	84.6	53.4	58.8	70.0	31.2	157.4	25.1	27.9	81.3
63.3	348.1	337.2	433.9	305.3	173.1	254.2	151.7	190.8	81.6	123.5
89.5	38.8	33.7	61.2	55.8	23.9	46.7	31.8	47.8	32.8	51.9
59.7	1512.1	1706.9	1546.2	1779.6	1627.9	1022.0	2070.4	1581.3	818.6	1121.8
1341.2	3133.8	3487.9	4392.3	2320.2	3794.4	3070.7	3323.7	1453.4	1149.8	2154.4
3290.6	6393.7	6246.1	7166.7	6347.6	5650.8	7736.5	6174.0	5387.3	3359.4	4898.0
40.5	117.0	314.5	251.7	49.7	82.0	88.8	181.5	160.7	25.6	93.6
88.6	1965.6	1617.4	2201.7	1399.0	1817.7	2422.5	2094.0	557.2	267.4	1238.8
44.8	172.5	216.7	239.9	221.1	132.4	245.7	118.6	79.3	71.0	145.4
565.1	4802.1	5571.1	6819.9	4722.3	4194.6	5857.5	4754.8	4235.1	3289.9	4081.8
549.8	1216.8	1380.6	1429.3	1388.7	1051.0	1460.6	998.8	662.2	257.1	899.6
470.9	6459.6	7599.2	8659.8	7879.1	6234.4	9719.5	6003.4	2090.7	1340.5	3950.2
1510.2	682.7	1010.2	1084.9	682.6	852.1	1142.3	964.0	768.9	570.8	761.6
815.8	5068.5	6167.6	7648.1	2540.9	4635.4	5275.7	4862.4	1677.4	1006.8	3400.3
1569.9	5168.1	5497.5	6257.1	5711.3	5225.5	6195.6	4716.9	5638.7	5564.4	6112.4
103.4	2706.8	3609.4	4406.5	981.0	2798.7	2850.4	2647.5	851.7	327.6	1880.4
653.6	6385.0	7645.6	9423.2	2274.6	5858.7	6387.7	5989.6	1491.9	996.1	4195.7
19583.8	12533.1	11101.9	12958.0	13962.9	11974.5	14940.7	11013.0	15854.7	12911.8	14128.6
153.4	3228.5	2976.7	3437.1	2497.6	2459.3	4145.1	2522.8	1685.1	1216.1	2770.6
2804.1	3484.1	3413.6	3366.1	2865.7	3496.7	3550.8	2851.8	4078.9	3395.2	4230.0
210.1	2430.1	2538.3	2923.0	1242.3	1835.2	1764.5	2765.6	924.1	554.4	1749.7
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251.8	2650.1	2953.5	3344.1	1711.6	2454.6	3049.6	2650.7	1386.1	1012.1	1782.6
1636.7	1878.6	1775.1	2324.2	1342.1	2020.7	1473.9	1998.0	1359.0	850.0	1387.7
851.0	4315.2	5594.9	6364.1	2205.3	4192.3	4383.5	4263.0	1271.9	845.0	2944.1
500.5	3907.6	3692.4	4416.0	3402.7	3885.4	4184.9	4381.5	5032.1	4042.0	4654.0
53.9	101.1	113.7	114.2	75.2	110.7	73.7	69.8	73.5	60.6	63.3

4923.1	5866.4	6571.6
5966.4	5362.5	8012.3
3622.5	3131.1	4765.7
27.0	34.4	20.1
6303.2	5612.5	3537.6
1780.9	2114.6	2003.0
5042.2	3935.0	4669.3
2072.3	2286.6	2058.2
883.1	616.1	989.2
855.4	735.8	1189.2
3844.0	2594.1	1684.0
1877.4	904.9	442.3
1879.7	906.4	441.6
66.6	65.2	43.7
319.2	293.5	301.6
44.8	40.9	39.4
1758.2	1565.5	1006.6
4563.7	2799.1	3602.9
7069.0	6425.0	6159.4
206.4	129.9	57.1
2514.3	1330.4	737.0
178.2	196.0	173.9
6103.8	5330.2	4280.9
1540.3	1419.3	822.5
7351.4	5296.0	8027.0
827.4	1575.6	902.8
8439.8	4638.7	3924.0
4873.9	4779.1	4783.5
4836.1	2316.7	1272.6
10526.0	5204.7	4045.4
11075.9	11018.2	13629.8
2894.7	2415.4	2995.5
2768.0	4662.5	2691.4
2724.7	2158.5	800.7
5125.3	4480.4	6515.1
6357.2	4495.5	6179.6
3341.6	2618.4	2630.9
2276.8	2515.1	2056.8
7263.7	3815.0	2343.0
3986.1	3686.7	3425.9
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DQ797120.1 gg_id:193805 human fecal clone RL386_aao87c04 DQ797
AY349401.1 gg_id:92942 human oral cavity clone IK053 AY3494
AM420032.1 gg_id:239506 Noma subgingival plaque clone 201G02(oral) AM420
EF445275.1 gg_id:211356 dairy cow rumen clone NED5F5 EF4452
EF097566.1 gg_id:178558 mouse cecum clone SWPT19_aaa04e03 EF0975
FJ684982.1 gg_id:529185 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
GU302978.1 gg_id:583107 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ682998.1 gg_id:528890 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
FJ557802.1 gg_id:522669 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
FJ674216.1 gg_id:522084 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ365605.1 gg_id:360621 feces adult twins and mothers; TS20 clone TS20_a04h03 FJ3656
GQ491765.1 gg_id:581537 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU460026.1 gg_id:287974 mammals their gut microbes eastern black and white colobus feces clone COL_aai13 EU460
L16483.1 gg_id:2193 Prevotella disiens L16483
EU461736.1 gg_id:291589 mongoose lemur feces clone ML_aaj28a06 EU461
GQ448975.1 gg_id:578219 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
EU748460.1 gg_id:348149 neotropical folivorous flying bird adult hoatzin crop clone hoa61_09b11 EU7484
NR_029284.1 gg_id:576355 Prevotella dentalis str. ES2772; DSM 3688 NR_02
DQ799957.1 gg_id:193335 human fecal clone RL247_aaj22c11 DQ799
FJ678896.1 gg_id:526034 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
AF371892.1 gg_id:44821 swine intestine clone p-2517-18B5 AF3718
AY836508.1 gg_id:109626 Prevotella loescheii str. NCTC 11321 AY8365
AF371877.1 gg_id:28413 swine intestine clone p-1310-a5 AF3718
FJ673401.1 gg_id:520866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
GQ491454.1 gg_id:539050 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ363048.1 gg_id:367089 feces adult twins and mothers; TS148 clone TS148_a02d02 FJ3630
EU467386.1 gg_id:291328 chimpanzee feces clone CHIMP12_g09_1 EU467
EF445259.1 gg_id:212167 dairy cow rumen clone NED5D8 EF4452
AB185757.1 gg_id:104511 rumen clone U29-B08 AB185
DQ801361.1 gg_id:187628 human fecal clone RL388_aao94e03 DQ801
EU747951.1 gg_id:339093 neotropical folivorous flying bird adult hoatzin crop clone hoa11_70F09 EU747
FJ671740.1 gg_id:532041 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
DQ801635.1 gg_id:180138 human fecal clone RL117_aae93b10 DQ801
FJ681316.1 gg_id:519417 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ684766.1 gg_id:529366 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
FJ681390.1 gg_id:531139 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ797096.1 gg_id:186007 human fecal clone RL386_aao86h09 DQ797
FJ679785.1 gg_id:510855 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
EU773488.1 gg_id:335634 Bonobo feces clone BNO_aaa04a03 EU7734
EU467084.1 gg_id:303306 mongoose lemur feces clone ML_aae87f08 EU467
GQ491976.1 gg_id:573810 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491

