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DQ795033.1 gg_id:185560 human fecal clone RL310_aam39d05 DQ795
GQ493530.1 gg_id:580564 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU748168.1 gg_id:329933 neotropical folivorous flying bird adult hoatzin crop clone hoa33_17A03.F EU748
EU778985.1 gg_id:307174 Prevost's squirrel feces clone SQ_aah82a04 EU778
EU887831.1 gg_id:321459 and RFLP slurry Nisargruna biogas plant aerobic predigester clone 9B EU887
EU472954.1 gg_id:295831 douc langur feces clone DL_1aaa02f02 EU472
FJ684479.1 gg_id:523276 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
FJ683769.1 gg_id:530979 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6837
EU531892.1 gg_id:272726 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
GQ044807.1 gg_id:375044 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ044
EU462153.1 gg_id:302183 black-handed spider monkey feces clone SPIM_aaj36a09 EU462
AY978038.1 gg_id:117846 human cecum mucosal biopsy clone LH81 AY978
AY976203.1 gg_id:123983 human ascending colon mucosal biopsy clone LW22 AY976
FJ673016.1 gg_id:519306 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
AB270095.1 gg_id:164946 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU773649.1 gg_id:336924 Capybara feces clone CAP_aah97f08 EU773
FJ683145.1 gg_id:527471 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
EF534315.1 gg_id:224539 Prevotella genomosp. T3 str. W1609 EF5343
DQ797184.1 gg_id:174975 human fecal clone RL386_aao88b01 DQ797
FJ685119.1 gg_id:526943 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
GQ492563.1 gg_id:538485 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ673913.1 gg_id:520460 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ685238.1 gg_id:528077 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
EU461757.1 gg_id:292547 mongoose lemur feces clone ML_aaj28d02 EU461
FJ673610.1 gg_id:532039 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ364375.1 gg_id:357830 feces adult twins and mothers; TS15 clone TS15_a02b10 FJ3643
GQ006801.1 gg_id:502863 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu87h07c GQ006
EU475110.1 gg_id:301251 visayam warty pig feces clone VWP_aaa01c09 EU475
FJ362948.1 gg_id:364157 feces adult twins and mothers; TS148 clone TS148_a01b05 FJ3629
FJ678342.1 gg_id:522618 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
AY982503.1 gg_id:118916 human sigmoid colon mucosal biopsy clone MN09 AY982
EU461703.1 gg_id:295287 mongoose lemur feces clone ML_aaj27d08 EU461
EU775112.1 gg_id:326403 Francois Langur feces clone FL_2aaa02g04 EU775
FJ679733.1 gg_id:518773 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ685476.1 gg_id:517719 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ684568.1 gg_id:529076 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU778816.1 gg_id:336769 Black-handed Spider Monkey feces clone SPIM_aaj35h09 EU778
FJ685495.1 gg_id:530925 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
FJ674081.1 gg_id:513870 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EF401398.1 gg_id:214549 human fecal clone SJTU_D_09_79 EF4013
FJ680457.1 gg_id:516274 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804

42.9	2494.0	3173.7	4021.7	1568.3	2317.0	2157.4	2293.0	710.1	497.7	1532.3
55.9	4099.0	5316.3	6611.8	1319.2	4161.6	4363.8	4408.9	954.2	470.6	2506.5
12288.4	6172.8	6740.3	7788.2	5675.5	5771.8	7502.5	6312.1	5750.8	3729.1	6975.0
3990.0	6842.6	6440.6	7578.1	6682.0	6974.4	7670.9	6072.4	5915.6	5126.8	6141.5
44.7	30.0	45.6	46.1	32.1	39.3	32.1	39.4	28.6	26.3	35.1
204.0	1632.0	1841.9	2288.2	969.1	1016.9	1809.1	1179.5	905.0	395.5	657.2
139.9	4602.5	5714.4	7508.4	1382.3	4377.3	4464.7	4417.3	1057.8	447.2	3045.3
3136.4	6447.4	6776.0	8213.0	7875.5	6398.8	8758.5	5699.5	3685.0	3151.9	4988.1
43.5	3873.4	4389.2	4493.7	1415.4	3506.9	3751.7	3738.7	1369.4	910.3	2255.9
38.8	48.0	43.4	42.3	42.3	42.9	34.6	36.1	31.1	25.5	28.5
453.1	901.6	1012.2	942.1	989.3	919.0	1057.6	867.1	550.9	1219.7	758.2
375.1	4944.3	5074.9	5792.1	5718.1	4571.9	6344.9	4171.9	1701.0	1139.4	2746.2
403.9	4217.7	3736.9	4459.8	7409.2	3991.0	5859.5	3346.0	1664.5	1033.1	2212.0
101.0	2229.5	3046.7	4129.6	966.0	2304.3	2253.8	2272.2	806.6	270.2	1562.0
51.7	387.9	465.2	705.9	18.9	27.2	31.2	93.5	31.7	13.7	32.1
1598.2	4336.1	5295.9	6588.6	2691.2	4117.3	4286.2	4524.7	3368.7	2981.9	3268.2
320.3	5687.9	6961.7	8523.3	4198.3	5644.9	6719.7	5223.9	2030.8	1130.8	3751.8
47.3	388.9	613.5	610.3	170.0	458.1	427.7	390.4	98.0	54.9	252.3
1106.4	2677.8	3555.6	4411.4	1192.4	2653.2	3039.5	2691.8	785.0	327.8	1693.8
818.2	6832.0	8358.5	10289.2	3033.7	6342.5	7246.1	6575.1	1844.1	1038.8	4574.3
283.5	3737.5	4937.2	6374.7	3578.2	4283.4	4357.2	4513.2	1707.8	716.4	2342.2
85.2	988.8	1432.5	1767.9	421.4	902.0	1137.1	1011.2	396.4	40.0	635.8
120.2	4034.4	4855.3	5876.4	1092.5	3752.0	3120.7	4794.9	1213.5	525.8	4522.2
409.2	5543.0	6185.7	8565.1	5431.2	5513.4	7342.4	5358.4	1394.1	1880.1	3848.8
104.1	835.3	1417.4	1493.4	618.0	797.6	890.0	949.4	120.3	73.9	298.6
3126.3	4643.7	4441.5	4910.5	5203.8	4190.0	5985.9	4687.5	3725.2	2748.6	3485.3
991.2	2585.9	2166.3	2248.2	1634.6	1604.4	1854.7	1693.9	1339.1	745.7	1502.4
54.7	1175.6	1584.9	1682.1	507.0	1107.3	863.3	1349.9	887.0	397.2	690.2
50.2	639.6	962.6	1156.1	191.7	559.4	499.5	762.4	193.1	79.5	326.3
3005.8	2623.5	2949.1	3781.0	2742.1	2720.1	3023.2	2547.4	2040.9	2073.8	2736.1
1294.6	3716.7	3981.0	4552.2	1896.1	3082.0	2941.7	3577.7	1332.2	688.6	2156.5
39.2	872.1	1130.8	1566.1	280.0	825.6	1338.0	848.2	147.2	110.2	512.7
300.2	3329.7	3942.9	5000.4	2440.3	3793.8	3968.6	3478.3	2345.2	1156.0	2917.9
111.9	2856.4	3349.5	4800.5	1978.6	2610.6	2859.4	2934.4	1966.4	640.0	1966.2
54.9	808.7	650.0	788.8	234.1	407.4	298.2	511.8	199.8	209.1	302.6
877.6	3434.2	3999.7	4955.7	3033.0	3113.7	3717.5	3004.5	1966.4	1270.3	2923.5
298.9	3014.5	2909.7	3664.1	4146.9	2526.0	4291.2	2587.7	1179.8	921.9	1866.4
1767.9	2630.8	3292.3	3974.0	2382.4	2883.8	3210.6	2741.1	1444.5	1842.8	2468.5
12271.6	6974.9	7094.0	7916.3	6453.2	6496.7	8068.3	6097.7	7313.0	6424.8	7309.5
52.4	33.6	36.9	48.2	29.2	40.5	45.2	66.4	35.2	20.9	34.5
1254.4	4510.6	4637.5	5436.3	2445.9	4446.6	4584.4	4154.7	2032.1	924.6	3192.9

3296.0	2433.7	2819.2
7638.4	4012.2	2601.9
7601.3	7189.2	7128.4
6462.0	6792.1	6991.0
38.8	38.9	23.4
1845.0	1274.3	951.0
7842.2	3867.3	2682.5
7381.9	5913.7	7998.8
4679.5	2963.6	1151.0
41.5	61.9	40.0
520.7	1420.8	835.5
4858.9	3924.9	4547.3
3222.6	3253.5	4365.6
4167.8	2243.7	1139.0
240.8	169.2	26.1
6041.7	4840.9	4628.5
8425.3	4866.3	4874.7
708.2	297.8	262.0
4633.1	2608.6	1226.8
11576.5	6027.9	4602.6
7235.9	4611.9	3629.1
1938.7	1050.4	441.7
5895.5	3824.3	5201.4
7574.3	5044.2	4103.4
857.4	915.6	637.7
4135.8	5846.9	4339.8
2471.6	1897.7	1764.0
1744.3	1636.3	2481.1
1132.2	565.3	248.2
3297.2	2735.9	2557.2
4530.1	3325.9	1437.5
1697.4	549.3	286.7
4470.5	4035.3	3508.4
5209.6	3086.2	2152.3
466.4	840.6	1177.9
3748.5	3258.9	3103.5
2662.4	2236.4	2924.2
3759.0	2406.2	2121.5
8945.2	6596.3	6402.8
59.1	34.7	53.4
5856.5	5572.2	3776.1

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EU462275.1 gg_id:291569 chimpanzee feces clone CHIMP1_aaj38h09 EU462
EU773152.1 gg_id:333756 BigHorn sheep feces clone BHSD_aaa03c01 EU773
EU467242.1 gg_id:288050 black-handed spider monkey feces clone SPIM_d08_1 EU467
EU462271.1 gg_id:294573 chimpanzee feces clone CHIMP1_aaj38g12 EU462
FJ685406.1 gg_id:523949 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
GQ031818.1 gg_id:370841 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ031
EU467643.1 gg_id:299524 naked mole-rat feces clone molerat_2d12_1 EU467
DQ795931.1 gg_id:174318 human fecal clone RL202_aai49b03 DQ795
FJ685510.1 gg_id:515077 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6855
DQ796855.1 gg_id:185708 human fecal clone RL179_aao55e05 DQ796
EU778070.1 gg_id:328035 feces clone RL388_aao93b02 EU778
FJ676072.1 gg_id:511424 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6760
DQ800980.1 gg_id:191586 human fecal clone RL387_aao90c07 DQ800
EU462605.1 gg_id:294610 Sumatran orangutan feces clone orang2_aai66a04 EU462
FJ681247.1 gg_id:523957 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
EU458766.1 gg_id:296943 Goeldi's marmoset feces clone CAL_a04_1 EU458
EU461954.1 gg_id:299764 white-faced saki feces clone Saki_aaj64c08 EU461
EU459724.1 gg_id:300135 ring-tailed lemur feces clone RT_aai11f02 EU459
GQ072794.1 gg_id:381205 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw201c04c GQ072
AM420217.1 gg_id:247034 Noma subgingival plaque clone 601D02(oral) AM420
AY979721.1 gg_id:121586 human transverse colon mucosal biopsy clone M462 AY979
FJ673616.1 gg_id:525181 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
AY979544.1 gg_id:123488 human transverse colon mucosal biopsy clone M201 AY979
FJ684156.1 gg_id:525306 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
DQ801513.1 gg_id:174844 human fecal clone RL388_aao96e04 DQ801
EU461652.1 gg_id:288795 mongoose lemur feces clone ML_aaj26d01 EU461
FJ685070.1 gg_id:518228 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
FJ673390.1 gg_id:513417 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
DQ794957.1 gg_id:183105 human fecal clone RL310_aam38d09 DQ794
EU469446.1 gg_id:298451 black lemur feces clone BKLE_a06_2 EU469
EF510408.1 gg_id:219995 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
DQ796298.1 gg_id:186364 human fecal clone RL179_aah25d08 DQ796
GQ493728.1 gg_id:588151 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EF436381.1 gg_id:216511 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC95 EF4363
EU773561.1 gg_id:334610 Goeldi's Marmoset feces clone CAL_g04_1 EU773
GQ021950.1 gg_id:487718 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
FJ683508.1 gg_id:515712 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
EU562293.1 gg_id:267244 Prevotella genomosp. E3 str. 4D22 EU562
EU381837.1 gg_id:271262 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU462041.1 gg_id:296442 black-handed spider monkey feces clone SPIM_aaj33g08 EU462
FJ674185.1 gg_id:527333 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741

979.2	4462.9	4830.1	5753.8	3515.7	3755.5	5027.3	4110.1	2016.9	1255.9	3232.2
149.7	2405.0	2756.9	3260.0	2672.1	2157.6	2864.4	2334.3	1305.9	674.9	2083.9
2254.3	6478.2	7365.2	8399.7	6280.2	6549.1	6912.5	5913.5	2469.0	1010.1	4533.9
53.3	2128.1	2725.6	3889.8	1569.8	2037.9	2171.9	2019.9	797.5	431.1	1347.1
1173.1	1925.4	2628.4	2714.8	2401.6	2215.4	2873.5	1740.8	1104.4	1021.7	1634.9
163.3	1554.7	1661.2	2140.4	1153.8	1728.7	1621.0	1929.9	507.7	309.8	1010.5
872.9	4867.4	4711.1	5473.9	3235.0	3423.4	3125.8	4161.9	4054.2	3336.2	2943.3
1038.0	1107.7	1328.7	1954.7	709.0	1166.4	1266.1	1258.1	544.1	195.1	700.6
2540.1	4670.0	5444.6	6527.8	2554.2	4674.1	5438.5	4999.6	1651.6	956.3	2998.0
2542.5	5706.9	5805.1	8110.9	7087.0	4936.7	6518.6	5405.7	2592.4	1362.5	4140.8
36.3	24.2	29.8	37.0	28.7	21.4	33.9	29.8	22.2	15.4	17.3
78.5	4529.2	5781.2	7886.9	1355.8	4145.7	4312.1	4768.6	839.3	369.0	2902.4
30.3	1606.8	2376.5	2774.1	665.6	1813.4	2423.6	1675.8	224.9	156.2	849.3
371.2	3749.8	4056.1	4533.8	6225.0	3387.3	5712.1	3122.7	1640.1	1151.5	2149.9
620.5	2921.6	3405.1	3604.6	2137.6	2320.9	4099.9	3208.9	1322.0	1589.7	2931.8
230.5	1782.2	2290.3	2840.3	214.4	345.6	303.4	1252.8	220.6	73.7	365.1
54.0	4083.5	3984.0	5047.9	1982.1	3712.4	3309.7	4079.1	2539.2	1754.2	2250.5
110.0	5660.7	4798.7	5542.4	4153.9	3596.1	4069.7	5181.1	6700.1	4954.2	3848.9
1838.7	2015.3	1834.6	2306.1	2861.1	1842.5	2765.2	1831.9	1501.0	1301.2	2216.9
96.0	2222.1	2834.4	3456.7	619.8	1534.4	1846.9	1811.8	303.4	170.8	883.8
218.2	1408.6	1785.5	2047.7	1295.1	1372.9	2309.7	1564.8	510.5	233.2	1642.8
467.5	3759.3	4992.6	5606.4	2850.6	4023.8	4288.0	4414.6	1756.4	1084.5	4645.4
4036.1	3109.9	2782.5	2742.3	3402.1	2217.2	2501.0	1868.8	2957.9	2735.2	3542.7
89.1	1902.2	2658.1	3219.4	709.8	1879.7	2276.4	1904.8	537.9	157.4	1238.7
1714.8	5390.5	5067.6	6239.2	8508.0	4555.1	6964.4	4072.1	2234.0	1407.6	3194.7
46.0	905.4	753.8	846.6	980.0	959.9	1008.8	929.2	303.0	266.4	646.8
126.9	3685.4	4697.1	6138.9	1092.2	3532.5	3647.5	3569.8	745.1	357.4	2313.7
432.1	2725.7	2962.2	3161.4	947.4	2687.0	2093.3	2580.0	1654.7	1121.7	2089.9
53.2	3712.6	4830.9	5975.5	1299.9	4247.7	3813.5	4117.7	731.5	400.4	2110.0
53.7	2839.7	3884.3	5079.8	1421.9	3424.4	2958.3	2789.5	890.5	479.1	1519.6
225.1	1076.2	1266.7	1555.0	1247.9	1064.4	1565.7	1268.6	788.2	323.6	943.4
4710.6	4252.9	5130.3	5767.9	2647.2	4183.9	4480.5	4225.8	2973.2	1445.3	3010.4
37.8	1882.0	1260.1	1625.7	1188.2	1508.8	909.6	1572.4	2200.8	1474.5	901.6
196.8	1187.0	1173.0	1423.6	650.1	493.5	625.4	987.8	1308.6	780.7	700.8
110.1	3366.1	3179.3	3661.8	2605.1	3214.3	4791.0	2669.8	1796.9	1662.3	2969.3
4372.2	3222.1	3256.8	3447.5	3642.9	3178.9	3962.0	3041.8	2910.5	1675.0	2576.5
6868.5	3355.5	3681.2	4499.8	3599.4	3265.5	4294.6	3379.1	2715.3	2293.7	3857.5
35.0	820.0	1126.4	1347.5	627.8	1016.0	955.0	1001.3	212.0	227.0	348.8
65.7	543.0	929.6	1235.8	596.5	587.0	737.0	754.9	553.1	116.0	302.9
64.0	866.5	862.3	1023.0	502.1	819.4	581.6	728.7	682.8	565.1	306.2
73.4	1226.4	1534.3	1667.4	360.5	1058.9	908.3	1645.6	432.3	261.7	1540.4

4929.5	3877.6	2748.9
2547.2	2515.2	2166.8
5734.0	5509.3	4019.5
3172.5	2105.6	2821.5
2276.2	1790.2	1819.3
2926.5	3062.8	3191.5
5683.1	3774.1	2798.3
1882.1	1620.2	797.8
7197.4	4520.3	3661.8
6305.1	5416.9	4706.6
17.5	29.9	26.6
8207.5	4131.0	2345.4
3974.4	1289.5	879.0
3636.6	3329.8	4527.2
3376.5	2888.7	3403.3
3476.3	1575.3	446.6
5317.4	3376.3	1518.8
5150.4	4182.2	2490.6
2623.3	2214.8	2033.2
3767.6	1812.7	653.7
1320.4	1580.1	2400.9
5329.8	4163.8	4485.3
2049.8	2701.7	2980.1
3633.2	1686.8	787.9
4825.7	4336.7	5206.6
884.2	872.5	1065.0
6468.8	3131.9	2166.8
2850.9	2974.7	1090.1
6617.2	3428.2	2331.7
4472.5	2934.6	3388.6
1490.4	1201.9	1434.3
6096.3	4312.1	2239.4
1391.2	1832.5	624.1
1664.4	1310.2	1247.2
3087.4	2818.8	5807.0
2952.3	3495.1	2864.1
4551.7	3655.2	3241.9
1675.0	1190.4	484.8
789.7	748.2	320.3
928.3	1012.5	423.4
1591.0	1181.2	1889.1

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FJ673268.1 gg_id:527231 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU381920.1 gg_id:274228 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ682676.1 gg_id:527516 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
AB009196.1 gg_id:2125 rumen clone RFN40 bacterium AB009
EF097252.1 gg_id:188712 mouse cecum clone SWPT18_aaa03g12 EF0972
EU462081.1 gg_id:293554 black-handed spider monkey feces clone SPIM_aaj34f04 EU462
GQ493799.1 gg_id:560836 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ104049.1 gg_id:462552 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw562d0 GQ104
EU464389.1 gg_id:301956 hamadryas baboon feces clone AFBAB_aai04b11 EU464
FJ678814.1 gg_id:517885 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
FJ172886.1 gg_id:310111 Qinghai Yak Ruminal and Fungi China rumen clone RB-2H4 FJ1728
GQ491485.1 gg_id:562839 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ684576.1 gg_id:519453 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU774533.1 gg_id:305603 Douc langur feces clone DL_2aaa02f12 EU774
AF371878.1 gg_id:46566 swine intestine clone p-863-a5 AF371
EU843543.1 gg_id:352418 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF510800.1 gg_id:226942 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5108
GQ491127.1 gg_id:593125 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ801467.1 gg_id:186617 human fecal clone RL388_aao95h07 DQ801
EU771473.1 gg_id:325802 Hamadryas Baboon feces clone AFBAB_aai01f01 EU771
FJ681094.1 gg_id:519110 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
FJ673559.1 gg_id:521157 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
FJ683451.1 gg_id:513649 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
FJ982992.1 gg_id:393419 Aspects Oral Microbiome root canal clone OPEN_ROOT_39 FJ9829
EU469550.1 gg_id:303304 western lowland gorilla feces clone GOR_aad32f07 EU469
AY980771.1 gg_id:120305 human rectum mucosal biopsy clone LN69 AY980
FJ684111.1 gg_id:531103 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
FJ678631.1 gg_id:522413 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6786
FJ677781.1 gg_id:520447 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6777
FJ674195.1 gg_id:520294 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ678568.1 gg_id:517889 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
GQ492008.1 gg_id:540051 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
GQ491649.1 gg_id:589891 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU475447.1 gg_id:302303 springbok feces clone SBSD_aaa03e02 EU475
AY982235.1 gg_id:126297 human sigmoid colon mucosal biopsy clone MH51 AY982
AF481227.1 gg_id:68339 Prevotella sp. str. E9_34 AF481
FJ683584.1 gg_id:519069 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6835
FJ678992.1 gg_id:526388 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
DQ797126.1 gg_id:188652 human fecal clone RL386_aao87c11 DQ797
GQ492677.1 gg_id:588173 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ683185.1 gg_id:517978 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831

9387.6	11335.9	10433.7	11813.5	9554.0	10782.8	13213.2	10529.4	11485.1	9573.1	14006.3
206.7	2275.2	3222.9	3637.1	1281.4	2070.7	2319.4	2644.2	1399.0	1049.9	2967.4
898.0	6066.2	6638.9	6970.8	5281.6	6463.9	6474.8	6216.6	7976.1	7626.1	6594.8
511.6	483.5	499.8	483.0	342.1	360.7	365.8	325.5	467.5	468.6	259.9
44.2	79.8	162.0	200.2	47.0	110.5	95.6	122.4	127.0	29.4	57.4
228.0	1682.0	1821.9	2408.7	3731.7	1747.2	2992.8	1286.2	601.6	463.5	1002.7
58.8	2392.9	3567.4	4521.0	827.9	2706.2	2525.3	2800.6	263.9	203.1	1262.7
460.5	2871.2	3374.3	3868.7	3186.4	3137.7	3921.8	3024.6	1942.6	1411.7	2250.4
1317.8	6029.4	6586.5	7153.1	5406.4	5993.5	7188.3	7588.8	5587.1	5465.4	6808.6
141.0	3987.8	5321.6	6630.9	1218.7	3705.1	3980.5	3796.4	1083.0	389.5	2568.3
158.9	649.8	899.5	1001.1	259.3	442.4	460.7	554.6	228.0	90.4	269.3
41.3	2859.3	4179.4	5329.6	953.4	3281.4	2934.7	3358.7	461.9	208.8	1645.7
141.5	1939.3	2824.4	3289.2	393.6	2161.1	2149.4	2090.9	466.5	96.1	1238.5
3296.4	5948.7	5681.9	7070.2	5995.3	4923.7	5915.1	5834.9	7489.9	4577.8	7718.8
41.2	36.5	50.5	49.7	33.9	28.5	38.9	41.3	23.9	20.0	38.6
702.3	4010.0	4287.9	5043.8	3229.1	3160.0	3477.0	3779.3	2422.0	894.0	2640.1
915.3	1816.3	2090.2	3065.7	1529.4	1966.7	2339.3	1959.7	761.5	687.9	1258.4
54.5	3585.3	5061.0	6275.9	989.6	3663.7	3580.9	3699.1	552.5	249.7	2015.5
65.7	3539.5	4147.0	4814.1	1987.1	3493.9	4565.9	3936.2	897.5	585.0	2556.4
78.3	1387.1	1717.0	2241.1	257.3	1163.5	819.7	1476.5	261.9	173.4	497.7
463.7	4713.0	5456.2	7371.4	1764.9	4192.8	4460.0	4728.8	1325.2	601.0	3073.0
61.3	3666.5	4003.4	3496.0	2342.5	3276.4	3746.0	2821.8	4208.7	4061.1	3416.3
4041.2	3876.6	4529.1	4733.6	2477.7	3497.2	3806.6	3554.9	2760.0	1869.5	2776.1
52.2	242.0	380.6	498.4	71.6	274.8	206.0	285.6	65.7	45.8	73.9
3127.9	1459.8	1606.5	1671.3	1371.4	1407.7	1383.1	1588.2	1009.3	608.3	888.9
187.4	1480.0	1252.0	1365.4	1859.0	1234.5	1850.4	1132.3	641.7	400.8	789.8
163.9	668.3	692.5	1305.9	690.4	589.8	787.1	824.5	135.2	49.0	307.8
176.1	3940.9	4760.5	5458.0	1741.2	3367.9	3549.9	3931.4	981.3	640.1	2404.4
2704.3	4377.4	5097.6	4845.2	5376.7	5248.8	6190.4	4921.7	3234.0	1930.6	4752.8
1125.1	4110.3	5185.9	5371.8	2923.2	4157.4	4291.3	3885.5	2185.6	1981.7	2952.8
762.3	5316.2	6318.9	7597.4	2400.9	4835.7	5683.3	5037.6	1443.4	965.8	3660.8
59.8	3698.6	4859.5	6107.4	1089.0	3853.3	3929.0	3939.8	649.7	335.1	2122.9
83.1	5389.3	7267.8	8532.6	1943.3	4930.6	5600.0	5148.0	1176.2	749.3	3657.4
122.1	3203.5	3969.6	4638.2	1182.8	2502.9	2638.6	2813.9	1624.8	1607.6	1514.8
500.5	5131.1	4567.8	6298.6	7197.7	4556.8	6280.2	4473.6	2123.8	1310.9	3125.3
299.2	3403.4	3099.9	3430.0	1715.1	3081.3	2765.3	2753.6	1198.7	2990.7	2191.9
25.6	1406.5	2056.0	1371.8	761.0	1411.9	1651.9	1351.4	149.2	140.9	502.1
1636.6	1624.6	1874.1	1906.3	1249.0	1490.9	1464.4	1603.3	1182.4	867.0	777.8
24.0	717.8	710.1	1650.5	225.8	866.9	858.5	841.3	103.3	74.5	460.0
73.8	3468.9	4651.3	5844.2	1022.3	3744.8	3713.7	3787.4	877.9	512.2	2054.5
176.2	3211.0	4206.8	5095.5	1517.0	3105.1	2997.9	3391.1	1293.5	445.9	2324.3

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6815.1	6253.4	6448.5
501.1	477.6	344.7
243.5	110.0	40.3
1253.5	1259.8	2306.8
5621.2	2450.5	1311.8
3106.6	3605.2	4222.8
5850.2	6359.4	6283.7
6934.2	3486.8	2431.8
1101.7	836.5	1326.1
6600.5	2946.8	1502.6
3671.7	1991.6	1168.1
5380.3	6739.4	6980.4
54.2	41.7	30.9
5211.2	4115.0	3478.8
3698.8	1995.9	2094.0
7556.5	3059.3	1701.1
4659.6	3204.6	2764.3
2581.7	1737.3	480.2
7154.1	4219.2	3079.5
4933.3	2911.5	2543.5
4762.4	3743.4	2169.6
411.7	540.1	93.4
1444.5	2462.0	1608.2
1159.6	1384.8	1759.1
1253.1	1562.3	30.0
6200.2	3414.0	1407.6
4825.7	5623.1	5195.6
6413.9	3918.1	2845.6
8349.3	4526.0	4052.1
7096.2	3413.9	1736.0
10172.0	4388.2	3063.5
5020.6	2639.3	2199.6
5029.2	4201.5	4663.7
3392.8	3598.5	3038.3
3350.5	1322.8	877.0
2267.0	2107.6	1026.0
2041.5	808.1	252.6
6722.1	3342.9	2384.9
6217.5	3273.1	2103.4

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FJ676640.1 gg_id:522859 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6766
AF385515.1 gg_id:73324 tongue dorsa clone DO045 AF3855
AB009237.1 gg_id:2081 rumen clone RFN90 bacterium AB0092
EU469378.1 gg_id:292751 black lemur feces clone BKLE_f01 EU4693
FJ674026.1 gg_id:522462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
GQ402134.1 gg_id:512265 alpacas and sheep forestomach clone SH17 GQ402
EU776030.1 gg_id:305514 Spotted hyena feces clone HY1_h05_2 EU7760
EU748036.1 gg_id:321154 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43f07 EU7480
DQ797187.1 gg_id:195206 human fecal clone RL386_aao88b05 DQ797
EU778991.1 gg_id:341295 Prevost's squirrel feces clone SQ_aah82h08 EU7789
FJ681588.1 gg_id:517965 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
FJ683293.1 gg_id:524838 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
EU432416.1 gg_id:261404 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU4324
FJ684258.1 gg_id:510384 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ685374.1 gg_id:512261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
FJ673204.1 gg_id:517714 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EF510603.1 gg_id:227118 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
AF414823.1 gg_id:72550 Prevotella intermedia str. 6-PIN AF4148
FJ557883.1 gg_id:531961 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5578
EF445236.1 gg_id:210346 dairy cow rumen clone NED4D2 EF4452
EU462076.1 gg_id:300872 black-handed spider monkey feces clone SPIM_aaj34e01 EU4620
AB078826.2 gg_id:147308 Bacteroidales str. KB3 AB0788
EU850530.1 gg_id:314206 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF318 EU8505
FJ681842.1 gg_id:518692 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ440093.1 gg_id:554296 Megamonas hypermegale colonization correlates Campylobacter jejuni exclusion pou FJ4400
DQ801108.1 gg_id:176761 human fecal clone RL387_aao92c09 DQ801
FJ879770.1 gg_id:455452 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8797
EU774591.1 gg_id:327684 Douc langur feces clone DL_1aaa03a10 EU7745
FJ674210.1 gg_id:510200 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
FJ678888.1 gg_id:525355 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6788
AF371882.1 gg_id:46017 swine intestine clone p-408-o3 AF3718
EU458688.1 gg_id:291144 Goeldi's marmoset feces clone CAL_b09 EU4586
AB185507.1 gg_id:103209 rumen clone F23-A04 AB1855
FJ684554.1 gg_id:529883 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ683093.1 gg_id:519998 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
AB185648.1 gg_id:102695 rumen clone F24-H04 AB1856
EU461639.1 gg_id:301048 mongoose lemur feces clone ML_aaj26b02 EU4616
GQ004014.1 gg_id:505648 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbu67e0 GQ004
AY349397.1 gg_id:92496 human oral cavity clone GI059 AY3493
EU461584.1 gg_id:287542 mongoose lemur feces clone ML_aaj25a06 EU4615
EU774976.1 gg_id:323239 Flying Fox feces clone FF_c03 EU7749

1294.7	2500.2	3906.6	4026.0	1414.4	2909.5	2922.1	3578.3	1107.2	373.9	1997.0
299.5	543.4	458.7	398.8	471.3	1471.2	381.9	759.8	220.4	175.1	280.6
112.8	1089.0	1487.4	1649.5	333.1	736.2	794.3	986.3	282.1	182.2	771.9
881.7	2681.5	3416.3	3712.9	2225.1	2789.7	2752.4	2706.9	1613.0	931.4	1929.2
1327.9	4400.2	6005.2	6959.3	1630.1	4299.3	4191.6	4550.7	1097.3	511.8	2646.6
1003.1	1873.1	2194.6	2823.4	2659.6	2071.8	2523.4	2809.1	2396.9	1860.8	1548.5
28.8	1868.1	2915.8	3648.9	658.2	1893.2	2304.1	2187.5	253.6	161.2	874.5
123.0	2747.0	3269.5	4524.1	705.5	2423.7	2269.4	3417.0	773.1	603.2	2182.0
48.1	365.0	527.1	275.1	115.9	329.8	346.5	332.6	88.4	56.4	203.0
251.4	3659.1	3849.9	4856.7	2085.2	3285.4	3871.1	3472.0	866.1	451.5	2225.6
81.1	4215.3	5692.8	8122.8	5466.2	4012.4	8460.5	4999.6	2817.7	2617.1	6366.3
1537.1	4388.5	5981.8	6708.3	2330.0	4336.9	4642.6	4595.6	1462.6	558.2	2924.8
1726.9	7215.0	6301.8	6339.3	7726.3	6144.1	6540.8	6019.1	8768.5	6687.1	6519.4
66.0	1697.4	2551.7	3894.5	1012.6	1838.4	2183.7	2340.1	611.2	171.1	1417.0
53.5	3340.3	4332.1	6317.5	1204.1	3156.8	3358.9	3556.0	599.3	220.7	2152.7
180.5	6120.5	6898.9	7924.9	2221.5	5468.3	4714.0	7016.8	2276.2	1242.2	7834.7
256.5	1081.2	1270.9	1562.9	1172.5	993.9	1462.2	1189.9	791.9	330.5	948.3
53.5	1467.8	2090.3	2646.3	1087.8	1503.9	2005.8	1627.4	873.9	659.9	951.1
702.1	2939.5	3149.2	3876.9	2491.3	3340.0	3691.9	3307.2	1953.6	1475.1	2321.1
34.1	23.5	16.9	20.3	16.2	18.5	15.3	16.9	19.1	14.5	18.7
98.2	2625.1	2179.8	3118.1	3670.5	2089.4	2597.4	2184.2	1181.1	800.8	1752.3
55.5	371.1	465.1	394.9	88.5	511.9	418.6	385.2	82.8	54.0	374.7
142.8	1672.6	2187.7	2441.1	1317.9	1594.5	1881.0	2154.6	760.5	797.3	1561.1
111.9	3195.4	4344.9	5095.7	1193.6	3356.1	3332.1	3389.4	974.2	372.5	2175.8
146.7	2068.3	2889.5	3022.9	913.9	2350.4	2187.7	2856.0	906.7	568.9	1958.6
57.7	3377.1	4631.2	5887.0	940.6	3368.3	3244.4	3478.8	547.5	255.1	1910.6
52.9	80.9	117.0	143.1	61.7	67.7	76.8	97.3	61.1	45.5	89.7
136.2	3067.6	3274.8	2826.1	2516.3	2723.1	3220.0	2673.3	4390.1	3067.5	2660.1
1204.8	3631.4	3802.6	4441.5	1845.0	2851.0	3043.5	3283.5	1382.0	1265.6	2294.8
3118.1	3968.4	4615.1	4945.7	2863.4	3649.8	4398.4	3157.1	3411.3	4684.7	4804.2
278.0	2275.5	2361.8	3120.4	1549.6	1633.5	1808.0	1876.9	504.1	245.0	962.8
89.2	3082.8	2687.7	3464.9	2187.5	2910.0	4700.7	2548.4	1276.4	1336.5	3085.5
3593.1	3331.8	3428.3	3854.3	3193.6	3273.2	3735.7	3175.5	3469.6	2540.5	7279.7
182.8	4551.8	5863.7	7168.2	3114.6	3989.0	6113.3	5037.5	1510.3	548.8	4319.1
1123.8	2631.2	3199.2	3665.4	1100.5	2580.3	2447.4	2721.3	1105.4	331.1	1661.5
1322.2	655.6	721.4	702.8	489.2	746.4	563.3	623.3	430.7	505.3	485.0
48.3	886.6	1225.7	1690.4	105.3	968.0	1068.2	1021.2	240.6	181.2	484.6
44.8	525.9	587.0	670.1	350.8	401.1	570.3	439.9	119.2	72.3	232.6
60.8	2101.1	1586.2	1743.5	1408.3	1494.6	1507.0	1550.0	1422.5	1004.9	947.8
1145.3	4092.3	5046.2	6619.2	1737.8	3800.9	3939.5	3958.5	1371.1	451.0	2599.0
44.3	33.4	33.5	41.2	28.3	19.4	20.5	31.9	23.5	23.3	26.6

5235.7	3065.8	1554.5
496.7	655.0	484.3
1286.3	871.7	333.3
4026.9	2768.0	1883.3
7822.8	4361.8	2678.6
2758.6	2294.4	2503.0
4785.4	1777.9	1750.6
4296.5	2823.2	2816.9
721.6	494.5	202.2
4028.1	2806.3	1952.9
5253.9	4248.5	6843.3
7541.8	4565.8	2234.3
5788.0	6551.6	6279.8
3758.8	1897.9	958.5
6126.5	3090.2	1235.8
8327.9	5033.6	9161.3
1491.6	1205.5	1338.7
3147.0	2011.7	1314.0
4120.0	3751.4	4961.8
17.9	18.1	14.0
2529.9	2143.6	1771.0
1266.5	243.5	113.6
2813.2	1852.6	2994.9
5969.9	3105.8	1487.9
3159.6	2909.7	4205.0
6853.3	3061.1	1643.0
81.0	141.4	54.4
2445.6	4290.3	2528.9
4569.7	3002.2	1625.7
4946.2	4417.5	3562.8
3444.7	1835.7	1381.4
2780.8	2505.4	6219.8
3434.1	4737.8	3563.9
6012.6	5363.1	7127.3
4392.2	2489.1	1320.8
656.7	843.1	435.5
2184.2	957.0	1102.6
750.5	764.6	559.9
2360.3	1546.4	1557.1
6617.1	3828.0	1829.5
29.9	38.9	19.6

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EU778908.1 gg_id:317337 Black-handed Spider Monkey feces clone SPIM_aaj36f08 EU778
FJ683280.1 gg_id:521175 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
GU302957.1 gg_id:553043 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GQ000713.1 gg_id:469277 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
DQ801533.1 gg_id:196806 human fecal clone RL388_aao96g03 DQ801
AB185623.1 gg_id:100680 rumen clone F24-F01 AB185
EU461508.1 gg_id:290453 black rhinoceros feces clone RH_aaj91c02 EU461
EF445269.1 gg_id:214082 dairy cow rumen clone NED4H12 EF4452
FJ679524.1 gg_id:527726 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ672981.1 gg_id:511974 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6729
FJ676996.1 gg_id:524240 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
AB286442.1 gg_id:205607 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
DQ801283.1 gg_id:185287 human fecal clone RL388_aao93d08 DQ801
DQ797016.1 gg_id:190025 human fecal clone RL386_aao85g10 DQ797
EU871411.1 gg_id:351351 Genetic Bovine (Bos taurus) Rumen Thailand clone CF383 EU871
AF371903.1 gg_id:20534 swine intestine clone p-817-a5 AF371
GQ491301.1 gg_id:593822 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
AM420031.1 gg_id:252889 Noma subgingival plaque clone 201F12(oral) AM420
FJ673999.1 gg_id:517123 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ679715.1 gg_id:530240 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
FJ685341.1 gg_id:526489 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
EU458726.1 gg_id:289980 Goeldi's marmoset feces clone CAL_d03 EU458
FJ685375.1 gg_id:525880 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
DQ801483.1 gg_id:177789 human fecal clone RL388_aao96b05 DQ801
FJ673420.1 gg_id:523261 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
FJ673272.1 gg_id:515189 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU472979.1 gg_id:301030 douc langur feces clone DL_1aaa03f03 EU472
EU459530.1 gg_id:294458 capybara feces clone CAP_aah99c08 EU459
FJ678717.1 gg_id:526104 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
GQ492292.1 gg_id:583770 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
DQ796504.1 gg_id:192562 human fecal clone RL179aan73e10 DQ796
EU463048.1 gg_id:296766 naked mole-rat feces clone molerat_aai69a04 EU463
GQ458218.1 gg_id:577260 Microbial structure co-digestion anaerobic bioreactors treating cassava pulp and pig GQ458
AY977971.1 gg_id:125607 human cecum mucosal biopsy clone LH01 AY977
EU777022.1 gg_id:352470 Naked mole-rat feces clone molerat_2b06 EU777
DQ801587.1 gg_id:188149 human fecal clone RL117_aae92a12 DQ801
GU174055.1 gg_id:586099 Microbial Bactrian camel estimated rumen clone XJC84 GU174
FJ673023.1 gg_id:521137 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
FJ680545.1 gg_id:511256 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6805
EU843073.1 gg_id:329796 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ448611.1 gg_id:572743 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_6wks_gr GQ448

58.2	1967.5	1432.8	1832.5	1670.0	1559.4	1697.9	1602.4	2483.6	1834.7	1228.4
964.1	3675.0	4428.1	5451.6	2659.8	3507.8	3929.4	3476.6	1879.2	1194.4	2898.4
647.1	1025.4	787.0	1141.0	781.7	715.4	875.8	675.3	1031.6	1004.3	1497.1
36.1	24.3	46.6	40.7	34.9	26.9	35.4	41.3	22.4	19.3	25.0
244.1	3198.5	3839.5	4460.4	4200.8	2776.4	6277.1	3666.9	1955.6	1430.1	3649.5
47.3	68.1	135.0	172.7	85.7	60.3	123.0	137.0	55.0	26.1	50.2
51.2	524.1	378.3	355.0	129.3	428.2	250.1	752.7	153.0	182.0	427.3
37.4	32.7	25.0	39.4	25.2	15.8	23.1	19.2	21.4	14.8	16.8
922.9	1092.2	1220.9	1088.2	974.9	1110.9	948.3	958.8	1216.5	1427.8	1164.8
754.6	4907.7	5811.1	7194.0	2319.2	4497.8	5361.9	4674.4	1447.2	952.6	3451.3
1414.0	4487.3	4737.2	4919.2	4824.2	4806.2	4290.5	4047.0	4810.6	4540.6	4183.3
36.4	196.0	308.7	455.7	81.6	174.1	189.1	235.6	60.3	34.6	126.7
51.6	1391.7	1109.0	1303.6	552.9	1320.4	747.9	1001.3	608.7	299.6	516.5
2063.3	6079.7	6436.4	8115.6	6541.7	6544.4	8153.0	6068.7	2243.5	2821.1	6436.3
31.1	194.7	344.4	339.0	46.3	168.9	172.0	285.9	128.4	13.6	82.8
51.8	79.6	105.7	134.4	46.4	43.3	46.2	49.5	43.7	25.7	54.1
50.6	3821.2	4704.5	5859.9	2034.2	3523.0	3514.4	3844.3	1926.4	1333.6	2365.0
514.5	4783.5	4784.1	5966.2	5442.9	4195.7	6346.0	4827.5	4378.0	1895.9	4327.4
686.1	5472.8	6634.1	8157.3	2011.6	5078.4	5575.2	5146.5	1182.2	877.5	3465.2
303.3	2588.2	2890.2	4160.5	2161.3	2744.7	2778.6	2857.8	1184.6	1110.7	2136.6
135.1	3179.5	3533.2	3252.9	1227.3	2565.0	2599.4	2687.4	1662.0	636.2	2185.8
396.3	4594.5	6351.9	5421.3	4867.7	4796.1	6983.3	5113.3	2455.8	1962.5	4193.4
101.3	2682.5	3568.6	4353.3	983.6	2611.6	3035.4	2634.3	849.8	277.6	1874.5
152.7	2124.7	2450.2	3295.2	2689.4	2170.1	2523.2	2068.5	1324.1	684.2	1840.6
1255.8	6072.6	6372.8	7716.6	3284.7	5324.8	5624.2	6992.8	2156.2	1673.7	7309.8
1163.2	3771.0	4147.6	4544.8	2629.4	3571.4	3805.7	3912.0	2140.2	1822.0	3898.6
80.6	2125.7	2544.8	1974.6	741.7	2295.3	2093.5	2053.0	439.3	120.7	1185.1
255.9	2533.5	3291.6	3755.9	3740.7	2719.7	4010.8	2791.6	1759.8	776.6	1827.8
688.2	4563.0	5085.2	6010.9	1949.1	3749.3	4259.8	4032.0	1210.6	867.2	2727.6
66.5	3938.9	3993.4	4810.2	2366.6	3506.1	3088.6	3915.2	3189.4	1883.1	2306.0
2409.2	3600.1	4625.7	4411.7	4808.1	3568.7	5428.8	3048.5	1910.8	1369.8	2428.4
38.1	202.9	278.4	338.5	61.8	118.0	81.3	258.5	39.0	57.6	77.9
102.2	306.0	730.1	781.8	115.2	318.7	228.6	327.7	97.1	46.4	132.9
133.7	3451.8	4879.4	6130.9	2739.9	3577.0	5495.8	4473.1	1225.1	798.9	3706.0
857.3	2205.4	2629.1	3221.5	993.3	988.7	1047.9	1815.7	490.6	450.4	1111.3
56.8	1905.9	3166.0	3203.3	483.8	2101.8	2198.1	1979.2	309.4	160.7	1027.5
123.2	1164.6	1602.4	1871.0	768.7	913.9	1207.6	1468.7	884.8	592.8	926.5
5173.6	3413.9	3844.7	4100.3	2864.2	3102.3	3410.9	3250.4	3258.3	1419.3	2720.2
2029.8	5042.4	5575.2	7073.9	3242.5	4860.9	5167.9	4647.6	2217.3	1108.9	3572.8
102.1	1941.9	2743.9	3537.3	653.9	1803.2	1660.3	1765.7	371.7	216.0	876.9
86.5	3160.8	3810.0	4570.2	755.7	2808.2	2278.5	3474.4	612.3	365.5	2014.6

1316.8	1939.3	1299.2
6266.0	3299.9	2560.2
819.9	882.7	1082.5
37.5	43.3	36.9
3443.7	3126.0	4919.8
147.4	162.7	102.9
442.5	353.6	184.1
23.5	29.3	43.6
826.9	1985.7	864.7
8064.8	4288.7	3887.0
3942.3	5049.5	4179.7
479.1	350.5	92.2
1730.1	1129.0	1927.4
6910.2	7259.3	6725.0
495.7	311.1	45.9
45.3	73.6	35.7
6733.1	3033.9	2582.2
5225.4	5461.3	5509.4
9158.9	4472.5	3532.1
3426.7	2367.1	2043.9
4763.0	2776.0	2222.6
4386.7	4560.3	7812.5
4795.0	2299.4	1270.4
2558.8	2221.7	2168.1
7323.4	5462.5	7468.4
5354.7	3517.8	4344.1
3599.8	2021.3	778.3
3195.7	3221.8	3357.0
6972.4	3605.7	1929.2
5483.9	3060.9	1616.1
3199.7	3438.6	2999.8
319.0	235.7	105.9
643.6	407.9	95.4
5745.9	4017.9	3179.5
3570.9	2175.7	1634.8
3632.2	1676.3	724.4
2086.6	1347.8	1252.0
4279.6	3579.8	2281.7
7849.4	5179.2	3725.4
3718.0	1684.5	853.6
4854.6	2721.3	887.4

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FJ683294.1 gg_id:510878 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
GQ492269.1 gg_id:587839 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
FJ682799.1 gg_id:526362 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6827
GQ448340.1 gg_id:545061 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ674237.1 gg_id:516332 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6742
EF096999.1 gg_id:183035 mouse cecum clone SWPT13_aaa04a03 EF0969
EU344585.1 gg_id:277290 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3445
EU459966.1 gg_id:292284 Prevost's squirrel feces clone SQ_aah82a11 EU4599
AY983899.1 gg_id:116299 human descending colon mucosal biopsy clone MA96 AY9838
AB009236.1 gg_id:2128 rumen clone RFN9 bacterium AB0092
FJ678725.1 gg_id:523005 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
FJ674139.1 gg_id:523308 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ681767.1 gg_id:526763 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
GQ491722.1 gg_id:579740 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ825149.1 gg_id:546934 Prevotella genomosp. T1 str. D033B-12-2 FJ8251
EU473721.1 gg_id:290880 douc langur feces clone DL_2aaa03h08 EU4737
EU777602.1 gg_id:342638 Sumatran orangutan feces clone orang1_aai53g06 EU7776
FJ673613.1 gg_id:523947 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU459973.1 gg_id:301649 Prevost's squirrel feces clone SQ_aah82b10 EU4599
DQ797212.1 gg_id:189542 human fecal clone RL386_aao88d09 DQ797
EU532001.1 gg_id:275566 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5320
FJ673603.1 gg_id:517360 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
FJ676526.1 gg_id:518330 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6765
EU344676.1 gg_id:273149 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3446
FJ684906.1 gg_id:524143 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ683408.1 gg_id:514719 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU871373.1 gg_id:307197 Genetic Bovine (Bos taurus) Rumen Thailand clone CF192 EU8713
EU850476.1 gg_id:328246 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF64 EU8504
AY028443.1 gg_id:70217 mpn-isolate group 2 AY0284
EU842796.1 gg_id:346503 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8427
FJ557915.1 gg_id:517411 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5579
EU773693.1 gg_id:346189 Capybara feces clone CAP_aai00e05 EU7736
FJ685108.1 gg_id:516580 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
GQ492062.1 gg_id:589329 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EU344418.1 gg_id:264746 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3444
DQ797162.1 gg_id:198733 human fecal clone RL386_aao87g05 DQ797
FJ684477.1 gg_id:515660 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
FJ685323.1 gg_id:524619 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
GQ073309.1 gg_id:441328 Topographical and Temporal Human Skin Microbiome skin palm clone nbw207e09c1 GQ073
EU381895.1 gg_id:261646 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3818
AB278593.1 gg_id:192814 Prevotella pleuritidis str. JCM 14110 AB2785

49.4	1225.6	1648.7	2088.9	301.0	1125.3	1089.5	1138.4	180.1	114.9	664.6
858.3	4048.3	4709.2	5951.8	2494.8	3691.6	4240.4	3879.2	1822.2	1102.9	2802.5
931.3	3675.4	4630.9	5507.4	2377.0	3450.6	3944.2	3364.7	1932.8	1330.7	2989.6
69.9	2562.3	3480.6	3726.4	782.1	2170.9	2077.2	2358.7	973.6	564.9	1950.9
979.4	939.9	1013.4	1308.5	880.0	598.5	921.3	943.9	1044.0	583.8	869.0
94.5	2740.2	4027.0	4138.1	514.6	1273.8	912.5	1870.3	718.9	215.7	1068.1
673.2	2954.4	3724.6	4482.7	1506.5	2069.8	2336.7	3630.2	1588.0	852.5	2546.0
252.5	4538.4	4754.5	5802.5	3015.2	5177.0	4780.0	4592.5	1649.9	832.3	3519.1
1508.0	6677.5	7534.6	8304.6	9069.2	6493.1	10492.1	6147.2	2674.9	1605.2	4286.4
50.1	32.7	40.4	51.0	40.2	30.5	39.3	33.9	27.0	27.9	21.4
276.7	2390.3	3498.1	3521.2	878.6	2250.9	1881.3	2496.1	988.1	775.1	1835.8
348.8	4164.3	4328.5	5713.4	794.9	3662.2	3444.7	4648.1	1442.2	792.8	3633.9
76.4	2765.6	4476.4	4832.7	1152.2	2942.0	2820.4	3301.7	1915.6	1125.5	1576.1
1169.8	7125.8	6960.3	6866.4	6405.1	6820.3	7510.7	7152.4	9089.6	6321.1	6649.4
4935.9	4350.9	4593.7	5543.2	3547.1	4248.4	4673.9	4726.6	4116.5	1345.0	2641.5
1146.7	3760.2	3286.5	3569.9	2860.6	2947.0	3204.3	3024.2	4080.8	3764.9	3223.3
216.8	2026.8	2030.8	2733.9	1076.5	1229.8	1493.6	1605.6	674.0	427.1	1644.9
5163.1	3525.8	3734.0	4086.3	2699.1	3208.5	3637.3	3421.0	3305.1	1412.4	2711.0
197.1	6088.8	4557.1	5407.5	4336.8	6042.9	4689.9	6019.2	5150.1	3663.7	4011.2
1346.9	7604.6	7920.8	8931.6	11626.3	7336.6	10827.8	6249.5	3871.4	2602.4	5331.7
31.4	1748.2	1822.8	2373.3	824.2	1764.6	1574.8	1565.5	1143.3	1017.1	845.6
3086.2	3284.3	3053.9	3404.4	2976.4	3030.4	3594.6	2863.9	2116.3	1927.1	3115.1
293.6	7038.5	7111.3	8080.4	5920.1	6347.7	7188.1	6984.9	8492.7	7704.0	8431.0
99.7	3475.6	4708.5	5765.0	1455.2	3224.0	3321.4	4211.2	1253.2	577.6	2902.6
111.1	4410.1	5994.1	7268.4	1383.4	4337.2	4878.1	4232.8	1019.6	358.6	2929.2
65.3	2121.8	2900.0	3251.7	641.3	2123.7	1982.0	2168.7	329.1	132.4	1095.3
214.6	1175.1	1205.5	1293.5	772.4	678.1	1221.5	802.9	842.1	714.5	796.9
128.6	257.2	469.9	570.8	113.0	231.0	320.2	344.5	98.1	57.1	312.2
52.3	440.2	526.8	536.8	186.5	203.1	157.0	359.2	103.6	46.2	120.1
123.4	101.6	115.0	95.1	127.3	99.7	71.7	71.9	61.8	62.6	61.6
1330.8	1605.1	2037.7	2373.3	997.5	1564.7	1935.7	1673.9	799.7	383.6	1040.1
128.2	597.0	626.8	811.2	919.4	487.7	817.3	532.5	280.4	293.6	480.6
1303.9	3909.0	5258.0	5787.3	1935.9	3785.6	4146.3	4011.6	1358.3	531.1	2596.1
95.3	2061.9	2949.7	3300.2	1160.4	2119.9	2578.6	2604.1	672.0	343.5	2254.8
81.4	2358.0	2907.9	4101.4	831.4	2016.5	1825.5	2277.1	477.8	189.7	1004.6
46.3	65.9	79.9	87.6	34.0	43.3	54.7	51.4	38.8	22.4	41.2
48.4	3467.2	4628.5	6646.9	1227.6	3419.7	3762.5	3742.9	562.6	253.0	2309.6
4107.8	9680.6	9227.1	12599.9	10190.0	10229.2	10073.9	8928.3	12198.9	9588.7	10961.6
1018.9	3596.2	3881.5	4278.5	3277.7	3578.6	4300.4	3564.7	3875.1	4595.8	3633.3
181.4	777.1	935.0	1133.2	216.5	519.8	463.4	639.3	190.5	81.6	287.6
49.8	59.5	95.5	99.7	96.4	49.3	165.1	52.1	26.2	20.3	43.9

1996.3	948.4	403.0
6365.1	3820.1	3892.1
6091.2	3348.1	2962.7
4083.4	1956.7	2747.3
983.5	1810.8	687.1
3948.1	1851.0	922.8
4689.1	3580.9	2442.3
5336.8	4222.5	2718.3
6601.9	5693.1	7404.7
34.4	42.6	37.8
3984.6	2292.0	1159.5
6991.0	2763.2	1413.6
7382.3	2770.8	3479.3
7551.6	7355.5	6757.9
6349.4	4219.9	4075.2
3605.7	4054.2	3188.8
1923.3	1549.2	594.4
3868.2	3774.2	2981.4
6406.9	4996.0	4631.5
7612.4	6367.3	9491.2
2362.2	1613.4	618.8
3273.6	4112.8	2713.3
8187.7	6930.2	6280.6
5937.1	3735.6	2717.0
7779.4	3671.1	1798.7
4364.3	1773.2	760.1
920.0	1196.9	942.4
641.8	482.6	140.6
605.6	493.4	218.5
95.6	146.6	75.3
2470.9	2026.7	1946.9
783.2	622.5	602.6
6420.4	3921.3	1992.3
3754.7	2239.3	2762.2
3884.0	2647.8	1081.0
72.2	87.6	49.3
6688.9	3083.7	1275.6
9944.4	8752.6	10755.0
3449.2	4257.7	4836.7
1356.9	874.4	395.9
70.4	54.0	46.0

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DQ801262.1 gg_id:196661 human fecal clone RL388_aao93b05 DQ801
AB009187.1 gg_id:2074 rumen clone RFN29 bacterium AB009
GQ493694.1 gg_id:583126 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ673887.1 gg_id:528706 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6738
DQ113737.1 gg_id:132480 dog colon clone C5-17 DQ113
FJ683202.1 gg_id:532413 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6832
FJ673229.1 gg_id:523833 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
FJ678986.1 gg_id:517816 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
AY976458.1 gg_id:124114 human ascending colon mucosal biopsy clone LZ62 AY9764
EU777604.1 gg_id:326108 Sumatran orangutan feces clone orang1_aai53c03 EU777
AY981014.1 gg_id:126778 human rectum mucosal biopsy clone V184 AY981
FJ682579.1 gg_id:523551 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6825
AF001759.1 gg_id:2118 rumen clone RF27 AF001
EU463171.1 gg_id:303058 naked mole-rat feces clone molerat_aai71a10 EU463
EU844794.1 gg_id:332263 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ978771.1 gg_id:436201 feces clone CL_F_479 FJ9787
EU774243.1 gg_id:319679 Chimpanzee feces clone CHIMP1_aaj38d06 EU774
NZ_ACKS01000100.1 gg_id:470823 Prevotella bergensis str. DSM 17361 NZ_AC
GU303916.1 gg_id:532681 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AB269970.1 gg_id:170418 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
FJ673304.1 gg_id:526031 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU774217.1 gg_id:342890 Chimpanzee feces clone CHIMP1_b03 EU774
FJ673265.1 gg_id:530447 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU467085.1 gg_id:291677 mongoose lemur feces clone ML_aae87f09 EU467
FJ682897.1 gg_id:516731 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6828
GQ493224.1 gg_id:582888 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ684189.1 gg_id:519697 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU773408.1 gg_id:356625 Black lemur feces clone BKLE_e03_2 EU773
EU778865.1 gg_id:347831 Black-handed Spider Monkey feces clone SPIM_c03 EU778
FJ675931.1 gg_id:529907 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
AB477014.2 gg_id:528418 Prevotella dentasini str. NUM 1903 AB477
FJ684108.1 gg_id:511379 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
DQ797074.1 gg_id:197763 human fecal clone RL386_aao86f07 DQ797
FJ673773.1 gg_id:519762 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
FJ673620.1 gg_id:521737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
EU467225.1 gg_id:300603 black-handed spider monkey feces clone SPIM_g12 EU467
EU778888.1 gg_id:339561 Black-handed Spider Monkey feces clone SPIM_c02 EU778
FJ681726.1 gg_id:509358 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
FJ682972.1 gg_id:521760 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GQ101478.1 gg_id:457738 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw495f GQ101
EU473086.1 gg_id:293009 douc langur feces clone DL_1aaa02f01 EU473

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42.2	68.5	114.4	159.9	42.9	91.7	70.5	85.9	32.3	25.3	53.9
190.5	3462.6	4165.6	5245.0	1895.1	3683.3	3646.2	3666.4	2542.0	1250.9	2004.9
463.2	6162.1	7241.6	8669.4	6118.7	6240.4	7918.5	5485.2	2562.3	1297.2	4219.0
2525.0	3490.0	3759.7	4443.6	4065.5	3815.1	4466.1	3666.8	1660.7	782.7	2540.6
68.1	1734.7	2019.3	2938.2	415.9	1684.3	1465.3	1778.3	194.4	161.1	836.9
1556.0	2962.8	3801.0	4267.2	2431.9	2949.7	3182.1	3588.7	1321.8	581.7	2559.4
1335.3	4384.4	5631.0	6998.3	3118.2	5027.9	4720.2	4068.0	2717.6	2560.3	2974.2
338.0	4639.9	5153.4	5937.6	5591.5	4569.0	6192.2	4091.7	1501.6	912.2	2555.9
1700.5	2816.3	2706.7	3540.9	3492.0	2995.0	3651.1	2751.7	1284.7	594.1	2155.1
172.1	3722.9	3103.8	4106.4	3258.7	2813.4	3486.5	3252.2	2329.7	1744.6	2591.7
1380.5	2873.7	3877.1	4470.3	1722.1	2843.1	3185.5	3075.8	1251.2	446.1	1994.1
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3430.5	4104.8	3604.5	3957.3	2108.4	3425.3	3170.8	3157.8	2920.2	2302.0	3305.5
47.0	175.7	187.3	61.6	135.6	103.5	170.0	138.8	77.8	33.4	70.3
3036.9	2787.0	2431.1	3028.7	3435.3	2864.3	3019.2	2921.4	3002.0	3026.6	2416.4
1444.5	3628.3	4119.8	4619.4	5843.6	3586.6	4916.7	3043.4	1628.9	984.2	2244.5
58.2	26.5	27.9	30.9	31.9	21.1	28.6	23.9	26.9	22.9	42.2
108.6	2054.8	1927.8	2557.1	442.9	1253.1	908.1	2198.1	588.5	292.5	1532.3
76.3	911.7	1246.1	1671.3	282.8	514.4	502.1	914.9	248.3	142.6	356.8
1124.9	4294.0	4884.1	5491.2	2725.7	4032.4	4361.5	3825.7	2644.8	1819.8	3150.3
36.4	2718.0	3191.4	4333.2	1763.6	2834.2	3682.4	2658.0	572.4	428.4	1807.5
358.2	1685.5	2279.6	2062.3	1081.6	1585.1	1558.3	1807.7	1552.1	929.1	1411.2
1889.7	979.5	905.8	843.3	817.3	966.7	930.2	1044.5	842.0	317.9	576.5
1386.7	5416.7	6248.8	7594.3	2874.8	4624.4	5208.4	5222.6	1966.2	1008.8	3647.2
81.4	2845.1	3693.9	4662.2	812.4	3104.1	3020.3	3131.8	800.9	475.2	1598.2
65.1	3612.4	4763.1	7058.5	1147.3	3360.6	3494.7	3855.4	637.8	243.5	2280.7
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1721.8	5847.9	5998.6	7293.6	9658.4	5807.4	9047.0	5080.7	2877.4	1682.4	3862.4
225.7	2054.5	2434.0	3075.1	3688.2	2150.6	3807.8	1844.5	696.5	528.6	1250.0
86.1	1121.0	1533.6	1818.3	489.4	992.0	1342.7	1104.4	369.2	138.8	733.5
513.6	4615.8	5838.9	7042.3	4642.8	5104.6	5055.8	4131.4	2371.5	1319.8	3574.3
49.3	32.4	33.9	32.8	34.6	25.1	31.1	24.9	43.7	27.3	28.0
420.5	1259.5	1299.1	1546.0	1229.0	1254.1	1112.6	1453.2	1465.5	722.8	799.3

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3569.6	2315.5	523.1
4714.9	3778.2	2420.6
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2302.0	976.9	1287.2
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765.4	1532.4	913.1
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4840.3	3816.7	3203.1
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5815.2	5264.1	7120.3
2386.4	1872.4	2712.9
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32.1	33.3	25.4
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EU473077.1 gg_id:295048 douc langur feces clone DL_1aaa02g02 EU473
EF436341.1 gg_id:211784 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC55 EF4363
EU845194.1 gg_id:335548 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU845
FJ679778.1 gg_id:528866 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
GQ491879.1 gg_id:551635 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU462152.1 gg_id:287783 black-handed spider monkey feces clone SPIM_aaj36a08 EU462
FJ683682.1 gg_id:526922 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
GQ046497.1 gg_id:431396 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ046
GQ493811.1 gg_id:556757 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY244896.1 gg_id:85799 cow rumen clone BF18 AY2448
FJ681232.1 gg_id:530653 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ364421.1 gg_id:357005 feces adult twins and mothers; TS15 clone TS15_a02g04 FJ3644
FJ172820.1 gg_id:312373 Qinghai Yak Ruminal and Fungi China rumen clone RB-5B5 FJ1728
AF132249.1 gg_id:72142 adult human fecal matter clone adhufec235 AF1322
FJ681368.1 gg_id:510300 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ801321.1 gg_id:194164 human fecal clone RL388_aao93h08 DQ801
EU773571.1 gg_id:313753 Goeldi's Marmoset feces clone CAL_c04_1 EU773
FJ680901.1 gg_id:511091 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
DQ801556.1 gg_id:181943 human fecal clone RL117_aae91a12 DQ801
FJ674135.1 gg_id:524891 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ797023.1 gg_id:188921 human fecal clone RL386_aao85h09 DQ797
FJ683138.1 gg_id:515532 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
AF371875.1 gg_id:24907 swine intestine clone p-2190-s959-3 AF3718
FJ673391.1 gg_id:530487 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ680203.1 gg_id:518851 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6802
FJ678765.1 gg_id:517558 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6787
AF018480.1 gg_id:2142 rumen clone 12-101 AF0184
AY244930.1 gg_id:100068 cow rumen clone BE13 AY2449
DQ456110.1 gg_id:157597 pre-adolescent turkey cecum clone CFT114E7 DQ456
FJ674173.1 gg_id:524836 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ683154.1 gg_id:516852 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ684879.1 gg_id:525835 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ028800.1 gg_id:567752 Microbial Taiwan water buffalo rumen fluid clone TWBRB87 FJ0288
DQ795861.1 gg_id:178434 human fecal clone RL245_aai83e09 DQ795
FJ558443.1 gg_id:518217 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5584
DQ796011.1 gg_id:196481 human fecal clone RL202_aai50c04 DQ796
EU871377.1 gg_id:322023 Genetic Bovine (Bos taurus) Rumen Thailand clone CF199 EU871
EU778079.1 gg_id:316570 feces clone RL388_aao93f04 EU778
FJ678203.1 gg_id:509498 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
EU467097.1 gg_id:288393 mongoose lemur feces clone ML_aae88b06 EU467

940.3	3459.9	4459.7	5172.5	2329.4	3496.2	3681.8	3469.9	1757.4	1086.0	2697.6
736.2	5695.6	5078.7	6137.9	6121.5	4765.2	6564.6	5036.4	6908.6	6108.4	5541.9
774.1	799.9	860.5	1050.3	653.3	620.4	1024.2	717.6	747.3	463.9	981.4
120.7	3456.0	4177.4	5555.8	2897.4	3319.0	3425.3	4866.3	3077.0	944.7	2863.9
95.8	2495.4	3497.3	4085.6	854.5	2468.1	2900.3	2444.3	535.0	219.5	1618.3
44.1	2407.7	3535.9	4450.0	686.4	2765.7	2462.2	2804.2	400.5	151.0	1336.9
4366.1	2359.6	2212.8	2460.0	2217.6	1945.8	2205.1	2000.1	2625.8	1374.9	1861.1
199.9	4188.1	4728.9	5756.2	1987.7	3378.8	3788.7	3938.1	1051.4	708.4	2584.3
41.1	103.0	163.2	193.7	55.1	89.9	121.4	107.6	21.9	21.5	56.5
247.0	4820.4	6149.5	6929.7	5749.3	4475.7	8031.3	5610.2	3958.2	2178.6	6176.3
39.4	88.2	153.3	150.0	67.5	35.6	90.2	125.4	35.6	23.7	60.0
805.8	4430.7	5251.3	6580.6	2472.3	4103.5	4885.9	4332.4	1457.1	931.2	3207.3
44.0	3601.7	4171.5	4930.9	2362.0	3430.4	3449.4	3622.2	1432.0	762.6	2241.9
1651.7	2439.9	2701.8	2521.8	1432.7	2144.2	2458.4	2053.1	1263.1	1218.0	1783.4
59.8	225.4	336.4	68.6	168.7	221.7	251.4	216.9	216.1	68.8	203.8
467.3	5710.4	6756.4	9184.7	2001.4	5143.8	5480.7	5740.7	1520.2	616.8	3695.9
1897.2	3731.9	3564.7	4930.1	4622.7	3968.8	4844.4	3651.2	1592.2	729.2	2853.5
1269.2	3352.9	3895.7	4107.1	1889.5	3673.6	3256.5	3252.4	2850.0	1452.7	2518.6
2183.5	4438.8	4857.6	5991.2	3098.6	4034.2	4738.1	4285.3	3985.0	2717.7	3743.8
36.1	1652.8	2570.8	2153.5	1167.3	1775.5	1845.7	1847.4	1695.4	1282.2	1020.1
101.4	2187.9	3366.0	3682.7	1459.0	2224.2	3052.5	2657.4	1081.5	1366.3	2074.8
1327.7	3386.5	3126.6	3855.4	3721.2	2489.8	3815.5	3438.0	2053.7	1163.0	2957.0
955.0	6026.4	6816.2	8258.1	5829.4	5710.9	7463.9	5398.5	2273.8	1585.7	4121.1
54.9	29.6	26.7	33.4	46.0	31.0	35.1	23.1	34.2	19.1	27.3
4386.7	5930.5	7515.2	8491.3	3156.7	5648.4	5808.9	5883.6	3281.0	1712.7	4044.5
665.9	4202.5	5276.8	6285.6	1968.4	3922.6	4756.9	3928.0	1113.4	739.4	2924.4
3107.4	6171.3	5851.0	5298.2	5408.5	5767.7	6717.7	6547.5	9981.2	6893.3	8539.0
42.8	24.2	31.0	30.0	26.0	25.8	22.6	33.2	27.1	20.7	31.7
38.0	343.7	587.8	659.3	156.4	153.6	492.5	371.1	170.4	62.4	182.9
54.3	45.2	56.9	55.8	49.3	33.6	46.8	40.4	28.5	38.9	43.2
113.7	3208.3	3851.5	4476.0	1172.2	2711.1	2708.5	3156.5	714.6	439.4	1921.7
5170.7	3480.3	3733.2	4135.3	2577.8	3260.3	3471.3	3317.9	3282.9	1291.2	2491.2
174.8	1764.8	1717.9	2201.3	1427.1	1590.6	1928.8	1855.0	568.2	596.2	934.9
121.8	3069.1	3955.7	5569.9	1945.1	2339.4	2413.0	2772.1	1124.3	1379.9	1488.1
4066.2	5397.1	5462.5	6250.5	3742.1	5367.6	5745.4	4663.5	3660.2	1646.5	3769.9
5160.5	7376.6	6822.4	6164.7	7245.7	7838.3	8860.5	7879.6	10929.6	7124.4	7644.8
1407.3	5119.8	5710.4	6881.1	7559.2	4792.7	7811.2	4381.6	2342.0	1509.8	3355.3
101.1	1062.3	1510.3	1503.0	1202.0	1250.6	1538.3	1066.7	512.3	341.0	620.0
3901.1	3324.3	3533.8	4172.3	4749.1	4429.2	3668.8	3420.9	2598.3	5771.4	3572.3
68.4	1040.3	1633.6	2867.6	400.7	1021.1	1106.0	1263.3	175.3	88.7	578.4
155.0	2934.8	3827.2	3911.4	2256.6	2741.8	5153.8	2613.9	685.6	627.2	1789.3

5931.7	3288.5	2395.4
4476.2	5892.0	5643.9
622.7	1092.3	615.4
5191.0	3994.1	3057.7
4389.1	2090.2	997.0
5544.2	2336.2	1289.8
1932.7	2429.9	1447.3
6552.4	3425.3	1513.6
170.2	147.7	120.9
5084.6	4535.4	8263.5
122.4	149.1	39.8
7375.5	4100.3	3827.7
5139.1	3249.8	1898.6
2453.6	2908.9	2421.7
427.9	166.7	132.3
9169.2	5064.1	3363.7
3613.0	4207.0	3124.0
4011.4	4136.7	2788.9
5935.7	5400.8	3598.9
2095.2	2358.0	794.0
2336.0	2163.8	2055.8
3366.5	3318.0	2383.4
7747.3	5127.1	6000.5
25.8	35.5	31.5
9199.7	5861.4	3802.4
6434.7	3320.9	2179.1
5367.9	6557.4	5463.5
20.7	28.9	23.7
216.4	174.5	215.3
39.8	56.6	49.2
5152.1	2602.1	1167.1
3855.9	3580.1	1889.9
1929.8	1952.6	1627.2
4601.0	2991.5	1839.9
5973.3	4807.2	3420.8
6231.9	7817.2	7004.5
5399.5	4600.2	6242.4
1478.9	907.7	1770.9
5976.9	4393.7	3843.3
2477.0	1321.1	457.5
4243.0	2148.4	2159.6

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EU459941.1 gg_id:300536 Prevost's squirrel feces clone SQ_aah81f03 EU459
EU459830.1 gg_id:294537 Prevost's squirrel feces clone SQ_aah79f05 EU459
GQ897764.1 gg_id:585756 Diets enriched fructans and/or can alter dominant fecal humans but do so non-cons GQ897
EU778293.1 gg_id:325046 feces clone RL388_aao96b06 EU778
EU458706.1 gg_id:296262 Goeldi's marmoset feces clone CAL_f10 EU458
FJ679626.1 gg_id:524036 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
EU461627.1 gg_id:296932 mongoose lemur feces clone ML_aaj25g09 EU461
FJ675967.1 gg_id:515381 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU473861.1 gg_id:292246 douc langur feces clone DL_2aaa02g03 EU473
FJ685261.1 gg_id:514444 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
GQ047279.1 gg_id:377975 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1010h GQ047
FJ683431.1 gg_id:520737 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AY244912.1 gg_id:83758 cow rumen clone BF34 AY244
AJ315483.1 gg_id:26715 human colonic sample clone AJ3154
AY977626.1 gg_id:124820 human cecum mucosal biopsy clone LC71 AY977
GQ491841.1 gg_id:538267 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ801569.1 gg_id:192124 human fecal clone RL117_aae91f01 DQ801
FJ681522.1 gg_id:532396 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6815
GQ433639.1 gg_id:577211 Prevotella sp. str. WAL 2039G GQ433
EU531920.1 gg_id:259433 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
GQ030288.1 gg_id:463032 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw876a GQ030
GQ422744.1 gg_id:532929 Prevotella sp. oral taxon 781 str. F0055 GQ422
EU459927.1 gg_id:299240 Prevost's squirrel feces clone SQ_aah81d02 EU459
FJ364568.1 gg_id:360096 feces adult twins and mothers; TS15 clone TS15_a04e03 FJ3645
FJ684510.1 gg_id:517196 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU469364.1 gg_id:293011 black lemur feces clone BKLE_b11 EU469
FJ684867.1 gg_id:523851 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ673336.1 gg_id:515720 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ685365.1 gg_id:511813 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
EU462253.1 gg_id:294521 chimpanzee feces clone CHIMP1_aaj38e05 EU462
AM420262.1 gg_id:236167 Noma subgingival plaque clone 701G08(oral) AM420
EF510678.1 gg_id:224575 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5106
FJ557727.1 gg_id:521268 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5577
FJ673253.1 gg_id:511743 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6732
EU462056.1 gg_id:293402 black-handed spider monkey feces clone SPIM_aaj34a11 EU462
FJ675551.1 gg_id:531487 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
FJ684653.1 gg_id:528818 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
FJ680910.1 gg_id:518747 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6809
GU303995.1 gg_id:542145 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AY982518.1 gg_id:117749 human sigmoid colon mucosal biopsy clone MN41 AY982
FJ674199.1 gg_id:527095 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741

224.8	4681.0	4842.0	6853.3	4628.6	4621.9	4542.5	4190.9	3509.8	1936.2	3320.1
544.9	5083.3	5640.3	6874.5	4427.5	4760.0	6009.2	4453.3	3195.3	1627.5	4184.1
37.6	58.2	98.2	91.0	37.0	68.3	64.0	119.2	43.8	17.4	37.9
118.4	1406.1	1740.5	1502.1	1575.9	1492.3	2027.3	1135.6	460.2	286.0	910.0
144.9	3184.0	4170.2	5060.0	2669.7	3162.4	4518.6	2844.2	903.1	343.1	1918.7
139.1	4123.5	4845.3	5267.0	1824.8	3465.8	3422.6	3722.5	822.3	561.7	2569.4
32.6	592.2	885.7	1440.0	167.7	456.4	522.0	593.3	104.5	53.9	209.4
305.4	3109.2	2740.6	3281.9	1348.0	2182.9	1993.6	2354.2	1615.3	1231.7	1634.9
64.1	1965.1	2774.6	3638.1	200.7	887.8	455.5	1141.8	754.2	288.0	412.3
761.4	5270.1	6306.1	7727.4	2332.8	4739.3	5483.2	4957.0	1470.6	947.2	3549.2
112.6	1731.6	1950.4	2590.7	285.0	921.5	600.6	1443.8	273.1	162.3	516.8
4630.8	3623.9	3487.9	3690.1	2880.2	2787.4	3109.4	2845.5	3591.5	5120.1	3205.5
45.0	99.7	89.6	102.0	114.7	93.2	95.1	83.7	32.3	30.3	38.9
68.5	1644.6	2198.4	2734.3	772.7	1797.4	2013.3	1846.0	460.6	207.0	800.3
45.1	90.6	215.1	235.5	36.4	47.9	80.4	69.1	26.4	15.3	57.1
48.1	2766.7	4082.8	5129.1	698.2	3131.6	2879.3	3168.2	378.2	217.3	1427.2
11218.2	4681.4	4856.3	5455.4	4204.0	4952.2	5580.7	4490.2	4627.2	2248.8	3618.3
4363.6	3502.1	3698.4	4054.3	2512.1	3177.5	3607.7	3383.0	2894.9	1498.4	2682.6
29.7	594.4	1086.3	1184.1	126.9	713.4	711.5	771.6	104.9	52.8	312.9
1138.2	1631.6	1846.6	2504.9	1503.9	1483.0	1615.8	1572.7	847.4	474.9	1061.2
193.3	4685.3	4890.9	5071.0	2881.4	3564.8	5713.1	3742.7	3056.6	1686.2	3740.0
172.2	1914.4	2264.3	3137.3	1771.9	1721.9	2817.0	1978.1	1200.8	477.2	1130.4
329.3	4303.2	5014.5	6068.3	4787.5	4250.2	6227.9	3835.0	1687.0	1010.6	2976.6
690.1	1358.0	1407.4	1556.1	1270.9	1322.8	1742.1	1311.5	540.4	347.6	647.4
502.4	5001.2	5917.4	7471.1	1870.5	4505.8	4800.5	4980.2	1520.3	664.6	3209.0
4736.1	4240.5	5075.8	5097.0	3046.4	4087.4	3945.3	4186.0	3279.6	1431.9	2778.2
2817.7	2617.0	3184.3	3772.8	2941.2	2713.7	3248.6	2541.4	2038.4	2067.8	2731.7
558.5	3685.9	5317.0	6221.0	2451.1	4216.0	3993.9	3659.2	2083.5	1027.4	2843.4
25.4	284.7	362.3	365.2	110.2	174.9	132.3	144.2	22.8	30.1	28.3
62.0	1841.6	2502.9	2805.5	474.3	1804.7	1813.1	1642.6	281.6	136.5	1138.9
38.3	224.7	341.7	469.0	108.5	254.0	224.7	319.6	64.0	46.1	110.8
1320.4	2370.5	2435.6	2705.2	2404.2	2570.9	3178.0	3387.3	1706.0	1018.2	1722.3
1909.7	3580.7	3840.8	5293.4	3628.9	4260.0	4872.0	4110.5	1786.0	859.3	2639.6
902.5	2848.8	3389.5	3993.6	2155.9	2925.5	3047.0	2857.8	1606.9	949.6	2116.1
59.1	740.4	702.8	877.4	1128.6	770.3	919.4	646.0	265.4	188.0	516.1
38.8	352.6	576.7	837.3	108.3	436.3	446.3	437.5	45.0	39.2	238.9
1261.2	8374.7	8498.4	10040.7	4839.8	6821.2	9977.4	7149.6	3067.1	4489.7	6093.0
406.1	3120.7	3946.9	5027.2	3496.3	3356.5	4552.8	3668.4	2301.7	984.2	3739.3
34.9	157.1	348.3	465.3	44.6	202.8	146.2	218.6	30.1	31.7	96.7
150.9	2342.0	2204.4	3255.0	1799.0	1786.1	2905.5	1947.7	760.8	507.7	2312.1
1188.4	6624.8	9108.4	10751.9	3918.0	7366.3	7214.9	6213.4	1828.2	1661.0	4381.8

5932.1	4047.6	4577.8
6756.0	5156.2	4441.3
93.8	143.0	55.6
1558.1	1404.7	1450.9
4775.0	2896.1	4549.9
5847.0	3493.0	2020.3
1150.3	667.6	934.1
3052.2	2750.4	1098.6
2365.7	1948.0	2371.7
8430.1	4642.9	3962.2
2516.3	1415.9	340.2
4601.7	2988.9	2813.8
93.0	140.9	160.0
3229.4	1856.6	1109.3
161.1	213.7	45.0
6306.5	2529.3	1357.9
5258.6	4881.2	2965.3
3810.4	3665.8	2968.2
1478.6	521.1	240.9
2161.6	1761.9	919.6
4625.0	3580.3	2669.9
3052.4	1863.6	1865.0
5317.0	3499.7	3727.8
1591.8	1508.7	1285.0
8030.1	4433.6	3152.9
4974.9	4471.6	2111.8
3287.0	2732.0	2553.2
6102.0	4142.2	2294.5
474.8	243.7	104.5
2863.5	1753.3	643.7
528.6	492.8	226.3
3412.5	3390.6	4770.9
5137.8	4118.7	3926.0
4207.6	2763.2	2030.5
705.2	772.4	963.3
744.0	339.3	131.3
9971.1	5374.3	5601.8
4115.8	3710.7	4978.1
1146.9	155.0	34.0
1917.5	1797.2	2394.5
10288.6	5337.5	3612.8

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EU472622.1 gg_id:294714 Angola colobus feces clone EAC_2_aaa02c04 EU472
FJ681868.1 gg_id:530508 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6818
FJ683006.1 gg_id:516303 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
EU850571.1 gg_id:339973 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF383 EU850
FJ364385.1 gg_id:357152 feces adult twins and mothers; TS15 clone TS15_a02c08 FJ3643
EU850455.1 gg_id:313890 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF24 EU850
EU473048.1 gg_id:292699 douc langur feces clone DL_1aaa03e11 EU473
FJ557945.1 gg_id:521803 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5579
FJ365334.1 gg_id:364193 feces adult twins and mothers; TS20 clone TS20_a01f07 FJ3653
EU773458.1 gg_id:321145 Black lemur feces clone BKLE_e03_3 EU773
FJ673184.1 gg_id:524964 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
GQ493590.1 gg_id:564755 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ365512.1 gg_id:362089 feces adult twins and mothers; TS20 clone TS20_a03g02 FJ3655
AY977674.1 gg_id:117761 human cecum mucosal biopsy clone LD28 AY977
EU381854.1 gg_id:271680 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ684203.1 gg_id:519003 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU777028.1 gg_id:323411 Naked mole-rat feces clone molerat_aai72d04 EU777
FJ683074.1 gg_id:509587 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
DQ796936.1 gg_id:185170 human fecal clone RL179_aao56f06 DQ796
FJ682022.1 gg_id:511530 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU462168.1 gg_id:296780 black-handed spider monkey feces clone SPIM_aaj36c09 EU462
FJ680885.1 gg_id:527286 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6808
EF096023.1 gg_id:190522 mouse cecum clone lean2_aaa02c05 EF096
GQ402129.1 gg_id:584509 alpacas and sheep forestomach clone ALP23 GQ402
EF096104.1 gg_id:180524 mouse cecum clone lean2_aaa04c04 EF0961
FJ673318.1 gg_id:517304 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ685049.1 gg_id:512224 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
EU473854.1 gg_id:292234 douc langur feces clone DL_2aaa04b06 EU473
AY244933.1 gg_id:86315 cow rumen clone BE15 AY244
FJ674171.1 gg_id:510530 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
GQ422745.1 gg_id:570119 Prevotella sp. oral taxon 782 str. F0012 GQ422
FJ363234.1 gg_id:366561 feces adult twins and mothers; TS148 clone TS148_a04g10 FJ3632
DQ794918.1 gg_id:191249 human fecal clone RL310_aam37h08 DQ794
AY980875.1 gg_id:116049 human rectum mucosal biopsy clone LQ01 AY980
EU462285.1 gg_id:302389 chimpanzee feces clone CHIMP1_aaj39c08 EU462
GQ492017.1 gg_id:581481 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AB270138.1 gg_id:168429 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
FJ683497.1 gg_id:511597 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AY349394.1 gg_id:92629 human oral cavity clone FW035 AY349
FJ558099.1 gg_id:521761 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
FJ673305.1 gg_id:524963 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733