1414.7	3017.1	2834.9	3264.6	2920.1	2692.9	2900.4	3001.2	1445.2	865.4	2102.0
59.8	3228.4	2561.2	2498.5	1835.0	1993.7	2356.5	2244.8	4271.7	2126.3	2368.1
119.2	2960.6	3586.4	4705.9	997.7	3221.8	2645.3	3082.6	792.1	375.0	1919.6
49.2	18.9	26.0	25.0	25.2	21.7	26.3	22.2	28.4	19.7	28.2
39.9	520.8	1129.7	1259.8	242.2	373.2	466.8	629.8	268.2	45.3	339.4
1307.6	4357.9	5555.7	6646.7	2327.0	4053.0	4648.2	4295.2	1580.7	602.8	2929.0
43.2	25.9	27.1	20.3	26.5	21.5	23.2	22.7	22.2	20.5	17.6
1037.2	2780.9	3490.1	4021.8	2422.4	2753.3	2983.3	2792.5	1698.7	1075.8	2321.5
1280.6	1035.7	1500.1	1737.2	582.1	1138.7	1444.3	1212.8	509.2	225.3	651.3
1407.7	3904.5	5243.2	5767.6	1938.0	3781.1	4135.3	3998.6	1269.5	533.6	2590.5
98.9	2020.8	2208.7	2633.4	1281.2	2117.3	2440.9	1819.0	369.8	246.1	1124.0
47.5	3581.4	5056.5	6271.5	983.2	3903.4	3578.4	3941.7	588.4	245.8	2011.5
45.7	202.4	399.3	547.2	52.0	89.7	52.5	147.3	61.7	27.9	60.5
47.2	150.8	156.8	145.1	54.2	37.4	58.2	155.5	28.1	20.3	22.6
52.2	25.8	24.2	30.9	17.2	19.5	18.9	22.4	30.8	28.2	28.7
97.3	1658.1	1877.8	2027.3	1405.5	1281.6	1843.9	1602.3	472.1	322.0	865.9
1054.9	3760.2	4663.2	5476.6	2091.3	3661.3	3505.7	5511.0	2976.4	4059.1	5122.2
55.8	210.0	403.5	427.8	84.3	286.7	233.7	289.8	47.6	33.4	127.4
337.9	3553.5	4027.8	4896.0	5253.9	3985.7	6902.6	3639.3	1168.3	870.0	2082.4
129.0	2527.4	3338.7	3984.0	1027.9	2387.9	2148.5	3141.2	726.9	533.5	3037.9
172.3	5050.4	5348.2	7208.4	3908.4	3184.5	4263.7	3759.4	3438.0	2859.6	3846.2
31.7	42.0	70.1	67.7	39.6	43.8	46.1	38.5	25.3	26.9	34.8
34.6	420.3	656.0	806.8	93.5	494.4	501.7	476.4	57.2	40.0	196.1
1041.3	1998.8	2639.8	3005.1	2059.1	1957.7	2257.9	2048.8	1579.8	900.3	1628.8
151.5	2762.3	3545.4	4494.4	1300.3	2883.4	3070.7	3056.9	1182.9	439.5	1874.1
2350.8	4733.8	5707.1	6472.2	4637.8	5192.2	5935.1	4963.4	7460.9	6041.1	5582.0
149.2	2837.5	3403.0	4147.2	1542.1	3009.9	3269.0	2964.7	707.7	1036.9	1760.7
58.2	742.2	1044.0	1143.2	201.5	667.4	642.4	690.4	127.7	53.5	456.6
39.2	35.0	31.7	53.7	49.4	32.1	42.0	39.8	27.6	35.9	26.0
2935.2	2656.5	4631.3	5253.2	2087.4	2364.1	4369.1	2974.6	1070.6	894.7	3144.3
46.5	1316.5	1687.5	2222.2	589.0	1506.7	1147.6	1317.0	1103.8	886.7	672.7
8959.4	6477.3	7230.9	7733.8	5263.4	5661.1	6561.1	5519.2	5774.9	5010.3	8308.5
101.5	2082.1	3493.7	4391.4	1932.5	2844.0	5331.4	3082.5	809.4	671.0	2876.4
131.6	3279.6	4313.8	5324.6	1055.6	3051.9	3449.7	3203.1	890.2	355.1	2256.4
115.7	445.6	511.3	684.5	378.7	372.9	458.6	402.2	244.1	179.9	596.4
3544.8	9327.2	8008.6	9203.8	8351.0	7183.2	9887.3	7396.2	7463.8	7812.6	7670.3
3767.7	3669.7	4307.0	4818.4	2674.6	3316.5	4302.0	3348.3	2471.7	1383.8	2826.7
61.3	661.2	975.6	1056.4	793.1	778.6	1059.3	745.8	335.7	142.5	687.2
118.8	971.0	906.4	994.9	713.7	781.2	858.2	753.4	699.4	475.4	795.9
127.2	1004.5	879.6	1098.7	801.4	687.6	872.2	885.5	435.9	275.1	633.5
819.4	4638.1	6104.6	7612.2	2186.3	4644.8	4857.8	4671.9	1257.3	826.8	2880.8

2975.8	2949.9	1973.5
2094.8	2209.6	2150.1
6061.8	3017.5	1964.9
24.8	33.5	27.7
843.5	1030.2	448.9
7476.9	4251.8	2238.9
23.9	24.4	23.0
4613.0	2713.2	2274.7
1977.9	1461.3	624.7
6412.2	3909.4	1988.8
2123.2	1509.2	1340.6
7552.0	3259.9	1698.9
216.3	344.5	94.7
56.6	89.3	31.1
37.0	36.6	35.7
2203.4	1475.1	811.0
5115.0	5033.2	5877.5
319.8	440.6	98.6
3892.8	3368.7	5174.7
4043.0	2374.6	4035.2
5317.1	4381.6	2668.0
55.5	66.9	90.1
818.3	517.8	140.6
3520.5	2207.6	1910.7
5018.8	2894.9	2100.5
5457.7	5714.0	4194.3
4485.6	3114.7	2637.8
1539.3	781.1	273.1
35.1	64.0	29.5
4222.5	3245.0	4536.6
2716.9	1219.5	1419.4
7632.4	6371.8	6070.7
3902.5	2231.8	2887.5
5654.7	2784.9	2242.5
363.1	800.4	309.7
7796.9	7115.1	8194.6
4942.3	3388.2	2117.4
901.2	882.3	734.5
735.2	1000.7	715.6
1117.5	1129.1	994.9
8541.4	4252.9	2956.9