82.1	2497.7	2937.8	3410.6	1482.6	2279.5	2790.3	2673.5	1729.7	1224.7	3334.9
632.2	888.6	382.7	819.6	537.1	835.0	1015.8	643.3	738.3	686.1	1068.2
1752.8	3439.9	3564.8	3989.6	3173.3	3413.3	4005.3	4042.8	1882.9	1722.5	2725.5
26.2	146.3	103.1	128.6	32.4	74.5	88.7	72.6	20.3	14.8	55.7
1189.0	2867.1	3132.5	3803.4	2190.5	3273.4	3004.9	3079.0	942.2	508.7	1764.6
117.6	1159.8	1588.5	1742.7	344.3	754.0	742.5	1187.5	315.1	178.8	619.7
884.8	3970.7	3160.2	3650.2	2917.7	2812.8	2903.0	3064.0	2940.8	1818.2	2350.4
103.6	1349.4	1359.3	1267.1	1128.1	1086.2	2030.2	1232.4	1323.2	514.7	1398.2
51.7	2076.5	2965.6	3447.2	900.4	2521.4	2284.1	2467.0	444.7	334.6	1158.0
2606.3	4858.5	4315.1	5248.6	3503.5	3994.1	5982.4	4651.4	2056.7	1306.4	3158.0
327.8	695.8	690.1	746.3	472.4	571.3	587.6	635.2	459.8	425.3	479.4
46.1	2591.1	3741.6	4593.8	828.1	3038.2	2629.2	3043.0	559.9	268.1	1383.6
817.1	3725.7	4728.9	6021.6	1928.7	4030.5	4387.6	4020.3	1202.7	977.4	2287.6
41.9	25.9	69.7	47.0	29.7	23.7	25.6	25.6	19.8	26.0	23.3
47.3	108.0	238.9	341.6	37.8	37.3	57.0	61.5	30.7	20.4	42.7
111.6	954.4	1910.3	1718.8	1364.2	1345.8	1964.7	1537.4	490.7	478.2	1553.9
150.4	2886.7	3481.9	4127.3	2075.4	2636.6	3106.1	3270.2	1211.1	576.1	2833.6
1839.9	3364.3	4499.6	3469.1	3864.1	3768.6	4868.5	4199.9	2102.6	2077.6	3726.3
104.6	1393.0	1327.1	1288.5	668.1	1393.8	1006.7	1174.5	439.9	518.6	728.9
713.2	2710.1	3198.9	3648.9	1897.0	2669.7	3160.6	3063.6	1262.5	707.7	1934.6
220.0	2283.5	3023.7	3787.2	3686.0	2429.4	3647.3	1980.8	825.3	567.5	1352.9
1886.0	13980.6	13606.5	15362.0	10992.3	14830.6	13517.5	12135.0	14649.3	13528.3	14796.0
7087.4	2577.9	3639.4	2980.8	2282.8	2565.2	2867.2	2277.7	3232.8	1170.5	3343.1
37.4	66.5	128.6	75.0	52.0	44.2	42.1	142.9	83.1	42.5	30.7
49.6	520.0	1015.7	683.4	275.8	504.5	584.4	497.3	720.3	134.6	420.3
803.4	4905.9	5824.0	7177.6	2308.4	4498.9	5355.8	4663.0	1394.3	940.1	3429.8
89.5	1902.7	2658.6	3218.3	712.5	1879.5	2276.6	1905.0	540.5	157.3	1240.1
38.6	194.4	333.1	400.0	122.7	111.2	180.3	135.0	87.3	33.1	61.8
34.0	388.9	249.3	130.4	187.3	133.4	136.0	110.8	134.2	126.2	49.5
692.0	4798.4	5824.0	7163.3	1888.6	4452.7	4894.0	4519.7	1260.5	877.2	3042.2
42.4	2749.6	3194.2	2689.3	691.5	2507.8	2942.2	2250.0	460.7	267.9	1713.5
342.9	5150.2	5241.0	5763.7	3994.4	4892.6	4239.9	4930.6	7475.0	5500.2	4365.0
66.7	1469.0	1827.6	2117.8	510.7	1260.5	1197.3	1644.4	341.2	201.4	834.5
1346.8	2567.8	2936.8	3475.3	2135.4	2419.6	3657.1	2716.9	1214.8	547.3	2471.8
1113.2	3159.2	2968.1	3634.2	2911.8	2670.1	3590.1	2971.3	1347.1	853.2	2230.9
53.8	3640.8	5092.8	6406.0	967.3	3813.2	3671.1	3753.8	560.5	245.1	2030.8
445.5	1086.8	1462.7	1679.1	1228.0	985.0	1231.5	1244.6	640.4	1360.1	1265.4
69.7	789.7	1000.8	1189.0	396.4	702.2	692.4	842.4	143.0	69.8	297.6
209.1	2272.0	2853.4	3979.4	2045.2	2462.5	2988.3	2953.9	933.3	352.8	1487.2
119.3	2543.0	3278.4	5011.6	1130.2	3799.7	3148.4	3487.5	2001.4	877.8	1338.8
277.1	4669.9	3777.1	3665.1	3472.8	3974.7	3528.5	3600.9	7622.7	4392.2	3174.8

2671.9	2544.3	3020.0
676.9	1283.3	730.1
4466.6	3594.8	3957.4
153.6	137.8	44.8
4084.1	2671.9	1761.0
2642.0	1291.7	1211.5
3625.6	3475.1	6566.4
1039.2	1639.4	1328.3
3937.6	2077.6	1848.0
5070.8	4975.5	4434.2
841.1	1254.8	424.9
5720.9	2500.4	1629.6
6774.6	3550.7	3681.2
32.5	39.2	24.9
81.7	170.4	38.2
1483.6	1323.8	1236.3
3610.1	2361.8	2284.0
4413.2	3781.1	4368.0
1678.5	1724.8	956.0
4037.3	2977.2	3666.0
2699.6	1966.9	3307.6
10985.3	11604.2	10435.5
2805.3	2708.2	1975.8
52.7	175.7	68.4
856.5	597.6	243.5
8015.7	4226.3	3873.3
3632.5	1688.2	787.5
154.5	241.5	148.8
139.5	264.2	212.6
8028.9	3927.6	3313.4
4028.7	3020.5	1015.1
5123.0	5592.7	3474.9
2606.1	1208.5	483.2
2520.8	2891.7	3987.3
3071.0	2860.1	2028.9
7662.2	3135.2	1713.0
1504.7	1462.9	929.1
1787.5	715.1	378.2
2917.1	3905.9	2802.8
5805.5	2258.3	2496.9
4925.7	3709.8	2398.6

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GQ493098.1 gg_id:579123 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ684917.1 gg_id:520350 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU471536.1 gg_id:302793 Asiatic elephant feces clone AE1_aaa04b08 EU471
AF153866.1 gg_id:2190 faecal clone adhufec41.25 AF153
EU462594.1 gg_id:297847 Sumatran orangutan feces clone orang2_aai65g11 EU462
FJ673968.1 gg_id:522803 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
FJ682169.1 gg_id:517050 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6821
FJ684805.1 gg_id:531509 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ674182.1 gg_id:528488 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EU381939.1 gg_id:259544 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
DQ795908.1 gg_id:188629 human fecal clone RL245_aai84f03 DQ795
EU462333.1 gg_id:299235 chimpanzee feces clone CHIMP1_aaj40c12 EU462
EU462125.1 gg_id:298189 black-handed spider monkey feces clone SPIM_aaj35d03 EU462
FJ673154.1 gg_id:512933 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6731
EU467184.1 gg_id:298007 white-faced saki feces clone Saki_c01 EU467
EU776856.1 gg_id:313152 Mongoose lemur feces clone ML_aaj27h04 EU776
FJ684967.1 gg_id:523945 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ363033.1 gg_id:368725 feces adult twins and mothers; TS148 clone TS148_a02b08 FJ3630
AY976024.1 gg_id:117319 human ascending colon mucosal biopsy clone LT70 AY976
EU381986.1 gg_id:260514 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ684292.1 gg_id:515980 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
FJ364562.1 gg_id:357744 feces adult twins and mothers; TS15 clone TS15_a04d08 FJ3645
AB034103.1 gg_id:31669 rumen clone 4C3d-5 AB034
FJ684836.1 gg_id:521597 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
EU467230.1 gg_id:289953 black-handed spider monkey feces clone SPIM_a09 EU467
FJ673684.1 gg_id:519820 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ801406.1 gg_id:175562 human fecal clone RL388_aao95b04 DQ801
GQ493827.1 gg_id:550372 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ677459.1 gg_id:527153 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
FJ364488.1 gg_id:366536 feces adult twins and mothers; TS15 clone TS15_a03e09 FJ3644
AB269982.1 gg_id:165485 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB269
FJ685211.1 gg_id:521837 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
AF414822.1 gg_id:70907 Prevotella intermedia str. 5-PIN AF414
AB009225.1 gg_id:2079 rumen clone RFN78 bacterium AB009
FJ364288.1 gg_id:364886 feces adult twins and mothers; TS15 clone TS15_a01b09 FJ3642
AY944134.1 gg_id:114813 Prevotella genomosp. P4 str. P4P_53 AY944
FJ685000.1 gg_id:512387 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6850
EU462169.1 gg_id:297270 black-handed spider monkey feces clone SPIM_aaj36d01 EU462
AB185513.1 gg_id:107586 rumen clone F23-A10 AB185
FJ673935.1 gg_id:531755 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6739
AY980608.1 gg_id:116069 human rectum mucosal biopsy clone LK41 AY980

79.8	2113.7	2680.7	3282.1	624.8	2048.6	2122.6	2251.6	722.7	347.8	1252.3
904.9	3980.8	4568.5	5060.7	2280.2	3556.9	4008.7	3489.5	1849.0	1600.8	2770.0
1932.4	2299.1	3387.5	4272.7	1735.9	2534.5	3657.5	3566.4	2566.2	2896.7	2469.3
359.3	3499.2	2514.8	3571.6	4869.7	2181.5	3433.6	2707.7	1321.0	1123.9	2089.5
250.2	1252.3	1614.7	1742.6	639.1	817.2	994.3	1465.2	603.7	253.7	635.6
478.9	5590.0	6432.8	7863.8	6362.4	5616.9	7510.2	4947.1	2181.1	1411.5	3523.0
109.1	3265.9	4637.8	5291.9	1408.1	3218.1	3376.6	3431.3	549.3	271.0	1926.9
1617.0	6428.1	5445.6	5103.7	6038.7	5162.2	5643.3	5022.0	6443.1	5136.6	4743.6
5650.7	3197.0	3454.4	3186.8	2491.0	2889.0	3227.6	2808.0	3351.5	2087.1	2378.2
57.9	617.0	564.8	717.0	265.7	366.5	248.4	265.5	206.9	71.1	136.2
152.2	1556.0	1796.0	2047.7	2175.3	1557.6	3241.9	1558.8	677.1	393.0	1203.8
1051.9	1528.1	1678.8	2089.8	2321.9	1724.2	2097.5	1485.8	863.3	431.3	1161.5
56.6	2036.7	1654.9	2379.6	1487.0	1447.8	1992.5	1748.1	894.9	570.7	1274.8
72.9	1279.5	2086.4	2859.8	1045.8	1347.3	2248.3	2097.2	369.7	298.7	1536.7
157.6	2540.1	2612.4	1728.9	1518.5	2854.8	3298.1	1934.9	1618.0	2559.0	1694.5
52.4	1846.4	2126.1	3123.6	552.5	1662.3	1879.0	1853.1	630.6	396.9	1038.7
1405.2	4386.2	5978.6	6705.8	2321.8	4333.6	4639.3	4592.7	1459.9	601.0	2921.4
1973.3	3116.0	4134.0	4467.8	2084.5	3569.1	3277.2	2977.6	4110.7	2325.2	2612.0
261.3	4142.1	4607.8	5258.9	4258.6	3885.0	4900.4	3700.9	1356.6	831.2	2347.8
123.0	1951.7	2595.7	3270.5	2631.7	2429.9	2501.2	4438.7	2383.5	953.1	1926.7
1914.2	4168.1	4565.4	6050.8	1532.0	3072.1	3198.6	3428.0	1292.6	390.3	1938.0
1366.2	3687.2	3513.0	3897.4	4491.8	3581.5	4772.2	3333.8	1934.1	1079.2	2297.7
49.6	343.6	720.6	1006.0	119.0	98.8	104.8	192.2	67.8	47.4	90.0
1000.0	2341.8	2655.6	2926.6	2400.6	2112.7	2702.7	2238.6	1526.3	1038.3	1785.6
1210.4	1936.8	1686.8	2259.2	1436.1	1558.7	1380.0	1929.3	1048.8	580.6	1247.6
2023.7	3043.7	3758.9	4680.5	2336.8	3168.6	3372.9	2952.5	2413.3	2247.2	3173.0
622.7	7025.2	6004.4	6708.4	6835.6	6669.0	7593.4	6170.0	8601.2	6638.8	5716.8
142.4	3825.1	4716.5	5997.2	3140.7	3820.4	4895.1	4480.4	1707.2	1367.4	5020.6
75.2	1101.3	1619.5	1433.6	911.3	1173.4	1498.7	1421.1	954.3	656.8	854.1
2750.2	4330.3	4627.3	5301.8	1283.4	4202.4	3722.2	5123.7	1576.2	706.5	3029.6
35.7	79.5	146.2	201.4	103.4	64.8	158.7	168.2	28.6	21.2	46.4
2810.7	3746.2	3672.0	4141.5	4258.9	3327.6	4876.3	3246.1	2557.6	1052.4	2514.8
1278.8	1826.3	2541.2	2824.7	1417.2	1768.0	2502.5	2001.4	1788.5	1166.8	1322.3
133.4	2053.2	2568.6	2986.2	593.4	1577.8	1555.7	1892.1	629.8	243.8	1131.7
109.5	3707.1	4730.8	5751.8	1816.5	4473.0	3994.7	4143.7	1075.8	465.7	2353.9
32.9	61.2	110.4	145.4	49.2	49.1	63.3	59.0	23.6	30.1	41.6
1386.2	4165.4	5050.6	5104.2	3334.9	4231.7	5251.7	3782.0	4141.0	2069.4	4076.6
92.1	3381.0	3809.8	4801.0	1144.7	3185.1	3525.4	5032.2	1037.2	305.3	4710.4
43.6	248.5	234.4	270.6	188.1	159.1	187.6	152.3	208.9	99.4	99.9
111.0	3331.4	4574.1	5698.3	996.1	3226.8	3642.0	3282.7	745.8	292.2	2099.6
1757.5	5330.4	4644.9	6058.7	7771.4	4866.5	7126.4	4434.0	2498.3	1548.9	3402.7

3452.9	2207.3	1949.0
6077.8	3412.2	2548.3
4698.9	3244.1	2981.8
2792.6	2651.5	2095.6
1613.3	1363.6	1266.8
7069.8	4820.0	6102.8
6353.4	3301.8	1303.2
6952.9	5066.6	5213.0
3803.7	3340.8	2186.7
443.7	496.1	109.0
1810.9	1599.2	1778.5
1478.6	1750.7	1540.7
2082.4	1665.4	1661.1
1971.4	1289.5	1644.9
3029.7	2372.3	2114.7
2803.0	1931.0	2930.4
7539.0	4563.7	2232.0
3891.6	3780.5	2297.2
4766.0	3466.7	3169.4
3127.3	2826.5	2111.4
6352.9	3892.1	1749.1
3263.7	3233.0	3443.5
198.6	363.2	101.7
2946.6	2372.8	2086.6
1831.1	1832.9	857.6
4483.2	2970.3	2164.3
5876.0	6206.6	7429.5
5543.6	4091.2	5549.2
1836.8	1828.2	833.8
7103.8	4082.7	1657.8
123.2	152.5	164.0
3558.3	3772.9	4012.2
3030.3	2520.2	1283.4
3088.4	1782.7	558.2
6408.4	3489.1	2003.2
77.8	162.8	43.1
4815.7	4163.4	3388.9
4552.7	3136.6	5664.6
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6177.9	2892.1	2008.9
4452.8	4572.4	5296.7

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FJ682684.1 gg_id:512004 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6826
EU382007.1 gg_id:270749 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU382
EU462051.1 gg_id:291409 black-handed spider monkey feces clone SPIM_aaj34a03 EU462
EU462357.1 gg_id:287476 chimpanzee feces clone CHIMP1_aaj40h06 EU462
FJ684936.1 gg_id:523487 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
EU794130.1 gg_id:343453 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_B15 EU794
FJ685499.1 gg_id:525684 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
GU303863.1 gg_id:576321 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ678990.1 gg_id:531015 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6789
FJ558006.1 gg_id:524930 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5580
EF510785.1 gg_id:221716 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5107
AY244942.1 gg_id:82965 cow rumen clone BE28 AY244
DQ113761.1 gg_id:130336 dog ileum clone I8-18 DQ113
AY323522.1 gg_id:89232 Prevotella oralis str. ATCC 33269 AY323
FJ880100.1 gg_id:432904 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
AJ011683.1 gg_id:2200 Prevotella albensis str. M384 AJ0116
DQ795952.1 gg_id:196360 human fecal clone RL202_aai49d04 DQ795
FJ676816.1 gg_id:523904 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6768
EU776890.1 gg_id:327728 Mongoose lemur feces clone ML_aaj26a07 EU776
FJ682269.1 gg_id:518097 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6822
EU461706.1 gg_id:294811 mongoose lemur feces clone ML_aaj27e01 EU461
EU531921.1 gg_id:270686 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
AF385509.1 gg_id:70671 tongue dorsa clone DO014 AF385
FJ684180.1 gg_id:531562 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
FJ685141.1 gg_id:514801 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EF510841.1 gg_id:224824 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5108
FJ364461.1 gg_id:368482 feces adult twins and mothers; TS15 clone TS15_a03c04 FJ3644
EU461648.1 gg_id:298929 mongoose lemur feces clone ML_aaj26c05 EU461
GQ491758.1 gg_id:590857 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EF510440.1 gg_id:218082 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
FJ681717.1 gg_id:511017 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
GQ491904.1 gg_id:567987 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ674037.1 gg_id:530649 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6740
EU344275.1 gg_id:260187 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ677005.1 gg_id:523019 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6770
EU475262.1 gg_id:299882 bonobo feces clone BNO_aaa03c06 EU475
FJ557663.1 gg_id:525105 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5576
FJ680794.1 gg_id:517921 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
FJ673656.1 gg_id:513815 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
GQ010629.1 gg_id:499036 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ010
FJ028784.1 gg_id:510871 Microbial Taiwan water buffalo rumen fluid clone TWBRB69 FJ0287

17364.4	7296.2	6590.1	7015.5	7017.9	6552.8	7916.0	6653.0	10288.5	10667.4	10331.4
41.9	367.9	504.3	732.0	160.8	68.3	119.8	269.7	96.4	38.5	59.0
397.0	4236.2	5076.0	5829.1	3718.7	4077.6	4210.2	3526.4	2364.6	1781.8	2889.1
1125.1	1796.7	1983.3	2142.9	2042.7	1868.3	2332.0	1622.7	899.6	444.9	1456.4
600.6	6054.0	6666.6	7992.1	8422.7	6293.1	8984.6	5274.9	2518.2	1669.3	3995.3
59.8	768.6	738.9	914.2	410.3	447.3	431.4	792.0	480.7	213.9	402.7
92.0	761.9	1233.9	1525.2	1164.8	1254.3	1581.6	1847.9	378.8	320.7	812.6
57.0	886.5	860.7	612.7	160.4	674.2	458.9	527.3	200.3	139.7	212.5
69.0	4656.1	6077.6	8190.9	1377.6	4408.6	4715.8	4955.5	802.5	355.4	3025.7
2907.1	2971.9	3235.3	4599.5	1929.7	3496.8	3716.1	3701.8	2644.8	2056.5	2181.9
3512.8	4197.1	4715.7	7095.2	3934.9	5581.7	5214.9	5027.0	4190.7	2955.0	4323.6
44.6	73.7	76.4	99.1	24.1	22.3	25.2	29.3	24.3	15.3	26.3
791.9	2347.8	2520.1	3064.0	2788.1	2342.4	3063.9	2745.1	2043.6	433.3	2530.2
37.9	39.6	43.1	62.0	30.9	25.9	33.1	39.9	19.7	18.9	26.3
534.1	3888.0	3571.2	4417.7	5271.2	3652.3	5520.7	3536.8	2250.9	1409.0	3141.1
24.9	39.5	63.8	57.2	27.2	39.2	43.2	45.2	18.0	17.5	27.6
329.7	2079.4	1994.9	2821.0	3113.8	2001.0	2520.3	1872.4	1308.1	930.5	2086.0
86.9	4532.4	5785.4	7330.7	1359.4	4149.7	4316.2	4771.7	840.7	371.5	2906.5
390.2	2191.5	1449.0	1948.2	1826.2	1792.4	2043.2	1661.9	1968.9	991.5	2001.0
4734.6	3090.9	3151.7	3128.4	2803.5	2848.2	3090.0	3013.3	2956.0	1489.1	2191.0
3533.8	3287.3	3933.6	4406.7	2542.2	3190.9	3805.8	2963.4	2427.2	1364.6	2514.9
2599.6	6612.9	6962.4	8322.1	8865.9	6668.5	9435.8	5998.5	3066.9	1547.2	4194.6
44.3	30.5	29.5	31.2	20.6	21.3	29.9	30.8	27.6	23.6	26.5
160.7	1036.2	1529.4	1728.8	442.2	980.3	822.3	1197.6	581.4	212.8	663.1
54.6	376.9	617.6	627.0	115.1	351.9	297.1	356.9	80.0	26.2	172.5
5193.3	4461.0	4088.1	6423.0	5200.6	6853.4	6978.1	6421.5	4061.8	2420.3	4401.1
128.0	4498.2	5891.5	7238.0	2051.5	4975.5	4697.2	4679.8	1239.0	633.9	2798.3
975.4	2947.4	3885.7	4455.6	1050.1	2811.6	3543.6	2852.0	729.4	345.6	1811.1
58.1	2507.9	3151.7	4112.0	799.0	2681.5	2691.9	2825.3	520.2	321.8	1405.2
3749.0	3096.0	3350.5	4461.6	3451.7	4178.0	4680.4	3793.5	3989.4	1882.2	3075.0
715.2	6309.3	7614.1	9275.6	2616.0	5782.5	6699.3	5973.7	1611.7	1047.4	4235.6
58.8	3268.1	3791.0	4591.2	1400.9	3207.7	3652.8	3501.4	1365.1	818.8	2095.4
456.0	4304.5	5013.6	6936.9	1677.5	3854.9	4147.4	4424.4	1329.5	558.7	2847.3
170.6	2118.0	3169.0	3804.3	803.2	1657.9	1284.1	2137.6	351.1	643.7	787.8
919.9	5391.8	5608.9	6818.4	4554.0	6094.7	5789.1	5984.0	6523.5	4915.2	6092.5
158.5	2517.3	3406.2	4686.4	943.6	2580.6	2444.4	2467.4	1862.6	1074.1	1596.5
497.4	1945.6	2255.9	2906.6	2780.1	2077.2	3345.4	2559.2	1574.5	1195.2	2132.1
2702.6	6935.9	6114.9	6910.8	6817.7	5894.0	7468.8	5692.3	8791.1	6207.3	7401.7
5684.9	4706.5	5149.7	5432.3	3405.5	4112.1	4711.3	4048.9	3818.8	2340.1	3351.1
995.3	3054.1	3865.2	3934.0	2855.4	3130.1	3153.0	2906.9	3993.2	2568.9	3578.0
95.2	1455.1	1897.7	2253.5	852.7	1246.4	1334.5	1381.3	581.2	532.2	1484.1

6393.2	7142.7	6771.5
904.6	227.7	157.7
4918.9	3631.4	4857.2
1866.6	2134.2	1545.5
6627.6	5063.4	7024.1
776.0	954.7	1132.9
2618.3	1576.9	950.6
906.4	607.5	177.0
8769.8	4124.5	2198.3
4695.2	4325.7	2184.3
7558.2	5196.9	4601.8
84.7	74.8	24.9
2823.3	3364.7	1475.8
29.4	62.6	66.6
3646.7	3804.9	5425.4
88.8	80.8	22.6
1782.8	2267.1	2590.8
8212.2	4131.9	2347.8
1465.0	2553.1	1976.7
2775.6	3488.0	2662.2
3806.9	3054.8	1798.2
7300.8	5752.2	6518.6
26.4	38.8	23.7
1540.6	1233.6	393.0
791.4	626.0	135.3
6380.1	5519.3	5884.6
8007.6	4081.3	2978.1
4363.6	2543.6	1247.6
4855.7	2429.0	1612.0
4223.6	3583.5	3653.2
10359.5	5368.6	4354.6
5227.3	3319.0	2166.9
6869.7	3981.8	2925.4
3851.3	2184.8	2047.2
5551.6	7423.9	5646.4
4404.5	2486.2	1504.1
2565.5	2068.3	2043.2
5971.7	6827.6	4519.0
5991.5	4423.2	2779.8
2730.3	4196.3	3007.9
2173.1	1898.0	967.8

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FJ677433.1 gg_id:519738 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6774
EU778264.1 gg_id:304166 feces clone RL388_aao96b11 EU778
FJ678298.1 gg_id:526911 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
FJ683687.1 gg_id:517784 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6836
GQ491551.1 gg_id:570360 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ797060.1 gg_id:176028 human fecal clone RL386_aao86d10 DQ797
GQ493297.1 gg_id:536652 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
GQ491577.1 gg_id:577157 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
EU473009.1 gg_id:300879 douc langur feces clone DL_1aaa03d07 EU473
EU778133.1 gg_id:337656 feces clone RL117_aae91e03 EU778
FJ684992.1 gg_id:519598 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
AY982422.1 gg_id:118345 human sigmoid colon mucosal biopsy clone ML25 AY9824
FJ673340.1 gg_id:526514 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
EU475054.1 gg_id:295322 visayam warty pig feces clone VWP_aaa04a01 EU475
EU871406.1 gg_id:351650 Genetic Bovine (Bos taurus) Rumen Thailand clone CF367 EU8714
EU467067.1 gg_id:296772 mongoose lemur feces clone ML_aae87a02 EU467
AF001708.1 gg_id:2172 rumen clone RC17 AF0017
DQ794897.1 gg_id:197293 human fecal clone RL310_aam37f10 DQ794
FJ683479.1 gg_id:514486 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
AB009178.1 gg_id:2124 rumen clone RFN19 AB009
AY978052.1 gg_id:115991 human cecum mucosal biopsy clone LI04 AY978
GU303838.1 gg_id:534756 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
CU926909.1 gg_id:558189 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU926
FJ678284.1 gg_id:525581 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6782
GQ493375.1 gg_id:592705 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
EU468932.1 gg_id:290509 Speke's gazelle feces clone SP2_d12_1 EU468
FJ675854.1 gg_id:525223 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6758
FJ674162.1 gg_id:530021 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
DQ794878.1 gg_id:189711 human fecal clone RL310_aam37d12 DQ794
AB270080.1 gg_id:163689 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU843355.1 gg_id:336569 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU469846.1 gg_id:294896 western lowland gorilla feces clone GOR_aag72d07 EU469
EU467431.1 gg_id:295620 chimpanzee feces clone CHIMP12_g01 EU467
FJ577255.2 gg_id:588912 Prevotella sp. oral taxon 317 str. F0108 FJ5772
FJ365600.1 gg_id:364196 feces adult twins and mothers; TS20 clone TS20_a04g08 FJ3656
FJ684735.1 gg_id:517701 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6847
DQ795814.1 gg_id:185522 human fecal clone RL245_aai82g09 DQ795
EU850541.1 gg_id:326121 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF335 EU850
FJ673386.1 gg_id:510064 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ681684.1 gg_id:526867 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6816

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142.3	4601.8	6153.6	6973.9	1290.2	4378.2	4807.5	4418.2	1057.8	447.1	3046.1
1977.8	3887.6	5032.3	5044.9	1541.1	3731.5	3928.6	4289.0	1210.7	1283.6	2607.3
1220.7	7559.5	7739.9	9492.8	5893.8	9161.9	6333.9	6827.6	6347.8	5046.5	6194.6
1428.3	3605.5	4998.6	5662.0	1624.4	3629.6	3590.2	3765.5	931.2	402.8	2150.9
106.5	3360.1	4101.9	4947.4	1768.0	3006.1	3456.9	3451.7	1418.8	878.8	2017.8
71.6	381.5	362.3	399.3	548.0	449.4	993.1	342.9	221.6	47.1	149.4
75.7	3036.1	3875.7	4828.6	875.3	2990.9	3059.8	3174.8	889.1	390.5	1783.6
51.0	2712.5	3923.2	4803.0	768.0	3019.8	2689.4	3068.0	396.1	217.6	1475.0
382.3	4159.2	5215.9	6605.7	2239.5	3092.8	4071.2	3640.4	1730.9	1042.4	2522.6
956.7	6563.8	8187.6	6604.3	5689.1	6071.8	7527.8	5978.3	8901.6	7145.8	5056.7
804.8	4384.7	5238.6	6651.0	2399.3	4007.1	4685.8	4251.8	1488.1	910.2	3095.7
537.4	3119.1	3105.1	3357.5	3148.9	2794.0	4226.2	2473.6	2331.4	1879.8	2915.4
4908.9	2025.2	2273.8	2401.5	1838.4	1919.8	2235.8	2275.8	2373.3	1846.5	2388.9
63.8	129.0	172.3	126.2	113.6	89.0	187.8	121.7	75.6	56.3	81.4
57.6	1741.5	2042.1	2190.0	1024.4	727.5	1059.6	1133.0	441.8	444.5	658.5
53.1	2291.4	2201.6	3412.3	1214.6	1642.0	1656.7	1790.9	735.4	585.7	1317.7
60.3	133.3	134.1	118.3	46.0	104.7	65.8	60.2	59.7	31.1	62.3
44.3	2782.1	3795.6	4699.8	1508.0	2990.8	3406.1	2812.0	770.8	538.5	1697.5
68.8	1692.7	2173.7	2490.3	605.0	1651.2	1549.8	1764.2	339.9	91.0	851.7
180.7	1753.7	2496.2	3296.2	1107.6	1553.1	1524.3	1847.6	1108.7	1048.1	1301.3
3692.9	9329.0	8268.4	9215.5	8480.6	8297.7	9763.3	8439.2	11818.5	8527.7	8051.0
126.4	1086.2	1499.7	1664.7	1013.8	1409.4	1105.7	1585.6	827.2	695.8	778.4
639.9	5929.0	5866.9	6956.5	5380.1	5456.3	6603.6	5277.6	2005.6	1980.9	4358.6
2879.4	3213.5	3271.0	4088.9	1531.8	2795.3	3714.7	3690.0	1407.6	804.2	2232.0
573.7	4808.1	6454.8	7741.4	2189.4	4681.5	4948.2	4985.3	1255.0	740.5	3270.5
78.2	2620.9	3384.1	4622.1	568.6	1418.0	1218.6	2051.0	713.1	324.3	770.2
8157.4	5776.8	6728.7	7293.6	5280.7	5626.2	6799.3	5773.5	4503.3	3329.3	5621.6
208.6	3035.7	3484.3	4607.3	3044.5	3213.4	3159.0	2879.2	2704.9	1820.2	2664.2
697.0	3013.3	3573.0	4301.3	1728.3	3185.8	3290.3	3341.6	1108.7	929.1	1832.2
864.1	1253.2	1331.8	1697.2	1024.1	906.5	1274.9	1066.9	897.4	621.3	1233.5
30.9	150.4	431.1	350.5	67.8	170.5	208.6	427.9	29.5	143.4	111.9
40.2	239.7	275.3	236.5	222.7	170.4	139.1	275.6	195.4	105.2	104.9
52.9	1354.7	1420.6	1097.2	937.1	1515.2	1672.5	1148.1	597.5	325.0	855.8
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76.4	1545.9	2302.8	2490.7	322.8	1363.3	1432.7	1244.6	436.7	205.8	1167.0
2451.9	3638.9	4610.5	4424.2	4824.6	3147.5	7625.2	3059.4	1936.0	1187.0	3253.4
42.8	20.9	22.0	33.0	22.6	22.2	22.9	23.3	24.0	21.0	19.1
137.5	3406.6	3819.9	4708.6	1337.3	2721.9	2891.2	3163.1	766.9	489.3	2067.1
106.5	1794.7	2383.3	2688.0	487.6	1614.8	1532.7	1773.6	390.9	224.2	1013.7

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8472.3	6465.2	5730.8
6418.4	3667.5	1551.0
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5320.9	3038.0	2228.0
5793.1	2473.5	1434.3
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6309.3	6428.9	5523.2
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2279.1	2737.8	1681.2
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2169.8	1325.3	1377.5
2601.6	1732.6	1433.3
79.1	74.9	56.1
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3436.7	1464.0	650.0
3824.7	1828.5	2641.9
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2403.9	1459.3	1804.7
7878.7	4801.9	4400.4
4312.2	3728.3	4038.8
8916.5	4880.6	3481.7
4733.7	2219.3	1395.4
6948.3	5953.9	4398.9
3603.9	3282.0	2415.5
5026.7	2816.7	3359.4
1178.0	1281.2	912.4
391.0	270.2	89.6
288.0	365.5	149.8
1802.7	1468.7	1272.3
4372.6	4056.4	3503.0
1180.9	2498.1	1310.7
2390.4	1311.5	1016.0
3214.6	3999.3	4056.8
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5434.5	2613.5	1250.0
2871.4	1642.3	754.8

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GQ491516.1 gg_id:582363 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
DQ797245.1 gg_id:197149 human fecal clone RL386_aao88h03 DQ797
EU344463.1 gg_id:266559 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU461321.1 gg_id:302729 red kangaroo feces clone KO2_aai17a11 EU461
FJ683039.1 gg_id:523539 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6830
FJ680423.1 gg_id:529428 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
DQ801086.1 gg_id:192723 human fecal clone RL387_aao91h11 DQ801
EU461617.1 gg_id:288217 mongoose lemur feces clone ML_aaj25f05 EU461
EU473029.1 gg_id:288876 douc langur feces clone DL_1aaa02c09 EU473
FJ681266.1 gg_id:519342 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812
FJ684520.1 gg_id:521258 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
EU773471.1 gg_id:318181 Bonobo feces clone BNO_aaa02b05 EU773
EU381791.1 gg_id:262164 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
GQ054111.1 gg_id:429229 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1098g GQ054
AB185521.1 gg_id:103448 rumen clone F23-B08 AB185
FJ365568.1 gg_id:360196 feces adult twins and mothers; TS20 clone TS20_a04d07 FJ3655
EU461697.1 gg_id:300106 mongoose lemur feces clone ML_aaj27c11 EU461
FJ681358.1 gg_id:517926 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
DQ796007.1 gg_id:193455 human fecal clone RL202_aai50b11 DQ796
FJ792538.1 gg_id:535359 Prevotella melaninogenica str. ATCC 43982 FJ7925
FJ676936.1 gg_id:519070 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
AY916271.1 gg_id:113370 human rectum biopsy clone N064 AY916
EU381908.1 gg_id:276131 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
FJ557682.1 gg_id:529630 Survey Approach Assess Endotracheal Tube Biofilms and their Origins biofilm extubat FJ5576
EU773685.1 gg_id:312051 Capybara feces clone CAP_aah97b02 EU773
FJ365308.1 gg_id:361498 feces adult twins and mothers; TS20 clone TS20_a01d03 FJ3653
EU469497.1 gg_id:295421 black lemur feces clone BKLE_h09_2 EU469
AB009235.1 gg_id:2080 rumen clone RFN89 bacterium AB009
GU302844.1 gg_id:575618 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU794188.1 gg_id:321621 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_D02 EU794
EU462042.1 gg_id:301550 black-handed spider monkey feces clone SPIM_aaj33g10 EU462
FJ364538.1 gg_id:361284 feces adult twins and mothers; TS15 clone TS15_a04b06 FJ3645
DQ795899.1 gg_id:191319 human fecal clone RL245_aai84c09 DQ795
EU776846.1 gg_id:343094 Mongoose lemur feces clone ML_aaj26g04 EU776
FJ679787.1 gg_id:515802 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6797
AY982452.1 gg_id:117045 human sigmoid colon mucosal biopsy clone ML81 AY982
EU461621.1 gg_id:295934 mongoose lemur feces clone ML_aaj25f12 EU461
EU773517.1 gg_id:354322 Bonobo feces clone BNO_aaa02g04 EU773
EU778818.1 gg_id:336258 Black-handed Spider Monkey feces clone SPIM_aaj33e11 EU778
EU472955.1 gg_id:295175 douc langur feces clone DL_1aaa03d10 EU472

158.1	2576.7	3042.1	3769.8	2202.6	2726.6	3729.3	2412.8	600.4	446.3	1900.7
480.3	4112.6	5140.4	5934.1	2201.6	3928.5	4320.0	4126.3	1024.3	675.6	2668.3
144.2	3695.5	3750.4	4536.9	2215.5	3094.5	2632.9	3519.7	1465.1	1964.0	2033.5
4543.4	4941.6	5244.9	6364.8	5003.1	4626.0	5933.0	5827.5	3885.5	2091.8	5171.5
69.1	2381.1	3196.8	4201.9	1075.0	2464.7	1984.6	2814.4	1784.0	1042.3	1145.2
1690.1	3791.9	4301.9	4866.4	3305.4	3764.2	4550.6	4467.3	2089.5	1781.4	2972.0
2010.8	3927.6	3527.0	4380.0	3713.4	3480.7	4303.9	3216.5	2663.0	1288.4	3238.7
38.8	484.6	768.5	962.9	21.7	459.9	557.9	661.7	43.9	46.8	258.9
937.2	5122.2	5077.7	6116.1	3083.3	4232.3	5716.6	4996.7	2010.4	1337.2	3607.2
88.5	1238.0	1629.2	1961.6	296.5	648.5	654.4	954.8	263.1	106.2	384.0
1313.3	5353.5	6917.5	8544.6	4446.2	6083.6	6069.9	4954.4	3295.5	2340.3	4154.8
79.4	2135.6	2713.5	3312.6	682.7	2063.7	2136.3	2269.3	668.4	332.7	1265.9
1605.9	3209.5	3560.4	4517.2	4777.2	3488.6	4005.3	3136.2	1778.9	1701.9	2396.2
137.1	1585.4	1868.9	1796.0	771.1	1016.6	1250.9	1356.9	1286.8	1187.3	1065.1
57.7	51.9	57.7	47.2	49.9	44.2	43.8	48.6	33.5	32.0	35.7
59.8	99.8	119.1	181.7	85.8	47.3	74.1	73.0	39.0	67.0	67.8
79.0	4098.4	5076.8	6066.4	1447.4	3895.4	4339.5	4182.3	1418.5	658.1	2357.8
143.2	4163.1	4724.9	6371.4	1908.9	4124.1	4156.4	4400.1	1421.0	1144.2	2847.1
176.3	2945.3	2726.5	3524.7	2545.1	2610.2	2711.8	2592.5	2751.5	1192.7	2694.8
1291.7	2829.2	2663.8	3084.6	2559.5	2506.5	2716.5	2794.3	1351.0	804.4	1969.3
3117.2	3203.4	3242.8	4400.5	1721.8	3302.4	2923.4	2988.9	1155.4	535.8	1844.8
2865.1	3619.7	4330.3	5488.6	2898.8	3777.1	4257.4	3444.5	2392.6	2360.3	3378.6
181.5	2857.8	2544.3	3029.4	2146.0	1886.7	3319.5	2424.8	1249.8	407.6	2028.9
55.6	155.5	275.6	391.6	131.6	114.4	136.2	295.1	161.0	36.5	96.3
87.6	353.8	496.3	719.2	117.3	487.4	362.9	589.2	102.5	53.4	131.3
468.9	1500.6	1537.9	1727.7	1134.8	1245.8	1419.5	1545.9	1290.1	700.2	1090.1
67.5	685.6	532.1	539.2	271.8	279.7	357.4	650.4	356.2	300.9	373.3
79.8	2408.9	1815.2	2271.6	1292.3	1729.3	2333.0	1855.6	1205.2	761.6	1307.5
38.9	39.8	49.8	55.1	29.2	20.1	28.3	24.5	26.4	16.1	22.8
89.8	2137.7	3553.0	2785.4	3030.6	1819.0	4043.1	2449.3	1189.7	746.9	3237.6
197.3	2497.5	2750.7	2939.8	1287.0	2022.8	1822.4	2320.7	2537.9	1922.7	1787.1
1352.2	3751.7	4092.9	4862.2	5009.5	3544.5	5534.9	3260.9	1744.6	973.9	2608.5
3482.5	4518.8	5290.8	6323.6	2966.6	4312.5	4383.2	4587.6	4098.7	2860.9	3451.7
6214.4	7542.0	8316.3	9121.9	6699.8	7532.5	9105.0	7610.5	7751.6	5855.5	8318.5
462.8	3908.2	3925.3	5411.0	5038.1	3364.3	4496.2	3354.8	2361.7	1446.0	2847.9
41.8	20.1	18.9	22.2	22.5	17.3	21.4	13.4	14.5	18.6	24.2
231.1	3909.8	5356.3	5954.7	2668.2	3315.1	4704.8	4063.4	1243.8	826.9	2143.4
169.1	2613.5	4649.9	4693.3	2661.9	2982.2	4384.7	2367.7	527.0	497.3	1457.3
164.5	1963.9	2168.9	2514.3	2475.1	2090.4	3173.2	2547.0	769.3	344.3	1416.2
48.1	2232.1	3272.1	4118.9	1595.4	2509.7	2235.1	2174.6	703.1	497.9	1382.9
88.7	1547.3	2002.6	2458.2	1089.2	1439.2	1946.4	2320.6	797.4	783.7	1431.0

3052.9	1885.1	2181.2
7007.7	3948.8	2310.3
4589.4	3600.4	8391.5
5551.7	6041.8	5828.3
3519.7	2337.6	1539.6
5354.5	4185.0	5050.3
4402.0	4006.6	4086.8
891.4	439.3	168.9
5789.8	4181.8	2675.7
2166.9	1401.7	328.1
7696.3	4937.7	5864.7
3508.3	2278.8	1956.9
3856.7	3231.7	4421.4
1025.8	1482.4	1366.5
52.1	53.7	40.3
72.6	187.2	78.0
6531.1	3975.2	2334.1
6867.5	5196.6	3714.1
2427.4	2890.3	2022.6
2813.4	2733.4	1849.1
5321.2	3760.5	3034.1
5144.6	3387.3	3146.8
2427.6	2380.9	3454.4
311.3	241.4	188.7
932.3	658.2	158.1
1635.4	1955.2	3228.7
382.9	730.8	47.2
2278.5	1814.8	1537.1
67.2	38.8	35.9
2365.9	2305.2	4383.1
2944.1	2185.3	2831.2
3727.1	3313.3	3778.9
6301.0	5427.4	4779.9
9320.4	8738.9	7292.7
4539.8	3369.3	3042.8
16.9	16.2	16.4
5810.6	3630.3	5125.4
4404.6	2167.1	1745.2
2167.9	2262.7	1751.6
3445.9	2342.5	3742.9
2692.5	1639.3	2119.5

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FJ681780.1 gg_id:511401 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
AY323524.1 gg_id:88701 Prevotella denticola str. ATCC 35308 AY3235
EU469385.1 gg_id:295406 black lemur feces clone BKLE_g01 EU4693
FJ673578.1 gg_id:527874 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6735
GQ402133.1 gg_id:562683 alpacas and sheep forestomach clone ALP25 GQ402
EU531893.1 gg_id:274980 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5318
EU850503.1 gg_id:311462 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF273 EU8505
FJ684973.1 gg_id:520181 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6849
FJ680670.1 gg_id:509720 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
FJ363100.1 gg_id:370036 feces adult twins and mothers; TS148 clone TS148_a03a10 FJ3631
AY992930.1 gg_id:135660 mouse cecum clone C22_j09 AY9929
FJ684658.1 gg_id:517908 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6846
AF371884.1 gg_id:42406 swine intestine clone p-185-o5 AF3718
FJ028751.1 gg_id:552400 Microbial Taiwan water buffalo rumen fluid clone TWBRB27 FJ0287
AY984123.1 gg_id:122625 human descending colon mucosal biopsy clone MF93 AY9841
GQ493958.1 gg_id:568261 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ673365.1 gg_id:510239 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ676140.1 gg_id:520810 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6761
FJ680416.1 gg_id:509703 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6804
FJ682033.1 gg_id:518528 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6820
EU842487.1 gg_id:351813 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8424
EU842548.1 gg_id:326333 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU8425
FJ681995.1 gg_id:522422 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6819
FJ679583.1 gg_id:528902 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6795
FJ676423.1 gg_id:523360 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6764
FJ681009.1 gg_id:525734 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6810
EF510457.1 gg_id:226400 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
FJ675976.1 gg_id:509430 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6759
EU461709.1 gg_id:292318 mongoose lemur feces clone ML_aaj27e04 EU4617
FJ685142.1 gg_id:514269 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6851
EU469532.1 gg_id:298360 black lemur feces clone BKLE_f09_3 EU4695
GQ493814.1 gg_id:592612 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
DQ278861.1 gg_id:154641 Prevotella sp. 152R-1a DQ278
FJ678573.1 gg_id:526174 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6785
AY983829.1 gg_id:119916 human descending colon mucosal biopsy clone M919 AY9838
GQ038538.1 gg_id:412937 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
FJ684244.1 gg_id:513431 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU531891.1 gg_id:276145 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU5318
FJ673624.1 gg_id:513335 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6736
DQ796978.1 gg_id:195574 human fecal clone RL386_aao85c07 DQ796
EU773521.1 gg_id:340253 Bonobo feces clone BNO_aaa02c12 EU7735

103.8	3769.6	4205.4	5477.5	1092.3	3452.3	3642.9	4668.6	1295.0	601.3	4418.9
47.8	20.4	20.1	19.4	24.2	18.8	18.6	17.1	18.7	14.2	23.8
7633.1	5823.3	5487.7	5573.2	4022.4	5631.2	7503.0	5476.5	7329.4	6745.6	8053.0
1011.8	5165.3	6046.3	7064.7	2875.5	4680.3	5217.3	4600.6	2202.2	1866.1	3541.1
43.4	626.9	927.1	1007.1	380.5	470.3	425.2	682.4	172.1	88.7	240.6
46.3	1236.3	1340.0	1358.3	936.0	935.3	986.2	1173.7	569.9	473.2	825.5
79.6	1026.7	1125.5	1554.5	169.0	877.2	765.2	1148.6	200.0	141.8	555.2
1559.0	6500.8	6806.4	8061.8	3602.8	6107.9	7914.8	5314.9	6788.3	6274.3	7838.0
2258.8	3318.1	3478.6	4911.8	3052.3	3308.6	3864.7	3317.0	2785.1	2274.6	2989.7
102.8	1119.4	1535.2	1916.1	592.1	1336.7	1155.3	1397.5	916.3	636.6	571.2
46.9	128.7	358.8	311.2	80.8	166.2	183.4	246.4	165.4	34.4	104.7
70.3	3048.5	4347.8	4881.8	1319.0	2772.9	2988.3	3637.9	419.6	268.5	1675.4
68.2	110.2	85.3	88.7	61.3	62.8	65.9	54.3	45.6	39.9	45.1
63.7	236.2	333.5	477.6	85.4	68.1	115.1	213.5	71.4	42.8	95.6
379.7	5922.5	5523.6	5737.0	6049.6	5249.2	6027.1	5144.4	5879.9	3705.9	4562.0
912.8	2495.0	3056.9	3891.3	1637.2	2320.5	2584.3	2341.6	1088.5	748.3	1669.9
643.5	1758.8	2245.4	2595.5	1628.6	1380.7	1879.9	1593.1	1247.8	893.6	1274.8
1233.2	5526.5	5228.3	6894.2	8461.6	5260.3	7692.3	4449.6	2849.2	2182.9	3984.5
1477.6	1076.9	1351.6	1460.3	821.8	944.3	1134.1	1324.8	1005.1	627.7	875.8
432.1	6201.1	6264.4	7160.1	6129.5	5694.9	6651.2	5943.8	7207.2	8212.3	9642.0
54.8	147.0	285.7	296.8	71.9	68.1	137.7	88.0	43.5	30.7	39.9
38.8	941.4	1108.5	1106.6	485.8	589.4	718.7	551.5	333.9	156.1	288.7
2945.9	1145.1	1184.8	1238.7	1343.9	1160.3	1026.0	1268.6	1471.8	975.9	1364.8
219.0	4162.8	5454.4	6938.5	4247.3	4225.2	6540.5	5315.4	3007.4	2092.5	3491.7
764.2	6314.5	7620.5	9993.3	2625.8	5786.7	6703.2	5978.8	1616.4	982.8	4239.9
120.3	1218.6	1157.8	1498.1	813.8	526.6	973.9	860.3	956.2	547.3	852.4
941.1	1841.4	2047.8	3051.0	1743.4	1997.2	2427.2	1968.3	810.8	745.8	1323.6
4402.1	2767.4	2985.5	4566.4	3733.6	3169.4	3769.4	3098.4	1222.1	581.0	1853.1
1120.0	1562.1	1729.3	1882.9	2143.8	1724.4	2263.7	1598.3	868.0	462.7	1164.5
71.1	4655.6	6543.9	8191.1	1377.3	4408.8	5077.6	4956.0	802.4	329.3	3025.3
3013.6	4340.8	4398.4	4192.7	3756.7	3576.8	4776.9	3288.7	3492.0	4367.7	4120.7
67.7	1614.3	1252.1	1568.9	697.3	1318.5	1357.5	1437.9	989.3	833.2	911.1
36.4	24.6	30.2	30.7	40.8	33.5	28.3	29.4	19.8	17.8	21.9
1938.2	3090.1	4005.7	4276.0	2893.7	4196.5	2898.8	4504.3	2335.9	2372.0	4380.0
552.1	5370.6	5161.8	6067.0	7247.4	4975.3	6578.5	4661.1	2524.1	1617.4	3308.6
100.9	2308.9	2671.1	3396.1	1501.8	2048.1	2757.6	2309.7	1593.3	1240.5	1938.5
403.3	5201.1	5770.6	7307.7	3524.7	4402.8	5839.1	5312.2	3887.3	2167.6	4572.0
479.2	3909.5	4486.1	5408.8	5039.8	3924.6	4493.2	3357.4	2366.4	2023.5	2848.7
77.3	2755.5	3502.8	4559.3	909.9	3160.2	3073.8	3197.6	544.3	378.0	1483.7
46.4	62.3	97.6	72.0	38.2	55.1	49.3	56.3	63.7	28.0	39.4
1206.8	1669.9	2100.5	2630.8	1353.9	1726.1	1979.7	1801.8	816.6	454.6	1078.3

5551.0	3556.2	5461.6
22.7	23.9	19.4
5163.2	6419.6	5626.2
8320.4	4407.3	2927.9
1494.2	952.6	1704.2
1039.3	1282.0	1119.8
1514.8	995.6	621.6
6997.8	5894.3	4800.6
3727.9	3580.8	3988.2
1954.7	1436.0	873.8
393.7	170.4	82.2
6378.1	3032.3	1359.5
86.6	71.9	45.5
414.7	298.2	342.5
4280.5	5667.8	5481.1
4219.5	2381.7	2163.1
3286.3	2160.6	1584.7
5513.8	4575.8	6400.3
1873.2	1918.5	1764.2
7007.0	5423.8	5355.7
126.6	175.6	128.8
532.4	878.1	260.2
1103.6	2269.2	62.9
6124.7	4839.8	5286.1
10366.3	5373.0	4357.9
1070.4	1335.7	816.8
3627.9	1976.2	2230.3
3845.9	3816.7	2251.3
1553.1	1898.9	1650.4
8769.5	4124.2	2197.1
3792.3	4638.8	5239.3
1520.0	1265.4	1258.1
27.3	46.2	53.8
3880.9	4406.0	4075.5
5053.0	4392.8	5093.6
2717.9	2222.8	2360.0
6881.9	5171.3	7411.5
4540.8	3371.5	3042.0
5352.3	2639.5	1724.2
68.4	93.7	43.2
2409.2	2074.8	1682.0

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EU774082.1 gg_id:333598 Chimpanzee feces clone CHIMP1_a07 EU774
FJ172825.1 gg_id:337278 Qinghai Yak Ruminal and Fungi China rumen clone RB-5E1 FJ1728
EU779070.1 gg_id:331015 Prevost's squirrel feces clone SQ_aah79c10 EU779
AB264070.1 gg_id:196997 Fecal microbial (dugong dugon) determined genes Dugong feces clone dgD-75 AB264
EU773564.1 gg_id:354491 Goeldi's Marmoset feces clone CAL_g07_1 EU773
EU778855.1 gg_id:305145 Black-handed Spider Monkey feces clone SPIM_a10 EU778
DQ797036.1 gg_id:188089 human fecal clone RL386_aao86b06 DQ797
FJ683399.1 gg_id:513249 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6833
EU774602.1 gg_id:328946 Douc langur feces clone DL_1aaa01f04 EU774
FJ683172.1 gg_id:514517 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6831
FJ685379.1 gg_id:515705 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6853
EF096662.1 gg_id:198204 mouse cecum clone SWPT11_aaa02g08 EF0966
FJ677113.1 gg_id:528726 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6771
AF371896.1 gg_id:45645 swine intestine clone p-1933-s962-3 AF371
EF436315.1 gg_id:213152 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC29 EF4363
GQ074351.1 gg_id:438260 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw161 GQ074
EU467104.1 gg_id:288753 mongoose lemur feces clone ML_aae88c11 EU467
FJ364571.1 gg_id:364967 feces adult twins and mothers; TS15 clone TS15_a04e06 FJ3645
AY244928.1 gg_id:86283 cow rumen clone BE11 AY244
GQ491858.1 gg_id:576234 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ491
FJ684133.1 gg_id:516225 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6841
EU381758.1 gg_id:267845 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU778194.1 gg_id:351168 feces clone RL117_aae92b12 EU778
FJ685436.1 gg_id:521152 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6854
GQ073116.1 gg_id:415792 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205c07c1 GQ073
FJ674116.1 gg_id:529679 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
FJ673357.1 gg_id:521841 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733
FJ676939.1 gg_id:520450 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
FJ676966.1 gg_id:519529 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6769
FJ679668.1 gg_id:530373 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6796
AF218619.1 gg_id:69910 Prevotella ruminicola str. TC2-28 AF218
FJ684336.1 gg_id:509425 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6843
EU531867.1 gg_id:269138 Predominant role host genetics controlling gut microbiota FMF remission stool clone EU531
FJ673775.1 gg_id:531273 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6737
EU774268.1 gg_id:335697 Chimpanzee feces clone CHIMP1_aaj40g11 EU774
FJ685256.1 gg_id:523620 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6852
AY244914.1 gg_id:82967 cow rumen clone BF36 AY244
EU473005.1 gg_id:296243 douc langur feces clone DL_1aaa02e07 EU473
FJ684814.1 gg_id:528993 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6848
FJ684515.1 gg_id:525810 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6845
FJ673375.1 gg_id:523090 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6733

45.6	559.9	582.2	695.1	29.4	538.4	738.6	554.7	218.2	181.5	314.5
102.1	508.5	662.4	718.1	222.8	601.5	360.9	539.9	135.7	127.5	251.9
148.0	3903.4	4469.5	4008.2	2279.9	3796.6	3946.2	4091.6	1779.4	689.4	3066.5
57.3	148.8	127.5	141.6	104.1	95.0	170.2	160.9	67.9	30.6	161.1
478.7	4323.3	5403.6	6232.6	4189.4	5026.9	5426.3	4166.4	2915.9	1021.8	4544.2
217.7	1715.2	1867.8	2314.4	3417.1	1743.4	3223.4	1381.6	605.0	497.6	1002.0
1351.1	5165.6	5721.9	7551.3	5960.1	4947.9	6623.7	4693.2	2219.0	1128.8	3458.1
992.0	5329.4	6893.4	7928.2	2872.3	5349.1	5562.2	5362.2	2211.5	1201.1	3767.5
105.1	2749.9	2861.6	3146.9	1067.4	1835.1	2251.0	2245.8	878.3	456.6	1788.7
47.1	2296.5	2411.0	2482.4	1519.8	2124.3	2202.9	2235.7	1973.6	2529.5	2249.9
109.6	3412.8	4592.9	5455.0	1144.6	3312.8	3780.4	3292.2	847.7	318.5	2349.9
53.0	223.7	250.9	292.0	171.2	198.9	189.2	178.9	76.7	56.8	132.1
71.6	1722.8	2415.2	2986.2	354.4	1571.5	1533.5	1321.5	438.0	227.3	1330.9
50.2	51.8	68.0	84.6	33.4	58.3	50.4	43.3	13.3	24.8	37.9
65.5	23.2	24.4	31.1	21.4	19.5	25.6	17.9	23.0	15.4	24.7
3765.6	2631.6	3013.1	2874.6	2501.1	2382.6	3045.2	3114.3	2250.0	1341.3	1949.0
1001.2	7119.8	6434.1	7258.6	6582.8	6917.0	8867.0	6365.5	8640.3	5471.6	7527.7
3854.9	2940.5	2792.2	3691.7	2349.0	2693.5	2843.5	3284.2	2596.2	2288.4	2278.3
34.7	31.1	34.6	36.5	29.5	22.8	23.0	36.2	16.8	13.0	22.4
92.4	1427.4	1887.6	2114.5	390.0	1298.1	1235.5	1326.5	220.9	153.0	757.0
110.7	1242.3	1534.5	2904.7	739.5	1183.7	1046.8	1664.5	624.3	232.0	1244.3
98.8	1762.4	2603.7	3501.8	435.1	1190.4	1128.4	1611.1	316.0	131.1	738.8
409.9	2953.5	3069.5	3783.5	3881.5	2982.6	4150.8	2881.0	1793.0	873.9	2064.7
69.6	4656.3	6076.8	8871.5	1482.7	4408.0	4715.6	4954.9	802.5	329.4	3024.4
35.7	1119.9	941.1	908.6	795.0	1193.7	186.0	1436.7	1716.7	679.9	915.2
1542.3	7075.7	8940.5	9031.1	8451.8	8733.4	8316.0	7801.6	4579.6	4492.2	7378.0
3971.2	5272.3	4958.5	5564.3	4521.3	5331.1	6273.2	4579.9	4451.0	2944.9	5034.5
704.8	2578.2	3345.1	4072.0	1681.2	2343.8	2828.7	2262.0	1121.1	820.2	2101.7
976.7	4985.4	6113.9	7397.0	2985.1	4796.7	5181.0	4692.0	2057.2	1209.2	3686.0
53.3	66.8	123.1	149.2	96.8	70.5	73.7	16.5	34.6	28.6	14.6
44.5	533.3	641.5	709.3	45.4	71.0	73.1	314.6	63.2	16.2	63.2
764.9	5526.2	6668.6	8123.3	2457.0	5064.7	5867.3	5232.2	1612.9	1049.3	3711.5
119.9	4777.2	5298.6	7440.9	4923.1	4269.5	5700.7	5664.2	2194.3	1662.2	3424.4
77.0	2031.1	2394.4	3209.7	547.3	1449.9	1191.6	1725.7	373.1	126.1	708.0
3743.9	4620.7	6481.8	7087.2	1597.6	4338.3	4538.3	4331.2	1346.5	457.5	2981.1
1873.8	4518.6	3804.1	4368.8	4256.1	3868.6	4313.3	4361.7	6948.8	4845.2	5066.1
49.6	135.5	170.5	168.4	30.7	57.6	58.7	79.6	30.4	29.0	48.6
1102.1	4436.9	4315.8	5306.3	5215.8	3748.0	5680.2	3894.1	2340.9	1529.6	3234.2
286.2	3291.1	4391.1	5288.3	3710.7	3494.7	4991.2	3529.1	2609.9	934.7	3827.8
1465.4	4008.0	5785.0	5686.1	3378.5	5031.7	4605.1	5210.0	2333.1	2039.6	5827.8
138.6	3609.8	3259.7	3848.5	2688.1	2843.7	2647.5	2810.1	3426.9	3229.8	1717.7

638.7	604.5	1044.5
777.3	466.8	380.3
6086.3	3703.4	3184.3
70.3	131.5	101.9
5696.8	4137.3	4035.0
1323.6	1372.0	2468.6
6502.0	4713.6	4291.8
8631.1	5139.2	4353.1
3318.6	2055.6	1560.4
3267.2	1785.7	1462.4
5762.5	2825.6	1512.9
135.8	231.5	406.3
2642.5	1375.0	1088.9
80.0	128.8	75.0
21.3	25.1	21.9
3337.9	4032.4	3231.9
6136.6	6570.8	8581.8
3317.8	3962.8	2112.9
24.9	32.7	110.7
2315.4	1143.2	456.0
1594.0	1472.1	1191.7
3047.8	1725.4	956.8
3074.2	2660.1	3282.4
8768.4	4125.0	2198.3
1059.0	1060.7	617.7
6245.9	7261.9	8544.8
4993.5	7022.3	6720.4
3875.7	2505.1	2206.7
8410.5	4309.8	2998.6
109.7	153.6	56.3
1204.3	280.8	81.3
9071.7	4701.3	4063.2
6710.6	4826.8	6580.4
3019.6	2075.9	578.8
7570.8	4493.0	2021.8
3781.5	4375.6	3997.6
195.7	173.2	42.6
4223.0	3942.9	3900.7
3543.1	3744.8	4208.9
4959.5	5062.9	4664.4
3836.4	2740.3	1596.1

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s__Alistipes putredinis	69794

EF510444.1 gg_id:227436 Loss During Antibiotic Treatment 1 Intubated Patients Colonized Pseudomonas aerug EF5104
FJ681799.1 gg_id:520235 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6817
AB009191.1 gg_id:2174 rumen clone RFN35 bacterium AB009
GQ493040.1 gg_id:543667 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
FJ683495.1 gg_id:523862 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6834
EU461634.1 gg_id:300957 mongoose lemur feces clone ML_aaj25h12 EU461
EU777984.1 gg_id:304278 Rock hyrax feces clone RHSD_aaa01h11_1 EU777
FJ682963.1 gg_id:525654 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6829
GQ448332.1 gg_id:585048 Microbiome neonatal calves: shedding microorganisms fecal clone calf783_2wks_gr GQ448
FJ684257.1 gg_id:530209 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6842
EU472972.1 gg_id:287921 douc langur feces clone DL_1aaa04f11 EU472
EU469531.1 gg_id:293939 black lemur feces clone BKLE_f08_2 EU469
GQ492787.1 gg_id:563840 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
AJ005635.1 gg_id:2181 Prevotella enoeca str. ATCC 51261 AJ0056
EU843354.1 gg_id:334051 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU461752.1 gg_id:301489 mongoose lemur feces clone ML_aaj28c05 EU461
FJ363067.1 gg_id:368969 feces adult twins and mothers; TS148 clone TS148_a02f01 FJ3630
EU774603.1 gg_id:353551 Douc langur feces clone DL_2aaa02f02 EU774
GU304031.1 gg_id:539999 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU304
FJ684484.1 gg_id:531065 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6844
EU467281.1 gg_id:298841 black-handed spider monkey feces clone SPIM_g05_2 EU467
GU303561.1 gg_id:541984 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
FJ370118.1 gg_id:362555 feces adult twins and mothers; TS55 clone TS55_a04f03 FJ3701
EU777261.1 gg_id:308029 Okapi feces clone OK3_h06_2 EU777
EU461552.1 gg_id:298770 black rhinoceros feces clone RH_aaj92c09 EU461
EU777995.1 gg_id:326540 Black rhinoceros feces clone RH_aaj91c03 EU777
EU475391.1 gg_id:293472 springbok feces clone SBSD_aaa04f08 EU475
AB034021.1 gg_id:34809 rumen clone 4C0d-8 AB034
EU463261.1 gg_id:295357 naked mole-rat feces clone molerat_aai72e06 EU463
EU871385.1 gg_id:304289 Genetic Bovine (Bos taurus) Rumen Thailand clone CF231 EU871
EU459498.1 gg_id:293135 capybara feces clone CAP_aah98e04 EU459
EU474589.1 gg_id:302013 bighorn sheep feces clone BHSD_aaa04a07 EU474
AB009211.1 gg_id:2201 rumen clone RFN64 bacterium AB009
AB331897.1 gg_id:362169 Paraprevotella xylaniphila str. YIT 11841 (= JCM 14860 = DSM 19 AB331
EU468730.1 gg_id:302334 okapi feces clone OK3_b01 EU468
EU773683.1 gg_id:347680 Capybara feces clone CAP_aah98f08 EU773
EU461370.1 gg_id:300691 red kangaroo feces clone KO2_aai19b05 EU461
EU462623.1 gg_id:299230 Sumatran orangutan feces clone orang2_aai66c05 EU462
FJ880903.1 gg_id:379362 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
AJ518874.1 gg_id:109956 Alistipes finegoldii str. ANH 2437 AJ5188
NZ_ABFK02000016.1 gg_id:469639 Alistipes putredinis str. DSM 17216 NZ_AB

156.8	1274.9	1675.2	2459.8	760.6	1319.1	1514.5	1465.7	478.2	198.4	725.1
128.8	3684.9	5057.1	6139.0	1091.9	3532.4	3926.7	3570.2	745.0	332.9	2313.2
54.9	870.6	886.3	649.4	730.9	932.5	923.3	891.1	530.1	429.3	268.6
56.0	3168.0	4571.2	5687.0	1047.6	3318.7	3164.4	3399.8	425.4	275.1	1787.7
450.7	2897.1	3817.5	4147.3	1538.7	2568.9	2769.8	3071.5	589.5	558.4	2014.8
1099.8	1015.4	1378.2	1730.5	745.9	1105.9	1087.1	1112.7	424.4	207.1	661.6
284.8	4391.4	5405.8	4691.8	3291.6	4002.4	4817.5	5413.6	4696.9	2612.3	5241.9
241.6	5435.0	5554.0	6345.8	5954.9	4978.3	6187.8	5267.8	2682.4	2537.9	5608.0
61.0	1092.0	1024.0	1001.3	1295.5	1135.8	1361.5	1149.3	343.7	277.4	663.9
135.7	3565.9	4793.7	5997.4	1284.7	3333.2	3531.9	3492.9	1037.4	431.4	2351.1
77.5	3613.8	4903.1	5468.3	1042.1	3028.6	3119.1	3289.6	627.6	298.2	1920.4
4053.9	4750.9	5312.6	5982.6	2704.0	4298.2	5315.5	4334.9	3197.4	1377.8	3350.3
77.0	2419.5	3227.3	4692.4	1319.9	2483.8	2942.3	3624.4	651.2	329.0	3297.6
293.0	4406.3	4069.1	5045.8	1837.2	3909.8	3318.9	3870.6	1812.8	2855.6	4075.4
107.9	5088.3	6689.2	7945.0	1733.7	4600.0	4776.9	5330.9	1730.4	691.7	3293.0
79.9	536.5	465.9	626.1	104.1	357.6	174.7	443.5	182.8	128.7	284.7
617.2	4796.6	5359.2	6692.2	4174.3	4946.2	5630.8	5359.6	4417.2	3061.4	4187.7
59.3	389.2	667.3	885.9	314.6	382.3	304.6	654.5	141.1	206.7	260.5
5347.9	3285.4	3077.1	3392.3	2880.9	2539.7	3535.2	2634.2	3219.8	2056.2	3015.5
161.5	3280.8	3834.5	4718.5	1384.5	2995.1	2714.8	3861.0	981.5	457.0	3798.6
4065.5	4006.1	4490.5	4958.7	3883.9	3958.5	4361.2	3889.8	3138.6	1583.9	3020.2
1759.1	4523.6	4263.9	5368.4	2704.4	3826.9	3819.3	4741.9	3233.1	2863.5	4479.6
41.9	52.0	51.8	51.1	63.0	56.8	47.0	59.4	29.8	24.5	31.1
195.0	3170.6	3162.1	4128.7	2571.5	2309.4	2810.9	2942.6	3430.4	969.1	1299.1
3415.2	6518.9	6514.9	6380.6	6548.3	6120.0	7013.1	6320.0	6203.0	8537.2	5542.5
3471.4	3271.4	4106.9	3814.5	3946.2	3519.4	3808.4	3532.8	3702.7	4421.5	3095.0
173.7	2038.2	2448.8	3298.6	872.4	1413.4	1676.4	2138.9	1147.4	565.4	970.8
37.8	296.2	377.0	491.6	161.0	202.1	301.3	266.3	92.0	43.7	125.0
116.5	3456.6	3886.8	5324.3	3107.7	2881.2	4167.9	3981.0	5615.3	1695.7	2124.1
138.5	3464.7	3243.3	3687.0	1938.1	3372.7	2771.4	3330.1	4612.5	4091.3	3090.5
2375.6	4104.8	5639.5	3546.5	2549.6	3972.9	2910.0	3985.5	4677.8	2385.2	4440.8
231.9	4870.8	5609.2	5660.0	6209.4	4939.6	7652.4	4938.4	2712.3	4407.4	6063.8
43.3	185.3	318.9	396.1	193.5	172.8	303.5	184.8	56.2	27.6	74.2
52.8	163.4	123.3	199.7	38.9	28.6	36.6	145.5	39.1	24.6	33.6
57.9	1680.6	2011.7	2478.0	1059.9	1542.4	916.8	2067.5	782.4	759.0	1623.0
107.2	4333.2	3506.3	3876.1	3320.0	3848.6	4368.7	3605.9	2798.4	1109.3	2214.2
527.4	3316.9	3538.6	4009.9	2600.5	2950.5	3561.5	3801.3	2789.8	2791.1	4257.9
472.5	3550.7	2987.3	3350.8	2769.0	3531.9	3180.4	3460.8	4888.8	2707.3	3123.1
41.4	34.1	71.8	192.9	47.0	72.6	22.3	49.2	37.5	35.6	44.0
148.3	337.2	768.7	323.6	312.0	440.2	299.5	338.6	223.4	161.0	258.3
94.9	794.8	647.4	835.8	1233.1	732.4	1170.6	693.8	210.4	79.3	417.9

3071.6	1584.3	1321.5
6468.6	3131.5	2165.6
719.0	620.1	803.0
6853.9	2894.6	1649.3
5043.8	3261.7	1560.1
1634.6	1376.5	582.1
4070.6	4406.4	5257.9
5547.9	4654.8	6575.7
1056.3	1093.2	1078.6
6226.1	3319.2	2377.5
5804.7	3375.3	2012.0
6053.8	4282.9	2421.8
4638.2	2428.2	4048.4
5180.8	3618.1	4528.1
8753.9	4624.0	3285.6
455.5	347.5	60.4
6359.5	5727.7	5503.7
835.5	732.9	1396.5
3106.3	3205.2	3075.9
5201.1	2735.0	5004.8
4572.9	4410.0	4241.0
5363.0	3973.0	2373.7
36.5	56.9	43.9
4565.6	2998.8	1879.0
5836.0	5942.0	6847.3
3397.9	4854.5	4824.2
2910.9	2050.1	2195.1
415.6	478.6	170.1
3166.8	3538.8	3808.2
3213.9	3237.3	2643.8
3349.4	4934.1	2825.2
4488.2	4773.7	8550.3
164.8	343.2	297.5
88.7	180.1	42.0
1447.2	1526.7	2746.2
3511.5	3684.5	3624.4
3706.7	3059.9	4000.3
3594.1	3576.1	5455.8
41.0	43.6	50.4
417.9	459.4	976.0
963.2	947.5	1867.9

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EU655882.1 gg_id:286948 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
AY979218.1 gg_id:122365 human transverse colon mucosal biopsy clone Z358 AY979
FJ680633.1 gg_id:518598 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6806
EU452123.1 gg_id:324193 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU452
AY643082.1 gg_id:128182 Alistipes finegoldii str. 4401054 AY643
EF098147.1 gg_id:185451 mouse cecum clone SWPT14_aaa02b11 EF0981
EU468718.1 gg_id:301755 okapi feces clone OK2_e10_2 EU468
EU456567.1 gg_id:320525 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU456
DQ456413.1 gg_id:158550 pre-adolescent turkey cecum clone CFT214G5 DQ456
AY992622.1 gg_id:135560 mouse cecum clone C23_l20 AY992
AY547271.1 gg_id:107044 Alistipes massiliensis str. 3302398 AY547
EU469334.1 gg_id:296168 springbok feces clone SBK_f08_1 EU469
EF603936.1 gg_id:227834 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
EU655823.1 gg_id:280240 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EF096138.1 gg_id:175375 mouse cecum clone obob1_aaa01b08 EF0961
EU655761.1 gg_id:286907 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU453026.1 gg_id:329877 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74 EU453
EU455627.1 gg_id:347069 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU455
EU456350.1 gg_id:319372 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU456
EU773364.1 gg_id:323400 BigHorn sheep feces clone BH1_aao27a03 EU773
EU655981.1 gg_id:286067 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU505566.1 gg_id:259196 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa02g06 EU505
EU455346.1 gg_id:316883 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU455
DQ798086.1 gg_id:179688 human fecal clone RL302_aal95d02 DQ798
EU468557.1 gg_id:298464 okapi feces clone OK1_f10_1 EU468
EU655977.1 gg_id:283716 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
AJ518876.1 gg_id:104780 Bacteroides sp. str. DSM 12148 AJ5188
AY974072.1 gg_id:138006 Alistipes sp. WAL 8301 AY974
GQ043010.1 gg_id:396409 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw1012a GQ043
EU655719.1 gg_id:282072 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU468653.1 gg_id:288382 okapi feces clone OK2_e11_1 EU468
EU468891.1 gg_id:296840 Speke's gazelle feces clone SP2_f11 EU468
GQ493426.1 gg_id:579595 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ493
AY993266.1 gg_id:129437 mouse cecum clone C21_l17 AY993
AY991744.1 gg_id:133452 mouse cecum clone C20_b22 AY991
AY991932.1 gg_id:133674 mouse cecum clone C20_l18 AY991
EU505322.1 gg_id:262704 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02e02 EU505
DQ794029.1 gg_id:192724 human fecal clone RL176_aah46h06 DQ794
AY992915.1 gg_id:134775 mouse cecum clone C22_i11 AY992
EF402636.1 gg_id:213671 human fecal clone SJTU_B_10_51 EF402
FJ681251.1 gg_id:515059 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6812

159.6	4884.0	4670.5	4054.5	3653.1	3520.7	5248.0	4444.8	3481.1	6193.1	3422.4
49.8	2600.3	2654.7	2683.0	2078.1	2117.6	2717.3	2203.5	1008.8	325.0	978.2
4848.7	8706.3	9381.5	9866.5	9816.7	7557.6	9148.3	7297.2	9246.1	10132.3	7797.2
4160.5	3556.7	3414.2	3568.6	3735.8	2964.5	4190.1	3102.6	5306.7	3889.8	4866.8
132.1	2196.0	2289.2	1852.8	1389.9	1255.2	2546.1	1711.7	1456.6	555.4	1443.9
2359.2	2909.7	4004.2	4600.4	2087.7	2332.5	2654.9	4024.3	1749.0	4423.1	3816.8
750.3	4661.5	3992.0	4311.5	3633.7	4457.6	3805.6	4214.6	4446.9	3780.8	3728.9
1129.8	4932.6	4487.1	5038.4	4913.5	4587.9	5095.7	4766.2	4725.6	4177.9	5445.5
294.1	1925.2	2300.6	2976.4	2384.6	2039.5	2668.4	1753.7	921.1	563.1	1135.4
3861.9	3206.4	3360.4	4047.0	2662.5	2641.1	3268.2	2799.5	2286.0	1955.0	3503.7
196.3	1799.1	1953.6	2140.7	1774.4	1769.1	2212.7	1629.8	1038.5	774.7	1343.1
1190.3	3632.5	3803.3	4639.2	3403.0	3347.8	3831.2	4196.2	3663.6	2790.7	4240.1
1342.1	3282.8	2925.1	2719.7	3378.9	2739.3	3389.7	2935.4	3332.1	1906.8	2354.7
84.6	1416.0	1166.6	1434.1	1444.0	1825.7	1292.8	1380.4	297.2	108.4	742.3
143.9	4530.2	5582.5	6753.3	5092.2	5093.0	6296.8	5482.2	3916.8	2659.8	6495.6
2815.4	2946.7	3488.6	2922.3	3318.5	2877.9	3317.4	3277.2	2535.0	2280.8	2463.9
1226.1	2661.5	2600.8	2800.6	2973.0	2562.8	2863.3	2731.0	2279.2	2304.6	2827.4
3903.0	5832.2	5548.9	6244.7	5854.0	5856.4	6191.7	5733.4	6285.9	5505.2	6548.8
4181.8	6191.2	6471.0	6589.9	6244.4	6181.6	6707.1	6214.1	9324.3	7235.4	7020.0
173.1	1145.8	2333.1	3038.0	1587.4	1672.7	1807.5	2212.2	795.6	807.7	1939.3
151.1	2130.1	1728.5	1682.0	2504.3	1403.3	2465.3	1949.4	1059.8	2183.0	1231.0
9713.0	5058.7	4303.0	4500.1	4491.2	4306.9	4817.8	3994.4	6155.6	5731.8	5200.6
1204.6	7671.2	6931.2	7432.7	5888.9	7029.2	7157.9	6887.8	11011.4	8280.3	7318.9
688.0	5798.3	4536.9	5502.6	5872.4	4323.2	8151.8	4467.5	2995.2	1436.1	4864.2
894.3	5085.6	3936.4	4564.1	5329.2	4582.9	4714.3	4794.9	2915.5	2538.0	3225.9
2117.2	4821.3	4685.2	4954.7	5342.2	4002.7	5530.1	4806.5	4002.6	4879.5	4172.2
47.4	226.0	152.1	223.3	197.9	120.9	54.2	215.9	84.7	183.8	65.8
48.4	1332.4	1052.4	1026.2	1219.4	845.0	795.5	1033.4	302.3	295.8	617.3
48.0	107.8	173.3	169.8	62.2	95.8	72.1	133.1	69.2	106.1	55.1
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7224.2	5395.0	4875.7	4778.9	4435.4	4158.3	4858.1	4923.8	6106.3	6062.1	5812.2
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5275.3	9220.1	9956.8	10506.4	10718.3	9101.1	11484.5	8517.4	11792.5	10855.4	10091.4
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2176.4	3385.6	4263.4	3523.9	3777.2	3666.3	4232.5	4415.8	4433.6	4678.1	3539.4
372.6	4271.9	4013.1	4442.4	4674.2	4280.0	4907.8	4202.5	4140.5	2981.7	4836.3
39.7	895.2	890.3	760.6	1007.1	880.9	791.8	907.7	1410.7	1307.2	798.6
527.3	4358.2	3464.0	4405.2	4536.0	4082.2	5342.2	3719.5	5500.1	2393.4	2945.5
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9132.3	9158.0	8402.8	8916.0	7248.1	6307.5	7986.8	6108.9	11464.9	6971.7	8255.1

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8191.5	9754.0	8460.7
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1397.9	2010.5	1875.6
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2628.3	2950.3	6805.6
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6487.3	6595.0	5916.7
2952.7	1812.7	1351.1
1805.9	1832.7	2851.4
4176.5	5137.4	5012.0
7248.6	7455.7	7164.6
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4461.3	5664.3	6115.3
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784.6	968.7	1286.3
347.1	158.7	89.6
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4706.5	4634.8	5936.3
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EU655721.1 gg_id:287165 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU764925.1 gg_id:337670 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B2 EU764
EF602837.1 gg_id:227692 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6028
EU453554.1 gg_id:317407 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
DQ815959.1 gg_id:173573 mouse cecum clone aab24g11 DQ815
EU452946.1 gg_id:316354 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU452
AY992841.1 gg_id:131061 mouse cecum clone C22_e18 AY992
EF603815.1 gg_id:256742 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal m EF6038
FJ681306.1 gg_id:520462 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6813
EF099892.1 gg_id:198614 mouse cecum clone SWPT5_aaa01h03 EF0998
DQ800969.1 gg_id:197995 human fecal clone RL387_aao90b01 DQ800
EF100039.1 gg_id:190844 mouse cecum clone SWPT5_aaa03g11 EF1000
EF096012.1 gg_id:194490 mouse cecum clone lean2_aaa01h09 EF0960
EU656031.1 gg_id:284620 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
EU655858.1 gg_id:286968 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU452427.1 gg_id:322395 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
EU505657.1 gg_id:270391 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa04c04 EU505
EF603125.1 gg_id:230784 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6031
EU510227.1 gg_id:267812 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03c01 EU510
GQ031018.1 gg_id:465433 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ031
EF097211.1 gg_id:190026 mouse cecum clone SWPT18_aaa03b10 EF0972
AB234408.1 gg_id:149167 termite gut homogenate clone MgMjD-026 AB234
DQ307714.1 gg_id:143926 termite intestinal tract clone MTG-47 DQ307
GQ175524.1 gg_id:569030 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EF400613.1 gg_id:205226 human fecal clone SJTU_E_15_74 EF4006
DQ307718.1 gg_id:144574 termite intestinal tract clone MTG-60 DQ307
EU655943.1 gg_id:282931 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU656070.1 gg_id:283288 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
EU009842.1 gg_id:251257 intestinal microbiota domestic and wild turkeys turkey cecum clone WTB_S10 EU0098
AB088945.1 gg_id:77794 termite gut homogenate clone Rs-F73 bacterium AB088
GQ175488.1 gg_id:512098 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
EU791148.1 gg_id:418501 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology MMP7++ mou EU791
EU760448.1 gg_id:355301 Mouse fecal microbiota feces clone 3E1 EU760
EF401874.1 gg_id:211541 human fecal clone SJTU_D_11_42 EF4018
EU655844.1 gg_id:281630 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
DQ307715.1 gg_id:144995 termite intestinal tract clone MTG-56 DQ307
FJ374191.1 gg_id:366302 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindgu FJ3741
AB234412.1 gg_id:149950 termite gut homogenate clone MgMjD-045 AB234
AB234442.1 gg_id:150403 termite gut homogenate clone MgMjW-42 AB234
FJ362627.1 gg_id:362179 feces adult twins and mothers; TS13 clone TS13_a01c04 FJ3626
CU927011.1 gg_id:565304 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU927