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FJ365580.1 gg_id:357467 feces adult twins and mothers; TS20 clone TS20_a04e08 FJ3655
FJ681551.1 gg_id:515734 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
EU773702.1 gg_id:340238 Capybara feces clone CAP_aah97c05 EU773
FJ365485.1 gg_id:368449 feces adult twins and mothers; TS20 clone TS20_a03d11 FJ3654
FJ681706.1 gg_id:516236 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ678113.1 gg_id:509724 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6781
EU459803.1 gg_id:296515 Prevost's squirrel feces clone SQ_aah79b04 EU459
AB270064.1 gg_id:170559 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ674011.1 gg_id:532013 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU461722.1 gg_id:301626 mongoose lemur feces clone ML_aaj27g01 EU461
EU467113.1 gg_id:292253 mongoose lemur feces clone ML_aae88e08 EU467
FJ681046.1 gg_id:521640 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
AB185633.1 gg_id:105738 rumen clone F24-F12 AB185
EU748247.1 gg_id:304355 neotropical folivorous flying bird adult hoatzin crop clone hoa45_54F07 EU748
GU302809.1 gg_id:536141 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU771540.1 gg_id:321723 Hamadryas Baboon feces clone AFBAB_aai01e04 EU771
GQ493961.1 gg_id:561151 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GU303821.1 gg_id:570979 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU531871.1 gg_id:272155 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
GQ025673.1 gg_id:396867 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ025
EF445225.1 gg_id:204190 dairy cow rumen clone NED5D2 EF445
FJ679994.1 gg_id:528287 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6799
EU777529.1 gg_id:324283 Sumatran orangutan feces clone orang1_b04 EU777
FJ682571.1 gg_id:516854 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
FJ673303.1 gg_id:515870 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ673617.1 gg_id:525511 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
AJ009933.1 gg_id:2170 Prevotella aff. ruminicola Tc2-24 AJ0099
FJ364399.1 gg_id:360425 feces adult twins and mothers; TS15 clone TS15_a02d11 FJ3643
GQ492549.1 gg_id:545761 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU461619.1 gg_id:300684 mongoose lemur feces clone ML_aaj25f10 EU461
FJ364599.1 gg_id:358738 feces adult twins and mothers; TS15 clone TS15_a04h05 FJ3645
GQ449130.1 gg_id:544926 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ449
AB269968.1 gg_id:171872 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
GQ491322.1 gg_id:582462 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
GQ867327.1 gg_id:573688 and prevalence blaTEM genes Arctic seals colon content clone WSp68 GQ867
EU463137.1 gg_id:295917 naked mole-rat feces clone molerat_aai70d12 EU463
GQ493782.1 gg_id:588929 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ673118.1 gg_id:521450 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
FJ678505.1 gg_id:523335 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GU302532.1 gg_id:587640 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU459683.1 gg_id:299215 ring-tailed lemur feces clone RT_aai10g09 EU459

50.5	2235.9	2992.5	3794.2	492.7	2659.8	2510.1	2704.9	482.9	322.2	1201.6
1501.1	4750.5	6105.8	7299.6	3988.4	5098.9	5911.9	5198.4	2130.2	1576.3	3793.7
42.0	254.1	504.7	674.5	84.7	363.9	284.0	327.6	57.6	31.9	160.6
40.8	2605.1	3341.3	4503.9	290.2	2106.5	2249.5	2647.9	421.3	296.3	1095.0
138.4	3558.0	4737.8	5835.0	1070.1	3249.2	3492.1	3396.7	913.6	350.0	2354.3
10057.6	5783.3	6474.1	6528.1	4954.9	5139.1	8069.7	5878.9	4197.7	4303.2	7186.3
109.7	4293.6	4782.8	5890.3	1262.0	3607.1	3856.6	4013.6	817.9	470.8	2643.6
41.6	58.0	66.0	62.3	27.1	35.3	36.2	39.9	31.8	18.2	24.8
105.4	3141.6	4271.4	5306.1	1273.2	3351.5	3321.5	3164.3	969.2	400.6	2166.0
1899.1	2190.5	2731.4	3831.9	1260.0	2010.7	2228.2	2189.1	1151.2	545.9	1337.6
1322.2	2735.4	3121.6	3662.5	4367.0	3005.5	4132.6	2465.2	1318.3	788.0	1796.0
500.5	1358.3	1447.1	1840.5	1124.3	787.2	1182.5	1086.2	1371.4	710.0	1351.4
58.8	50.5	65.6	68.2	51.4	42.3	52.9	47.3	30.7	19.1	31.6
552.0	4480.9	4890.6	5948.5	4932.0	4686.8	5985.9	4924.0	3525.3	1180.2	3306.7
143.6	5666.0	7374.5	9166.2	1597.7	4672.8	5037.7	5403.8	945.1	482.8	3096.5
974.2	4710.6	5209.2	5805.4	4811.2	3987.0	7078.8	4995.8	5864.0	2841.7	4690.3
65.4	4363.9	5833.0	7375.2	1327.7	4448.1	4498.3	4589.1	903.4	461.5	2510.7
186.7	927.3	1120.5	1277.8	1299.4	1115.9	1407.4	1019.5	703.7	306.0	828.2
171.8	599.0	844.0	1077.3	454.0	360.5	574.7	644.5	521.8	27.7	342.4
1606.0	4082.9	4081.2	4970.0	4504.0	5418.7	5346.8	4417.3	3622.6	2374.4	3950.8
46.6	32.8	32.9	32.0	30.6	25.6	28.1	27.4	25.7	21.6	28.1
1451.2	2037.1	1987.5	2137.5	1520.9	1892.5	1926.9	2218.9	1189.2	628.6	1233.2
352.1	485.2	456.3	320.8	234.9	392.3	306.0	282.3	262.9	125.0	289.0
862.2	3891.2	4950.4	5581.3	2263.5	3768.0	4249.2	3864.3	1355.1	882.8	2685.6
1287.9	4960.5	5600.5	6709.7	2497.3	4137.3	4731.7	4698.7	1722.1	1021.8	3334.6
1224.4	5436.4	5646.1	7211.1	2820.5	4585.7	5123.0	4722.7	1907.6	1988.2	3809.5
39.2	31.5	36.6	33.9	29.0	17.1	32.0	22.8	24.0	15.3	30.7
255.7	2385.6	2267.9	2607.8	3462.7	2335.2	3284.8	2095.5	1072.7	691.1	1391.2
66.7	3903.6	5198.6	6513.0	1134.6	4142.7	4158.6	4222.8	674.1	361.7	2224.9
32.5	21.2	20.5	29.9	12.8	20.9	26.5	27.5	19.3	8.0	15.8
1109.4	2679.8	3143.2	3567.4	2049.0	3277.6	3009.7	3080.7	943.3	475.0	1656.8
807.6	3960.1	4725.7	5303.7	3061.0	3984.8	4075.6	4551.8	5173.0	3268.3	4172.3
73.6	496.2	514.2	794.1	320.7	487.4	619.6	652.9	157.0	126.3	248.7
69.7	3452.0	4555.2	5633.4	835.6	3659.2	3686.1	3703.0	588.5	304.0	1935.4
116.5	2758.6	2888.8	3034.8	2543.3	2447.2	3113.1	2629.8	3082.0	976.8	2323.7
163.7	2107.5	2781.6	3572.4	1208.3	2032.5	2328.2	2136.3	530.9	534.7	1340.1
1878.3	3700.4	4548.0	5043.0	1680.8	3496.3	3986.8	3332.7	3602.2	2607.8	3788.4
155.9	1515.5	1980.2	2173.2	1255.1	1414.7	1631.1	1425.0	662.4	418.5	635.7
4732.3	3658.8	3749.8	4660.4	2805.7	3026.7	3567.4	3084.8	2862.3	1663.2	2731.9
3434.8	2091.2	3546.0	3032.0	1978.4	903.8	2796.8	2130.0	2805.7	2901.8	3755.7
308.0	1551.1	1891.3	1971.3	672.6	1148.5	1393.4	1218.2	1091.9	512.1	839.4