1438.4	9069.1	7980.8	7890.1	7335.6	7064.6	8307.4	6805.0	11284.6	7071.7	6634.5
1434.6	2364.5	2821.5	2772.4	2555.4	1848.3	3335.2	2264.1	1535.2	1061.7	1954.2
80.7	1872.8	2505.4	2938.5	2135.1	2359.6	2798.6	2319.2	1732.8	1628.0	2662.7
1750.7	4746.9	4474.0	5043.5	4710.0	4411.4	5496.7	4502.0	4124.5	4540.4	5378.7
46.0	157.0	149.8	274.9	93.3	177.6	65.6	118.6	59.0	33.9	81.0
58.6	2335.6	2421.9	2643.6	2926.8	2434.7	2592.9	2474.2	1711.0	1529.7	2057.5
59.8	346.6	457.0	302.9	446.2	313.8	435.3	252.1	168.1	225.6	178.9
229.1	4677.6	5495.5	6491.9	3790.1	3868.2	3418.0	4399.6	5296.0	4309.2	3437.5
35.3	1520.5	1529.3	1387.2	1807.3	1428.2	2704.5	1201.8	661.2	164.8	1060.3
579.5	3276.2	2801.9	4153.9	4870.7	3096.3	4388.4	3947.4	3851.2	4120.2	3096.0
2768.8	4111.2	4683.8	5731.9	4328.9	4597.1	5347.9	3933.3	6124.2	5409.3	4981.5
35.6	18.0	22.6	24.0	20.3	21.6	16.1	21.4	13.7	8.4	11.9
6982.1	4487.4	4823.2	4881.8	4611.0	4163.4	5167.7	4551.0	6444.6	6004.6	6248.1
3030.5	8601.4	8799.5	8235.5	7698.0	7918.1	8780.4	7970.4	11463.4	12216.8	8735.0
64.6	1130.1	1421.9	1685.6	802.8	1158.6	1359.8	1406.4	454.0	425.5	820.0
78.0	1307.0	1150.1	1493.6	1575.6	1302.6	1447.2	1646.9	819.2	834.9	1148.8
93.8	1903.1	1549.2	1605.5	1708.8	1291.6	2387.6	1397.9	981.4	369.5	1125.4
140.6	3809.0	2833.8	2389.6	2249.1	2815.8	4262.1	2550.0	6002.3	3469.3	1822.8
444.4	4413.9	3678.7	3711.0	3755.8	3060.6	4367.0	3572.4	3251.8	3149.5	3213.3
32.4	247.4	237.9	220.0	74.4	113.5	205.2	113.3	49.1	26.6	73.9
694.3	3431.8	4077.0	4000.8	3175.0	3557.8	3355.4	5141.5	3279.8	1815.1	5211.3
51.8	1577.3	1785.3	2191.2	1671.2	1730.9	1466.8	1467.8	871.6	1268.0	925.9
579.4	5107.6	4428.0	5829.4	5134.5	5185.5	6330.1	4957.9	3548.3	2224.4	3171.1
122.7	4471.9	3028.4	2920.4	2009.7	3472.2	2987.6	2988.1	4272.6	2937.1	2091.3
121.0	1207.6	1580.5	1307.5	1171.4	1246.9	1423.0	1206.8	3025.5	1755.3	1650.6
38.9	2163.6	2720.1	3244.6	1767.1	2562.1	2363.1	3165.5	1813.8	1593.9	2252.2
2697.7	5797.6	5537.1	5904.9	6299.3	5192.7	6271.8	5522.1	7432.6	3837.4	6651.8
1585.2	7264.4	6784.9	7844.3	7808.8	6734.6	9140.8	7646.2	10513.5	5406.6	7346.1
102.8	3884.1	3597.9	3829.5	2776.0	3232.7	3881.4	3915.0	2032.8	1552.1	2002.6
88.7	463.2	547.2	697.6	849.8	397.4	1060.9	884.5	202.7	320.3	338.4
1450.7	6011.7	5883.2	5833.5	5268.7	5771.6	5764.8	5092.9	4603.7	3884.0	5841.1
3534.2	7802.3	7381.5	8718.2	8684.1	6921.0	9938.1	7560.2	10853.2	5245.4	7805.4
1197.1	5209.8	5191.6	5455.2	5284.4	4919.1	5974.0	6246.8	6770.5	3887.6	6208.1
39.9	1914.1	3240.0	3226.3	3832.5	2605.0	5205.4	2910.5	3787.4	162.9	2588.1
199.1	2133.8	1958.2	2226.3	1705.1	2103.5	2098.3	2272.3	3942.1	2210.2	1747.3
3778.4	3725.8	4669.6	5544.5	3729.9	3762.9	4706.2	4126.6	2728.2	2549.3	3557.4
136.3	3317.4	3054.9	3239.9	2209.9	2025.9	3100.0	2956.9	3311.4	4520.7	2321.9
42.8	37.9	58.6	72.5	89.5	47.0	84.3	54.6	36.4	20.0	44.2
167.9	3649.9	3426.5	3861.6	3877.2	3540.2	3756.0	3592.2	3491.6	1997.2	3387.6
634.7	2807.8	3398.6	3393.6	2689.0	2649.6	3871.7	3009.8	2159.3	2461.6	2053.5
137.3	760.0	836.9	951.6	749.3	782.3	1329.8	912.9	390.1	272.7	412.3

6280.3	6726.7	7947.5
1573.5	2355.3	2762.6
2629.2	2488.7	3065.2
4258.0	4830.2	4224.9
310.5	233.2	880.4
2450.8	2162.3	2401.2
216.8	393.8	469.9
4277.7	4788.6	3265.8
1283.6	1212.9	1624.1
4571.7	2933.0	2955.2
3840.0	4762.5	4517.7
24.1	21.4	38.2
3920.7	5784.3	4200.3
7293.1	7982.6	8774.2
1977.8	1573.6	2467.0
1635.1	1082.4	935.3
1806.7	981.7	1552.5
2996.5	2706.6	2769.6
3978.0	3873.9	4999.9
230.4	207.7	209.1
3886.8	4330.8	8957.1
1780.7	1791.9	2758.0
4590.0	4722.7	4404.3
3033.0	2688.0	4181.5
1159.9	1118.4	1159.0
3035.1	2408.5	3250.3
4491.8	5553.8	4985.0
7415.4	8287.6	8063.3
4460.9	3972.5	6214.3
615.3	653.3	633.3
4996.4	4421.1	5276.2
7206.3	8889.1	7886.5
5535.3	5449.9	5791.1
2048.5	1793.8	2127.7
1960.4	2469.9	3107.7
4114.8	3312.2	3683.3
2575.3	2588.1	3826.6
50.0	82.0	72.0
3747.6	3792.6	5598.4
3142.8	4373.6	4100.3
842.1	1013.6	1367.5

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EF603250.1 gg_id:233124 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6032
EU655868.1 gg_id:285292 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6558
GQ175465.1 gg_id:569831 Chicken intestinal microbiota modulations various feed supplementations DGGE and GQ175
AB288900.1 gg_id:203209 termite gut homogenate clone BOf4-04 AB2889
AB234381.1 gg_id:147812 termite gut homogenate clone MgMjD-085 AB2343
AB234430.1 gg_id:145163 termite gut homogenate clone MgMjR-034 AB2344
DQ307694.1 gg_id:143794 termite intestinal tract clone MTG-1 DQ307
AB234413.1 gg_id:148704 termite gut homogenate clone MgMjD-055 AB2344
AB234444.1 gg_id:146402 termite gut homogenate clone MgMjW-65 AB2344
AB234440.1 gg_id:147387 termite gut homogenate clone MgMjW-41 AB2344
DQ307716.1 gg_id:144084 termite intestinal tract clone MTG-58 DQ307
DQ307722.1 gg_id:144258 termite intestinal tract clone MTG-85 DQ307
EU778281.1 gg_id:307742 feces clone RL117_aae92a01 EU7782
EF515393.1 gg_id:226691 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23g10 EF5153
FJ825571.1 gg_id:562180 Microbial during start-up mesophilic biogas plant clone 43_BS5_8 FJ8255
EF436336.1 gg_id:212713 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC50 EF4363
EU771218.1 gg_id:352631 Asiatic elephant feces clone AE3_aaa01a05 EU7712
AY188307.1 gg_id:80463 marine? clone KD3-67 AY1883
GQ502510.1 gg_id:558040 Effects Geographic Location on Formosan Subterranean Termite (FST) gut clone Cf2- GQ502
EU850557.1 gg_id:306219 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF365 EU8505
AM086105.1 gg_id:145424 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
CT574141.1 gg_id:152067 Evry municipal wastewater treatment plant clone 061A06_B_SD_P93 CT5741
EU358741.1 gg_id:310915 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU3587
AB244308.1 gg_id:143645 Microbial mesophilic chemostat cultivation long-chain fatty acids-degrading methan AB2443
FM179909.1 gg_id:315021 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
EU871403.1 gg_id:343959 Genetic Bovine (Bos taurus) Rumen Thailand clone CF343 EU8714
U81709.2 gg_id:1878 fluidized bed anaerobic digestor fed vinasses (waste wine distillery) clone vadinHA21 U81709
DQ330455.1 gg_id:159438 Guerrero Negro hypersaline microbial mat clone 062DZ68 DQ330
FJ484700.1 gg_id:535284 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4847
EU662616.1 gg_id:592227 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems floating microb EU6626
AY838556.1 gg_id:109402 fruiting body Pleurotus eryngii clone PE01 AY8385
EU407205.1 gg_id:258955 household biogas digester clone GW-20 EU4072
CT573994.1 gg_id:154079 Evry municipal wastewater treatment plant clone 009A01_B_SD_P15 CT5739
DQ395033.1 gg_id:151832 harbor sediment clone VHS-B5-15 DQ395
EF454472.2 gg_id:219599 termite hindgut clone 290cost002-P3L-2184 EF4544
FJ230923.1 gg_id:329546 under Level Antibiotic Selection Pressures river water clone F12 FJ2309
AJ534684.1 gg_id:75921 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
GQ377114.1 gg_id:590965 structure two reactive PCE degrading enrichment s stimulated OU Duck Pond Norm GQ377
FJ437992.1 gg_id:548813 Benthic okenone production Fayetteville New York Green Lake surface sediments 16. FJ4379
CT574155.1 gg_id:152565 Evry municipal wastewater treatment plant clone 060G05_B_SD_P93 CT5741
CT573934.1 gg_id:154809 Evry municipal wastewater treatment plant clone 012A08_B_SD_P15 CT5739

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33.8	1391.4	1059.2	920.4	852.0	1060.9	863.6	1104.4	2531.9	1231.7	807.8
301.1	7470.6	7444.6	7816.0	7094.2	7076.9	8042.7	6986.2	6312.4	7686.9	6944.2
81.1	1328.0	1188.5	1113.0	554.8	1531.1	680.3	1183.5	812.2	1072.8	1495.1
263.0	3897.3	4525.6	4687.7	4645.0	3977.0	6325.4	4641.5	2961.0	2235.8	4531.8
35.0	92.4	119.5	98.8	48.7	52.6	58.1	57.5	124.7	16.5	69.2
52.8	2565.5	3037.0	3388.7	1121.4	2234.7	2020.2	2589.2	1830.6	1824.1	1968.4
35.0	42.9	68.6	46.9	54.0	55.3	37.0	59.0	25.6	22.6	33.8
179.5	3944.5	4040.8	4667.9	4454.3	3539.0	5258.2	4211.7	3032.7	2571.5	4569.8
55.1	623.8	1458.1	1536.6	489.6	1005.6	1104.5	1227.5	432.9	149.1	981.0
26.4	277.2	256.9	202.6	211.7	384.3	288.8	358.0	101.8	45.3	165.1
41.6	2034.4	2365.9	3554.8	2154.7	1743.8	2781.1	2830.1	690.4	733.8	806.3
631.7	1265.3	1159.2	1012.8	714.9	953.0	775.7	794.7	1063.7	662.9	1000.4
78.2	1853.5	2079.2	1944.4	1853.8	1627.4	2922.5	1551.0	872.5	422.8	1322.7
98.1	3372.1	4099.4	3825.0	3451.1	3338.8	3110.3	3875.7	2272.2	1550.8	2427.9
45.9	196.4	225.4	239.3	328.5	196.0	379.0	191.2	27.3	30.0	169.5
571.3	3736.1	3600.6	3668.1	3502.9	2732.3	4365.9	3883.7	2381.3	963.2	3706.0
37.4	78.4	104.0	94.4	83.6	47.1	107.4	30.8	24.1	16.4	36.2
242.2	2845.8	5099.0	4075.1	4129.1	3042.6	5733.5	4294.3	3246.9	1502.8	3902.0
294.5	2562.1	3093.5	3092.4	3594.7	2686.6	3875.9	2959.3	1891.4	1117.9	2007.5
296.5	1901.5	1927.6	1824.5	1716.9	1442.9	2391.0	1250.2	1673.2	915.1	960.2
235.9	2555.8	2447.8	2818.8	2423.7	2552.6	2485.2	2281.9	1783.6	2064.8	3350.9
110.0	955.2	1197.0	1352.6	1810.5	1028.1	1575.4	1549.7	663.2	290.5	549.5
39.0	26.9	43.6	45.2	47.2	38.4	62.7	20.4	13.9	16.0	22.0
89.6	1672.2	3014.3	3122.6	2950.7	2380.4	4251.9	2788.7	1227.6	535.8	2296.3
6994.6	10897.6	9143.5	9544.8	10554.5	9478.9	10798.7	9563.2	12560.7	11792.6	9981.3
39.2	354.8	705.4	523.6	866.0	752.8	1208.8	717.2	293.4	478.2	384.4
127.2	4060.5	5914.9	6315.2	5146.7	5668.2	6411.5	4835.7	4943.9	1561.3	4077.4
7310.9	8479.7	9444.6	10600.5	9670.0	8657.0	13090.0	8669.5	11099.1	7878.1	11887.4
245.9	6531.8	6620.1	6628.9	6719.2	6352.8	8216.8	6064.8	4379.9	4996.3	4688.7
55.3	353.4	494.1	400.4	376.3	490.3	189.5	498.2	145.8	50.0	164.0
126.3	4382.4	2579.4	2493.9	2289.0	2972.8	2220.5	3116.4	3216.5	2495.9	2462.5
25600.4	5214.1	4906.4	5330.2	4584.4	6106.4	5529.6	4348.6	7047.5	7096.2	9197.9
119.3	2532.4	3039.3	3584.0	2685.8	3341.8	2579.1	2435.8	1137.9	1067.2	1541.9
142.4	2339.2	2461.8	2982.9	2701.5	2767.8	3171.3	2576.4	2296.2	2104.2	1975.3
62.5	766.4	712.5	641.2	1324.0	816.0	3090.2	1429.2	682.6	209.4	571.0
90.0	756.8	859.2	912.8	1338.3	787.9	1976.2	715.2	817.6	256.1	633.8
1011.0	3345.3	4264.0	4756.8	5581.2	4297.0	5277.2	4712.3	6622.3	1412.1	3275.4
2443.3	3262.4	3419.8	3578.9	5099.0	2809.3	5556.8	2472.6	3183.3	2279.6	3524.4
110.8	500.2	535.4	586.4	534.9	477.4	558.0	550.1	644.9	582.3	323.6
117.2	166.7	141.8	158.9	214.9	147.7	150.5	150.5	108.9	133.4	109.8

3772.6	4266.3	6725.2
863.7	1453.3	1874.4
7976.8	5913.6	8271.4
1353.6	1171.7	1583.0
4821.6	4447.0	7414.0
59.3	43.8	43.1
3223.2	1771.7	2840.9
54.9	105.1	48.8
3804.2	3300.4	4908.1
770.3	1147.1	1259.6
373.8	207.4	603.8
2615.5	2734.7	4520.6
714.6	1319.5	1382.0
1088.9	1629.2	2138.0
5234.2	2589.5	3151.8
179.5	213.7	171.6
2857.3	2596.2	3272.9
34.0	127.7	1593.1
2864.1	3769.8	3690.1
2399.6	3083.6	2331.7
1078.3	1228.7	828.6
2789.1	2669.6	2441.5
1729.0	2038.6	5653.1
24.1	29.3	22.1
1939.3	1839.0	2887.0
9525.9	9677.4	8587.4
377.6	638.6	1269.9
4149.7	3670.5	3973.8
7256.7	8403.5	10499.0
6865.6	4858.3	6193.4
415.9	1120.0	870.1
2525.7	3308.0	8364.6
5457.4	6281.6	4975.6
2250.3	1415.0	1618.8
3183.3	2790.0	2926.3
1101.9	363.3	387.3
668.6	903.3	607.2
2582.3	4750.9	2801.3
2466.1	2751.5	3024.5
499.3	1257.2	446.9
179.8	260.6	205.9

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EF467569.1 gg_id:214814 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
DQ080187.1 gg_id:134023 sediment clone A42 DQ080
AM982612.2 gg_id:277958 microbial and slurry pig saw dust spent bedding clone PISD-AJA05 AM982
AY426454.1 gg_id:101910 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone E1 AY4264
AY160848.1 gg_id:97753 termite intestinal tract clone COB P4-1 AY1608
GU293181.1 gg_id:558868 Microbial contents and mucus yel catfish (Pelteobagrus fulvidraco) stomach content GU293
EF520593.1 gg_id:230769 structure lakes: what controls ? acid-impacted lake clone ADK-IHh02-08 EF5205
EF436380.1 gg_id:212612 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC94 EF4363
GU303885.1 gg_id:560011 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
EU773671.1 gg_id:342691 Capybara feces clone CAP_aah99e07 EU773
AY208811.1 gg_id:83262 cave microbial mats clone LKC2.127-25 AY2088
DQ018797.1 gg_id:130615 anaerobic swine lagoon clone C-85 DQ018
AJ441241.1 gg_id:57445 hydrothermal vent polychaete mucous clone P. palm A 249 AJ4412
AY586396.1 gg_id:108442 fatty acid-degrading consortium clone FA-PB6 AY5863
FJ269080.1 gg_id:337780 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2690
AB234391.1 gg_id:148295 termite gut homogenate clone MgMjD-027 AB2343
AY571428.1 gg_id:114514 termite gut clone RsaHw538 AY5714
EU461538.1 gg_id:289776 black rhinoceros feces clone RH_aaj92a07 EU4615
EU037344.2 gg_id:272261 structure landfill sediments receiving long-term augmentations wastes chromium co EU0373
AM086137.1 gg_id:146292 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone (AM086
EU644095.1 gg_id:282866 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU6440
EU461439.1 gg_id:291256 black rhinoceros feces clone RH_aaj89d12 EU4614
AJ488099.1 gg_id:66165 chlorobenzene-degrading consortium clone IIIB-28 AJ4880
FJ269057.1 gg_id:313117 dissimilatory ferric iron reducers arsenic contaminated Hunan south China paddy soil FJ2690
DQ415785.1 gg_id:157878 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
AM162485.1 gg_id:151096 and situ identification acidic sphagnum peat bog clone B114 AM162
AY571426.1 gg_id:114648 termite gut clone RsaHf415 AY5714
FM877978.1 gg_id:557739 Bacillus sp. str. IST-38 ALISIMBF05R02 FM877
AJ431253.1 gg_id:107777 Cytophaga sp. str. Dex80-37 AJ4312
AY188300.1 gg_id:80683 marine? clone KD2-33 AY1883
AB088921.1 gg_id:77751 termite gut homogenate clone Rs-E47 bacterium AB0889
AY216454.1 gg_id:81597 temperate estuarine mud clone KM66 AY2164
EU475307.1 gg_id:299959 rock hyrax feces clone RHSD_aaa03e02 EU4753
CT574192.1 gg_id:151076 Evry municipal wastewater treatment plant clone 060C01_B_SD_P93 CT5741
FJ901804.1 gg_id:584556 phreatic limestone sinkholes northeastern Mexico water column surface cenote La Pa FJ9018
DQ206420.1 gg_id:150564 Sulfide oxidation coupled arsenate reduction microbial soda lake water clone ML-S-1 DQ206
EF648025.1 gg_id:241699 dynamics during produced water treatment aerobic activated sludge clone HB14 EF6480
AB255913.1 gg_id:165659 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB2559
FJ712490.1 gg_id:518764 Prokaryotic structure and sediments active submarine mud volcano (Kazan MV Sea) k FJ7124
CU922535.1 gg_id:537422 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9225
EF648023.1 gg_id:242143 dynamics during produced water treatment aerobic activated sludge clone HB12 EF6480

67.8	315.2	525.9	528.5	607.1	314.5	931.6	267.1	151.8	117.6	219.4
835.3	4598.3	4847.8	3536.3	3583.1	3259.5	4410.0	3262.7	3745.6	2424.4	2724.7
10570.0	8220.4	7797.9	9030.2	7384.0	7102.3	8657.4	7376.3	9994.9	8287.6	9847.7
1237.7	4989.6	6314.9	7652.5	6919.4	5137.0	9804.9	6208.3	5739.5	1979.9	5654.3
5758.8	6472.8	6506.3	6914.7	5372.9	6413.4	6424.8	5962.6	7036.8	4723.9	7580.8
75.8	1296.4	2635.3	1903.8	2118.2	1143.8	3191.0	1307.0	754.5	247.4	1044.3
2713.0	6675.8	6507.4	6791.2	7093.8	5516.3	7780.0	6058.0	7212.6	7178.1	7096.1
34.1	49.1	35.5	71.3	80.9	55.9	87.7	72.3	28.7	28.2	53.7
49.3	470.5	584.7	780.4	545.2	426.9	633.7	682.1	193.5	99.4	301.4
1773.2	8919.0	8607.4	10562.9	9902.5	8186.1	11023.7	8605.6	8036.5	9030.9	9274.7
2172.6	7489.3	8502.8	7623.1	9866.6	7525.2	10458.8	6720.7	5725.9	7577.0	7012.0
47.8	390.0	914.4	824.6	704.2	408.1	1449.0	441.2	151.8	90.0	343.3
55.0	116.8	280.9	205.8	172.0	182.5	383.5	196.6	93.2	37.5	156.2
206.3	3109.7	3720.1	3530.7	3698.4	3804.0	4539.0	3376.9	3453.2	683.9	2902.5
217.2	2336.7	3192.8	2521.0	2066.8	2553.1	2056.9	2640.4	1596.0	653.1	1661.3
39.9	136.0	276.1	186.0	198.4	233.8	198.6	256.7	135.9	62.8	113.2
162.0	1798.5	3492.8	1687.3	2857.7	1694.2	3374.0	2158.5	1234.1	548.4	1323.2
47.8	683.0	1085.2	1164.8	1148.8	1331.6	772.6	1408.3	457.2	785.2	732.0
1035.0	5717.8	3557.9	3354.0	4367.4	3623.2	4333.5	3949.0	4153.5	4129.5	2331.1
245.0	2811.3	4072.9	3739.7	5383.6	3370.4	5777.3	2644.3	2088.7	1336.4	2302.6
75.9	3735.7	4660.6	4924.7	6528.3	3264.4	7274.9	3011.1	2225.1	852.9	3323.6
4254.2	3143.1	3776.4	3971.9	4973.4	3904.7	2942.3	3931.2	3439.0	3506.5	3340.9
1053.7	4137.7	5592.4	4619.5	6321.0	5410.4	4551.9	4857.9	8624.1	5844.1	3938.7
372.1	4702.1	5973.1	6408.3	7236.0	6102.5	7204.7	6061.0	9727.9	3991.3	4582.0
44.3	941.2	1659.1	1273.4	1353.3	493.3	4738.7	526.7	212.7	129.0	372.2
613.6	3845.3	4915.6	5343.1	4791.9	4544.5	6870.3	4538.9	2446.3	1663.4	4163.8
36.1	3272.5	2745.3	2271.4	2740.3	3012.5	2809.6	2832.9	3134.2	2539.2	2325.8
30.6	1485.2	701.8	875.8	780.4	885.2	652.3	1025.5	1536.6	1317.9	693.9
114.1	1997.4	1777.4	2175.8	1715.2	1764.8	2086.2	2064.9	1874.5	853.8	1711.6
4321.2	5315.4	5139.1	5057.8	5219.1	4395.8	6552.1	5224.3	8029.1	4641.9	3989.8
215.1	3245.4	3037.1	3247.9	2439.5	2960.0	3986.0	3417.2	4054.2	2414.6	3654.8
1828.1	7409.4	8418.0	9179.6	7745.9	7345.9	9723.1	6811.7	6116.0	4822.7	7791.1
1227.2	4682.3	4627.0	4629.5	3571.6	4611.2	4249.7	4697.0	6002.0	4382.7	4676.2
1250.3	5562.5	4108.8	4686.7	4764.4	5526.6	4371.3	4080.6	5184.0	5573.3	5002.8
6033.0	5328.9	5055.6	5501.7	5730.4	5357.1	6048.7	4933.8	6972.0	5439.9	4726.3
34.0	64.8	83.6	77.1	87.7	76.9	117.8	136.5	47.5	134.2	42.6
5398.2	5421.7	5545.9	5546.7	5500.9	5354.5	6146.3	5297.4	5966.3	4872.4	6664.9
5821.6	6651.3	5355.3	5830.7	5597.7	5602.3	6849.5	5540.9	6430.7	5284.0	4639.1
5032.0	4336.6	5513.7	5829.8	5098.6	5379.2	4899.9	4379.7	4525.1	3025.2	5494.1
988.6	3631.6	5755.5	6074.6	5551.5	3385.4	9931.3	4711.9	5918.6	1957.0	5186.0
2568.4	5352.1	6801.2	6553.9	7289.4	5102.7	8351.6	6222.9	7809.3	3189.5	5257.0

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4208.2	3018.7	3506.2
6721.8	7806.1	7099.2
5801.5	5893.2	5966.1
6242.2	6492.0	5762.8
732.7	929.6	860.8
6874.5	6545.5	6343.4
37.8	59.5	35.9
542.8	665.9	533.2
7586.3	8334.5	8656.4
6990.6	8115.0	7710.8
146.1	301.0	343.1
151.4	174.9	115.4
1749.1	2844.0	2395.6
2348.9	2583.6	4153.6
123.5	234.6	448.3
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1380.6	1380.9	779.9
3506.6	3806.7	3674.0
2557.9	2427.8	3145.1
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2855.6	4766.4	6747.3
5020.1	4881.6	4618.6
4637.1	6534.1	6475.9
135.3	201.7	207.2
3917.1	5740.7	7424.2
2669.3	3473.2	2577.2
929.1	892.3	625.8
1743.2	1759.0	2073.5
4636.2	4767.0	4614.8
3186.7	2409.2	1929.9
6584.4	6465.4	9689.4
3890.5	5766.6	7708.0
5938.0	4052.9	3802.1
5108.3	5371.7	4741.7
70.6	97.5	69.4
5585.2	6061.3	5538.5
5352.5	7012.4	7887.0
4481.6	3639.7	2900.7
3764.2	4086.1	4569.0
5900.6	6354.3	5478.1

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AB447626.1 gg_id:587106 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
EU778007.1 gg_id:340733 Black rhinoceros feces clone RH_aaj91g09 EU778
AB234373.1 gg_id:148765 termite gut homogenate clone MgMjD-040 AB2343
GU196223.1 gg_id:593277 Bioaugmentation improved recovery digesters after toxicant exposure lab-scale ana GU196
AB288897.1 gg_id:202388 termite gut homogenate clone BOf3-20 AB288
EU381867.1 gg_id:274261 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EF648053.1 gg_id:248589 dynamics during produced water treatment aerobic activated sludge clone HB45 EF648
EU461561.1 gg_id:296651 black rhinoceros feces clone RH_aaj92e07 EU461
EU461511.1 gg_id:301495 black rhinoceros feces clone RH_aaj91c11 EU461
FJ437917.1 gg_id:564635 Benthic okenone production Fayetteville New York Green Lake 25 m water depth clo FJ4379
AY548930.1 gg_id:99570 ANAMMOX sludge clone 1-1 AY548
EF562574.1 gg_id:239593 stable microbial consortia capable degrading complex organic matter paper pulp colu EF5625
AF449768.1 gg_id:80791 CFB group clone ML1228J-9 AF449
EU777479.1 gg_id:350728 Sumatran orangutan feces clone orang1_aai53c10 EU777
AB530243.1 gg_id:570855 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB530
AJ306736.1 gg_id:66951 DCP-dechlorinating consortium clone SHA-5 AJ3067
EU459441.1 gg_id:297220 capybara feces clone CAP_aah97a09 EU459
AJ488097.1 gg_id:66167 chlorobenzene-degrading consortium clone IIIB-1 AJ488
AF449769.1 gg_id:79827 CFB group clone ML1228M-4 AF449
EU461428.1 gg_id:300713 black rhinoceros feces clone RH_aaj89b10 EU461
EF648037.1 gg_id:251918 dynamics during produced water treatment aerobic activated sludge clone HB25 EF648
EF148839.1 gg_id:187075 sp. str. OF1 EF1488
EU778256.1 gg_id:323736 feces clone RL388_aao96a11 EU778
CR933168.1 gg_id:109928 Evry municipal wastewater treatment plant clone 009C01_B_SD_P15 CR933
EU871349.1 gg_id:340817 Genetic Bovine (Bos taurus) Rumen Thailand clone CF24 EU871
EU778270.1 gg_id:347138 feces clone RL388_aao94a06 EU778
EU843687.1 gg_id:344506 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU463641.1 gg_id:294443 domesticated horse feces clone horsej_aai90c05 EU463
FJ172810.1 gg_id:336477 Qinghai Yak Ruminal and Fungi China rumen clone RB-4G9 FJ1728
EU473846.1 gg_id:300815 douc langur feces clone DL_2aaa02f04 EU473
EF436357.1 gg_id:204894 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC71 EF4363
EU458001.1 gg_id:326858 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83 EU458
DQ777884.1 gg_id:162338 rat feces clone R-1153 DQ777
EU748358.1 gg_id:327696 neotropical folivorous flying bird adult hoatzin crop clone hoa5_05g04 EU748
EU461240.1 gg_id:288278 hamadryas baboon feces clone BAZ_aah91c04 EU461
EU453832.1 gg_id:339637 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75 EU453
EU006270.1 gg_id:245595 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU791114.1 gg_id:437229 Enteric Defensins are Essential Regulators Intestinal Microbial Ecology HD5-- mouse EU791
DQ823995.1 gg_id:198761 human fecal clone RL204_aaj57h05 DQ823
EU504520.1 gg_id:275108 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa01g06 EU504
FJ880426.1 gg_id:443609 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804

45.8	1002.5	1557.3	1519.6	1967.6	1256.3	2217.5	1126.6	742.2	142.5	1026.1
4445.8	6107.7	5813.5	6350.1	6393.3	6048.8	5278.9	6640.0	5844.9	6515.6	5922.0
138.5	2555.6	1678.3	1765.2	1802.5	1985.8	1750.8	1665.8	1965.6	1144.3	1269.8
4450.7	4632.6	5779.8	6893.0	7293.4	4678.2	8512.5	6178.8	8741.0	2056.5	5412.6
47.0	1002.7	1488.6	1780.9	1852.2	1232.6	2171.1	1087.0	258.8	154.0	787.7
94.8	10560.1	9770.1	7208.7	8267.8	10260.7	7630.4	9287.1	14106.0	11297.0	8876.8
2500.6	4353.7	4558.5	4574.0	4795.2	4058.4	5709.3	3681.3	4685.6	3208.3	4173.2
953.3	7584.7	8177.7	9269.0	8381.7	8463.2	9111.6	8772.2	10342.2	7473.3	8723.0
3612.8	5832.3	6298.9	7549.5	7446.2	6650.2	6399.5	7107.7	6553.2	5783.8	5634.1
6031.9	5632.8	5043.1	5410.0	4782.0	5518.9	5731.1	4588.2	5881.8	2997.3	7349.0
42.9	244.7	545.3	271.5	288.5	240.5	461.8	300.5	85.6	93.7	144.0
570.4	3009.0	3214.3	3372.0	3554.9	2410.6	4879.1	2644.2	2214.0	1297.4	3215.5
41.2	48.8	56.9	70.9	36.8	24.6	44.5	57.4	25.1	19.6	35.6
1950.3	1825.7	1733.5	2140.4	2561.1	1685.8	3562.9	1338.5	1840.3	1486.7	2399.9
45.9	1580.9	2315.6	2259.8	1613.5	1955.7	2573.6	1720.0	943.5	362.3	1138.4
63.6	711.5	1025.6	971.8	1577.1	1099.8	2194.4	1095.5	578.6	293.9	605.3
4134.6	5459.9	6307.2	6584.6	8776.8	6435.0	6729.7	6902.6	5502.4	4203.3	5567.8
191.4	6004.5	7142.3	7500.8	7810.7	5645.7	9136.5	6182.5	3314.2	4020.0	6125.0
41.4	114.6	225.7	268.1	297.1	138.9	569.5	246.9	66.5	51.6	104.3
77.4	3718.1	3107.7	3714.6	3557.2	2688.8	3849.4	3971.1	2462.0	3972.3	2661.0
2133.9	7011.7	7505.3	8129.2	8653.3	6326.7	9511.3	7059.9	9138.0	4094.8	6846.4
52.1	68.1	65.4	51.3	32.7	83.1	176.3	45.8	32.1	25.5	31.4
94.6	1803.1	1846.1	2342.6	1197.6	1812.2	1947.9	1675.7	537.8	484.7	1296.7
87.1	808.4	682.8	815.4	671.4	819.6	766.8	1052.8	243.8	88.2	633.6
99.4	2913.5	2987.1	3196.2	1316.5	3047.8	1985.1	3716.4	1528.6	865.3	2316.9
143.1	1187.2	1676.8	1481.2	934.0	1333.7	1195.5	1349.1	668.0	186.9	966.2
14692.0	6616.3	6591.4	7600.4	4426.2	6125.3	5619.1	6581.3	6984.8	6498.2	6028.0
983.6	5517.8	5288.5	5993.4	4469.8	5912.8	5799.8	5672.6	8751.9	5781.2	4588.4
419.9	3451.0	3977.4	4899.0	1739.7	3465.6	3000.0	4114.3	2625.8	1801.3	3204.7
4733.6	5065.6	4026.6	5010.1	4557.4	4854.3	4140.9	5355.8	3770.7	2430.8	3445.4
39.5	110.2	208.0	250.1	128.1	172.3	123.2	277.6	69.4	99.0	96.0
396.8	3618.3	4212.9	4780.1	3000.1	3030.1	1979.2	3082.6	3009.2	3232.4	2858.0
51.4	169.6	242.3	421.9	211.0	149.0	153.3	392.1	68.0	58.2	119.1
12519.8	8497.7	8893.9	10474.1	8570.2	8415.4	9867.1	8462.5	11003.0	7797.2	11330.2
77.8	1667.9	2389.9	2938.0	933.1	1515.4	1209.1	2108.0	1146.1	928.8	1479.7
40.9	236.3	277.9	457.7	454.8	186.5	249.4	149.7	53.8	28.1	115.0
179.2	1227.0	2144.0	2611.4	1019.1	1096.8	915.4	1133.1	739.0	281.3	779.2
746.7	1180.6	1314.0	1716.6	1078.1	927.0	1954.6	1163.7	1374.9	524.7	1747.8
45.1	116.6	119.7	122.2	93.6	118.4	116.7	157.9	66.7	44.4	160.5
72.4	1104.2	1292.1	1248.1	1045.6	819.4	806.9	998.5	552.7	707.0	922.4
375.4	1928.7	2543.8	4182.3	1068.2	1625.6	1083.1	1729.6	444.8	1001.5	1386.6

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1496.8	2057.9	2245.9
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1254.6	1048.1	1625.8
9981.6	8695.9	8397.1
3607.4	4361.0	4496.5
7908.5	8827.0	7734.0
6150.1	7122.8	6998.6
4022.9	4722.4	6341.7
313.3	236.3	252.8
1822.0	2480.2	2553.8
29.0	26.7	17.6
1443.0	2001.8	4495.2
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872.3	542.2	301.4
5958.9	7788.7	6560.7
5978.6	6064.3	11349.2
228.8	148.8	213.5
2685.6	2642.6	3085.6
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73.0	63.3	36.1
2078.4	2060.5	2536.9
781.9	1452.7	7254.0
3946.4	2445.7	1698.3
1580.7	1349.9	1742.6
7633.6	7419.3	6255.1
5764.2	5921.5	7081.2
4989.9	3393.7	7355.2
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221.8	203.2	226.2
3837.5	3922.0	2528.5
230.5	352.8	334.5
8075.3	8818.4	8507.9
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EF603052.1 gg_id:232866 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF098294.1 gg_id:193974 mouse cecum clone SWPT14_aaa04c11 EF0982
EF100060.1 gg_id:190816 mouse cecum clone SWPT5_aaa04b05 EF1000
AY990250.1 gg_id:129831 mouse cecum clone C3_E23 AY9902
EF604853.1 gg_id:235135 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048
FJ879160.1 gg_id:460476 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
FJ880190.1 gg_id:447761 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU455049.1 gg_id:335280 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU4550
EU452048.1 gg_id:319794 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4520
EU474325.1 gg_id:290142 western lowland gorilla feces clone GORSD_aaa04b01 EU4743
EU344221.1 gg_id:276488 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3442
EU461555.1 gg_id:291173 black rhinoceros feces clone RH_aaj92d08 EU4615
EU454885.1 gg_id:308212 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4548
EU451421.1 gg_id:318052 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU4514
FJ674167.1 gg_id:518896 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6741
EF099942.1 gg_id:187037 mouse cecum clone SWPT5_aaa02e06 EF0999
DQ015647.1 gg_id:133444 mouse cecum clone M3_f04_3 DQ015
EU748033.1 gg_id:333767 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44d08 EU7480
EF603021.1 gg_id:232374 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF098597.1 gg_id:191252 mouse cecum clone SWPT16_aaa01h11 EF0985
EU843235.1 gg_id:324417 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8432
EF614890.1 gg_id:235223 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF604748.1 gg_id:228472 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EF096266.1 gg_id:192712 mouse cecum clone obob1_aaa03g06 EF0962
DQ809192.1 gg_id:182039 human fecal clone RL308_aal83b07 DQ809
EF400350.1 gg_id:211699 human fecal clone SJTU_E_11_94 EF4003
FJ880902.1 gg_id:439512 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8809
EF096823.1 gg_id:186342 mouse cecum clone SWPT13_aaa01c04 EF0968
EU452288.1 gg_id:355245 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4522
EU505008.1 gg_id:272333 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01e09 EU5050
EU510319.1 gg_id:259347 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak04f07 EU5103
FJ880449.1 gg_id:379255 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8804
EF603912.1 gg_id:228791 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EU622716.1 gg_id:278265 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6227
EF603985.1 gg_id:233000 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6039
EU474208.1 gg_id:288634 western lowland gorilla feces clone GORSD_aaa01a08 EU4742
EF603044.1 gg_id:227767 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
AF371911.1 gg_id:45604 swine intestine clone p-2445-18B5 AF3719
EU456979.1 gg_id:314956 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU4569
DQ014909.1 gg_id:130514 mouse cecum clone M1_1c08 DQ014
EF604467.1 gg_id:231927 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044

253.1	2901.3	2606.9	3034.4	2361.9	2433.8	2550.3	2557.5	2769.8	1757.3	3320.9
40.5	94.4	174.2	222.1	26.3	45.7	50.3	215.4	31.0	15.1	38.7
104.8	1375.8	1216.4	1520.8	846.5	1145.0	771.5	1063.2	2010.1	1676.7	758.9
60.8	3301.7	3155.4	3439.6	2633.7	3913.8	2852.9	3189.2	4164.8	3189.4	2941.5
33.0	1101.6	1366.4	1462.2	681.7	948.4	696.3	1117.2	1523.3	322.4	936.3
46.6	1140.4	1693.8	2781.6	220.5	306.8	317.7	919.7	312.0	49.1	273.8
172.5	457.8	751.4	1100.7	483.4	429.5	519.6	642.7	291.0	134.6	358.0
33.8	1139.9	1690.5	2393.7	541.9	1341.4	1330.6	1854.9	617.8	339.5	2644.3
33.5	2771.4	2308.0	2777.3	647.0	1445.5	722.3	2523.5	934.0	4403.9	1770.4
34.9	713.6	763.3	1187.6	105.8	247.0	118.6	489.6	70.5	39.4	117.7
2910.2	5951.7	6075.8	7272.1	4950.4	5081.4	5375.0	5225.3	6395.6	2590.3	4423.6
1124.8	3932.8	4166.0	4870.8	4203.2	4094.7	4968.0	3666.6	4689.3	2707.6	3681.5
4470.9	3329.5	3622.5	4591.2	3035.3	4196.6	3232.3	3487.3	2800.2	2565.3	3268.8
57.3	403.9	320.6	422.9	332.6	464.8	207.1	394.3	521.0	339.2	279.9
100.3	1399.1	1567.6	1925.9	715.2	568.4	816.7	983.0	520.1	242.5	607.4
1300.5	3009.8	3431.7	3589.7	2846.5	2881.3	2887.6	3329.1	3326.9	5012.0	3190.2
221.5	1072.3	1188.2	1389.6	1698.7	932.2	1669.5	1342.9	557.3	279.6	759.3
1052.4	8219.9	8617.8	9158.9	7592.5	8974.8	8827.9	8279.1	12287.1	6012.5	10159.7
256.1	3158.7	3962.9	4851.9	4231.8	4348.0	4456.3	3571.9	3472.7	1338.0	2479.3
56.2	113.0	258.6	438.5	56.4	51.9	42.2	110.8	55.2	82.2	79.2
1725.1	5222.3	5779.9	6547.1	5862.5	5273.5	6698.7	6115.3	7450.3	3167.0	6998.0
191.9	1633.7	2075.7	2154.5	2455.5	1630.6	2895.9	1528.4	1269.3	1741.0	1477.6
237.3	561.9	583.7	933.3	356.9	330.8	453.2	412.0	290.0	303.5	322.3
61.3	135.1	120.2	146.3	73.1	131.2	108.9	114.7	85.5	49.6	92.3
580.3	1018.9	755.2	847.5	888.4	1053.1	850.2	844.2	812.8	417.1	895.1
36.4	15.5	13.6	13.0	14.7	11.8	10.5	14.8	15.2	19.5	11.5
119.7	3618.9	3905.0	5230.4	2225.6	2521.9	1080.3	3239.6	2099.8	736.9	2701.7
28.7	30.4	39.0	45.3	24.3	19.8	37.5	25.9	21.3	15.8	26.6
212.9	444.8	82.0	85.0	547.6	420.0	35.3	483.3	439.8	494.1	107.0
45.1	41.5	35.6	63.2	31.6	15.5	28.2	32.1	30.2	21.2	21.3
84.5	353.9	456.6	876.1	246.7	258.2	40.2	987.9	154.8	34.1	584.5
36.3	121.4	157.3	211.6	159.7	64.8	191.2	87.6	31.7	30.9	37.2
105.1	727.1	1206.5	1518.0	1141.1	1026.0	1009.0	1570.1	584.7	203.5	777.3
481.4	1908.0	2580.1	4135.4	988.7	1023.4	787.6	2287.5	537.2	623.9	987.7
143.3	181.0	199.5	198.5	188.8	182.5	173.5	100.6	117.7	175.2	60.9
349.2	6444.3	5967.3	7561.2	5576.9	5211.5	5798.5	5750.9	4818.2	2322.9	5757.4
2501.3	2803.7	2274.3	2920.1	2308.1	2263.6	2172.1	2464.6	1502.4	1283.2	1631.9
111.7	4836.9	4444.9	5346.4	4772.3	4412.7	5231.6	3753.7	3742.0	3245.9	3745.5
387.4	3499.6	2812.7	3334.1	2848.1	3009.5	6357.4	3335.8	3953.4	4404.3	3917.9
402.3	1300.1	1743.5	1856.8	993.7	1320.4	1263.0	1566.9	521.3	301.5	1147.0
310.4	2535.7	2628.0	3580.2	2286.9	2871.3	2709.6	2424.7	3635.5	2818.0	2713.3

2473.2	2548.3	2742.3
78.1	122.1	22.7
1057.2	1254.4	392.3
2889.2	3272.6	2289.4
889.9	693.4	349.9
1031.7	1151.7	258.1
394.8	641.7	894.3
1135.7	1070.8	1756.5
2331.4	1331.9	1449.3
357.9	564.2	312.0
5601.7	5678.5	4810.3
3581.6	4763.3	4222.5
4057.9	3308.0	3468.5
301.2	572.3	286.1
1225.0	1332.7	898.8
3135.9	3704.4	2851.8
876.9	1695.1	1039.1
7282.2	8344.9	8464.1
3408.2	4107.6	3003.6
148.7	175.8	40.6
5506.3	6149.7	6624.5
1178.8	1370.1	1935.0
469.3	724.0	293.8
81.4	184.0	188.1
912.6	1404.6	575.1
14.0	16.8	16.9
3273.7	3526.5	2614.6
28.8	39.5	21.2
481.9	609.8	101.3
28.5	30.2	24.2
396.5	476.1	237.0
72.2	105.0	150.9
1197.2	977.7	1102.4
2413.9	2278.7	991.6
123.6	458.6	201.1
5724.6	5717.5	3607.1
2516.6	2591.7	2640.8
3082.2	5249.6	4226.1
3546.8	3122.4	3054.3
1661.2	1820.1	1949.2
2249.5	2963.4	2859.5

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EU743928.1 gg_id:325933 Mouse fecal microbiota feces clone 3B6 EU743
FJ879269.1 gg_id:416233 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8792
EU656018.1 gg_id:282023 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
EF097726.1 gg_id:189531 mouse cecum clone SWPT20_aaa02g09 EF0977
EU474718.1 gg_id:300665 takin feces clone TAK_aaa03g01.Contig2 EU474
EF099096.1 gg_id:174741 mouse cecum clone SWPT2_aaa02b08.Contig2 EF0990
EU504956.1 gg_id:259835 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04g08 EU504
EF099937.1 gg_id:178306 mouse cecum clone SWPT5_aaa02e01 EF0999
FJ879522.1 gg_id:402704 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8795
EF097748.1 gg_id:184865 mouse cecum clone SWPT20_aaa03b05 EF0977
EU622752.1 gg_id:279579 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU765785.1 gg_id:309629 Pervasive effects antibiotic on human gut microbiota deep sequencing fecal clone B4 EU765
EF603581.1 gg_id:229522 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6035
FJ673460.1 gg_id:516479 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6734
EF100007.1 gg_id:191621 mouse cecum clone SWPT5_aaa03d12 EF1000
EU510274.1 gg_id:264605 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak03h10 EU510
EU504962.1 gg_id:267331 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04h04 EU504
EF097884.1 gg_id:193106 mouse cecum clone SWPT12_aaa01c08 EF0978
EF603896.1 gg_id:231210 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
EU458061.1 gg_id:321671 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79 EU458
EU504777.1 gg_id:276032 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02a05 EU504
FJ880859.1 gg_id:420373 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8808
EU622655.1 gg_id:278105 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF097203.1 gg_id:192034 mouse cecum clone SWPT18_aaa03b01 EF0972
EU463064.1 gg_id:291639 naked mole-rat feces clone molerat_aai69c07 EU463
EF097265.1 gg_id:195543 mouse cecum clone SWPT18_aaa04a12 EF0972
EU464141.1 gg_id:288655 reticulated giraffe feces clone gir_aah94g07 EU464
EU843556.1 gg_id:341053 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF096036.1 gg_id:182345 mouse cecum clone lean2_aaa02e05 EF0960
FJ880763.1 gg_id:387968 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8807
EU504616.1 gg_id:266075 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa03c07 EU504
EU459736.1 gg_id:298057 ring-tailed lemur feces clone RT_aai11h09 EU459
EF099380.1 gg_id:189985 mouse cecum clone SWPT3_aaa02e04 EF0993
DQ014612.1 gg_id:131899 mouse cecum clone M1_f05 DQ014
EF614858.1 gg_id:228861 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF6148
EF604593.1 gg_id:230920 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EF097497.1 gg_id:187537 mouse cecum clone SWPT19_aaa03e02 EF0974
EU457205.1 gg_id:307427 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77 EU457
EU504683.1 gg_id:264752 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04e01 EU504
FJ880214.1 gg_id:424255 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8802
EF603737.1 gg_id:233584 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037

79.5	2343.2	2997.8	4474.0	824.6	1523.9	1693.4	2640.3	840.4	315.4	2436.5
1060.2	6133.5	6526.7	7145.4	5720.6	5435.1	7501.5	5612.3	4883.2	4731.4	6740.8
40.1	735.0	836.6	1325.5	365.3	459.1	517.4	620.3	181.4	69.6	331.6
86.0	287.5	659.8	1030.1	113.3	91.9	161.7	412.3	41.0	17.9	104.7
54.6	315.2	320.1	431.8	85.7	74.8	86.1	217.2	56.7	29.2	62.2
66.1	1071.6	1775.4	1732.0	1046.7	754.0	1348.6	1537.9	972.0	531.6	2184.5
448.4	3929.7	4504.5	5077.6	5418.0	4486.0	4655.6	4427.7	5866.1	4035.3	5052.1
54.5	38.6	35.4	41.6	42.3	26.5	26.0	33.1	34.7	18.8	27.2
167.6	3875.6	4644.9	5441.6	3761.6	4157.3	3697.4	4287.2	2882.7	3496.6	2806.8
54.6	60.7	69.1	87.5	62.6	45.9	46.6	54.5	26.7	13.6	49.3
232.0	276.4	140.6	516.6	174.0	194.8	147.8	211.3	90.7	56.2	151.8
70.8	2149.1	1766.7	2147.2	1009.8	1688.7	1526.9	1819.5	2778.7	1735.1	2227.1
1041.0	1504.5	1365.9	1243.2	1079.8	1537.3	1312.7	1377.1	2245.2	2518.3	1464.6
37.7	793.8	680.7	1272.7	273.8	529.6	372.4	725.0	556.1	140.1	220.1
30.2	19.7	20.0	19.3	25.3	19.2	25.6	17.1	16.8	22.4	19.9
81.6	607.8	680.0	1075.1	120.0	128.3	136.5	335.5	42.5	45.4	115.0
85.7	1364.0	1121.5	1258.4	352.9	1125.8	1822.3	1912.6	1524.3	1153.5	3208.8
34.6	28.0	27.6	26.6	31.6	30.8	28.1	34.1	22.5	20.2	37.3
2084.6	2787.9	2957.2	3221.6	1113.2	1326.2	1319.8	1981.6	2119.5	1505.5	1700.6
373.3	2204.9	2439.8	2633.3	956.8	2043.2	1521.5	3165.7	1019.8	536.8	3658.1
185.0	1306.1	1963.1	1863.6	993.8	1867.1	1686.1	1609.9	638.6	3317.9	1052.0
93.9	733.7	1262.0	1901.8	434.5	682.3	617.6	813.8	230.0	276.4	343.3
289.4	1264.2	1560.5	2082.9	1373.9	1068.8	2157.2	1850.1	1313.6	1070.6	766.3
191.1	898.4	1364.7	1971.7	596.6	795.4	953.0	1360.3	850.2	579.2	1158.7
115.1	1790.0	2528.9	3123.6	1780.5	1893.9	1998.0	3426.7	1448.4	1040.2	2931.9
51.6	3609.1	4445.8	5925.9	1300.6	1888.1	1683.2	2944.9	1692.3	1832.6	2092.6
495.5	7957.9	7723.7	7852.2	7692.0	8957.3	9508.8	6521.8	6491.1	5721.2	7004.6
459.1	5016.4	5897.5	6782.0	2955.8	4416.2	4104.7	4827.4	4224.9	2291.3	4244.6
89.5	1187.5	1163.8	1829.1	951.8	1073.9	1332.8	1195.7	1179.9	724.3	899.9
365.8	3881.6	4619.9	6645.7	1942.2	2197.5	2505.1	3813.6	1599.8	2520.4	2439.8
63.2	60.8	62.7	64.2	38.6	21.2	25.0	27.6	24.6	25.3	25.2
1138.6	2952.6	3535.7	3636.7	2411.4	2556.3	3224.2	2627.9	3180.3	1511.6	1798.0
485.3	4540.7	5514.1	5805.9	5247.9	5500.9	5495.1	4903.7	9098.9	5362.8	3961.5
67.1	211.9	402.3	427.2	103.3	75.9	94.8	327.0	61.1	44.4	93.5
32.4	153.1	323.7	560.3	27.0	21.8	27.2	119.6	26.2	29.3	61.3
3430.3	3340.1	3326.0	4444.1	2037.8	2333.7	2572.9	3323.1	2976.2	2325.8	3103.8
296.7	9269.0	6893.8	7357.0	7612.8	7474.0	8198.0	7070.3	12686.9	8403.4	7892.0
68.5	2563.1	2634.7	4366.2	1344.5	1473.2	1167.2	2631.9	2159.7	1433.0	2158.7
137.1	1445.8	1527.3	2383.3	588.8	513.0	1222.8	1214.6	284.1	292.6	515.8
41.8	1842.1	2518.6	4105.1	674.3	647.2	930.9	1581.3	385.8	338.3	677.5
37.9	90.5	99.1	163.9	25.3	13.3	16.6	127.0	27.8	16.1	29.0

2628.1	1938.2	3081.9
5415.0	5724.4	5348.5
558.2	552.2	629.4
346.3	401.1	135.5
180.3	225.9	103.2
1372.5	1608.6	1818.6
4954.6	5296.7	6046.1
26.8	43.9	28.5
4925.6	4219.8	4149.1
50.1	79.6	56.7
233.6	310.3	432.7
1896.7	1704.5	988.6
1348.6	1723.4	1729.6
487.0	666.5	253.7
23.2	26.6	24.4
325.9	445.5	253.7
1665.3	1962.9	1178.1
146.7	44.3	81.2
2345.9	2500.2	1064.5
2814.8	1726.8	1741.3
1791.6	2055.8	2010.7
771.7	888.1	601.1
1010.8	1071.9	500.8
1085.1	1564.7	1382.8
2762.8	2997.3	2421.3
3211.0	3821.6	2103.1
7328.1	6179.1	7535.8
5541.2	4538.1	3888.5
1712.2	1091.3	1913.9
4264.1	3543.1	2432.8
41.5	42.0	25.8
2952.7	3104.5	2310.2
4388.1	5046.7	4021.1
249.1	278.8	114.9
180.0	133.7	33.0
3097.9	3295.9	2215.3
6090.9	8201.4	6858.0
2185.1	2381.9	871.8
1103.0	938.5	564.4
1789.0	1590.0	605.7
43.6	65.8	19.6

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EU454778.1 gg_id:344046 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU454
AY993146.1 gg_id:133160 mouse cecum clone C21_g03 AY993
EU453593.1 gg_id:339017 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU453
EF605028.1 gg_id:234539 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF605
EF096010.1 gg_id:179716 mouse cecum clone lean2_aaa01h07 EF096
EU455009.1 gg_id:325057 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU455
EU381853.1 gg_id:262581 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU622648.1 gg_id:278171 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF603749.1 gg_id:230641 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EF603903.1 gg_id:233923 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF603
EF097895.1 gg_id:196913 mouse cecum clone SWPT12_aaa01e08 EF097
EU777326.1 gg_id:326627 Okapi feces clone OK1_f07_1 EU777
EU655810.1 gg_id:284926 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU748090.1 gg_id:333975 neotropical folivorous flying bird adult hoatzin crop clone hoa2_41a07 EU748
DQ014853.1 gg_id:132181 mouse cecum clone M1_e03_3 DQ014
EU510694.1 gg_id:269241 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak39e04 EU510
FJ879490.1 gg_id:453275 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ879
EF096626.1 gg_id:177452 mouse cecum clone SWPT11_aaa02b12 EF096
EU748352.1 gg_id:310634 neotropical folivorous flying bird adult hoatzin crop clone hoa5_07d02 EU748
EF604769.1 gg_id:228242 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF604
EU504951.1 gg_id:277259 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04f11 EU504
EU467659.1 gg_id:300634 naked mole-rat feces clone molerat_2c03_2 EU467
EU655851.1 gg_id:284911 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EU455289.1 gg_id:326297 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU455
EU471874.1 gg_id:293854 Asiatic elephant feces clone AE3_aaa04c09 EU471
GQ492835.1 gg_id:552779 Effect Diet on Human Gut Microbiome: Metagenomic Humanized Gnotobiotic Mice GQ492
EF099271.1 gg_id:176215 mouse cecum clone SWPT2_aaa04h04 EF099
AY993118.1 gg_id:132569 mouse cecum clone C21_e21 AY993
EF099246.1 gg_id:185948 mouse cecum clone SWPT2_aaa04e07 EF099
EF097178.1 gg_id:180387 mouse cecum clone SWPT18_aaa02e07 EF097
AY993254.1 gg_id:132331 mouse cecum clone C21_l04 AY993
EU453748.1 gg_id:305789 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU453
EF604468.1 gg_id:229055 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF604
EF614680.1 gg_id:234291 Obesity alters gut microbial ecology cecum mother 1 mouse offspring genotype ob/o EF614
EF096743.1 gg_id:179168 mouse cecum clone SWPT11_aaa04a05 EF096
EU505586.1 gg_id:263664 cecal contents Mus musculus strain C57BL/6J; myd5 clone myd5_aaa03b02 EU505
FJ684583.1 gg_id:517722 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ684
EF406717.1 gg_id:204158 mouse colon clone infected_14days-B10 EF406
EU463180.1 gg_id:290181 naked mole-rat feces clone molerat_aai71c03 EU463
EF096320.1 gg_id:188845 mouse cecum clone obob1_aaa04h02 EF096
EU461002.1 gg_id:288628 red kangaroo feces clone KO1_aai42a08 EU461

22282.5	9094.5	9820.6	11734.8	10227.3	8767.9	10777.5	8861.8	12788.9	11771.4	12711.9
45.1	29.9	56.8	78.6	22.8	17.7	18.6	24.2	17.7	13.8	22.9
75.7	2763.2	2485.8	2377.7	1923.5	2699.2	1841.7	2441.5	3080.5	2326.5	1868.7
170.5	1289.5	1121.9	1322.5	681.4	1121.8	1055.5	732.9	1115.7	812.8	1388.2
634.8	1005.3	1224.7	1551.1	1023.3	970.3	1305.4	1436.1	584.2	618.7	1041.4
387.6	6199.3	6961.0	7601.3	5635.9	5796.6	6054.7	6794.8	7343.3	6944.2	7032.3
836.4	3761.6	4263.0	5254.7	3888.4	4444.2	4057.0	3430.0	5639.2	1935.7	3801.8
43.9	101.3	154.0	198.5	38.8	31.3	31.2	113.3	33.1	59.2	41.4
104.3	5774.1	5114.2	6612.5	3941.0	2739.4	3320.0	5636.6	5733.9	5388.8	3621.5
164.1	3339.1	3127.4	4491.5	813.4	3251.0	1960.8	3140.3	1403.8	520.2	3575.9
518.3	1898.9	2546.9	2749.5	1555.5	2093.0	2008.2	1958.1	1402.1	2057.2	2194.1
1222.2	4630.8	5153.8	6910.7	3925.4	3628.7	4549.9	4431.3	3181.1	3459.4	4622.0
62.4	1299.8	1559.2	1851.1	1024.4	1529.5	1476.4	1857.1	640.2	787.4	1676.2
107.9	3276.7	4783.8	6252.7	2155.9	3246.3	3317.7	4429.4	2337.1	1117.0	3366.6
48.8	1321.2	1605.6	1346.9	885.9	1062.8	1141.6	1295.7	1771.0	1197.4	784.5
122.2	1799.8	1949.9	2579.9	1827.7	1734.9	2040.8	2435.1	1633.8	794.1	1335.0
2573.4	5453.7	5362.8	7171.8	3665.3	4349.3	4530.8	5639.6	2536.3	2047.2	5038.9
76.6	136.8	267.2	372.2	159.7	85.1	169.2	246.3	67.6	80.2	123.2
282.1	4784.6	5701.1	6894.1	3841.7	4820.0	6086.9	5999.4	3358.0	3312.5	5926.5
6817.6	5705.3	5275.0	5827.7	5084.5	6018.1	6305.7	5271.1	9467.3	5492.3	6831.6
43.6	243.8	377.2	380.4	180.5	142.8	216.5	156.4	70.3	141.0	242.2
95.9	3882.2	3422.6	4171.3	2697.8	3346.2	2801.3	2740.8	5232.0	1539.2	2622.6
44.4	2258.3	2635.0	3008.3	3395.5	2303.3	3212.3	2253.3	1700.3	1007.4	2019.6
42.4	924.1	1174.4	1427.9	1338.7	1054.0	1438.3	1402.2	425.1	364.1	702.2
1989.3	7131.1	7778.9	8294.9	6832.9	6846.6	8807.5	7431.2	7211.3	5233.1	7445.0
27.7	33.4	47.9	35.6	43.5	32.0	103.4	19.0	44.0	17.5	32.8
174.5	2648.0	3153.6	4066.9	2442.0	2361.9	3315.6	2865.8	1920.5	1123.8	3937.8
81.5	1592.0	3155.2	3396.4	1698.0	1360.5	3150.2	2198.4	1347.0	390.9	1652.9
45.8	36.8	28.5	38.3	30.1	18.8	32.4	24.7	13.8	15.7	18.9
15721.3	6918.4	6538.6	6469.8	6517.3	7381.0	8322.2	6891.5	12376.5	9258.7	7491.0
13453.3	8645.0	7858.0	8146.6	8486.7	7846.0	9089.1	7181.6	13709.5	10789.0	9397.3
43.2	995.9	1276.2	1885.0	251.6	376.0	439.1	667.4	460.1	247.9	381.0
136.0	489.2	534.3	416.8	422.8	397.4	636.0	479.6	510.8	395.5	399.2
663.7	3282.5	3066.9	2730.8	2674.3	3799.6	2201.8	3422.1	6429.1	3763.0	2620.5
1506.3	1011.8	1180.0	1647.3	839.9	861.3	609.7	2078.0	728.9	326.8	856.2
1516.1	1941.0	1820.1	2210.7	2089.2	1772.1	4352.0	2175.1	2819.9	1454.3	2350.5
493.7	5911.0	5222.9	6522.5	3609.4	5668.6	3398.8	6283.2	6708.5	3672.3	5512.5
124.6	1637.3	1852.0	2929.1	1344.3	1125.9	1137.1	1724.9	963.2	673.1	750.2
3061.6	4776.4	5039.4	6648.8	3900.5	4321.9	4993.5	4643.7	5069.3	3375.6	4160.3
31.2	284.9	462.2	570.0	87.8	103.1	241.0	396.3	85.0	29.5	320.0
1307.4	3577.4	3983.8	4814.0	4059.6	3731.6	5540.0	4830.1	2455.8	4110.4	3823.7

8673.4	9177.1	9884.5
37.7	70.3	26.5
2226.4	1753.5	1128.4
609.2	692.2	602.5
1084.2	1645.4	1468.4
6038.4	5465.9	5003.8
3625.3	4803.9	4037.9
133.6	118.2	30.4
5231.2	3772.7	2190.7
2629.4	1884.6	2497.5
2038.6	1076.3	1862.6
4532.8	5074.7	3952.8
1953.1	1872.4	1712.3
3686.8	3562.5	4481.7
1245.9	2229.1	480.4
2005.8	3203.7	2206.1
5013.0	4724.9	4461.7
218.5	294.7	184.2
5533.9	5458.6	4561.1
4867.5	6764.2	6553.3
203.1	239.9	145.7
2554.5	2825.1	3235.9
1990.0	2431.5	2628.8
955.1	1066.8	1561.5
7694.3	7167.3	7887.0
26.2	50.3	29.2
2933.4	2732.4	4502.3
1464.4	1713.8	1258.2
24.6	36.1	27.9
5732.6	7060.5	8571.7
7124.7	8363.7	6905.9
911.9	940.8	269.6
379.2	649.7	462.7
2884.8	3340.4	1493.8
935.1	2161.1	1400.8
2323.7	2870.7	1981.6
3855.3	4111.5	3496.4
2119.2	1711.2	861.7
4059.9	4923.1	4301.6
179.8	206.3	87.9
3077.3	5145.7	4774.0

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EU456212.1 gg_id:327235 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU456
EU510723.1 gg_id:261177 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40a08 EU510
EF096578.1 gg_id:193790 mouse cecum clone SWPT11_aaa01d03 EF0965
EU504735.1 gg_id:260998 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa01c10 EU504
EU455272.1 gg_id:325298 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU455
EU777255.1 gg_id:316469 Okapi feces clone OK1_h10_1 EU777
EF097583.1 gg_id:177900 mouse cecum clone SWPT19_aaa04g02 EF0975
EF097303.1 gg_id:194893 mouse cecum clone SWPT18_aaa04g05 EF0973
EU507656.1 gg_id:270583 cecal contents Mus musculus strain C57BL/6J; MD23 clone MD23_aaa02f06 EU507
EF096992.1 gg_id:182524 mouse cecum clone SWPT13_aaa03h01 EF0969
DQ015383.1 gg_id:129623 mouse cecum clone M3_d10 DQ015
EU508829.1 gg_id:272700 cecal contents Mus musculus strain C57BL/6J; MD4 clone MD4_aap51g10 EU508
AM265434.1 gg_id:160942 Oligonucleotide Probes intestinal flora BB-DP rat colon clone ratAN010102C AM265
EU776378.1 gg_id:328822 Red Kangaroo feces clone KO2_aai18b04 EU776
EU844667.1 gg_id:336446 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU844
FJ879438.1 gg_id:377036 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
EF406804.1 gg_id:205553 mouse colon clone infected_28days-B10 EF4068
EF406606.1 gg_id:204111 mouse colon clone control_28days-H1 EF4066
EF604589.1 gg_id:233662 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6045
EU344268.1 gg_id:269168 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
FJ172865.1 gg_id:355949 Qinghai Yak Ruminal and Fungi China rumen clone RB-5H11 FJ1728
EU655724.1 gg_id:283486 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
EF406445.1 gg_id:209552 mouse colon clone control_7days-H4 EF4064
EF603601.1 gg_id:234512 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6036
AY993115.1 gg_id:135674 mouse cecum clone C21_e18 AY9931
AY991908.1 gg_id:134681 mouse cecum clone C20_k09 AY9919
EF100118.1 gg_id:181786 mouse cecum clone SWPT5_aaa04h11 EF1001
EU504837.1 gg_id:274905 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa03a06 EU5048
EF098594.1 gg_id:191158 mouse cecum clone SWPT16_aaa01h07 EF0985
EF099203.1 gg_id:182945 mouse cecum clone SWPT2_aaa03g11 EF0992
FJ671760.1 gg_id:517293 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
EU450961.1 gg_id:329268 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU4509
EU467621.1 gg_id:289406 naked mole-rat feces clone molerat_2a08 EU4676
EF097867.1 gg_id:176637 mouse cecum clone SWPT12_aaa01a07 EF0978
AF153865.1 gg_id:1960 faecal clone adhufec77.25 AF1538
EU468452.1 gg_id:298560 black rhinoceros feces clone RH_aad13e05 EU4684
EF096969.1 gg_id:193510 mouse cecum clone SWPT13_aaa03e05 EF0969
EU465575.1 gg_id:292867 argali sheep feces clone AS1_aao38c06.Contig1 EU4655
EU655727.1 gg_id:287113 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU655
FJ879109.1 gg_id:396796 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8791
EU622642.1 gg_id:279248 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU6226

47.1	2534.2	2748.4	3502.2	2235.8	2221.6	2202.8	2287.0	3330.9	1739.1	1745.9
50.3	510.3	926.1	1544.9	48.8	55.7	69.4	336.1	42.5	26.2	78.7
4908.7	3418.9	3431.4	4311.8	2311.2	2905.7	3921.1	2944.0	4221.0	3012.3	3475.5
1596.4	3645.8	2991.6	3789.0	2471.3	2152.2	2488.3	1808.5	3806.8	2816.3	2473.4
535.3	1618.5	2008.4	2121.9	1679.3	1522.2	3913.4	1618.0	3276.4	798.5	1714.8
859.0	7448.4	8986.8	9659.9	11301.9	7142.9	12248.0	7928.7	8528.7	5838.6	8077.7
99.2	892.0	1115.7	1847.2	689.8	738.6	757.7	1115.5	761.9	672.4	920.2
83.1	197.4	399.6	441.1	214.6	218.4	239.1	585.5	82.4	86.8	552.4
73.2	1411.1	2277.4	2627.0	1929.1	2011.3	2025.3	2082.2	717.5	274.8	1683.4
76.9	638.0	687.4	944.3	389.7	574.5	550.8	801.0	407.1	857.4	648.1
104.2	1922.2	1887.5	1942.6	1678.1	1889.4	2134.1	1891.1	2083.3	1810.8	1757.2
103.9	245.3	371.8	438.2	83.6	145.0	159.2	274.9	130.9	62.4	137.9
61.3	56.2	85.8	87.4	73.1	63.6	75.2	52.3	49.9	55.8	71.3
660.5	4799.3	5956.8	6543.0	4405.4	5204.4	8054.4	6173.2	5227.1	4561.8	8428.6
83.4	5687.5	3748.7	4323.0	2284.4	4443.8	3078.7	3936.9	4666.4	2282.0	3616.2
592.7	1240.9	1523.9	1623.6	1027.1	1491.8	1236.4	1472.2	913.9	451.4	1000.7
36.3	167.9	353.3	563.7	26.9	70.2	164.6	217.5	27.5	16.7	57.2
34.4	202.8	277.0	475.9	83.3	33.4	113.4	174.5	27.5	28.3	65.6
6413.1	2611.6	2823.8	2650.8	1777.1	2475.6	2921.7	3021.9	3099.6	2050.7	2986.4
2933.3	10028.6	9358.0	12143.7	6884.2	8987.1	8614.4	9261.1	7530.1	7387.7	11070.2
709.9	5404.4	5123.5	6149.5	3916.2	5585.4	4787.8	4512.7	7295.5	2619.8	5431.3
62.3	1295.2	2013.5	2913.7	697.7	1095.8	1185.0	1600.0	627.6	269.2	1158.2
130.3	1271.9	932.4	1305.0	1505.2	900.5	1154.0	1327.3	554.5	430.6	792.5
41.9	65.5	90.8	151.4	39.0	41.0	34.3	65.1	29.8	21.5	34.3
51.7	35.0	47.9	47.3	52.8	38.5	49.5	33.9	25.8	28.9	33.8
2346.9	4183.7	3595.5	3916.5	3015.4	3452.2	4738.3	4850.1	5262.8	3686.7	8325.9
1580.0	4001.3	3728.1	4326.8	4773.9	3638.8	4324.1	4375.6	4483.1	3638.1	4624.7
60.6	27.0	32.1	48.7	24.6	25.5	32.8	31.7	31.8	17.2	52.4
1754.9	3388.6	3716.4	4860.0	3381.3	3004.1	3754.1	3237.0	3292.2	2740.5	3502.6
29.6	696.1	1278.0	1678.4	57.1	42.0	91.5	597.2	50.8	41.5	240.7
46.5	347.1	718.3	1189.8	184.7	207.3	159.8	578.4	127.3	36.5	300.5
697.9	5573.6	4573.2	4717.2	4435.1	4961.7	8466.9	4674.3	8550.4	6071.5	5956.2
155.8	4457.5	4539.7	5825.9	2785.5	4391.2	2707.0	4284.4	4705.6	2708.6	3685.9
109.2	1083.8	1085.7	1536.6	1328.7	1239.4	1884.4	1648.7	596.3	772.2	834.9
2242.6	2949.2	2675.1	2222.3	2427.3	2746.1	2528.3	2433.1	3809.0	2224.1	2517.0
1087.2	3722.2	3877.7	4098.8	3822.4	3888.6	4314.2	3287.1	5460.6	3829.4	3933.0
19.7	70.0	134.1	161.7	42.1	38.5	41.4	46.8	55.9	21.5	39.5
653.2	4285.8	4385.0	6316.9	1302.5	2921.1	1996.2	3634.5	1276.7	1044.8	2431.1
61.0	1818.9	2515.4	3294.8	952.8	1427.8	1827.8	2125.7	1244.0	257.5	1725.5
155.2	2358.5	2653.3	3954.0	1837.1	2475.3	2071.2	2809.3	2418.7	798.7	2496.9
1872.2	3211.4	3408.2	4538.0	2699.4	2941.3	3602.7	3783.0	2082.9	2659.0	2872.9

2274.5	2999.7	2500.6
548.3	415.2	117.4
2966.8	3540.2	2217.3
2204.3	2289.8	1860.3
1361.3	2023.5	2433.0
6360.1	7458.5	7765.6
997.5	1288.7	598.2
506.5	462.0	300.5
1958.3	1972.8	1980.1
458.9	756.5	558.0
1569.3	1880.5	1080.4
262.8	565.1	197.3
52.5	81.7	86.3
3841.1	5192.0	5310.8
3330.3	2904.2	4038.5
1049.1	1574.8	986.7
76.9	204.2	113.5
162.3	244.7	67.5
1575.3	3491.2	3374.7
9266.5	7679.0	8773.5
4494.9	5066.4	4493.3
1201.6	1113.4	667.4
1181.0	959.0	1787.9
56.5	150.0	41.8
29.2	56.1	64.4
4844.4	5023.6	4026.9
3694.8	4926.8	4255.2
47.8	31.6	27.8
3234.3	3722.9	2754.7
666.2	545.2	75.1
498.2	455.9	357.0
4936.3	5003.4	4719.5
3352.5	3972.1	1458.1
1117.7	1968.9	2525.5
2272.0	2771.0	1769.3
3279.2	4494.8	3488.4
79.3	129.1	45.1
4714.7	3501.0	2658.4
1503.0	1458.5	1548.4
2827.6	3041.2	2318.6
4112.8	4074.7	3506.5

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DQ815337.1 gg_id:168732 mouse cecum clone aab45h10 DQ815
DQ815534.1 gg_id:167078 mouse cecum clone aab42d05 DQ815
EF100100.1 gg_id:189237 mouse cecum clone SWPT5_aaa04f10 EF1001
EU452919.1 gg_id:338076 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H77S EU452
EF099201.1 gg_id:192206 mouse cecum clone SWPT2_aaa03g08 EF0992
EU453409.1 gg_id:314284 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU453
DQ815707.1 gg_id:168880 mouse cecum clone aab21c02 DQ815
EF097001.1 gg_id:196067 mouse cecum clone SWPT13_aaa04a06 EF0970
EU469598.1 gg_id:302042 flying fox feces clone FF_e10 EU469
EU456444.1 gg_id:346997 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EF406463.1 gg_id:214715 mouse colon clone control_14days-B6 EF4064
EF096007.1 gg_id:197522 mouse cecum clone lean2_aaa01g12 EF0960
EF098272.1 gg_id:191723 mouse cecum clone SWPT14_aaa04a04 EF0982
EU504985.1 gg_id:263232 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa01b12 EU504
EU344438.1 gg_id:272858 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU510551.1 gg_id:274125 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak37a08 EU510
AF371913.1 gg_id:49015 swine intestine clone p-251-o5 AF371
DQ905202.1 gg_id:173773 human fecal clone 013-b11 DQ905
EU463693.1 gg_id:294182 domesticated horse feces clone horsej_aai91b06 EU463
EU451397.1 gg_id:344901 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU451
EU456545.1 gg_id:329371 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU456
DQ015199.1 gg_id:133109 mouse cecum clone M2_h12_2 DQ015
EU794078.1 gg_id:345791 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O4 EU794
EF603895.1 gg_id:228588 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6038
EF098910.1 gg_id:177453 mouse cecum clone SWPT1_aaa03b06 EF0989
EU510197.1 gg_id:259625 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02g09 EU510
EU771635.1 gg_id:351900 African elephant feces clone AFEL3_aao16g05 EU771
EU457393.1 gg_id:356389 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU457
EF099960.1 gg_id:180240 mouse cecum clone SWPT5_aaa02g11 EF0999
EF097016.1 gg_id:186680 mouse cecum clone SWPT13_aaa04c04 EF0970
EF604781.1 gg_id:228568 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6047
EF603098.1 gg_id:228267 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF406790.1 gg_id:214904 mouse colon clone infected_14days-H6 EF4067
EU510156.1 gg_id:264835 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak02b12 EU510
EU453039.1 gg_id:321735 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU453
AY239399.1 gg_id:97196 rat feces clone rc3-52 AY2393
EU510721.1 gg_id:265939 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak40a04 EU510
EF096055.1 gg_id:198382 mouse cecum clone lean2_aaa03a09 EF0960
EF097021.1 gg_id:192035 mouse cecum clone SWPT13_aaa04d01 EF0970
EU775301.1 gg_id:343616 Reticulated giraffe feces clone gir_aah96d03 EU775
EF098930.1 gg_id:190976 mouse cecum clone SWPT1_aaa03d08 EF0989

37.1	18.2	14.0	36.7	17.9	15.6	17.6	12.3	16.0	16.2	14.2
54.9	68.9	116.5	176.7	92.7	72.3	102.8	64.4	30.8	44.4	88.4
61.7	1841.1	1762.9	2240.9	1326.2	1267.8	1551.8	1277.8	2004.1	786.5	1026.9
291.5	3683.2	4482.2	4692.9	3494.9	3257.6	4503.8	4333.2	3544.3	3339.8	4717.5
33.9	261.8	375.8	794.5	186.2	786.5	137.9	345.6	140.7	262.1	207.4
50.1	14.9	14.5	16.3	15.0	12.4	12.2	15.5	15.2	20.3	16.7
68.1	843.1	1319.0	1650.7	378.4	823.0	914.4	1083.8	293.9	132.5	862.3
43.9	272.2	183.0	232.6	203.4	138.1	170.1	224.2	60.7	69.5	255.9
232.6	5144.6	4085.1	3095.7	3382.7	2901.4	4656.7	3155.7	4088.8	6002.8	3412.7
45.7	747.4	1188.2	1615.7	727.8	725.8	960.1	937.0	323.6	581.6	577.9
58.8	1567.8	2047.8	2501.6	805.2	1909.9	1137.5	2064.1	1945.6	853.2	1843.5
71.6	82.7	111.6	165.4	106.5	57.2	73.5	173.8	57.6	37.0	80.8
2487.6	6792.6	6115.7	7204.6	5834.1	6830.3	7262.4	6570.3	9871.4	9037.9	9013.3
82.2	3479.4	4203.9	5686.7	1763.8	2515.8	2818.3	3331.2	1759.6	1792.2	3433.4
314.3	4060.6	5407.1	5567.5	2938.0	5038.9	4432.7	5304.9	4091.8	1878.6	5871.1
53.2	54.4	84.8	136.2	48.4	40.7	46.5	59.3	33.5	31.9	49.2
55.4	152.8	190.4	237.7	158.3	164.4	184.8	344.5	64.2	62.2	156.3
34.3	219.7	281.1	430.5	65.5	58.4	48.5	104.0	24.3	24.4	48.2
7373.2	5260.6	5113.8	5513.1	5102.1	4689.5	5740.5	4714.0	6870.0	3673.0	5325.3
155.5	2198.8	2122.9	2394.5	1706.1	1721.6	2164.3	2034.5	2062.0	1551.5	1503.3
1133.1	2176.5	2499.2	2415.1	2568.4	2252.1	2910.1	2057.8	3222.3	1171.7	1846.0
36.4	212.4	178.0	198.5	139.9	200.7	121.3	228.7	124.7	84.9	50.9
89.6	2950.1	3455.1	4807.9	925.0	1701.8	1573.4	2452.6	692.2	678.3	1403.7
316.5	5590.1	5201.7	4984.2	4006.3	3303.6	5327.8	4054.4	7215.3	6481.6	4188.4
28.3	373.6	363.9	692.3	53.5	25.8	57.1	122.6	25.3	25.9	60.8
36.2	45.8	74.9	59.9	36.4	32.3	34.8	26.8	37.0	29.4	25.7
84.3	2598.7	3292.0	4527.6	1659.2	2059.4	2183.1	3453.3	1277.1	700.5	3915.0
595.7	980.2	937.7	1351.9	1251.4	719.7	905.9	862.8	611.2	473.9	838.6
181.8	1570.9	1864.3	2178.4	1355.9	1376.6	62.1	1496.2	1457.7	727.9	1568.6
60.7	172.9	465.5	845.1	140.9	89.8	85.1	288.0	44.1	29.9	114.5
196.3	3025.5	3339.8	3645.0	2652.2	3015.6	3543.8	4328.0	3189.5	2042.9	4405.9
65.9	2572.8	3635.2	4487.5	1227.4	1598.0	2249.2	3027.9	914.0	358.4	2299.8
42.4	587.2	758.5	1190.7	161.7	231.1	174.4	318.1	103.9	34.4	133.7
2979.9	5765.0	6241.4	6976.5	5429.4	5903.5	6835.0	5582.5	7169.1	5494.0	7983.2
626.2	4735.1	4153.9	5186.2	2892.2	4096.2	3331.6	4374.2	4398.7	2483.2	4256.8
46.4	381.5	628.2	1003.5	102.0	130.1	78.8	364.3	50.9	55.4	146.8
92.1	1073.9	1493.6	2009.0	218.5	250.7	220.2	704.6	109.2	91.2	278.6
39.1	22.3	22.7	38.2	30.6	19.7	23.5	20.9	20.1	18.0	20.7
41.0	321.9	353.3	636.3	181.1	185.2	161.2	314.2	79.8	49.3	224.3
2460.9	5096.3	5127.2	5778.9	3113.5	3673.4	6634.7	5107.1	2465.3	2513.6	6153.7
57.9	140.9	238.4	304.9	51.9	169.2	133.0	230.5	51.4	46.0	86.5

15.7	15.7	12.9
118.0	164.6	130.2
1189.2	1971.4	747.5
3954.2	3823.9	4438.5
551.4	381.6	537.5
17.1	14.4	15.4
769.7	1475.5	1477.8
176.3	257.9	239.7
2513.4	2752.9	3014.9
978.2	906.4	961.0
1634.6	1441.1	1491.9
104.0	223.4	245.5
6935.3	6339.0	6941.8
3558.4	2792.4	3093.8
4690.7	5216.3	7531.8
55.7	87.4	39.3
150.7	175.7	122.0
124.2	196.6	60.3
5130.0	5880.2	4978.9
1786.0	2382.1	1920.3
2198.8	2539.0	3084.9
167.8	179.9	124.4
3247.3	2632.8	1354.3
4049.8	4048.0	3170.9
234.6	195.8	37.1
35.0	40.4	32.2
2841.6	2355.2	1711.7
1022.4	1096.6	752.6
1469.6	1635.8	1612.2
229.1	435.3	153.1
2946.8	3780.2	7226.5
3110.9	2741.4	3036.4
475.6	773.9	1255.9
5215.3	6383.4	5641.1
3216.3	3306.7	2835.7
471.4	292.9	103.9
946.9	972.4	309.4
21.6	29.2	20.4
260.3	300.9	212.4
4187.9	4280.2	5641.4
194.0	179.7	73.7

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EF406462.1 gg_id:204003 mouse colon clone control_14days-B5 EF4064
EU381754.1 gg_id:262779 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EU455232.1 gg_id:311914 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU455
EU453264.1 gg_id:335050 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU453
EU510491.1 gg_id:263168 cecal contents Mus musculus strain C57BL/6J; WD4 clone WD4_aal39f05 EU510
EF096961.1 gg_id:175646 mouse cecum clone SWPT13_aaa03d04 EF0969
AY239412.1 gg_id:97151 rat feces clone rc2-4(2) AY2394
EU456177.1 gg_id:322237 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EU748162.1 gg_id:305473 neotropical folivorous flying bird adult hoatzin crop clone hoa33_63G08.F EU748
EU656086.1 gg_id:286179 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU656
FJ879486.1 gg_id:388276 Diets enriched oat or wheat bran temporally and alter fecal rat feces animal fed contr FJ8794
EU456228.1 gg_id:336363 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K77S EU456
EU452724.1 gg_id:342392 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU452
AY991887.1 gg_id:132083 mouse cecum clone C20_j11 AY9918
AY993727.1 gg_id:135206 mouse cecum clone C15_J03 AY9937
EU457424.1 gg_id:320200 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU457
AY239409.1 gg_id:95688 rat feces clone rc2-30(4) AY2394
EU774274.1 gg_id:323139 Chimpanzee feces clone CHIMP12_e05_3 EU774
DQ777906.1 gg_id:172976 rat feces clone R-1233 DQ777
EU622708.1 gg_id:278550 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF603253.1 gg_id:230919 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6032
EF096068.1 gg_id:198621 mouse cecum clone lean2_aaa03d04 EF0960
EF604564.1 gg_id:230346 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6045
EF099086.1 gg_id:174420 mouse cecum clone SWPT2_aaa02a08 EF0990
EU777229.1 gg_id:313410 Okapi feces clone OK2_c05_1 EU777
EU779037.1 gg_id:334720 Prevost's squirrel feces clone SQ_aah81f10 EU779
EF445234.1 gg_id:206507 dairy cow rumen clone NED4C7 EF4452
EU455879.1 gg_id:307731 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU455
EU474278.1 gg_id:294646 western lowland gorilla feces clone GORSD_aaa04g10 EU474
EU510141.1 gg_id:265808 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01h09 EU510
EF097720.1 gg_id:186508 mouse cecum clone SWPT20_aaa02g03 EF0977
EU457872.1 gg_id:327559 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H83N EU457
EU510115.1 gg_id:258247 cecal contents Mus musculus strain C57BL/6J; WD3 clone WD3_aak01e12 EU510
EF099277.1 gg_id:188940 mouse cecum clone SWPT3_aaa01a01 EF0992
EU451846.1 gg_id:343032 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU451
DQ015345.1 gg_id:135894 mouse cecum clone M2_1g02_1 DQ015
AY239469.1 gg_id:98087 Enterococcus sp. cL10-2b-4 AY2394
DQ014936.1 gg_id:135808 mouse cecum clone M1_1g10 DQ014
EF602765.1 gg_id:234140 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6027
EF604753.1 gg_id:231289 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6047
EF096360.1 gg_id:183770 mouse cecum clone obob2_aaa01e10 EF0963

476.6	1570.7	1648.8	1966.3	1334.4	1242.5	1323.6	1161.9	1524.0	762.0	1261.1
32.5	2808.5	3247.0	3762.3	2704.2	3646.1	2865.1	3225.3	3155.7	2626.5	2204.7
2925.5	9271.4	8165.2	8787.8	10389.1	8077.6	8718.8	7501.6	8719.4	7684.3	7950.1
3209.1	4294.1	3977.3	4810.0	4243.0	4118.4	4560.9	4248.8	4091.3	4566.8	6088.4
801.7	676.4	891.6	1067.8	532.3	623.1	1006.3	1122.1	595.6	508.1	1723.4
28.7	18.5	17.6	18.4	19.3	19.5	15.3	14.0	26.9	17.1	18.8
64.2	260.3	591.5	758.4	225.7	121.9	354.8	310.4	208.4	35.9	129.5
3646.0	3858.0	3746.9	4045.4	3258.1	3642.1	4020.4	4322.2	4931.1	5788.4	6847.5
309.6	5895.2	7246.4	8804.3	3775.7	6040.0	6606.1	6506.2	5586.0	2865.7	7145.5
236.2	760.2	1210.6	1875.6	528.6	568.7	468.5	977.9	176.6	262.6	403.1
3270.7	7022.9	7304.2	8888.8	6755.0	6874.3	8492.0	6891.1	7602.8	7585.9	10544.3
1078.7	7753.3	7282.3	7055.4	5857.1	6638.8	7403.9	6767.1	8202.7	6531.8	7477.8
38.0	333.9	645.5	978.9	120.0	229.0	239.1	407.1	78.4	45.8	168.5
5446.0	4097.3	4126.8	4508.4	3557.3	4279.7	3935.7	4993.0	6315.0	3989.9	4126.4
42.3	647.3	1299.3	2320.8	62.4	49.7	64.4	617.6	63.0	52.4	182.1
4750.5	2292.1	2211.6	3228.9	1772.7	2645.3	2303.5	2316.9	3334.4	3986.8	2492.8
103.1	1321.4	1755.3	2772.3	432.9	405.3	289.4	1609.1	343.5	92.1	563.1
212.3	1842.5	2596.5	2920.8	1428.1	2280.6	1888.1	2413.2	2269.8	1022.9	2015.5
27.7	181.2	284.8	442.6	61.7	52.5	101.2	152.7	47.4	25.5	78.8
29.0	89.3	162.9	272.9	22.1	24.7	49.9	92.8	20.9	20.4	38.2
6183.0	5987.1	6048.0	7540.1	5779.0	5378.4	7629.7	5885.2	5165.2	3107.8	6032.8
212.3	1187.1	1285.8	1839.8	1790.3	1254.1	1807.2	1878.6	570.1	286.5	1500.1
221.6	402.2	477.5	623.9	395.6	395.9	155.9	527.5	303.0	151.7	419.2
45.3	42.2	81.0	79.5	53.5	73.8	45.9	70.3	67.1	23.0	44.2
1734.1	3088.1	3474.4	4660.2	2437.8	2650.3	3056.5	2723.1	3251.9	2794.7	3631.0
27.9	735.0	1129.8	1741.7	207.7	247.9	290.4	639.2	120.5	40.1	347.5
69.7	4511.1	3047.1	3859.3	1589.3	4242.6	2521.7	3140.2	4348.6	1690.7	3577.7
660.8	2790.2	3955.3	3640.2	3583.3	3047.8	4347.7	3278.4	4727.3	4628.1	3540.7
181.4	1991.5	1981.6	2773.2	1664.2	1296.3	1573.7	1724.3	1355.8	1001.0	1480.2
39.6	241.9	519.7	959.8	378.7	144.5	342.1	213.9	32.2	26.5	97.5
80.3	207.9	465.8	763.9	97.9	69.4	77.5	331.9	37.7	25.0	104.8
752.8	2591.3	3276.5	3709.3	1750.6	1937.3	2031.1	2180.4	2573.0	1229.6	1478.7
9534.5	5825.3	4918.7	5798.0	5011.7	5567.2	5434.2	5928.8	5898.3	4719.3	7500.7
61.9	2647.2	2256.9	2593.2	2692.4	2637.6	2425.5	2416.7	3034.3	1768.0	1419.1
8513.9	3149.3	3561.3	3869.7	2722.1	2746.3	3635.4	3212.3	2981.4	2664.2	2276.3
44.0	89.9	150.4	264.5	47.3	32.1	33.3	107.6	33.8	25.0	33.7
35.3	24.2	18.2	21.3	20.8	19.4	20.5	17.3	19.8	20.8	19.1
52.0	122.1	165.4	186.1	34.8	54.8	41.4	64.7	52.9	41.5	55.5
172.5	539.1	594.5	1134.2	440.3	560.9	563.5	756.7	163.6	96.8	567.0
103.7	4188.3	4792.1	5587.2	1245.4	3809.8	3153.2	5348.7	1383.6	684.2	5777.4
42.3	25.0	24.1	24.7	21.1	19.0	20.1	19.4	21.6	19.6	17.5

1363.9	1398.3	1090.8
3732.7	3959.0	5218.7
7465.8	8270.0	8150.8
4647.8	4762.9	4430.8
1061.8	1574.3	1080.6
13.0	17.7	17.3
195.6	319.2	546.4
3219.7	4121.9	3907.8
8418.2	6236.4	8119.5
683.7	884.8	883.6
7318.6	7950.3	6454.7
6542.7	6939.2	7469.9
517.8	508.4	164.7
3956.1	4422.4	4169.6
816.0	685.0	68.6
2474.8	3109.0	2321.9
1211.7	1331.0	501.8
1951.2	2778.8	2292.8
154.9	182.2	99.9
110.3	208.7	25.4
6881.9	5640.3	7235.1
1471.2	2052.8	1790.2
357.9	666.6	482.3
58.7	178.5	36.2
2847.7	3278.0	2594.9
644.4	722.3	200.0
3223.0	2269.3	3411.6
2218.3	4436.0	4418.7
1720.3	1916.8	1116.7
375.4	229.9	63.9
285.2	280.0	91.4
2582.3	3094.1	1622.2
5128.9	6273.5	5520.9
2123.4	1813.8	983.2
2690.0	3605.0	4184.8
89.7	134.8	37.6
23.7	21.5	14.9
70.2	135.4	34.2
937.5	542.4	806.3
5356.9	4179.3	7379.3
21.7	26.4	19.8

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EU462383.1 gg_id:296340 Sumatran orangutan feces clone orang1_aai53d11 EU462
EU453863.1 gg_id:320397 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H75N EU453
EF099732.1 gg_id:199177 mouse cecum clone SWPT4_aaa03e12 EF0997
EF406520.1 gg_id:203844 mouse colon clone control_14days-H2 EF4065
EU454981.1 gg_id:317771 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H78S EU454
EU511943.1 gg_id:262228 cecal contents Mus musculus strain C57BL/6J; WD2 clone WD2_aak11f05 EU511
EU775557.1 gg_id:311186 Western lowland gorilla feces clone GORSD_aaa02g11 EU775
EU454465.1 gg_id:329502 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU454
FJ880106.1 gg_id:374577 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8801
EU622750.1 gg_id:278712 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
FJ880357.1 gg_id:386729 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8803
EU006116.1 gg_id:256157 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
AY993090.1 gg_id:135711 mouse cecum clone C21_d17 AY993
EU464528.1 gg_id:291463 African elephant feces clone AFEL_aai30f04 EU464
EU503874.1 gg_id:269368 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa01h06 EU503
EF098000.1 gg_id:174102 mouse cecum clone SWPT12_aaa03g10 EF098
EU454477.1 gg_id:317652 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H79S EU454
FJ880507.1 gg_id:451901 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8805
EU508941.1 gg_id:272168 cecal contents Mus musculus strain C57BL/6J; MD6 clone MD6_aap39g09 EU508
GQ077868.1 gg_id:404145 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw1212f0 GQ077
EF099759.1 gg_id:180997 mouse cecum clone SWPT4_aaa03h07 EF0997
EU457095.1 gg_id:305059 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU457
DQ014795.1 gg_id:131465 mouse cecum clone M1_g07_2 DQ014
EU504667.1 gg_id:270707 cecal contents Mus musculus strain C57BL/6J; myd1 clone myd1_aaa04c02 EU504
EU794137.1 gg_id:351182 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_AA13 EU794
EU458102.1 gg_id:336454 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K75N EU458
DQ777907.1 gg_id:170395 rat feces clone R-1234 DQ777
EU505050.1 gg_id:263586 cecal contents Mus musculus strain C57BL/6J; myd3 clone myd3_aaa02b08 EU505
AY916251.1 gg_id:112848 human descending colon biopsy clone NO50 AY9162
EF099541.1 gg_id:185723 mouse cecum clone SWPT3_aaa04f07 EF0995
EF097592.1 gg_id:185533 mouse cecum clone SWPT19_aaa04h07 EF0975
EU454725.1 gg_id:312854 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU454
FJ879812.1 gg_id:419444 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8798
EU453931.1 gg_id:334800 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EF603758.1 gg_id:231587 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
AY979637.1 gg_id:121159 human transverse colon mucosal biopsy clone M344 AY9796
EU452889.1 gg_id:338324 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K80N EU452
EF099578.1 gg_id:199707 mouse cecum clone SWPT4_aaa01c12 EF0995
EF603107.1 gg_id:232033 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6031
EU453884.1 gg_id:321729 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EF604835.1 gg_id:231806 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6048

1003.2	766.3	1003.5	1556.8	593.2	554.6	616.9	868.0	464.6	328.8	443.1
4877.6	4395.6	4781.1	5625.3	5412.2	3205.2	6520.5	3919.1	3409.3	4740.5	4646.4
292.6	740.1	950.3	1498.0	491.1	660.0	653.7	892.8	440.0	295.1	590.6
268.4	638.0	1316.7	2095.1	1040.0	555.5	842.9	821.6	302.5	321.3	576.9
19220.1	6003.8	5133.0	6409.8	6449.4	6508.1	6486.8	5764.0	5896.5	5731.3	8157.9
167.4	3702.3	4366.2	4978.3	2041.1	3490.5	3581.8	4424.1	2717.7	1318.2	5280.3
29.0	46.2	57.9	52.6	35.2	37.5	60.6	37.0	23.6	17.5	36.8
317.8	865.2	912.6	1261.6	767.3	715.5	799.6	790.6	816.7	604.0	716.8
169.9	824.4	1418.9	1279.3	614.7	955.1	867.8	1481.3	696.1	485.0	787.4
42.2	203.1	475.8	413.5	65.1	54.3	127.6	131.6	32.8	74.9	74.8
15559.6	8946.9	8406.9	8707.1	8058.0	6989.1	9752.8	7609.3	8547.6	7668.3	8659.2
31.4	34.1	81.1	226.9	23.1	22.0	22.4	27.6	20.6	22.2	26.4
621.8	2090.2	2462.8	3149.4	2439.8	1968.6	3399.3	2570.4	1255.4	1334.7	2145.2
474.9	3651.4	4033.8	5308.0	3142.6	2818.1	3730.8	3586.5	2020.3	863.9	3070.0
41.5	661.9	1015.3	1710.4	126.0	128.4	128.7	667.4	98.3	47.1	190.4
199.6	3397.3	3423.7	4125.0	1213.7	2808.3	2997.1	3848.7	1412.4	719.7	4041.2
38.3	1197.1	976.1	1721.7	165.6	449.1	192.2	609.9	97.4	70.5	199.3
54.2	456.3	1073.9	1175.9	171.7	445.3	155.3	1155.3	238.3	304.6	291.3
66.1	106.7	112.5	68.1	75.3	52.6	72.4	67.5	53.1	67.1	84.1
1046.9	1864.6	2193.4	2019.3	1354.8	2797.2	2419.0	3045.3	1200.0	1273.3	3171.9
317.4	5042.4	4802.3	5562.5	3960.0	5053.0	6207.5	5205.3	5625.5	3449.4	6893.7
2407.1	3040.4	3645.6	4060.3	2989.5	3000.2	4103.0	4256.5	4037.7	3023.6	5121.3
40.5	922.5	1237.2	1029.8	632.5	852.6	396.4	904.6	2121.9	631.1	534.1
694.2	1479.3	1485.9	2157.8	1584.4	1676.1	1958.7	1657.8	1162.0	859.0	1247.4
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4613.0	1972.1	1780.0	1651.7	1195.9	2292.2	1555.8	1426.7	1970.5	2218.4	1678.5
72.9	613.0	1441.2	1259.2	608.0	553.0	667.8	943.8	802.2	691.7	660.6
223.3	801.9	936.8	1418.2	502.4	525.6	573.9	764.0	398.0	315.5	564.8
44.2	87.5	111.6	169.5	62.1	50.0	62.4	74.0	46.6	25.6	45.9
78.0	257.7	459.2	599.4	177.0	243.1	220.4	426.3	73.7	183.3	304.7
30.4	109.2	174.0	160.6	66.3	69.3	111.0	125.9	67.9	36.7	185.3
8836.2	5831.8	4428.3	5820.5	5971.7	4529.1	4970.0	4570.5	5038.5	3175.0	4408.7
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40.2	61.3	84.1	158.6	62.9	27.8	44.9	45.0	21.2	19.8	26.1
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29.5	303.2	233.7	625.5	27.9	28.5	119.8	107.0	20.1	22.5	36.4
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50.3	283.5	301.2	479.3	45.9	172.5	305.4	173.8	26.5	25.8	74.0
105.1	1355.0	1231.5	1451.8	1604.0	854.2	1631.9	973.3	582.6	517.2	900.1

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1103.3	1488.4	1205.5
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4003.3	3720.1	4981.0
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722.2	1006.7	845.5
1218.9	1551.1	2025.0
114.5	209.3	72.7
7488.2	8598.4	8933.7
19.0	58.0	16.8
2628.5	2113.8	3563.0
3384.0	4061.6	4283.9
796.0	582.5	180.1
3786.5	3206.9	4955.2
609.5	878.8	631.1
1458.0	694.9	1135.5
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2574.4	2708.5	2037.5
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571.1	1691.2	225.4
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802.8	1865.1	1187.7
884.5	1188.8	444.2
75.2	187.4	55.4
324.9	508.5	269.8
64.8	174.1	79.7
5121.1	4826.7	4863.8
29.2	45.3	27.6
2317.7	2040.7	1864.4
9498.7	10033.1	8529.1
76.8	63.2	33.9
4164.0	3675.4	4516.6
428.5	378.0	42.8
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235.9	304.8	69.9
1019.1	771.8	1806.9

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EU452310.1 gg_id:331475 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU452
EU006217.1 gg_id:240633 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EF603916.1 gg_id:228458 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF603
EF097679.1 gg_id:189127 mouse cecum clone SWPT20_aaa02b09 EF0976
EF100062.1 gg_id:196923 mouse cecum clone SWPT5_aaa04b07 EF100
EF602770.1 gg_id:230836 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6027
EU504920.1 gg_id:269859 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa04b11 EU504
EF098360.1 gg_id:193807 mouse cecum clone SWPT15_aaa01e07 EF0983
EU463191.1 gg_id:294221 naked mole-rat feces clone molerat_aai71d07 EU463
EF604640.1 gg_id:230453 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6046
EF604939.1 gg_id:231349 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6049
EU776950.1 gg_id:309676 Naked mole-rat feces clone molerat_aai70b02 EU776
EU467647.1 gg_id:289805 naked mole-rat feces clone molerat_2g10 EU467
FJ880096.1 gg_id:442846 Diets enriched or wheat temporally and alter fecal rat feces animal fed oat bran diet; FJ8800
GU302930.1 gg_id:550070 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
FJ880583.1 gg_id:426735 Diets enriched oat or temporally and alter fecal rat feces animal fed wheat bran diet; FJ8805
EU622730.1 gg_id:278940 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU843395.1 gg_id:312272 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU455328.1 gg_id:320024 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU455
EU505320.1 gg_id:271280 cecal contents Mus musculus strain C57BL/6J; myd4 clone myd4_aaa02d10 EU505
EU381897.1 gg_id:275175 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
AM265425.1 gg_id:159925 Oligonucleotide Probes intestinal flora BB-DP rat colon clone ratAD060301 AM265
GQ896847.1 gg_id:578799 Diets enriched fructans and/or soy protein can alter dominant fecal humans but do GQ896
DQ015356.1 gg_id:135834 mouse cecum clone M3_b02 DQ015
EF099751.1 gg_id:195475 mouse cecum clone SWPT4_aaa03g10 EF0997
EU456256.1 gg_id:304541 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K78S EU456
EF406449.1 gg_id:211595 mouse colon clone control_7days-H9 EF4064
EU779312.1 gg_id:354876 Visayam Warty Pig feces clone VWP_aaa04h02 EU779
EF406819.1 gg_id:217096 mouse colon clone infected_28days-C3 EF4068
EF097253.1 gg_id:181680 mouse cecum clone SWPT18_aaa03h02 EF0972
DQ015015.1 gg_id:131469 mouse cecum clone M1_1g04_2 DQ015
EU474374.1 gg_id:292591 western lowland gorilla feces clone GORSD_aaa03h06 EU474
AY239406.1 gg_id:98683 rat feces clone rc3-37 AY239
DQ015629.1 gg_id:133346 mouse cecum clone M3_d06_3 DQ015
EU006237.1 gg_id:247154 Salmonella enterica serovar typhimurium exploits inflammation compete intestinal r EU006
EU468776.1 gg_id:290077 okapi feces clone OK3_f06 EU468
AY993195.1 gg_id:131253 mouse cecum clone C21_i12 AY993
AY990304.1 gg_id:132871 mouse cecum clone C3_F09 AY990
EU474328.1 gg_id:297768 western lowland gorilla feces clone GORSD_aaa02h05 EU474
EF096109.1 gg_id:187153 mouse cecum clone lean2_aaa04c11 EF0961
EF097070.1 gg_id:190752 mouse cecum clone SWPT18_aaa01a03 EF0970

114.8	3312.5	3056.4	4182.3	1243.6	2330.3	1921.9	2818.3	1469.3	1572.8	2936.2
6385.7	6941.6	6486.9	6877.1	6073.7	6629.2	6621.2	5906.6	9415.1	8747.7	7869.0
147.3	3105.7	3288.2	3951.1	2688.2	3226.1	3918.1	3366.1	1822.7	1939.0	2626.2
45.6	55.0	51.7	102.3	19.7	28.5	39.5	47.8	20.0	9.1	24.4
5958.0	6924.2	5973.9	6619.8	5899.8	6496.5	8042.6	6111.9	9655.1	8038.5	8743.7
466.0	6588.2	7395.0	8354.1	6803.6	6507.5	7145.2	6202.0	8479.4	6730.2	6175.0
1687.0	1634.9	1490.6	2147.6	1318.8	1204.4	1636.2	1451.8	1188.6	1632.5	1090.0
47.5	384.1	514.1	726.3	126.4	150.5	166.2	372.0	71.5	66.5	123.2
3322.8	6058.5	6452.7	7258.0	5296.2	6213.5	7656.0	7116.8	8309.9	6061.4	7799.8
55.7	1024.3	1375.3	2377.7	700.5	1240.2	1381.2	1758.9	1132.1	343.3	721.5
31.9	184.0	458.7	764.4	66.5	31.0	40.9	191.8	31.5	19.2	80.7
60.8	2434.7	3234.8	5213.0	355.3	709.0	508.0	1790.4	1108.1	351.3	836.6
981.8	5217.3	6108.4	7350.3	6250.9	5336.4	7753.2	6622.2	5004.3	3561.1	6184.2
37.7	172.2	287.4	357.9	158.9	214.5	220.9	349.8	77.2	29.4	170.2
351.5	1611.6	1841.5	2668.5	935.1	1305.1	1633.7	1586.5	627.6	504.3	994.3
66.5	850.3	1071.8	1557.4	351.0	709.0	636.7	796.6	246.8	282.6	465.8
252.5	2161.8	3568.6	4098.5	2919.2	2791.5	3188.3	3202.7	1527.0	1835.2	2783.2
247.4	1518.1	1812.0	2325.8	1179.5	1303.1	1320.3	1493.8	494.2	520.6	1106.6
71.9	264.7	866.7	1352.2	391.7	275.2	305.5	508.2	85.3	83.8	226.5
5097.0	6102.0	6663.5	7669.8	4595.0	6502.7	7586.4	6094.9	6543.9	5621.4	6012.8
338.9	2177.0	2621.6	4119.6	1839.5	2421.0	2407.3	1972.5	3129.5	1501.2	1570.2
921.6	2472.7	3486.5	5358.5	1536.3	1054.4	1557.4	2917.6	621.6	514.2	1188.5
322.8	2614.9	2985.3	4234.5	2233.7	2887.6	3457.8	3790.3	2444.5	1473.6	4550.1
60.3	96.4	76.7	150.3	42.2	34.4	32.0	45.8	37.4	17.2	30.2
42.1	104.5	152.5	284.5	58.7	59.8	38.0	93.1	37.5	52.7	61.0
40.5	3294.4	3972.3	4774.0	1606.8	2026.6	1958.7	2275.4	3059.4	1633.5	1623.9
41.5	473.5	619.8	774.2	274.5	342.8	242.8	329.6	592.9	543.7	169.7
1910.0	2911.4	3243.5	4379.9	1910.0	2771.2	2365.4	2892.8	2275.0	1356.1	2245.6
35.4	167.3	247.9	304.3	228.7	29.5	294.0	218.5	112.3	189.3	164.7
503.1	1617.5	1829.5	2063.7	1976.9	1556.3	2245.5	2015.3	1786.9	1460.8	2282.1
40.3	64.0	53.0	59.7	32.6	31.2	23.3	20.3	33.8	20.7	34.1
234.6	1090.8	1438.5	2004.8	1107.5	955.8	1151.1	1422.1	698.5	290.2	999.4
68.5	110.7	174.1	223.2	118.2	169.0	129.3	139.2	59.2	36.9	69.4
35.5	170.5	188.3	309.0	58.7	45.9	72.5	94.5	43.2	26.0	47.3
21683.5	12772.2	11141.5	14604.5	12365.0	12873.5	15396.3	12256.9	19014.2	16277.4	15682.1
1858.9	7170.9	8338.4	9253.1	9030.4	7931.9	10393.9	9621.0	9174.4	7987.2	9489.3
206.0	2391.5	3214.7	5223.0	687.6	466.2	655.1	2601.8	280.8	181.2	730.8
43.2	95.3	155.4	249.2	33.4	24.2	40.9	124.0	24.5	25.9	35.4
62.2	211.8	339.8	464.4	148.7	196.4	183.3	316.4	62.0	106.5	168.4
36.2	64.9	90.5	174.5	39.8	53.0	44.0	64.9	24.0	40.7	38.6
49.9	1314.2	872.5	997.8	201.0	872.4	554.7	1208.0	327.7	197.0	950.6

2909.8	2093.2	1880.2
5677.5	6931.2	5016.3
3560.7	2885.2	3829.6
69.4	35.2	10.2
6526.5	5284.7	6815.5
6562.9	7445.4	8006.6
1483.7	2200.5	1612.6
544.3	331.9	169.1
5832.5	7268.7	6028.1
1449.9	1421.5	1034.9
217.6	301.1	49.3
2298.7	1768.7	558.3
4150.1	5690.6	7160.3
165.8	163.3	158.5
1683.2	1826.3	2951.3
1121.5	1190.5	828.2
2970.6	2879.2	3942.2
1581.2	1844.6	2794.8
665.2	793.3	743.9
7895.5	7075.8	4253.3
2493.1	2884.4	3078.5
3096.3	2523.7	1733.4
2821.2	2437.4	3270.0
66.6	81.2	97.0
49.5	116.5	85.8
3084.8	2836.0	1217.8
394.5	713.0	219.1
2904.8	3045.9	2950.3
148.6	318.9	483.1
1677.9	2031.3	2149.6
37.1	49.1	26.3
995.4	1125.1	1267.1
125.1	147.0	217.1
74.6	161.3	56.0
12902.4	11730.2	13536.4
7621.0	7082.4	4318.4
3058.9	1713.7	639.0
76.3	134.1	30.1
256.5	364.6	218.1
100.5	142.4	37.1
1074.8	674.0	525.1

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EU622651.1 gg_id:278675 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EU452936.1 gg_id:319699 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K79S EU452
EU760449.1 gg_id:329026 Mouse fecal microbiota feces clone 3H3 EU760
EF097246.1 gg_id:194729 mouse cecum clone SWPT18_aaa03f12 EF0972
EU504203.1 gg_id:264534 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa04b01 EU504
EF406703.1 gg_id:204375 mouse colon clone infected_7days-H7 EF4067
EU506168.1 gg_id:259557 cecal contents Mus musculus strain C57BL/6J; MD18 clone MD18_aaa01h02 EU506
EF099144.1 gg_id:189700 mouse cecum clone SWPT2_aaa02h11 EF0991
EU453346.1 gg_id:337004 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone K74N EU453
EU504144.1 gg_id:265567 cecal contents Mus musculus strain C57BL/6J; CRWD5 clone CRWD5_aaa02b07 EU504
EU507923.1 gg_id:260460 cecal contents Mus musculus strain C57BL/6J; MD24 clone MD24_aaa03e08 EU507
EU510603.1 gg_id:268107 cecal contents Mus musculus strain C57BL/6J; WD5 clone WD5_aak38a07 EU510
EU381784.1 gg_id:273277 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU381
EF097715.1 gg_id:187391 mouse cecum clone SWPT20_aaa02f10 EF0977
EF604469.1 gg_id:228370 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6044
EU775447.1 gg_id:307242 Western lowland gorilla feces clone GORSD_aaa02h07 EU775
EF099844.1 gg_id:175658 mouse cecum clone SWPT5_aaa01b12 EF0998
EU622740.1 gg_id:278240 -feed administered sub-therapeutic chlorotetracycline alters structure and but not a EU622
EF604644.1 gg_id:233540 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6046
EF406383.1 gg_id:211771 mouse colon clone control_7days-B5 EF4063
EF602759.1 gg_id:231387 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6027
EU504036.1 gg_id:277555 cecal contents Mus musculus strain C57BL/6J; CRWD4 clone CRWD4_aaa04d01 EU504
EU471547.1 gg_id:288578 Asiatic elephant feces clone AE1_aaa03g07 EU471
EF099334.1 gg_id:176935 mouse cecum clone SWPT3_aaa01h05 EF0993
EF603018.1 gg_id:231681 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6030
EF096871.1 gg_id:184698 mouse cecum clone SWPT13_aaa02a03 EF0968
FJ368943.1 gg_id:369063 feces adult twins and mothers; TS4 clone TS4_a02d06 FJ3689
EU474297.1 gg_id:299687 western lowland gorilla feces clone GORSD_aaa03g11 EU474
AY993275.1 gg_id:134248 mouse cecum clone C21_m04 AY9932
EF097825.1 gg_id:183755 mouse cecum clone SWPT20_aaa04d06 EF0978
EF097844.1 gg_id:194048 mouse cecum clone SWPT20_aaa04f09 EF0978
EF097131.1 gg_id:180152 mouse cecum clone SWPT18_aaa01g11 EF0971
AB370251.1 gg_id:274244 Barnesiella intestinihominis str. YIT 11860 AB370
EF603725.1 gg_id:229158 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mouse EF6037
DQ015238.1 gg_id:133103 mouse cecum clone M2_f09_1 DQ015
EF096489.1 gg_id:180290 mouse cecum clone obob2_aaa03f10 EF0964
EF096452.1 gg_id:192586 mouse cecum clone obob2_aaa03a10 EF0964
FJ678385.1 gg_id:528459 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6783
EU504803.1 gg_id:262102 cecal contents Mus musculus strain C57BL/6J; myd2 clone myd2_aaa02d08 EU504
EF098085.1 gg_id:193878 mouse cecum clone SWPT14_aaa01c07 EF0980
EF099615.1 gg_id:198966 mouse cecum clone SWPT4_aaa01h05 EF0996

4355.7	1564.6	1804.5	2656.8	1070.7	1407.1	1820.4	2106.4	1144.4	515.1	1317.9
38.8	25.0	36.2	39.4	38.3	30.8	29.1	31.5	23.1	18.7	28.3
593.1	1802.8	2124.4	3132.8	1518.9	2257.7	1905.2	2274.9	789.0	1393.3	1450.0
3155.5	6053.1	5269.7	6284.0	4153.5	6555.2	6132.5	5399.0	9279.7	7305.7	6177.5
75.8	428.3	312.5	401.5	144.7	410.7	250.5	247.9	297.8	89.5	136.4
858.7	2904.4	2859.7	4173.0	2601.7	3412.9	3709.9	3322.2	3576.5	3053.2	3632.6
54.6	99.3	209.4	241.4	41.1	64.5	71.5	110.2	33.6	52.9	117.6
896.3	3636.0	3143.0	3412.0	2557.2	3386.3	2879.0	2871.6	3938.6	4334.4	4236.7
3505.8	1630.5	1636.4	2057.4	2249.3	1745.2	2122.9	2235.3	3075.3	1487.2	2131.1
85.7	1211.1	1313.7	1985.2	1373.2	970.1	1257.2	1084.8	676.9	742.4	879.5
73.2	242.5	387.8	296.3	148.6	216.0	170.3	176.2	288.6	518.5	169.1
38.1	1770.5	2098.2	2302.5	1508.3	1537.3	1941.0	1613.0	2668.3	2467.5	2266.2
4189.0	7125.2	7510.9	8848.3	5708.5	6939.3	8246.2	7496.0	9143.3	8757.6	9136.7
41.4	59.9	185.6	249.0	29.2	41.0	41.3	145.3	33.3	24.4	52.7
123.7	799.1	1223.8	1109.9	733.7	864.4	1012.5	794.3	2302.5	583.5	837.3
54.5	44.7	70.7	180.0	66.1	33.1	66.8	98.5	33.2	22.8	54.7
45.1	729.1	745.9	805.2	264.5	556.2	324.1	651.5	224.3	371.5	529.0
39.9	212.9	266.1	425.6	55.8	57.8	70.9	91.8	26.1	22.2	44.8
4933.0	3303.1	3384.2	3921.7	3584.2	3608.7	4566.2	3306.5	6089.4	3064.5	3463.4
57.6	748.8	930.4	1191.2	571.2	743.0	912.6	679.8	725.2	398.9	805.8
2440.0	2848.9	3688.6	5500.7	3060.1	2347.2	2687.6	3625.8	1578.2	1828.1	2107.6
42.7	532.6	787.0	1700.2	43.9	56.6	48.8	455.2	58.3	88.7	124.7
233.1	1366.7	1574.6	1586.5	1265.9	1155.1	1390.2	1847.4	1146.5	575.3	1403.4
73.0	77.5	80.7	111.7	74.4	65.1	77.6	84.3	116.8	52.2	43.2
218.2	3673.7	2699.3	3541.1	3142.3	2696.9	3118.9	3553.6	2062.0	1990.6	2443.4
82.1	734.0	1003.8	1603.6	238.4	756.6	687.4	1440.9	141.8	413.4	1424.9
43.0	36.2	21.3	25.4	21.5	17.2	24.6	20.3	28.2	24.8	34.5
312.7	2208.8	2320.6	3309.2	1797.2	1279.1	1844.3	1996.7	701.6	404.2	1196.9
239.2	250.1	300.5	306.1	182.1	196.2	209.7	209.0	320.4	241.7	180.9
202.3	250.4	376.1	437.3	415.9	365.1	381.8	378.4	190.0	141.0	237.8
215.4	3358.9	2814.0	3827.4	3422.2	3275.0	3220.7	2546.1	5045.0	3768.0	3243.9
107.4	2677.6	2175.9	2660.7	3572.6	2132.1	2295.9	2429.8	3286.6	1877.6	1758.5
78.2	838.3	838.8	899.4	1137.9	739.5	1150.4	711.0	910.7	457.0	1171.3
36.1	610.1	1001.1	1534.4	384.9	418.5	336.0	953.0	312.5	69.8	246.1
56.5	44.0	74.0	65.4	55.4	59.9	48.7	38.7	45.9	35.7	47.7
58.8	475.2	500.0	921.9	165.3	113.6	235.1	341.3	75.6	49.3	118.8
152.8	3094.2	4061.6	4838.8	210.3	2060.2	1608.9	2676.3	769.3	304.0	1597.3
728.5	3271.6	4024.5	4643.7	2667.2	3225.6	2857.0	3197.2	3096.3	3343.9	2653.1
59.5	3498.9	3458.6	4791.8	3204.4	2792.2	3708.3	3156.2	812.9	1488.6	1760.0
10107.1	3468.5	3493.1	4774.6	3478.5	4043.0	4028.5	4448.3	4925.9	3713.0	3786.6
52.0	53.5	72.6	141.5	29.4	35.3	29.5	139.6	30.9	15.4	46.1

1713.4	1894.5	1126.5
31.8	33.3	30.3
2097.7	2407.9	1980.5
4737.5	5368.0	3334.0
299.4	329.6	114.8
3091.1	4004.2	3058.3
126.9	148.7	56.6
2625.4	4017.8	1909.7
2049.3	1686.5	2003.1
1057.1	1008.6	1207.6
233.4	405.5	252.0
1201.6	1828.9	1845.5
7285.8	7070.9	7628.5
100.8	153.9	53.9
669.5	899.9	788.1
114.8	95.7	36.3
690.8	875.4	29.0
88.5	154.3	93.5
3123.2	4482.8	4589.4
573.2	840.1	811.2
3525.1	3658.2	2756.6
681.4	388.2	73.0
1370.9	2206.4	1670.9
70.0	140.1	90.0
3068.3	2699.5	3259.9
871.3	729.3	851.3
15.7	23.5	24.7
1850.0	1943.5	1158.3
190.5	326.4	234.8
317.3	471.1	346.6
2426.2	2809.3	2868.3
1735.6	2442.1	1619.6
657.8	823.1	39.3
955.8	1001.7	410.6
55.1	65.7	55.3
211.4	454.9	251.0
4467.5	2092.0	503.0
3203.8	4149.9	3200.5
3991.8	2798.7	3738.0
4164.6	3280.0	4203.5
44.8	113.7	51.8

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EF097565.1 gg_id:184222 mouse cecum clone SWPT19_aaa04d11 EF0975
EF406845.1 gg_id:206367 mouse colon clone infected_28days-E7 EF4068
EU451626.1 gg_id:316383 Innate immunity and intestinal microbiota Type 1 diabetes mouse cecum clone H74N EU4516
EF099279.1 gg_id:187557 mouse cecum clone SWPT3_aaa01a05 EF0992
EU773067.1 gg_id:346845 Banteng feces clone BG_aaa02d07.Contig1 EU773
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EU459488.1 gg_id:288014 capybara feces clone CAP_aah98c03 EU459
AB192163.1 gg_id:142693 termite gut homogenate clone RsTz-83 AB192
EU522664.1 gg_id:268892 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU522
EU474844.1 gg_id:298225 takin feces clone TAK_aaa03c10 EU4748
AB447622.1 gg_id:582590 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
FJ832886.1 gg_id:589986 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q401_33A05 FJ8328
GU322884.1 gg_id:568069 Metaproteomics -temperature anaerobic granular sludge cultivated temperatures c GU322
CU922971.1 gg_id:570947 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
FJ502273.1 gg_id:508913 Co-occurrence denitrification and nitrogen fixation meromictic lake (Switzerland) Lak FJ5022
AB240349.1 gg_id:143752 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
EU101168.1 gg_id:241983 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
EU887841.1 gg_id:344827 Bacteroides nordii str. H6 EU8878
AJ249101.1 gg_id:16567 SHA-25 clone AJ2491
EU777142.1 gg_id:308111 Okapi feces clone OK3_c06_2 EU777
EU775257.1 gg_id:312978 Reticulated giraffe feces clone gir_aah93g11 EU775
DQ168847.1 gg_id:139337 Fermentative biohydrogen production heated anaerobic sludge clone J3 DQ168
EF467522.1 gg_id:215462 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
EU626628.1 gg_id:277641 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
AM086143.1 gg_id:149805 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
EU626717.1 gg_id:278621 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
EU469991.1 gg_id:299307 trancaspain urial feces clone TU1_aaa03a07 EU469
EU344633.1 gg_id:265199 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
GU454901.1 gg_id:524763 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU454
FJ612117.1 gg_id:573374 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.1.10 FJ6121
DQ330407.2 gg_id:159129 Guerrero Negro hypersaline microbial mat clone 02N1A277 DQ330
FJ672357.1 gg_id:518436 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
GQ844375.1 gg_id:562395 Microbial anoxic tank full-scale water treatment plant influent produced wastewate GQ844
AB447707.1 gg_id:587341 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
AJ969457.1 gg_id:157758 Microbial black smoker s Mid Atlantic Ridge ecological implications rock fragments ch AJ9694
EU358743.1 gg_id:311025 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
FJ680373.1 gg_id:509073 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6803
EU283476.1 gg_id:278938 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A840 EU2834
EU775874.1 gg_id:344007 Horse feces clone horsem_aai94d01 EU7758

37.9	221.9	279.5	435.6	98.5	50.6	98.9	97.5	27.1	26.7	68.1
29.2	453.4	554.6	903.5	45.6	26.8	78.3	187.9	16.9	21.1	54.5
96.7	1566.1	2170.4	2521.4	1855.1	2564.4	3013.2	2383.9	1302.7	483.8	1130.1
31.8	555.3	869.1	710.7	368.9	773.3	336.7	703.2	468.6	201.6	340.5
42.6	246.3	202.8	382.5	225.5	125.8	333.0	271.0	87.9	49.0	118.4
26.7	33.3	63.2	43.1	43.6	29.2	48.8	39.6	17.1	27.3	26.4
546.2	2760.6	3112.0	3679.5	2009.6	3030.9	2445.5	3215.4	2387.0	1386.8	2739.1
158.0	2568.0	3266.9	3253.5	3322.2	2674.6	5384.3	2779.7	1703.7	1703.8	2663.7
393.4	8186.9	6786.7	6819.7	7986.2	9121.6	8600.8	7630.0	10956.9	9001.7	6988.5
41.0	38.5	58.5	59.2	57.0	94.6	47.2	39.1	33.8	28.2	52.0
181.4	945.4	1197.6	1432.2	835.9	631.4	1488.0	844.2	780.6	445.7	987.3
91.0	2515.8	2952.4	3324.8	1894.0	2950.8	2487.2	2611.7	1074.1	1245.6	2239.3
218.1	8627.0	8461.0	7391.7	7961.9	7779.3	9720.3	7842.2	6797.6	8088.1	6975.5
67.4	4339.2	5001.5	5451.4	1338.9	4168.0	3789.7	4582.7	2105.7	1203.6	3433.2
5628.5	7361.2	7830.8	8234.7	9904.2	7749.5	10072.8	7336.8	5680.0	3773.6	7853.3
25574.8	9796.3	9783.8	10388.1	10537.2	9100.7	12674.0	8559.9	11848.9	10246.4	11475.5
54.4	1411.9	2255.5	2005.6	5645.2	3389.5	4154.6	1964.6	879.5	279.2	1425.6
54.5	1619.3	3072.3	2156.7	5171.5	3523.1	3292.4	2416.0	1164.6	92.0	2682.5
71.5	455.7	607.7	423.5	433.4	388.3	427.9	506.4	314.4	1448.0	299.7
61.0	3205.6	2657.5	2780.4	1319.5	2055.1	2085.5	2576.6	1966.4	2266.4	1732.7
38.1	2813.7	3717.7	4296.4	3324.4	1545.7	4601.7	2442.8	856.6	1380.4	1728.3
192.6	4826.4	6309.2	7201.3	4743.5	4841.9	6243.6	5700.0	3109.7	1834.8	3435.7
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94.8	2116.7	2422.4	3107.5	1645.0	2009.3	2496.3	2006.0	1101.5	671.9	1717.7
60.0	1187.0	1600.7	1354.3	1240.6	1064.2	1765.5	2495.7	514.0	283.6	1336.7
72.3	2267.4	3290.9	3551.1	3321.5	2252.2	3761.6	3247.4	2803.2	713.7	2689.3
28.0	1733.1	2446.7	2091.1	1965.2	425.4	3955.1	906.3	290.0	288.8	1021.1
186.4	4243.2	5970.4	5213.3	5749.2	4346.5	6068.2	5194.9	4498.9	3437.7	4526.1
2352.7	4086.6	4204.8	4629.3	3942.2	4305.4	4700.6	4788.5	4299.0	3633.2	4528.6
791.6	6712.2	5952.1	6999.1	5923.7	5888.8	6875.6	6951.3	5777.3	5796.1	6887.0
3097.1	7288.7	7724.1	9017.5	9392.5	6724.9	10464.8	6609.0	7599.7	5183.9	7855.4
57.1	375.2	525.8	742.3	134.1	253.5	291.5	321.9	124.5	67.7	384.4
250.1	1362.6	1476.7	1341.4	890.6	1070.3	1104.3	1848.9	1011.3	1573.5	1140.1
2173.6	2509.9	1759.8	1456.9	1706.1	2059.1	2008.0	1542.9	2173.3	2069.8	1903.0
436.4	7374.5	8777.8	10124.4	8088.9	6708.8	9719.3	7864.9	5336.7	1860.5	7291.1
224.7	3998.9	3997.9	4617.7	3571.2	3696.5	4233.3	5117.9	4896.0	3316.5	4116.2
3486.3	4313.4	5361.5	5023.4	5410.3	4598.0	6730.5	4734.7	4327.9	3524.8	3585.9
823.2	4621.4	4765.0	5202.2	5610.1	4402.1	7516.5	4539.8	2169.4	1239.1	3467.6
137.6	4247.8	3845.1	3897.9	2465.0	4349.6	2811.7	3554.1	2589.9	2161.4	2531.0
150.8	3295.8	5411.3	3925.3	3993.9	2585.3	7983.2	2962.4	2405.9	1477.1	2814.1
104.2	3032.7	3215.2	3707.2	4385.9	3191.4	5693.6	2982.0	1566.1	832.1	2180.8

153.3	276.4	100.9
328.0	314.8	36.7
1223.6	2336.7	4300.6
705.7	614.0	635.6
294.8	496.9	425.8
31.5	44.7	35.0
2979.9	2839.9	4716.2
2724.0	2630.4	2997.3
7736.9	6919.6	5866.4
39.7	107.8	120.2
842.4	840.7	775.4
2974.4	2805.0	6650.1
6579.6	6302.4	6327.5
6384.2	3360.0	2583.0
7139.7	7713.3	10374.7
8877.7	9686.1	8944.2
1928.7	1646.3	1168.6
1378.7	1092.8	1034.9
397.2	649.0	479.0
2868.0	2222.1	5356.4
1280.7	723.2	949.4
6564.1	4799.0	5197.1
3061.1	3300.1	3564.5
2936.3	1893.3	2616.0
1396.3	844.5	2118.6
2098.1	2729.7	3470.0
192.5	449.2	812.4
4619.0	5223.9	4477.4
3342.9	4110.9	5724.5
6133.9	5683.7	9463.0
5815.0	6337.4	6871.5
302.1	428.5	2444.9
1443.9	1451.0	1637.0
3071.7	2127.0	2262.0
6196.4	6009.2	7879.1
3094.9	3533.6	3445.2
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EF520437.1 gg_id:231844 structure lakes: what controls ? acid-impacted lake clone ADK-HDh02-17 EF5204
AB240375.1 gg_id:142380 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
EF515640.1 gg_id:217292 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5156
EU617865.1 gg_id:334161 Seasonal variation microbial Yel Sea sediment clone C13S-108 EU6178
EU234211.1 gg_id:237249 receiving river and un techniques effluent WWTP treating penicillin G production wa EU2342
GU174049.1 gg_id:566383 Microbial Bactrian camel estimated rumen clone XJC123 GU174
AM086153.1 gg_id:149981 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
AB189373.1 gg_id:113650 cold seep sediment clone JT75-304 AB1893
EU488084.1 gg_id:533148 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU4880
EF632714.1 gg_id:237093 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
GU180191.1 gg_id:592210 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
EU471659.1 gg_id:291030 Asiatic elephant feces clone AE1_aaa01b02 EU4716
AJ249107.1 gg_id:27268 SHA-54 clone AJ2491
GQ354965.1 gg_id:592485 structure between two geochemically distinct springs Alum Rock Park spring clone 4 GQ354
EU471662.1 gg_id:296114 Asiatic elephant feces clone AE1_aaa02a07 EU4716
EF515716.1 gg_id:225096 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5157
AB062847.1 gg_id:22095 termite gut homogenate clone BCf9-17 AB0628
EU460992.1 gg_id:301069 red kangaroo feces clone KO1_aai41g02 EU4609
EU794245.1 gg_id:319354 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_M14 EU7942
GU061301.1 gg_id:534403 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AJ007873.1 gg_id:1909 cytophagales clone LD21 AJ0078
EU344456.1 gg_id:259929 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3444
EU283479.1 gg_id:278289 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1892 EU2834
GQ339154.1 gg_id:525962 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
EU468706.1 gg_id:290252 okapi feces clone OK2_a07 EU4687
EF208683.1 gg_id:202437 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.C EF2086
CU927762.1 gg_id:550552 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9277
EU644260.1 gg_id:281260 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6442
CU927382.1 gg_id:569229 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9273
FJ374189.1 gg_id:361803 Inter- and intraspecific humivorous scarab beetle larvae (Pachnoda spp.) larval hindg FJ3741
EU468800.1 gg_id:300785 okapi feces clone OK3_d07 EU4688
FJ716481.1 gg_id:511725 Uncultivated archaea sulfate-reducing biofilm Frasassi cave system anoxic lake water FJ7164
AY340833.1 gg_id:91285 sulfate-reducing fluidized-bed reactor clone SR_FBR_E99 AY3408
AJ441238.1 gg_id:57446 hydrothermal vent polychaete mucous clone P. palm A/C 22 AJ4412
FN396675.1 gg_id:537712 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V FN3966
AJ633981.1 gg_id:114657 hlpd: Llgnd and Idspd) hst's accssr ndmntl glnd cln T66ANG1 AJ6339
EF687372.1 gg_id:281446 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
FJ670687.1 gg_id:523843 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6706
EU794308.1 gg_id:347016 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H34 EU7943
GQ449224.1 gg_id:537070 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_ GQ449
FJ672548.1 gg_id:515828 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6725

31.4	534.1	3301.0	4282.9	2440.9	395.1	1870.9	178.7	122.2	28.2	615.9
46.8	2496.9	3764.8	4654.3	4470.9	2428.3	5006.2	2214.5	1583.5	417.9	1592.2
45.6	1953.0	2374.4	2811.3	2073.8	2280.6	2882.8	1627.1	565.1	1192.1	1039.9
36.6	731.8	1981.2	2104.9	559.9	570.3	2038.8	1367.3	497.2	249.8	661.2
827.1	6255.0	7450.6	5070.6	8167.9	6881.8	7289.0	6637.7	3243.6	8504.1	4282.2
3575.4	7673.8	7931.4	8109.8	7811.2	7133.7	9227.9	7052.1	4534.9	3611.9	6907.3
56.3	882.7	841.3	1114.2	444.5	654.1	602.2	1984.5	137.9	141.8	1098.7
61.0	2587.9	2300.5	1458.6	1961.3	2218.6	1303.5	2715.1	6395.1	2488.9	1511.0
13066.8	5862.0	5686.6	6124.3	5744.0	5573.4	7416.4	5031.6	7246.8	4952.1	6120.3
197.0	4426.8	2813.7	2949.5	3537.0	2550.1	3969.8	2811.1	1827.5	1460.2	2853.4
128.1	5745.8	7384.2	8502.4	6310.7	4869.3	8735.7	6242.0	4945.6	2913.5	6168.1
229.1	2863.2	3876.4	4481.2	2707.5	3569.6	3559.9	3737.9	2619.0	3323.0	3268.1
45.7	56.6	87.6	103.4	76.7	53.3	209.3	70.9	72.7	50.6	37.0
37.9	490.5	1227.4	1276.5	1229.0	601.1	963.6	615.0	270.7	169.0	391.4
596.2	5005.3	6088.5	6315.2	5816.1	4624.4	6703.3	4709.8	5630.5	4517.5	4526.3
29.8	15.9	12.7	23.0	22.5	13.0	19.9	14.6	13.2	13.2	19.3
46.9	35.8	31.8	28.0	34.7	21.8	29.9	31.0	30.4	25.8	34.7
848.5	3741.3	4762.0	5274.9	2945.6	4014.6	3829.1	4864.8	4188.7	2461.8	4190.4
6060.9	5398.3	5508.1	6576.0	5404.5	6082.8	5740.8	5776.7	5711.7	3905.9	5386.8
2311.1	8057.0	10149.2	9220.5	8769.0	7044.6	14009.5	7670.4	5841.0	7461.1	10908.2
8454.9	6824.6	7527.9	7976.8	6288.3	5450.2	7536.5	6809.0	6092.5	5260.1	7701.1
316.4	4558.2	5079.8	5811.5	4316.1	4442.4	5731.6	5003.8	3914.3	3600.5	3267.0
55.7	3672.4	4793.8	5385.3	5283.5	3700.6	7051.5	2881.9	1360.4	2007.2	2523.3
373.7	3924.7	4635.1	4814.2	4721.6	3709.3	6411.4	3286.0	2710.5	966.3	2424.4
176.1	1949.7	1617.1	1812.5	1788.6	1758.6	1429.1	1598.0	2129.0	717.4	1146.0
55.4	568.1	1048.3	943.5	1302.1	751.6	1552.3	770.6	234.4	405.5	429.6
10687.9	4953.6	4912.6	5358.9	5195.6	4170.3	7924.5	4189.6	4214.6	4169.8	4082.4
141.6	3950.9	4969.0	6425.0	5095.3	3570.2	7875.5	3904.9	3150.5	1350.3	3964.3
174.1	1020.2	1850.4	1638.9	1491.5	998.0	1855.6	1330.1	908.9	306.5	818.6
63.2	224.0	249.9	240.5	376.0	273.9	433.0	230.7	148.0	130.6	142.0
768.9	4992.1	4802.6	4969.4	5800.5	4708.9	4808.1	5320.6	3196.0	4040.5	4045.8
3425.4	4846.3	5967.9	5773.2	6792.2	5493.6	7741.3	4056.1	3565.0	3633.1	3867.4
5865.0	5207.5	5748.6	6380.1	5746.6	4758.0	8842.4	5160.0	6435.8	4204.3	5639.0
83.2	5237.2	6383.0	5466.4	3523.5	4197.2	6799.5	4425.3	2685.4	2640.2	4439.0
159.4	4019.1	5690.2	5737.3	6095.5	4764.7	7544.1	4564.8	4154.2	3318.0	3925.0
113.3	2913.0	3228.6	2822.6	3370.4	2597.5	4189.9	2387.3	3091.2	1620.7	3605.2
293.6	6304.1	7039.4	8340.3	8084.7	6797.9	10113.4	7033.9	5903.2	3137.8	7157.4
87.7	1837.7	2876.1	3136.8	2027.1	1222.5	3293.6	2189.9	926.9	485.1	2134.5
114.7	2254.8	2403.2	2834.4	1077.3	1406.9	1238.5	2255.8	770.8	415.9	1067.0
110.9	5562.5	5632.3	5963.4	4950.1	5376.4	5018.5	5577.0	6429.7	3209.0	5356.3
105.1	1609.0	1038.3	859.9	1716.7	710.9	1567.1	1056.5	815.9	304.6	689.8

35.4	183.3	1742.6
1130.7	1158.9	1809.8
2022.0	1461.8	2162.5
799.6	201.3	606.6
7143.7	7116.9	12921.9
8322.0	7332.5	9489.0
579.9	217.7	101.6
1411.0	1818.7	1139.8
5302.2	5105.6	6659.1
2271.5	3430.6	3281.8
4384.8	4228.6	4554.6
3826.9	3877.2	3464.2
42.2	44.8	23.2
478.1	545.8	292.1
4701.3	5051.8	3936.8
12.8	12.4	14.2
28.0	30.5	35.4
4375.0	4658.7	3302.2
6171.7	5975.0	5636.2
6614.3	6794.4	7481.8
5195.5	6070.0	4388.6
5269.1	5141.8	4973.9
2388.6	1368.8	2115.2
2452.6	3064.1	3793.4
2163.0	1764.6	2142.9
1015.7	784.8	903.2
3389.7	4217.6	4222.7
3182.7	3219.3	4315.1
1009.7	1817.7	2196.9
267.2	281.0	342.7
5317.6	4799.0	4861.6
5035.8	3977.8	3698.6
3517.0	4871.9	7184.5
3116.6	2384.3	3448.2
4400.1	4749.2	3806.7
1640.3	2483.0	2649.4
5341.3	5794.0	8844.0
1124.1	1356.2	1797.4
2253.2	2499.7	3337.4
4620.1	4745.5	3647.3
2068.9	843.7	1267.5

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FJ716918.1 gg_id:570877 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7169
EU474496.1 gg_id:302981 bighorn sheep feces clone BHSD_aaa04g01 EU474
AM883180.1 gg_id:349092 Endosymbioses between and deep-sea siboglinid tubeworms arctic cold seep (Haak AM883
AY082459.1 gg_id:69791 neutral pH mine biofilm clone 44a-B1-14 AY0824
GQ360012.1 gg_id:559138 Microbial intestinal contents and yel catfish (Pelteobagrus fulvidraco) intestine muc GQ360
EU773616.1 gg_id:354389 Capybara feces clone CAP_aah97h09 EU773
EU775144.1 gg_id:341051 Francois Langur feces clone FL_1aaa01g03 EU775
EU775249.1 gg_id:321527 Reticulated giraffe feces clone gir_aah93b08 EU775
AB240242.1 gg_id:141996 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU245226.1 gg_id:246041 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-D05 EU245
FJ674366.1 gg_id:514574 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
AB195895.1 gg_id:109183 Anaerobic sludge clone S15 AB195
EU472280.1 gg_id:289823 francois langur feces clone FL_2aaa04a07 EU472
AB186817.1 gg_id:106460 polychlorinated dioxin dechlorinating microcosm clone TSBX12 AB186
AB191998.1 gg_id:142777 termite gut homogenate clone M1PL1-52 AB191
AF419687.1 gg_id:72909 Guaymas Basin hydrothermal sediment clone CS_B045 AF419
AB504929.1 gg_id:554505 structure microorganisms reddish-brown iron-rich snow clone oze05B24 AB504
FJ202099.1 gg_id:342229 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2020
EU644099.1 gg_id:284431 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
EU777992.1 gg_id:335513 Black rhinoceros feces clone RH_aaj92b02 EU777
DQ394963.1 gg_id:152831 harbor sediment clone VHS-B3-78 DQ394
EU772007.1 gg_id:310931 Argali sheep feces clone AS2_aao33a07 EU772
AJ011042.1 gg_id:1910 strain clone R1 AJ0110
AF371924.1 gg_id:16915 swine intestine clone p-2534-18B5 AF371
EU472140.1 gg_id:300246 francois langur feces clone FL_1aaa03b03 EU472
EF454492.2 gg_id:227458 termite hindgut clone 290cost002-P3L-2216 EF4544
FM955631.1 gg_id:551607 Study Prokaryotic Some Selected Niches Western Ghats India water clone BCWCSP1 FM955
EU475381.1 gg_id:296470 rock hyrax feces clone RHSD_aaa02b12 EU475
EF420217.1 gg_id:211333 Mature fine processing harbour methanogenic oil sands tailings pond clone 24-9G EF4202
GQ448662.1 gg_id:509560 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EU474792.1 gg_id:291587 takin feces clone TAK_aaa02d05 EU474
AB363973.1 gg_id:236772 Bacteroides sp. str. XDT-1 AB363
AF320926.1 gg_id:70586 Lake Michigan sediment clone LMBA49 AF320
GQ448729.1 gg_id:557275 Microbiome neonatal calves: shedding microorganisms fecal clone calf784_10wks_g GQ448
EF688234.1 gg_id:338749 Detection microbial sludge anaerobic wastewater treatment system clone 5F10_con EF6882
EF420216.1 gg_id:204265 Mature fine processing harbour methanogenic oil sands tailings pond clone 12-3C EF4202
EU472043.1 gg_id:297059 francois langur feces clone FL_1aaa03a10 EU472
AM176862.1 gg_id:160787 Recovery mangrove sediment clone SZB26 AM176
FJ516976.1 gg_id:546673 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
EU101284.1 gg_id:238631 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU101
AB192158.1 gg_id:142988 termite gut homogenate clone RsTz-24 AB192

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1245.8	6530.0	6988.8	7869.6	6789.5	5157.2	9018.5	7297.7	8737.9	2615.6	6682.7
1160.4	5544.9	5838.0	6073.9	5673.7	4592.5	6954.5	5605.4	4684.2	2819.4	4152.5
5673.4	4307.9	5169.4	4326.2	3574.4	2236.8	7067.1	3270.9	3678.3	2454.2	2982.5
37.6	1600.9	2495.0	2534.7	1061.9	1571.0	2266.1	1848.4	1267.6	535.3	2121.7
792.2	7978.5	6892.6	8137.1	6721.6	6860.2	9501.0	7574.8	6047.8	10054.5	8092.4
1814.0	5246.0	5354.5	4372.5	4900.5	5153.2	3776.9	5051.2	7453.9	4161.5	4058.5
155.4	638.7	447.8	448.7	474.3	510.3	221.2	656.3	211.6	92.3	148.9
243.5	984.0	2239.4	2588.8	2603.8	1294.7	4115.6	1271.7	395.5	396.1	759.8
1747.3	4663.4	4014.8	5274.3	3995.7	4429.1	5289.0	5350.8	2642.3	3139.0	3883.5
117.4	1984.6	874.8	869.7	1485.7	976.7	1256.1	899.4	1059.4	1251.4	743.3
168.3	508.2	777.5	498.5	583.1	367.2	799.9	496.6	255.2	106.6	475.8
120.6	2003.2	2693.2	3378.9	3114.3	1945.6	4207.6	2433.8	1576.4	1513.6	2978.7
33.2	407.7	954.5	1056.0	435.7	265.5	393.6	468.1	120.9	55.6	224.5
49.4	151.4	272.7	298.4	143.3	205.2	260.6	287.1	121.4	28.4	215.8
73.8	479.1	619.8	612.2	510.0	436.2	491.0	670.4	518.1	371.1	276.5
243.3	6271.4	7966.0	7543.0	6656.7	5936.9	9381.2	5866.9	4936.2	2207.2	6628.2
117.9	1611.7	2210.3	2601.9	794.6	3319.6	1270.4	2370.5	949.9	362.0	2154.9
138.3	980.3	4888.8	5389.7	4337.2	1844.0	4702.6	1575.3	892.3	531.5	1429.7
506.1	10086.0	8711.9	9436.7	8775.6	9348.8	8782.7	9914.0	12064.7	9528.1	9764.0
201.6	1984.1	2174.4	1731.6	1732.9	2325.3	1348.4	2327.8	2192.4	937.9	4420.1
2074.5	10406.1	8670.3	8918.0	9202.1	9117.3	9159.6	9170.5	12068.5	8927.6	10542.7
159.8	4569.3	5973.3	6172.9	5744.4	3644.1	7258.5	4614.3	3214.8	987.0	4254.2
59.7	107.7	169.0	205.4	34.9	162.5	239.1	271.3	60.0	31.3	128.3
1530.6	3742.4	3604.7	4226.9	3422.8	3600.6	3915.7	3628.0	3383.6	2505.2	4010.1
39.2	149.3	258.9	324.9	253.2	77.4	533.0	80.3	37.6	19.1	60.0
112.8	2205.7	2562.5	3082.1	3124.7	1855.6	3833.6	2355.7	1582.9	685.5	1806.6
57.5	436.9	613.5	539.5	223.0	669.8	559.1	492.6	202.3	161.1	286.5
101.1	3405.4	4459.0	4604.9	3937.3	2155.3	5862.4	3459.2	2133.1	795.5	2790.3
668.4	1115.1	1700.4	831.7	1214.6	1433.0	1438.7	1135.0	690.8	531.1	924.4
97.8	2396.9	2822.5	3094.6	2559.1	2229.9	3215.4	2950.7	1603.8	639.0	1992.5
416.7	3394.8	1010.2	1013.7	303.6	1003.5	296.7	1245.9	754.4	952.1	715.2
5850.0	4942.7	4910.5	4962.9	5701.9	4255.4	7102.6	4303.1	4072.5	3428.4	4660.1
324.2	2810.8	3034.5	3382.6	3222.6	2970.7	4015.0	3346.9	1494.4	1301.3	2205.7
59.2	1599.6	2322.9	2407.7	2474.0	2190.3	3750.8	1712.8	358.9	834.3	943.6
28.6	770.3	1372.3	1912.0	1266.6	688.5	2413.0	1383.5	1285.2	139.6	763.0
454.1	2858.1	2877.2	3315.4	1628.6	2574.1	2795.4	2839.2	2172.7	1787.9	2781.9
45.3	920.6	1261.5	1249.5	1643.1	726.8	1988.1	1423.1	633.1	95.7	821.0
57.0	3826.9	4546.2	5043.5	5413.3	4602.7	6354.9	4251.9	2827.3	1738.6	3850.5
45.3	153.1	244.1	203.8	169.2	260.9	330.3	111.4	92.5	54.8	128.6
24.1	123.6	203.2	333.2	669.5	390.8	396.0	288.6	116.1	124.0	145.6

6076.0	6209.7	4955.2
5358.3	8404.3	6596.9
4611.4	4422.8	4234.5
1952.0	2832.1	2534.3
1849.8	1355.9	3461.3
8241.5	6137.2	8070.6
4746.1	5328.1	6441.9
1225.3	287.5	444.5
1068.2	1251.2	2197.2
4416.1	4832.2	4419.4
1678.4	1284.8	1514.2
376.7	681.7	502.2
2629.3	2381.0	3746.1
199.2	583.5	308.5
104.8	324.0	303.6
404.8	1060.1	552.0
4418.4	3890.0	3744.3
1253.4	977.7	1404.7
1070.7	1650.5	3970.5
9224.2	8634.5	9178.4
1315.4	3611.4	531.1
8937.4	8088.4	7863.7
3150.8	3179.3	3891.7
54.5	152.7	51.4
3719.1	5136.9	4409.8
240.0	117.3	117.5
1637.4	1974.3	3744.7
693.0	664.6	1420.9
2087.6	2270.2	2508.5
1644.5	1329.6	1100.7
2093.9	2393.3	3028.2
5782.7	699.5	194.0
4004.2	4697.8	5015.3
2874.9	3355.9	3639.7
1357.8	872.9	974.2
612.2	1377.3	1968.5
2836.8	3317.8	2708.6
852.6	725.5	1020.7
3451.5	3737.3	5227.0
102.5	136.1	101.5
336.8	366.0	236.9

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AB088920.2 gg_id:105182 termite gut homogenate clone Rs-N39 AB088
EU700166.1 gg_id:302703 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU24 EU700
EU842222.1 gg_id:356426 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
FJ484663.1 gg_id:548668 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4846
AJ306737.1 gg_id:101390 DCP-dechlorinating consortium clone SHA-13 AJ3067
FJ462124.1 gg_id:544483 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4621
EF097027.1 gg_id:177669 mouse cecum clone SWPT13_aaa04d07 EF097
DQ676360.1 gg_id:225388 Archaeal sediment and plankton freshwater pond suboxic freshwater-pond clone M DQ676
EU644165.1 gg_id:284946 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
EU468504.1 gg_id:294848 okapi feces clone OK1_d05_1 EU468
AF029039.1 gg_id:1921 Benzene mineralizing consortium complete clone SB-1 consortium AF029
AF050539.1 gg_id:1896 contaminated aquifer clone WCHB1-53 AF050
CU918213.1 gg_id:558606 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AJ240979.1 gg_id:1914 Norway:(Svalbard)Hornsund clone Sva1038 AJ2409
FJ672351.1 gg_id:525055 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6723
FJ172812.1 gg_id:312412 Qinghai Yak Ruminal and Fungi China rumen clone RB-4G11 FJ1728
EU463478.1 gg_id:291681 domesticated horse feces clone horsem_aai94f08 EU463
EU592422.1 gg_id:561608 Seasonal changes Salton Sea hypersaline sediment clone SSS23N EU592
AY572027.1 gg_id:114774 termite gut clone RsaPv13 AY572
EU234164.1 gg_id:244201 receiving river and un techniques effluent WWTP treating penicillin G production wa EU234
DQ824495.1 gg_id:183618 human fecal clone RL304_aal76g04 DQ824
AY168724.2 gg_id:76102 arsenite-oxidizing biofilm clone Hot Creek 27 AY168
DQ799357.1 gg_id:178148 human fecal clone RL305aal85c11 DQ799
AB234433.1 gg_id:145246 termite gut homogenate clone MgMjR-050 AB2344
AM490701.1 gg_id:584987 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
GQ461682.1 gg_id:588344 Coupling -ITS Clone Libraries and Automated Intergenic Spacer Microbial Bioremedi GQ461
EU245060.1 gg_id:240986 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-C07 EU245
EU925908.1 gg_id:325319 sediments sediment station DBS1 northern Bering Sea clone 137I1 EU925
EU644161.1 gg_id:282325 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
FJ680730.1 gg_id:521139 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6807
AB191984.1 gg_id:141874 termite gut homogenate clone M1NP1-14 AB191
EU461421.1 gg_id:288259 black rhinoceros feces clone RH_aaj89a08 EU461
EU644268.1 gg_id:282750 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
EU828421.1 gg_id:564444 Microbial effects changeover without CO2 sparging two-stage biological and methan EU828
EU773667.1 gg_id:333804 Capybara feces clone CAP_aah97h05 EU773
EU528260.1 gg_id:285668 Seasonal Dynamics Mudflat Mouth Major Kentucky Lake Reservoir Tributary sedime EU528
AB426186.1 gg_id:277035 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
AB234394.1 gg_id:147476 termite gut homogenate clone MgMjR-007 AB2343
EF520436.1 gg_id:228557 structure lakes: what controls ? acid-impacted lake clone ADK-MOh02-18 EF5204
EU473455.1 gg_id:288119 Somali wild ass feces clone WA_aaa02g08 EU473
EU573107.1 gg_id:279087 and Dependent Microbial Oil Reservoir North Sea Ekofisk oil field Norwegian sector c EU573

37.0	1602.0	2011.4	1284.5	1541.9	1526.0	1155.6	1937.5	2523.9	2081.8	930.9
354.7	3835.6	4295.1	3865.2	4493.8	3283.2	5185.3	3410.0	2940.6	2305.0	3173.2
1116.5	6607.3	6254.6	7414.8	5524.5	6423.9	7256.4	6683.4	8189.9	6261.9	7726.9
162.5	2839.3	3433.8	4176.5	4040.1	2474.7	5194.8	2490.9	2604.2	661.6	2094.0
6884.7	7101.4	7731.0	8000.7	6487.3	4670.9	10166.2	5753.2	6404.6	4114.0	6530.2
1505.7	6878.0	7294.0	8606.0	8828.2	5524.6	11451.2	5658.5	5644.5	4481.6	5490.5
40.3	538.6	910.3	958.1	189.4	452.2	275.7	683.5	409.3	115.7	221.4
48.0	1563.0	3062.4	4379.8	293.1	1551.4	1573.2	3662.7	591.6	50.3	3379.0
56.2	1675.1	2649.4	3724.0	6009.0	1472.2	6824.6	1802.0	297.3	603.2	972.5
513.0	3502.0	3913.6	4383.5	2980.6	3311.2	3086.7	4833.8	3063.6	1495.9	2974.0
224.7	5042.9	5040.1	5430.3	6173.1	4578.6	7076.6	4179.3	4742.0	4685.6	3976.0
316.7	1750.4	2264.9	2979.5	3861.0	1054.4	5218.0	1329.2	292.7	59.0	939.0
6296.0	8376.7	10047.1	10954.0	11077.0	6862.4	14661.8	6980.8	7229.5	7817.6	9498.5
54.0	2344.8	4365.7	3430.4	3796.0	2487.3	5950.1	2064.8	1180.5	279.4	2116.7
3146.2	2709.0	2193.0	2384.2	1792.7	2273.6	2492.4	2193.2	2859.3	2278.6	2618.4
399.0	4571.5	4669.9	4865.8	5980.4	3900.7	6797.6	4191.0	3197.5	2712.0	2667.4
5223.0	4520.4	4419.0	4840.7	4658.6	4486.2	5305.0	4087.6	7517.1	7354.2	5087.6
166.6	4901.2	5538.6	5511.6	5039.8	4188.4	6677.5	3871.8	3471.1	3095.8	6587.2
147.0	1078.8	1233.5	1565.4	2060.0	1619.4	1808.8	1383.5	662.4	664.7	803.8
1994.5	4640.8	7794.2	5663.8	5866.2	3382.5	11760.9	4402.7	3515.3	3102.0	5019.2
7709.2	3783.7	5466.4	4494.5	4546.4	4279.8	3450.4	5478.2	3911.9	9046.0	3349.0
522.8	7860.4	8624.3	10187.8	8996.2	9697.3	9311.4	8241.7	8022.8	8973.1	8118.1
48.7	372.3	595.5	678.9	172.3	432.8	327.3	542.7	198.2	40.1	444.0
45.1	576.2	1466.2	1760.4	415.4	625.2	1135.6	1881.9	446.7	609.5	2771.2
81.6	2074.8	1823.6	1764.8	2161.8	2785.7	2923.7	1858.5	1188.0	854.0	1155.1
1566.3	10120.0	6558.9	6803.1	8319.4	7403.2	9147.3	6150.2	6704.3	5056.5	5527.0
379.8	1548.9	1966.6	2276.2	2764.4	1553.4	3449.4	1637.7	862.5	328.4	882.8
1480.4	4657.0	5183.2	5833.7	4679.5	4527.4	7016.7	4721.7	4769.2	3113.1	4317.1
674.8	8145.5	10792.9	10962.2	10683.5	8056.0	14515.9	8237.2	7763.4	3913.8	9911.7
110.3	4239.5	3965.5	4397.3	3896.0	3740.7	4079.0	4270.9	3985.3	3012.0	3899.1
54.1	126.3	207.6	208.4	130.7	136.1	133.1	117.4	62.7	80.9	77.3
16221.9	8093.6	8108.0	8927.4	9305.1	7630.8	10408.1	7476.8	12161.5	10910.1	10320.3
72.4	1730.8	2773.9	3435.8	2913.2	2324.7	3768.8	2045.2	1219.1	1323.9	1283.4
30.1	1148.1	964.3	1070.3	253.5	854.6	500.9	1138.1	295.2	111.2	444.4
3059.1	11931.6	9389.8	10170.8	9688.0	9814.1	11647.0	9665.4	17040.5	14302.4	12984.0
48.6	3009.9	4677.0	5099.2	4569.8	3214.6	6184.9	3078.9	1362.0	1458.1	2707.6
34.0	888.7	1108.9	1262.9	1961.3	414.1	3038.2	367.6	89.2	53.4	215.5
22.7	215.4	492.2	717.4	157.2	259.1	314.4	713.0	255.8	312.1	716.8
3432.9	3900.0	4766.6	5035.7	3546.7	3842.2	5032.5	3985.7	4494.7	3736.2	2922.2
35.0	135.8	105.7	81.6	67.1	77.3	66.2	93.1	99.3	55.9	55.9
63.7	280.9	687.8	613.6	703.4	426.5	673.9	433.4	200.2	237.3	201.7

1641.7	2367.7	724.4
2612.9	2596.0	3496.7
5871.2	6315.0	7154.5
2151.1	1405.1	1481.5
4803.2	4659.1	5509.0
4980.6	4295.1	4561.6
934.6	520.2	512.7
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872.4	899.6	1146.8
4992.4	3202.5	2953.4
4017.5	4703.3	4319.6
941.2	914.3	618.9
5946.4	6953.2	8068.4
959.4	1135.7	1974.9
2264.1	2673.9	3195.8
3238.4	3360.9	4508.5
4018.4	5674.3	4460.2
3644.7	3876.1	4322.6
1246.4	1226.3	1641.9
4048.8	3101.9	3670.7
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8672.2	7190.6	7753.3
562.7	574.7	228.8
781.0	554.4	479.3
1726.3	2293.1	1754.9
6669.4	6121.3	8858.3
1333.0	1174.2	2553.8
3561.9	4358.4	4666.4
6421.4	7394.4	9869.4
3880.2	3583.8	2618.8
153.4	179.1	293.2
7895.9	9853.7	9527.8
1511.8	1648.9	1981.1
1413.1	798.1	725.7
8906.7	11012.4	10399.1
2757.6	2362.3	3198.0
140.6	135.4	465.8
403.0	405.0	97.8
3373.9	4527.9	3248.4
74.8	108.3	44.4
514.7	698.7	356.9

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GQ451287.1 gg_id:584405 Fecal Yunnan snub-nosed monkey feces clone J288 GQ451
AB240279.1 gg_id:144088 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU771159.1 gg_id:310626 Asiatic elephant feces clone AE2_aaa02f05 EU771
AB234241.1 gg_id:148180 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
EF203178.1 gg_id:216042 phylotypes sediments Lake Kastoria Greece sediment clone Kas15B EF2031
DQ807536.1 gg_id:196757 human fecal clone RL307_aam07h03 DQ807
AB240489.1 gg_id:144918 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
AB234242.1 gg_id:150133 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
CR933182.1 gg_id:110176 Evry municipal wastewater treatment plant clone 008F09_B_SD_P15 CR933
DQ404822.1 gg_id:153943 contaminated sediment clone 655950 DQ404
AB243253.1 gg_id:148980 acetone-preserved termite gut clone M2PB4a-005 AB243
EU462500.1 gg_id:293970 Sumatran orangutan feces clone orang1_aai55h06 EU462
EF515298.1 gg_id:223902 Electricigen Enrichment MFC upf microbial fuel cell anode clone 22e09 EF5152
EU465874.1 gg_id:298588 African elephant feces clone AFEL3_aao13d03 EU465
GQ354954.1 gg_id:578372 structure between two geochemically distinct springs Alum Rock Park spring clone 4 GQ354
EU470170.1 gg_id:297727 trancaspain urial feces clone TU2_aaa04c11 EU470
FJ189544.1 gg_id:325619 digester anaerobic sludge clone EUB_23 FJ1895
FJ976448.1 gg_id:575621 Interindividual healthy human oral microbiota mouth clone SB41 FJ9764
AB240238.1 gg_id:141243 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB240
EU246146.1 gg_id:239867 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-C08 EU246
AY667262.1 gg_id:102227 TCE-dechlorinating groundwater clone TANB60 AY667
EU644241.1 gg_id:283400 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
EU101242.1 gg_id:242725 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing w EU101
AY532557.1 gg_id:105221 uranium-contaminated aquifer clone 1013-1-CG49 AY5325
AB015525.1 gg_id:1911 deep-sea sediment clone BD1-16 AB015
EU468899.1 gg_id:288433 Speke's gazelle feces clone SP2_h01 EU468
EF687374.1 gg_id:281862 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
GQ048278.1 gg_id:453933 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ048
AJ229236.1 gg_id:1907 str. PB90-2 AJ2292
FJ437786.1 gg_id:545634 Benthic okenone production Fayetteville New York Green Lake chemocline 20.5 m w FJ4377
EU778706.1 gg_id:335446 Springbok feces clone SBSD_aaa04e06 EU778
AM086159.1 gg_id:150297 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
DQ003617.1 gg_id:125230 human mouth clone MB2_G17 DQ003
CU922957.1 gg_id:547444 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
AY188304.1 gg_id:80197 marine? clone KD3-17 AY1883
DQ799481.1 gg_id:195926 human fecal clone RL305aal86g08 DQ799
FJ716929.1 gg_id:533819 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7169
AB231022.1 gg_id:146449 termite gut wall clone HsW01-040 AB231
EF467587.1 gg_id:214170 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strea EF4675
EF686598.1 gg_id:253230 Sequences Manifest Rumen Yunnan Yel Cattle (Bos Taurus) rumen fluid clone YNRC8 EF6865
FJ484845.1 gg_id:510959 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4848

580.3	3092.4	3728.3	3903.6	3385.8	3220.5	4105.3	3676.0	3001.0	3394.7	3436.6
31.8	1090.6	912.0	479.5	73.0	432.3	1410.3	113.1	571.8	114.0	106.2
336.1	7926.6	6044.5	6907.6	7661.9	5309.2	7518.2	6622.5	5351.7	8116.5	5529.6
39.7	523.3	538.4	552.4	325.1	196.0	918.1	357.2	203.2	70.1	312.8
805.0	5639.6	5375.5	5600.8	6324.7	5221.7	8250.7	4693.8	3627.5	2620.5	4042.1
2149.0	1441.3	1640.9	2235.0	1787.1	1830.7	1664.1	1491.6	2726.1	1964.8	1322.2
5994.9	7734.3	8823.9	10307.3	9154.8	8724.7	9853.6	8336.4	7437.8	4786.0	9381.2
35.8	1800.1	2260.2	2048.7	1999.2	1003.9	2836.1	826.7	776.6	133.6	655.6
61.7	644.6	1141.1	830.7	1104.8	585.9	943.0	769.9	1036.2	152.2	790.4
44.5	1808.1	4204.3	4558.1	3764.1	3125.0	4768.3	2799.9	1330.1	612.2	1957.2
46.6	62.4	108.8	98.9	126.3	200.3	118.9	72.5	41.7	159.4	71.7
8941.9	8141.1	8609.0	9656.5	8797.6	8286.7	10091.5	8622.1	8505.0	9441.7	10220.5
36.8	78.5	122.6	125.0	115.6	97.8	339.1	154.6	51.2	24.8	52.1
4645.9	7258.9	6343.3	6996.1	7546.9	6876.3	7306.1	6526.7	11317.6	7115.8	7923.2
77.0	1786.1	2461.4	3444.5	4163.0	1193.5	5364.8	1328.8	643.7	85.4	1005.1
52.4	3612.0	2824.5	3341.5	2326.2	2858.2	2260.9	3535.5	3078.5	2149.9	2984.7
73.3	2073.3	2350.3	1903.2	1789.0	1642.7	2624.7	1712.6	1708.6	1832.8	3864.6
1280.7	164.2	1048.9	1125.7	1344.3	1493.4	1099.0	1451.5	967.1	668.5	570.7
954.4	5876.2	4962.2	4225.4	4991.6	5633.5	6177.9	4045.8	6060.4	4890.6	4517.8
55.4	1131.2	1523.3	1817.8	2016.1	1233.2	2839.2	1294.4	329.5	281.8	694.4
37.0	164.6	298.2	401.0	85.9	227.5	384.5	127.4	58.9	24.7	136.6
26686.3	11613.2	11908.9	13084.4	11679.2	10831.9	14484.6	10510.9	15385.6	11079.7	16556.2
5588.7	2356.1	3465.5	3865.9	3858.9	2834.9	4946.8	3531.0	1806.0	1040.2	1975.0
338.6	1388.5	2256.8	2234.5	2012.5	1956.5	2710.4	2215.2	2083.1	284.4	2820.1
51.5	412.7	726.3	1075.1	1116.3	457.2	1103.2	486.4	242.0	202.9	319.8
208.3	4734.1	4655.9	5440.3	4321.2	4346.4	5178.2	5440.4	2295.0	2916.5	4508.0
41.4	1897.3	3033.2	2407.5	2557.5	2668.4	3251.0	2919.2	1222.1	1597.5	1632.0
2130.9	2518.8	2811.6	2547.4	2054.9	3310.8	3662.6	3282.2	1912.2	772.6	2560.6
440.4	5877.8	6001.7	5762.3	4899.3	5723.7	7134.6	5748.4	6677.5	4629.0	5626.5
1175.9	7467.8	10314.1	9969.5	9528.5	6617.7	14494.3	7231.5	5377.2	1985.5	8593.4
161.7	6456.9	5450.7	6279.6	5389.1	5231.1	5749.0	5620.1	7063.6	2162.9	4468.0
42.7	2577.9	3772.5	3947.5	4070.1	2927.0	4809.9	2812.1	1650.6	972.7	2088.8
30.9	129.6	338.7	195.5	173.3	173.4	235.2	121.3	93.4	18.7	149.3
1579.7	6810.1	8233.4	8605.9	8792.1	6809.8	10030.3	6630.3	6534.1	5010.4	6188.1
60.9	1059.4	2275.5	2998.8	1915.8	898.3	4396.5	1356.8	515.2	631.6	889.1
2158.5	1655.9	1747.2	2165.6	1655.4	1640.8	1404.3	2164.3	2436.9	1308.1	1724.6
819.1	4816.5	4297.1	4274.2	5461.2	3760.4	5780.7	3676.4	3199.6	2921.0	3248.8
42.1	514.5	574.5	739.0	164.5	558.6	49.2	520.1	525.1	153.8	497.9
54.5	19.5	90.7	16.5	13.4	14.0	7731.0	285.3	19.3	22.3	258.6
83.3	181.5	372.7	435.6	238.7	266.9	232.5	226.9	143.0	321.8	193.6
701.6	5450.0	5376.1	6017.6	5557.7	4845.2	7060.7	5352.4	5430.6	4294.0	4737.1