4327.0	2281.0	1970.9
7210.9	4801.3	3801.4
1163.9	239.6	155.9
4047.9	2173.1	1723.1
5906.3	3138.0	2312.7
6608.1	7333.0	4728.0
6621.9	3189.7	1379.3
25.9	62.7	52.4
5860.2	2879.5	1484.6
3401.1	2628.6	3049.3
2357.9	2642.3	3126.2
1239.2	1777.1	1036.3
53.7	79.4	118.1
5510.4	5591.6	6663.1
9545.9	5152.8	3553.6
4960.7	4870.1	5514.5
8446.7	4076.0	2677.5
1094.5	1066.4	734.3
1044.6	978.5	392.5
4390.6	4851.8	4941.5
30.9	27.8	34.0
2232.8	2296.4	1686.6
369.9	559.0	195.2
6060.7	3675.5	2271.0
7245.8	4287.1	2277.7
7375.5	4792.4	5636.0
19.9	25.7	17.4
2135.9	1943.3	2551.9
7566.4	3687.9	1798.4
27.4	37.8	20.7
4091.0	2696.4	1827.6
5473.3	4696.8	3602.7
1033.3	633.6	824.4
6510.0	3115.4	1585.6
2267.4	1887.0	1697.7
4597.4	2487.8	1859.6
5113.8	3588.9	1954.3
2718.8	1401.2	1132.9
4550.2	3296.4	1973.0
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EU773599.1 gg_id:314731 Capybara feces clone CAP_aah98f07 EU773
EU458702.1 gg_id:290109 Goeldi's marmoset feces clone CAL_f02 EU458
DQ308594.1 gg_id:150163 sheep rumen enrichment clone 196.F11 DQ308
AF018486.1 gg_id:2208 rumen clone 12-109 AF0184
EU748085.1 gg_id:303751 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44f02 EU748
EU469471.1 gg_id:297749 black lemur feces clone BKLE_d11_1 EU469
FJ684964.1 gg_id:523901 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU850591.1 gg_id:329927 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF415 EU850
GU302651.1 gg_id:549174 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ493350.1 gg_id:583870 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ557580.1 gg_id:520942 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5575
EU462060.1 gg_id:292785 black-handed spider monkey feces clone SPIM_aaj34b09 EU462
FJ680644.1 gg_id:518150 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
FJ364333.1 gg_id:357026 feces adult twins and mothers; TS15 clone TS15_a01f12 FJ3643
EU460000.1 gg_id:301320 Prevost's squirrel feces clone SQ_aah82f08 EU460
FJ681471.1 gg_id:524449 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
FJ678726.1 gg_id:516894 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ682499.1 gg_id:521915 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
FJ673331.1 gg_id:524827 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU773472.1 gg_id:356372 Bonobo feces clone BNO_aaa04h04 EU773
EU462114.1 gg_id:301147 black-handed spider monkey feces clone SPIM_aaj35c02 EU462
GU302758.1 gg_id:581246 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ179741.1 gg_id:453900 Heterogeneity vaginal microbial within individuals vagina clone VE62D04 GQ179
FJ674220.1 gg_id:513326 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
EU778215.1 gg_id:304851 feces clone RL388_aao93e08 EU778
AY244911.1 gg_id:84913 cow rumen clone BF33 AY244
GU302695.1 gg_id:542879 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ365296.1 gg_id:367816 feces adult twins and mothers; TS20 clone TS20_a01c03 FJ3652
EU531869.1 gg_id:261330 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
FJ557908.1 gg_id:522663 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5579
EU462176.1 gg_id:289542 black-handed spider monkey feces clone SPIM_aaj36e11 EU462
GQ493115.1 gg_id:581089 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ801307.1 gg_id:195099 human fecal clone RL388_aao93g04 DQ801
EU259409.1 gg_id:251069 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC33 EU259
EU774357.1 gg_id:319810 Chimpanzee feces clone CHIMP1_aaj39a04 EU774
FJ683112.1 gg_id:516530 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EU463602.1 gg_id:300061 domesticated horse feces clone horsej_aai89e10 EU463
FJ674149.1 gg_id:516591 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
AY977838.1 gg_id:120596 human cecum mucosal biopsy clone LF34 AY977
FJ681877.1 gg_id:532296 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
DQ518919.1 gg_id:181627 Prevotella sp. str. 4401737 DQ518

97.7	3344.2	3325.0	3984.3	3463.9	2971.8	4311.7	3283.6	1344.4	869.5	2116.8
403.9	4714.0	5059.7	6191.8	5771.0	4445.0	6349.4	4107.5	1794.7	813.3	3035.7
216.6	510.7	679.1	921.0	233.9	389.8	273.8	581.1	252.7	74.2	273.1
73.7	147.2	128.4	268.2	36.4	63.4	75.4	80.2	25.6	29.8	48.1
45.6	656.4	886.1	949.6	222.9	623.5	487.8	728.1	602.1	86.0	539.9
1442.9	3382.4	3816.1	4602.8	5349.5	3331.9	5263.5	3028.6	1623.0	851.2	2233.7
549.7	3876.4	3890.8	4982.9	4245.0	4033.6	4299.8	3560.6	2664.5	899.1	2953.4
165.1	5334.3	4384.9	5587.3	3770.3	3476.9	4408.7	3529.1	2569.5	1680.9	3236.5
138.0	2481.0	3116.1	3704.8	2212.2	2559.8	2970.6	2376.3	1746.0	3365.4	1566.7
374.7	5133.8	6296.9	7452.0	2718.5	5281.2	5462.1	5243.7	2490.9	1399.2	3523.0
1385.2	537.4	645.9	672.0	421.6	584.2	700.6	652.4	430.5	151.7	354.0
1402.6	3898.2	3942.2	4239.3	3581.5	3155.0	6103.3	3338.5	1716.0	1630.0	2923.2
249.4	5505.7	6255.1	7574.2	3264.2	5152.7	6122.6	5817.5	3562.5	2164.1	6360.3
223.8	4207.1	5137.7	6094.2	3036.4	4009.2	4458.6	4089.3	2090.3	1370.8	3301.0
140.4	1468.4	1676.5	2622.1	1030.7	1289.3	1250.5	1559.8	457.1	460.9	1397.8
926.3	2885.6	3481.9	4117.7	2552.9	2755.3	3578.8	2866.7	1620.2	1040.5	2194.7
808.0	3879.8	4902.2	6142.8	2468.8	3830.8	4276.4	3793.0	1455.9	995.8	2807.9
61.1	1179.0	2198.2	2675.9	1324.4	1282.4	2205.8	2073.9	397.0	274.4	1535.7
1119.8	4623.0	5417.6	6133.7	3005.8	4353.4	4756.9	4158.2	2689.8	1962.8	3456.5
3862.4	8034.0	8275.8	8832.2	8962.1	7825.2	10172.6	6928.9	4348.4	2237.4	5427.3
80.4	2026.6	1734.1	2169.4	1258.5	1762.8	1493.1	2224.8	718.1	471.8	1528.7
40.0	132.0	296.7	424.2	20.0	20.1	16.1	67.6	19.6	16.1	14.7
57.0	26.8	33.3	43.3	24.6	33.6	27.1	38.4	24.4	26.5	24.4
1333.2	3050.0	3598.5	4005.2	2838.7	2941.8	3348.2	2803.4	2500.6	1807.3	2351.5
244.1	6337.4	7287.9	9377.1	5941.3	6246.7	8417.1	6852.7	2077.2	683.2	7029.2
29.8	91.7	101.2	142.5	57.8	39.4	75.0	75.0	34.4	22.1	35.2
986.1	2185.8	2057.0	2336.0	976.3	1530.9	1496.6	1908.9	1120.5	795.8	1852.7
54.7	4132.8	5280.5	6374.5	1661.9	4197.3	4736.9	4528.1	882.5	572.4	2462.4
14339.7	11843.8	10809.3	11495.5	10745.3	10549.7	11192.7	10056.6	20935.8	13410.1	12377.5
2314.7	4762.1	4435.2	5580.1	4689.5	5142.1	5418.8	5041.4	4924.4	3082.7	3568.2
217.1	3980.0	3240.6	4545.3	5450.4	3115.5	4633.0	3314.7	2919.8	2197.8	2504.2
56.7	3606.4	5100.8	6318.5	1057.8	3678.2	3600.1	3724.2	551.6	252.3	2030.2
5737.8	6043.8	5972.0	5993.6	4698.3	5200.7	6057.1	5315.1	6343.7	4588.1	5707.4
93.0	468.6	679.0	993.8	74.6	197.8	100.9	250.2	72.8	29.2	86.7
259.6	1049.1	1160.7	1310.5	361.0	693.0	515.1	849.8	337.1	202.1	603.5
1327.3	3808.5	4613.0	5699.1	1989.9	3384.6	3835.3	3780.1	1681.2	657.9	2786.0
475.9	1749.0	1850.8	2038.5	1668.0	1991.7	1841.6	1785.7	1250.9	769.1	1550.0
97.7	2347.5	3341.1	4144.3	989.4	2575.8	2620.9	2437.9	660.6	247.0	1534.3
444.5	5190.9	5524.3	5728.8	5302.6	4577.3	6886.7	5124.6	5149.5	3250.8	4555.7
814.6	5790.4	7047.3	8738.2	2725.5	5296.0	6026.4	5555.5	1680.1	1009.7	3884.5
49.8	109.8	205.0	219.0	180.0	146.4	170.7	107.4	41.6	33.7	96.0