3688.7	4636.6	4516.4
304.5	229.7	160.6
5886.7	5481.6	6434.8
97.9	206.7	556.1
4229.0	3453.4	5119.1
1419.7	1934.6	1358.1
9126.4	8016.3	7813.6
562.9	748.0	862.1
472.5	1018.0	6627.4
1605.3	2306.2	5355.1
183.9	249.7	327.3
9333.7	7662.8	8027.2
277.8	109.7	156.8
6144.6	7537.3	7721.9
565.8	537.7	539.5
2810.0	2780.8	1987.1
1136.7	1150.2	2119.7
1831.2	1745.0	1435.0
3866.7	3823.7	3740.6
762.5	922.3	2442.0
156.1	140.9	77.4
9791.4	10872.2	10866.1
2702.9	2568.4	2075.6
1221.2	1153.0	855.7
374.0	336.1	145.9
4606.1	3277.7	7214.5
2325.3	1564.8	1811.0
2092.5	3119.6	3011.4
4427.7	4216.4	3387.4
4915.3	5990.6	7319.8
6390.3	4199.1	3672.0
2269.5	2037.7	2924.3
159.9	180.9	188.8
5918.4	5197.2	5637.9
652.7	615.8	739.3
1490.0	2164.2	1611.7
3012.3	3619.3	5951.4
327.5	377.4	629.5
16.4	22.7	11.9
322.2	338.9	167.6
4822.7	5263.6	6020.9

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EU468501.1 gg_id:295553 okapi feces clone OK1_c12_1 EU468
EU748271.1 gg_id:325978 neotropical folivorous flying bird adult hoatzin crop clone hoa46_78F10 EU748
EU464332.1 gg_id:292562 hamadryas baboon feces clone AFBAB_aai02h06 EU464
DQ441269.1 gg_id:194238 human intestinal biopsy clone CD18 DQ441
EU470323.1 gg_id:298928 Grevy's zebra feces clone GZ_aaa01f03 EU470
EU776309.1 gg_id:307692 Red Kangaroo feces clone KO1_aai44h10 EU776
AB185511.1 gg_id:107298 rumen clone F23-A08 AB185
DQ456060.1 gg_id:157620 pre-adolescent turkey cecum clone CFT112H10 DQ456
EU471630.1 gg_id:298746 Asiatic elephant feces clone AE1_aaa03f12 EU471
DQ673532.1 gg_id:162741 rumen fluid clone GRC67 DQ673
AB185713.1 gg_id:101584 rumen clone U28-F04 AB185
AB299527.1 gg_id:238682 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
AB494861.1 gg_id:582555 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
FJ462067.1 gg_id:556399 Microbial ecology industrial digestor mesophilic anaerobic reactor fed effluent chemi FJ4620
EU779085.1 gg_id:327330 Takin feces clone TAK_aaa03d02 EU779
EU748049.1 gg_id:343180 neotropical folivorous flying bird adult hoatzin crop clone hoa2_42a07 EU748
EU779143.1 gg_id:349018 Trancaspian Urial feces clone TU2_aaa02a06 EU779
EU281854.1 gg_id:256305 Eubacterium sp. str. F1 EU281
EU843102.1 gg_id:356053 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EF559120.1 gg_id:225848 mesophilic anaerobic digester clone C35_D7_H_B_F09 EF5591
GU302845.1 gg_id:533344 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
GU083693.1 gg_id:576540 Microorganism Xiarinur soda lake sediment clone x214 GU083
EU461318.1 gg_id:296205 red kangaroo feces clone KO2_aai17a06 EU461
EU748217.1 gg_id:353608 neotropical folivorous flying bird adult hoatzin crop clone hoa32_93E12.F EU748
EU468592.1 gg_id:298415 okapi feces clone OK1_f03_3 EU468
EU778052.1 gg_id:334221 Rock hyrax feces clone RHSD_aaa01f03 EU778
CT573848.1 gg_id:152954 Evry municipal wastewater treatment plant clone 013F06_B_SD_P15 CT5738
AF001767.1 gg_id:1957 rumen clone RF36 AF001
FJ833082.1 gg_id:591925 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q301_01A01 FJ8330
EU474585.1 gg_id:301884 bighorn sheep feces clone BHSD_aaa01f06 EU474
EU779171.1 gg_id:314276 Trancaspian Urial feces clone TU2_aaa02c08 EU779
FJ497327.1 gg_id:577375 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EU747933.1 gg_id:327526 neotropical folivorous flying bird adult hoatzin crop clone hoa12_45E06 EU747
GU303464.1 gg_id:578586 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen epithelium GU303
EU864494.1 gg_id:326247 structures under selection pressure levels antibiotics Xiao River receiving treated ox EU864
AB270021.1 gg_id:169316 Influence temperature and humidity on heifers rumen contents Holstein heifer (Bos AB270
EU843815.1 gg_id:335661 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
AY922190.1 gg_id:114259 whalefall clone 131610 AY922
EU470289.1 gg_id:297914 Grevy's zebra feces clone GZ_aaa03b07 EU470
CU922385.1 gg_id:565660 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
GQ347687.1 gg_id:563702 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347

1133.4	2816.6	2918.3	3938.9	2968.4	2868.2	3166.4	3592.4	2863.8	4409.7	3082.5
830.0	1535.9	1236.6	1693.5	1126.8	856.8	1234.0	943.1	1132.0	1188.5	1229.0
43.2	888.5	537.2	917.5	316.2	1095.6	220.5	326.5	209.2	69.8	267.9
37.4	139.7	128.5	186.1	165.2	96.0	229.2	221.1	50.7	69.4	123.2
5161.0	3907.4	3474.5	4045.8	4331.1	3939.0	4657.7	3977.4	5168.9	4583.5	4379.2
1026.5	1994.7	2105.4	2592.8	1645.4	2184.4	2621.2	1816.6	2242.9	4014.2	2195.5
55.2	878.5	726.5	610.9	548.0	664.9	712.3	492.7	1609.0	1469.3	630.3
237.2	2029.5	1529.2	1150.2	1338.6	1388.1	1120.1	983.3	1203.6	830.9	822.5
6569.1	8287.0	8168.9	11327.8	10562.5	8257.3	9931.3	8495.5	11554.6	8642.6	9768.0
133.1	1256.3	1297.5	1113.6	2507.0	1713.7	2015.7	1691.7	607.0	1168.3	1049.5
34.3	58.6	97.6	117.9	68.3	55.8	59.2	62.3	28.6	28.9	29.6
73.6	3218.5	2304.8	2886.0	2626.6	2384.1	1641.0	2895.4	2048.2	1603.2	1546.7
57.5	55.1	88.8	93.1	101.1	68.1	45.4	52.3	45.6	44.3	44.6
64.9	552.2	581.1	633.0	812.2	451.3	1086.1	429.2	215.0	95.4	175.0
99.3	1342.2	1537.8	1521.0	274.9	1323.5	1023.2	1432.5	438.2	832.6	1063.4
72.1	1806.5	1943.7	1808.1	1190.7	1584.4	1669.8	1654.4	2049.5	2109.9	2076.9
10099.0	7175.7	6835.3	8254.7	6963.1	7172.5	7254.0	7226.9	8147.8	5510.8	10597.6
5297.7	7099.6	7204.6	7617.7	8129.0	7309.1	7998.6	6475.6	5537.9	8375.7	6215.0
393.7	2492.2	2970.8	3423.9	2884.4	2433.3	3321.8	2678.1	2471.2	2084.5	2328.3
44.3	1401.5	1851.0	2504.6	1894.4	1349.2	1873.1	2394.0	558.1	206.7	1733.7
2348.7	6691.3	7099.7	7496.0	8837.0	6207.1	6827.8	6456.6	9495.7	6220.1	7742.6
5086.7	9951.8	8139.3	8442.4	9428.4	6944.4	10053.7	6768.2	9260.1	7501.9	8725.3
730.3	5140.7	5624.9	6413.7	7325.4	5992.9	8963.8	5006.4	2929.0	1770.4	4230.9
206.6	3635.3	4457.3	5637.5	1439.4	3060.3	2737.2	4465.1	1181.2	573.3	3721.3
67.5	826.9	1048.8	1507.1	538.2	995.8	508.6	1056.4	351.3	737.7	484.2
1848.8	5828.0	5523.3	6273.7	5736.7	5602.9	5673.7	5628.6	3778.3	4122.5	5078.3
133.3	870.1	777.7	893.7	719.2	1097.9	524.5	440.6	416.7	240.7	497.2
312.4	806.2	966.1	1223.5	880.0	899.7	1011.4	1012.8	911.2	314.2	1011.6
707.2	3280.9	3777.9	3715.5	3072.7	3344.1	3737.8	3633.2	2357.9	5116.7	2625.1
2078.0	4032.4	4649.3	5214.5	2912.1	4485.9	4991.7	3686.3	4998.2	5591.3	8006.8
533.1	3148.8	3941.0	4502.4	2935.4	3957.5	3257.2	3725.1	1918.1	1904.2	4264.8
38.4	2737.5	3016.4	3657.8	1726.5	2202.6	1614.4	2988.9	4278.8	933.0	2479.2
2454.8	3039.8	2978.8	3193.0	2718.3	2905.8	3335.3	2722.4	3098.7	1886.7	2792.0
224.8	1830.7	2434.0	2591.8	1558.0	2006.0	2363.0	2607.0	1089.7	2015.3	1966.5
12184.1	6064.0	6337.6	6520.3	4354.2	5714.8	7830.5	6148.2	8615.5	6185.5	7875.4
39.3	192.2	150.4	200.8	165.3	156.4	109.5	129.2	151.9	52.3	121.6
146.9	1507.4	1667.3	1734.4	1252.3	1007.4	1635.9	1563.9	1045.4	1277.6	1600.1
36.3	29.8	130.9	68.4	87.8	116.1	73.5	50.2	28.7	24.4	28.2
3316.4	3056.8	2920.9	3838.5	3006.7	2866.4	3078.7	3472.1	2898.0	1880.7	2126.8
53.0	2922.3	4506.5	4958.8	5331.5	2519.0	6336.8	3155.2	1145.7	445.4	3122.1
613.1	4817.4	5930.2	7106.4	5892.7	5446.2	7760.8	6136.0	5924.0	3906.0	5959.5

3836.8	3449.5	5243.2
1380.8	1619.7	1256.7
859.4	1813.0	7211.9
180.6	212.5	223.7
4108.2	3748.6	3585.1
2420.6	2550.9	3150.2
443.8	754.2	1075.8
1257.3	1764.8	2385.6
7939.0	8171.9	8691.4
1391.5	1595.7	3286.6
76.6	109.2	80.8
2544.3	3141.7	10649.0
62.6	57.3	60.7
409.2	302.9	1045.0
1381.4	1158.4	979.6
1614.0	1657.7	2971.5
6299.3	6677.8	7108.5
7799.3	7123.8	12863.8
3061.4	2901.7	2998.1
1846.3	1853.3	4643.0
5913.9	8279.7	6728.4
7450.1	6607.7	7202.4
4853.7	4960.0	10892.3
5501.9	3642.2	6605.9
1404.4	990.6	1705.9
5143.5	7439.9	6630.0
407.0	1488.9	3833.8
799.8	1028.7	1007.6
4142.7	4300.3	4400.7
4223.0	4053.7	4681.5
3781.8	3807.5	4256.8
2326.7	2440.9	2070.3
3403.8	3146.2	3526.9
2601.6	2510.5	2914.7
5001.5	6538.4	6492.6
147.7	119.0	140.4
763.8	1111.8	4473.6
35.3	169.4	65.5
4352.9	4367.1	5080.5
1945.0	2339.6	4552.6
6203.5	5877.7	6491.5

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EU487946.1 gg_id:540386 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
DQ394587.1 gg_id:154077 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
FJ716944.1 gg_id:545501 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United King FJ7169
CU925689.1 gg_id:559384 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EU774568.1 gg_id:312881 Douc langur feces clone DL_1aaa03h05 EU774
EF436442.1 gg_id:216099 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC156 EF4364
AM420249.1 gg_id:237268 Noma subgingival plaque clone 701B10(oral) AM420
AM086109.1 gg_id:146275 Abundance and archaea mesotrophic Lake Kinneret lake profundal sediment clone AM086
EU794185.1 gg_id:351627 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_B46 EU794
CT573907.1 gg_id:153033 Evry municipal wastewater treatment plant clone 012F02_B_SD_P15 CT573
FJ675350.1 gg_id:526207 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6753
EU771153.1 gg_id:311581 Asiatic elephant feces clone AE2_aaa03c09 EU771
EU842960.1 gg_id:308429 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU842
EU776461.1 gg_id:336579 Red Kangaroo feces clone KO1_aai42c10 EU776
EU472392.1 gg_id:289225 Angola colobus feces clone EAC_1aaa02b05 EU472
AM176864.1 gg_id:160369 Recovery mangrove sediment clone SZB56 AM176
AY542556.1 gg_id:113450 Gulf Mexico seafloor sediment clone GoM GB425 12B-2 AY542
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EU470230.1 gg_id:301941 trancaspain urial feces clone TU2_aaa01g11 EU470
AC160630.1 gg_id:137403 Fosmid Clone clone zdt-25h14 AC160
AB487860.1 gg_id:579376 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNSR0 AB4878
EU467513.1 gg_id:292321 Sumatran orangutan feces clone orang1_f02_2 EU467
GU303765.1 gg_id:591227 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
DQ394647.1 gg_id:156519 on -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindee DQ394
GU174038.1 gg_id:578661 Microbial Bactrian camel estimated rumen clone XJC75 GU174
EU771109.1 gg_id:319120 Asiatic elephant feces clone AE2_aaa02b11 EU771
DQ811911.1 gg_id:169882 mangrove soil clone MSB-5A10 DQ811
AB307635.1 gg_id:271588 clay wall used Japanese traditional buildings clone B22 AB307
GQ347420.1 gg_id:568514 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
GQ402123.1 gg_id:591233 alpacas and sheep forestomach clone ALP16 GQ402
FJ832931.1 gg_id:574718 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q101_43C06 FJ8329
AB299528.1 gg_id:248049 Motility Symbiont Termite Gut Flagellate Caduceia versatilis Member 'Synergistes' G AB299
DQ394583.1 gg_id:156411 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
EU779386.1 gg_id:326906 Somali Wild Ass feces clone WA_aaa02e05 EU779
AJ535255.1 gg_id:77623 marine sediment above hydrate ridge clone Hyd89-65 AJ5352
AF001701.1 gg_id:1880 rumen clone RC9 AF001
EF208704.1 gg_id:201885 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2087
FJ833658.1 gg_id:578259 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q402_75C10 FJ8336
EU468305.1 gg_id:294655 domesticated horse feces clone horsem_d07 EU468
AB255907.1 gg_id:167008 Localization Cell Morphologies Members Candidate TG3 and Subphylum Phylum Fibr AB255

236.5	4399.2	4963.8	5085.7	5208.4	3393.6	6647.4	3602.2	3148.6	1267.8	3450.3
114.1	5140.2	4991.3	6031.3	5510.3	5155.8	5933.3	4739.0	5723.5	2298.5	4465.1
380.6	6480.1	7076.1	7500.8	7419.8	6288.8	9451.9	6839.1	4976.6	4373.6	9374.2
1574.2	1312.3	1248.4	1364.9	1270.1	1610.1	1160.3	1085.5	1717.2	1558.3	1744.8
49.1	1271.9	1059.6	1156.6	1180.4	789.5	1331.0	1188.9	667.4	1207.7	883.5
44.2	70.1	106.3	112.8	51.1	48.0	57.2	33.4	37.6	19.2	46.0
39.7	45.1	41.7	47.2	30.8	38.6	33.5	30.4	25.3	19.5	28.8
29.8	1122.6	3366.4	2722.2	1732.1	1352.0	4102.1	1896.9	1341.2	164.8	1448.7
2165.4	5879.9	6543.1	7773.4	6417.7	6772.6	7113.1	7536.6	7017.0	8275.9	6522.8
9122.8	8783.9	9812.8	9170.3	10379.4	8783.0	9814.8	8193.1	12600.8	7656.6	12428.0
62.1	3512.7	3641.8	4277.9	2137.4	2684.6	2488.2	2861.3	1573.7	1110.4	2280.9
94.0	830.3	1000.9	778.8	421.9	519.6	845.8	663.1	436.0	292.7	424.4
4053.7	4468.5	3612.8	5460.0	4018.5	4102.3	4209.8	3774.4	5749.0	3682.2	4236.9
395.6	3265.2	4110.9	4970.8	3452.6	3766.3	4225.4	3680.5	2288.3	1046.7	3189.6
9822.8	5447.5	4876.6	5175.7	5459.7	5140.1	5360.4	5546.2	6947.0	6139.9	5781.6
55.1	424.1	844.2	874.2	597.4	641.6	880.1	497.5	248.6	65.9	502.5
229.3	4630.5	5449.0	6418.5	6053.1	4537.5	8469.9	5058.7	3257.2	2032.2	4639.9
168.2	2446.3	2769.5	3049.5	2866.5	2606.0	3826.2	2807.7	1167.0	680.5	1803.7
228.2	1803.9	1860.3	2066.4	2397.3	1584.7	1831.8	1557.2	1493.5	450.4	955.9
244.1	2407.4	2254.7	2095.7	2103.5	1969.8	2350.2	1990.9	2276.9	2504.6	2190.1
79.7	532.7	625.6	555.7	889.9	1042.3	1131.3	522.7	155.8	92.5	344.3
72.2	3948.3	4079.9	4460.3	4988.1	3545.6	6544.3	3464.9	3078.0	2049.0	3432.7
444.0	4155.0	3197.1	4016.2	2780.9	3159.1	3332.8	3825.5	5662.4	3649.4	3796.0
362.3	3515.3	3328.2	3582.5	2478.9	2868.8	2844.7	3291.4	3136.8	2237.0	3232.5
33.5	51.1	42.9	88.0	22.3	19.3	24.7	19.2	33.0	17.3	36.9
207.7	1949.5	2183.8	2372.7	2973.3	2082.3	2195.4	2070.8	828.9	324.8	1131.9
375.1	5198.6	5844.2	6362.5	6161.1	5773.1	6657.1	6124.5	5322.8	4252.6	5357.7
28.7	229.0	553.1	688.4	722.1	154.0	776.9	260.8	51.2	16.5	126.9
4554.7	7298.6	6818.6	8076.5	7406.7	6996.2	8975.1	6614.0	7635.8	4670.1	8074.0
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60.4	45.9	64.3	74.9	43.5	37.3	39.0	38.6	26.4	27.0	40.3
334.9	3929.8	3616.4	3846.9	3469.7	3976.3	4129.2	4010.6	2650.0	6893.2	3190.7
155.9	2739.3	3709.0	3738.7	3233.9	3178.7	2534.8	3113.1	3018.1	2030.8	3131.3
37.0	173.6	148.5	167.3	113.2	145.2	82.5	313.3	195.4	128.7	53.2
7510.1	4403.3	4347.9	4846.1	3904.0	5316.3	3841.7	5320.7	3722.7	6837.5	6498.6
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36.4	135.1	211.2	260.1	110.2	211.0	113.0	170.2	84.7	53.2	87.9
193.8	3426.0	2657.4	1383.4	1856.7	2665.6	2212.8	2903.9	2363.3	1827.3	1881.6
3003.4	3393.4	2888.7	3133.5	2772.1	3327.3	3898.4	2843.6	2682.5	1390.6	3222.3
9268.7	2106.4	2996.3	2748.0	2969.2	2374.4	3026.1	2504.3	1443.8	1170.1	2053.4
124.0	1343.7	1832.2	2070.5	961.9	1291.0	2241.8	2075.4	1621.3	400.9	2500.9

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5326.5	5950.2	5969.8
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851.4	996.9	2177.9
93.8	125.3	202.6
35.9	55.5	73.8
658.0	768.7	1226.8
8015.7	7291.0	11791.7
7989.3	10270.4	11695.2
2518.8	2830.6	6111.0
532.2	1708.8	389.5
3925.8	5455.9	4291.8
4099.6	3439.7	6082.3
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520.9	471.1	602.8
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2631.4	2219.5	3368.2
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1607.8	2675.2	2021.2
326.0	1453.7	7724.2
3291.7	3400.0	4441.6
3065.5	3966.9	3249.9
2599.5	3041.8	4334.2
36.0	42.5	57.0
1885.3	2858.1	5251.2
4902.7	6377.2	12866.9
163.2	60.3	607.0
7116.4	5758.7	7799.9
4965.2	5071.0	6515.1
57.2	90.9	50.2
4470.1	4011.8	5268.1
2043.9	3471.5	4373.2
189.4	627.9	425.1
6102.0	5423.9	6129.6
1260.7	1321.3	1694.2
214.6	111.2	79.2
1618.6	2044.9	1742.4
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AB494854.1 gg_id:563560 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB4948
FJ832681.1 gg_id:545050 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q401_46F06 FJ8326
EU259440.1 gg_id:238999 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC64 EU2594
EU775732.1 gg_id:346144 Horse feces clone horsem_c07_1 EU7757
EU771161.1 gg_id:305635 Asiatic elephant feces clone AE2_aaa01g12 EU7711
AB185529.1 gg_id:104649 rumen clone F23-C09 AB1855
AF275923.1 gg_id:70875 anaerobic digester clone AA39 AF2759
EU245277.1 gg_id:250289 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B10 EU2452
EF436316.1 gg_id:215985 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC30 EF4363
AB195879.1 gg_id:109166 Anaerobic sludge clone S37 AB1958
EU472605.1 gg_id:292349 Angola colobus feces clone EAC_2_aaa03e12 EU4726
AB192156.1 gg_id:143966 termite gut homogenate clone RsTz-94 AB1921
EU794261.1 gg_id:330660 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_H28 EU7942
EU777058.1 gg_id:328258 Okapi feces clone OK2_c01_3 EU7770
AF371921.1 gg_id:47049 swine intestine clone p-1026-a5 AF3719
EU465732.1 gg_id:293211 argali sheep feces clone AS2_aao34c12 EU4657
EU381985.1 gg_id:258985 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3819
FJ673057.1 gg_id:512290 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6730
EF031097.1 gg_id:189900 Prokaryotic Tirez La Macha Spain endorheic hypersaline atalasohaline lake clone SalB EF0310
CU922295.1 gg_id:554191 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9222
CU922121.1 gg_id:558102 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9221
AB494902.1 gg_id:593289 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB4949
GQ259275.1 gg_id:509761 Microbial activities coastal marine sediments and water column Svalbard deep sedir GQ259
FJ833868.1 gg_id:547889 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q402_91C12 FJ8338
EU469060.1 gg_id:299149 Speke's gazelle feces clone SP2_f08_2 EU4690
EU470252.1 gg_id:295171 Grevy's zebra feces clone GZ_aaa02g09 EU4702
GU302647.1 gg_id:587980 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
EU774538.1 gg_id:305859 Douc langur feces clone DL_1aaa01a05 EU7745
EU734985.1 gg_id:343763 assemblages sediment station DBSE Northern Bering Sea clone 079B21 EU7349
FJ534992.1 gg_id:559276 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5349
EU748041.1 gg_id:337169 neotropical folivorous flying bird adult hoatzin crop clone hoa2_41a11 EU7480
DQ018802.1 gg_id:129393 anaerobic swine lagoon clone C-102 DQ018
AB240491.1 gg_id:143744 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB2404
EU344372.1 gg_id:276301 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU3443
EU779130.1 gg_id:331919 Trancaspian Urial feces clone TU2_aaa01a05 EU7791
EF559197.1 gg_id:217858 mesophilic anaerobic digester clone A35_D28_L_B_D03 EF5591
FJ202260.1 gg_id:337337 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
EU773072.1 gg_id:314825 Banteng feces clone BG_aaa02h03.Contig1 EU7730
AB177222.1 gg_id:133354 seafloor methane hydrate clone ODP1230B6.31 AB1772
AB185691.1 gg_id:99984 rumen clone U28-D05 AB1856
GQ347553.1 gg_id:558459 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347

5870.7	3706.0	3881.5	5246.9	4177.1	4393.4	4986.6	5065.8	4310.6	2480.5	4193.4
92.2	3661.3	3287.8	3857.7	2517.3	2657.4	3805.3	2952.4	1731.4	1441.2	3246.7
2311.5	4396.4	3689.6	3750.5	3393.0	3678.3	3477.8	3390.3	4500.8	2615.7	5011.3
1723.4	3895.3	4376.0	4250.0	3083.8	3460.1	5137.4	3178.7	3260.8	1814.4	4867.5
239.5	6889.1	8748.2	9479.6	8362.0	8075.7	9585.2	8478.9	5821.6	5754.8	7619.5
95.0	2196.7	2463.7	2720.2	2653.0	3367.8	3124.5	2456.3	1378.2	1392.7	2122.5
13374.4	4284.8	4733.1	5172.1	5046.2	3673.3	5478.7	4411.4	4417.4	4704.3	4641.3
1677.0	4114.1	4256.2	4927.1	4417.3	4069.4	5507.1	4770.7	2768.9	2208.6	3620.8
48.8	28.4	30.1	23.3	27.2	26.9	32.6	22.8	19.3	26.8	31.4
27.6	904.8	989.3	1054.0	216.6	729.8	321.8	555.3	281.3	181.0	684.0
935.9	3458.9	3402.3	4520.2	2506.0	3248.8	4233.1	2809.5	3850.6	3349.1	3935.3
97.1	2127.3	3047.3	3525.5	2460.6	2615.3	3226.9	2741.9	1252.6	869.9	1602.4
631.0	3591.0	4192.0	4696.7	4537.0	3927.6	5084.6	4860.4	3957.5	1695.1	3258.4
257.3	5546.3	5537.8	5909.7	6752.6	5520.0	7474.4	5247.9	2831.7	5782.0	4899.0
75.9	163.7	103.6	233.0	199.9	264.3	87.1	136.1	55.7	51.4	73.6
138.8	3581.6	4681.3	5476.3	3971.9	4430.2	4979.7	3987.9	2845.6	1918.7	3842.3
161.3	2175.0	2291.7	2786.1	2310.6	2093.4	3468.8	2422.6	1721.6	964.8	1933.0
165.2	2198.6	3352.3	4091.6	2574.6	2797.7	3597.4	3256.8	1187.9	1481.6	2514.8
67.8	713.0	914.6	693.9	645.5	641.1	1030.6	601.9	110.1	214.0	715.0
2180.1	4771.7	4127.0	3985.1	4100.2	3939.2	3828.0	3260.0	3825.0	1746.0	4217.4
59.1	2490.8	2197.6	2680.8	2912.1	3071.9	2325.9	1289.0	602.8	521.2	1018.5
34.6	1538.3	602.9	630.9	452.3	1016.4	170.1	1072.6	1445.0	550.5	569.7
6392.2	7555.2	6303.1	6844.4	6340.9	5466.7	8257.2	6120.1	8272.9	6829.6	5752.0
3138.1	4364.1	4618.0	4826.4	3982.1	4277.3	5615.0	4338.9	3982.1	4237.9	4323.2
113.2	2759.8	3657.2	4289.7	3586.8	4613.3	3544.6	2626.0	2278.1	1191.4	2225.9
386.8	3889.8	3280.2	3383.6	5172.0	3712.9	4362.5	4217.7	3378.8	3834.3	2476.5
24587.5	4916.6	4475.5	5431.8	4256.8	5398.1	4900.6	4257.5	7886.0	5347.1	6885.7
223.0	2078.5	1742.5	2157.1	2278.2	1790.9	1490.7	1867.4	1587.2	649.2	1032.5
563.0	8035.3	9590.0	10478.9	10435.5	8214.2	13172.7	7951.1	8511.3	4914.7	9806.2
116.2	2322.1	2958.5	3819.4	2895.8	2555.2	4434.1	3407.7	1441.3	289.5	2197.5
122.8	1784.4	2223.2	2747.5	826.0	949.8	830.6	1674.9	375.3	240.4	1163.3
140.2	74.0	116.6	1129.2	363.6	537.9	1086.0	128.5	32.1	889.4	65.1
2899.7	2006.9	2529.7	2310.0	2553.8	2003.2	3329.2	2270.5	3395.5	2311.4	3405.4
614.2	3550.1	3231.5	3220.7	3255.7	2896.4	4248.8	3009.8	3918.9	5315.2	4106.3
526.3	2002.5	1594.1	2144.2	1732.5	1622.1	1862.5	2047.5	1609.4	2311.1	1309.9
39.3	1168.5	967.4	1319.8	820.8	1654.7	455.1	634.9	321.3	1660.3	695.4
25.2	569.4	1056.3	1251.5	949.6	382.7	1528.5	573.9	149.6	212.5	511.6
957.9	5470.1	5540.8	5881.5	6004.1	5284.3	6795.0	6287.9	4024.3	3940.8	5201.1
31.0	379.4	617.9	654.6	700.0	651.7	640.2	651.4	578.6	268.8	331.5
2686.8	6096.2	3844.2	3149.1	2636.1	3981.1	2917.5	2831.0	4736.0	3160.4	2459.4
138.5	2819.6	2380.5	2216.4	2737.1	2682.0	2985.0	2145.0	2837.7	1903.6	2583.0

3241.2	3863.5	4984.7
2976.0	2837.3	4498.1
2911.5	4251.9	3703.7
2650.2	3604.7	4495.8
8676.3	7320.5	13764.3
2795.1	2068.3	8339.4
3958.7	4787.2	5002.9
4655.8	3689.1	7593.5
26.3	32.8	26.4
619.8	1186.6	2355.5
4268.3	3528.7	4003.7
2239.3	2283.5	5056.2
3428.3	4858.7	7853.1
4951.0	4786.3	6463.2
176.1	737.3	1065.6
4459.2	3927.2	7886.5
2197.0	2258.2	3244.7
3464.5	3288.0	4564.6
452.8	953.0	2313.6
2924.2	4316.1	7057.4
986.6	3327.7	11410.4
594.4	921.8	548.7
4373.0	5012.0	5518.0
5710.7	4558.4	5583.2
3511.9	2744.8	5909.6
4562.7	2894.5	4614.3
4350.0	5243.0	4558.2
2205.2	2313.4	6308.5
6309.7	8152.3	10142.6
2744.1	2342.9	3664.2
2261.9	1748.2	2504.6
83.9	906.0	2766.4
1437.2	1614.9	2130.8
2595.8	3601.5	3903.7
1943.9	1938.0	2373.9
1303.8	2079.9	10953.0
315.5	238.9	434.2
5944.3	6452.7	7028.9
471.9	794.7	972.6
2599.0	3006.9	4754.5
1872.7	2052.7	1913.9

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AB191989.1 gg_id:142446 termite gut homogenate clone M2PB4-72 AB191
EU473576.1 gg_id:298864 Somali wild ass feces clone WA_aaa01e11 EU473
DQ456031.1 gg_id:159032 pre-adolescent turkey cecum clone CFT112E7 DQ456
FJ172845.1 gg_id:345477 Qinghai Yak Ruminal and Fungi China rumen clone RB-2B7 FJ1728
EU463760.1 gg_id:303347 domesticated horse feces clone horsej_aai92d02 EU463
EU463415.1 gg_id:291060 domesticated horse feces clone horsem_aai93e04 EU463
CU925021.1 gg_id:563507 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
EU469023.1 gg_id:297758 Speke's gazelle feces clone SP2_b01_3 EU469
CT574143.1 gg_id:156107 Evry municipal wastewater treatment plant clone 061A01_B_SD_P93 CT574
AB234243.1 gg_id:149156 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB234
AM157648.1 gg_id:141722 Cytophaga sp. str. -BI4 AM157
EF436314.1 gg_id:207085 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC28 EF4363
DQ673498.1 gg_id:166526 rumen fluid clone GRC33 DQ673
FJ203657.1 gg_id:351676 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
FJ716343.1 gg_id:513117 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7163
EU259441.1 gg_id:254541 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC65 EU259
AB231048.1 gg_id:150102 termite gut wall clone NkW01-004 AB231
GQ347492.1 gg_id:544518 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AB240481.1 gg_id:142435 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
DQ673480.1 gg_id:173669 rumen fluid clone GRC15 DQ673
EU843787.1 gg_id:342384 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
EU463453.1 gg_id:289260 domesticated horse feces clone horsem_aai94c04 EU463
DQ330518.1 gg_id:159207 Guerrero Negro hypersaline microbial mat clone 09D2Z20 DQ330
EU468496.1 gg_id:294059 okapi feces clone OK1_b09 EU468
AB494915.1 gg_id:563403 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
EU469327.1 gg_id:301613 springbok feces clone SBK_f02 EU469
EU626625.1 gg_id:278732 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
AF001746.1 gg_id:1956 rumen clone RF14 AF001
FJ832802.1 gg_id:585003 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q201_30F04 FJ8328
FJ832848.1 gg_id:548307 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q301_49A07 FJ8328
DQ856504.1 gg_id:245820 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1G DQ856
EU471879.1 gg_id:291143 Asiatic elephant feces clone AE3_aaa01c04 EU471
EU843500.1 gg_id:308739 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU843
GQ347395.1 gg_id:591978 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EF562552.1 gg_id:257527 stable microbial consortia capable degrading complex organic matter paper pulp colu EF5625
EU470313.1 gg_id:299488 Grevy's zebra feces clone GZ_aaa02a08 EU470
GU174039.1 gg_id:556899 Microbial Bactrian camel estimated rumen clone XJC76 GU174
EU748062.1 gg_id:313687 neotropical folivorous flying bird adult hoatzin crop clone hoa2_44b05 EU748
FJ834259.1 gg_id:512857 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A2Q401_31G04 FJ8342
DQ351806.1 gg_id:149262 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
EU779179.1 gg_id:328981 Trancaspian Urial feces clone TU2_aaa02c10 EU779

482.9	1362.0	1532.9	1693.7	1731.7	1519.8	2258.8	1427.2	1797.4	1051.8	1781.9
108.8	2227.9	2794.3	3171.4	821.0	1925.6	1536.9	3502.1	698.6	534.2	2903.6
5848.8	2617.1	2575.6	2683.4	1731.0	2332.4	2991.7	2625.8	2726.3	1576.6	2669.5
39.9	345.2	259.7	582.6	41.7	18.2	36.7	234.7	31.1	18.4	43.3
2031.3	2117.0	2377.9	2793.9	2098.5	1851.5	2966.3	2110.0	1104.0	1571.0	1804.7
2475.7	2428.5	2370.7	2640.7	3056.3	2096.6	2667.8	2400.9	2540.4	2053.6	2515.7
15068.1	7883.4	6704.5	7329.8	7634.0	6789.8	7683.3	6885.0	10640.8	7490.8	10490.1
624.3	2580.9	2837.9	3307.7	2620.5	2908.9	2450.8	3688.3	1391.3	2391.4	2007.9
12716.5	6555.1	6788.6	5430.3	6350.7	6283.0	6644.4	6080.4	10019.6	6146.4	8736.1
90.7	3232.1	3434.2	4123.3	7553.5	2368.9	11755.0	2645.1	1072.9	275.0	1531.5
182.9	713.9	1048.8	1105.6	766.3	676.5	1102.4	933.8	699.8	139.3	691.1
39.3	76.3	136.9	247.8	292.2	64.0	432.2	88.8	30.6	24.0	38.6
54.7	46.1	63.9	67.8	48.9	62.0	48.7	41.2	46.7	35.6	41.3
1897.1	3318.2	4101.8	3377.9	3488.6	2816.6	5718.6	2383.8	2896.3	2432.8	2419.5
64.1	1174.7	1376.2	1484.1	2149.8	2143.8	2739.4	1364.3	609.8	222.3	682.9
151.2	248.5	366.5	259.8	198.4	288.2	243.7	252.8	159.9	136.8	314.9
65.2	3090.9	1848.0	2493.0	2267.4	2181.8	1401.6	2328.3	2077.5	1322.6	1048.9
362.6	3911.5	4353.6	4485.0	5087.8	3776.7	5533.9	4130.5	3319.6	2928.9	4030.5
44.5	2057.8	3779.9	2943.5	1379.3	1412.2	3265.3	1786.3	898.7	227.0	1772.9
21.1	299.5	472.1	243.5	214.8	333.9	249.1	542.1	130.5	82.7	259.5
584.1	4840.8	5100.1	6052.5	4442.5	4571.5	6817.4	4775.3	3724.5	3500.5	5818.7
370.3	3275.5	3963.1	2976.8	4653.4	3147.6	4256.6	3013.0	3024.2	3526.8	3128.9
59.2	2738.1	2309.2	2438.4	1674.8	1174.6	2809.0	1581.9	1618.7	481.5	955.9
361.4	2660.2	2896.5	3409.5	2097.6	3060.8	2536.9	3164.6	1368.3	1478.7	2439.8
39.9	151.4	202.5	285.2	85.8	154.0	146.7	281.5	125.9	42.6	237.6
117.8	3289.4	3002.0	3768.6	2922.2	3158.9	4136.4	2681.1	1380.3	1491.2	2550.2
217.1	4955.2	5934.8	6251.5	6013.1	4618.3	7680.7	5869.0	4341.8	3529.4	5333.9
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1071.8	7283.4	6743.7	7578.2	8107.9	7471.7	6721.4	7386.8	6773.3	8089.8	7415.4
48.1	2552.5	4065.7	3643.5	4038.3	2377.0	5692.9	2779.3	1211.3	564.2	3501.9
1488.5	2940.2	3872.0	4711.4	3345.9	3579.8	4064.2	2887.9	2525.0	528.3	3697.2
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508.7	3595.1	4570.0	4808.8	5235.5	3869.2	5505.1	4398.6	3632.3	1986.3	3888.7
5902.6	7243.1	6721.7	7265.7	6165.9	6880.7	7078.0	7015.0	7632.8	5839.0	7789.3
87.5	909.9	1578.4	1223.3	646.7	1194.9	837.1	1051.6	325.5	1555.7	534.0
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679.2	1439.5	1226.4	1604.1	856.7	1114.6	1356.5	2219.6	798.3	521.6	2320.3
475.0	1199.8	1572.8	1533.2	998.2	1109.5	2112.7	1309.2	731.8	628.1	1437.6
137.1	4303.6	5624.0	6285.0	4440.3	5020.7	5390.5	5149.8	3158.5	2096.6	4865.6

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2252.3	2018.9	2056.5
2335.3	3097.9	2948.4
6788.6	8675.8	11025.0
2776.6	3402.1	4105.0
5951.2	7251.3	8310.8
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56.1	51.4	37.5
125.6	76.1	77.1
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287.9	296.5	568.5
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2646.2	4060.3	6070.3
926.2	1013.4	1643.9
3474.9	2950.8	5422.6
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3012.4	2875.0	7042.9
4045.4	5023.4	4803.6
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1769.2	2192.8	1933.8
6190.8	6294.3	7077.9
2175.8	1964.9	3400.2
3562.2	3041.9	5057.5
5064.7	7379.2	10666.8
3871.5	3019.0	4055.4
7491.2	7091.4	7916.0
2257.9	1103.9	1418.9
2769.4	2430.7	2473.5
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610.8	1441.8	1304.0
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EU462559.1 gg_id:293458 Sumatran orangutan feces clone orang2_aai65b03 EU462
AB231046.1 gg_id:150318 termite gut wall clone NkW01-010 AB231
EU776268.1 gg_id:335713 Red Kangaroo feces clone KO1_aai43e05 EU776
EU461047.1 gg_id:302016 red kangaroo feces clone KO1_aai43a10 EU461
EU468838.1 gg_id:296958 okapi feces clone OK3_f06_2 EU468
AB494857.1 gg_id:588984 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB494
FJ832825.1 gg_id:536508 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J3Q201_76D10 FJ8328
FJ497383.1 gg_id:549719 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4973
EF445286.1 gg_id:207764 dairy cow rumen clone NED4H2 EF445
EU850526.1 gg_id:341942 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF312 EU850
EU259388.1 gg_id:247308 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC12 EU259
CU919638.1 gg_id:559287 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
AM420001.1 gg_id:250872 Noma subgingival plaque clone 102F04(oral) AM420
GU302721.1 gg_id:549765 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
DQ018790.1 gg_id:130880 anaerobic swine lagoon clone C-16 DQ018
EU842535.1 gg_id:329727 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
EF453830.2 gg_id:226064 termite hindgut clone 290cost002-P3L-1187 EF4538
FJ833406.1 gg_id:542721 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J1Q101_65A09 FJ8334
EF436451.1 gg_id:207769 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC165 EF4364
AF419690.1 gg_id:42167 Guaymas Basin hydrothermal sediment clone C1_B008 AF419
AB519265.1 gg_id:531670 Identification Major Acidogenesis Methane Fermentation Reactors Ambient Temper AB519
FJ833110.1 gg_id:588658 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q301_54F07 FJ8331
EU358698.1 gg_id:317871 structure archaeal denaturing gel electrophoresis and sequencing mesophilic biogas EU358
EU461939.1 gg_id:293725 white-faced saki feces clone Saki_aaj64b03 EU461
EU473583.1 gg_id:291747 Somali wild ass feces clone WA_aaa04h08 EU473
EU470042.1 gg_id:300082 trancaspain urial feces clone TU1_aaa01c10 EU470
EU464195.1 gg_id:299917 reticulated giraffe feces clone gir_aah96a03 EU464
AB185695.1 gg_id:100612 rumen clone U28-D09 AB185
EU465542.1 gg_id:291169 argali sheep feces clone AS1_aao37c10.Contig1 EU465
EU771187.1 gg_id:348911 Asiatic elephant feces clone AE3_aaa01d12 EU771
AB243257.1 gg_id:148372 acetone-preserved termite gut clone M2PB4a-094 AB243
EU344342.1 gg_id:260440 Foregut Fermentation Birds: Hoatzin Crop Supports Case Convergence Ruminants ad EU344
EU462709.1 gg_id:295701 Sumatran orangutan feces clone orang2_aai67f12 EU462
EF436305.1 gg_id:214424 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC19 EF4363
EU470020.1 gg_id:288652 trancaspain urial feces clone TU1_aaa04a04 EU470
EU748102.1 gg_id:305543 neotropical folivorous flying bird adult hoatzin crop clone hoa2_43b07 EU748
EF436356.1 gg_id:209931 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC70 EF4363
EU842409.1 gg_id:332099 metagenomics random sampling pyrosequencing rumen fluid pooled liquid phase mi EU842
CT573886.1 gg_id:152026 Evry municipal wastewater treatment plant clone 013A02_B_SD_P15 CT5738
EU464524.1 gg_id:301331 African elephant feces clone AFEL_aai30e11 EU464

67.2	1243.1	1482.3	1267.5	2421.6	1338.1	2585.2	1035.3	486.0	264.9	607.7
1555.2	2946.5	3256.8	3685.7	3406.1	3228.4	3626.8	3969.0	2376.3	1063.3	2809.4
3685.0	7926.3	7681.8	8122.7	6884.6	7483.9	6664.3	8356.7	8859.7	8953.1	9208.9
57.5	2034.7	2871.4	3688.1	1844.9	2213.8	2554.9	2597.6	756.1	597.0	1453.3
126.7	3428.3	4546.2	5357.5	3594.5	4243.2	4631.1	3873.7	2804.8	2054.7	3798.7
1488.7	5385.4	6645.1	7713.9	5634.6	5993.7	7345.1	6854.5	3722.2	4458.9	6007.5
56.2	608.2	1077.4	946.3	1325.7	870.2	982.8	1046.9	476.4	334.8	413.1
493.4	3285.0	3551.4	4117.0	3012.1	4021.7	3551.0	4568.7	4807.3	2440.5	3431.5
36.7	40.4	46.9	42.5	29.1	19.9	50.4	33.2	25.7	23.3	37.8
1744.1	457.2	422.6	379.0	483.5	352.7	342.9	421.3	696.7	678.1	404.2
7655.6	3498.0	4368.6	4241.1	4226.9	3547.6	4866.2	3843.2	3336.7	2276.0	4666.4
60.5	2545.6	2559.2	3356.9	1578.7	2570.7	1601.0	2115.9	937.4	1938.6	1948.3
95.3	1423.0	1449.3	1646.9	1426.1	2033.9	1780.6	1004.1	896.2	321.1	1269.9
37.8	160.1	288.4	440.6	202.2	178.5	301.5	200.7	47.0	31.6	55.1
60.2	638.9	960.2	990.5	712.1	741.3	140.1	884.7	491.2	455.7	465.5
50.6	586.9	1404.4	1234.4	1880.8	1730.5	1546.9	1187.6	936.0	897.9	843.1
58.5	2593.8	2775.8	3149.5	2454.8	2826.9	3375.9	2892.4	1772.8	1275.4	2556.6
87.9	1512.0	2076.5	2138.8	2075.1	1172.3	3806.8	1919.2	653.3	143.6	1143.8
4901.5	6872.7	7931.5	8921.4	7980.4	7438.5	8920.4	7545.2	6837.8	7148.1	8407.1
979.7	3051.2	3592.7	3873.2	2951.4	2939.8	3387.8	3544.2	2753.6	3753.7	3237.1
38.9	841.5	1171.6	1297.8	1916.2	997.0	2110.0	1092.0	1326.4	118.7	891.5
632.8	4183.9	4433.3	4678.8	3476.0	3634.8	4509.7	5266.2	3254.1	2258.5	5345.6
173.3	3630.0	4247.4	4641.4	3575.0	3938.3	4501.4	4342.6	3005.2	3139.3	3583.0
51.7	1862.5	3333.0	2511.7	2251.0	2322.7	3836.4	1989.4	2263.5	349.8	2175.8
144.1	842.0	946.0	1305.3	602.7	932.0	859.0	1246.9	311.5	260.8	550.9
250.6	1855.7	3070.4	2249.4	2724.5	2500.4	2882.6	2769.9	1207.9	2578.0	1847.1
5863.8	7720.7	5930.1	6273.3	5861.2	6297.3	6248.9	5730.3	7254.1	3873.0	7888.7
370.5	1470.0	1447.6	2264.6	1450.5	1601.4	1896.1	2199.8	1345.3	1219.2	1238.1
50.0	198.7	165.3	171.4	58.2	86.3	36.0	78.0	23.8	25.5	37.9
272.2	3884.7	4696.7	5059.1	5518.5	4392.9	5262.8	4417.3	5057.5	3344.9	3723.4
92.8	2526.1	2777.4	3159.8	1154.3	2196.7	1534.5	3180.2	1058.3	681.2	2395.3
34.1	523.2	493.4	604.6	351.5	334.6	358.6	563.1	311.6	206.4	276.4
6657.0	7043.0	6646.3	6920.0	7933.2	6901.1	7057.2	6565.7	10145.3	6965.0	7333.6
118.6	2491.7	3397.5	3761.0	2664.6	2776.6	3717.9	3167.3	1554.9	1913.1	1970.2
45.4	43.5	59.2	76.4	85.5	65.3	67.3	56.9	43.6	31.0	37.6
52.2	1186.4	1118.7	1633.8	251.1	552.6	313.8	563.6	287.2	220.3	376.4
1071.8	705.7	511.6	715.0	293.1	383.0	193.4	557.4	208.5	274.3	191.4
74.1	42.1	53.1	65.8	51.5	33.9	49.9	86.9	39.5	22.4	46.2
810.3	1430.7	1836.5	2129.2	1249.8	1319.1	1382.9	1281.5	991.3	413.5	1385.6
7102.8	6027.0	6758.8	6458.4	6392.9	5629.3	6654.3	5609.5	5303.4	3324.5	7517.9
1806.0	4586.6	4419.7	4515.5	4331.0	4485.2	5548.8	4635.4	3547.0	5198.1	4160.2

756.6	1576.3	2011.8
2693.5	3595.5	3798.9
6553.9	6836.8	7718.0
3650.2	2479.6	3198.9
4445.0	3713.9	7309.8
7207.2	6293.8	9816.7
820.9	1258.0	851.3
3018.4	4183.3	5579.6
34.1	45.2	24.5
341.4	241.2	620.4
4128.1	3783.1	4465.0
3792.1	2995.9	6430.3
945.0	2456.0	4284.1
195.6	164.0	374.0
1136.1	829.2	1107.0
691.8	2787.6	5637.6
3172.1	2945.7	4004.1
885.4	914.2	1390.5
7886.9	7133.8	9406.9
3921.0	5033.8	8028.8
782.6	717.6	816.7
2954.4	3058.0	6593.6
3953.4	3993.1	6557.9
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1556.7	1722.6	1483.5
2652.7	2799.1	3565.1
5164.0	6146.2	5786.5
1896.9	1936.8	3183.0
199.6	472.3	1570.7
3611.6	3332.1	5534.3
2700.2	2577.3	8105.5
449.7	487.6	924.0
6293.5	7712.5	8558.1
3249.0	3221.4	4141.0
97.7	108.0	92.7
1345.9	1444.6	2346.9
750.8	779.4	2343.1
51.5	108.7	62.5
1791.0	1308.2	1441.6
4790.1	5713.7	7386.9
3884.9	5263.7	11770.9

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EU259395.1 gg_id:246553 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC19 EU259
EF105951.1 gg_id:203509 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 2 EF1059
GU303987.1 gg_id:578597 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU303
AB231019.1 gg_id:145206 termite gut wall clone HsW01-015 AB231
GQ261754.1 gg_id:510100 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
EU871375.1 gg_id:345149 Genetic Bovine (Bos taurus) Rumen Thailand clone CF196 EU8713
EU474816.1 gg_id:300128 takin feces clone TAK_aaa02a08 EU4748
AY160852.1 gg_id:104105 termite intestinal tract clone COB P3-5 AY1608
FJ264575.1 gg_id:323109 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2645
EU474478.1 gg_id:287662 bighorn sheep feces clone BHSD_aaa02g12 EU4744
AF050544.1 gg_id:1884 contaminated aquifer clone WCHB1-29 AF0505
EU469956.1 gg_id:296260 trancaspain urial feces clone TU1_aaa04d11 EU4699
EU245190.1 gg_id:254208 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-G12 EU2451
CU918047.1 gg_id:570261 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
GQ348451.1 gg_id:546087 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EU843373.1 gg_id:345767 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
CU917556.1 gg_id:547076 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU917
EU458663.1 gg_id:291841 European rabbit feces clone RA_d06_1 EU458
DQ455992.1 gg_id:158008 pre-adolescent turkey cecum clone CFT112A3 DQ455
EU246069.1 gg_id:252310 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-G07 EU246
AY280418.1 gg_id:105877 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
EF687321.1 gg_id:283513 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) s EF6873
EU469052.1 gg_id:300161 Speke's gazelle feces clone SP2_e07_1 EU469
FJ833148.1 gg_id:565398 Microbial Ecology Crop Folivorous Hoatzin crop contents clone A1Q401_40H05 FJ8331
CT574088.1 gg_id:153576 Evry municipal wastewater treatment plant clone 053C03_B_DI_P58 CT574
FJ152986.1 gg_id:338988 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
EU245179.1 gg_id:243547 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H3-F07 EU2451
CU918811.1 gg_id:569212 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
GU302875.1 gg_id:569543 inhabiting epithelial tissue ruminal digesta -DGGE and sequencing rumen contents c GU302
AB175367.1 gg_id:103316 mesophilic anaerobic BSA digester clone BSA1B-13 AB1753
AB288907.1 gg_id:202195 termite gut homogenate clone BOf6-19 AB2889
EF603097.1 gg_id:227778 Salmonella typhimurium Exploits Inflammation Compete Intestinal Microbiota mous EF6030
CU466749.1 gg_id:341960 Evry wastewater treatment plant anoxic basin clone CU466
EU777829.1 gg_id:311444 European rabbit feces clone RA_f05_3 EU7778
GQ357018.1 gg_id:509437 Metal Dependent Marine Methane Oxidation methane seep sediment clone FeOrig_ GQ357
DQ330405.1 gg_id:159414 Guerrero Negro hypersaline microbial mat clone 02N1A225 DQ330
EU662472.1 gg_id:533502 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU6624
CR933139.1 gg_id:110799 Evry municipal wastewater treatment plant clone 012E05_B_SD_P15 CR9331
AB494948.1 gg_id:583826 Fibrobacter succinogenes dominated consortium on hay stems sheep rumen clone N AB4949
AB185523.1 gg_id:103729 rumen clone F23-B11 AB1855
EU465836.1 gg_id:289466 argali sheep feces clone AS2_aao36e06 EU4658

46.7	459.9	214.1	191.3	210.9	290.5	224.0	300.2	120.4	122.5	193.4
71.4	449.9	798.9	850.3	759.4	360.7	1336.2	402.9	187.0	86.7	495.2
207.9	2151.0	2947.7	3610.5	3537.2	2194.6	4453.5	2565.3	1750.9	1296.2	2625.6
3774.0	3500.7	4210.1	4042.5	3831.1	3425.9	5590.6	3795.1	2146.8	3965.3	2619.8
43.3	327.8	451.1	440.1	435.8	226.9	455.2	364.5	224.1	66.5	225.7
2941.0	3296.5	3547.0	2962.3	3095.4	2895.7	3167.3	3767.9	3837.1	3150.6	4780.5
95.0	1361.0	1846.4	1688.5	1160.7	1605.2	1274.9	1436.9	768.5	537.6	1124.4
52.8	28.8	55.4	34.5	77.7	36.4	116.9	38.6	31.6	31.0	51.0
359.8	4648.6	3455.5	3608.9	4005.6	3465.6	4443.5	4288.6	4700.2	3132.1	3003.9
12765.0	3386.1	3025.9	3822.1	3523.6	3213.7	3293.3	3684.4	4072.7	5911.4	3015.4
49.3	86.9	87.9	82.5	76.2	41.5	63.0	46.1	36.0	24.8	38.2
1426.1	4774.0	5368.6	6326.9	4501.5	5954.8	5369.6	5732.1	3295.9	4030.3	5330.6
325.7	3624.3	5266.3	5080.0	5524.1	4945.1	8237.2	4578.0	4465.2	2448.7	3404.9
636.3	1624.3	1795.7	1751.3	1814.8	1643.3	1772.7	1781.3	1570.2	2468.5	1798.3
12182.6	8673.0	8292.6	8558.3	9337.1	8341.4	9398.3	7731.4	14896.5	12430.8	11803.6
36.4	525.4	493.9	905.4	120.3	225.3	238.7	307.4	30.0	44.2	99.8
47.3	228.3	501.1	411.6	220.2	546.5	247.9	620.9	456.5	742.8	458.4
539.1	6161.4	6402.1	7759.1	2971.2	5357.6	5831.5	7131.9	3042.3	2848.0	7193.9
140.8	4679.1	4711.8	6220.8	1531.4	3668.5	3103.1	5082.1	1529.9	849.1	5891.2
474.9	5092.0	6022.1	6887.3	6662.5	4930.7	9029.6	5761.4	4905.0	2736.3	6547.8
75.5	42.0	37.1	73.5	52.9	31.3	53.0	35.2	42.0	28.5	65.0
83.6	319.6	408.4	500.5	604.0	373.0	692.8	688.0	265.4	45.3	234.8
65.7	350.1	649.7	1026.9	244.0	266.6	193.2	477.0	88.1	213.1	332.7
474.1	6596.0	6740.5	8103.9	4599.3	6001.0	6445.1	7102.9	4024.5	4459.6	7152.0
52.9	252.9	256.0	277.2	566.3	872.8	91.0	120.9	72.2	37.1	86.5
38.7	2559.7	3879.4	3853.5	3282.3	1974.7	5126.4	2842.2	1026.3	281.7	2005.1
53.7	1719.9	2350.2	2291.5	1919.0	2328.4	3390.7	2173.0	640.0	974.2	1321.0
11296.3	5153.5	5017.0	5529.3	4856.5	4606.9	5209.6	4793.7	5731.0	4533.1	6732.6
1989.8	2698.5	3231.3	3711.7	3347.2	2787.6	2765.4	2442.1	4088.6	2266.5	2856.9
439.2	616.7	649.4	669.5	615.3	876.4	594.2	525.6	476.3	296.3	319.1
64.0	1359.4	1572.5	1947.6	1956.5	1186.4	2257.6	1515.8	946.1	597.7	1129.1
40.5	526.7	412.7	419.9	337.9	241.9	415.0	208.9	374.0	64.2	84.8
7260.4	4428.8	4505.6	4564.2	3387.1	4192.1	3865.7	4219.5	5881.3	5305.5	4497.7
19220.3	15463.1	14678.7	15621.8	14918.4	14070.1	17092.8	13500.4	20706.1	19251.3	18141.3
103.3	1861.2	2309.4	1821.6	1986.6	1604.9	2520.2	2525.2	767.7	843.6	1125.4
45.7	275.4	463.1	402.2	164.6	66.3	265.6	177.1	56.2	29.2	65.4
51.4	421.4	773.8	1922.2	656.5	520.9	2696.0	648.7	119.4	28.2	347.2
38.8	27.4	25.3	25.3	30.1	32.8	25.4	26.0	29.0	27.0	22.4
894.9	6010.6	6410.8	7163.9	5822.0	6809.2	6147.3	6697.0	5170.9	4696.4	6067.2
866.9	804.2	786.7	800.7	769.7	715.8	1059.0	610.4	695.3	771.7	838.2
112.9	916.8	1481.9	1652.2	1446.4	793.8	1842.5	1408.1	2752.6	124.7	787.0

225.6	621.2	4725.6
274.8	410.6	872.4
2856.5	2281.9	4670.5
3273.4	4342.5	4470.6
218.2	466.8	310.5
3595.5	3734.1	3926.6
1482.0	1957.2	4646.3
60.2	47.8	29.4
3556.9	3521.6	3853.2
4248.1	5345.4	4824.0
46.8	131.8	74.1
6494.0	5435.7	8727.0
3966.4	4475.6	4453.9
1625.6	2528.0	11891.5
7570.6	8930.8	9361.3
878.6	336.6	333.4
458.3	500.9	2613.1
7448.1	5848.8	10135.5
5311.7	3913.0	8629.0
4655.7	4588.7	6408.5
26.3	27.2	20.0
341.7	710.5	485.6
875.2	486.8	853.3
7735.2	5790.2	9913.0
104.1	1378.6	5089.8
1172.3	1536.2	2160.0
1541.7	1136.7	912.2
4839.5	5523.8	6091.4
2191.7	3880.2	2413.6
374.1	1686.5	2468.4
1419.1	1982.4	4636.2
194.6	224.3	95.6
4091.3	4809.1	3891.5
13948.0	14363.1	16666.1
1847.5	1533.1	1966.9
47.9	49.8	118.2
321.4	220.1	580.6
24.7	27.0	718.1
6043.4	5969.1	10053.6
607.0	1393.1	862.1
948.3	2134.0	2444.2

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AY160853.1 gg_id:203506 Abundance and Axial Intestinal Tract Two Soil-Feeding Termites (Cubitermes spp.) te AY1608
AF029041.1 gg_id:2476 Benzene mineralizing consortium complete clone SB-5 AF0290
EU779275.1 gg_id:303504 Trancaspian Urial feces clone TU2_aaa02g06 EU7792
FJ172867.1 gg_id:356189 Qinghai Yak Ruminal and Fungi China rumen clone RB-3B2 FJ1728
EF436379.1 gg_id:211575 library-based ruminal water buffalo (Bubalus bubalis) rumen fluid clone BRC93 EF4363
FJ832615.1 gg_id:510752 Microbial Ecology Crop Folivorous Hoatzin crop contents clone P3Q302_51C07 FJ8326
FJ497446.1 gg_id:534938 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4974
EU472504.1 gg_id:299841 Angola colobus feces clone EAC_2_aaa03b12 EU4725
EU644103.1 gg_id:280540 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU6441
FJ833777.1 gg_id:581418 Microbial Ecology Crop Folivorous Hoatzin crop contents clone J2Q301_45E06 FJ8337
EU771454.1 gg_id:311474 Hamadryas Baboon feces clone AFBAB_aai01g05 EU7714
AB294310.1 gg_id:209429 Microbial structure deep coal seem groundwater clone YWB41 AB2943
EU794094.1 gg_id:342089 bovine microbiota via oligonucleotide fingerprinting genes fecal clone EMP_O10 EU7940
EU843760.1 gg_id:342684 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8437
AY244963.1 gg_id:84869 cow rumen clone BS9 AY2449
AB121104.1 gg_id:100286 cold seep sediment clone JS624-9 AB1211
EU850501.1 gg_id:311418 Genetic swamp buffalo (Bubalus bubalis) rumen fluid clone BF271 EU8505
EU843362.1 gg_id:347678 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8433
FJ517042.1 gg_id:565133 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
AY667260.1 gg_id:101918 TCE-dechlorinating groundwater clone TANB53 AY6672
CU924843.1 gg_id:567660 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9248
EU655924.1 gg_id:285831 influence dietary flavonoid-containing extracts on gut microbiota mouse feces clone EU6559
EU843935.1 gg_id:336049 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8439
AJ534683.1 gg_id:75351 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
EU779491.1 gg_id:330732 Grevy's Zebra feces clone GZ_aaa04h10 EU7794
FJ679020.1 gg_id:524048 Synecology primary and secondary habitats Escherichia coli O157:H7 fecal MARC bee FJ6790
EU748268.1 gg_id:347900 neotropical folivorous flying bird adult hoatzin crop clone hoa45_25A04 EU7482
EU246065.1 gg_id:250662 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P2-F12 EU2460
EU772481.1 gg_id:307991 Hamadryas Baboon feces clone BAZ_aah90e10 EU7724
GU455026.1 gg_id:529619 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
AB185756.1 gg_id:104352 rumen clone U29-B07 AB1857
DQ673584.1 gg_id:161764 rumen fluid clone GRC119 DQ673
EU382048.1 gg_id:264591 Rumen eubacterial implicates Bacteroidetes major phylum rumen particulate phase EU3820
EU472952.1 gg_id:302010 douc langur feces clone DL_1aaa03h01 EU4729
DQ415754.1 gg_id:157385 Dominant microbial limestone-corroding biofilms system Italy Frasassi sulfidic cave s DQ415
FJ516916.1 gg_id:554336 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled upper s FJ5169
AB243255.1 gg_id:148852 acetone-preserved termite gut clone M2PB4a-023 AB2432
EU461358.1 gg_id:300177 red kangaroo feces clone KO2_aai18f05 EU4613
AB240370.1 gg_id:141173 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403
EU468998.1 gg_id:302775 Speke's gazelle feces clone SP2_e12_2 EU4689
DQ334621.1 gg_id:175084 Impact metals on sediments heavy metal polluted marine sediment clone HB2-15-3(DQ334

614.7	1998.9	1701.6	2315.3	2728.4	2001.7	1926.4	1871.9	1712.7	1035.5	3886.7
36.0	340.0	688.3	686.1	782.9	391.5	1344.6	498.0	194.3	175.8	295.5
1280.4	5021.9	5159.0	5640.9	6248.1	4945.6	6411.7	5348.6	6664.5	5540.2	6044.1
490.8	1901.9	2243.2	2137.3	2026.8	1876.6	2311.9	1830.1	1316.4	932.7	1663.2
564.3	2992.6	2635.2	3160.8	3296.1	2731.9	1884.5	2260.7	2561.9	1280.2	1548.8
1580.2	4676.7	4934.6	5065.6	4454.5	4075.3	4304.2	4315.1	6047.9	4706.7	4844.1
876.8	8327.5	6861.6	7443.0	6200.6	7076.5	7394.8	7259.1	11705.9	9462.1	7640.8
4438.2	3588.7	3973.6	4535.1	3590.2	3703.0	4805.1	3749.8	3814.6	3519.6	3738.3
504.4	3371.2	4238.1	4358.0	3239.6	3206.3	4819.6	3829.9	4474.7	3170.7	4095.7
925.5	4555.4	5285.7	5191.4	4676.9	5054.7	4833.3	5177.5	7337.3	4858.3	5527.0
561.7	3218.5	3546.9	4073.9	3830.0	2978.0	4422.7	3574.8	2111.2	1296.1	2924.0
326.5	583.4	465.1	363.2	541.5	457.6	464.9	418.2	268.8	278.8	457.6
146.4	2770.6	3185.9	3806.8	2705.7	3353.8	2622.0	2594.4	1311.4	1233.8	2085.5
4091.6	7818.9	7859.8	9029.6	8156.5	7679.1	9886.8	8016.5	8726.9	8266.3	8510.1
131.1	2984.9	2970.2	2130.8	2592.2	2918.5	3382.3	2991.7	3803.1	3162.9	2983.5
68.0	1589.5	1817.5	1939.5	2442.2	1579.9	3303.6	1401.6	735.6	674.3	966.5
42.7	76.8	87.9	128.9	45.6	98.5	27.7	41.9	29.4	30.7	44.8
1281.0	1585.7	1285.2	1312.7	1944.7	1252.0	1914.5	1267.2	1161.7	859.9	1228.1
209.9	4161.7	5115.0	6376.7	7179.6	4555.5	9695.7	4781.3	3584.1	3181.2	5335.6
1187.1	4053.4	4308.9	4038.2	4900.6	3907.0	4503.6	4492.4	4068.5	2823.2	4688.9
40.0	999.2	951.7	1204.0	1409.2	2616.8	374.4	336.6	287.8	118.3	342.4
39.0	336.6	495.1	666.4	228.1	267.1	262.1	425.8	173.8	397.1	269.4
2859.0	2879.7	2734.6	3080.4	2818.5	2859.4	3417.1	2963.5	308.9	2774.4	2303.0
111.8	554.0	889.8	1099.8	455.6	548.2	767.6	865.1	767.3	429.2	919.3
106.1	2072.6	2494.3	3073.5	684.2	1805.0	1588.6	2713.6	749.8	514.3	2551.9
223.4	968.9	995.8	874.2	800.5	788.3	1080.0	991.2	821.9	3531.9	977.0
51.0	1592.6	2080.4	2718.7	754.6	1318.4	1076.4	1464.7	334.9	293.4	666.4
43.1	32.0	38.8	50.1	47.1	37.8	36.2	38.6	39.3	26.3	39.1
420.3	3007.5	3045.6	4238.9	2895.6	3128.1	3720.8	3986.8	2047.9	904.0	2464.8
1112.3	2537.3	2718.6	2506.1	2086.2	3159.9	2033.4	3471.1	3719.0	3423.9	2551.1
36.8	65.0	91.7	103.4	77.4	109.5	36.3	152.1	35.0	25.7	57.9
75.6	466.1	267.7	332.6	308.5	363.3	622.1	255.4	216.2	135.7	158.8
55.8	2230.5	2105.1	2427.8	1543.8	1690.7	1840.7	2274.7	2081.0	1669.5	1942.2
682.5	5247.9	4321.6	4621.0	4664.3	4513.4	4979.7	4308.8	6755.6	5298.6	5434.3
35.3	1122.7	1310.7	1257.9	1569.5	1395.4	2455.7	1372.8	467.5	209.5	692.7
1347.6	10408.9	9762.9	11760.6	12309.5	9099.9	12201.1	10828.3	11284.3	5980.3	11093.0
5366.3	6098.8	5356.0	5773.3	7005.1	6213.0	7787.2	5621.1	7130.6	4839.9	5844.9
109.4	2430.9	2980.7	3495.6	1433.6	2533.3	2440.2	3133.5	1002.9	1059.0	2247.3
75.3	200.8	333.7	345.3	394.1	343.6	543.4	290.3	117.0	101.2	216.9
494.3	3877.7	4955.5	4191.7	3935.6	5013.7	4089.7	3921.5	3863.9	4188.9	3674.7
40.7	1355.6	2159.7	2681.5	2908.9	955.0	4070.8	1427.8	420.0	338.7	916.6

1752.3	2217.4	1821.2
378.9	431.4	431.2
4603.3	5550.0	7561.9
1695.6	2220.1	3165.2
2117.2	3763.7	9475.1
3984.1	5080.8	5968.2
5703.4	6693.2	5733.1
3941.6	3812.0	4343.5
3028.7	2869.9	3523.9
4311.8	4960.1	4321.5
2967.9	3593.5	5346.9
428.2	614.9	405.0
3352.3	3116.5	4952.2
7304.0	7980.5	7271.3
2597.5	3479.3	4348.3
1302.5	1564.0	2774.7
86.0	222.4	957.0
1141.1	1937.0	2504.0
3531.3	3845.8	3888.4
4068.5	4172.7	3116.6
375.5	3474.1	15673.0
606.2	410.1	188.3
2975.1	2544.0	2735.9
388.5	1413.8	1753.2
3126.9	2165.1	3752.5
1027.4	942.8	785.6
2898.7	1841.2	1761.8
35.5	62.0	40.3
3602.1	4114.9	5911.1
1493.8	2591.6	1754.2
96.9	512.1	384.4
265.6	266.2	314.0
1644.6	1735.9	1286.5
3944.8	5027.5	5206.6
882.1	1247.9	1985.3
9084.7	10117.3	10096.9
5688.2	5903.3	5120.7
3413.0	2974.9	5327.6
270.4	241.9	109.3
4238.7	4337.8	6019.6
594.1	993.2	1479.2

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AF481204.1 gg_id:55917 oral endodontic infection clone MCE3_262 AF481
FJ497505.1 gg_id:539608 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
EU259389.1 gg_id:237728 Rumen yak (Bos grunniens) sequences rumen fluid clone YRC13 EU259
DQ394624.1 gg_id:152221 -Arctic peninsula Svalbard Norway determined genes and rumen isolates reindeer o DQ394
CT573936.1 gg_id:153085 Evry municipal wastewater treatment plant clone 012A05_B_SD_P15 CT5739
EU474777.1 gg_id:292120 takin feces clone TAK_aaa04h09 EU474
AY244968.1 gg_id:83719 cow rumen clone BS14 AY2449
EU245071.1 gg_id:242715 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-E01 EU2450
EU468816.1 gg_id:301037 okapi feces clone OK3_h07_1 EU4688
EU843666.1 gg_id:305138 metagenomics random sampling pyrosequencing rumen fluid fiber adherent microbi EU8436
GQ347477.1 gg_id:536407 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
EU981245.1 gg_id:334455 sulfate reducing living bench scale aquifer packed bed clone D23_FB EU981
GQ350920.1 gg_id:583859 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU472521.1 gg_id:299958 Angola colobus feces clone EAC_2_aaa02d03 EU4725
AB198479.1 gg_id:135780 termite gut wall fraction clone RsW01-047 AB1984
EU778712.1 gg_id:343538 Springbok feces clone SBSD_aaa03f04 EU7787
AB100009.1 gg_id:79430 inactive deep-sea hydrothermal vent chimneys clone IndB4-4 AB1000
X75622.1 gg_id:2243 Blattabacterium species X75622
Z35665.1 gg_id:2237 Mastotermes darwiniensis endosymbiont Z35665
X96730.1 gg_id:2236 Blattabacterium sp X96730
Y13889.1 gg_id:2240 Coleomegilla maculata male-killing endosymbiont male-killing Y13889
AJ009687.1 gg_id:2241 Flavobacterium sp AJ0096
AJ318122.1 gg_id:28868 Waste-gas biofilter clone BIfcii9 AJ3181
DQ395551.1 gg_id:154321 deep-sea octacoral clone ctg_CGOCA86 DQ395
U87105.1 gg_id:2252 Ornithobacterium rhinotracheale str. LMG 14578 U87105
GQ350671.1 gg_id:573049 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
FJ710777.1 gg_id:544037 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
AM930294.1 gg_id:539275 gradual cooling stage mass and its spatial composting clone SMG46 AM930
AY947955.1 gg_id:141673 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
EU801225.1 gg_id:356497 It's all ranking aquatic Chesapeake Bay MD clone 3C002472 EU801
EU005803.1 gg_id:271719 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU0058
AY948068.1 gg_id:141750 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY9480
AY225660.1 gg_id:95582 organic-rich substrate exposed to Mid-Atlantic Ridge vent clone AT-co1 AY2256
AF314421.1 gg_id:49398 aerobic phosphorus-removal ecosystem clone PHOS-HE28 AF3144
DQ071117.1 gg_id:132660 marine surface water clone SJC3.17 DQ071
AB125062.1 gg_id:100077 Owenweeksia hongkongensis str. UST20020801 AB1250
GQ351219.1 gg_id:590041 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
AY947978.1 gg_id:141856 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
GU230411.1 gg_id:585843 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal water clone A GU230
EU283529.1 gg_id:278327 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1856 EU2835
EU544839.1 gg_id:276455 free-living particle- aggregate- archaeal and Laptev Sea 1.0-60 um size fraction (susp EU5448

52.5	300.7	366.1	417.6	239.4	219.5	313.0	314.0	202.1	184.2	247.8
55.6	7030.8	4283.2	4544.0	5540.5	6471.1	4893.9	6456.7	8416.1	7488.6	5484.0
9030.1	3417.4	2835.2	2781.9	2520.3	2532.1	2956.6	3124.4	3846.4	3546.3	3881.4
34.3	65.3	141.4	88.5	94.4	49.8	86.7	59.0	43.0	39.8	51.0
312.6	1509.5	892.5	731.6	901.3	842.8	944.8	908.4	2172.4	952.7	702.3
1002.0	3810.7	4348.9	5081.2	3968.4	4377.2	4420.3	4517.5	3764.5	4183.7	3726.7
43.0	110.5	180.4	270.3	116.0	108.1	83.0	170.4	62.9	32.0	209.8
352.5	6141.9	7240.0	8073.0	7840.8	5959.7	9544.0	6374.6	6668.9	3828.1	6938.6
466.1	2803.0	3533.1	4584.9	3758.4	3379.8	4563.3	3968.1	2215.0	2875.0	3551.0
51.4	714.0	678.7	753.0	651.0	752.2	479.3	959.4	1012.3	468.9	496.4
834.8	5082.0	4460.3	4384.2	5239.2	4335.6	4615.8	4461.1	4685.7	6016.3	4276.0
454.8	3264.5	2687.8	2688.6	2905.6	3249.9	1943.8	3177.1	1721.1	2320.6	1801.1
1692.0	4726.0	4273.4	4278.4	4723.9	4179.9	4510.9	3756.6	4426.9	4302.9	4753.8
12464.0	11890.7	11810.9	13081.2	13328.9	12122.8	13439.8	11726.5	14370.8	13161.6	14211.9
38.0	416.7	345.0	280.6	589.3	254.0	468.5	287.7	268.8	898.5	123.1
2620.3	4524.8	4607.6	4812.4	4055.1	4334.7	4642.3	4345.3	4889.0	3973.5	4461.8
52.4	3133.8	2830.5	3056.2	3746.4	3458.9	4549.7	3365.8	2899.4	6255.5	2071.4
138.9	4222.5	4969.8	5099.9	5241.7	4676.6	6577.2	4733.2	5080.6	3572.1	4059.3
2537.7	3755.6	3374.8	2953.6	2861.1	3730.4	3586.1	2982.4	5542.9	3739.2	3120.6
2565.0	5302.9	5402.1	5597.0	5337.1	4844.9	5730.6	4864.3	5934.1	4087.4	5735.2
43.4	736.3	692.6	722.5	474.4	1037.0	455.8	1191.2	766.4	3225.6	670.5
2248.8	9204.6	7709.9	7092.9	6249.4	6797.3	6425.5	7134.1	10985.4	9992.4	7498.3
117.8	1224.3	1404.0	1222.0	2734.9	1098.5	2405.3	1234.2	532.8	357.8	1050.8
726.1	1190.8	1450.5	1449.4	1873.5	2009.0	1583.7	1383.3	1594.2	1554.2	1906.0
121.7	498.8	550.2	625.4	404.3	604.8	323.5	397.0	419.9	1995.1	320.1
3190.3	14312.1	14046.3	15617.0	15019.2	13276.0	16125.4	13730.3	18152.2	16270.4	17788.1
889.6	7153.9	6933.3	7522.1	6471.4	7291.2	8163.9	7481.3	6659.3	7820.8	8346.0
148.0	3309.0	4088.8	4795.4	3980.0	3059.6	5111.5	4263.1	3617.1	3589.6	2744.0
1659.6	7805.1	7248.8	9444.3	5908.0	7872.6	6004.7	8170.9	9662.0	7214.8	8081.4
63.9	695.6	1089.0	1156.8	1331.3	947.2	1319.4	1242.8	580.9	390.9	735.6
310.6	6249.8	5745.8	6164.3	6694.8	6095.1	6767.3	5572.4	6754.0	8261.9	5205.1
116.1	4107.4	4146.2	6696.1	4228.7	4692.3	3636.9	4656.8	5314.1	1270.2	3152.7
3104.5	5081.7	5811.1	7691.1	4984.4	4674.1	4653.8	5976.6	3870.3	2543.8	7661.5
55.9	348.7	207.5	244.2	4245.7	984.3	2947.8	298.5	62.6	61.2	43.2
38.9	1072.6	1011.7	1145.1	514.8	654.5	512.3	831.5	1042.7	1302.6	1245.7
44.1	263.6	274.8	349.4	197.8	224.5	169.1	514.1	203.5	69.7	150.2
1042.8	5811.4	5661.9	6035.3	5619.7	4758.1	6741.9	5640.6	5733.7	5236.6	5052.6
41.5	1058.2	1872.0	3336.9	1300.6	1997.3	1611.5	2224.3	1261.8	101.4	878.5
131.9	1486.9	2090.5	1845.7	1874.2	1932.2	1679.7	2261.5	2922.0	1327.9	1786.8
892.3	5406.8	4082.2	3947.3	5686.6	4818.7	6536.1	4236.3	4915.9	3313.6	2662.9
33.6	1051.3	1268.5	1428.2	1361.5	1082.4	1634.6	1496.7	959.4	1063.6	774.9

312.9	454.7	523.0
5990.1	4566.4	2871.6
2348.6	3590.2	2614.2
61.0	103.9	223.2
630.0	1800.4	2510.6
4987.1	4593.2	7993.1
136.6	299.2	117.8
5785.4	5812.9	7473.3
3925.5	3625.3	5897.2
505.7	1028.5	799.5
3972.6	3804.8	4263.7
3195.0	4209.4	8706.8
3455.6	4177.0	4709.1
12038.9	12068.7	14024.2
244.1	395.0	100.8
3830.4	4561.9	10566.6
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4210.9	4985.6	4621.3
2482.2	3491.8	2143.4
5224.7	5700.0	5976.7
1142.5	1261.7	471.7
6339.6	7361.0	6788.7
1295.6	1096.2	1022.2
1457.7	1707.6	1364.7
425.5	468.0	432.6
13336.2	13495.8	13532.1
6594.6	6721.4	10595.4
3626.7	3087.2	3527.3
5925.8	6286.5	4641.4
991.0	329.4	457.8
5449.4	5414.5	5505.4
3724.0	4070.4	2843.7
4782.9	5168.3	4785.0
115.3	83.4	62.7
752.5	502.7	517.9
287.7	506.8	125.2
4852.9	4712.5	5027.7
1816.6	897.9	555.5
2977.8	1783.2	1380.5
3677.2	4227.3	4250.0
1073.1	1168.9	588.5

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o__Flavobacteriales	f__Corymorphaceae
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GQ350649.1 gg_id:556934 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
FJ152979.1 gg_id:319175 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
GQ349547.1 gg_id:572077 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU801442.1 gg_id:326250 It's all ranking aquatic Chesapeake Bay MD clone 3C002735 EU801
EF108212.1 gg_id:192107 Coccinistipes vermicola str. IMCC1411 EF1082
EF572500.1 gg_id:231342 Coco's Island site 23 marine clone S23_599 EF5725
EF659422.1 gg_id:240929 mixed granule anammox reactor clone KIST-JJY049 EF6594
GQ350126.1 gg_id:563364 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GQ037609.1 gg_id:374923 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ037
EF648062.1 gg_id:254309 dynamics during produced water treatment aerobic activated sludge clone BH58 EF6480
AF468278.1 gg_id:80562 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKIA-105 AF4682
EU133759.1 gg_id:256454 tallgrass prarie soil clone FFCH3291 EU1337
EF646134.1 gg_id:243514 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
AM279205.1 gg_id:171966 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
EF572825.1 gg_id:232976 Coco's Island site 23 marine clone S23_924 EF5728
EF645943.1 gg_id:257079 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6459
AY907766.1 gg_id:136952 identification picoplankton contrasting waters Arabian Sea water clone A712014 AY9077
EF572198.1 gg_id:228608 Coco's Island site 23 marine clone S23_297 EF5721
GQ349023.1 gg_id:567825 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
GQ350545.1 gg_id:579668 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
DQ395555.1 gg_id:156530 deep-sea octacoral clone ctg_CGOCA81 DQ395
GQ350398.1 gg_id:589627 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EU005823.1 gg_id:265044 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU0058
AB239762.1 gg_id:146507 isotopic evidence ectosymbiosis between filamentous and stalked barnacle (Cirriped AB2397
AY693832.1 gg_id:103624 anaerobic sludge clone EUB72-2 AY6938
GQ350620.1 gg_id:537682 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
DQ071031.1 gg_id:131321 marine surface water clone Chl1.10 DQ071
GQ349831.1 gg_id:535025 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AY922203.1 gg_id:113227 whalefall clone 131637 AY9222
AF452594.1 gg_id:63864 CFB group clone ML110J-8 AF4525
GQ259251.1 gg_id:511108 Microbial activities coastal marine sediments and column Svalbard surface water clo GQ259
EU801471.1 gg_id:337438 It's all ranking aquatic Chesapeake Bay MD clone 3C002767 EU801
AM279183.1 gg_id:163266 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
GQ340290.1 gg_id:571029 Prokaryotic Marathonas Reservoir Greece water column clone B08-115-BAC GQ340
EF645942.1 gg_id:245184 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6459
GQ348600.1 gg_id:561299 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
DQ009096.1 gg_id:122966 bacterioplankton clone SPOTSAPR01_5m129 DQ009
GQ356156.1 gg_id:585736 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
GQ348151.1 gg_id:549398 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ169200.1 gg_id:305331 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1692
AB189346.1 gg_id:113820 cold seep sediment clone JT58-23 AB1893