4129.8	3045.1	6826.2
5082.7	3851.5	5415.2
757.7	636.1	411.5
170.2	209.9	35.9
780.4	898.8	472.4
3578.3	3239.2	3492.2
5267.2	4625.1	4728.6
4206.3	4248.8	6012.6
2846.1	3303.5	2869.6
7899.0	5003.5	3904.7
718.3	853.3	467.0
4211.6	3209.0	2938.5
5905.6	5834.4	7091.4
5855.8	4370.0	4396.5
1882.6	2204.5	1397.0
3509.4	2749.9	2197.2
6455.0	3589.2	3569.1
1882.8	1367.3	1834.5
7186.5	4122.5	3159.0
7522.2	6883.2	6830.6
1951.4	1746.4	1272.5
123.2	258.2	23.5
42.9	33.7	23.8
5183.9	3112.0	2481.5
7282.0	5774.8	9581.3
119.1	72.9	45.0
2123.2	1907.3	834.9
6625.8	4127.0	3442.7
10707.1	11877.7	10392.3
5751.0	5104.7	5053.8
3343.0	3020.6	3011.7
7611.4	3130.1	1709.1
6132.1	6369.9	6997.9
748.4	423.0	99.4
1146.6	1320.7	690.1
6344.0	3824.6	3190.3
2129.4	2279.6	3721.1
4671.7	2263.1	1006.4
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9644.0	5300.0	4209.2
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GQ492115.1 gg_id:560771 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ684931.1 gg_id:516464 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU467101.1 gg_id:291438 mongoose lemur feces clone ML_aae88c02 EU467
FJ684855.1 gg_id:524957 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU774233.1 gg_id:335566 Chimpanzee feces clone CHIMP1_aaj37h12 EU774
FJ673972.1 gg_id:520856 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
AY979519.1 gg_id:120419 human transverse colon mucosal biopsy clone M167 AY979
FJ684201.1 gg_id:528619 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU776852.1 gg_id:341421 Mongoose lemur feces clone ML_aaj27a05 EU776
EF603058.1 gg_id:235046 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
FJ674046.1 gg_id:530392 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
FJ683175.1 gg_id:510416 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ673465.1 gg_id:532179 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
EF445226.1 gg_id:211557 dairy cow rumen clone NED5H5 EF4452
FJ684873.1 gg_id:529031 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU467249.1 gg_id:296720 black-handed spider monkey feces clone SPIM_h08 EU467
AY982301.1 gg_id:117207 human sigmoid colon mucosal biopsy clone MI62 AY982
FJ673599.1 gg_id:530725 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
EF097294.1 gg_id:187934 mouse cecum clone SWPT18_aaa04e10 EF0972
DQ797179.1 gg_id:190072 human fecal clone RL386_aao88a06 DQ797
DQ796159.1 gg_id:198715 human fecal clone RL202_aai52d10 DQ796
EF097208.1 gg_id:180282 mouse cecum clone SWPT18_aaa03b07 EF0972
DQ796142.1 gg_id:187055 human fecal clone RL202_aai52b12 DQ796
EU459673.1 gg_id:299368 ring-tailed lemur feces clone RT_aai10f06 EU459
GU470887.1 gg_id:539347 Prevotella sp. oral taxon 302 str. F0323 GU470
FJ676106.1 gg_id:515850 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6761
FJ682447.1 gg_id:520581 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6824
FJ834265.1 gg_id:510667 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_48H06 FJ8342
EU459943.1 gg_id:290924 Prevost's squirrel feces clone SQ_aah81f06 EU459
AM422125.1 gg_id:245050 Prevotella amniotica str. CCUG 53648 AM422
DQ795906.1 gg_id:178860 human fecal clone RL245_aai84e05 DQ795
EU778318.1 gg_id:347953 feces clone RL388_aao93f08 EU778
FJ678522.1 gg_id:512781 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
EU776927.1 gg_id:316941 Naked mole-rat feces clone molerat_aai71d05 EU776
FJ673642.1 gg_id:520686 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU850466.1 gg_id:338302 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF44 EU850
GQ492508.1 gg_id:571918 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ681312.1 gg_id:527502 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
FJ684758.1 gg_id:524124 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
EU473087.1 gg_id:299362 douc langur feces clone DL_1aaa02g12 EU473
DQ801633.1 gg_id:198472 human fecal clone RL117_aae93b07 DQ801

68.6	3168.2	4166.2	5259.7	999.8	3144.0	3204.7	3374.1	716.0	402.5	1835.5
138.9	1215.2	1957.0	2162.3	566.6	1001.8	1394.1	1284.8	549.6	105.8	705.8
152.5	1111.5	1048.2	1336.6	1968.1	920.4	2317.3	815.8	464.1	393.8	589.5
78.2	3964.6	5059.0	7324.2	1352.1	3628.3	3774.3	4133.8	837.1	366.6	2516.1
249.3	1879.7	2299.8	2746.1	2211.3	2269.4	2279.9	1860.3	1372.1	1097.7	1501.7
1173.9	5164.1	5885.4	6976.9	4252.8	4597.2	6037.2	4929.1	5820.1	3726.8	6139.0
1423.7	3736.4	3985.9	4859.0	2035.0	3297.2	3143.8	3833.5	1446.7	694.2	2300.2
121.7	909.4	1462.6	2251.3	814.2	539.3	1130.6	1293.8	538.6	47.1	563.8
42.2	713.8	1026.4	1246.6	848.2	1015.0	1464.9	856.3	628.3	289.2	627.2
69.5	46.4	92.9	153.2	65.8	58.8	59.4	66.7	39.3	38.1	39.3
4277.4	5982.2	4162.3	4089.2	4992.7	4293.0	4890.3	4079.6	5487.4	4159.8	3726.2
104.3	3370.6	4042.2	4251.8	1150.9	2955.2	3027.0	3167.5	1458.7	450.0	2101.5
359.0	5157.5	6223.5	7538.3	4558.3	5108.6	6223.8	4708.6	1990.4	1121.4	3471.0
35.5	20.6	22.9	25.6	19.7	16.4	20.1	16.5	21.1	22.6	13.6
64.3	4135.4	5335.7	7692.0	1150.9	3851.3	4170.8	4310.5	703.2	289.2	2663.7
197.4	2449.1	2522.7	3435.6	2550.2	2052.9	3183.3	2068.8	925.6	527.0	1681.7
208.5	4760.7	6825.3	6447.2	3058.8	4230.1	6535.8	4944.5	977.7	626.0	2621.9
1614.5	3050.0	3495.4	3887.9	2698.4	3060.5	3582.7	3637.4	1659.2	1609.2	2296.2
57.7	365.8	1060.5	880.9	218.9	518.2	533.4	603.9	563.7	182.9	304.4
918.8	5575.4	6006.0	7148.8	5092.7	4991.7	6767.9	5249.4	2447.9	1514.9	4206.7
1036.7	5465.5	6383.4	6808.5	4089.5	5065.3	6731.1	5483.5	1884.5	1353.0	3608.2
4656.0	6303.2	7644.2	6919.9	5793.7	5749.8	7696.8	5391.6	7783.8	7060.5	6665.3
1289.3	5324.8	6061.0	8091.4	3968.0	4743.1	5659.9	4912.7	2042.3	1012.5	3499.2
1269.8	4658.9	5460.3	6736.9	3092.6	4200.7	4784.8	4351.4	2799.3	1451.1	3416.4
45.1	31.7	51.6	49.1	22.4	22.6	19.4	146.7	21.0	12.4	20.3
732.6	5125.0	6171.6	7374.6	2402.3	4798.4	5750.9	4852.6	1404.8	913.5	3544.8
1316.6	2686.7	3096.4	3121.6	1963.8	2403.9	2574.7	3435.3	1360.0	820.2	2220.8
59.5	1937.4	3064.6	3355.1	634.6	1524.6	1857.2	2168.7	645.5	253.2	1145.8
556.6	5507.4	5525.2	6698.3	6603.8	5268.2	7232.8	4770.8	2415.2	1376.8	3849.6
37.8	66.8	111.9	132.0	37.2	91.5	85.5	102.3	32.5	22.0	42.3
56.3	1566.6	2661.9	3260.9	287.8	2004.9	1559.8	1790.8	173.5	110.7	812.0
68.6	173.7	190.8	303.0	50.1	73.8	73.2	141.0	59.8	45.5	77.6
3239.9	5111.6	5369.6	6189.9	4174.1	5162.1	5308.2	5893.7	4140.5	6191.4	7561.3
653.4	2921.6	3812.7	4641.9	1502.4	2816.9	2747.7	3146.8	1298.5	777.2	1789.7
112.3	3860.7	5196.0	6301.5	1288.3	3760.2	4230.4	3705.0	1017.2	355.8	2564.4
96.5	3231.9	4882.4	5898.1	1491.6	3103.0	3461.0	4283.9	1222.6	633.5	2398.1
743.1	4924.5	6149.3	6639.6	3447.9	4548.4	5228.5	5033.6	2901.8	1880.8	4382.6
5909.6	3443.3	3448.1	2795.6	2377.4	3367.0	3257.0	2669.4	3407.3	3605.2	2831.4
157.7	3566.5	4638.1	5595.6	1491.8	3377.1	3568.0	3416.4	1138.1	334.8	2394.8
36.2	64.2	133.9	72.4	108.7	143.1	76.8	87.4	40.4	25.7	62.1
28.9	898.5	1703.1	1830.8	228.8	1265.5	1265.6	1219.9	98.7	73.9	457.2

5912.3	3019.8	2300.2
2584.2	1461.4	698.7
969.9	923.6	1538.2
7182.0	3616.1	2195.6
2337.7	2585.1	2705.6
6098.7	5578.3	4743.1
4832.3	3573.2	1528.7
2693.1	1570.7	572.4
1094.8	1022.1	1112.1
90.5	88.6	72.6
4648.1	4524.3	3354.4
5854.2	2990.8	1685.0
7119.9	4434.5	4919.3
16.3	19.0	20.3
7554.9	3467.6	1969.1
3017.4	1969.7	2183.3
6076.6	3753.5	2886.5
4236.5	3373.1	4254.7
1301.3	761.2	247.0
6063.3	4967.5	4204.7
7192.9	4920.7	4184.0
5042.6	6081.6	6803.2
7722.3	4926.4	4225.0
7174.1	4765.5	4664.8
30.4	42.8	22.4
8286.2	4330.5	2661.2
4131.3	2666.7	1644.2
2844.2	2169.7	1272.3
5530.7	4395.8	5378.3
152.8	229.2	220.9
3698.2	1991.9	397.2
280.3	299.7	61.5
7094.0	6154.9	5936.9
4860.5	3585.0	2047.6
6808.3	3213.4	1682.0
6234.4	3537.0	2655.6
6546.1	4509.3	4510.1
3725.2	4213.0	3016.7
6622.0	3207.3	1762.7
162.9	114.6	59.8
2424.9	961.1	385.5

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GQ080000.1 gg_id:426220 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ080
DQ308599.1 gg_id:149030 sheep rumen enrichment clone 196.G09 DQ308
EF445249.1 gg_id:211987 dairy cow rumen clone NED6C6 EF4452
EU842865.1 gg_id:313080 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8428
FJ682084.1 gg_id:529577 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
AF018460.1 gg_id:2051 rumen clone 12-16 AF0184
EF510668.1 gg_id:220889 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
FJ673367.1 gg_id:519509 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
AY278625.1 gg_id:88035 Prevotella genomosp. C2 AY2786
FJ673762.1 gg_id:516492 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
AM420076.1 gg_id:244669 Noma subgingival plaque clone 301G11(oral) AM420
AF001777.1 gg_id:2121 rumen clone RFN1 AF0017
AF018482.1 gg_id:2143 rumen clone 12-103 AF0184
AB185747.1 gg_id:99412 rumen clone U29-A10 AB1857
FJ364552.1 gg_id:363513 feces adult twins and mothers; TS15 clone TS15_a04c09 FJ3645
DQ801414.1 gg_id:198573 human fecal clone RL388_aao95c01 DQ801
DQ796381.1 gg_id:187532 human fecal clone RL179_aah26e05 DQ796
GQ492443.1 gg_id:547386 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU843990.1 gg_id:353232 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8439
GQ448254.1 gg_id:587185 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ680952.1 gg_id:529311 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
GQ006634.1 gg_id:503030 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu85h01c GQ006
AM420252.1 gg_id:237394 Noma subgingival plaque clone 701D05(oral) AM420
EU467139.1 gg_id:291194 mongoose lemur feces clone ML_aae89d04 EU4671
DQ796032.1 gg_id:189776 human fecal clone RL202_aai50e04 DQ796
FJ685231.1 gg_id:526617 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
GQ491487.1 gg_id:582564 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AB009184.1 gg_id:2073 rumen clone RFN26 bacterium AB0091
FJ558104.1 gg_id:526949 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5581
FJ682743.1 gg_id:516402 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
FJ674157.1 gg_id:520484 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU775095.1 gg_id:334392 Francois Langur feces clone FL_2aaa01e10 EU7750
FJ679127.1 gg_id:525990 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6791
AY093462.1 gg_id:63123 deep marine sediment clone MB-A2-107 AY0934
FJ674138.1 gg_id:520780 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ682119.1 gg_id:528609 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
FJ364458.1 gg_id:364074 feces adult twins and mothers; TS15 clone TS15_a03b11 FJ3644
EF510483.1 gg_id:222154 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
EU461603.1 gg_id:294196 mongoose lemur feces clone ML_aaj25d04 EU4616
AB270111.1 gg_id:168200 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB2701
FJ674044.1 gg_id:525357 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740