6709.3	5212.0	5426.4	5843.1	5375.0	5689.6	6630.4	5122.2	7601.6	6022.5	7288.9
130.4	2962.7	3128.2	3043.3	3918.8	3173.9	4087.8	3754.8	3024.8	585.0	3480.5
73.9	4383.1	6260.3	8927.7	2812.9	3351.3	3809.5	6640.4	2385.4	1566.1	4766.2
252.7	2177.2	4487.3	3186.9	3066.6	3669.9	2503.9	3199.5	3172.6	2483.3	2763.6
54.0	84.8	138.3	106.2	112.8	138.7	106.0	109.9	112.9	34.4	67.2
559.0	1534.2	1785.2	2206.7	2036.7	1649.8	1393.9	1952.2	2177.3	929.8	1189.5
301.5	5464.6	5567.6	6096.9	4813.4	5041.6	5614.1	5225.8	5764.3	4259.0	5175.8
16149.0	9214.6	6558.8	7250.9	7307.7	9246.4	6490.7	8157.5	8872.3	5789.9	9982.2
697.9	5079.7	4634.6	5869.8	6057.0	5770.8	4881.2	4572.5	4512.7	4444.6	3872.3
3782.4	5264.9	6222.8	6276.0	5296.8	4807.7	7287.5	5897.3	4571.7	4755.0	4264.3
342.2	1129.1	1567.9	1404.7	1969.3	2511.9	1747.7	1772.0	1561.5	1265.6	823.1
52.8	528.5	867.1	899.9	1933.5	560.0	1031.3	461.1	162.1	69.8	450.0
32.4	2459.6	2531.6	2932.8	2418.0	2321.2	2044.5	2653.9	2567.6	1808.1	1840.2
12962.4	7648.4	7577.6	8435.6	8788.8	9066.0	9594.9	7552.1	11553.2	9263.1	12353.4
60.6	231.2	325.5	250.9	439.3	335.0	423.5	198.6	580.6	186.6	200.8
22904.8	7711.2	7870.5	7673.9	7894.0	8406.6	9474.4	7326.4	12757.4	7295.4	10584.6
75.7	71.1	97.3	95.5	64.3	69.5	56.5	81.8	49.2	60.9	103.0
83.7	1333.4	2249.9	1901.8	1033.0	1299.3	1381.3	1954.8	1753.5	356.4	1498.1
1804.0	5552.3	6217.0	6546.9	7163.5	5951.4	7591.6	4808.5	6818.8	5263.4	5789.1
362.3	4894.4	4201.0	3758.8	3352.8	5538.2	2997.0	5006.6	5038.7	2855.4	4560.4
110.8	2326.7	1443.7	1871.6	1516.4	1562.5	1344.3	1632.2	2785.8	1688.7	1619.7
344.2	1612.4	1078.5	1249.4	365.1	1796.2	1851.2	1148.2	1780.6	850.8	835.8
42.5	115.5	207.9	191.8	85.0	114.3	90.4	174.6	101.1	79.3	108.6
1916.6	3482.6	3777.5	4526.8	3885.5	3383.8	3185.5	4801.1	2747.2	2369.9	5301.1
38.3	1054.2	821.0	1003.8	8927.1	1837.2	4085.4	470.9	112.2	150.9	119.3
125.9	5571.0	4740.2	3181.9	4196.6	5452.4	3767.0	5808.1	7628.4	4625.1	6031.6
112.6	1192.2	1558.4	1104.1	1853.8	1708.6	1375.0	1237.9	1752.6	1567.4	965.7
306.8	3317.8	3041.5	3127.2	2251.4	2570.1	2722.5	3528.7	3337.3	2025.5	4064.0
56.6	843.5	1713.9	2125.5	851.2	1075.6	2309.3	2595.4	473.7	336.9	857.9
66.9	525.6	957.4	893.4	1248.3	678.3	1310.7	713.6	290.8	94.8	437.9
8460.0	6049.8	5606.4	6110.1	6212.1	5550.9	5771.0	6930.8	4989.1	4564.6	6787.1
893.7	4202.4	5159.3	5303.6	3767.6	3823.4	5176.0	4793.5	3061.9	2493.5	4217.5
56.7	1520.2	1957.3	2367.2	1452.5	1309.2	1865.7	2104.1	771.4	574.7	1137.7
2576.8	9020.7	7183.0	5615.8	9141.4	8389.4	8884.7	6477.6	6359.7	7242.5	6319.9
538.6	9592.0	9615.7	11916.7	7372.3	9328.4	9392.0	9512.7	9137.8	10526.9	10122.3
326.6	6276.2	3393.9	3386.7	3985.0	6648.5	2684.3	5411.3	6596.9	3946.3	4056.5
35.9	600.9	718.9	630.5	704.9	619.4	1475.4	689.7	334.8	241.5	322.8
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1210.8	3737.0	3111.2	2071.2	4044.2	2769.4	2313.4	3548.3	3500.2	1848.3	1962.8
3883.9	5922.6	6856.4	6942.8	6603.2	6051.1	7406.7	6151.0	3838.1	5673.6	5338.7
1685.7	5098.3	4716.3	5432.3	5738.5	4849.5	7146.1	4402.9	3829.9	4001.5	4023.6

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4413.1	2329.3	2935.9
2887.6	3399.9	3301.9
136.3	213.2	576.1
1329.4	1160.1	1453.0
5629.6	5612.8	5232.6
6630.4	7479.0	5679.5
5081.7	4901.6	4868.0
4927.5	5033.9	8639.6
2399.3	2978.6	1389.1
778.9	278.9	314.5
1966.2	2105.7	2802.0
7986.0	9555.7	7541.0
163.7	526.1	194.6
6825.8	7309.0	7455.4
80.1	148.1	77.6
1739.4	1606.9	1101.5
5819.7	5146.9	6509.2
3189.7	3590.9	2053.7
1602.7	1344.1	1112.8
1195.3	839.4	881.7
144.1	345.5	832.6
4059.2	5255.6	3486.9
533.7	133.9	254.9
3834.3	3150.6	2147.1
1311.9	1922.9	1864.1
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1200.3	957.0	997.1
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4117.8	4236.6	4336.0
1963.5	2085.1	2048.3
8154.5	6385.9	7756.0
8028.9	8811.3	9698.4
4187.1	4091.9	1452.1
572.9	808.1	892.3
3014.8	4053.8	3423.7
2171.7	4178.7	2676.1
5542.6	6026.5	6430.9
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GQ452884.1 gg_id:590564 Biodiversity planktonic surface water Northern Bering Sea clone s7 GQ452
FN433409.1 gg_id:591187 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
EU328017.1 gg_id:278158 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
EF572761.1 gg_id:227744 Coco's Island site 23 marine clone S23_860 EF5727
GQ350114.1 gg_id:576702 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
AF170738.1 gg_id:2474 Cryomorpha ignava str. QSSC1-22; ACAM 647T; CIP 107453T; LMG 21436T AF170
FJ744818.1 gg_id:556891 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
GQ349882.1 gg_id:592642 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EF646132.1 gg_id:242779 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
DQ103639.1 gg_id:130262 hypersaline endoevaporitic microbial mat clone E4aF11 DQ103
FN433415.1 gg_id:574728 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
FJ916091.1 gg_id:575472 Evidence structuring organic carbon source temperate lakes integrated lake epilimnic FJ9160
EF646121.1 gg_id:248998 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
FJ203530.1 gg_id:339642 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
DQ015777.1 gg_id:140681 Antarctic lake water clone ELB25-042 DQ015
FN433404.1 gg_id:556785 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
GQ351157.1 gg_id:563664 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Eastern GQ351
EF573969.1 gg_id:228350 site S25 near Coco's Island marine clone S25_313 EF5739
AY678524.1 gg_id:107797 estuarine sediment clone C319a-R8C-E8 AY6785
AY344418.1 gg_id:91513 Lake Kauhako 30 m clone K2-30-6 AY344
EF646127.1 gg_id:252859 Potential interactions particle- anammox and archaeal partners namibian Namibian u EF6461
FN433355.1 gg_id:542989 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
GQ350397.1 gg_id:575543 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
EF575268.1 gg_id:230500 site S25 near Coco's Island marine clone S25_1612 EF5752
GU119321.1 gg_id:535182 Threatened Corals Provide Microbial Habitats reef water clone Reef_L02 GU119
EU919764.1 gg_id:334050 Kongsfjorden western Spitsbergen Svalbard ocean water clone b22 EU919
EF092242.1 gg_id:268391 Persistent Axinella corrugata Flavobacteriaceae clone B276_B9 EF0922
AF382110.1 gg_id:79316 bacterioplankton clone ZA2515c AF382
FJ403071.1 gg_id:363690 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
FJ203162.1 gg_id:352599 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
EF016472.1 gg_id:196863 Near real-time autonomous detection marine on coastal mooring Monterey Bay Calif EF0164
AY947919.1 gg_id:142782 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
EU638919.1 gg_id:345656 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6389
EU703443.1 gg_id:457098 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH35 EU7034
EF471629.1 gg_id:271550 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay (EF4716
EU394563.1 gg_id:324593 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU3945
FJ615174.1 gg_id:592284 Microbial dynamics seasonally fjord: British Columbia Saanich Inlet depth 10m anoxic FJ6151
AF361205.1 gg_id:20456 mesoeutrophic reservoir clone 06 AF3612
EU010171.1 gg_id:239916 Biogeography Singapore seawaters seawater clone B82 EU0101
AY947908.1 gg_id:142739 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
DQ501345.1 gg_id:187558 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501

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832.5	7349.7	5035.9	4106.9	5503.7	5500.1	4956.3	6225.5	6093.1	4807.8	3812.2
31.4	1175.6	1181.2	1099.3	852.7	965.1	1992.0	1203.3	332.0	191.4	796.6
121.4	486.6	422.3	509.8	144.0	207.0	153.5	473.7	381.1	179.2	359.5
141.6	8222.7	7221.2	6218.0	7205.1	6928.7	6836.2	7389.2	9275.0	6803.1	8263.0
45.7	248.0	327.6	389.5	443.8	233.0	287.7	327.2	326.8	46.4	165.9
74.7	3957.4	5372.4	6362.1	6745.0	4894.3	8103.8	4798.7	3126.6	1887.1	4030.5
1562.1	4452.8	4560.9	4519.0	4624.1	5723.2	4694.6	5130.3	4798.5	3957.7	4097.2
115.2	3352.8	3167.7	3003.1	3906.7	2786.1	3281.8	3390.2	2236.9	1575.2	2546.8
46.9	152.0	269.5	315.3	262.5	213.9	243.5	199.0	114.8	54.1	83.2
80.8	2218.0	2806.8	2892.1	1941.1	2276.0	3139.7	2594.9	1959.5	3146.1	2497.6
924.1	5185.5	7730.2	9909.9	5953.5	6411.8	5212.5	7217.4	6626.6	4264.9	5246.8
860.7	9830.9	8494.0	9002.3	8722.1	8641.1	10375.6	8148.8	8779.6	6032.7	8444.3
10337.8	7668.3	8097.3	8217.3	7610.2	7462.9	7629.8	8292.5	9654.7	7719.9	9424.8
33.8	392.5	765.0	697.4	917.0	809.2	810.7	567.4	261.2	33.2	195.1
17186.8	13778.9	11877.4	11356.2	13131.5	13090.7	12945.1	11864.7	19503.3	12620.7	13068.2
1408.2	6974.8	5838.1	7219.6	5868.7	5124.7	5137.5	6178.3	4336.1	4991.1	5235.6
6723.9	3508.1	3512.4	4108.5	3073.1	3735.1	3461.2	3316.1	5005.5	2213.2	5009.2
2835.8	5789.6	6339.5	5678.7	5480.4	5668.1	6817.9	5782.8	11257.8	7422.5	7464.4
63.7	624.3	603.1	668.3	1051.1	699.0	1042.5	638.1	387.1	465.6	409.4
125.2	3746.2	4267.2	4726.5	4867.9	4844.5	6316.7	4170.3	3824.5	1492.0	3001.1
2003.9	5915.9	6177.8	7485.1	6097.2	5953.1	4813.5	6931.5	8305.6	3234.2	4908.4
127.7	4059.9	1869.7	1823.5	2740.8	3947.6	1830.8	3823.1	3943.0	3607.0	2011.8
36.1	107.0	204.1	245.5	146.7	138.6	86.3	772.4	143.4	27.4	222.6
790.0	4008.2	4455.9	4611.5	3154.6	4334.3	2934.0	4645.0	7754.6	3041.4	5183.0
1264.1	4521.8	4355.5	4474.3	4096.3	4192.0	4686.5	4686.0	4509.8	6756.9	3817.1
96.1	3268.3	3075.5	2833.4	3567.0	3379.9	4128.5	3474.5	4814.4	2174.6	2935.7
18922.9	9816.7	10483.9	10486.6	9917.1	9043.3	10800.9	10576.7	16317.2	13528.1	14537.5
326.0	5306.3	3465.4	2945.2	3987.0	8172.8	2776.5	4960.0	8121.2	5357.1	4235.3
2211.7	9866.4	8478.9	8503.6	8701.2	8766.9	9206.5	8503.2	9314.1	10495.5	9480.0
51.3	785.5	970.5	1173.6	1202.1	758.4	1356.4	810.1	877.6	175.9	1004.9
81.7	3853.3	4126.9	3672.4	2912.0	3852.0	2810.7	4360.1	4612.7	2758.4	5225.8
413.2	2995.6	3663.6	3752.8	3034.5	2743.6	3637.8	3420.8	2379.9	1552.5	3115.0
10091.7	6666.0	6146.2	6228.8	5302.2	6608.4	5189.7	6349.8	9371.8	5076.2	8221.3
320.7	7975.4	9191.0	10438.0	6933.0	6653.7	8019.1	9170.1	7949.7	6539.7	9400.1
177.4	2858.0	3303.1	3152.1	2637.8	2552.3	1408.1	2867.6	1846.5	1499.2	3230.1
1946.0	7738.7	7629.6	6899.6	8179.9	6957.7	6309.0	6995.8	10596.4	9129.2	8083.0
52.9	4584.0	4917.4	5774.1	2658.9	2873.3	3813.2	5151.9	2572.2	1500.7	3403.7
183.0	1738.5	1834.4	1358.9	1772.0	1569.3	1154.8	2050.5	1519.8	674.9	630.2
15443.3	8120.0	7613.0	7770.7	7421.9	7346.9	9838.4	7282.1	9946.5	7215.2	9819.5
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918.3	600.1	429.1
292.9	345.6	118.1
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267.9	350.3	144.2
4502.6	5202.0	6594.9
4677.0	5072.3	4604.3
3863.1	3175.6	3129.3
152.9	277.0	143.3
2369.4	2613.8	1852.5
6433.7	5109.3	4056.9
7162.4	7692.2	10046.0
7516.5	7604.1	7470.0
325.8	292.3	285.4
11133.1	10233.6	10198.6
4801.3	4589.8	3443.2
3123.6	3252.4	2698.5
4773.6	6069.8	6651.1
604.6	826.0	983.9
3691.5	3039.1	3730.7
5343.3	6017.4	4196.7
2863.4	3275.8	1351.7
125.5	285.1	181.2
2274.7	4678.1	2758.3
4059.2	4807.5	5474.4
2865.2	2883.8	1554.7
9414.4	12281.5	9566.5
4299.5	3103.7	2199.9
8689.5	7100.6	6253.7
547.1	701.6	951.1
2865.5	2906.7	1838.7
2465.3	2483.2	3267.2
4691.0	5009.2	4083.9
6233.3	5953.6	5330.7
1665.0	1408.5	1164.7
6342.6	7478.4	6967.1
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1558.4	1445.5	1254.3
6621.6	7383.5	7214.2
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EU703391.1 gg_id:426117 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH39 EU703
EU703232.1 gg_id:449826 lakes on Eastern Tin Plateau oligosaline lake altitude 4718 masl clone XZNMC14 EU703
EU700187.1 gg_id:293440 Study on Shantou Bay Marine Sediments Microorganisms sediment clone STU45 EU700
AF289153.1 gg_id:73378 freshwater clone PRD01a005B AF289
DQ906732.1 gg_id:162765 and marine microorganisms Antarctic sea water 20 m clone AntCL1F6 DQ906
DQ501310.1 gg_id:179461 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
DQ103637.1 gg_id:131164 hypersaline endoevaporitic microbial mat clone E4aE04 DQ103
CU466753.1 gg_id:340884 Evry wastewater treatment plant anoxic basin clone CU466
EU133760.1 gg_id:237434 tallgrass prarie soil clone FFCH3806 EU133
DQ015842.1 gg_id:140107 Antarctic lake water clone WLB13-202 DQ015
GU061224.1 gg_id:553384 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AF507867.1 gg_id:62693 Mono Lake at depth 17.5 m station 6 July 2000 clone ML617.5J-5 bacterium AF507
AM279209.1 gg_id:166763 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
AY532584.1 gg_id:102122 uranium-contaminated aquifer clone 1013-28-CG47 AY532
AF449770.1 gg_id:80707 CFB group clone ML310M-46 AF449
EU801202.1 gg_id:328847 It's all ranking aquatic Chesapeake Bay MD clone 3C002449 EU801
EU236348.1 gg_id:295497 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A10 EU236
EU246821.1 gg_id:242251 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU246
AF521195.1 gg_id:69811 Brumimicrobium glaciale str. ACAM 644 AF521
AM930454.1 gg_id:260035 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
FN433447.1 gg_id:588456 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
EU592398.1 gg_id:564878 Seasonal changes Salton Sea hypersaline water clone SSW85N EU592
EU652656.1 gg_id:277616 Seasonal variation microbial Yel Sea sediment clone B8S-139 EU652
AB078042.1 gg_id:58645 Crocinitomix catalasitica str. IFO 15977 AB078
EU803886.1 gg_id:351352 It's all ranking aquatic Lake Gatun clone 5C231539 EU803
AM930461.1 gg_id:264938 involved Tripneustes gratilla (Echinoidea) cloning and FISH host body wall lesions cl AM930
NR_025031.1 gg_id:545908 Aequorivita sublithincola str. QSSC9-3; ACAM 643 NR_02
AY027806.1 gg_id:39184 Aequorivita crocea str. Y12-2T AY027
EU642844.1 gg_id:279541 Vitellibacter sp. JC2436 str. JC2436; IMSNU 14137 EU642
FJ889654.1 gg_id:547999 Aequorivita sp. str. ZS1-6 FJ8896
NR_028631.1 gg_id:544761 Vitellibacter vladivostokensis str. KMM 3516 NR_02
AM279207.1 gg_id:171297 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
EU727254.1 gg_id:308741 Winogradskyella sp. str. KMM 6211 EU727
AY187689.1 gg_id:80619 Algibacter lectus str. KMM 3902 AY187
AY612758.1 gg_id:140533 Formosa sp. str. 18III/A01/079 AY612
AM946640.1 gg_id:265850 Tamlana sp. Aga22 AM946
EU221275.1 gg_id:245619 Tamlana agarivorans str. JW-26 EU221
AY608407.1 gg_id:106561 Aquimarina muelleri str. KMM 6021 AY608
DQ660387.1 gg_id:172234 Aquimarina sp. str. HJ055 DQ660
FJ490365.1 gg_id:547485 Aquimarina sp. str. CNURIC 011 FJ4903
FN554605.2 gg_id:540893 Aquimarina latercula str. HJ5 FN554

6775.9	6108.8	5705.9	4444.3	3975.6	4839.2	3832.6	5249.5	5095.4	4188.4	5984.6
1882.9	3821.8	3665.6	3599.5	2914.9	3351.3	3261.6	3661.6	3580.9	2166.0	4485.2
51.4	2529.1	3692.6	2758.8	1156.3	1522.5	2330.1	3133.0	1851.7	349.7	2258.1
47.0	6272.0	8598.0	10822.5	582.7	2609.9	1088.6	8886.2	1395.7	123.0	8633.1
38.0	66.6	143.2	91.7	86.8	79.8	131.4	229.4	59.4	101.4	71.2
55.8	212.9	1197.2	763.5	393.0	774.5	74.5	2089.7	824.8	20.8	276.4
53.3	1446.4	2012.3	1570.1	1806.2	1092.6	2388.4	1590.6	737.0	347.4	647.5
353.7	4626.0	3918.8	3275.0	3935.0	3544.5	4416.1	4159.1	3905.7	4724.2	3024.1
63.2	2523.2	2586.4	2676.2	1618.1	2255.8	1604.2	2819.7	2006.9	272.0	1374.1
9540.3	6008.5	6757.8	6857.5	5573.7	5322.4	4923.1	6702.7	6894.9	2967.1	8053.1
3562.4	7008.5	7258.5	7712.5	8207.7	6860.0	7872.4	7134.6	7829.6	2320.5	6256.3
1389.1	3793.3	5425.2	4738.5	4383.4	4389.0	3633.1	6397.4	7158.9	5141.0	3567.3
25.9	343.4	325.1	180.2	209.4	192.4	189.3	234.7	487.2	115.6	165.8
2270.9	5003.1	4618.0	6476.0	5358.7	4214.5	4167.1	5767.1	7111.0	2583.4	5924.6
301.7	2076.7	4048.1	3599.3	2557.4	2641.6	2504.2	4077.2	3000.1	2594.0	1901.9
81.5	2291.6	3652.0	3650.4	1679.6	1578.1	1344.0	2543.9	2434.5	606.6	1651.4
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84.7	3110.8	4113.1	4282.7	2078.2	3150.2	2209.9	3824.2	2265.9	2230.9	3526.9
64.8	2564.6	3448.9	3680.0	1386.0	2004.7	1967.5	3376.1	1765.3	1748.8	2305.1
304.4	5362.6	6165.2	5658.7	4832.2	4980.0	3222.8	7003.2	6239.5	2312.4	6150.8
439.8	4371.0	4831.4	5022.9	4424.4	4260.6	3283.5	5457.6	3597.2	4555.8	4138.2
55.7	1847.2	2181.5	2336.4	1278.5	1442.7	838.5	2349.5	1361.5	230.4	1446.0
36.4	557.1	947.0	661.7	550.6	761.4	525.4	857.8	674.3	462.9	485.5
983.7	7288.1	6670.3	6186.3	5443.6	5769.8	5110.9	5324.0	8275.8	4791.0	4110.9
76.6	1517.3	1466.5	1660.6	1667.4	1304.8	1769.8	1790.9	996.1	239.7	977.1
4612.6	2157.4	2340.8	3064.1	2732.1	2109.6	2397.8	1968.8	3442.7	2496.0	2499.6
11807.1	4316.0	4443.8	5074.8	3820.2	3907.9	4247.9	4053.5	6364.0	5735.3	7068.0
354.9	3238.9	3753.2	3251.4	3644.9	3352.5	3418.8	3446.3	3751.8	3751.3	3237.5
169.7	1911.7	2218.3	2312.3	3308.4	2398.7	3648.0	2330.5	1608.4	1939.5	1802.0
34.2	438.4	370.0	253.9	607.4	524.3	478.9	349.1	210.9	154.4	223.7
65.6	2577.8	2962.9	3368.8	3645.6	2918.9	3635.5	3938.3	1056.7	978.6	4904.4
296.3	1173.6	1799.4	1986.4	1605.1	1459.7	2441.6	1825.7	907.3	403.6	1240.7
72.5	1231.7	2673.2	2928.3	1773.1	2757.2	1666.0	3421.6	2017.1	1599.3	2293.5
30.5	630.3	1126.0	952.6	839.2	796.2	1212.4	1457.7	492.6	186.1	494.7
3139.2	6225.7	7381.5	5863.5	7369.6	6102.0	6266.1	6697.5	13209.3	7122.2	6365.4
252.2	2130.3	2827.1	2399.7	2549.3	3048.6	2170.7	2773.3	3835.5	2919.3	1745.5
44.3	2988.4	3065.4	2837.5	2363.7	2736.3	2101.2	3292.9	3920.0	4813.6	3447.4
38.0	3940.9	3986.1	2613.0	3802.9	4692.2	3308.5	4570.8	6463.8	4650.5	3047.6
44.0	2160.5	2581.9	2298.0	2339.2	2894.8	1656.0	2962.0	2152.5	1863.3	3178.0
131.6	3262.6	3896.8	2859.8	3195.2	3733.7	2658.9	4394.7	2709.5	4850.1	4865.0

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3019.4	1015.4	403.3
209.3	284.8	93.6
630.0	351.5	487.7
913.3	1165.1	1405.5
4086.9	3803.8	3348.0
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6647.1	5756.3	6073.7
4426.4	3746.8	4291.8
132.3	209.8	149.8
4746.4	6434.9	4087.6
2521.0	2461.0	4615.7
1669.6	1625.5	1803.5
1219.8	1440.2	868.9
9850.0	9810.1	7841.2
3556.1	3080.0	3422.2
2335.1	1803.8	1659.0
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5133.5	3143.6	4310.3
2838.0	1200.3	1668.2
642.2	1113.0	493.4
4586.2	3523.1	4412.2
1239.8	983.8	1166.1
2140.3	2863.0	2263.9
3537.4	4603.2	3733.5
3643.6	4540.2	4282.6
1906.2	2919.5	3306.3
319.7	454.8	713.6
2510.5	2076.6	1245.0
2371.3	1581.6	3179.5
2877.9	2305.0	1278.7
1588.2	856.3	369.1
7090.0	7600.0	6398.8
3591.6	3649.2	1939.4
3381.4	2717.8	2943.1
3816.5	2442.0	3564.1
2932.6	2287.8	3341.3
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s__Cellulophaga lytica	66502

AM113977.1 gg_id:160694 Aquimarina intermedia R-28470 AM113
DQ357763.1 gg_id:149899 Aquimarina sp. SW42 DQ357
AY987367.1 gg_id:122067 Gaetbulimicrobium brevivitae str. SMK-19 AY9873
AM259874.1 gg_id:207314 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-29 AM259
DQ357758.1 gg_id:146214 Marine Hatchery: Balance Between Pathogenic and Potentially Probiotic Strains adu DQ357
EF536748.1 gg_id:253613 Arenibacter echinorum str. KMM 6032 EF5367
NR_024790.1 gg_id:561384 Arenibacter troitsensis str. KMM 3674 NR_024
AY398697.1 gg_id:99911 Bergeyella sp. h1890 AY3986
AY694005.1 gg_id:102654 Calefactosor saleffrenus str. HFD AY6940
NR_025827.1 gg_id:555628 Bizionia paragorgiae str. KMM 6029 NR_025
AF513399.1 gg_id:55449 Gelidibacter sp. str. 13-4 AF5133
AY694004.1 gg_id:102497 Calefactosor gelidisalsuginis str. IC164 AY6940
AY643075.1 gg_id:129359 Capnocytophaga canimorsus str. CIP 103936 AY6430
DQ009624.2 gg_id:125969 Capnocytophaga haemolytica str. A0404 DQ009
U41350.1 gg_id:2363 Capnocytophaga ochracea str. ATCC 27872 T U41350
GQ000769.1 gg_id:469333 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
AM179907.1 gg_id:149379 Identification microflora (Oncorhynchus mykiss) rainbow trout intestine clone G3-1: AM179
FJ976269.1 gg_id:582773 Interindividual healthy human oral microbiota mouth clone 7BB410 FJ9762
AF538853.1 gg_id:59534 Capnocytophaga sp. oral strain str. P4G_35 P4 oral AF5388
AF543298.1 gg_id:56144 Capnocytophaga ochracea str. ChDC OS48 AF5432
X67609.1 gg_id:2373 Capnocytophaga sputigena str. ATCC 33612 X67609
FJ976207.1 gg_id:577305 Interindividual healthy human oral microbiota mouth clone 3405 FJ9762
AY643076.1 gg_id:133677 Capnocytophaga cynodegmi str. CIP 103937 AY6430
AF385494.1 gg_id:71957 subgingival plaque clone DZ074 AF3854
AY429469.1 gg_id:102901 Capnocytophaga sp. P2 oral strain str. P4P_12 AY4294
DQ009623.1 gg_id:125439 Capnocytophaga leadbetteri str. AHN8855 DQ009
AM420201.1 gg_id:249209 Noma subgingival plaque clone 502H07(oral) AM420
AY005076.1 gg_id:70616 subgingival dental plaque clone BB167 AY0050
AF118419.1 gg_id:31284 Coenonia anatina str. 726-82 AF1184
GQ110815.1 gg_id:465094 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ110
EU432438.1 gg_id:270675 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU4324
AY008312.1 gg_id:73803 Capnocytophaga sp. oral clone EL043 AY0083
FJ773364.1 gg_id:530224 biofilm incipient early childhood caries dental plaque clone SK117 FJ7733
AM420168.1 gg_id:245563 Noma subgingival plaque clone 501C07(oral) AM420
X67610.1 gg_id:2370 Capnocytophaga ochracea str. ATCC 33596 X67610
GU410280.1 gg_id:533210 Human Oral Microbiome oral cavity GU410
EU000223.1 gg_id:323900 Cellulophaga algicola str. KOPRI_22146 EU000
NR_028661.1 gg_id:569170 Cellulophaga algicola str. IC166; ACAM 630 NR_028
AB032512.1 gg_id:28162 Cellulophaga lytica str. IFO16021 AB0325
DQ311648.1 gg_id:147086 Cellulophaga sp. str. QY201 DQ311
AB032510.1 gg_id:23812 Cellulophaga lytica str. IFO15986 AB0325

114.5	1559.0	2533.8	1996.7	1847.7	2621.5	1524.5	2633.3	992.5	5191.4	1611.6
45.4	1584.4	2154.4	1960.5	1434.6	2113.5	1593.4	2346.0	1093.1	2312.2	2427.4
63.9	96.7	127.6	155.9	103.3	62.6	82.6	151.7	48.4	59.0	77.2
58.0	1944.4	1627.0	1011.7	1379.1	2218.2	1224.3	1626.7	4983.5	1823.3	855.8
25.8	2014.3	3294.3	3179.7	2460.0	3503.6	2357.8	3400.6	1454.5	5661.3	2425.1
43.1	614.5	894.9	699.3	572.1	671.5	484.9	531.2	791.5	573.6	377.8
40.8	127.6	252.6	220.1	163.0	123.5	111.6	124.4	65.6	56.5	102.5
156.7	3374.7	2302.5	1943.8	2216.0	2182.0	2314.9	3098.8	2493.2	4290.2	1813.2
2332.5	9846.0	9144.5	8741.9	8280.5	11107.1	7726.0	9743.6	15860.6	12094.7	10892.8
52.2	1160.8	1093.9	852.9	758.9	1303.4	411.8	1160.5	1194.4	1676.7	855.3
190.2	5772.6	6550.1	5697.7	5921.4	5869.2	4051.4	5546.9	4316.8	5594.1	4849.5
56.0	1252.4	1151.7	1045.9	1213.6	1745.0	1375.3	1802.0	1716.4	1563.3	852.9
261.1	4271.9	2976.8	3199.7	3736.2	4021.6	3385.6	4231.5	2792.3	4880.0	3198.9
29.6	480.7	478.7	341.2	533.4	631.2	255.8	406.3	357.2	372.3	251.0
60.5	2128.8	2090.8	1751.9	2119.1	2186.0	1834.0	2398.1	2514.7	4430.4	1463.8
68.9	963.9	843.1	567.8	506.8	671.7	700.9	1128.4	1749.4	2192.8	629.1
2523.3	1923.0	1651.4	1862.8	1512.1	1699.7	1768.0	1720.7	2548.4	2219.6	2022.5
50.8	1873.3	3982.3	973.0	1043.2	1733.9	979.8	3771.6	897.0	4523.3	1276.2
33.4	92.7	221.4	194.3	278.1	246.5	116.1	343.2	243.0	341.4	100.4
46.4	50.0	205.4	97.0	168.8	241.9	102.8	100.0	34.7	12.3	51.6
42.1	15.7	15.5	19.9	14.9	13.1	23.3	12.2	13.1	10.3	17.0
58.3	61.9	95.5	121.1	107.8	95.1	115.1	102.4	107.8	282.0	43.8
113.1	5326.2	4541.9	5343.5	5740.5	4636.2	5721.3	5556.5	4917.8	6199.5	5129.4
57.7	29.2	41.0	54.3	44.9	32.7	36.2	32.7	29.1	21.2	34.4
64.0	722.6	881.4	762.5	719.5	742.6	575.8	936.9	1034.6	1553.8	631.3
91.0	851.1	1335.6	1452.4	2671.6	1068.1	1282.5	1479.1	656.2	358.1	685.8
28.0	96.5	208.4	205.6	515.9	133.2	204.0	114.9	44.7	24.9	53.3
116.5	1197.6	1374.6	1360.4	1171.7	1169.9	886.0	1719.1	1420.1	1138.1	1056.2
68.2	1122.6	809.8	402.6	636.7	1050.4	293.8	662.2	1115.1	643.0	426.2
155.5	2792.3	3250.0	2577.0	2945.4	3355.5	2188.2	2856.9	2152.9	3164.8	1752.8
75.5	561.1	600.3	536.3	505.9	504.3	503.0	1209.3	850.3	749.6	535.8
8831.6	3208.4	3044.0	3284.9	3646.1	3202.8	4034.6	3386.2	4592.7	1822.4	3150.2
842.9	10313.4	8216.6	8100.7	7960.8	9178.2	8416.2	8771.2	15245.8	11760.7	9759.4
529.4	4746.3	3438.0	3736.5	3997.1	5038.2	3362.0	4589.6	4718.6	6278.0	4695.0
121.6	1428.7	1081.7	1793.1	1639.0	2015.4	1715.1	1840.9	1850.8	2329.7	1253.1
61.1	703.8	824.0	680.0	729.5	714.7	448.8	1125.8	826.3	1335.3	634.5
51.4	1951.2	2618.8	2387.2	1996.1	2145.6	1785.7	2857.1	1488.5	2789.9	1663.3
152.0	1960.5	2166.4	2257.7	1784.3	2431.3	375.0	1831.1	2405.4	2347.5	2015.7
39.0	699.3	663.3	585.4	534.2	662.3	789.0	805.5	451.6	77.0	394.7
8349.3	3851.7	3300.9	3165.8	3069.2	3924.5	3415.1	3549.1	4718.9	3602.6	3610.3
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5054.7	2452.7	3124.6
1513.4	658.0	898.7
545.2	94.8	579.5
2209.6	2624.8	1418.7
8465.9	10138.4	6035.4
872.0	801.9	426.3
5570.6	3951.1	3200.9
1649.2	1095.0	634.2
3438.4	3819.8	3839.5
359.9	447.3	98.0
2931.2	3133.0	1522.9
851.1	1467.9	433.7
1595.8	3251.4	1491.9
1918.8	1447.0	826.6
250.4	464.1	155.8
229.1	143.9	884.6
14.1	15.2	11.3
136.8	309.6	38.3
4021.4	5164.5	3100.7
63.6	32.0	25.6
810.9	1307.4	672.4
1025.6	1426.9	864.6
99.2	133.1	248.6
1110.7	1761.3	576.8
882.4	615.6	232.3
3320.7	3117.5	2388.7
628.4	765.8	509.2
3194.1	4298.9	4382.8
7909.0	8660.4	7371.0
3569.9	4438.5	2971.3
2428.7	2221.5	4018.9
759.7	1070.6	632.8
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s__unclassified	66543
s__Chryseobacterium bovis	65191
s__Chryseobacterium daecheongense	63257
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s__Chryseobacterium joostei	65255
s__Chryseobacterium luteum	64787
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s__unclassified	63180
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s__unclassified	63286
s__unclassified	63300
s__unclassified	63359

AB100840.1 gg_id:99263 Cellulophaga pacifica str. KMM 3664 AB100
AB100842.1 gg_id:99572 Cellulophaga pacifica str. KMM 3915 AB100
DQ356486.1 gg_id:145374 Cellulophaga sp. str. CC11 DQ356
DQ357766.1 gg_id:146410 Cellulophaga sp. SED18 DQ357
AF539754.1 gg_id:83115 Cytophaga sp. str. E46 AF5397
EU443205.1 gg_id:272395 Cellulophaga sp. str. EM41 EU443
FJ439599.1 gg_id:362021 Cellulophaga sp. str. KT8 FJ4395
AF235118.1 gg_id:45411 Cytophaga sp. str. KT02ds20 AF235
EU626632.1 gg_id:278303 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
DQ357768.1 gg_id:149157 Cellulophaga sp. SED13 DQ357
NR_025287.1 gg_id:568483 Cellulophaga fucicola str. NN015860; LMG 18536 NR_02
EF204446.1 gg_id:201471 Chryseobacterium sp. H9 EF2044
FJ455451.1 gg_id:571052 Chryseobacterium daecheongense str. BF-Y6 FJ4554
NR_028942.1 gg_id:584982 Chryseobacterium defluvii str. B2; DSM 14219 NR_02
FJ887959.1 gg_id:434553 Chryseobacterium gleum FJ8879
AY468478.1 gg_id:102517 Chryseobacterium sp. str. LMG 19914 AY4684
GU296676.1 gg_id:585426 Chryseobacterium sp. str. ANSL GU296
AY770428.1 gg_id:128035 insect gut clone AY7704
DQ117545.1 gg_id:138622 structure (Citrullus vulgaris SCHARD.) -based approaches and terminal fragment len DQ117
AB264127.1 gg_id:162873 Chryseobacterium sp. str. TDMA-39 AB2641
AY468481.1 gg_id:106431 Chryseobacterium indologenes str. LMG 12856; NCTC 11409 AY4684
AJ843132.1 gg_id:102871 Chryseobacterium taichungense str. TWGS-8 AJ8431
EU221399.1 gg_id:256453 Chryseobacterium indologenes str. H2S10 EU2213
EU598809.2 gg_id:580026 Chryseobacterium sp. str. CH8 EU5988
AM232813.1 gg_id:161516 Chryseobacterium indologenes str. LMG 8337 AM232
EU121860.1 gg_id:238528 Chryseobacterium letacus str. CW-H EU1218
AY468467.1 gg_id:106164 Chryseobacterium sp. LDA39 G1966 12a AY4684
AY468479.1 gg_id:102672 Chryseobacterium joostei str. LMG 18208 AY4684
AM489609.1 gg_id:188834 Chryseobacterium aurantiacum str. DSM 18605 = LMG 237 AM489
EU999734.1 gg_id:345921 Chryseobacterium sp. str. KM EU999
DQ673671.1 gg_id:167569 Chryseobacterium sp. str. RHA3-1 DQ673
AY468458.1 gg_id:101293 Chryseobacterium sp. JIP 108/83 AY4684
EU862562.1 gg_id:328172 Chryseobacterium sp. str. ABc1 EU8625
EU057840.1 gg_id:250695 Chryseobacterium sp. WOF18(2)-4 EU0578
AY468460.1 gg_id:105095 Chryseobacterium sp. JIP 16/96 AY4684
EU057841.1 gg_id:251504 Chryseobacterium sp. CH33-3 EU0578
GQ225686.1 gg_id:392179 Chryseobacterium sp. str. HMC6043 GQ225
DQ166169.3 gg_id:155194 Chryseobacterium sp. str. TSBY-67 DQ166
GQ070524.1 gg_id:422863 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ070
GQ098998.1 gg_id:372442 Topographical and Temporal Human Skin Microbiome skin interdigital web space clo GQ098
EF591302.1 gg_id:230912 Chryseobacterium sp. str. JS6-6 EF5913

423.4	4614.8	4117.3	3049.9	3775.7	4736.1	3927.1	4338.0	7295.9	5544.8	3755.4
3799.9	7164.5	6653.8	7352.9	7388.6	8004.2	7360.1	7396.2	13434.7	9733.6	7704.8
52.2	1503.4	1008.7	790.1	905.0	1505.5	866.2	1067.5	2553.8	1467.7	718.1
38.4	39.5	65.4	59.0	46.2	41.9	74.9	61.0	33.9	13.6	47.4
53.0	2981.9	1748.9	1595.7	1713.2	1964.4	1748.2	3430.5	1623.8	4224.1	2831.9
46.1	395.5	512.5	271.7	583.0	873.5	386.0	473.1	706.8	838.2	264.2
60.8	3757.4	2120.6	1713.6	2055.3	2590.5	1993.9	3994.8	3105.1	5932.4	3435.0
83.8	5303.7	3233.3	2469.7	3461.0	4018.5	3380.1	5317.5	5386.7	6331.8	4814.2
538.6	2404.1	1700.7	1211.6	1796.7	2004.1	1424.0	1864.0	2837.5	2481.5	1454.4
689.5	4391.0	3801.9	2534.9	3335.7	4046.9	3735.3	3939.2	6638.1	3263.2	2189.2
47.4	580.0	702.5	832.6	616.8	818.6	689.2	816.3	331.0	230.4	446.4
1522.6	3355.6	3469.9	3534.4	2874.0	4342.7	2701.5	3342.1	2562.5	12745.8	2766.7
143.1	10546.4	7293.3	5973.2	7453.6	9087.9	6392.1	8798.9	11807.4	16985.3	7365.8
458.3	4353.8	3024.5	2802.0	5530.9	4517.5	3452.7	3243.0	3044.1	8577.6	1707.2
126.3	4730.8	3150.7	2780.5	3204.4	4614.3	2573.7	3015.8	2318.9	10785.7	1470.4
1775.5	7142.8	4514.8	4306.9	6576.6	5186.2	4616.5	4366.9	5350.6	11022.6	3266.1
1906.7	4532.0	3917.7	4066.8	6573.2	5187.0	3968.3	3877.7	5051.0	8641.2	2596.9
130.1	4325.1	3134.8	2755.7	2291.0	4675.8	1485.7	4696.2	4764.6	13580.6	2839.3
380.6	4258.7	4031.5	4074.6	5853.7	5280.6	4159.8	3573.2	2999.0	10373.8	1927.6
1539.1	8754.9	7081.7	6485.9	6330.5	8394.0	5809.4	7766.8	10203.5	16711.4	7232.8
60.0	860.3	801.5	699.2	367.5	1924.2	212.2	1130.5	294.0	7904.7	333.7
2313.0	11379.9	5658.4	4966.0	5001.7	7125.1	4856.3	7561.7	11938.1	13515.7	6436.3
1113.8	3376.2	2739.5	2497.2	1641.0	4852.8	1013.0	4101.9	1915.4	14516.9	1259.3
2767.4	8249.5	7161.0	5493.3	5170.5	7337.4	4770.4	7088.3	10074.5	17535.1	5811.5
49.0	5450.7	3461.1	2858.9	2046.4	4847.1	1511.1	4199.7	2103.5	16160.7	1902.5
68.5	4145.9	4620.8	3974.5	3530.0	5884.5	2902.9	5260.6	4747.8	15370.6	3154.4
167.4	8732.7	6556.2	3418.2	3059.5	5732.5	4155.9	5279.2	3351.3	10529.4	2570.3
163.9	6005.3	4573.4	4364.6	3661.4	4983.6	4911.1	4721.6	6662.4	7355.8	4102.1
210.5	7166.5	4527.5	4082.6	3720.9	4765.3	3525.2	6388.9	3552.1	11614.7	3927.7
3144.4	9821.4	5556.7	3798.6	2621.7	5095.9	3024.7	5207.6	4815.4	12834.8	4487.1
2339.9	7879.8	6349.2	5445.4	5439.7	7555.1	5525.8	6817.4	8527.1	14575.4	6680.1
132.9	8309.2	6133.6	4962.7	4448.4	6931.0	4434.3	6770.8	7988.0	16242.3	4157.0
3399.7	9738.3	7796.6	7295.6	6818.9	8608.7	7411.1	8139.1	10348.6	14809.1	7844.7
661.5	10375.9	6113.7	6200.6	5355.0	7139.1	4932.3	7690.9	9980.7	18449.3	5555.7
269.7	8459.9	7242.9	6263.5	6228.9	9009.9	5745.4	7840.8	11610.2	18247.4	6799.3
3372.4	8336.9	7626.3	8058.4	6080.5	8032.4	6677.8	7959.9	9853.1	15294.7	6462.8
133.8	7160.2	6183.7	4993.7	5245.6	7858.7	4482.1	6555.2	9684.1	16134.9	5835.9
1708.2	6400.9	4746.1	2793.5	2572.1	3818.9	2524.7	3397.5	5906.4	7993.9	3227.4
645.7	12807.5	9643.4	8201.1	8957.5	10656.9	8647.2	10677.5	15797.6	18188.4	10027.4
165.1	7272.1	6288.0	5415.9	5413.2	7938.8	5063.1	6853.0	11028.4	13580.7	6091.6
140.7	4652.2	4270.2	4418.6	3210.8	4160.3	3659.2	4351.3	2836.8	9399.6	2603.1

3895.4	3771.8	2420.4
6764.3	7554.0	6401.0
1009.3	1367.3	569.3
37.9	35.7	164.1
2916.6	1069.8	787.1
949.1	566.6	240.7
3502.4	1712.4	1353.8
4361.6	2772.1	1755.0
1728.0	2109.2	1533.5
2862.3	3556.5	2238.0
962.4	969.7	1161.4
5423.1	3515.7	4022.2
8832.8	6380.5	5084.0
4308.7	2719.6	1793.6
5379.1	2691.8	1816.9
5598.3	3932.7	3155.9
4157.8	3328.7	2498.3
4851.1	2154.4	1780.6
5526.6	3271.4	2576.8
8200.2	6646.6	5909.3
1447.8	413.9	211.1
6776.5	4854.4	4359.2
4910.2	2376.0	1198.4
7759.6	5589.7	3820.7
5715.9	2484.7	1476.9
5173.7	3152.8	2951.8
3559.8	3071.6	3341.0
3965.2	4107.8	4429.1
5403.1	3322.8	3372.2
4360.0	3436.3	2803.6
8035.9	6232.3	4549.8
8073.0	5061.3	4585.0
7875.5	7362.2	7053.3
7574.0	5319.2	5171.7
8699.4	6110.4	4227.0
8295.2	5533.9	4819.5
8152.3	6124.6	3224.6
3238.9	3974.4	2279.6
9860.2	7708.3	6093.2
7911.2	6593.9	3799.2
6133.2	3602.5	2709.0

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AM748691.1 gg_id:254510 Chryseobacterium sp. str. 10-106 AM748
AJ871397.1 gg_id:113156 Chryseobacterium sp. str. R-23566 AJ8713
EU538611.1 gg_id:282420 profile human microbiota antecubital fossa (inner elbow) skin clone nbt233g03 EU5386
AJ715377.1 gg_id:105032 Chryseobacterium formosense str. CC-H3-2 AJ7153
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DQ530068.1 gg_id:161519 Chryseobacterium sp. CI06 DQ530
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AM232806.1 gg_id:153966 Chryseobacterium sp. F-Fue-04IIIaaaa AM232
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EF077177.1 gg_id:258002 Chryseobacterium daejeonense str. RB-18 EF0771
EF591303.1 gg_id:229762 Chryseobacterium sp. str. JS17-8 EF5913
AY427792.1 gg_id:102191 Chryseobacterium sp. str. UOF CO294 AY4277
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EU999735.1 gg_id:345793 Chryseobacterium sp. str. CTM EU9997
GU451165.1 gg_id:519304 Chryseobacterium sp. str. BMC-1 GU451
GU458265.1 gg_id:526859 Chryseobacterium sp. str. HT4B GU458
DQ530076.1 gg_id:160293 Chryseobacterium sp. CI09 DQ530
DQ301786.1 gg_id:146939 Chryseobacterium sp. str. PHD-9 DQ301
EF077176.1 gg_id:240678 Chryseobacterium moechotypicola str. RB-02 EF0771
EF601827.1 gg_id:232408 Chryseobacterium sp. str. NX12 EF6018
GU272226.1 gg_id:554707 library dichlorvos treatment rape phyllosphere clone TF6 GU272
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DQ869047.1 gg_id:243833 Chryseobacterium sp. str. WO DQ869
EU375848.1 gg_id:264030 Elizabethkingia miricola str. L99; CGMCC 2295 EU3758
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DQ314742.1 gg_id:147749 Chryseobacterium stagni str. 10-59 DQ314
EF601823.1 gg_id:229949 Chryseobacterium sp. str. HX31 EF6018
AB193101.1 gg_id:112081 Chryseobacterium shigense str. GUM-Kaji AB1931
AY751083.1 gg_id:99776 Chryseobacterium sp. AUR9 AY7510
EU598813.2 gg_id:578292 Chryseobacterium sp. str. CH34 EU5988

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75.4	5385.0	5303.6	5262.9	3289.8	5192.8	3845.8	5167.0	4568.2	14398.8	3576.6
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53.4	8058.6	4437.1	2753.1	2450.0	5275.7	2153.8	5827.4	5748.3	16427.7	3271.5
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AY230767.1 gg_id:82614 Flavobacterium sp. 'Smarlab BioMol-2300973' str. Smarlab BioMol-2300973 'Smarlab AY2307
EF644913.1 gg_id:248031 Chryseobacterium kwangyangense str. CW9 EF6449
DQ673672.1 gg_id:162999 Chryseobacterium sp. str. RHA2-9 DQ673
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AY883415.1 gg_id:143124 Chryseobacterium soldanellicola str. PSD1-4 AY8834
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EF608166.1 gg_id:554568 Chryseobacterium sp. str. HT11 EF6081
AB024308.1 gg_id:32882 Flavobacteriaceae str. 2 AB0243
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FJ671737.1 gg_id:515176 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
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DQ394928.1 gg_id:153040 harbor sediment clone VHS-B3-5 DQ394
AF217562.1 gg_id:32560 Chryseobacterium sp. str. FR2 AF2175
GQ103633.1 gg_id:389542 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
AB245373.1 gg_id:149000 Chryseobacterium ginsengisoli str. Gsoil 248 AB2453
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AM159183.2 gg_id:150743 Chryseobacterium hispanicum str. VP48 AM159
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EU057843.1 gg_id:253242 Chryseobacterium sp. 3Ablue EU0578
AY163576.1 gg_id:75119 Croceibacter atlanticus str. HTCC2559T; KCTC 12090T; ATCC BAA-628T AY1635
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DQ481462.1 gg_id:176649 Dokdonia donghaensis str. MED134 DQ481
AF207075.1 gg_id:27969 Chryseobacterium meningosepticum str. CIP 6057 AF2070
AM945588.1 gg_id:275181 Eudora adriatica AM945
AY154889.1 gg_id:57759 Flavobacterium sp. str. SR1 AY1548
AB016515.1 gg_id:2312 Flavobacterium columnare str. EK-28 (IAM 14820) AB0165
AB010952.1 gg_id:2311 Flavobacterium columnare str. FK 401 AB0109
EU431785.1 gg_id:544271 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
AB010951.1 gg_id:2310 Flavobacterium columnare str. IAM 14301 (NCMB2248T) AB0109
DQ005505.1 gg_id:129444 Flavobacterium columnare str. Kokanee-94 DQ005
AJ318907.2 gg_id:77276 ED5 earthworm gut AJ3189
EU599190.1 gg_id:278190 Flavobacterium denitrificans str. JS14-1 EU5991

51.2	5843.5	5237.6	4151.5	2632.9	5108.1	2756.4	6333.7	4309.6	14589.4	3986.7
2352.0	8381.1	5374.8	5306.2	4605.0	6996.8	4261.3	7277.1	8267.8	15963.6	5507.6
34.3	9158.6	5127.9	3686.4	3490.5	5624.4	2872.2	7261.9	5965.3	14733.3	4471.2
1251.1	6308.0	4031.8	3720.7	3063.0	5710.0	2928.2	5223.9	4744.7	15085.5	3039.2
784.3	5327.5	4560.2	4028.8	3132.7	5132.7	2805.8	4361.4	4490.7	15444.8	3331.9
109.8	5519.9	2971.8	2319.7	1610.8	3268.6	2294.5	3727.5	4968.9	11811.8	1882.6
96.3	6381.4	4578.7	3035.9	2467.6	4699.2	2618.4	4554.5	6119.7	14399.5	2742.2
422.6	4353.8	3585.7	3590.2	2895.3	3539.9	3862.9	3293.0	3458.6	7394.2	3646.4
396.5	5706.5	5217.2	5486.9	4673.6	7129.7	4461.4	5980.7	7214.2	16440.5	4225.1
85.0	3485.3	3623.6	3813.5	2351.6	3253.6	2501.6	4258.3	3455.4	6100.5	2667.8
813.0	9579.2	7416.7	6731.1	6363.3	8970.7	6170.9	8181.1	12971.7	18811.0	6822.1
100.8	7087.6	6972.5	6114.5	6063.4	7186.9	5565.6	6789.6	8974.7	15824.8	6044.6
1658.1	3896.7	3002.6	2642.3	2297.1	3768.5	2166.6	3211.1	2709.4	11235.6	2809.4
52.3	3225.9	2605.3	1974.7	1033.2	2590.5	1807.0	2316.3	1914.4	8454.1	1269.2
98.4	5910.1	4441.7	4050.3	3404.9	6597.8	3268.3	5783.7	5155.2	15817.2	3625.6
3704.3	13074.4	8544.6	7404.1	7143.2	8726.2	7614.4	9335.5	11194.5	18956.4	8333.9
2288.0	13415.6	6888.5	6189.6	6158.0	8560.4	4605.9	9809.4	11318.8	20085.2	7570.2
1216.0	4807.4	4034.2	4055.0	3043.2	4745.7	3223.0	4282.2	3754.8	13455.3	3092.3
312.3	3986.4	3651.9	3813.3	1936.6	2995.5	2388.1	3585.4	2455.0	8989.0	3336.1
7056.9	5213.1	5677.0	4943.6	5599.1	5083.4	5950.0	4420.4	5028.5	7668.3	4890.9
3223.6	13176.7	7915.4	5898.3	6261.7	9075.1	5461.6	9617.5	14273.5	19295.0	7819.4
76.2	3946.9	2379.0	1353.1	871.8	2859.5	1362.6	2298.1	1641.4	8504.8	1084.3
386.1	6042.8	4057.5	3860.8	4811.5	5672.1	3920.1	5523.0	5035.1	12220.3	3611.8
408.8	8802.7	8692.4	7865.6	6155.4	7643.1	7996.7	8074.5	12660.2	12389.8	7970.6
165.3	8771.7	6580.8	6002.5	5844.5	7449.6	5310.6	7211.7	9371.4	15349.0	6539.5
108.3	6028.1	4774.7	4151.5	3519.3	5517.5	3402.9	5030.0	5755.3	13605.2	3995.0
3864.3	12022.7	10100.5	8733.0	9645.8	11659.2	9395.9	10866.8	17488.1	17588.4	11012.1
4061.6	12712.2	9235.9	7641.9	8518.0	10340.4	7880.9	10151.5	14011.2	20819.4	9208.3
209.9	2036.7	2077.7	2015.2	2286.7	1793.8	2978.6	2469.3	1431.8	2691.0	1235.3
53.3	35.9	75.6	86.6	91.8	69.6	72.8	107.5	43.6	49.3	56.3
357.4	2882.6	1338.7	1072.8	1775.1	1652.1	941.5	3354.1	1620.9	4440.1	3199.4
40.7	590.0	1309.4	690.7	1020.8	1329.5	789.1	1082.5	227.1	15496.0	501.9
477.7	2071.2	1991.4	2486.6	2836.4	1895.9	2215.8	3089.5	1768.4	2043.9	1428.3
2834.6	12757.7	10384.9	11958.7	10869.3	11629.5	13011.3	11225.9	19814.6	16088.2	13484.7
2155.1	7019.6	4848.8	4507.0	5391.5	5591.4	4939.5	5609.7	8212.4	7971.6	5647.6
194.6	12265.9	8559.0	7476.4	9510.2	10809.7	7335.7	9064.4	12975.4	11425.9	9677.4
6171.6	9028.3	8448.0	8502.0	9562.4	8065.9	8568.4	8586.2	11426.5	11306.6	6971.9
106.4	7418.0	6211.3	5232.0	6017.1	5638.2	4503.4	6226.3	9526.1	8981.9	5510.7
62.4	6429.9	4898.4	3923.2	5459.4	5991.0	3682.6	6478.8	6702.1	9306.3	5220.5
47.6	3840.4	3871.8	3249.7	4272.4	4979.6	3186.2	3929.8	5284.3	7241.0	2560.9
46.4	4270.4	3439.4	3356.3	5970.7	5836.6	3759.8	4913.4	13887.3	9243.9	2697.2

6801.8	3438.6	2201.3
6541.5	5065.8	5743.6
7487.0	3444.4	2846.4
6355.3	3907.5	3015.8
7307.2	3842.4	2697.3
3431.3	2588.4	2920.3
5764.5	3291.6	1896.0
3746.7	3755.5	3754.5
6916.8	4764.5	4367.4
4528.2	3468.4	2335.3
9009.1	6311.1	5278.2
6727.8	5733.5	5548.3
4102.8	2828.9	3000.7
3327.1	1927.1	2163.3
7464.7	3788.8	2290.7
10121.8	6898.4	6108.5
8133.1	5514.6	4819.0
5783.7	4005.3	3945.8
4723.8	2907.2	2165.6
4531.4	5177.6	5271.3
10082.4	6308.0	4377.4
2938.3	1584.2	1633.2
6122.8	4413.0	3710.1
8031.1	6843.3	5135.5
7772.9	5606.3	3854.9
7316.1	4203.5	3349.4
10302.7	8620.7	6772.2
10755.9	7392.2	5690.4
3443.2	1974.8	1857.5
124.2	78.9	74.1
2455.9	1306.8	480.7
2091.6	847.9	1120.9
2027.9	2274.3	1726.7
10536.2	10612.0	12051.8
4916.1	4994.1	4247.0
9687.1	6422.2	4148.9
9018.7	8668.8	6301.2
5755.0	5950.8	2424.5
6141.4	5088.9	3164.6
5631.6	4480.4	2728.3
5609.3	4692.5	1194.8

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EU046269.1 gg_id:236177 Flavobacterium anhuiense str. D3 EU046
EU037341.2 gg_id:277429 structure landfill sediments receiving long-term augmentations wastes chromium co EU037
AB455257.1 gg_id:333236 Flavobacterium frigidarium str. NBRC 102676 AB455
AY771738.1 gg_id:144927 Flavobacterium frigidarium S5-15 AY771
AF321008.2 gg_id:37648 Flavobacterium sp. str. GOBB3-C101 AF321
AF235124.1 gg_id:28033 Cytophaga sp. str. KT0234A AF235
AF468425.1 gg_id:80437 Arctic sea ice ARK10164 AF468
AF321019.2 gg_id:19998 Flavobacterium sp. str. GOBB3-C103-3 AF321
AB275999.1 gg_id:222700 Flavobacterium kamogawaensis str. KG12 AB275
GU073293.1 gg_id:580196 Flavobacterium sp. str. LW30 GU073
AB455260.1 gg_id:311116 Flavobacterium psychrolimnae str. NBRC 102679 AB455
AB078060.1 gg_id:58629 Flavobacterium psychrophilum str. IFO 15942 AB078
AM177631.1 gg_id:149279 Flavobacterium sp. str. WB 4.3-34 AM177
AM265623.1 gg_id:159982 Flavobacterium hercynium str. WB 4.2-33 AM265
GU138376.1 gg_id:558897 Flavobacterium sp. str. THG 81 GU138
EU431710.1 gg_id:544153 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU431
FJ958328.1 gg_id:418781 Flavobacterium sp. str. Tibet-YD5000-3 FJ9583
EU057853.1 gg_id:237807 Flavobacterium sp. 20I EU057
AJ551174.1 gg_id:93705 Cytophaga sp. An36 AJ5511
AM230488.1 gg_id:152029 Flavobacterium johnsoniae str. DSM 425 AM230
EU707556.1 gg_id:333324 Flavobacterium sp. str. YC6718 EU707
AM921624.1 gg_id:245846 Flavobacterium pectinovorum PhyCEm-99 AM921
DQ640006.1 gg_id:161549 Flavobacterium sp. str. PR01 DQ640
AM934631.1 gg_id:264229 Flavobacterium sp. str. WB2.1-16 AM934
AB496407.1 gg_id:543988 Flavobacterium sp. str. S22202a AB496
AJ557888.1 gg_id:88003 Flavobacterium micromati str. LMG 21919 AJ5578
FN397666.1 gg_id:382056 Flavobacterium sp. str. PON14 FN397
AM230490.1 gg_id:151743 Flavobacterium pectinovorum str. DSM 6368 AM230
DQ778315.1 gg_id:172143 Flavobacterium sp. YO51 DQ778
EU057848.1 gg_id:257608 Flavobacterium sp. 19C EU057
EU636033.1 gg_id:279577 Antarctic str. L10 EU636
AM921621.1 gg_id:250589 Flavobacterium johnsoniae PhyCEm-72 AM921
AM934672.1 gg_id:267882 Flavobacterium sp. str. WB4.3-66 AM934
AY599656.1 gg_id:102856 Flavobacterium sp. str. TB4-4-II AY599
AY550033.1 gg_id:104940 Sporocytophaga cauliformis str. 9726R AY550
EF395377.1 gg_id:222394 Cytophaga sp. str. 4D9 EF3953
FJ786050.1 gg_id:539182 Flavobacterium sp. str. I-111-19 FJ7860
EF640932.1 gg_id:254023 Chryseobacterium sp. str. GR15 EF6409
EU099872.1 gg_id:257508 Flavobacterium sp. str. CJ4 EU099
EU057845.1 gg_id:257586 Flavobacterium sp. CH16-1 EU057
EU057851.1 gg_id:245636 Flavobacterium sp. PR30-9 EU057

40.5	2278.7	2506.1	2577.8	3457.9	3561.3	2630.0	3059.0	1895.4	9850.8	1664.7
351.2	6838.0	5760.1	5656.5	6718.0	8354.8	5963.7	6120.0	10333.8	9129.7	6201.7
61.6	4786.2	5371.3	4100.2	5294.1	6088.4	4759.3	4699.1	8970.6	6291.1	2743.6
61.4	4244.6	3727.2	2955.6	3348.2	4129.0	3274.1	5303.9	5850.5	6048.7	3505.0
82.6	7170.3	7321.2	5495.2	7077.3	7361.4	6275.6	8040.2	13896.8	11430.4	5709.5
170.7	2515.8	2732.0	2400.1	2733.7	2739.3	2564.0	2225.7	3257.4	3361.3	2354.1
73.0	7733.6	8262.0	5081.1	7025.4	7422.1	5865.0	6574.1	17271.3	10460.8	3420.6
338.7	6555.4	7219.2	5309.6	6712.9	7154.0	5997.7	7757.8	9239.9	10647.6	5568.7
39.9	7553.2	9322.0	6929.7	7918.1	7909.2	5297.5	7190.7	15267.4	9263.7	6043.5
340.9	5186.6	3387.4	3116.8	1916.7	4800.7	2101.7	4078.5	4429.0	3047.8	2947.7
31.5	5508.0	4197.8	3389.2	5417.8	5456.9	5377.0	5559.6	11628.3	5492.0	3550.2
42.2	5557.3	5178.2	4332.7	6555.6	6605.3	5797.5	6037.1	14903.0	8120.7	4210.6
50.6	6706.5	6762.8	5262.2	6596.5	6420.5	5965.9	6739.0	9600.2	8373.2	4843.6
53.9	6649.8	6762.6	5183.6	6895.5	6485.5	5893.2	6123.3	12318.7	8432.8	4506.0
44.1	7327.4	5781.5	2585.5	5252.6	5955.6	5021.7	5887.7	11204.9	7572.1	6306.7
756.1	10696.0	11294.6	9891.1	13564.2	10735.5	11249.5	9822.8	20047.5	13532.9	7879.2
53.2	8005.4	7853.3	5989.1	8013.6	8001.1	7699.0	7975.8	12585.9	11183.2	6685.0
45.4	7917.1	6841.1	5364.5	7410.0	7303.8	6298.7	7257.4	17237.9	8756.9	5549.7
34.2	8597.2	8244.3	5290.9	6543.9	6898.5	5543.9	8409.7	12201.8	9559.2	6780.5
51.1	8713.0	8809.5	7325.2	9100.7	8529.0	8105.0	8374.3	14599.4	12462.3	6773.2
46.5	10518.1	10479.9	7901.6	9829.0	10165.4	8787.7	11222.1	14664.3	15109.9	8499.8
46.0	6267.4	5623.7	4231.8	5664.3	5896.6	5040.4	6010.4	8822.2	8353.2	4042.6
36.4	4444.5	4971.6	4838.4	5470.3	5196.9	5126.5	5123.6	10649.9	5776.0	3036.7
58.7	9091.3	8775.9	6596.6	8523.5	8316.6	7727.1	8416.3	13544.1	12264.3	7479.7
33.4	5977.9	6310.9	3655.3	7499.7	7009.1	4597.7	6418.6	15431.2	7526.7	4431.0
34.1	6631.0	5791.0	3594.3	6987.0	6791.8	4082.2	6490.3	13121.5	7374.6	4589.9
45.1	6519.2	6324.8	5136.4	6835.1	6624.2	6232.4	6654.0	12350.9	8147.4	4593.1
35.5	5047.3	4187.2	3041.4	6641.4	6526.3	4517.4	5933.0	17488.8	7486.8	3449.1
39.3	4406.7	4937.2	3958.4	4848.0	4678.1	3859.8	4948.4	6314.5	6524.0	2983.7
2941.9	9476.1	9459.5	7097.2	8814.8	9643.2	8727.9	9048.7	13218.2	11128.2	9229.3
51.7	7883.4	6941.5	4099.4	5610.8	5434.3	4152.5	5795.6	11184.2	9327.8	3364.8
1359.2	5732.4	5122.2	5369.7	4600.6	5731.4	3890.6	6208.7	8097.9	6483.3	4329.8
34.3	6710.0	6932.8	5134.8	6844.6	6867.4	5916.5	6334.7	12722.7	8020.5	4324.7
44.3	3174.9	2271.0	1537.7	2308.1	2277.0	2004.3	2450.2	4615.1	3244.6	2452.1
50.5	8928.9	8854.5	6839.1	8501.2	8373.1	7440.9	8347.9	13717.8	12660.4	6861.6
47.6	9462.5	7781.2	5485.8	7579.1	7727.6	6135.7	7927.0	13543.6	9971.3	6739.0
64.9	11245.4	11330.5	9103.7	11065.8	10590.8	9515.0	10928.3	18434.1	16011.6	8609.5
42.1	6740.3	4907.1	2824.2	6441.3	6398.0	3655.9	5826.2	14377.7	5780.7	4267.0
270.9	9245.5	6311.0	5348.5	6291.1	7281.1	5310.2	7069.7	13106.2	6502.1	6383.4
44.9	5665.1	5718.9	4366.0	5509.4	6011.4	5082.0	5992.2	8023.1	8551.8	3820.9
49.5	9242.6	8528.7	6856.5	8437.2	8248.5	7572.1	8407.5	13849.7	12028.0	6868.5

4081.2	5348.5	1339.3
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6094.8	5654.5	2251.4
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8620.4	9186.8	3474.0
2291.2	3657.9	1985.6
7572.7	7114.7	3058.1
7237.3	7755.4	4347.6
6923.9	6662.1	3044.4
4129.2	2413.6	2032.8
4733.4	5484.8	1685.9
5938.0	7819.1	2440.8
6770.6	7971.4	4117.5
7168.6	7796.1	3473.5
5505.4	6333.2	3024.5
10904.3	9977.5	8086.5
8673.3	8719.5	4915.5
7347.5	7664.8	3391.4
6664.8	8450.4	4070.3
9529.6	8967.9	5037.7
10565.7	10116.1	5759.6
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5018.8	5841.4	3234.5
9672.3	9172.3	5134.9
5710.4	5841.5	2790.1
5852.9	5528.2	2271.2
7049.3	7699.5	3547.8
6137.7	5235.7	1655.7
5518.8	5612.5	2437.4
9834.9	10140.8	7249.9
5178.3	5205.0	3044.9
5080.6	5605.9	3417.1
6709.5	7377.5	3972.2
2430.7	2707.9	1210.1
9622.4	8512.8	4064.8
7658.3	7601.5	3947.1
11307.7	10459.2	6488.5
5533.4	4756.0	1564.0
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DQ856547.1 gg_id:256080 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3A DQ856
AM167558.1 gg_id:143877 Flavobacterium sp. str. WB 2.1-30 AM167
DQ778316.1 gg_id:167810 Flavobacterium sp. YO60 DQ778
GQ339900.1 gg_id:545188 Flavobacterium sp. str. PB002 GQ339
DQ628945.1 gg_id:168173 Flavobacterium sp. SOC A4(51) DQ628
EU860081.1 gg_id:336431 Flavobacterium johnsoniae str. A3 EU860
DQ778318.1 gg_id:169203 Flavobacterium sp. YO66 DQ778
AJ551150.1 gg_id:93577 Cytophaga sp. An11 AJ5511
EF653586.1 gg_id:256294 water s Dong Tinghu clone DTH16 EF6535
EU104118.1 gg_id:320418 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
AY599655.1 gg_id:102705 Chryseobacterium sp. str. TB4-8-II AY5996
DQ530073.1 gg_id:161601 Flavobacterium johnsoniae CI04 DQ530
GU291857.1 gg_id:547948 Flavobacterium sp. str. HMD1071 GU291
GQ069169.1 gg_id:434593 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
EF601819.1 gg_id:231100 Flavobacterium sp. str. WX3 EF6018
DQ478946.1 gg_id:158263 Flavobacterium sp. QLX6 DQ478
AB075231.1 gg_id:36697 Flavobacterium limicola str. ST-10 AB075
AB075232.1 gg_id:34165 Flavobacterium limicola str. ST-92 AB075
AJ601392.1 gg_id:95581 Flavobacterium xanthum AJ6013
AF030380.1 gg_id:2327 Flavobacterium xanthum str. ACAM 81(T) AF0303
GQ009789.1 gg_id:499875 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU431833.1 gg_id:561092 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
DQ228399.1 gg_id:142636 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EF019396.1 gg_id:211062 aspen rhizosphere clone Elev_16S_629 EF0193
GQ249374.1 gg_id:555934 Research on biodiversity sludge bioflim Biological Aeration Filter clone B16 GQ249
AY212736.1 gg_id:99774 water 5 m downstream manure clone 41ds5 AY2127
EU432473.1 gg_id:266040 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU4324
FJ716000.1 gg_id:588086 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
GQ084774.1 gg_id:445836 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
GQ249524.1 gg_id:579829 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 6-8 cm layer clor GQ249
AM934667.1 gg_id:268494 Flavobacterium sp. str. WB4.1-56 AM934
AF289165.1 gg_id:71577 freshwater clone PRD01b005B AF2891
DQ264555.1 gg_id:144460 universal microarray broader than typical library when sampling subsurface groundv DQ264
DQ856509.1 gg_id:252738 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C1M DQ856
EU431740.1 gg_id:563689 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4317
AM934683.1 gg_id:263519 Flavobacterium sp. str. BF134 AM934
EF424395.1 gg_id:210562 Flavobacterium sp. str. IP10 EF4243
DQ628917.1 gg_id:173779 sequences Arctic glacier subglacial water ice or sediment clone BFA 7C DQ628
AM110990.1 gg_id:140778 Flavobacterium sp. str. 3037 AM110
AM230493.1 gg_id:156139 Flavobacterium succinicans str. DSM 4003 AM230
DQ501350.1 gg_id:198748 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501

62.4	11599.7	11337.6	8842.1	10917.1	10606.9	9667.8	10597.4	18033.2	16386.1	9849.5
43.7	8283.6	7000.4	5670.6	7474.5	7837.4	6891.9	7677.1	15498.0	9501.1	5670.1
45.0	7653.5	6814.8	5188.0	7272.9	7631.3	7070.5	7800.8	15506.9	9688.7	6344.8
48.2	4966.9	5332.8	3605.9	5240.6	5550.7	4077.0	5407.1	7454.9	7087.1	3195.6
35.5	6246.7	5247.6	3247.2	3970.6	4726.0	3463.3	6421.7	7447.0	5653.2	4406.0
43.0	7227.3	6929.0	4755.7	6884.3	6749.2	5262.2	6537.4	12280.1	8657.3	4942.7
51.5	8562.2	9281.3	7723.7	9145.9	8863.6	8310.6	8864.1	13097.0	12791.9	6406.3
34.6	5057.9	4788.8	3224.8	3818.5	3875.0	3412.5	4591.6	9586.7	4821.3	3143.1
36.9	4673.7	4045.8	2533.4	4961.3	4170.3	3286.9	4164.4	10972.1	3768.2	3099.2
48.2	7515.0	7334.4	5558.9	8076.6	7331.7	6572.0	7034.2	14228.7	9787.0	4578.9
63.7	6740.2	7258.1	5012.3	6696.6	6856.7	5352.5	6427.8	9439.3	8410.5	4425.1
30.5	7111.6	6464.1	4798.2	6396.1	6453.6	4541.2	6928.4	10589.3	9031.7	4671.3
51.8	3828.8	4991.6	4619.7	5755.5	5913.9	5584.2	5275.8	7498.3	8856.4	2866.6
29.6	3169.3	3812.5	2175.3	3645.7	3407.4	2566.8	2975.8	8259.8	5288.4	1765.0
57.4	9126.0	9187.5	6745.2	8963.8	8708.3	8043.1	8427.7	14301.9	13223.8	7465.0
6510.2	4156.3	4161.6	4297.1	4670.6	4865.0	4715.1	5043.8	4555.2	7150.2	3533.4
60.5	5321.1	3756.9	2909.0	4764.8	5776.3	6154.7	4941.7	6703.6	5018.1	3208.8
47.2	5617.5	4578.2	4225.4	5372.0	7124.8	6118.9	5497.2	10057.5	6592.2	3411.1
56.4	7843.6	5742.0	3791.3	5585.5	5983.3	6021.7	5843.4	9605.9	7288.4	3629.9
1420.5	5406.8	4855.1	4208.9	5211.6	6139.4	5534.5	6474.4	7541.6	7290.1	4744.7
172.4	3540.7	2740.6	2270.7	2925.3	3863.1	2379.3	3204.6	5638.8	3118.4	1859.1
18267.1	8788.9	9361.0	8967.7	9965.8	9634.9	9728.6	8639.3	15226.6	13115.7	8805.6
47.6	7635.2	7720.2	5757.6	7543.8	7988.7	7168.3	8327.2	18371.5	9085.0	4954.8
399.5	7001.6	6253.5	5483.4	5598.3	7326.0	5945.0	6279.9	10329.0	8282.0	4917.3
3555.8	7742.2	6121.2	5903.2	6785.1	8780.0	6421.0	7225.1	11686.2	9323.3	6783.9
46.3	13913.5	12186.5	8612.7	10956.1	11085.1	9190.8	11523.9	21556.0	14421.9	8360.6
147.9	8286.2	8324.7	6990.1	10053.6	9415.8	9401.5	8177.3	15774.0	9123.0	7131.8
947.7	5643.9	6221.9	5232.6	5589.1	5566.7	5711.7	5426.0	9009.6	6852.0	5109.1
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454.1	8838.1	7655.2	5447.2	6001.6	8353.4	6368.1	7313.9	8264.8	7548.8	5951.0
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40.0	34.6	120.5	115.8	344.0	187.8	215.9	175.8	45.0	135.6	103.3
30.9	6713.3	7376.0	4604.6	6055.2	6136.7	5803.1	6092.1	14609.2	7994.9	3717.4
47.9	9287.4	7933.9	6331.4	8157.8	8163.9	7258.1	8273.4	13650.1	8559.7	6181.9
52.1	6672.3	6602.8	4985.5	7355.1	6318.7	7224.6	7485.3	8759.8	7512.9	5123.0
11032.2	8353.3	7366.4	7690.7	7134.7	7847.4	7414.8	7722.8	12637.5	9167.9	8077.1

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7777.9	8235.9	3620.2
7277.7	8671.1	4210.5
4510.1	6434.4	2408.8
3676.4	4951.2	2687.7
6861.3	6522.9	2971.5
9905.4	9544.0	5232.3
4010.9	4614.8	1840.0
3659.7	3831.9	1734.8
7668.8	7392.1	3736.3
6713.5	7628.5	3861.1
7010.8	6862.4	2897.0
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3694.8	3084.0	1434.6
9922.8	8869.3	4779.7
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4914.3	4242.1	1539.5
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3452.9	3083.0	1826.3
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7732.8	8615.3	4455.3
7316.8	7563.8	4323.3
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11358.6	10024.0	5317.6
8255.9	9202.7	5439.5
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7601.5	6616.6	4741.9
4384.8	6587.3	2311.5
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AM934649.1 gg_id:268495 Flavobacterium sp. str. WB2.3-63 AM934
NR_025202.1 gg_id:548212 Flavobacterium omnivorum str. 1.2747; JCM 11313 NR_02
GQ354998.1 gg_id:509233 structure between two geochemically distinct springs Alum Rock Park spring clone 4 GQ354
GQ389164.1 gg_id:509696 quality deterioration drinking system during serious red water outbreak clone D32 GQ389
FJ517669.1 gg_id:510071 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e FJ5176
FN421997.1 gg_id:586494 proteogenomics physiology phyllosphere clover clone 5_H09 FN421
EF648152.1 gg_id:250428 dynamics during produced water treatment aerobic activated sludge clone XJ104 EF6481
DQ264580.1 gg_id:142257 universal microarray broader than typical library when sampling subsurface groundv DQ264
DQ021903.1 gg_id:136136 Flavobacterium saliodium str. 1.3801 DQ021
EU037363.2 gg_id:268227 structure landfill sediments receiving long-term augmentations wastes chromium co EU037
AM712887.1 gg_id:542078 Salibacter luridus str. KSW-1 AM712
AF502205.1 gg_id:59360 EBPR sludge lab scale clone HP1A39 AF502
EU373337.1 gg_id:274547 Cytophaga sp. str. HNR01 EU373
EU008825.1 gg_id:248249 Flavobacterium sp. str. CC-YMW-3 EU008
DQ628951.1 gg_id:169102 Flavobacterium sp. SOC A4(12) DQ628
AM888191.1 gg_id:247605 Flavobacterium sp. str. THWCSN34 AM888
AM167559.1 gg_id:141447 Flavobacterium sp. str. WB 2.1-78 AM167
DQ310736.1 gg_id:148060 Recurring seasonal dynamics microbial stream habitats riverine sediment clone WC(DQ310
DQ856559.1 gg_id:256046 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3L DQ856
AM934646.1 gg_id:260813 Flavobacterium sp. str. WB2.3-15 AM934
EU109724.1 gg_id:248774 Flavobacterium sp. str. H7 EU109
GQ406174.1 gg_id:511461 Benthic submerged sinkhole ecosystems sediment clone -45-4 GQ406
GU305854.1 gg_id:558583 Research on changes structure during algae outbreak oligotrophic lakes (YangHe res GU305
AJ318198.1 gg_id:21369 Waste-gas biofilter clone BIwi5 AJ3181
EU802008.1 gg_id:340945 It's all ranking aquatic Chesapeake Bay MD clone 3C003394 EU802
AM934637.1 gg_id:277267 Flavobacterium sp. str. WB2.1-50 AM934
AB180738.1 gg_id:102656 Flavobacterium granulensis str. Kw05 AB180
DQ222427.1 gg_id:141129 Flavobacterium sp. str. GH1-10 DQ222
FJ535187.1 gg_id:556344 Contamination risk vegetables Arcobacter during post-harvest processing water carrc FJ5351
AM934669.1 gg_id:274086 Flavobacterium sp. str. WB4.3-36 AM934
EF467491.1 gg_id:204202 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
FJ979858.1 gg_id:372941 Flavobacterium sp. str. tsz28 FJ9798
DQ658240.1 gg_id:168113 Flavobacterium arcticum DQ658
DQ256316.1 gg_id:141407 subsurface water clone EV818BHEB5102502SAR27F80 DQ256
FJ979863.1 gg_id:425968 Flavobacterium sp. str. tsz35 FJ9798
DQ178976.1 gg_id:139119 Flavobacterium dokdonense str. DS-6 DQ178
GQ000816.1 gg_id:469382 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ000
GQ079017.1 gg_id:413256 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ079
EF632770.1 gg_id:244921 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
FJ593904.2 gg_id:538912 Flavobacterium sp. str. -8 FJ5939
L39067.1 gg_id:73974 Flavobacterium hibernum str. ATCC51468 L39067