141.8	2763.0	2891.5	3130.8	2858.4	2323.4	3256.0	2575.1	2071.9	1184.1	3071.0
601.2	2220.5	2519.4	3272.5	1707.4	1994.4	2632.2	2123.7	1529.9	763.7	1809.0
57.1	376.0	629.3	815.7	156.7	451.8	430.9	518.9	86.8	53.3	206.5
41.9	31.5	37.2	36.5	31.7	20.3	26.4	27.1	19.5	18.7	20.7
1227.2	2599.3	3235.7	3687.0	1239.7	2492.5	2261.9	2717.1	1160.4	468.9	1648.5
45.6	213.3	466.2	519.9	74.9	229.6	182.9	219.7	53.9	64.1	168.7
416.3	2648.0	2667.5	3589.6	3496.7	3326.1	4629.1	2647.2	1594.5	733.1	2345.6
358.7	4194.5	5063.3	6410.7	2484.3	3795.3	4999.3	4657.9	3446.7	1984.9	4531.0
35.7	143.0	185.5	212.7	53.5	128.0	154.4	163.7	44.4	20.3	100.5
267.3	9672.2	8205.9	8529.2	7853.3	8423.4	8921.7	7816.4	9917.6	6663.0	8550.6
33.0	77.1	37.9	37.2	17.4	21.2	242.4	72.2	82.6	16.9	22.0
17570.1	8374.2	7766.6	8249.0	8114.9	8146.1	8889.8	6933.2	12020.7	6784.4	8279.1
103.0	1842.5	2234.7	2250.6	602.5	792.7	901.4	1260.0	623.3	299.7	532.8
51.9	148.3	160.5	261.5	61.4	27.9	97.7	135.1	64.5	36.3	80.5
91.2	3632.6	4537.4	6089.8	2406.8	3478.0	4416.6	4332.1	1812.5	1116.4	3214.1
48.1	42.6	39.9	47.3	33.3	45.4	31.5	54.8	33.4	26.3	30.4
314.8	3945.7	3794.7	5215.1	7571.7	4279.5	6103.8	3253.3	1842.8	1112.2	2504.8
51.4	1514.3	1944.9	2388.7	865.3	1558.7	1863.5	1701.8	218.4	131.8	797.0
347.1	2163.0	2832.0	3125.2	1600.2	2503.9	2476.5	2817.7	1381.9	492.0	1518.7
1254.6	2880.8	2992.3	3490.3	1869.3	2601.5	2813.9	2974.8	1338.3	868.6	1705.5
157.0	2715.1	3694.1	4414.1	1188.5	2596.9	2809.6	2629.4	757.0	196.5	1667.3
78.9	263.1	327.1	373.2	199.8	161.4	164.9	187.5	138.8	66.9	105.8
2177.1	2230.1	1856.4	1892.3	2441.5	1868.5	2171.9	2028.3	1695.8	1012.0	1426.2
2517.4	2956.9	3535.5	4479.9	1516.8	2890.7	2851.0	3190.8	1198.8	349.5	1841.6
2155.9	1145.3	1030.0	1312.0	963.8	1094.3	1084.9	1195.1	752.5	253.2	915.2
76.5	2695.5	4140.4	4767.6	788.8	2679.8	2479.3	2458.1	516.6	424.0	1841.5
52.2	3209.9	4425.4	5562.1	955.7	3279.8	3175.7	3370.4	592.4	273.5	1788.1
38.1	473.1	584.7	645.1	128.7	197.5	211.0	422.1	78.7	51.2	150.9
2220.1	2160.7	2297.9	3502.9	1679.5	2444.1	2361.4	2591.7	1043.3	394.0	1159.2
344.8	1447.6	2465.6	2451.9	1078.5	1264.5	1521.0	1611.3	845.2	960.7	847.8
1322.4	3178.1	4308.8	5155.2	1331.4	3104.5	3031.7	3350.1	977.2	407.4	1919.8
1317.7	3647.6	4435.9	5224.6	4359.4	4045.7	5194.9	3424.1	1460.5	943.5	2396.8
119.4	1906.6	2243.9	2746.4	890.3	2291.8	1412.3	2215.9	554.5	599.3	1887.0
824.6	3078.6	3023.5	3784.0	2966.5	2633.7	3225.9	3255.1	3003.5	212.4	3262.2
971.5	3213.3	3967.1	3958.0	2010.8	3061.7	3299.8	2938.6	1494.0	1486.4	2086.3
85.3	635.4	1003.1	1195.4	276.3	575.0	564.8	743.2	342.3	262.4	350.8
4078.0	6500.9	6792.0	7769.7	7262.8	6191.6	8428.0	6714.8	6261.4	3770.1	5259.6
257.3	2289.8	2792.0	4375.3	2147.9	2760.2	3074.1	3033.2	1272.3	409.9	1547.2
67.9	3038.7	4210.0	5410.5	818.3	3175.2	3015.4	3067.7	426.0	207.1	1453.7
37.5	570.3	944.3	1233.3	268.7	779.2	537.1	812.0	109.0	52.0	531.3
1008.6	3850.8	4864.7	5038.2	2561.9	3851.5	4022.9	3619.9	2047.7	1835.2	2750.1

2805.6	2207.9	3060.9
3191.7	2254.0	1866.8
1230.2	413.1	194.9
23.8	30.4	27.8
4517.8	2602.4	2128.2
629.1	208.9	278.6
3549.1	3154.7	3909.1
6129.0	3710.4	5828.1
245.6	155.2	82.9
7661.0	8668.3	6300.3
109.7	78.6	25.8
7203.6	7898.4	6179.1
1819.6	1016.7	562.2
243.3	197.9	186.1
5974.6	3240.0	3662.8
46.5	58.8	40.8
3996.5	3637.9	3784.9
2830.2	1267.4	977.5
3283.7	2740.5	2605.0
3744.1	2940.2	2993.3
5347.8	2526.7	1249.5
297.6	300.5	173.8
1888.3	2595.3	1583.1
4977.4	4931.6	1458.9
973.5	1678.7	759.2
4458.5	2202.9	1249.0
6744.9	2788.8	1773.1
577.3	353.2	94.0
4083.8	2863.6	2392.8
3172.5	1873.5	1188.4
5822.7	3365.0	2272.5
3993.0	3301.8	3398.7
2282.8	2601.6	2643.5
3752.2	3108.2	2959.9
4947.4	2975.0	2064.3
1369.3	1064.0	581.4
6591.6	7871.2	5803.8
4964.0	3005.3	2509.2
6247.6	2763.1	2102.9
1673.6	647.2	490.2
6033.3	3636.6	2665.1

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EU461994.1 gg_id:288204 black-handed spider monkey feces clone SPIM_aaj33a06 EU461
AY981001.1 gg_id:117786 human rectum mucosal biopsy clone V138 AY981
DQ015308.1 gg_id:132494 mouse cecum clone M2_1e09 DQ015
EU774114.1 gg_id:349352 Chimpanzee feces clone CHIMP1_aaj40h10 EU774
FJ683316.1 gg_id:509294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU537408.1 gg_id:285626 profile human microbiota antecubital fossa (inner elbow) skin clone nbt78a03 EU537
FJ674193.1 gg_id:521199 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ796131.1 gg_id:186388 human fecal clone RL202_aai52a06 DQ796
EU774309.1 gg_id:329650 Chimpanzee feces clone CHIMP1_aaj37f03 EU774
FJ673054.1 gg_id:524193 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ676833.1 gg_id:527419 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
GQ492186.1 gg_id:581344 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AF018469.1 gg_id:2140 rumen clone 12-51 AF018
FJ683139.1 gg_id:522450 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
AY581270.1 gg_id:114909 Prevotella sp. str. HY-36-2 AY581
FJ364584.1 gg_id:366904 feces adult twins and mothers; TS15 clone TS15_a04f10 FJ3645
EU461667.1 gg_id:302285 mongoose lemur feces clone ML_aaj26f07 EU461
AY978001.1 gg_id:117426 human cecum mucosal biopsy clone LH36 AY978
FJ674154.1 gg_id:520593 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ797117.1 gg_id:189432 human fecal clone RL386_aao87b12 DQ797
GQ491991.1 gg_id:546549 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ674224.1 gg_id:521529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
GQ031780.1 gg_id:380886 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
AY979701.1 gg_id:121507 human transverse colon mucosal biopsy clone M435 AY979
FJ681462.1 gg_id:519347 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6814
GQ037615.1 gg_id:374568 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
FJ364593.1 gg_id:361488 feces adult twins and mothers; TS15 clone TS15_a04g10 FJ3645
GQ448313.1 gg_id:541579 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ676933.1 gg_id:530238 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
EU467121.1 gg_id:293143 mongoose lemur feces clone ML_aae88g03 EU467
DQ801565.1 gg_id:194357 human fecal clone RL117_aae91e01 DQ801
EU778580.1 gg_id:339374 Ring-tailed lemur feces clone RT_aai09f10 EU778
FJ976203.1 gg_id:544617 Interindividual healthy human oral microbiota mouth clone 3083 FJ9762
FJ679660.1 gg_id:520962 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
GU302821.1 gg_id:582218 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU850584.1 gg_id:334521 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF403 EU850
EU459856.1 gg_id:299317 Prevost's squirrel feces clone SQ_aah80c01 EU459
EF445247.1 gg_id:214336 dairy cow rumen clone NED6C4 EF4452
AY976237.1 gg_id:123765 human ascending colon mucosal biopsy clone LW67 AY976
FJ557771.1 gg_id:528457 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
FJ680456.1 gg_id:530706 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804