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32.0	6646.5	6406.0	3655.7	5305.6	6409.9	4307.7	4981.7	8361.2	8886.0	2646.0
45.6	11173.5	8709.8	6902.7	7339.1	9328.5	5837.3	9518.7	17253.8	10550.3	8462.1
43.5	4102.1	2853.7	1954.7	2873.5	4906.9	1515.3	4758.2	3806.0	6676.3	3677.6
71.4	11735.3	10042.3	7145.5	10073.3	11164.1	8451.2	10014.9	19567.0	14373.8	9583.1
53.4	8287.1	7602.9	5872.1	9691.8	8958.5	7218.2	7501.6	14868.8	9676.4	6557.8
54.2	8803.3	8072.9	6788.9	8783.2	9125.4	8534.2	9106.0	18563.5	11698.2	7489.6
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117.2	6301.1	7216.7	2227.0	5071.1	3623.8	2443.4	2938.5	4602.4	5392.5	2153.8
2971.9	9218.1	9298.8	8126.0	8172.5	9516.4	8742.6	7925.3	14244.2	10407.3	8617.2
2366.9	4074.4	6082.1	3727.9	4726.4	4268.8	3706.2	4765.7	2870.8	9334.0	3745.9
803.7	12279.3	7770.1	5911.4	8884.1	12316.0	7064.0	8829.1	17261.6	11640.9	8927.8
136.7	9700.2	8170.0	8116.2	8859.3	9418.4	8684.5	9130.3	11133.1	8522.9	9028.6
157.2	7937.7	6822.7	5140.8	5519.4	6618.3	5698.9	6219.5	9968.9	9684.8	4255.3
41.2	3556.5	4962.7	3748.0	5093.4	5125.9	4814.1	4449.0	8800.6	4632.3	2430.0
56.0	6804.6	4416.5	4344.3	5694.0	7231.6	3762.5	7827.0	11563.0	9395.4	7413.9
43.0	9425.8	6890.1	4711.7	6252.7	6878.1	6105.6	7812.1	13045.8	6917.7	5660.3
97.5	1702.2	904.1	297.8	781.7	927.8	323.1	1712.4	3574.9	677.0	795.5
62.2	11925.1	11261.5	9008.6	11004.1	10622.4	9507.5	11791.4	19225.2	16293.8	9913.0
57.2	7798.8	9227.0	6939.5	8895.2	8261.4	7683.3	8431.4	15115.9	11342.6	5493.0
70.8	4090.4	4732.0	4317.0	5113.5	4142.7	5145.7	6027.6	4961.9	6705.8	3585.0
42.6	4498.5	4128.4	2585.7	3243.0	4128.5	2788.5	5141.4	5409.5	7687.2	3209.5
107.7	7177.6	6097.1	4767.6	6038.3	6831.7	5255.6	8000.9	8636.0	9956.3	6090.5
136.2	2213.1	2468.3	1776.5	1637.9	2289.3	2017.6	2038.6	2678.8	2644.1	1573.4
32.5	9417.5	7641.0	6300.3	4986.8	7881.0	3662.8	8338.4	16980.1	7488.7	6268.0
29.9	4970.5	5697.0	4120.1	5309.1	4813.3	4031.8	5539.5	6315.0	7141.0	3835.3
45.6	4028.2	4866.6	3932.5	4040.5	4253.9	3766.8	6692.6	7701.2	10114.8	3727.3
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38.1	3557.6	4506.4	4095.3	5289.5	5245.3	5295.6	4903.8	6610.2	4955.4	2587.6
37.6	4558.3	3700.2	2513.8	3704.5	4171.0	2708.3	4475.3	7415.5	6471.8	2192.8
48.2	5914.4	5227.1	4080.8	4007.0	5314.9	3373.4	5851.3	9274.3	4966.4	4312.3
14306.9	8114.9	9956.4	7307.7	8337.0	9042.5	8004.6	7650.8	17360.4	11433.7	8412.4
34.4	3210.7	4236.2	2708.0	4205.5	4530.2	3017.2	3476.9	5683.0	5272.0	2067.7
357.7	15419.7	12528.7	11813.4	12914.1	14124.3	11705.5	13376.1	21574.9	16990.8	15047.8
154.6	9314.3	8464.4	6949.0	7233.2	8035.0	6623.2	7922.8	13933.8	10905.6	8041.9
51.4	7303.2	6708.6	7208.4	6904.9	7674.6	6912.4	7672.0	12763.8	8120.8	5268.5
90.8	4596.8	4326.9	3245.2	6070.3	5844.6	5240.3	3892.2	4207.5	3664.0	3122.0
248.4	6942.2	5958.4	5539.4	8264.4	6725.3	6603.7	6895.2	9950.3	7265.4	6377.4
36.0	6473.1	6117.0	4141.4	6245.8	6350.7	4606.0	6425.1	13990.9	9384.4	4899.2
228.7	7006.7	4442.0	3176.8	5374.8	8276.2	3561.7	5521.6	8111.7	6727.1	4864.5
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2752.8	2287.7	1109.6
10716.7	10153.1	5042.8
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9428.9	9890.7	4711.7
10695.4	9086.2	6319.4
2970.5	3399.5	1256.8
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DQ372981.1 gg_id:151202 Flavobacterium sp. str. EMB34 DQ372
EF632859.1 gg_id:249853 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6328
FJ544921.1 gg_id:549166 Flavobacterium sp. str. KOPRI 25149 FJ5449
EF520552.1 gg_id:227962 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-29 EF5205
AM230492.1 gg_id:156027 Flavobacterium succinicans str. DSM 4002 AM230
AM230486.1 gg_id:152630 Flavobacterium flevense str. DSM 1076 AM230
AY212593.1 gg_id:99956 water 20 m downstream manure clone 142ds20 AY2125
GQ395239.1 gg_id:570635 Flavobacterium sp. str. XAS590 GQ395
FJ529995.1 gg_id:510944 Initial ammonia- and nitrite-oxidizing compromises successful nitritation counter-diffu FJ5299
CU466733.1 gg_id:350201 Evry wastewater treatment plant anoxic basin clone CU466
DQ521513.1 gg_id:193156 Antarctic lake ice cover clone ANTLV2_D10 DQ521
FJ716009.1 gg_id:566584 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
AF336355.1 gg_id:32387 Flavobacterium sp. str. Wuba46 AF3363
DQ298763.1 gg_id:143021 Effect Nutrient Periodicity upon Microbial Dynamics exposed 7-day nutrient flux DQ298
AM230494.1 gg_id:156296 Flavobacterium succinicans str. DSM 4001 AM230
FN547416.1 gg_id:574039 Flavobacterium sp. str. WG2 FN5474
AJ786797.1 gg_id:108074 Flavobacterium sp. R-21935 AJ7867
DQ298762.1 gg_id:142500 Effect Nutrient Periodicity upon Microbial Dynamics exposed 7-day nutrient flux DQ298
DQ521514.1 gg_id:186502 Antarctic lake ice cover clone ANTLV2_D11 DQ521
DQ256490.1 gg_id:144140 Flavobacterium johnsoniae Jm162a DQ256
AM934684.1 gg_id:269942 Flavobacterium sp. str. CL1.100 AM934
EF424249.1 gg_id:212836 Isolation and properties alginate-decomposing decomposer alginate rotten algae sun EF4242
AM177633.1 gg_id:148903 Flavobacterium sp. str. WB 4.3-96 AM177
AM412168.1 gg_id:257833 Flavobacterium sp. str. P-131 AM412
EF632769.1 gg_id:253814 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
CP000685.1 gg_id:220711 Flavobacterium johnsoniae UW101 str. UW101; ATCC 17061 CP000
DQ264616.1 gg_id:141431 universal microarray broader than typical library when sampling subsurface groundv DQ264
EU340154.1 gg_id:249417 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU3401
AM934651.1 gg_id:267818 Flavobacterium sp. str. WB2.3-68 AM934
EU104097.1 gg_id:348328 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
GQ144412.1 gg_id:439710 Flavobacterium sp. str. HMD1045 GQ144
AM934644.1 gg_id:264327 Flavobacterium sp. str. WB2.3-9 AM934
AM934665.1 gg_id:277605 Flavobacterium sp. str. WB3.4-82 AM934
AF090991.1 gg_id:2299 Flavobacterium psychrophilum str. ATCC49418 AF0909
EU703375.1 gg_id:456274 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH72 EU7033
FJ362499.1 gg_id:363931 Flavobacterium sp. str. AC17 FJ3624
EU636031.1 gg_id:278951 Antarctic str. N04 EU6360
AM230485.1 gg_id:150856 Flavobacterium aquatile str. DSM 1132 AM230
AJ534682.1 gg_id:76123 ground water deep-well injection disposal site radioactive wastes Tomsk-7 clone S15A AJ5346
DQ659445.1 gg_id:161600 Flavobacterium sp. W6-14 DQ659
GQ281769.1 gg_id:557941 Flavobacterium sp. str. 15C3 GQ281

46.8	3224.0	1921.5	1314.9	1619.3	3783.9	1199.9	2448.5	4928.1	3609.9	2154.8
40.8	7496.1	6545.6	5811.1	6670.8	8141.1	5221.3	7759.9	16746.6	10256.5	5790.8
60.2	5123.3	3993.9	3126.0	4187.2	4153.4	4172.2	4891.4	6737.4	4411.2	3139.2
60.3	7428.3	6425.6	4453.2	6933.7	8567.2	5191.7	7616.6	13552.2	7546.1	5270.7
40.0	9255.0	8714.7	5983.8	7709.4	7496.5	6436.7	8134.6	11567.3	11558.8	6038.2
70.6	7526.9	7588.3	5451.0	7672.3	7356.1	7075.5	7452.0	12731.0	10778.2	5119.3
49.2	10983.4	8690.6	7174.3	7961.4	8771.8	5298.2	9897.9	16031.5	9591.0	8396.7
59.6	5230.8	4477.8	3796.3	6092.6	5867.9	3618.4	5802.4	9773.7	11738.7	3089.0
3995.9	6218.0	5140.6	4173.2	5023.5	6630.8	4232.7	6400.2	6610.8	7565.0	6991.2
47.4	4423.6	4575.7	3421.9	4636.5	4537.3	3887.8	4537.5	6870.5	5666.1	3088.4
139.0	4575.9	4483.6	2148.7	4049.9	3092.9	3561.5	4140.7	3269.3	5248.4	3023.2
166.0	9356.8	9103.0	7191.6	8461.6	8188.4	7314.9	7618.1	12500.6	12034.5	8237.9
45.8	3232.2	4240.4	2703.5	3163.4	3666.1	3376.5	5793.6	4930.5	10724.3	3328.0
273.1	8969.5	6645.8	6565.8	7972.6	9266.9	6418.0	7635.3	12964.7	10219.2	8440.4
21.1	9679.6	8396.8	5645.7	5570.3	7038.9	4085.3	7411.3	8709.0	9807.5	4912.4
52.0	9073.7	4330.4	4339.1	5274.8	4061.0	3966.9	7469.3	5641.5	10907.9	7077.0
53.2	12407.9	10995.3	8346.3	10930.2	10383.1	8474.2	11629.4	16181.8	18607.1	9627.1
8030.2	8157.0	6793.7	7289.3	7352.3	7316.6	6900.3	8036.5	17721.2	9218.2	4139.3
44.1	4987.3	4734.0	4915.8	5062.0	6041.3	4330.4	6402.8	6555.3	7805.6	4036.9
108.7	5602.1	5274.8	5125.4	8239.9	6545.1	5492.5	5934.5	7595.1	11979.8	4576.9
62.7	7433.1	7710.5	5681.6	7202.5	6484.2	5998.8	7503.8	12338.2	8975.8	6009.1
137.7	8069.6	8324.5	6148.4	9001.1	7919.3	7305.4	7351.2	12438.1	7478.9	6091.2
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40.4	9764.0	8154.6	6543.7	8369.2	8540.4	6646.3	8433.1	14562.4	14012.6	7550.1
54.3	4599.0	5101.9	4249.6	5813.7	5212.5	5462.7	5673.9	11162.1	6294.1	3657.6
666.9	11912.2	9921.4	8107.7	11107.9	9377.9	8359.1	7721.3	13670.8	14386.4	6395.0
18536.5	8180.7	7577.4	8805.7	8196.4	8750.8	8868.2	8161.1	11295.3	6947.6	9329.6
53.4	15766.0	12352.1	9570.1	10354.2	11380.9	8468.4	11572.3	22490.7	15288.0	10602.7
54.4	3754.2	4588.2	3279.0	5558.0	4265.6	3824.8	4674.4	8452.7	5488.3	3760.4
208.4	4404.8	4272.7	2953.4	6014.4	5107.5	4068.5	3975.2	5618.2	5167.0	3937.8
63.1	8367.6	8260.3	6167.4	8732.0	7717.6	7764.7	8402.6	15362.2	10225.5	6876.0
72.3	12094.7	12622.1	9565.4	12241.4	11976.9	11042.2	11650.9	22317.1	16813.9	9951.3
41.7	4083.2	5045.6	3330.0	3849.8	4094.3	3392.3	5384.2	9519.6	6589.6	2674.5
2916.4	4653.9	3962.2	4142.9	2889.4	4489.4	3957.4	4911.9	7106.6	4795.3	5260.6
258.4	8287.1	7753.8	6832.9	6889.0	8017.2	6261.7	7309.8	12834.5	9730.1	7131.0
124.8	8047.7	8706.4	6360.3	8181.4	7571.9	7286.7	8891.3	15107.1	12081.0	5734.2
86.6	8571.3	4992.3	2983.9	4770.3	8512.8	3363.3	5907.1	12293.9	5698.7	4907.7
1297.9	3897.5	2950.0	2607.5	3646.0	4550.0	2519.5	4300.5	7026.9	4874.4	4159.4
32.6	1032.1	170.6	97.7	440.9	2015.0	160.4	710.0	533.5	2160.9	569.5
30.9	923.5	1463.2	529.6	868.6	1167.5	533.8	1137.7	909.4	2125.3	550.0
61.1	4700.0	4654.0	3563.9	5381.8	5532.7	3199.3	3912.1	6242.3	11925.9	2282.5

2028.3	1953.9	856.2
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3813.2	5434.7	1640.2
6191.3	6164.5	2891.0
7935.1	6756.0	5160.2
7860.0	6802.7	4511.9
7127.4	5700.0	2805.7
6002.6	5466.9	1845.6
4932.1	4041.1	3203.0
4030.4	6084.4	1449.0
3152.0	5189.6	2945.0
7336.3	8020.4	4392.7
4245.7	4197.8	3085.0
8898.2	6080.9	4471.3
5606.6	5675.7	3143.3
4427.6	2967.8	1307.4
11191.8	9245.6	5382.7
7912.6	8279.3	4696.5
5473.0	6114.7	2590.1
7015.6	6578.2	3018.2
8102.7	8531.1	3263.8
6544.0	8751.1	3810.7
2962.7	4385.1	2740.2
9473.9	7834.4	3151.4
4604.6	8459.8	2201.4
9480.0	7043.8	6143.1
8157.0	8113.4	5103.0
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4061.2	5190.8	1957.5
4818.5	3893.6	2708.8
7682.5	10153.6	4594.2
12497.1	12106.2	7546.8
4875.2	5085.7	2380.6
3618.7	5253.9	3490.1
7233.5	8648.8	4657.1
8364.6	8858.5	4721.3
5118.1	3666.4	1853.3
3604.4	2916.0	1328.0
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2166.4	1117.0	307.2
5921.9	4389.2	1975.2

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EU801647.1 gg_id:320416 It's all ranking aquatic Chesapeake Bay MD clone 3C002993 EU801
EU057846.1 gg_id:252975 Flavobacterium sp. PR6-3-11 EU057
EU340167.1 gg_id:253323 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY EU340
GQ079944.1 gg_id:429841 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ079
GQ406175.1 gg_id:552287 Benthic submerged sinkhole ecosystems sediment clone CR-36-44 GQ406
AY773135.1 gg_id:109636 swine manure biofilm developed sub-surface f constructed wetland AY773
CU466729.1 gg_id:339084 Evry wastewater treatment plant anoxic basin clone CU466
AY747592.1 gg_id:106211 Flavobacterium columnare AY747
GQ019803.1 gg_id:489865 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu207c06 GQ019
AY947917.1 gg_id:141253 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY947
GQ093968.1 gg_id:395787 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
EU801889.1 gg_id:329653 It's all ranking aquatic Chesapeake Bay MD clone 3C003266 EU801
DQ239767.1 gg_id:141821 Flavobacterium sp. str. CC-JY-6 DQ239
AY584585.1 gg_id:108336 Flavobacterium sp. HTCC554 AY584
AF321014.2 gg_id:52052 Flavobacterium sp. str. GOBB3-317_2 AF321
DQ372986.1 gg_id:151876 Flavobacterium sp. str. EMB117 DQ372
GU295966.1 gg_id:585224 Flavobacterium sp. str. ARSA-45 GU295
AY947924.1 gg_id:143141 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY947
AF368756.1 gg_id:111856 Flavobacterium sp. str. 3A5 AF368
GQ397015.1 gg_id:559612 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
AJ440988.1 gg_id:83757 Flavobacterium frigoris str. LMG 21471 AJ4409
GQ018496.1 gg_id:491172 Topographical and Temporal Human Skin Microbiome skin back clone nbu139f08c1 GQ018
GQ144413.1 gg_id:382914 Flavobacterium sp. str. HMD1001 GQ144
EU194891.1 gg_id:368794 Flavobacterium sp. str. B46 EU194
DQ677872.1 gg_id:246431 Flavobacterium sp. BF03-Tho3 DQ677
GQ103400.1 gg_id:465739 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
EF632773.1 gg_id:241587 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
EF632767.1 gg_id:240042 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6327
DQ889724.1 gg_id:189074 Flavobacterium terrigena str. DS-20 DQ889
EU937955.1 gg_id:318613 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU937
EU431729.1 gg_id:548887 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU431
EF523606.1 gg_id:233570 Flavobacterium sp. str. OW3-15-5 EF5236
GQ144414.1 gg_id:442300 Flavobacterium sp. str. HMDW1 GQ144
FJ979836.1 gg_id:426108 Flavobacterium sp. str. tsz03 FJ9798
EU662323.1 gg_id:558797 Productivity- Chemolithoautotrophically Based Sulfidic Karst Systems microbial mat EU662
AB542075.1 gg_id:570482 Formosa sp. str. MA3 AB542
U62915.1 gg_id:17502 Gelidibacter algens str. ACAM 550 A374 U62915
AY694009.1 gg_id:103250 Gelidibacter salicanalis str. IC162 AY694
AJ344133.1 gg_id:25577 Gelidibacter mesophilus str. 2SM29T CECT 5103T AJ3441
AY218549.1 gg_id:81654 penguin droppings sediments clone KD1-108 AY218
AF001369.2 gg_id:39592 Gelidibacter gilvus str. IC158 AF0013

120.9	6160.0	4248.3	3713.5	4015.2	6015.1	3835.9	6426.0	5230.0	7415.9	4938.4
36.2	3378.2	3442.3	2903.1	3584.4	3729.4	3458.3	4539.4	11914.8	7133.2	2408.1
46.9	10650.9	9179.2	6131.6	7544.6	8035.5	6525.4	8128.4	14607.7	10548.3	5433.1
186.8	11943.0	11813.9	9310.7	11242.1	10954.5	10621.6	10419.4	21329.8	15282.5	9446.6
56.6	7350.9	6475.6	4928.5	6210.9	5403.8	5637.6	6935.1	10164.4	8521.8	4574.8
85.8	3543.9	2111.4	1261.8	1929.1	4587.7	1747.1	2615.7	3420.3	2646.6	1976.3
97.5	10669.1	10785.6	8009.4	10094.8	10346.9	7658.6	9777.1	23586.9	11790.8	8001.3
34.4	3726.7	3048.8	2078.6	2370.8	2704.1	2181.5	4040.5	5494.9	5537.3	2476.0
69.2	2954.4	2947.9	2721.6	4159.3	4212.6	3196.8	3373.3	2863.0	3312.4	2486.3
174.5	8962.2	8896.0	6799.0	9238.2	7888.4	8824.0	7387.4	9642.3	10666.5	5112.6
29.4	8699.0	6917.8	5620.7	6917.1	7695.2	6631.0	8420.1	16966.6	8868.1	5450.2
61.3	7693.0	5684.5	4983.1	7213.6	7319.5	6984.5	6874.0	15677.3	7110.4	5796.2
42.7	3614.8	4484.2	1133.6	2513.7	4242.2	646.8	2085.7	5256.1	3335.8	1813.6
54.5	5917.9	6189.3	4757.4	6783.2	5630.7	6422.3	5835.2	13345.2	6896.4	4109.0
110.4	3280.0	3324.0	2567.0	2257.3	3412.1	2182.3	2743.1	5278.3	4036.0	3181.3
92.4	9294.1	7005.5	5584.8	9663.3	8629.5	6185.9	7766.8	16094.5	9043.1	6039.2
63.1	13125.1	7126.7	6732.5	10067.9	11566.9	5153.8	12085.6	24516.2	8644.2	11369.6
51.2	14139.8	11225.7	8152.9	10659.7	11358.9	7612.6	11751.8	24716.5	13892.7	9862.4
50.6	4820.7	3863.8	2326.3	3581.4	3292.0	2196.2	4876.6	3016.8	6636.8	3333.1
150.6	5108.6	4375.7	3349.9	4485.0	5749.2	3353.2	5830.0	7101.7	5017.1	3751.7
178.2	4018.3	4496.2	2480.1	3311.8	3478.1	3643.1	5056.9	4607.0	7094.7	3399.7
76.7	12097.0	10787.2	8905.6	11476.9	11557.6	9676.9	11405.6	22427.9	13678.8	9506.9
81.8	7434.9	7525.0	5056.3	8137.1	7055.9	7303.0	7728.1	15929.1	9223.4	5211.9
434.1	10785.6	8895.0	6559.5	9384.5	9672.1	7117.6	10032.2	14964.6	10721.3	8900.2
33.0	7523.5	6673.2	4885.4	6095.7	6758.2	5188.1	6933.8	13384.9	7701.9	4747.5
4489.0	6187.4	5694.7	4369.6	4682.7	5785.6	4386.9	5613.1	8671.4	6651.4	7133.8
51.0	9053.9	5858.5	3067.1	6149.2	9441.7	3663.7	6926.5	19657.9	7448.4	6440.1
609.5	11717.0	9976.3	7530.1	7806.9	9219.8	6770.8	9219.2	15831.0	12705.3	8904.3
37.7	6975.1	3879.8	3514.6	2295.2	6168.4	1557.7	7262.2	6447.8	5415.7	5898.9
34.6	7648.7	7723.6	7327.2	6496.0	7285.3	5167.2	8005.0	13446.3	7789.2	6107.1
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43.1	3270.4	4655.8	3412.6	3634.9	4062.2	3280.8	5121.4	6711.7	9196.5	2680.0
75.1	5862.3	3980.5	2517.7	4256.2	7614.6	2814.1	5763.7	7529.5	7566.4	5610.7
1670.4	4609.2	6887.5	5744.8	6879.9	5747.1	6530.2	6354.6	9677.7	6993.3	4193.5
74.0	6576.5	6458.7	4629.0	6630.8	7460.3	5340.1	6225.8	11661.0	7655.1	4328.6
324.7	1150.4	1606.0	1776.5	2329.9	1784.9	2434.6	1487.2	1173.6	1867.9	1384.4
90.4	2076.9	2211.5	1986.3	3911.8	2894.9	2760.5	2427.1	1933.2	2639.7	3307.2
53.3	6139.0	4945.2	3699.7	5941.8	6023.2	4182.1	5297.6	10348.3	8183.6	5071.9
67.6	3419.9	2252.5	1914.6	3046.8	4494.7	3694.7	2871.2	2735.7	3477.3	2070.3
33.0	4077.5	4952.2	3375.7	4334.6	3880.4	5189.6	4391.9	6606.2	6244.8	3688.8
44.8	267.9	617.1	680.5	746.3	338.4	1893.1	553.5	158.1	44.8	208.1

6241.5	7246.4	2656.1
3607.7	4696.7	1872.2
7705.0	7752.3	4776.6
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5661.3	7891.5	3246.8
2213.5	1606.4	1305.4
9651.2	8918.0	3964.9
2329.7	3587.0	1598.2
3571.5	2428.4	3022.5
8044.6	8504.2	5805.9
7347.2	8355.6	4059.4
6059.1	5381.3	3069.4
2504.5	1193.9	264.8
5929.7	6038.5	2761.7
2799.3	3937.3	2191.1
8048.5	5924.3	3811.9
6933.8	5043.3	4367.5
10305.8	8611.8	4370.1
3462.4	2408.4	841.4
3648.2	4110.1	2931.1
3739.6	6130.2	2014.2
11071.2	9960.4	5442.5
6339.4	7818.6	3374.6
9193.4	8549.4	5754.1
6670.2	6826.9	2954.1
4157.1	5144.5	3780.0
4760.9	3379.2	1229.5
8538.3	7573.0	4455.7
3313.0	2574.6	752.6
6152.7	7552.3	3660.7
11050.2	10644.6	6119.7
4200.5	4895.2	2750.1
3874.9	2699.3	1532.2
5884.2	8673.3	4164.0
6997.6	6832.1	2720.1
1625.1	1544.5	1376.4
3154.3	2817.3	3055.9
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3564.9	3953.7	2018.9
467.3	431.4	1365.9

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g__Gelidibacter
g__Gillisia
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g__Leeuwenhoekiella
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g__Lutimonas
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s__Leeuwenhoekiella marinoflava	66056
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AJ786810.1 gg_id:108084 nitrifying inoculum isolate R-22858 AJ7868
DQ202393.1 gg_id:140497 Gillisia sp. str. UST050418-085 DQ202
AY913287.1 gg_id:114195 forest soil clone DUNssu064 (-2C) (OTU#204) AY9132
AY694007.1 gg_id:102953 Gillisia sandarakina str. IC148 AY6940
DQ365988.1 gg_id:154376 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone 2C DQ365
EU735632.1 gg_id:315560 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU7356
NC_008571.1 gg_id:188892 Gramella forsetii str. KT0803 NC_008
NR_025824.1 gg_id:550580 Gramella echinicola str. KMM 6050 NR_025
AB279985.1 gg_id:223116 Gramella marina str. YM1 AB2799
AB035150.2 gg_id:45877 Haloanella gallinarum str. PS3 AB0351
AY294611.1 gg_id:90366 Kaistella koreensis str. Ko2 AY2946
GQ060011.1 gg_id:452349 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ060
AF385544.1 gg_id:72435 crevicular epithelial cells clone AY017 AF3855
EU104108.1 gg_id:345646 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
AY195836.1 gg_id:79767 Kordia algicida str. OT-1 AY1958
AB198086.1 gg_id:140181 Krokinobacter genikus str. Cos-13 AB1980
DQ328321.1 gg_id:155182 Dokdonia donghaensis 2.3 DQ328
AB198087.1 gg_id:140334 Krokinobacter genikus str. CKS-39 AB1980
AY694001.1 gg_id:102038 Lacinutrix copepodicola str. DJ3 AY6940
AY771723.1 gg_id:141174 Psychroserpens burtonensis S3-13 AY7717
AB261015.1 gg_id:166261 Lacinutrix copepodicola str. KMM 3967 AB2610
EU823298.1 gg_id:316012 Leeuwenhoekiella marinoflava str. P37 EU8232
EU823302.1 gg_id:322414 Leeuwenhoekiella marinoflava str. P7 EU8233
DQ294290.1 gg_id:143860 Leeuwenhoekiella blandensis str. MED217 DQ294
AJ780980.1 gg_id:102544 Leeuwenhoekiella aequorea str. LMG 22555 = KMM 6066 AJ7809
AY259509.1 gg_id:94012 Cytophaga sp. 'BSD 22' str. BSD S1 22 AY2595
EU239499.1 gg_id:250747 Aestuariicola saemankumensis str. SMK-142 EU2394
AM712898.1 gg_id:252605 Maribacter forsetii subsp. roscoffensis str. KT02ds18-4=CIP 10950 AM712
EU050897.1 gg_id:238825 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_12 EU0508
AY271624.1 gg_id:85665 Maribacter orientalis str. KMM 3947 AY2716
AY271626.1 gg_id:83608 Maribacter ulvicola str. KMM 3951 AY2716
EU287358.1 gg_id:238195 Pacific arctic surface sediment clone S26-58 EU2873
AY271623.1 gg_id:86570 Maribacter sedimenticola str. KMM 3903 AY2716
AF539757.1 gg_id:83542 Cellulophaga sp. str. E6 AF5397
AY258125.1 gg_id:136335 Zobellia sp. str. DG975 AY2581
AF235126.1 gg_id:46683 Cytophaga sp. str. KT02ds18 AF2351
EF536746.1 gg_id:278614 Maribacter sp. str. KMM 6025 EF5367
NR_025263.1 gg_id:543612 Mesonia algae str. KMM 3909 NR_025
DQ367409.1 gg_id:154938 Mesonia motionis str. KMM 6059 DQ367
EU369132.1 gg_id:333131 libraries oyster shell clone MBIOS-16 EU3691
EU328104.1 gg_id:279296 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU3281

55.4	2555.0	3245.4	3195.8	2919.1	2380.1	4751.0	3350.8	2802.8	1384.0	2588.0
58.5	65.2	74.5	65.2	72.6	73.0	53.3	103.8	43.7	26.3	47.5
98.2	3422.2	2857.6	2714.2	3232.4	3110.6	2645.5	3405.0	4407.9	3891.0	3116.1
54.5	67.4	49.6	47.9	98.1	41.8	156.5	43.3	33.0	23.1	51.6
29.8	1489.5	1722.2	1260.3	1037.9	1717.0	1195.6	1839.9	2395.7	1971.0	1680.7
62.7	707.8	771.0	768.0	808.0	756.6	797.4	800.5	1061.8	831.4	884.6
175.3	911.2	1242.8	1210.7	1028.5	1039.6	839.6	950.4	615.4	818.2	801.8
2949.8	7426.8	8144.6	4621.1	6972.1	7208.2	6776.0	6219.5	11766.7	8296.8	8208.0
307.3	1618.8	2821.4	2062.8	2148.9	1991.6	1659.6	1680.9	1482.7	2473.6	1293.2
83.5	7336.6	5548.5	3319.6	4274.2	5492.5	3444.3	5525.3	8716.6	10505.6	3409.9
100.5	2657.7	2420.8	2076.4	2475.8	2722.3	2324.0	2678.7	3338.6	5463.6	1388.2
55.6	2827.9	3936.9	4003.9	2255.9	2088.2	1887.7	3283.5	1380.2	423.9	3217.1
3773.8	7683.3	5302.9	4010.8	2680.1	4558.0	3515.1	3375.3	3915.0	11880.0	3115.3
81.2	5974.0	3846.5	3244.6	3232.0	4752.3	3142.1	4933.9	6040.8	10890.9	3733.8
1998.9	3503.9	4128.2	2691.6	3020.3	3917.8	3242.4	3678.9	3675.4	4164.3	3527.9
606.2	3535.5	1785.3	1552.9	2099.9	1736.2	1903.7	4699.5	2232.6	5060.4	3244.8
53.8	2149.8	1087.7	824.0	1178.7	1136.6	718.7	2441.1	1043.2	3142.6	2253.4
339.6	1449.4	1597.2	1389.7	1808.0	1412.1	1446.0	1893.9	1225.5	1271.5	1167.2
102.3	1923.3	2539.9	2231.1	2525.0	3100.7	2627.5	3038.4	4460.0	1872.2	2734.4
95.2	838.3	1742.3	440.5	762.3	1039.4	894.5	1456.6	157.6	1263.0	443.9
56.3	805.4	1378.3	695.9	1133.8	946.9	857.6	1000.8	690.0	926.1	400.3
15353.7	8494.3	9655.9	9347.6	9836.4	8854.6	9670.0	8876.0	18724.7	12689.4	10985.6
46.3	3950.5	4329.4	3953.1	3505.6	4254.6	3747.5	4153.7	4943.1	5489.7	3834.9
48.3	2271.2	1997.5	1505.1	3204.9	2990.3	1895.5	1867.5	1881.0	2509.2	1568.5
1207.2	4373.2	3995.6	4050.4	3844.6	5023.5	3404.9	5148.5	4487.9	4705.5	3609.0
66.7	2040.9	2023.3	2189.4	1739.1	2816.6	1672.8	2451.1	1257.2	2561.1	3140.6
65.0	3863.4	4089.0	3671.2	2707.4	3347.0	2509.2	3925.6	6933.3	2538.6	3976.1
702.9	3228.2	3605.8	3640.9	3765.0	3190.4	3692.8	3449.0	3616.5	3348.3	3134.0
3254.7	3334.1	4040.3	4742.3	3316.1	3147.9	3116.7	4178.6	4414.9	4284.0	4444.8
81.8	425.8	485.3	566.3	695.5	352.6	551.6	491.3	400.1	126.5	143.8
64.6	1428.0	1232.7	1021.4	1306.7	1288.9	1396.1	1300.8	1465.4	937.5	867.2
309.0	3140.4	3563.7	3726.8	3967.9	3246.0	4020.0	3853.2	4219.6	4557.2	3888.5
192.9	1360.7	1858.3	2410.2	1900.0	1507.2	2832.2	2019.6	739.6	315.7	1059.2
175.1	1757.6	1884.1	2216.0	1957.1	1747.2	2333.5	1982.5	1646.3	1309.6	1780.3
188.7	732.7	1222.3	978.6	1411.4	799.8	1302.0	970.7	572.3	514.6	594.3
680.9	4364.1	4731.7	4984.0	5362.9	4362.1	5941.1	4688.7	4604.0	3910.2	4139.7
567.2	2873.3	3386.0	3080.6	4088.6	3034.4	4548.6	3347.0	3120.0	2871.0	2708.3
52.1	2508.9	2360.7	2207.4	2329.3	2968.9	1961.1	2898.3	3948.9	2859.9	2137.8
44.9	326.5	744.1	607.7	363.6	460.4	607.1	625.1	286.7	380.3	363.9
46.4	1943.5	1408.6	1327.8	1473.0	1149.7	1837.1	1941.5	394.4	3189.0	1399.9
92.6	1241.7	1642.0	1542.9	1876.6	1250.5	1794.7	1122.8	1193.6	692.4	795.3

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1478.2	1845.7	777.3
772.5	561.3	1123.3
1024.4	1468.5	483.0
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2365.4	2123.6	1304.3
4812.0	4379.8	2452.0
2787.5	3266.8	2182.8
2319.7	2203.9	2004.5
5109.7	4583.2	3017.4
5837.8	3747.5	2565.8
3456.6	3207.3	2137.0
3146.0	1820.0	1137.2
2141.5	980.9	517.7
1671.1	1529.2	1225.7
2844.1	2417.4	2273.9
1278.3	492.2	434.4
1483.1	1124.9	445.9
9482.4	10080.3	7558.2
4841.5	4045.1	2656.5
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5143.1	3878.8	3974.7
2030.1	1819.6	838.6
2577.5	2285.4	1114.5
3101.2	3543.3	2543.3
4017.9	4587.8	2728.1
804.9	572.0	318.0
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3566.9	3970.0	2344.6
3274.2	1348.1	5382.2
1964.7	1489.0	1266.2
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AB073562.2 gg_id:70926 Cytophaga sp. str. MBIC04684 AB0735
AY576776.1 gg_id:139292 Muricauda sp. str. 3IX/A02/243 AY5767
AY445076.1 gg_id:100173 Muricauda aquimarina str. SW-72 AY4450
AB073566.2 gg_id:101291 Cytophaga sp. I-2029 AB0735
AM990884.1 gg_id:277744 Muricauda sp. MOLA 110 AM990
GQ348772.1 gg_id:582005 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ517032.1 gg_id:561872 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
AY445073.1 gg_id:99698 Muricauda flavescens str. SW-62 AY4450
EU311217.1 gg_id:255094 Myroides odoratimimus str. DB-3 EU3112
GU253339.1 gg_id:579933 Myroides sp. str. MY15 GU253
DQ346455.1 gg_id:154979 during composting libraries compost clone 1B23 DQ346
AY773141.1 gg_id:200923 microbial treated subsurface wetlands swine manure biofilm sub-surface f wetland AY7731
EU000228.1 gg_id:338486 Olleya marilimosa str. KOPRI_22310 EU0002
EF660466.1 gg_id:239512 Olleya marilimosa str. CAM030 EF6604
AY167317.1 gg_id:81957 Polaribacter irgensii str. ANT9210 AY1673
FJ425213.1 gg_id:366819 Polaribacter sp. str. K17-16 FJ4252
U73726.1 gg_id:2357 Polaribacter filamentus str. 215 U73726
GQ349584.1 gg_id:576701 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU626664.1 gg_id:278366 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
FN433361.1 gg_id:541258 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN4333
AF359539.1 gg_id:70110 Alexandrium tamarense PCC 173a AF3595
AM259822.1 gg_id:205919 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-94 AM259
GQ259215.1 gg_id:563333 Microbial activities coastal marine sediments and column Svalbard deep water clone GQ259
U85884.1 gg_id:2356 Polaribacter sp. str. IC066 U85884
AY922239.1 gg_id:113813 whalefall clone 131792 AY9222
AF468414.1 gg_id:79935 Arctic sea ice ARK10121 AF4684
GQ350084.1 gg_id:536354 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
GU061158.1 gg_id:575162 Evaluation culturing methods cultivate previously Yel Sea intertidal beach clone SF1 GU061
DQ356492.1 gg_id:148858 Polaribacter sp. str. AC3 DQ356
U85885.1 gg_id:2355 Polaribacter sp. str. IC063 U85885
FJ425215.1 gg_id:358831 Polaribacter sp. str. K17-17 FJ4252
FJ169204.1 gg_id:329178 microbial and polyketide biosynthetic potential palmerolide-producing tunicate Synoi FJ1692
U14586.1 gg_id:2352 Polaribacter franzmannii str. 301 U14586
AB234297.1 gg_id:141245 Pseudoscourfieldia sp. str. Nak AB2342
AY771712.1 gg_id:108685 Polaribacter irgensii str. S2-53 AY7717
EU703307.1 gg_id:457830 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH107 EU7033
DQ677858.1 gg_id:241336 Blood Falls Subglacial Outf Taylor Glacier Antarctica subglacial outf clone BF99_C105 DQ677
EU874390.1 gg_id:326705 Psychroflexus sp. str. ISL-14 EU8743
U62911.1 gg_id:2445 Psychroserpens burtonensis str. ACAM167 U62911
EU581702.1 gg_id:277351 Psychroserpens sp. MEBiC05023 EU5817

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38.0	24.3	18.4	24.9	18.6	18.4	22.9	20.2	28.7	21.5	30.3
133.8	767.4	1108.9	905.6	1129.3	828.2	1831.4	954.7	691.2	300.5	440.7
80.7	1991.8	2120.5	2043.8	2847.3	2310.6	2684.0	1980.7	2522.3	1746.8	1574.3
195.9	1717.5	3165.4	2922.8	2407.1	2366.4	2815.1	2551.7	1777.7	1411.2	1370.6
133.2	1164.3	2772.8	2348.0	2298.9	2100.8	3183.9	2235.2	1774.1	1251.2	1237.0
150.5	3134.3	4030.2	3299.2	3957.6	3691.9	3781.7	4335.9	3059.4	4517.0	3121.4
383.8	3138.9	4004.6	4519.2	4185.0	3437.8	5445.6	4049.0	2111.6	1275.9	2999.7
523.7	3441.9	3864.7	4462.7	4234.4	3920.2	4506.7	4168.1	3424.2	2611.6	3563.3
32.2	589.1	766.6	695.7	213.0	1330.3	80.5	380.9	112.1	153.9	150.4
480.8	6277.7	4657.2	4263.4	5201.9	6573.0	4178.4	5656.5	7463.5	6661.0	5148.4
40.9	134.9	251.6	227.2	83.9	109.7	230.9	132.4	73.0	130.3	56.4
299.2	4075.0	4524.2	1356.9	3163.3	3553.3	2700.7	4728.3	2766.7	5242.2	3180.5
94.8	411.6	861.3	987.5	658.2	502.3	912.2	1121.1	1387.3	176.3	388.2
53.5	3468.6	3562.6	2478.0	3514.4	2851.4	2483.6	3838.6	6414.7	4161.7	2757.5
53.7	647.8	810.1	800.0	484.0	434.3	426.6	661.9	531.5	159.3	473.4
46.5	498.7	703.0	471.6	828.5	526.8	688.3	576.6	290.2	277.2	275.9
235.0	1906.2	1865.6	1980.8	2669.1	2131.8	3316.6	2543.5	2322.0	1870.8	1291.2
2272.6	2675.5	3698.9	3955.7	3643.5	3322.6	3807.2	3494.1	3753.7	3051.1	3794.1
173.5	5705.5	4063.9	3038.3	4457.2	4864.6	3130.0	4257.4	6834.2	4435.7	4138.6
1135.4	2260.6	2626.0	2221.2	2384.4	2738.8	2307.9	2474.3	4074.9	2491.9	2467.1
68.2	1813.3	2470.4	1625.5	1519.0	2110.5	905.3	1639.6	1596.5	3627.8	1411.8
5551.0	1806.5	1267.9	1168.4	756.8	2379.5	850.0	2191.4	1009.2	1319.7	898.2
83.1	609.9	539.6	552.4	511.7	785.6	361.5	993.2	720.4	486.0	531.6
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2814.8	2523.3	2284.1	2274.1	2001.3	2865.4	1958.3	2711.9	2322.1	2010.6	1707.0
66.2	323.7	495.0	392.5	182.5	684.1	229.2	553.9	159.2	521.8	547.7
1462.0	3344.1	3267.5	3380.3	3680.1	3163.7	4227.6	4326.7	4831.3	3493.2	3044.7
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37.1	51.4	117.3	98.8	59.4	59.2	96.9	201.8	49.0	235.6	59.2
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2234.5	1852.5	2401.5	2244.2	1747.6	1989.6	2588.8	2159.5	2169.5	2165.6	2034.1
56.4	1004.5	1793.4	815.4	452.1	1664.7	533.0	1195.6	417.9	755.0	1354.9
40.6	2019.8	3242.7	2292.6	2232.2	2186.7	1737.5	2875.2	2416.0	2349.4	1961.7
42.5	34.9	49.4	40.7	42.3	40.4	50.5	50.3	36.2	24.1	37.5
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2009.1	2310.0	1830.5
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2738.0	2743.9	4858.8
3980.8	4042.1	4880.9
5663.9	3653.9	7867.0
4900.1	4083.3	4253.7
839.2	275.5	202.7
6940.0	4370.0	3526.4
206.8	431.4	125.4
3609.5	4223.8	2566.6
2819.3	635.2	1297.0
4168.9	2019.6	1259.1
919.0	588.5	1471.8
804.9	667.4	315.1
2549.4	1835.6	994.1
3262.1	3475.3	3032.5
3354.7	3168.1	3211.4
1339.7	2946.1	2249.8
1649.5	1325.1	831.3
1631.4	1781.8	1771.8
635.9	958.9	476.8
1549.0	1203.1	939.8
1837.8	1040.6	1554.7
3419.7	3876.5	2880.0
2451.5	1893.2	2762.8
249.9	674.4	197.2
3266.9	3707.2	3888.8
50.4	270.4	34.9
2493.6	1853.2	1453.2
58.7	244.9	126.1
4474.2	4922.4	3419.8
2126.9	2436.7	2133.8
742.0	1173.8	336.5
4235.9	2084.0	1510.7
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g__Psychroserpens
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g__Salinimicrobium
g__Sandarakinotalea
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s__unclassified	66485
s__unclassified	66719
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s__Riemerella anatipestifer	63325
s__Riemerella anatipestifer	63504
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s__Riemerella anatipestifer	64683
s__Riemerella anatipestifer	64847
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s__Riemerella anatipestifer	65103
s__Riemerella anatipestifer	65743
s__Riemerella columbina	65786
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s__unclassified	65897
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s__unclassified	66646
s__Sediminicola luteus	66707
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s__unclassified	66484
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s__unclassified	66712

FJ425226.1 gg_id:363441 Winogradskyella sp. str. K7-7 FJ4252
L10948.1 gg_id:2450 marine snow clone AGG13 L10948
AY167341.1 gg_id:81033 Psychroserpens sp. str. ARK10236 AY1673
AM040097.1 gg_id:145548 sandy sediments clone Sylt 1 AM040
EU715009.1 gg_id:313767 Riemerella anatipestifer str. RAf51 EU715
DQ995227.1 gg_id:182298 Riemerella anatipestifer str. RAf34 Minghou/FuZhou DQ995
AY920410.1 gg_id:114330 Riemerella anatipestifer str. RA-T2-122 AY9204
DQ995234.1 gg_id:191124 Riemerella anatipestifer str. RAf28 FuZhou DQ995
EU715007.1 gg_id:332013 Riemerella anatipestifer str. RAf43 EU715
EU715006.1 gg_id:322887 Riemerella anatipestifer str. RAf25 EU715
DQ995231.1 gg_id:184500 Riemerella anatipestifer str. RAf115 Weifang/Shandong DQ995
EU016549.1 gg_id:244701 Riemerella anatipestifer str. RAf46 Fuzhou EU016
DQ078779.1 gg_id:128148 Riemerella anatipestifer str. GDGZ-001 DQ078
DQ995226.1 gg_id:193890 Riemerella anatipestifer str. RAf17 Putian/Fujian DQ995
EU715002.1 gg_id:327523 Riemerella anatipestifer str. RAf10 EU715
AY871827.2 gg_id:112028 Riemerella anatipestifer str. D-28020 AY8718
EF641572.1 gg_id:240665 Riemerella anatipestifer str. RAf75 Fuzhou EF6415
AY871817.2 gg_id:112052 Riemerella anatipestifer str. D-26338 AY8718
U60101.2 gg_id:2261 Riemerella anatipestifer str. ATCC 11845T U6010
DQ995232.1 gg_id:187418 Riemerella anatipestifer str. RAf116 Minghou/FuZhou DQ995
AF181448.1 gg_id:2269 Riemerella columbina str. LMG11607 T AF1814
AF118416.1 gg_id:22221 Riemerella anatipestifer str. 4005 AF1184
EF641573.1 gg_id:243606 Riemerella anatipestifer str. RAf60 Fuzhou EF6415
EF641578.1 gg_id:242618 Riemerella anatipestifer str. RAf63 Fujian EF6415
DQ995233.1 gg_id:189735 Riemerella anatipestifer str. RAf2 Beijin DQ995
AY424899.1 gg_id:98563 Robiginitalea biformata str. HTCC2501 AY4248
DQ330448.1 gg_id:159349 Guerrero Negro hypersaline microbial mat clone 04D2Z14 DQ330
FJ872534.1 gg_id:544563 Robiginitalea sp. str. ZH09 FJ8725
FJ517119.1 gg_id:549936 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5171
DQ334626.1 gg_id:187417 Impact metals on sediments heavy metal polluted marine sediment clone HB2-21-1 DQ334
EF612764.1 gg_id:239789 Salegentibacter locisalis str. ISL-4 EF6127
AY682200.1 gg_id:107403 Salegentibacter flavus str. Fg69 AY6822
EF520007.1 gg_id:221915 Salegentibacter sp. str. BH206 EF5200
EU328085.1 gg_id:278201 dynamics during bioremediation crude oil contaminated moderate saline soil clone Y EU3280
FJ425217.1 gg_id:366927 Salinimicrobium sp. str. J14-12 FJ4252
AB206954.1 gg_id:161186 Sandarakinobacter sediminis str. CKA-5 AB2069
DQ514308.1 gg_id:160771 Flavobacterium sp. str. BSs20192 DQ514
EU802116.1 gg_id:323610 It's all ranking aquatic Chesapeake Bay MD clone 3C003523 EU8021
DQ015793.1 gg_id:139885 Antarctic lake water clone ELB16-036 DQ015
FJ203271.1 gg_id:338398 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
AY697923.1 gg_id:107130 Antarctica clone F4C78 AY6979

1724.3	7182.9	4980.9	4613.8	4412.8	5029.6	3836.1	6935.0	9660.8	5168.3	5301.9
96.6	2081.1	2757.3	2742.5	1699.9	2537.1	1784.0	3192.7	3035.5	2389.1	2732.5
1580.4	1756.3	1896.9	1976.5	1939.3	2266.1	2055.3	2072.9	2839.2	3078.1	2043.0
69.7	1340.2	1298.7	741.5	1012.3	952.3	691.6	1266.1	2826.1	1259.1	823.0
6660.8	12248.4	8744.8	8142.0	8040.0	9120.3	8132.8	9699.9	13169.4	14327.5	9774.4
1359.5	10441.5	7605.7	7031.3	6722.3	9064.9	6743.3	8649.1	11986.2	12027.3	8244.0
3105.1	10153.3	8053.6	7356.6	7257.4	7568.3	7433.1	8294.1	10380.5	11580.1	8240.7
7088.4	12316.6	8343.1	7478.3	8229.6	9422.8	8407.9	9352.4	13539.3	15211.9	9440.4
9576.8	11523.0	7781.3	8307.7	8553.5	9703.4	8520.9	9143.5	13572.2	12526.7	10528.5
7090.9	11777.5	8952.7	8593.0	8401.2	9480.1	8477.7	9750.8	13181.9	13510.8	10425.8
2586.6	9771.8	6401.3	7008.7	7029.9	6579.0	6635.9	7820.5	9114.9	10738.9	6240.9
7086.2	11455.6	8076.8	7966.6	7297.4	7938.8	7726.2	8951.4	10932.5	12725.7	9137.6
3802.1	6787.8	5077.9	5145.4	5104.0	5535.3	5866.8	5212.8	7274.9	8140.5	4822.2
6956.1	12177.5	8608.9	7931.6	8050.8	9134.5	7898.1	9577.1	12964.3	13458.7	9721.0
2896.3	8028.9	4518.5	4677.0	4645.1	5724.0	4409.0	6287.9	6868.9	7532.7	5156.5
1982.3	4269.3	4415.8	4773.8	4804.6	4712.6	5236.1	4375.0	3424.5	8475.4	3806.1
1382.4	10950.3	7779.4	7358.1	6927.0	9280.6	6924.4	9026.0	12158.9	13265.1	7969.0
3523.6	7018.5	4771.1	4460.3	4519.9	5291.2	3862.8	5871.2	6089.1	5011.7	6292.3
6211.0	11422.9	9080.7	8651.6	8493.8	9128.3	8777.7	9355.4	12410.9	13106.5	10028.9
3560.5	7356.2	3784.5	3187.0	3249.4	4479.0	3138.2	5335.0	5966.0	8508.7	4216.3
1362.0	11841.8	8194.1	7357.6	7036.9	9454.9	7148.5	9248.6	12847.3	13875.8	8521.3
1823.5	5338.6	3564.8	3336.3	4136.3	4785.7	3784.7	4399.7	5700.1	4961.0	3545.2
1861.3	5624.9	3947.7	3623.7	2854.0	6262.1	2936.1	4874.1	5730.8	11657.9	3248.2
3396.7	5568.6	5866.3	6078.6	5026.9	5930.0	5513.0	5688.5	5529.5	9304.0	5309.0
1872.8	8350.7	7178.7	7644.5	6291.7	7931.5	7409.4	7389.2	10564.5	10839.0	8478.8
926.3	2378.8	2651.0	2494.9	3272.7	2732.2	2958.6	3666.7	2472.9	4590.1	3268.4
50.4	4995.8	3639.1	3323.1	4770.3	3843.0	3790.3	5806.3	2876.1	1785.9	4908.7
66.5	342.2	521.1	554.2	267.7	289.7	302.8	332.6	131.1	250.5	206.4
49.1	1579.0	2309.3	2413.6	1352.2	1141.4	1780.1	1304.8	741.3	1072.6	1177.0
59.4	72.2	75.3	50.8	93.3	136.9	82.8	57.0	94.5	32.3	36.7
38.9	405.6	783.6	876.9	1008.9	555.6	1293.3	739.1	147.0	482.3	364.5
41.8	130.9	110.8	107.5	164.0	126.1	104.6	208.0	220.9	93.3	95.2
111.6	2321.4	2422.4	1862.9	1953.4	2405.3	1356.2	2604.1	1736.8	927.0	1395.8
154.9	587.8	1083.7	1087.5	1322.8	1295.7	680.1	1595.6	1012.2	1063.6	636.4
119.2	3172.2	3028.8	2689.0	2799.6	3116.1	3028.7	3339.6	4994.7	3953.6	2359.4
36.5	30.9	31.4	36.2	37.1	31.2	31.9	48.1	19.5	20.6	35.5
40.6	558.8	404.9	232.5	596.1	852.9	240.2	554.6	525.1	616.0	277.8
53.2	86.6	113.4	98.4	96.6	192.6	98.4	127.9	69.0	874.2	74.0
155.5	1773.6	2403.0	2572.8	2136.5	1839.8	2614.0	2276.4	1976.4	1411.0	1863.4
35.9	3787.0	3702.7	2658.5	3442.4	3100.6	2655.4	3697.3	1990.2	3776.5	3049.7
338.4	963.5	1226.5	1271.2	632.8	1280.2	1680.2	1335.1	642.9	1743.0	1580.6

5114.7	3947.0	2965.3
2128.0	1734.3	702.7
1997.5	2121.1	1908.6
1106.1	1092.7	605.8
8621.6	6961.0	6130.9
7125.1	6399.3	4974.0
7274.6	6080.0	5720.1
8704.6	7319.2	6380.7
9383.1	7940.0	7421.0
8730.6	7591.6	6609.6
7433.0	4989.3	5408.2
7778.5	6467.1	6430.0
4366.7	4116.7	3605.1
8452.1	6795.8	5837.0
5613.0	5238.2	4016.4
5405.2	5122.3	5875.3
7415.7	6717.8	6204.6
5013.2	4486.3	3206.4
8412.2	7411.6	6945.5
4437.0	4451.4	2481.8
7707.1	6590.6	5386.5
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6592.1	3909.4	2432.4
6622.8	7099.5	4681.3
8437.6	7445.3	7052.2
1304.2	1921.8	1610.6
3034.1	2975.1	2227.7
282.1	478.7	1763.9
1953.4	1569.4	4179.3
42.1	129.6	79.1
1429.4	817.8	1161.6
97.0	112.1	84.3
2362.2	2186.0	881.6
2170.6	1516.5	869.6
3497.4	3245.1	1797.4
52.1	70.6	23.0
536.7	403.2	164.7
330.1	241.7	67.8
3114.0	2493.2	2947.3
3455.1	3230.7	2718.0
1638.7	1716.9	769.1

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g__Sediminicola
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g__Sejongia
g__Sejongia
g__Sejongia
g__Sufflavibacter
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g__Ulvibacter
g__Ulvibacter
g__Ulvibacter
g__Ulvibacter

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s__Sufflavibacter maritimus	66479
s__Flexibacter echinicida	65967
s__Tenacibaculum aestuarii	66090
s__Tenacibaculum aestuarii	66734
s__Tenacibaculum lutimaris	66383
s__Tenacibaculum maritimum	66015
s__Tenacibaculum mesophilum	66618
s__Tenacibaculum ovolyticum	65941
s__Tenacibaculum soleae	65918
s__unclassified	65833
s__unclassified	65949
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s__unclassified	66614

EU799607.1 gg_id:329442 It's all ranking aquatic Newport Harbour RI clone 1C227226	EU799
EF108215.1 gg_id:190052 Aureimarina marisflavi str. IMCC3054	EF1082
GU345046.1 gg_id:550689 Chryseobacterium sp. str. Sa 1143-06	GU345
FN297836.1 gg_id:558661 Chryseobacterium sp. str. IMMIB L-1519	FN2978
DQ856545.1 gg_id:250944 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3D	DQ856
AJ244696.1 gg_id:70361 Flavobacterium sp. str. V4.ME.09 = MM_2295	AJ2446
AY006468.1 gg_id:45622 Flexibacter echinicida str. F8	AY0064
DQ868688.1 gg_id:165798 Tenacibaculum sp. str. SMB27	DQ868
EU419920.1 gg_id:277347 Tenacibaculum aestuarii str. RW33	EU4199
AY661693.1 gg_id:106077 Tenacibaculum marilutum str. TF-42	AY6616
AB078057.1 gg_id:58630 Tenacibaculum maritimum str. IFO 15946	AB0780
AB032504.1 gg_id:22718 Tenacibaculum mesophilum str. MBIC4357	AB0325
AB078058.1 gg_id:58631 Tenacibaculum ovolyticum str. IFO 15947	AB0780
AM746476.1 gg_id:233273 Tenacibaculum soleae str. LL04 12.1.7	AM746
AM259865.1 gg_id:207908 Spatial sponge- Mediterranean Tethya aurantium sponge cortex clone TAA-10-96	AM259
AM411030.2 gg_id:254395 Tenacibaculum discolor str. LL0411.1.1	AM411
DQ660385.1 gg_id:169324 Tenacibaculum sp. str. HJ103	DQ660
AB078044.1 gg_id:58642 Flexibacter aurantiacus subsp. copepodarum str. IFO 15978 subsp.	AB0780
GU124763.1 gg_id:541877 Tenacibaculum sp. str. 5136_F112_C_98	GU124
AB275606.1 gg_id:216158 Tenacibaculum japonica str. H2M8	AB2756
AM746477.1 gg_id:230495 Tenacibaculum gallaicum str. A37.1	AM746
AF530136.1 gg_id:61125 Tenacibaculum sp. str. MGP-10	AF5301
AM990757.1 gg_id:279493 Tenacibaculum sp. MOLA 533	AM990
EU428783.1 gg_id:259950 Tenacibaculum sp. str. JO-1	EU4287
EF416572.1 gg_id:204367 Tenacibaculum sp. str. a4	EF4165
AY353819.1 gg_id:92882 Flavobacteriaceae G121102s2_2	AY3538
NR_024737.1 gg_id:552292 Tenacibaculum amylolyticum str. MBIC4355	NR_024
GU289641.1 gg_id:562638 Tenacibaculum sp. str. MEBiC06102T	GU289
DQ314760.1 gg_id:145826 Tenacibaculum aestuarii str. SMK-4	DQ314
AF530150.1 gg_id:73960 Tenacibaculum sp. str. MGP-74/AN6	AF5301
DQ395657.1 gg_id:152840 deep-sea octacoral clone ctg_CGOF173	DQ395
FJ457296.1 gg_id:542003 Flexibacter sp. str. S4471	FJ4572
AM412314.1 gg_id:258128 Tenacibaculum adriaticum str. B390	AM412
AF469612.1 gg_id:22873 Tenacibaculum skagerrakense str. D30	AF4696
DQ334344.1 gg_id:150237 Microbial within ornate rock lobster (Panulirus ornatus) water column Panulirus orn	DQ334
AY353820.1 gg_id:92204 Flavobacteriaceae G121102s2_3	AY3538
AF468243.1 gg_id:80559 Arctic pack ice; northern Fram Strait; 80 31.1 N; 01 deg 59.7 min E clone ARKDMS-33	AF4682
AB476295.1 gg_id:542229 Compositional and functional transition epibiotic microbial hydrothermal vent galath	AB4762
DQ660381.1 gg_id:162582 Ulvibacter sp. str. AKS476	DQ660
DQ015799.1 gg_id:140731 Antarctic lake water clone ELB16-117	DQ015
DQ015819.1 gg_id:140527 Antarctic lake water clone ELB19-122	DQ015

34.8	751.3	1143.8	1056.2	923.2	935.4	1378.5	1436.9	603.0	434.6	425.8
40.2	92.8	174.0	191.0	144.8	106.2	334.6	161.9	43.7	42.9	61.1
66.0	9237.1	7385.8	6192.9	4864.4	6285.5	6044.6	7546.7	7019.9	10380.6	6281.0
143.1	12286.2	8468.4	3298.2	3415.2	6362.2	4880.3	5529.4	5985.5	10554.4	3854.2
3700.2	12853.4	8028.2	6548.4	6856.6	7700.6	7170.8	8716.2	10981.6	16338.8	7279.2
38.1	176.4	221.2	164.5	164.5	120.8	148.0	408.6	317.7	101.3	93.4
85.4	3897.4	2639.8	2140.2	3511.7	4084.3	2636.3	3458.6	5038.2	4467.1	2278.9
268.5	4477.3	3575.9	2491.8	2576.5	4405.5	2223.0	3636.2	5312.4	3090.3	3017.7
602.9	2155.3	1058.8	805.4	3447.5	1930.8	990.0	1158.6	2151.3	192.5	509.7
1038.4	3001.8	2742.8	2445.2	2071.0	2924.3	1877.5	2526.2	3790.1	1506.0	3276.1
40.6	320.7	503.6	420.5	347.3	358.5	369.5	558.3	142.6	146.5	221.4
263.0	5163.0	4499.2	4055.4	3923.1	4743.6	3590.7	4372.0	6292.5	3566.8	5061.2
140.2	5535.6	2940.9	2954.2	3468.5	6862.3	2033.3	5261.9	8365.5	4183.3	3927.7
191.5	5238.2	4290.6	4178.5	4040.9	3884.8	4286.2	4326.3	6028.0	4498.2	3435.3
74.8	1252.2	1591.9	1165.2	1712.2	1656.2	1354.4	1403.7	1057.9	1413.7	859.0
32.6	845.9	584.5	325.6	1171.7	844.7	402.5	651.5	824.2	75.1	219.9
157.4	4594.8	4361.4	2918.4	3217.7	4263.4	2631.8	4410.0	6795.6	2499.7	3570.6
61.6	4056.2	3213.4	2814.9	2993.1	3808.6	1589.3	4202.6	4068.7	2739.2	3805.9
233.7	5573.0	3839.7	3162.1	4354.8	6271.0	3652.2	5328.1	8276.0	4022.1	3509.5
76.1	2165.4	2307.6	1838.6	1569.9	2473.6	2203.5	2113.2	1159.5	1930.7	1495.7
46.0	2067.5	1496.0	1379.3	2336.2	2782.5	1798.8	2282.9	1826.9	845.6	1320.3
564.0	8868.1	5999.6	5065.3	5280.2	8510.7	3498.8	8022.1	13714.6	5312.8	6912.5
60.6	1030.2	1363.8	1118.9	1375.1	1385.5	1072.2	1269.6	754.5	1064.5	1002.3
39.0	278.2	405.6	385.1	352.3	306.4	322.0	581.0	160.6	42.0	173.9
1007.3	2051.5	3042.3	2604.8	2509.1	2161.2	2562.5	2298.4	1624.1	1374.9	1955.7
56.9	5034.8	4018.4	2939.3	2926.8	5438.6	1524.5	4736.4	4866.4	4644.6	3716.5
52.9	905.2	1371.3	1672.4	1900.9	1400.3	2159.7	1044.0	330.9	240.9	543.1
87.2	1847.5	1240.6	1037.7	1196.5	1721.8	1145.4	1712.7	2592.5	1520.2	941.5
548.1	6209.1	5272.5	4301.7	5211.1	5795.6	4339.3	5788.8	8845.6	6366.0	4848.7
62.5	2272.7	2559.8	1549.0	1400.4	1516.8	1042.3	2085.7	2913.2	813.4	1902.8
150.4	7667.1	3018.6	2153.9	2684.8	8046.2	1819.1	4429.5	9009.9	3693.1	3742.3
1181.3	3845.9	3260.2	2895.4	3180.6	3990.7	3037.9	4141.2	4822.3	3927.2	2928.5
1334.3	7463.6	6343.5	4917.9	4781.3	6950.6	4416.1	5578.5	10011.6	6427.0	6756.9
58.0	3352.7	3183.3	3181.3	3220.6	3303.2	3669.8	3481.7	3529.7	2540.0	3516.1
27.2	1433.9	279.6	114.2	339.3	491.0	191.4	1608.0	613.9	264.0	700.6
78.6	4388.5	3123.1	3165.8	3109.1	5601.5	1379.7	3715.7	4817.5	3042.5	3414.2
542.4	14742.4	12857.7	11569.5	12843.9	13489.7	12095.2	12599.1	22299.9	16216.2	15705.9
117.8	2838.3	2639.8	2875.1	3313.6	3796.1	2446.8	3043.0	4547.1	2095.8	2406.0
560.6	2667.6	2497.6	2690.6	2230.2	3109.9	1722.9	3695.4	3069.6	5045.1	2878.5
13224.6	2143.5	1867.0	1761.0	2030.9	2306.4	2044.2	2224.3	2617.5	3561.4	1725.8
9093.8	2519.5	2654.3	2696.0	1954.0	2309.6	2404.4	2436.2	1854.0	2816.8	2980.2

1865.7	1687.8	1354.4
76.9	99.1	32.3
6180.5	5438.1	4117.9
3896.0	3525.1	1891.8
8183.6	6371.8	6018.3
283.5	247.9	92.2
3289.7	3526.6	2098.8
3028.4	3130.4	2179.8
926.0	1540.5	1432.7
2079.2	2835.0	2232.5
638.7	622.6	625.8
3879.2	4021.4	3199.5
3788.6	2273.3	1382.2
4738.9	5035.5	4579.4
1659.9	1466.0	1187.1
467.9	647.6	547.2
3271.0	3338.6	2529.9
2827.7	1974.0	1267.3
5397.8	3993.1	5415.6
2900.8	1496.3	1763.5
1849.5	2038.4	1221.0
5134.4	4531.7	3693.1
1368.0	1236.5	991.6
373.1	342.7	304.8
1800.2	2016.0	3003.0
3928.9	1918.5	2468.0
865.3	548.7	1310.9
1549.8	1893.1	790.1
5568.2	5779.3	3738.6
920.6	969.3	662.9
3487.8	1902.7	948.8
3288.8	4268.2	2616.7
4971.4	5431.6	3863.6
2985.9	2520.1	2613.2
124.8	153.7	59.4
2867.3	1743.2	2369.3
12623.6	11380.7	8345.2
1922.7	2808.7	1709.3
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2210.2	2804.6	2394.9
2686.3	2581.5	2143.7

k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Flavobacteria
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k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Flavobacteria

o__Flavobacteriales	f__Flavobacteriaceae
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g__Ulvibacter
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EU394565.1 gg_id:323691 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU394
GQ022124.1 gg_id:487544 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GQ007109.1 gg_id:502554 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
GQ069658.1 gg_id:377516 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ069
GQ115370.1 gg_id:396621 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ115
GQ038972.1 gg_id:373580 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ095754.1 gg_id:421610 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ095
GQ023681.1 gg_id:485988 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ023
GQ039736.1 gg_id:402923 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu427f02 GQ039
GQ001629.1 gg_id:508030 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu175d0 GQ001
FJ544401.1 gg_id:428635 Cloacibacterium normanense str. tu29 FJ5444
GQ038764.1 gg_id:411419 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu522g0 GQ038
GQ038963.1 gg_id:387025 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ103650.1 gg_id:440607 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
GQ105575.1 gg_id:374740 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ105
GQ023597.1 gg_id:486071 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu320d1 GQ023
GQ022994.1 gg_id:486675 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GQ084334.1 gg_id:440552 Topographical and Temporal Human Skin Microbiome skin external auditory canal cl GQ084
GQ075556.1 gg_id:464611 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GQ099665.1 gg_id:417936 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ099
GQ114725.1 gg_id:393950 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ114
GQ039257.1 gg_id:435660 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
GQ111429.1 gg_id:403307 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw667c0 GQ111
GQ101729.1 gg_id:376177 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw498e09 GQ101
GQ039240.1 gg_id:461451 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
GQ106199.1 gg_id:392709 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ106
GQ021112.1 gg_id:488556 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2 GQ021
GQ075467.1 gg_id:425679 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GQ020806.1 gg_id:488861 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
GQ106534.1 gg_id:455925 Topographical and Temporal Human Skin Microbiome skin back clone nbw537a06c1 GQ106
GQ074932.1 gg_id:429345 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074
GQ072560.1 gg_id:433687 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw19 GQ072
GQ113784.1 gg_id:434333 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
GQ038713.1 gg_id:414341 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu521h0 GQ038
GQ022845.1 gg_id:486824 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
GQ083053.1 gg_id:391270 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ083
GQ102414.1 gg_id:370850 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ102
GQ106366.1 gg_id:374313 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ106
GQ104515.1 gg_id:440778 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ104
GQ023092.1 gg_id:486576 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ023
GQ074989.1 gg_id:378373 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ074

44.1	140.0	71.0	100.1	169.6	141.6	75.3	128.8	50.4	99.5	78.8
6240.7	11567.0	8124.8	8702.5	7075.6	8846.1	7891.5	9308.8	12262.5	14118.9	9647.7
1033.2	12932.5	7372.3	6013.2	6308.3	7393.5	6630.7	9489.5	10707.0	15715.3	7761.5
63.9	12926.6	7124.5	3021.2	4812.9	5033.5	2847.9	6519.6	4332.2	10812.5	3529.6
2639.5	13261.7	7120.1	5885.3	5659.2	6902.4	5943.1	9271.5	9637.1	16999.1	7472.6
2671.5	13125.6	7420.7	6549.8	6413.7	7636.5	6968.2	9683.9	10493.6	15986.7	7759.4
4539.6	12257.9	6594.0	4936.4	4422.4	6537.0	3840.1	7706.5	8189.0	14846.0	6020.6
2724.5	13332.1	7172.7	5612.7	5723.1	7194.8	6253.6	9479.2	9757.3	16472.4	7370.4
2761.4	14741.8	7904.0	6490.3	6226.1	7733.8	6470.5	10441.3	10776.0	18601.4	8265.9
4518.8	11734.9	6506.6	4744.4	4445.6	6483.7	3855.7	7853.8	7837.1	14277.5	6301.6
3010.6	14882.4	7559.3	6140.1	6012.7	7773.7	6046.0	10452.7	11267.7	18644.8	8079.2
1540.5	9255.4	6609.9	6461.3	6380.4	6738.0	6631.3	7573.6	11038.1	10055.3	7687.3
817.9	13237.7	6769.5	3415.5	4426.8	6365.4	3423.5	8453.9	11363.8	14020.1	5547.5
1710.6	9002.0	6783.0	6759.1	7116.4	6746.1	7466.3	7604.7	6184.5	10586.7	7138.7
17001.5	15906.7	10040.6	9354.8	9041.7	9997.6	9623.9	12149.1	14588.0	20579.0	12179.0
3860.9	11793.8	6869.4	4786.5	4669.0	6764.1	4858.9	7776.2	8530.8	14478.0	6578.3
12110.1	13316.4	9992.2	9203.3	9113.6	9594.4	10034.6	11462.2	13147.0	15488.8	11813.8
3331.6	14450.3	10392.3	9636.0	8861.2	10622.7	9612.0	11707.0	15324.3	16973.6	12248.3
4225.7	11255.3	6932.6	5130.6	5071.0	6660.7	4663.7	7771.2	7953.9	13798.1	6660.0
3924.4	11831.7	6884.0	5121.3	4747.3	6852.8	4186.7	7915.4	8762.9	13392.2	6506.9
952.0	8506.6	6448.3	6593.2	5935.2	6961.0	6690.7	8139.7	6666.7	11749.4	7198.2
990.2	10682.7	6155.4	5146.5	4766.6	6284.5	5243.3	8085.6	8237.9	12699.1	6406.0
10780.8	14217.2	11313.1	10995.0	10453.2	11794.4	12690.5	11354.0	19208.3	18642.0	13675.6
4995.1	11925.6	7553.9	5860.6	5513.9	7337.1	5143.4	8533.5	9366.8	14333.0	7522.3
2690.6	12694.8	8324.4	7624.0	7587.2	8370.3	8781.5	10292.5	11867.5	16200.1	9852.1
1794.5	11675.2	6437.7	4101.2	4106.4	6063.9	4499.3	7751.0	7565.3	12128.1	5556.9
8672.4	15104.1	8888.6	6799.0	6712.3	9312.0	7281.0	10580.3	13180.6	18118.2	9738.9
8370.6	7412.4	4187.4	3809.0	4321.5	4766.2	4212.3	5605.8	7079.3	7746.4	4616.4
125.0	9899.8	7173.0	6536.9	6519.4	7402.6	6538.5	7502.1	10551.6	10936.8	7189.9
1822.4	13986.8	8266.5	7386.6	5827.7	7591.4	6404.7	9913.4	11720.5	16287.8	8980.0
11961.1	13693.1	11343.3	10710.5	10382.4	10468.0	11663.1	11169.9	15777.8	17753.9	15143.7
1569.7	8712.7	6123.6	6342.1	4881.7	6440.7	7943.5	6337.8	10348.1	11879.0	9331.6
2694.0	12320.9	6158.5	5187.1	5111.4	6286.4	5769.5	8375.3	8015.3	15788.8	6532.9
1979.1	10453.3	4908.9	3641.5	4095.1	5578.1	3091.2	7085.7	9189.4	11779.2	5761.8
5426.8	15167.0	9241.5	8056.4	7905.3	8800.5	8657.9	10947.9	11721.2	19578.1	9831.5
16077.4	13621.6	9589.8	8453.8	7849.0	9218.5	9161.3	9389.3	14304.5	16551.9	11751.3
1113.4	14037.7	8581.3	5879.5	6175.5	7565.3	7657.8	9377.9	9281.2	16949.1	10556.0
9207.6	13881.9	8646.8	6982.1	6895.9	8649.3	6179.7	9619.1	11914.8	16169.0	8794.9
2296.6	10943.0	8107.4	8813.4	6378.6	7869.7	6536.5	9619.3	9309.0	12963.9	9391.9
13138.3	13915.0	8654.0	7756.5	7893.4	8807.9	8522.3	10461.5	12749.0	17403.0	9714.1
4592.4	14988.8	8571.8	7407.0	7372.1	8448.2	7727.5	10903.9	12317.8	18860.1	9537.2

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6523.2	5035.3	4851.0
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7124.2	5663.4	5939.0
6684.9	5197.8	5323.2
6711.7	4818.9	4730.0
7486.7	5268.2	4968.5
6646.1	5450.4	4247.4
7567.1	5153.8	4506.2
5875.5	7016.7	6081.9
5022.4	3159.8	2940.3
6467.8	6285.1	5919.4
10811.7	8264.6	8362.1
6738.0	4779.0	3341.3
9503.7	8678.4	9101.2
10365.4	9236.6	8819.1
6550.8	5790.1	5077.6
6834.9	5246.4	5040.0
6163.7	5507.4	5444.5
5263.5	4534.2	4279.3
11806.0	11863.5	10936.7
7398.8	6462.5	5306.3
7477.5	6738.1	6927.8
5779.7	4221.4	3501.3
9328.7	6225.1	5664.8
4218.9	5234.0	5411.0
6703.5	6972.1	4855.4
7639.7	5722.0	3503.6
9660.2	9766.6	9760.2
5483.2	5304.1	4959.1
6168.7	4188.1	4412.8
5242.3	3362.4	2536.3
9114.7	6720.6	6821.3
9050.8	9419.5	7621.7
7264.0	4979.2	4774.6
8351.9	7387.9	6487.6
7484.9	5452.5	4278.6
8321.7	7479.4	6931.6
7937.8	5792.3	6023.7

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GQ099555.1 gg_id:376250 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51 GQ099
GQ021336.1 gg_id:488332 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu27 GQ021
GQ099107.1 gg_id:460624 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ099
GQ104658.1 gg_id:442905 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nb GQ104
GQ092951.1 gg_id:462399 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw407b09 GQ092
GQ036826.1 gg_id:408836 Topographical and Temporal Human Skin Microbiome skin back clone nbu369g03c1 GQ036
GQ069211.1 gg_id:465358 Topographical and Temporal Human Skin Microbiome skin back clone nbw240f04c1 GQ069
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GQ106805.1 gg_id:454545 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw541b0 GQ106
GQ032425.1 gg_id:458095 Topographical and Temporal Human Skin Microbiome skin occiput clone nbu542g03 GQ032
GQ114290.1 gg_id:462604 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ037888.1 gg_id:429818 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ037
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GQ090454.1 gg_id:373899 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nb GQ090
GQ106015.1 gg_id:422686 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ106
GQ023053.1 gg_id:486616 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ023
GQ099578.1 gg_id:420908 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51 GQ099
GQ024558.1 gg_id:485112 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123g04c1 GQ024
GQ075966.1 gg_id:452569 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GQ096758.1 gg_id:437278 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ096
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GQ005439.1 gg_id:504224 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu92d11 GQ005
GQ105327.1 gg_id:458970 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5 GQ105
GQ111315.1 gg_id:384705 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw665b0 GQ111
GQ096196.1 gg_id:460445 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ096
GQ104509.1 gg_id:424223 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nb GQ104
EF419391.1 gg_id:208578 Substantial alterations cutaneous biota psoriatic lesions human skin clone 4P2-50 EF4193
GQ021940.1 gg_id:487728 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ097748.1 gg_id:459070 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw456b0 GQ097
GQ111381.1 gg_id:391245 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw666d0 GQ111
GQ106959.1 gg_id:397725 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw543a0 GQ106
GQ088492.1 gg_id:414456 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
GQ098069.1 gg_id:430687 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40 GQ098
GQ107006.1 gg_id:398179 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw543e1 GQ107
GQ105630.1 gg_id:380715 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ105
GQ088962.1 gg_id:417279 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ088
GQ095820.1 gg_id:468543 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ095
GQ104431.1 gg_id:384604 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ104

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4537.2	13995.1	7922.8	6854.6	6871.5	8403.3	7318.5	10022.2	10718.8	15960.0	8798.3
1081.2	8067.5	6020.6	5792.5	6255.2	5800.6	7051.4	6922.7	7006.2	10182.2	6409.2
4457.3	14853.7	8016.9	6578.5	6361.6	7895.8	6830.8	10374.1	11917.2	18602.3	8512.6
6706.9	14547.3	8396.0	7613.2	7808.4	8778.8	8347.8	10936.3	11484.3	18841.4	9429.0
2672.4	12419.9	5851.3	4682.1	4668.8	5807.3	5429.8	8494.9	7623.4	16028.9	6053.9
6254.9	15472.4	9680.4	8613.4	8283.2	9284.2	9112.7	11499.3	12175.4	20130.0	10722.2
1917.0	8844.2	5612.5	5768.5	2558.4	5122.1	2642.9	7803.6	4468.6	13834.9	4790.2
8009.7	13014.2	7185.4	6139.2	6435.9	7533.9	6817.4	9460.4	10440.6	17187.8	8152.9
240.7	5449.8	2735.8	2048.5	2457.9	3512.9	1918.1	4150.5	4308.8	7173.2	2886.5
2552.9	13203.2	6897.3	5211.1	5910.3	7035.0	5987.9	9193.1	9485.4	16095.3	7082.1
156.5	5366.7	3710.6	3087.8	3126.1	3809.1	3000.7	4409.1	4385.4	7410.5	3189.8
89.2	9067.2	4754.3	4586.1	4567.3	5076.9	3960.9	6782.9	5644.6	12098.2	5083.1
6914.2	14266.5	8732.3	6912.3	6248.9	8621.0	6127.0	10249.8	11931.5	17672.0	9638.5
3592.3	13592.1	7306.2	5956.5	5996.9	7660.1	6652.5	9711.6	10357.3	16978.8	7893.1
6846.2	14313.1	11447.3	10448.7	9435.2	10342.1	10568.7	11402.0	13878.6	17498.9	12814.7
2618.6	13963.9	7857.8	6694.0	6426.1	7622.1	6657.1	9984.9	10353.8	17723.0	8227.8
1971.0	9338.3	5988.0	4655.9	4461.5	5737.2	4888.5	6660.6	6214.5	11994.5	5723.2
791.8	6143.6	3897.3	2563.7	2163.0	3819.0	2461.5	3656.5	4350.6	8063.5	3507.9
611.9	6960.2	4203.7	3790.9	4132.9	4807.7	4583.2	4857.5	7659.7	6575.3	3160.6
1461.1	12646.8	10087.3	8487.4	8203.7	10521.5	9362.7	10636.0	15417.9	16309.0	11343.3
1959.2	9890.4	5891.1	6249.0	6081.8	6662.1	5771.0	8416.7	7227.9	13164.1	6506.5
5074.1	15467.9	9210.8	8188.0	7956.0	9244.9	8496.8	11389.7	13061.1	19397.8	10652.6
2391.0	14250.3	8017.9	6534.4	6384.6	7758.8	6864.3	9830.4	10532.7	17970.7	8392.2
8749.2	13990.5	9246.4	8521.2	6747.9	10069.2	7738.0	10176.8	15452.5	16180.9	10869.7
8089.2	12427.0	11025.5	10729.6	10803.6	10467.7	12163.9	10388.7	15759.9	15304.4	11316.8
940.7	14695.3	8533.7	7133.2	7692.5	9174.3	7673.3	11073.3	13778.1	18339.5	9534.9
16367.9	9230.2	6549.6	6605.2	6249.1	7120.6	7033.2	7028.5	11696.9	11078.2	8026.2
4560.8	13848.8	7444.7	5999.8	6131.6	7508.1	6780.8	9766.8	10734.7	17272.4	7950.9
62.8	2995.7	2039.1	1765.3	1771.7	1604.9	1829.8	2157.6	1516.1	3017.1	953.4
456.2	6881.2	5124.8	4908.5	4765.4	5559.7	5009.7	5417.6	5650.4	10200.8	5063.0
3208.3	15726.4	10255.0	7852.1	7369.5	9426.6	8910.5	11253.8	14462.4	20062.1	11957.1
1369.5	10836.5	6264.0	4753.7	4061.3	6080.3	4166.4	7236.3	6753.6	12757.7	5751.9
2549.1	11128.1	7033.0	6754.8	6893.4	7219.5	6928.1	8073.7	11234.7	12993.6	8224.5
1597.6	12597.1	6886.1	4366.7	4035.8	6711.2	4453.4	8494.6	7744.2	15388.2	6209.9
881.7	12461.1	6861.0	5671.8	4902.8	6697.0	5206.6	9520.3	8180.4	16978.6	6937.5
979.3	13286.8	7251.1	5856.6	6054.8	7075.1	5950.6	9442.7	10096.8	16168.8	7701.3
3919.8	10910.6	8164.4	7985.8	7869.1	7786.2	9180.7	8471.0	9764.7	12195.6	9743.2
8262.1	14193.1	8021.7	7084.9	7240.2	8485.3	7762.8	10392.0	11775.2	18068.3	8921.6
1012.3	13289.7	8979.3	8619.6	8602.0	8618.0	8640.5	10700.4	11219.5	16884.3	9602.8
6236.8	15183.2	8721.4	7600.0	7507.3	8631.8	7829.4	10982.1	12323.1	19412.3	9486.2

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8791.2	6627.9	7319.7
5439.5	3834.4	4105.7
9596.6	7264.6	7226.3
6779.8	3749.2	2467.0
7229.6	6201.1	5943.8
3461.1	2204.5	1294.7
6555.8	4441.5	4504.6
4306.2	3138.4	2398.4
4584.5	3906.0	3271.8
8750.5	6963.0	6489.3
7054.7	5257.8	4748.6
9818.0	8770.0	8124.8
7322.0	5562.4	5295.1
5715.4	5535.6	5018.0
3435.6	3215.7	2033.6
3864.6	3238.5	2516.2
9314.6	9215.2	8842.6
6000.2	4979.5	4318.9
9175.3	6765.8	6675.0
7650.5	5234.9	4761.4
9315.3	8475.5	5854.0
9362.1	10398.4	10583.0
8063.2	6141.9	5608.0
6250.2	8291.5	6405.5
7448.9	4767.5	4756.8
5079.9	1767.4	684.8
4990.0	5515.0	5003.0
9485.1	7113.4	5948.6
6143.4	4215.7	2729.6
6184.5	6604.6	6560.6
7062.7	4111.9	2388.2
6727.5	3765.6	3665.5
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7114.4	7412.1	6667.3
8196.0	6544.8	6560.6
8176.0	6408.9	6317.2
8674.9	6419.9	6622.7

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GQ065104.1 gg_id:458385 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw82h12 GQ065
EF554366.1 gg_id:218840 Sejongia marina str. IMCC3228 EF5543
GQ075589.1 gg_id:467227 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GQ098762.1 gg_id:461413 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw702c GQ098
GQ098090.1 gg_id:374684 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40 GQ098
GQ020899.1 gg_id:488768 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
GQ060012.1 gg_id:454184 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ060
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GQ038166.1 gg_id:452568 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbu38 GQ038
GQ047675.1 gg_id:454738 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137g03c1 GQ047
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DQ337009.1 gg_id:149122 subsurface water clone EV818CFSSAHH91 DQ337
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GQ106914.1 gg_id:454494 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw542e0 GQ106
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FJ375428.1 gg_id:579506 T-RFLP powerful tool rapid assessment cells microbial fuel cell sheet carbon cloth ano FJ3754
GU196264.1 gg_id:581231 Bergeyella sp. str. 405 GU196
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GQ098653.1 gg_id:423330 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw704h GQ098
GQ092053.1 gg_id:421736 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw405e03c GQ092
GQ089203.1 gg_id:462011 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ089
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GQ104342.1 gg_id:443508 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ104
GQ020682.1 gg_id:488986 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
GQ099206.1 gg_id:468454 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ099
GQ113829.1 gg_id:379522 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
GQ007418.1 gg_id:502244 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
GQ105778.1 gg_id:451356 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw5 GQ105
EF419388.1 gg_id:211708 Substantial alterations cutaneous biota psoriatic lesions human skin clone 4P2-33 EF4193