794.7	3626.8	3142.8	4239.0	4600.0	2945.3	4215.5	3074.3	2295.6	1499.0	2596.8
449.3	5118.6	4581.4	5898.7	6655.6	3999.7	5894.9	3929.2	1958.8	1306.5	2925.1
19524.1	6754.3	8749.7	7568.3	6678.7	6091.6	7978.1	6160.8	9614.1	5907.2	7051.9
974.7	4260.8	4174.8	5061.1	3733.0	3901.7	4571.9	3808.0	2265.5	1360.3	3067.6
709.0	3041.3	3487.9	4044.8	1787.9	2964.6	3165.1	3330.9	1223.3	713.6	2033.8
1400.3	970.1	1222.7	1622.8	547.4	1062.4	1136.2	1132.1	477.3	227.4	608.9
241.8	3208.9	4420.1	4726.4	1428.2	2938.5	3169.8	3293.5	1199.8	805.7	3246.4
38.1	238.1	468.5	502.7	127.1	251.3	168.8	223.3	30.0	12.6	46.2
371.6	3596.4	3332.0	4081.0	3038.7	2630.8	6151.4	3101.9	2217.1	1396.1	2876.8
853.6	2667.3	3236.7	3388.2	2771.9	2699.2	2884.1	2255.8	2136.1	2000.1	2139.1
466.8	5709.3	6755.6	8530.3	1999.1	5143.7	5480.0	5740.0	1518.9	663.3	3696.2
1001.2	4362.9	5491.6	6772.0	4575.9	4832.5	5712.1	4930.5	4072.9	1271.0	3983.1
42.1	1020.3	1127.8	925.8	513.7	561.2	633.0	1034.9	114.5	78.5	1032.6
2653.7	4286.2	4443.5	5235.9	4043.0	3425.4	5473.9	4527.8	2309.1	1911.5	3736.5
257.7	6483.9	8074.5	10348.8	2708.9	6180.8	7595.7	6345.1	2388.2	1213.9	4306.3
147.6	1659.5	1906.7	2419.1	1135.0	1293.6	1530.0	1598.5	1005.9	470.7	1033.8
830.6	3247.1	3523.5	4352.4	3698.8	3416.3	3801.9	3145.8	3458.8	2362.4	2936.9
4369.9	3786.6	3614.6	3843.4	4267.9	3290.3	3745.8	3156.1	2913.6	1678.8	2795.3
87.6	1903.0	2493.6	3218.2	712.8	1879.6	2135.4	1904.6	540.6	172.5	1240.5
1417.6	6074.6	6180.1	7232.1	6779.8	5727.0	8535.2	5180.6	2302.9	1268.8	4061.3
40.5	2516.5	3529.8	4563.6	709.1	3034.8	2605.8	3098.6	278.8	207.5	1353.2
567.1	1836.5	2320.5	2765.5	984.2	1824.5	1943.0	1727.8	943.3	764.1	1462.0
10206.3	4029.1	3663.6	4152.3	5218.3	4341.0	5439.4	4571.8	3948.6	4237.7	4369.5
444.4	4433.5	4059.0	5564.6	7015.3	4162.3	6035.1	3776.1	2073.7	1186.9	2688.0
108.2	3413.8	4594.7	5907.7	1149.2	3313.2	3779.6	3293.8	850.1	320.7	2350.6
184.5	1783.1	1598.2	1677.5	2765.6	1845.3	2531.6	1944.5	1598.3	1034.7	1439.9
1897.9	4145.6	4372.7	5421.3	5378.4	4442.8	5515.3	4156.1	2543.7	1502.0	3249.3
243.2	3627.9	4127.4	4415.4	3676.6	3290.8	4310.3	3712.7	2055.7	1196.0	2806.7
3176.3	4808.6	4963.0	6170.4	4289.3	5478.7	5199.9	5032.4	3924.9	2189.5	3338.6
1238.6	4125.5	4723.9	5519.5	4680.4	4052.2	6389.2	3652.2	1461.9	832.2	2739.3
41.6	1474.6	2196.4	2559.5	293.1	1964.9	1571.5	1906.9	128.9	119.0	713.8
1125.8	1527.6	1671.3	1933.7	2323.0	1723.6	2096.5	1487.1	865.1	465.8	1164.6
139.5	2510.2	3126.5	3678.0	1093.3	2366.0	2604.1	2792.7	1043.1	666.4	1738.4
1600.2	4081.3	4072.9	4529.7	3446.5	3894.9	4090.2	4625.0	2970.8	2268.4	3308.9
152.6	3285.6	4441.3	5707.9	3079.9	3474.7	4229.9	4790.6	2693.2	1108.5	3059.9
1064.0	2140.9	2793.3	2713.4	971.3	1766.0	1826.2	1829.0	911.4	694.2	1805.0
129.4	3058.4	3512.3	4310.0	2347.6	2802.1	3435.5	2811.9	1284.2	665.7	2187.3
61.7	1812.6	3783.1	5278.5	471.7	341.1	548.5	904.9	245.5	46.1	184.1
7568.5	4729.1	3527.8	5126.9	4991.3	3783.7	4731.5	4250.2	3329.1	1870.9	3197.6
62.2	672.4	917.2	914.2	385.4	569.0	721.3	614.2	340.0	321.5	564.4
111.9	2682.6	2936.4	3617.7	1745.7	2518.8	2804.3	2963.0	3064.1	848.1	2129.3

3324.7	3566.2	3010.1
4726.9	3680.5	4381.8
8212.9	6032.5	5966.2
4602.9	3903.0	4783.6
4499.3	3032.0	3569.3
1976.5	1267.6	586.3
5516.2	3222.3	2828.6
639.1	332.4	96.0
3766.5	3284.3	2045.8
3002.9	2432.8	2243.9
9169.0	5062.7	3364.2
6758.3	4304.0	4603.4
1145.7	800.2	387.4
4194.6	4246.7	3862.4
11585.2	5512.7	2936.9
2487.9	1725.0	1440.5
3363.2	3388.5	3255.6
3119.7	3668.8	3094.9
3632.6	1688.5	788.6
6497.2	5079.4	5748.4
5707.7	2325.8	950.5
2676.2	2058.2	976.2
4011.1	4418.2	5242.8
4402.3	3775.0	4568.7
5764.5	2827.6	1514.0
1502.1	1531.4	3067.7
6207.6	3969.4	4519.5
4063.3	3294.3	2781.0
5386.8	6105.1	4447.4
4484.3	3534.6	3707.3
3374.6	1355.4	531.9
1473.8	1725.5	1466.8
4304.7	1904.3	2344.4
4538.8	5314.9	5691.9
4912.1	4050.4	4999.6
2854.7	1866.1	1094.0
4146.3	2727.5	1777.8
1608.8	1320.6	478.3
4958.8	5166.8	5171.0
826.0	839.6	753.7
3200.0	2959.0	3949.2

k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
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k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
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