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15949.9	12633.5	8702.0	8529.9	7678.6	9235.6	8394.7	10576.3	13653.8	14739.7	10176.6
2236.3	13268.8	7778.6	6556.9	6240.3	7222.5	6627.5	9381.7	9729.4	16879.7	7827.7
34.6	44.3	63.2	45.6	31.8	34.1	38.9	42.6	25.7	53.2	41.1
2554.5	14369.3	7834.4	6205.3	5972.5	7609.0	6133.6	10031.3	10662.6	18214.5	7959.9
11149.2	11666.6	10328.4	9977.6	8975.1	10265.5	9992.2	10336.1	17081.8	14393.4	11510.4
4935.4	13880.6	7056.3	4952.5	4963.8	7371.7	5599.1	8636.8	11602.8	15161.4	7193.2
6370.4	10728.9	8107.4	8761.5	6906.3	8809.7	8178.7	8749.8	13291.5	12453.1	9834.9
28586.9	16405.0	13843.8	14143.8	14162.0	13911.4	14999.2	15999.5	22383.7	21068.5	18918.2
6186.7	14902.6	9230.6	8294.6	7820.2	9475.1	8885.1	11134.9	13330.0	18684.9	10987.3
1502.5	12674.5	8558.3	7637.5	7024.8	7905.3	7470.3	9211.0	9063.2	15581.4	8665.7
1753.9	9403.5	5714.3	4660.2	4862.3	5882.4	5466.2	7170.6	6679.6	12279.8	6155.6
11032.2	6412.4	4286.0	3783.1	3948.4	4914.8	4392.1	5218.0	8282.6	8025.2	5038.1
621.2	8292.5	5952.0	4831.2	4161.3	5542.0	3708.1	6079.1	9203.9	11113.8	5045.6
196.7	8909.2	6465.5	5403.2	4760.0	6456.4	4818.3	6854.4	6569.0	10344.1	6011.3
12974.6	11592.9	7927.3	7392.6	7179.8	8136.4	8218.7	9524.2	10976.9	14989.2	10043.6
2874.7	13600.0	7454.6	6388.5	6577.4	7856.9	6843.2	9673.2	10305.0	15325.6	8073.9
6738.2	12183.5	10256.7	10040.2	9579.5	9726.9	10455.5	9457.9	12047.0	15492.4	14110.5
2659.5	13163.6	7427.3	6390.3	6101.8	7381.5	6282.8	9151.9	10028.9	16759.1	7951.6
280.2	15229.0	7238.3	3628.9	4414.8	7020.8	4516.1	9544.9	12605.1	15097.3	6406.3
226.2	12254.4	7797.3	7291.9	8063.7	8014.1	7239.8	8276.3	12152.7	15860.8	7675.1
1348.9	7665.1	4007.1	2450.5	2070.6	4083.2	1969.2	4618.0	4471.0	8334.0	2990.8
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1423.1	12401.0	8685.2	8816.5	6875.2	8928.7	8638.1	10083.0	14023.1	12211.0	10462.7
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3010.6	14741.8	7904.0	6490.3	6226.1	7733.8	6470.5	10441.3	10776.0	18601.4	8265.9
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2593.5	14649.7	8377.4	6986.2	6845.2	8265.3	6926.2	10562.1	11862.5	18480.9	8836.5
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2042.8	12592.8	7759.2	6381.8	6605.0	8114.3	7096.8	9176.1	9997.4	14860.3	7696.5
1555.5	7334.8	4359.9	4112.5	4025.6	4176.2	4364.8	5522.3	7095.2	8078.9	3876.6
2623.7	13627.5	7400.6	6049.7	6199.1	7258.8	6052.5	9520.9	10102.1	16721.0	7650.4
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7843.9	5244.9	4884.3
8962.3	10497.3	9292.4
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4982.2	4671.0	3328.9
5976.8	5279.1	4630.8
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7173.6	5036.4	5291.0
8825.2	9533.8	11214.2
7388.5	5181.8	4823.8
5361.6	3650.1	2488.9
7852.1	6260.1	5609.6
4193.3	2986.0	2343.7
9626.9	10576.8	9790.7
7906.6	7407.5	6959.5
4092.9	2307.6	1174.1
7486.7	5268.2	4968.5
4944.9	4946.9	3743.1
8071.6	6482.9	3718.9
7848.3	5851.6	5626.3
8885.7	6279.0	6668.7
7288.4	5610.6	5354.0
7281.8	5413.7	3696.0
6910.0	5918.2	3587.2
10632.2	12877.8	13362.6
6241.3	4633.8	3998.3
7815.5	7238.0	5681.5
5212.5	5524.6	5057.8
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GQ106687.1 gg_id:380585 Topographical and Temporal Human Skin Microbiome skin back clone nbw539d04c1 GQ106
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1580.6	16326.7	10082.4	10276.9	9564.2	10631.4	8689.6	11807.6	18771.8	17842.0	12079.7
4524.3	14507.5	8762.4	7828.6	7526.1	8928.7	8409.8	10760.9	12916.2	18050.5	10262.9
1858.1	11876.6	8671.8	7982.8	7350.7	8862.8	8479.5	9488.7	11244.7	14136.5	9618.2
2038.2	11104.7	7430.0	6942.6	5117.9	7528.7	7159.5	8725.2	7733.5	10497.2	8522.0
1178.8	11677.1	6831.6	5059.1	4451.1	6837.4	5202.6	8057.0	8435.7	13789.2	6427.4
1090.0	12504.6	8525.1	8596.2	8492.4	8550.5	8073.5	10510.4	10795.6	15643.0	9193.8
3918.1	14009.3	9134.3	8424.6	8630.1	9025.5	9430.5	11414.1	11460.8	16138.0	10794.3
4474.0	13019.8	7744.5	6691.2	6950.7	6973.0	7882.8	9208.0	9379.3	16845.3	7520.4
3383.8	11387.8	8677.9	8785.9	7708.9	9296.2	9199.4	10091.7	15582.5	13237.8	10486.2
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4846.9	14899.1	8393.4	7282.2	7303.2	8231.5	7629.5	10843.7	11983.4	18632.4	9252.2
14146.8	13377.8	8211.3	7501.2	7499.9	8624.1	7988.9	10646.0	12341.7	16483.9	9601.6
2684.6	14256.9	7328.7	5531.9	5916.7	7478.1	6396.6	10063.1	10071.2	17886.3	7616.5
6238.9	14872.2	8857.1	7838.6	7658.4	8913.3	7583.6	10592.0	12472.4	19064.0	9467.4
2940.6	8715.8	4660.0	4500.6	4630.8	5366.4	5158.0	4807.2	9429.9	9438.7	5443.5
1172.8	12752.9	6915.1	4162.4	4379.1	6670.1	4471.6	8340.0	8841.7	15765.8	6014.5
6660.6	13635.0	8315.6	7470.5	7642.2	8084.8	7809.0	9745.4	11225.0	15892.2	8603.4
4519.1	13941.5	7604.2	6581.6	6712.7	8040.5	6945.2	9751.3	10310.4	15877.8	8022.9
1015.2	11598.0	8689.4	8744.3	8833.7	8459.9	9312.5	8532.1	11038.4	11435.3	9294.2
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3469.5	11696.7	6857.0	6193.0	6653.6	7584.6	7203.2	9216.9	10200.3	14462.6	7745.6
2668.3	11653.9	5833.3	4552.9	4721.8	5934.4	5037.5	7959.7	8087.2	14868.7	6047.9
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12624.0	9224.2	7196.1	6507.8	6291.5	6468.7	7420.9	8169.5	10884.4	11544.2	8571.1
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GQ103502.1 gg_id:400978 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ103
GQ106235.1 gg_id:385974 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ106
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GQ106659.1 gg_id:408181 Topographical and Temporal Human Skin Microbiome skin back clone nbw538h10c1 GQ106
GQ108173.1 gg_id:466316 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw603b07(GQ108
GQ038977.1 gg_id:414236 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu4 GQ038
GQ064890.1 gg_id:466017 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ064
GQ038848.1 gg_id:431402 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu523h11 GQ038
GQ109077.1 gg_id:377653 Topographical and Temporal Human Skin Microbiome skin palm clone nbw608b12c1 GQ109
FJ674757.1 gg_id:525819 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
GQ098258.1 gg_id:456403 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40 GQ098
GQ021913.1 gg_id:487755 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ001559.1 gg_id:508103 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu174e06 GQ001
GQ106034.1 gg_id:447124 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ106
GQ037522.1 gg_id:437251 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ037
GQ021725.1 gg_id:487943 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ020888.1 gg_id:488780 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ020
GQ021743.1 gg_id:487925 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ096238.1 gg_id:398950 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ096
GQ104500.1 gg_id:417558 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ104
GQ023536.1 gg_id:486133 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu319g06 GQ023
GQ023766.1 gg_id:485902 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ023
GQ070727.1 gg_id:431842 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
GQ114266.1 gg_id:423764 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw59 GQ114
GQ039046.1 gg_id:391867 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
DQ336714.1 gg_id:147046 Chryseobacterium caeni str. N4 DQ336
GQ104291.1 gg_id:381286 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ104
GQ007217.1 gg_id:502446 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
EU535726.1 gg_id:286716 profile human microbiota antecubital fossa (inner elbow) skin clone nbt10b01 EU535
GQ114067.1 gg_id:380870 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
GQ071987.1 gg_id:396996 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190g08 GQ071
GQ105856.1 gg_id:425298 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ105

2831.4	14803.5	8200.5	6822.3	7430.3	8289.8	7864.3	10649.1	11103.4	18030.2	8816.3
4845.0	12798.2	8644.0	8011.0	7500.9	8469.3	8815.8	9766.9	10189.7	15269.1	10009.0
100.6	9483.7	6160.0	4467.6	5865.5	5971.7	4558.0	6994.2	7840.3	11365.8	4560.6
778.5	13948.2	7373.3	3391.3	4481.3	6448.6	4468.0	8635.0	12563.3	14353.7	6287.3
3920.4	13692.9	8965.3	8034.7	8317.3	8593.6	9462.1	10794.5	11828.1	15083.9	10273.8
2181.1	9987.4	6332.7	4460.8	4792.5	6516.8	4954.2	7227.9	9397.7	12552.8	5355.3
2976.6	13274.0	7531.9	6206.3	6443.5	7577.1	6732.6	9567.7	10712.3	16267.4	7710.5
2445.3	15297.8	9576.5	9100.7	8752.4	10220.1	9896.8	12226.2	14998.3	18431.5	11745.3
4162.9	14373.1	8034.2	6640.0	6785.8	8133.0	7371.4	10352.9	11554.4	17971.3	8695.2
7937.0	9403.1	8571.8	8591.3	8114.8	8161.4	9266.4	7112.6	12693.5	11080.3	9688.1
1294.1	11313.5	6391.3	5480.1	5758.4	6328.0	5758.1	8494.8	7829.3	13610.0	6621.1
28089.1	10632.4	7895.5	7628.1	7693.0	8415.8	8389.3	9233.7	13508.5	13511.7	9731.3
2659.8	12999.7	7269.8	5768.4	5505.1	6833.2	6348.0	8922.6	10412.8	16027.3	7727.5
222.9	8467.1	6014.1	5677.4	5903.8	6180.5	6330.9	6431.9	9954.1	8251.4	6221.8
6914.2	13694.3	8355.4	6912.3	6248.9	8621.0	6127.0	9777.2	11206.5	15937.1	8691.8
9165.3	7976.6	5832.0	5244.4	4632.2	5941.2	5241.3	6098.7	9087.8	8665.4	6099.0
1233.4	9490.2	5569.5	4757.8	4849.9	5757.9	5525.5	6547.1	8527.8	10462.5	5172.9
23285.5	15755.4	11404.8	11082.3	11086.9	11543.8	12393.6	12294.4	18826.6	17995.7	16201.8
36.0	6606.9	5716.7	4027.9	1855.4	4557.9	2287.1	4390.6	4252.6	9202.7	3596.8
261.3	6514.8	4375.0	4647.8	3488.4	5180.3	4019.9	5152.5	7716.9	9636.5	4275.9
17326.9	8880.3	6410.4	6248.5	5922.0	6806.4	7254.2	7364.6	10600.3	10588.9	7617.0
6673.9	14989.9	8867.5	7708.0	7172.3	8840.7	8003.2	11078.2	12577.1	18963.7	10357.5
1159.1	13299.5	7219.7	5982.2	5833.5	7078.3	6375.1	9555.2	9919.3	16099.7	7785.8
14948.0	11439.7	7238.2	6546.3	6469.1	7535.8	7421.9	8938.7	11846.2	13817.6	9177.8
3750.5	13954.7	7737.6	6227.4	6609.4	7994.7	7121.8	9996.2	10848.6	17160.1	8388.0
4345.3	12413.2	6469.8	5010.9	5192.7	6708.7	5707.1	8780.1	9022.6	16098.2	7124.4
5361.8	12429.2	8847.1	9104.5	7172.0	8879.9	8402.1	9808.5	13795.7	14732.9	10597.4
3633.5	12531.2	6725.3	5595.8	5953.7	6656.8	6393.5	8964.2	8702.9	16074.5	6955.5
3680.6	11292.1	9425.0	9331.2	8826.9	9342.8	9667.8	9281.4	14293.4	12740.1	10389.6
1287.6	11644.8	6405.6	5485.8	5257.7	6418.8	5813.6	8060.6	9883.4	12896.0	6339.3
2483.6	13945.0	7331.0	5366.7	5701.8	7385.2	6068.9	9703.5	10045.9	17588.9	7391.7
4634.0	13085.1	8495.4	7844.6	7741.8	8580.2	8917.4	10382.7	11873.6	16886.5	9793.9
6283.1	12697.9	7722.1	5910.6	5565.2	7455.8	5983.2	8904.0	9935.9	15064.0	7761.4
2076.2	9323.3	6240.9	5046.0	4579.5	6192.1	5025.9	6918.7	7145.1	10601.1	5819.8
1926.1	9880.4	6804.5	5727.3	5424.9	8339.6	5074.7	7794.2	8868.7	19486.5	5983.0
259.7	10803.0	6937.2	6449.0	6571.1	7259.1	7230.3	8343.3	13176.2	11923.6	8673.2
1383.4	10962.9	6136.3	4332.8	4401.1	5855.8	4119.5	7099.6	7216.8	12905.1	4658.1
2224.7	11326.4	7730.6	7300.3	7844.7	7691.6	8464.6	8264.3	6662.3	13465.7	6696.8
730.7	12916.2	7132.1	3250.0	4214.9	5985.8	4376.7	8190.4	11226.7	13454.1	5668.7
8845.4	7548.8	5789.3	5044.8	4536.0	5171.8	5714.3	6143.2	7766.7	7994.5	7455.2
20772.9	15095.5	9998.8	9259.0	9373.9	10130.0	10176.3	11893.6	14841.5	18513.3	13389.9

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8305.2	6881.0	7529.9
5552.1	4993.2	3625.6
4858.5	3075.8	2571.7
7456.5	6376.9	7146.7
6097.4	4957.8	3561.4
7006.8	5662.9	5412.6
9005.5	7767.7	8202.7
7687.6	5783.7	5677.0
10237.1	8391.2	7820.5
5782.9	4229.3	4230.9
7867.2	8802.9	7087.4
6381.4	4762.6	4199.5
5593.0	5513.3	4536.9
8425.0	6963.0	6489.3
5413.0	5915.7	4716.1
5067.4	5210.8	4365.5
10594.9	10300.9	9475.3
4820.7	2997.9	1731.7
3880.2	5037.1	2556.8
6215.7	6839.4	5469.2
8320.6	6695.9	5881.1
6505.9	4492.8	4275.1
6376.8	7356.0	6317.1
7381.7	5686.0	5126.9
6088.2	4914.1	4131.8
8204.9	7829.2	5962.2
6343.6	4680.7	5079.7
7789.7	8773.4	7646.4
6204.5	4763.4	4296.5
7439.0	4619.4	4479.5
8277.4	7455.3	7569.7
7710.8	5757.3	4348.4
6247.9	5911.3	4774.9
10177.9	5740.0	3904.3
6113.8	6504.2	5062.3
5935.1	3716.7	2931.4
7738.5	4710.6	5394.7
4455.2	3041.4	2540.9
4159.9	6449.8	4162.0
9145.8	8872.0	8260.2

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k__Bacteria	k__Bacteria	p__Bacteroidetes	c__Flavobacteria

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GQ105160.1 gg_id:379891 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ105
GQ111425.1 gg_id:393239 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw667b1 GQ111
GQ096444.1 gg_id:422596 Topographical and Temporal Human Skin Microbiome skin back clone nbw388c07c1 GQ096
GQ097152.1 gg_id:423968 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ097
AJ853509.1 gg_id:110654 landfill leachate clone GZKB14 AJ8535
DQ856530.1 gg_id:248648 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C2K DQ856
GQ039375.1 gg_id:401021 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu420f11 GQ039
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GQ045525.1 gg_id:410600 Topographical and Temporal Human Skin Microbiome skin interdigital web space cl GQ045
GQ106282.1 gg_id:426560 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ106
GQ087626.1 gg_id:431329 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ087
GQ001382.1 gg_id:508279 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu17 GQ001
GQ021906.1 gg_id:487762 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ023440.1 gg_id:486228 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu318e1 GQ023
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GQ115270.1 gg_id:460924 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ115
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GQ047645.1 gg_id:427236 Topographical and Temporal Human Skin Microbiome skin palm clone nbw137c03c1 GQ047
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GQ024539.1 gg_id:485130 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123e07c1 GQ024
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GQ084721.1 gg_id:449384 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
GQ099437.1 gg_id:415250 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51 GQ099
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GQ099945.1 gg_id:424358 Topographical and Temporal Human Skin Microbiome skin alar crease clone nbw47 GQ099
GQ070644.1 gg_id:466041 Topographical and Temporal Human Skin Microbiome skin back clone nbw237a02c1 GQ070
GQ024441.1 gg_id:485229 Topographical and Temporal Human Skin Microbiome skin palm clone nbw122d10c1 GQ024
GQ007159.1 gg_id:502503 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ007
GQ005829.1 gg_id:503833 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbu97 GQ005
GQ098103.1 gg_id:429844 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw40 GQ098
GQ024383.1 gg_id:485287 Topographical and Temporal Human Skin Microbiome skin palm clone nbw121g11c1 GQ024

2629.8	13703.6	7527.7	6021.5	6185.0	7544.1	6860.9	9888.5	10097.7	17666.9	7818.9
389.8	6442.1	4018.7	3552.6	3181.6	4226.5	3440.9	4806.1	5815.8	5908.7	3360.1
14317.0	12322.3	8933.1	8062.1	7551.0	9031.6	8467.5	9550.8	13248.3	13958.8	11073.9
1598.0	10998.0	6649.5	5888.5	6234.8	5986.4	7616.0	8468.8	7231.3	12518.2	6177.7
13293.3	8610.1	5791.0	6181.1	5561.1	6187.0	5811.2	6544.3	10522.2	10725.6	5583.9
11682.9	13626.4	10116.0	9580.9	9019.7	9970.4	9312.2	11401.9	15673.9	16546.0	12298.8
922.2	4420.7	3095.5	3653.0	2423.3	2950.3	2328.1	3241.9	3712.2	5588.3	3023.9
1926.3	10673.5	3981.2	3175.7	3918.9	5147.6	3768.7	6500.7	9654.3	7183.9	3973.3
2599.0	9346.3	5051.7	4499.8	3629.1	4553.4	5781.0	6750.7	6802.4	12213.9	5630.3
2390.1	14556.2	8498.5	7011.9	6680.9	7926.5	7417.3	10401.8	10250.9	18790.9	8660.6
4436.5	12575.4	7122.8	5732.6	5309.3	6863.3	6176.8	8759.0	10415.0	15752.1	7947.5
1310.0	9238.5	4744.2	3665.1	3944.5	4953.0	4567.6	6408.2	8149.9	10709.1	5095.3
6254.9	15383.8	9040.0	7873.0	7666.1	8994.6	8202.7	11252.9	12731.6	19494.5	10261.6
1455.8	10952.1	8351.3	7982.5	7143.4	8617.9	8279.7	8655.9	12429.8	13930.3	9217.9
886.9	11312.4	5683.7	4359.8	4586.6	5750.8	4935.5	7881.5	8081.9	14316.5	6098.8
1088.0	12657.2	8536.5	8364.2	8208.6	8434.2	8107.0	10900.8	10812.2	15965.2	9490.2
11996.8	13379.7	10118.7	9232.6	8838.7	9563.3	9836.1	10596.1	15973.8	16778.1	13736.8
1263.8	10889.2	6092.6	4153.0	3729.4	5834.9	4100.5	7558.4	6827.8	12671.2	5536.3
3550.1	13918.6	7814.9	6710.1	6490.2	7643.2	6819.0	10055.5	10374.4	17701.2	8289.4
1338.8	11122.6	5895.4	3907.9	3424.1	5910.3	3716.3	7641.2	6235.6	14449.6	5228.5
6249.9	10004.5	7052.7	7686.4	5827.8	8174.2	7193.0	8380.3	12603.4	11611.3	8739.1
1397.5	12959.8	8786.6	8893.0	7393.9	8663.0	7631.4	10211.2	9262.6	13669.9	8720.7
6256.8	15231.3	9028.6	8105.0	7950.0	9111.0	8169.2	10862.5	12715.0	19172.3	9965.2
1070.0	12603.6	8217.9	8091.3	8049.8	8071.4	7733.8	10630.0	10403.7	15883.0	8714.8
2001.2	15842.0	7861.6	6355.2	6338.8	8725.4	6690.7	9323.7	13381.0	17532.7	8670.3
1296.7	11960.8	6611.2	4641.3	4150.2	6260.9	4528.6	7891.6	7859.7	13650.9	6002.3
3039.5	7843.3	5884.5	5466.3	5713.5	5344.3	6816.9	5928.0	6104.6	8810.5	5876.0
8804.2	10947.6	8967.6	8309.0	7772.6	8534.0	6909.9	8386.5	12373.5	13831.9	11173.3
6986.4	9963.7	6646.9	5807.6	5610.6	6515.8	6291.9	7885.6	8187.7	12240.6	8081.2
11471.8	7024.9	5188.5	5109.2	4812.8	5451.3	4627.8	5879.6	8648.2	8607.5	6009.8
1214.9	10838.7	5964.5	3973.2	3648.8	5885.7	4050.0	7348.9	6995.7	12461.5	5269.1
5412.2	13869.8	8494.1	7685.2	7483.6	8047.7	7737.7	10062.1	11004.8	17969.2	8856.2
2975.3	15796.6	9495.8	8592.6	8426.1	9224.3	8927.0	10938.2	13724.4	18210.0	9843.5
855.0	11843.1	6677.2	5218.2	5545.3	7006.0	5797.0	8752.3	10080.3	13913.5	6901.2
1173.6	10465.4	5582.8	3452.9	3263.9	6711.2	3488.3	6687.4	6452.8	12503.1	4885.0
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2522.6	14225.4	7874.0	6147.6	6574.5	8041.6	6861.5	10234.3	11245.8	17855.2	8268.3
243.2	9514.9	6661.5	6366.7	6381.2	6821.6	7140.8	7842.6	11568.7	10968.8	8005.4
1786.0	5829.1	3631.2	2985.8	3078.5	3752.5	3112.0	3841.9	6491.5	6078.7	3469.8
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8807.4	9506.2	8241.7
2308.5	2816.3	3065.1
2680.3	3279.0	2925.5
3216.6	3746.9	2917.6
7989.4	5611.9	5197.6
6215.3	5474.1	4216.6
3693.4	3124.5	3242.6
8939.9	6579.1	6448.2
8455.6	7898.8	7433.0
4994.1	3370.8	3492.6
7674.8	6239.4	5936.5
8454.9	8088.7	7632.5
6674.9	4061.1	3293.6
7198.8	5514.2	5441.8
6193.3	3652.7	2067.6
6822.0	7730.1	5144.8
6917.7	6139.2	7156.8
9404.1	6773.6	6950.3
7409.8	6080.2	6100.2
7811.2	5788.6	5937.4
6602.4	4236.0	2877.3
4856.3	6366.1	9298.6
7458.7	9350.9	6364.8
5713.3	6038.5	4781.4
5040.7	6172.1	4233.7
5963.8	3682.0	2743.1
8317.9	6540.1	6532.3
9241.6	7105.6	8032.0
5977.6	5220.1	4748.5
5527.3	3575.0	1888.0
7023.9	4553.3	4499.9
7514.0	5523.9	6651.9
7443.4	5226.1	5175.1
5740.8	6472.3	5027.0
2923.6	3825.5	2561.7
7409.9	6929.0	7301.2

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GQ073161.1 gg_id:381976 Topographical and Temporal Human Skin Microbiome skin palm clone nbw205g09c1 GQ073
GQ099471.1 gg_id:406373 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw51 GQ099
GQ104377.1 gg_id:422699 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ104
AY672523.1 gg_id:99413 hydrothermal vent 9 degrees North East Rise Pacific Ocean clone CH4_1_BAC_16SrRN AY672
GQ024700.1 gg_id:484969 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024
GQ086886.1 gg_id:378101 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw3 GQ086
GQ021036.1 gg_id:488631 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu2 GQ021
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GQ104692.1 gg_id:417321 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ104
GQ107052.1 gg_id:430947 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw544b0 GQ107
GQ107158.1 gg_id:446930 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ107
GQ019120.1 gg_id:490548 Topographical and Temporal Human Skin Microbiome skin retroauricular crease clor GQ019
GQ021806.1 gg_id:487862 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
GQ033033.1 gg_id:410066 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ033
GQ038701.1 gg_id:448920 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu521f11 GQ038
GQ039228.1 gg_id:460504 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbu41 GQ039
FJ674908.1 gg_id:527641 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
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GQ025181.1 gg_id:421544 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw1 GQ025
GQ098739.1 gg_id:435725 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw701h GQ098
GQ093307.1 gg_id:425608 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw42 GQ093
GQ106708.1 gg_id:465171 Topographical and Temporal Human Skin Microbiome skin back clone nbw539f05c1 GQ106
GQ002698.1 gg_id:506965 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ002
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GQ092643.1 gg_id:461919 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ092
FJ799162.1 gg_id:555128 Microbial Responsible Intermediates Degradation Anaerobic Digestion System Deterr FJ7991
GQ093037.1 gg_id:410778 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw408d06 GQ093
GQ075503.1 gg_id:419313 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ075
GQ071955.1 gg_id:374641 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw190d05 GQ071
GQ083237.1 gg_id:442868 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ083
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GQ023656.1 gg_id:486011 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ023
GQ115289.1 gg_id:444502 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ115
GQ110917.1 gg_id:443627 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ110

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1445.4	10100.1	7490.0	7183.6	6870.5	8040.7	7945.9	8618.5	12632.6	10819.9	9116.4
3993.0	11489.4	6525.3	4846.9	4596.5	6464.5	4090.7	8492.8	8027.4	12975.9	6268.1
1451.7	10714.4	5907.4	5017.4	5150.2	5956.5	5174.1	7418.2	7614.9	11111.3	5162.5
612.9	10352.9	6900.8	6174.7	6114.5	7378.8	7367.7	9190.7	10748.1	12454.1	7895.3
1194.4	14019.2	10164.0	10134.6	7789.7	9802.4	9502.3	11209.3	15807.1	15804.4	12225.7
106.6	7698.0	3894.0	3952.3	4438.3	4594.3	4697.4	5869.9	4889.6	8808.7	3556.5
2785.7	13297.3	7327.4	5758.6	5489.8	7032.3	6208.0	9189.9	10392.4	16523.9	7689.4
6168.7	14700.2	8912.0	8021.7	7661.4	9112.3	8511.8	10844.7	12921.5	18602.7	10211.9
2427.2	15095.4	9257.9	8827.7	8593.7	9857.3	9523.5	11955.4	14589.9	18349.3	10970.0
2691.5	13026.6	7727.9	7054.8	6856.4	8115.6	7307.9	9564.3	10885.5	15746.6	8238.4
8688.2	15307.4	9182.4	7939.7	7659.1	9050.2	8278.7	11284.8	12916.8	19527.5	10748.0
4239.0	14422.6	9009.2	8058.2	7773.7	7864.5	8854.3	9849.2	10932.3	18536.5	9042.9
3018.6	14056.9	7895.2	6649.7	6466.4	7781.1	6690.9	10085.3	10509.3	17537.2	8333.8
11327.7	14575.0	9474.8	7783.1	7272.2	9237.7	8143.2	10846.1	13008.2	17415.6	10971.7
23900.2	18100.5	13706.3	13737.2	13901.8	13600.8	15682.1	14331.6	21559.2	19861.5	19788.1
14148.8	13225.2	8199.9	7733.1	7783.8	8740.5	7955.3	10255.5	12325.1	16161.6	9305.2
2292.4	11786.3	8431.7	8596.0	7140.9	8859.2	9296.6	9631.5	15490.1	13433.2	9942.8
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2489.7	14425.4	8059.8	5986.5	6938.3	8542.8	7032.8	10555.9	11812.4	18399.9	8402.3
2120.6	13479.2	8111.2	7130.0	7434.0	8042.7	8058.6	10535.3	10646.4	15245.8	9045.3
80.1	5352.5	2903.5	2944.3	2351.6	3635.6	1947.5	3563.5	4701.6	8970.5	2801.1
4014.2	12603.7	8077.2	6523.9	6320.5	7712.4	6427.5	9402.9	10309.2	15451.7	8228.7
4550.7	11224.3	7586.1	6635.4	5636.2	7415.2	6152.2	8255.8	10633.9	15007.2	9258.8
3049.1	11193.2	6035.6	4876.0	4885.0	5866.4	5506.6	7278.2	8575.5	12736.9	6693.4
2047.6	12707.9	7204.6	5993.0	5790.1	7357.8	6174.1	9130.3	10820.0	15706.9	8159.2
4699.4	11804.8	6398.9	5241.5	5141.9	6602.9	6528.0	7798.2	8558.8	12820.1	6500.9
951.0	12027.7	7257.4	6128.0	6324.4	7711.5	6728.9	9442.3	10889.4	14253.5	8408.2
4416.2	12837.5	6973.2	5849.5	5463.4	6932.5	5771.8	9107.8	9639.3	16723.9	7692.6
1270.1	9911.6	5344.6	4067.3	3993.1	5299.9	4952.5	6763.7	8852.2	10447.4	5413.6
3960.8	11960.7	7028.1	5188.0	4742.1	7091.0	4553.7	7952.0	9480.1	15328.2	7081.1
2931.5	12713.5	7212.6	5785.2	6056.0	8181.4	6208.6	9678.0	12212.7	15388.1	7945.1
2658.3	13888.1	7467.8	5749.1	6218.5	7666.4	6744.7	9805.6	10490.0	17297.4	7784.7
4502.7	13722.3	7519.4	6055.5	6481.9	7601.8	6887.5	9844.2	10824.8	16898.7	8006.0
2234.7	11597.0	7045.0	5647.4	5156.5	7130.2	5646.4	8737.0	8007.3	14988.6	7216.4
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7395.9	10916.3	7089.7	6486.7	6146.1	6728.8	6966.3	8850.9	10928.1	13434.9	9226.8
2947.6	12289.5	6371.7	5103.2	5368.4	6440.4	5618.4	8634.5	8797.5	15589.4	6673.6
27357.2	10218.6	7839.6	7864.7	7747.6	8506.3	8242.1	8773.4	13785.2	13398.3	9764.4

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8740.5	7608.5	8366.3
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9670.4	6802.7	6374.6
7583.3	5855.3	5934.8
7370.8	5604.3	5375.2
9544.4	7010.3	6190.5
12739.0	12289.3	11880.6
8284.7	7504.4	7021.8
7987.0	7344.5	7508.7
9462.0	8051.7	7814.0
7756.3	5472.8	4640.6
7135.7	5247.4	5633.7
5232.5	2604.3	1700.6
7938.8	6310.4	3813.3
7626.6	6379.2	5673.5
6128.3	4521.6	3437.6
6340.9	4888.7	4146.0
6902.7	5317.2	4179.2
6524.5	5749.4	5525.8
6493.2	5539.6	4513.4
4143.0	3552.1	2417.2
6850.2	5606.8	4378.8
7439.1	5611.0	4639.5
6942.1	4694.0	4694.8
6952.7	4988.4	5363.5
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8439.2	7445.8	5196.8
8659.2	6064.4	4796.9
7326.0	8483.6	7081.8
7073.0	6098.2	5301.5
5838.9	4535.2	4478.6
7687.7	10095.7	8232.3

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GQ105500.1 gg_id:440386 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw! GQ105
GQ114636.1 gg_id:442397 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(GQ114
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GQ007898.1 gg_id:501767 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw: GQ007
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GQ114653.1 gg_id:449985 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(GQ114
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GQ103002.1 gg_id:373782 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ103
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133.3	7474.6	4425.8	3199.2	2864.0	4352.8	2797.3	5268.5	3781.0	9889.6	3905.2
231.0	10914.3	7828.5	5997.0	5861.2	7067.9	7467.7	7731.1	5744.0	13065.4	5716.5
2727.5	13895.8	7821.4	6563.5	6340.9	7563.4	6749.9	9944.4	10397.9	17520.3	8178.8
9506.3	8149.9	5909.1	5808.2	4960.9	6152.5	5880.8	6552.5	8167.6	8545.7	6689.5
20045.7	16374.5	11458.4	10866.7	10982.7	11439.4	12364.3	13342.2	15557.0	20305.8	15120.7
4959.5	13250.2	7229.0	6006.5	6406.9	7475.0	6674.9	9523.8	10643.0	16149.7	7834.1
988.9	13047.4	7219.8	5947.6	5994.0	7113.4	6420.5	9276.2	9432.4	15972.7	6884.8
4585.6	14253.1	8042.2	6967.0	6553.2	7857.0	7037.2	10288.6	11726.4	18572.1	8442.0
8250.7	14718.0	9106.2	8077.4	7969.3	8974.5	8701.6	10655.4	13658.9	17951.8	10339.8
3688.4	15136.2	10629.0	10310.8	9242.1	10771.2	10675.5	12232.0	17414.2	18329.2	12968.4
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194.1	3607.7	2851.2	3095.6	1901.3	5708.2	2571.7	3258.4	5210.5	5176.1	1829.9
3598.0	13858.7	7644.5	6413.6	6242.2	7539.2	6474.7	9803.4	10774.4	17602.8	8151.3
2926.9	13864.6	7171.9	5612.4	5735.6	7265.9	6130.4	9754.2	9745.9	17053.3	7383.8
7103.7	10273.5	9456.7	8198.1	7431.2	8928.5	7734.1	9798.0	14148.2	14375.9	9310.7
13514.4	10096.6	6230.8	5461.9	5505.6	6833.0	6238.5	7563.6	10696.9	12127.3	6809.1
127.0	2313.6	2804.3	1890.3	2085.4	3017.9	1459.4	2234.6	992.7	9042.5	1028.6
5595.1	14452.3	8573.4	7524.0	7670.0	8890.9	8548.0	10989.4	13289.8	17911.7	10210.3
2929.4	14025.3	6879.4	6169.6	4766.5	7141.8	4195.4	10016.1	13325.7	15504.5	8059.1
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932.9	11974.2	6938.8	5836.8	6165.7	7348.7	6355.6	9171.5	10480.9	14171.3	7632.8
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2678.9	12243.9	6094.2	4570.7	4994.2	6372.4	5118.9	8666.8	8230.2	15842.1	6072.4
1535.5	10864.9	6382.3	4667.3	4083.8	6292.0	4692.7	7824.7	6891.0	13909.5	6036.4
2867.7	9115.8	6264.6	5086.6	4355.9	5889.9	6538.7	6070.2	7700.2	10768.8	6574.2
2971.7	12026.6	6521.4	4986.3	5214.4	6371.3	6023.4	8285.7	9573.2	14617.6	6928.5
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21763.7	14915.0	10743.9	9861.1	9638.8	10931.4	9987.5	12054.3	14963.6	19679.2	12527.7
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3956.3	11510.6	6828.4	5334.5	4714.3	7388.2	4211.6	8199.1	7593.4	16451.0	6541.5
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6165.9	14905.1	8218.0	6761.4	7236.6	8408.1	7764.8	10654.4	11706.5	18786.6	8918.0
2377.5	10754.5	6285.6	4375.4	5214.9	6040.7	4686.6	7500.9	7217.0	11734.4	4862.5
2589.4	14456.8	8388.0	7285.5	6921.3	8173.1	7334.1	10602.4	12165.7	18044.8	9314.4

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10517.9	10852.4	9186.2
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5293.3	6148.1	4635.9
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7509.0	6709.5	4730.7
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3331.0	3794.8	2270.8
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8890.4	6452.0	5383.7
8270.0	5794.4	6109.3
6225.0	5025.3	3920.0
7609.0	5781.6	5562.6

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GQ101779.1 gg_id:450316 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw499c02c GQ101
GQ111365.1 gg_id:424203 Topographical and Temporal Human Skin Microbiome skin buttock clone nbw666b0 GQ111
GQ032981.1 gg_id:454425 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ032
GQ001507.1 gg_id:508155 Topographical and Temporal Human Skin Microbiome skin buttock clone nbu173h07 GQ001
GQ085281.1 gg_id:460617 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw273d07c GQ085
GQ023925.1 gg_id:485744 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbu GQ023
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GQ102865.1 gg_id:408591 Topographical and Temporal Human Skin Microbiome skin inguinal crease clone nbv GQ102
GQ115285.1 gg_id:390899 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ115
GQ102320.1 gg_id:452891 Topographical and Temporal Human Skin Microbiome skin axillary vault clone nbw7 GQ102
GQ021840.1 gg_id:487828 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021
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GQ101648.1 gg_id:386571 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw497f03c GQ101
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GQ037242.1 gg_id:438419 Topographical and Temporal Human Skin Microbiome skin palm clone nbu390g07c1 GQ037
GQ106388.1 gg_id:393677 Topographical and Temporal Human Skin Microbiome skin gluteal crease clone nbw GQ106
EF419408.1 gg_id:215975 Substantial alterations cutaneous biota psoriatic lesions human skin clone 4PN86 EF4194
GQ074377.1 gg_id:384774 Topographical and Temporal Human Skin Microbiome skin umbilicus clone nbw162c GQ074
BD175053.1 gg_id:82260 Slime control method in paper making step of neutral paper making. BD175
GQ022893.1 gg_id:486777 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
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GQ093359.1 gg_id:409635 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw408g06c GQ093
GQ024527.1 gg_id:485143 Topographical and Temporal Human Skin Microbiome skin palm clone nbw123d05c GQ024
GQ114694.1 gg_id:407171 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ114
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GQ070662.1 gg_id:448615 Topographical and Temporal Human Skin Microbiome skin popliteal fossa clone nbw GQ070
GQ084845.1 gg_id:377093 Topographical and Temporal Human Skin Microbiome skin manubrium clone nbw26 GQ084
AM279201.1 gg_id:162105 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
GQ112286.1 gg_id:444516 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ112
GQ024937.1 gg_id:484733 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ024

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4659.9	15005.9	8288.8	7306.0	7040.1	8472.6	7387.4	10524.3	11920.7	18378.3	8958.4
5385.7	13547.4	7957.2	6735.3	6943.3	8026.0	7251.7	9993.4	11127.1	17514.3	8353.0
1507.4	8430.9	4672.2	3275.3	3016.6	4683.0	2741.1	5386.7	5428.9	8849.5	3877.4
3113.2	14837.9	8231.1	7225.6	7603.1	8458.5	7955.6	10565.2	12411.2	16527.2	8421.6
2029.5	12653.4	6886.0	5720.0	5631.3	6995.0	5800.8	8859.5	10411.5	15624.7	7383.8
2888.5	10595.8	6962.5	6733.7	5684.8	7080.3	6637.7	8668.3	8982.2	14070.7	8172.7
15799.7	12860.1	10092.1	9851.0	8537.2	10252.4	10833.1	11113.2	17346.8	15910.7	13373.8
1989.1	12189.7	6575.7	5402.8	5818.5	6473.1	6291.5	8886.0	8697.6	15522.3	7006.4
11673.0	7736.2	5121.1	4767.7	4805.8	5726.6	4993.7	6013.5	9153.3	9170.1	5178.9
1042.2	11817.0	6109.3	4740.2	5304.9	6292.7	5410.7	8515.4	8231.0	14997.9	6301.0
1273.2	11577.4	7048.1	5304.9	4983.4	6743.5	5330.9	8072.7	7657.8	14434.7	6647.6
9925.1	14285.8	9124.3	7532.9	6838.9	9219.3	7829.6	10565.2	12944.5	17504.9	10715.0
1493.2	8930.8	4381.7	3301.9	3381.7	3981.6	4587.6	6290.6	7186.1	10018.9	4142.3
6914.2	14787.1	9905.2	8586.1	7627.3	9786.7	7691.6	11043.0	14317.3	18076.5	11904.3
3924.6	12524.0	7611.0	6163.8	5986.2	7773.4	5507.4	8738.0	10279.0	14716.0	7711.7
3924.3	12425.2	7740.1	6094.4	5920.4	7649.6	5436.1	8769.8	10175.5	14465.6	7611.5
3741.3	13275.9	7807.6	6542.3	6808.1	7842.4	7149.7	9915.2	11121.8	16962.1	8404.0
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2993.4	11508.0	7798.5	5662.6	6228.7	7650.2	7217.1	8792.2	12050.1	13942.9	8271.5
1993.3	11551.0	9361.3	8258.8	9021.0	8769.3	9146.3	8645.2	12046.7	12057.8	9756.7
1907.1	8895.1	5728.0	4819.6	4221.9	6369.2	4542.3	5875.6	8896.4	8863.1	5364.9
1454.4	12936.4	7943.3	5818.9	5392.4	7250.5	6377.5	8700.4	9682.9	15297.9	6043.9
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3315.7	11074.7	8015.0	7310.6	8202.2	8379.0	8489.1	9194.7	10872.6	12821.6	7929.3
3918.3	11676.3	6665.5	4926.9	4576.9	6763.5	4112.8	7786.4	8420.8	13177.8	6402.9
359.9	2428.1	2118.3	1799.2	1804.0	1932.1	2156.7	2252.7	1807.0	1871.8	1445.8
9544.3	6328.1	5105.5	5127.4	5701.2	5863.2	5836.3	5332.3	7281.8	8324.9	7618.4
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2722.2	14933.9	8683.3	7326.3	7827.8	9357.9	7775.2	11151.4	13783.4	18891.7	9484.0
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975.2	14406.6	6927.7	5136.5	5328.7	7203.1	5198.7	9932.4	10861.8	17834.9	7196.7
6355.1	10990.9	7959.8	8878.4	7060.3	8880.3	7824.0	9098.6	12515.8	13424.9	9580.0
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GQ095907.1 gg_id:390482 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw4 GQ095
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GQ104187.1 gg_id:382341 Topographical and Temporal Human Skin Microbiome skin glabella clone nbw564e1 GQ104
DQ241813.1 gg_id:142000 Bergeyella sp. str. AF14 DQ241
FJ529927.1 gg_id:558722 Initial ammonia- and nitrite-oxidizing compromises successful nitritation counter-diffu FJ5299
EF219000.1 gg_id:216031 and Eukaryotic Hydrothermal Site East Rise Ridge Flank Abyssal Hill hydrothermal site EF2190
AM040100.1 gg_id:145257 sandy sediments clone Sylt 4 AM040
EU804168.1 gg_id:339257 It's all ranking aquatic 250 miles Panama City clone 6C232064 EU8041
FJ416103.1 gg_id:364895 sediments sediment station NEC5 Northern Bering Sea clone 076L41 FJ4161
AY694008.1 gg_id:103103 Gillisia ilustrilutea str. IC157 AY6940
DQ334617.1 gg_id:179670 Impact metals on sediments heavy metal polluted marine sediment clone HB1-48-2: DQ334
AB198088.1 gg_id:140534 Krokinobacter eikastus str. PMA-26 AB1980
DQ312294.1 gg_id:149971 Algibacter gromovii str. KMM 6038 DQ312
AB377121.1 gg_id:552860 Poriferibacter numazuense str. HOY10-3 AB3771
FJ889677.1 gg_id:564481 Maribacter sp. str. ZS1-8 FJ8896
DQ811908.1 gg_id:171601 mangrove soil clone MSB-3B9 DQ811
FJ800033.1 gg_id:534732 Sediminibacter sp. str. KYW39 FJ8000
FJ264580.1 gg_id:351824 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedime FJ2645
EF644795.1 gg_id:302349 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6447
GQ349889.1 gg_id:576551 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
FJ425590.1 gg_id:356889 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata B FJ4255
GU289639.1 gg_id:573111 Psychroserpens sp. str. MEBiC05379 GU289
FJ516872.1 gg_id:510003 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled lower s FJ5168
EF467458.1 gg_id:203630 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4674
FJ425219.2 gg_id:358171 Algibacter sp. str. K17-8 FJ4252
AF530137.1 gg_id:61123 Zobellia sp. str. MGP-14 AF5301
AF359540.1 gg_id:73211 Alexandrium tamarense PCC 173a AF3595
GQ349607.1 gg_id:591190 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
EU010174.1 gg_id:256804 Biogeography Singapore seawaters seawater clone C11 EU0101
DQ462579.1 gg_id:157321 Bizionia palithoae str. KMM 6214 DQ462
EU626681.1 gg_id:278512 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
FJ675153.1 gg_id:526117 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
EU328015.1 gg_id:279641 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU3280
EF688382.1 gg_id:244377 soil clone F6-94 EF6883
DQ167246.1 gg_id:139202 Costertonia jungdongjinensis str. KOPRI 13342 DQ167
EU236356.1 gg_id:292328 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91B11 EU2363
FJ882164.2 gg_id:541534 Aquimarina sp. str. antisso-27 FJ8821

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153.8	10104.2	5040.4	3670.8	4516.2	4587.3	5436.2	7767.5	6539.9	12256.5	4897.6
2441.3	10809.7	4458.6	3375.7	5508.5	7153.8	3729.4	7759.0	13163.3	9852.1	5679.7
2568.6	12837.4	6616.7	5046.7	5388.5	6678.6	5878.4	8943.7	9020.4	16373.4	6904.4
3527.1	13434.4	7141.1	5575.0	5971.5	7315.4	6410.0	9475.7	10157.7	16977.1	7583.0
20520.8	11295.3	7406.7	7775.2	7755.2	8353.2	8754.8	9251.2	13231.9	13912.1	10699.8
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1410.8	7106.4	7773.9	8010.1	8545.5	7414.1	8513.4	7804.3	11662.8	9177.8	6784.9
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52.8	320.7	352.8	285.5	503.2	239.2	463.9	468.2	142.7	84.9	212.3
78.5	2499.9	2181.8	1623.6	2298.1	2177.3	2002.3	2964.0	7353.1	2092.3	3310.0
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45.7	3073.8	2964.6	2903.8	3780.7	2446.3	4104.8	3256.8	1899.2	2667.5	3956.6
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213.3	707.2	1006.9	705.3	741.2	697.0	1093.1	959.6	532.1	625.8	485.0
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6860.0	4962.3	4625.8
7798.5	8429.0	6591.4
679.4	781.0	307.7
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23.3	38.3	29.6
4307.7	4609.1	1955.9
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DQ334630.1 gg_id:187349 Impact metals on sediments heavy metal polluted marine sediment clone HB2-37-2 DQ334
FJ675086.1 gg_id:515439 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface FJ6750
EF688358.1 gg_id:253871 soil clone F4-161 EF6883
EU246690.1 gg_id:249383 Zobellia aquimaris str. KMM 3942 EU246
DQ071071.1 gg_id:130971 marine surface water clone PB1.19 DQ071
EU801540.1 gg_id:332561 It's all ranking aquatic Chesapeake Bay MD clone 3C002857 EU801
AB255369.1 gg_id:212182 Sediminibacter furfurosus str. MAOS-86 AB255
GU118604.1 gg_id:588842 Threatened Corals Provide Microbial Habitats clone Mfav_B01 GU118
DQ334647.1 gg_id:175223 Impact metals on sediments heavy metal polluted marine sediment clone HB2-4-7 DQ334
EU735616.1 gg_id:341915 archaeal structures and pristine soils China oil contaminated soil Jidong Oilfield clone EU735
GU369876.1 gg_id:518109 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
EU003227.1 gg_id:255704 variation and endosymbiotic phenotypically sea urchin Strongylocentrotus intermedi EU003
EU236412.1 gg_id:287759 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92F1 EU236
GU369875.1 gg_id:529450 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AF354619.1 gg_id:34569 marine clone Arctic96AD-4 AF354
DQ530476.1 gg_id:168278 Arenibacter sp. str. gap-e-67 DQ530
DQ009109.1 gg_id:123870 bacterioplankton clone SPOTSDEC01_5m8 DQ009
GQ872423.1 gg_id:590020 Gaetbulibacter sp. str. M1-7 GQ872
AM040105.1 gg_id:147529 sandy sediments clone Sylt 9 AM040
DQ513012.1 gg_id:161548 Microbial life fluids ridge flank crustal fluid clone FS140-164B-02 DQ513
FJ203619.1 gg_id:306527 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata FJ2036
AY701469.1 gg_id:108543 Bacteroidetes clone GCDE08_K AY701
AM162577.1 gg_id:150733 and role capsules Sepia officinalis host egg clone 3SOMBO82 AM162
AF406541.1 gg_id:56043 bacterioplankton clone AEGEAN_179 AF406
AY682383.1 gg_id:100578 Mesophilibacter yeosuensis str. NC1-5 AY6823
FJ889648.1 gg_id:571155 Subsaxibacter sp. str. ZS4-19 FJ8896
EU888117.1 gg_id:321134 Muricauda sp. str. CL-SS4 EU888
EU804390.1 gg_id:314108 It's all ranking aquatic 250 miles Panama City clone 6C232304 EU804
EU464970.1 gg_id:298323 African elephant feces clone AFYEL_aaj66a04 EU464
AY654825.1 gg_id:104306 Oculina mucus isolate 88 AY6548
DQ395462.1 gg_id:156104 deep-sea octacoral clone ctg_CGOAA74 DQ395
DQ154838.1 gg_id:139216 Diel Migration Restructures Hypersaline Microbial Mat hypersaline microbial mat cl DQ154
AM292800.1 gg_id:179042 Cetobacillus canariasensis str. 454-2 AM292
EU287304.1 gg_id:251312 Pacific arctic surface sediment clone S26-4 EU287
FN433422.1 gg_id:551808 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN4334
AM286230.1 gg_id:164896 Tamlana sedimenti str. HST1-43 AM286
AB073564.2 gg_id:69822 Cytophaga sp. str. MBIC04693 AB0735
GQ349775.1 gg_id:585849 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AJ535222.1 gg_id:78228 marine sediment above hydrate ridge clone Hyd24-2-2 bacterium AJ5352
EU432414.1 gg_id:263786 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU432

67.4	7620.0	2024.5	877.2	1415.0	2155.9	773.1	9893.4	1534.3	13087.2	7916.8
181.0	1757.0	1731.4	1143.1	2154.1	2582.4	2365.9	2130.5	3121.0	3506.4	954.5
1330.4	4367.4	3468.7	2249.9	3380.9	5467.5	2532.7	3170.0	6625.5	5005.4	2376.8
5602.7	5938.4	5217.4	5018.8	5210.6	5835.2	5135.8	5663.0	8990.4	7256.2	5260.7
1480.9	3987.1	3012.4	3474.8	2961.5	3538.0	4932.8	3556.3	3857.7	4310.2	2707.8
72.4	383.5	368.5	270.9	285.1	571.8	393.2	462.6	84.6	450.1	266.0
50.6	2693.8	2011.0	1597.7	1879.9	2750.9	1884.5	2234.8	3183.4	2570.8	1737.5
55.0	92.8	107.2	122.0	161.2	103.4	128.3	219.7	46.9	45.6	501.3
1594.5	2459.7	2536.8	2939.4	3457.4	2756.1	2942.6	3752.9	2590.4	1971.6	2300.9
68.1	3392.3	4886.9	3500.3	4337.9	3887.8	4005.5	3806.1	3530.4	3585.2	2685.0
77.2	3515.2	5268.7	3174.7	3869.8	3786.8	3526.3	3992.2	4940.1	7487.9	2649.4
212.7	4672.5	5366.0	5052.0	5325.5	5478.0	4866.6	5587.1	6964.9	6922.9	5105.2
2106.1	5726.1	4414.4	4113.7	4629.0	4193.9	4450.1	4853.1	6326.3	4225.8	4253.1
77.5	583.1	730.4	342.2	374.8	742.1	276.2	713.4	1153.3	691.0	506.3
49.1	2214.1	1943.8	2147.3	1369.4	1535.3	613.8	1778.3	1309.2	1544.5	1909.1
1290.1	3428.3	4182.9	3424.5	4467.5	3587.0	5190.7	3884.3	4564.7	4001.7	3151.8
72.2	1477.7	2913.0	2114.2	1564.6	1905.2	1839.5	2698.6	1979.1	1902.8	961.1
22745.1	3678.1	3494.0	3398.9	3616.9	3821.6	3505.8	3882.4	6786.4	6376.7	4350.3
157.0	2285.5	2509.1	2504.0	2689.0	3353.6	2334.6	2757.4	3451.3	4080.8	3013.3
1211.2	3203.0	3695.6	2932.7	2349.6	3223.3	2432.4	3211.7	2298.4	3833.5	5136.9
96.3	1982.5	2698.3	2667.8	2929.0	1851.8	3694.5	2076.0	1673.8	1517.6	1369.1
370.7	3214.6	3772.2	4011.3	4757.6	3159.4	5786.3	4016.7	2270.4	652.6	2643.7
57.5	33.6	116.0	277.4	100.9	96.9	202.8	178.4	73.1	44.4	49.7
211.0	1975.0	2522.8	3005.8	3124.6	2925.1	2584.4	2429.1	1583.7	1178.9	1841.7
389.7	2798.3	2476.0	2693.7	2186.8	2051.4	2899.0	2496.6	3256.6	2805.3	1322.7
329.2	839.9	1204.0	758.0	536.0	1003.1	670.3	1147.8	971.0	833.2	617.2
85.0	3533.8	5935.9	5117.5	5611.5	4740.4	6252.1	6037.1	8157.2	3241.3	3145.8
94.3	1398.3	2456.7	2947.6	2704.5	2216.9	3128.6	2720.9	2062.6	1337.1	1719.6
1042.8	2841.9	1100.2	1256.1	2108.6	1802.1	1176.9	3254.1	1710.3	339.9	1735.5
281.7	4325.4	4071.1	3664.6	3904.8	3685.5	4200.0	4580.9	4313.7	5025.2	3771.8
55.3	527.5	443.3	537.8	421.0	653.1	318.4	737.2	1307.8	561.0	340.2
30.4	1162.9	870.5	752.6	755.4	1273.9	431.5	1249.9	1840.1	1717.2	776.4
63.8	53.5	89.8	71.6	48.0	37.6	95.8	58.6	56.0	35.3	58.4
49.2	567.2	417.5	300.3	610.6	1028.8	175.2	350.2	899.4	1354.8	153.3
2248.5	2285.6	2548.2	3123.4	3183.9	2837.9	4323.8	3135.6	2896.5	2107.3	2623.7
39.4	2931.5	2657.9	919.6	1327.1	2117.3	930.7	3259.3	2774.7	2599.8	1961.8
38.3	200.2	611.4	296.8	359.8	271.1	138.5	341.4	233.9	226.8	155.4
193.4	707.5	1123.1	1018.6	1139.1	986.6	1121.4	1087.8	512.2	646.5	544.9
50.1	1905.7	953.4	594.0	981.6	1538.0	1087.5	2367.2	2213.0	972.7	1721.0
1689.3	2107.7	2452.4	2176.9	1694.6	2318.6	1659.2	2715.7	1864.8	1429.4	1586.4
50.0	1898.3	2917.0	1394.9	1371.0	2002.6	1060.1	2427.8	1531.9	3503.4	1264.8

2161.6	1678.7	624.8
2941.9	2780.5	969.8
3484.7	4018.1	3596.5
5231.3	6886.7	4845.3
3955.7	4456.9	5303.1
931.4	244.0	93.9
1618.5	2698.8	1107.5
91.0	108.5	154.1
2772.5	2974.4	3805.6
5531.5	3880.1	4407.1
4887.3	2632.1	2127.8
5831.6	4580.1	2607.1
4060.1	3594.7	4231.4
1032.4	820.6	253.3
1131.4	842.9	578.0
3594.7	3492.6	2646.0
5182.0	1286.5	1122.5
3586.7	5117.9	3577.2
2555.7	2477.0	2823.0
3335.0	2441.6	1656.8
1388.9	1898.7	1289.1
4423.8	3303.9	5297.9
156.5	74.4	30.4
2178.5	1921.4	2797.5
1827.3	2523.4	2393.0
2274.4	1007.8	406.5
6017.9	4757.0	8321.7
3473.1	2330.4	4768.2
1321.0	1303.4	940.9
3838.2	4246.2	3839.2
491.7	931.6	485.8
1085.7	1274.1	671.0
51.5	50.0	41.6
606.1	685.6	120.0
2098.0	2734.4	2520.6
2495.9	1156.6	695.1
168.7	880.7	442.0
1269.7	1447.2	1095.0
743.4	578.5	345.9
2050.8	2086.1	1987.1
2634.9	1194.6	653.7

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FJ229467.1 gg_id:330503 Siderophores Neighboring Organisms Promote Growth intertidal sand biofilm FJ2294
EF644800.1 gg_id:288165 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6448
GU061590.1 gg_id:578211 and function microbial mesoscale eddy perturbations South China Sea clone CE2-5m GU061
AY035869.1 gg_id:36799 Cellulophaga sp. str. ACEM20 AY0358
EU626667.1 gg_id:278558 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
EU369165.1 gg_id:323406 libraries oyster shell clone MBFOS-06 EU3691
EF092235.1 gg_id:267240 Persistent Axinella corrugata Flavobacteriaceae clone B2706_G2 EF0922
AJ244698.1 gg_id:61974 Flavobacterium sp. str. V4.BS.09 = MM_2428 AJ2446
DQ269118.1 gg_id:182252 marine macro-alga surface clone DPC244 DQ269
AF170737.1 gg_id:2313 Gelidibacter sp. str. QSSC1-21 AF1707
EU805333.1 gg_id:328149 It's all ranking aquatic 250 miles Panama City clone 6C233336 EU8053
FJ674613.1 gg_id:531182 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
EU003220.1 gg_id:243895 variation and endosymbiotic phenotypically sea urchin Strongylocentrotus intermedi EU0032
GU118755.1 gg_id:554611 Threatened Corals Provide Microbial Habitats clone Mfra_N17 GU118
AY907775.1 gg_id:136893 identification picoplankton contrasting waters Arabian Sea water clone A712034 AY9077
EF208678.1 gg_id:199798 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.A(EF2086
AB294106.1 gg_id:552203 Sediminitalea flava str. Mhi-72 AB2941
FN433418.1 gg_id:581484 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN4334
FJ675151.1 gg_id:518527 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
EU021293.1 gg_id:252313 Tenacibaculum sp. str. D38BY EU0212
DQ361033.1 gg_id:147647 Flaviramulus basaltis str. H35 DQ361
AF427479.1 gg_id:49407 Cytophaga sp. str. 41-DBG2 AF4274
DQ486480.1 gg_id:217732 Muricauda sp. str. DG1233 DQ486
FM179907.1 gg_id:330803 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
EU443206.1 gg_id:270202 Maribacter sp. str. EM44 EU4432
FJ674419.1 gg_id:510951 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6744
FJ416110.1 gg_id:356976 sediments sediment station NEC5 Northern Bering Sea clone 089L88 FJ4161
AY922250.1 gg_id:113758 whalefall clone 131854 AY9222
AJ575643.1 gg_id:133240 Pibocella ulvae str. LMG 21972 AJ5756
FJ672842.1 gg_id:527499 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6728
GU369879.1 gg_id:521453 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
GU119445.1 gg_id:556808 Threatened Corals Provide Microbial Habitats reef water clone Reef_K14 GU119
EF108217.1 gg_id:190536 Aureimonas pelagi str. HTCC2652 EF1082
EU010132.1 gg_id:236858 Biogeography Singapore seawaters seawater clone A40 EU0101
EU394577.1 gg_id:353843 Coccolithophore bloom dynamics shape (NE-Atl) northern Bay Biscay pelagic particle EU3945
EU626698.1 gg_id:278872 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
AM745157.1 gg_id:299050 Impact oil er hydrocarbons on microbial and activity Gulf Mexico cold seep marine s AM745
EU328022.1 gg_id:278042 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU3280
FJ674317.1 gg_id:512308 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
AM292396.1 gg_id:336602 Microbial investigations anaerobic nitrate-dependent utilization toluene and n-hexa AM292
EU000243.1 gg_id:310620 Donghaeana dokdonensis str. KOPRI_22265 EU0002

78.9	864.0	1100.8	1126.5	996.6	745.5	1110.8	1204.2	858.3	650.8	667.4
64.5	2313.6	2368.0	2272.7	1369.1	2003.5	998.1	1967.9	2767.8	1086.2	1082.7
75.6	4421.7	5738.8	6387.8	4176.1	4871.3	4676.2	6276.0	4471.6	5410.6	4769.7
38.4	1455.8	1144.6	441.2	699.3	1109.9	343.5	1778.4	2153.1	2674.6	1352.9
3379.4	7706.2	6475.9	6369.9	7633.4	6567.0	6995.5	5957.2	9859.3	4676.2	6305.0
44.1	2561.9	2138.2	1323.7	2280.9	1827.8	1417.0	1975.8	4510.2	2703.8	1277.5
61.0	7067.4	6974.6	7598.1	8367.1	7354.8	7231.6	8224.0	7299.1	5173.9	9887.4
50.5	4263.5	5977.7	2505.0	3551.6	4257.8	2813.2	5837.5	4926.5	7690.1	3304.9
35.2	688.9	769.2	691.7	478.5	910.9	636.6	966.7	571.2	912.9	849.0
2227.5	5465.7	4924.3	5107.6	4832.1	5128.2	5409.4	4578.0	9101.2	4956.2	6193.7
77.8	1511.6	863.5	500.4	809.0	1772.1	580.9	1207.7	2112.7	915.6	529.7
39.4	10279.0	7594.0	4372.0	6437.1	8615.9	3878.2	6938.8	15363.7	8774.2	5984.3
8830.2	10413.3	8257.9	8071.0	9466.0	8936.0	8350.8	7769.3	14003.4	7406.1	9615.2
78.1	2496.1	2803.0	3057.6	3422.4	3292.0	3504.6	2926.2	2186.8	1699.2	2990.6
42.2	311.1	320.3	415.2	238.0	178.8	238.5	400.9	80.0	48.3	253.8
39.2	46.9	65.1	54.2	84.6	43.5	55.6	58.9	22.0	42.9	32.1
40.4	1279.1	328.5	235.4	351.4	1686.8	440.2	811.4	575.7	591.4	463.8
1235.5	1754.1	1299.1	1087.9	1238.7	1609.4	1455.9	1400.2	2323.9	2156.6	1505.1
3089.4	5877.1	5149.7	4450.1	4421.3	6871.4	3948.2	4557.5	8839.0	5412.5	4427.5
214.8	4849.4	4930.7	5202.0	4330.4	4774.0	3598.0	5181.5	4832.4	3059.0	4833.8
56.2	5210.0	5946.6	5128.3	5111.1	5597.3	4928.6	5889.9	9471.4	7133.4	4517.7
176.6	9388.5	9530.3	7974.4	6785.0	8537.6	4911.7	8756.0	13472.8	11418.9	8294.3
563.0	1709.6	2711.0	2331.6	2160.6	1610.7	2271.0	1915.9	968.1	718.7	1112.4
70.3	1640.9	1917.5	1566.3	2063.8	1852.8	1633.8	2540.9	2053.8	2273.8	1580.7
2702.3	4711.5	4488.9	5142.9	4586.1	4280.6	4551.4	4365.1	7432.9	7539.6	4951.4
243.4	5708.9	5430.6	4014.8	4785.2	8248.0	3738.7	4799.2	7903.4	6002.5	4364.8
113.3	6211.4	7311.2	6317.8	5395.8	7050.9	4807.7	6996.0	8981.9	5811.1	5720.0
141.5	4325.2	3693.5	3455.0	2928.7	3675.8	1716.4	4273.1	6571.8	2586.8	3721.0
37.7	133.6	244.3	223.2	167.6	118.9	117.1	137.4	66.8	58.3	108.1
465.1	12387.2	9453.3	8787.3	9833.7	10202.6	8221.4	8935.4	15103.6	10781.7	10012.5
78.4	717.7	1221.4	988.8	1352.8	1833.1	1404.0	788.7	504.1	577.6	426.1
500.2	2174.0	2690.3	2498.3	2197.5	2567.4	2125.1	3199.1	2482.4	2078.0	2107.3
50.3	114.1	139.1	119.1	145.6	92.9	112.2	115.6	85.5	197.6	75.0
59.9	1820.6	2764.2	1231.2	982.8	2045.9	956.7	2502.7	1603.2	2954.9	1597.3
1233.0	4875.5	4092.2	3763.8	5331.6	5567.6	3450.8	6147.7	6156.5	7356.5	5170.7
38.1	299.8	173.6	127.8	249.3	194.8	107.1	397.5	66.1	252.6	175.0
282.6	1995.4	1709.3	2060.7	1454.0	1494.2	1574.1	1665.6	1247.5	2363.6	1455.4
4561.5	4928.0	4292.9	4532.2	4669.5	4659.8	4944.3	5567.3	6371.4	6625.2	3440.6
31.6	3163.4	7286.9	2509.2	4940.9	2280.9	1802.4	1750.9	7070.2	2402.3	1091.3
40.0	2737.2	2709.2	1601.2	1852.5	3396.2	2272.5	2510.2	4164.2	2986.5	1622.9
43.1	110.7	141.5	149.3	52.1	119.1	239.9	260.5	36.4	23.3	116.5

1001.8	1241.7	1422.7
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5784.0	5531.3	7210.5
2136.0	782.5	1397.0
5926.9	4600.7	3351.3
5017.4	3951.4	2331.0
678.8	904.1	710.1
4191.3	6178.3	4854.5
608.2	505.1	109.8
7206.9	5322.4	4000.4
7482.0	6775.6	6982.2
2852.8	2011.0	1683.4
159.3	240.1	376.0
59.0	76.7	51.6
809.9	442.9	127.7
1184.3	1521.9	1782.0
4235.9	4906.9	3400.5
3770.2	3961.8	3293.2
7496.0	5106.2	3246.4
7654.0	6739.8	3825.7
2863.5	2559.7	4182.7
1707.2	1899.8	1218.2
4349.5	4277.2	4362.5
4255.3	5208.9	3979.1
5801.6	5451.0	3749.5
2804.1	2879.9	1887.6
520.7	94.3	580.0
8694.4	8731.8	7492.9
614.4	1220.2	1136.4
2520.6	2926.6	3281.7
136.0	219.5	207.0
1732.4	1760.0	963.0
5653.1	3904.2	2912.4
326.8	335.9	144.5
2074.3	1838.7	1283.8
5251.4	5280.2	3741.1
1996.3	3066.7	1052.4
2775.1	1870.9	1112.8
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FJ674394.1 gg_id:532230 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
AB377124.1 gg_id:569055 Coralibacter albidoflavus str. 04OKA-3-121 AB377
DQ009098.1 gg_id:125945 bacterioplankton clone SPOTSAPR01_5m30 DQ009
EU626601.1 gg_id:277989 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
AB244984.1 gg_id:161450 Flavobacterium sp. str. MS-3 AB244
DQ103641.1 gg_id:129412 hypersaline endoevaporitic microbial mat clone E6aH07 DQ103
DQ395624.1 gg_id:151414 deep-sea octacoral clone ctg_CGOF071 DQ395
FJ155065.1 gg_id:348807 seasonal fluctuation coastal Bohai Bay sequencing and RFLP soil clone D FJ1550
GQ848410.1 gg_id:567371 Microbial sediments vents along East Lau Spreading Centre deep sea hydrothermal GQ848
FJ360684.1 gg_id:362896 Gaetbulibacter sp. str. NH57N FJ3606
EF574626.1 gg_id:230145 site S25 near Coco's Island marine clone S25_970 EF5746
EU328020.1 gg_id:277873 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
EU799445.1 gg_id:323173 It's all ranking aquatic Newport Harbour RI clone 1C227044 EU799
EU050901.1 gg_id:249428 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_87 EU050
GQ348530.1 gg_id:581353 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EU491703.1 gg_id:268530 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
CU467431.1 gg_id:345202 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
EU369144.1 gg_id:345475 libraries oyster shell clone MBIOS-28 EU369
FJ675599.1 gg_id:515649 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6755
EU434366.1 gg_id:260191 Flavobacterium sp. str. a306 EU434
DQ351761.1 gg_id:148990 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FN433358.1 gg_id:585425 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN433
EU626707.1 gg_id:281940 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
GU118801.1 gg_id:586182 Threatened Corals Provide Microbial Habitats clone Mfra_M18 GU118
U85886.1 gg_id:2403 marine psychrophile str. ACAM210 U8588
AF286039.1 gg_id:35713 mercury and PCB contaminated saltmarsh sediment clone LCP-72 LCP-72 AF286
DQ070805.1 gg_id:146853 Prokaryotic Structures Seafloor Basalts Varying Age and Juan de Fuca Ridge basalt gl DQ070
DQ514301.1 gg_id:160581 Flexibacter aggregans str. BSs20185 DQ514
AF468407.1 gg_id:80764 Arctic sea ice ARK10007 AF468
AJ704703.1 gg_id:109300 marine sediment clone HMMVCen-36 AJ7047
EU283513.1 gg_id:279132 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1530 EU283
AY936177.1 gg_id:113358 Flavobacteriaceae clone F1C24F AY936
AM945545.1 gg_id:267601 Pibocella sp. MOLA:312 AM945
AF406550.1 gg_id:60625 bacterioplankton clone AEGEAN_129 AF406
AF530135.1 gg_id:61127 Polaribacter sp. str. MGP-9 AF530
GQ348250.1 gg_id:581424 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
FJ416125.1 gg_id:361177 sediments sediment station NEC5 Northern Bering Sea clone 117O18 FJ4161
EU626639.1 gg_id:279125 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU626
FJ675281.1 gg_id:516393 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6752
EF016467.1 gg_id:176313 Near real-time autonomous detection marine on coastal mooring Monterey Bay Calif EF0164
AM259825.1 gg_id:211011 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-2-81 AM259

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38.8	433.0	642.6	670.7	634.5	734.4	755.7	643.9	455.8	218.7	451.3
52.9	3952.7	2967.2	2139.0	2483.8	3100.9	2988.1	2777.4	4400.5	3152.1	1720.4
7067.6	9684.3	8097.0	7593.8	9598.6	8490.2	8390.0	7267.9	13452.4	7923.1	8334.6
31.6	189.3	173.7	124.8	151.9	201.5	124.1	97.7	79.4	89.2	64.6
1041.1	2934.1	1968.4	1735.3	1886.2	2424.6	1502.8	2074.3	4335.4	2475.2	1953.2
3380.9	7117.8	5916.4	6407.0	6019.5	6416.3	6475.2	6416.7	8430.3	5287.2	6452.1
110.6	4038.9	5115.8	4663.6	3868.7	4149.1	4036.2	4813.2	4057.0	4148.2	4336.3
344.7	3259.1	4530.1	4633.7	4980.3	4559.1	5862.2	4192.4	3860.6	3020.9	3037.5
49.9	582.0	750.6	793.8	1568.3	669.7	514.9	670.6	571.3	224.8	480.6
42.8	91.6	394.8	262.7	271.7	65.4	181.4	384.8	338.9	298.2	226.2
54.6	1320.3	1373.7	793.8	1620.0	1602.0	1452.3	1705.9	2723.9	1689.6	974.5
148.8	3256.2	3836.2	3283.0	2772.3	3819.9	2417.8	3690.2	3475.1	4495.6	2654.7
448.7	1992.6	2002.3	1553.6	1607.5	2166.1	1409.5	1569.2	2585.2	1113.4	1924.5
46.4	614.5	696.1	586.5	728.8	780.5	957.8	633.1	189.7	573.1	415.0
107.0	897.8	1276.5	1225.7	1104.9	1397.1	1654.5	1404.1	1089.8	674.9	863.1
2668.4	11599.4	8156.6	9505.9	8685.4	10411.0	9638.3	8589.5	15074.6	10962.4	9528.5
56.4	2005.9	4035.2	2449.2	2657.9	2622.9	2401.9	2392.7	1310.2	2085.1	1421.7
17001.8	11057.3	9921.2	9875.6	11196.8	11621.0	10514.5	11163.1	19552.6	14784.9	12277.9
39.6	117.5	81.2	65.6	165.8	82.3	47.2	254.0	84.6	293.9	219.6
503.4	1714.3	1967.4	1395.8	1787.2	1606.3	1674.4	1538.8	2447.7	2106.4	1849.5
198.0	3807.4	3306.0	1104.3	3669.4	3326.5	4145.1	4100.2	5670.4	5571.4	4786.6
132.6	4984.3	4759.1	4519.6	4036.3	5146.2	2509.8	4677.7	4967.6	4883.5	4423.7
2336.1	1038.2	930.5	685.5	985.6	1058.8	964.1	891.0	1226.2	987.6	577.2
48.6	86.8	100.3	88.2	68.4	78.1	61.2	119.5	102.6	118.0	59.4
2957.3	7963.0	7500.9	7173.5	6498.0	7696.9	5891.7	8240.6	12326.1	7893.1	7667.7
28.2	2773.8	2410.1	2031.3	1780.5	2124.7	1323.2	3378.3	3792.1	2045.6	2207.8
46.0	734.2	869.5	537.0	834.0	857.1	663.1	706.3	1334.4	1011.5	284.9
1360.3	1791.8	2481.2	2281.3	1982.0	1519.7	2697.3	2216.7	2214.9	1848.6	2472.9
24240.6	7201.5	6804.0	5535.4	6879.1	6205.2	6432.2	6585.4	10352.8	13089.6	8685.8
212.0	2381.9	2149.5	2528.0	1748.1	2160.3	1762.5	2535.4	4330.1	2995.3	1498.4
72.2	1130.2	1410.4	1517.1	1151.3	1070.8	1582.1	1352.6	857.5	1129.4	941.0
64.9	429.1	669.0	776.0	659.9	512.0	429.5	682.5	246.8	270.5	510.0
777.4	808.4	1217.6	758.8	971.4	1068.3	659.1	1120.5	766.9	1253.2	489.8
41.8	287.9	423.7	325.1	185.5	324.3	245.1	352.8	284.1	270.0	209.1
77.2	3282.3	3499.4	2959.5	3989.7	3453.0	3232.8	4638.0	5543.8	5727.8	3990.7
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49.0	349.0	1404.2	1160.9	563.5	501.4	2360.1	1110.5	280.4	415.1	619.7
817.6	8416.6	6411.6	4928.9	6036.9	9000.3	4708.9	6134.2	10255.9	6264.4	5100.2
760.2	6487.0	6126.1	5191.6	4912.7	5802.4	6804.8	5002.4	8431.3	5596.8	5149.1
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1818.2	2015.2	1546.4
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195.6	291.5	270.6
1733.1	2873.7	1268.7
7144.6	4796.0	5673.0
4429.1	4313.8	2763.3
4066.8	4952.9	3994.6
503.9	656.9	1060.0
307.0	770.4	126.0
1348.7	898.3	767.4
3322.7	3181.0	2940.2
1365.2	1931.7	1014.6
713.6	546.5	395.9
1527.9	993.3	1468.7
7717.4	8103.1	7913.0
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11192.5	11605.8	8483.9
200.5	82.4	102.6
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3157.5	2874.0	2767.7
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764.3	1447.4	1419.3
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6432.1	6079.9	5319.6
2469.9	2667.7	1460.5
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3539.8	2075.7	1463.9
6501.5	7645.5	8179.9
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592.7	982.4	677.0
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271.5	446.5	245.0
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EF108219.1 gg_id:192374 Gelidibacter sp. str. IMCC1914 EF1082
EU581699.1 gg_id:262661 Flavobacteriaceae MEBiC05063T marine sponge Geomun-Island South Korea EU581
FJ196015.1 gg_id:340255 Donghaeana sp. str. ZS1-13 FJ1960
EF092186.1 gg_id:270683 Persistent Axinella corrugata Flavobacteriaceae clone Ax26_E2 EF0921
FJ595484.1 gg_id:543469 Winogradskyella sp. str. 022-2-26 FJ5954
DQ002871.1 gg_id:118184 Gramella portivictoriae str. UST040801-001 DQ002
AY162121.1 gg_id:136017 Cultivating Sargasso Sea clone GMD15A07 AY162
EF123625.1 gg_id:249295 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1236
GQ249588.1 gg_id:591430 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer cl GQ249
DQ334648.1 gg_id:175076 Impact metals on sediments heavy metal polluted marine sediment clone HB2-6-7 DQ334
AY694003.1 gg_id:102333 Calefactosor algoritergicola str. APA-1 AY694
EU925905.1 gg_id:353655 sediments sediment station DBS1 northern Bering Sea clone 131H30 EU925
AF449259.1 gg_id:61850 Riftia pachyptila's tube clone R103-B20 AF449
FJ791926.1 gg_id:537409 Unexpectedly archaeal species shift between rare and dominant over thousand year FJ7919
FJ675178.1 gg_id:520926 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6751
AY280421.1 gg_id:100925 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
EF157086.1 gg_id:250910 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF157
FJ825844.1 gg_id:569124 Succession during spring Sea filtered surface sea water period diatom bloom Yel Sea; FJ8258
EU491694.1 gg_id:267629 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ403056.1 gg_id:361407 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030
EU491713.1 gg_id:261907 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
AJ318193.1 gg_id:20776 Waste-gas biofilter clone BIvi22 AJ3181
EU236427.1 gg_id:293136 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92H7 EU2364
AB084261.1 gg_id:142361 Zobellia sp. str. KMM 3531 AB084
FJ675009.1 gg_id:517967 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6750
GU118746.1 gg_id:592672 Threatened Corals Provide Microbial Habitats clone Mfra_E01 GU118
GU118352.1 gg_id:540288 Threatened Corals Provide Microbial Habitats clone Gven_L09 GU118
EU465137.1 gg_id:295672 African elephant feces clone AFYEL_aaj68f01 EU465
AB362216.1 gg_id:324561 Leptobacterium flavescens str. 04PA2 Co4-8B AB362
EU626675.1 gg_id:277680 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
EU419942.1 gg_id:266863 Formosa sp. str. RW55 EU4199
EU021217.2 gg_id:254152 Bizionia argentinensis str. JUB59 EU0212
AY654759.1 gg_id:105219 Oculina mucus isolate 110 AY6547
EF687174.1 gg_id:286813 Biogeochemistry iron- and sulfur-precipitating microbial mats (Nile Mediterranean) ir EF6871
EF572248.1 gg_id:228698 Coco's Island site 23 marine clone S23_347 EF5722
EF108214.1 gg_id:179639 Croceimarina litoralis str. IMCC1993 EF1082
EU369134.1 gg_id:324541 libraries oyster shell clone MBIOS-18 EU369
AB255696.1 gg_id:186864 Orabacterium aurantiaca str. HSF3 AB2556
GU233518.1 gg_id:578850 Kordia sp. str. IMCC1412 GU233
GQ348644.1 gg_id:583466 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ348
EU443204.1 gg_id:265965 Gaetbulibacter sp. str. EM39 EU443

58.2	3511.6	3311.8	2841.4	2762.1	3161.6	2165.1	3816.1	4735.0	2612.8	2897.9
42.5	4129.2	4111.1	3595.3	3629.5	4137.9	3897.4	3766.5	7444.3	3810.0	3454.5
30.6	81.6	122.6	154.3	140.3	97.6	162.5	116.3	82.2	112.8	52.7
10908.0	12908.5	12527.0	12937.3	13904.0	11835.4	13949.7	11824.0	15807.2	10223.9	11928.3
94.0	929.0	871.8	1023.5	932.2	743.9	874.9	1364.8	1331.7	422.6	820.8
37.4	2090.6	4124.8	3093.9	1439.4	1945.3	3082.9	2937.8	1886.6	2555.6	2740.6
877.5	2480.5	3131.9	2432.4	3410.5	2598.4	2955.8	2661.7	3017.6	2745.3	2081.8
355.5	3992.3	4501.8	4661.5	3953.1	4323.8	4961.8	4133.5	5201.1	3330.9	3875.7
2965.8	7154.8	5879.5	4119.5	3083.6	6309.3	2846.5	4309.3	9061.6	3450.3	6415.6
3541.7	9121.8	7641.6	6909.9	7401.5	8294.9	7185.9	8250.3	11722.3	10456.1	9404.1
51.7	3975.3	3008.1	3048.9	3473.8	3977.3	1360.5	5025.6	2832.4	3842.6	4636.3
1297.9	5390.7	5622.2	6106.8	5781.8	5162.2	6799.0	5748.1	6518.9	5814.4	5085.2
95.8	656.4	580.3	974.3	982.6	619.0	1328.0	810.7	411.4	251.7	396.6
97.4	651.8	990.7	1104.3	456.5	890.8	651.1	1136.7	353.5	143.2	790.9
1381.6	9244.1	7778.2	7154.0	7774.3	9157.2	6732.2	9264.1	12804.7	11974.6	11203.7
82.1	1734.5	2125.8	2221.7	2456.5	1884.6	3485.4	2373.0	1049.3	1434.8	1743.5
142.1	1594.0	2839.5	1765.1	2501.9	1766.6	1455.2	1616.5	1311.1	1346.8	1093.6
7934.7	6381.0	7146.8	7341.7	7161.9	6858.7	5621.5	8118.7	7621.8	7575.9	6884.2
69.3	6395.2	3707.0	1874.1	4853.0	4982.0	4731.9	3777.6	8815.9	4997.7	4337.1
43.4	827.5	1094.5	1215.4	1067.9	1118.1	1098.4	1776.8	338.9	1867.3	789.5
1782.4	3779.7	4734.9	5782.9	3175.6	3051.9	3507.9	5188.3	4295.4	3096.3	4495.8
56.9	112.9	85.4	74.3	93.5	107.5	84.4	70.8	42.1	45.7	48.5
1355.1	1264.1	1390.5	1211.2	1201.3	1310.8	1374.2	1205.9	1521.6	1330.5	794.5
53.0	970.6	1073.8	1256.2	1045.6	1401.5	1137.9	1443.0	1429.6	522.1	811.1
82.9	3662.7	5815.1	2984.8	4600.5	3158.1	2831.6	2768.1	6619.7	3783.2	2539.2
11231.5	7787.9	7460.3	7742.9	8710.0	8145.3	8691.3	10382.3	10733.1	4825.7	10907.2
104.7	3203.5	3103.4	2927.7	4053.4	3791.5	3974.4	3464.5	4652.0	3626.1	3886.1
108.6	2466.3	2068.6	1351.8	1700.1	2679.1	1398.2	1827.7	2464.0	1667.5	1258.8
262.0	5193.0	5185.4	4154.6	4816.0	4918.9	3821.7	6333.1	5935.3	6685.0	5253.0
3376.2	10119.1	8832.5	8938.9	10237.5	8738.0	9601.8	7935.6	14132.6	7454.2	10904.4
54.0	141.1	214.2	200.1	259.3	255.8	144.7	176.6	115.9	92.3	114.7
56.0	4358.2	5001.3	4591.5	2702.5	3097.6	3026.9	5090.8	5561.8	3577.2	3687.4
23.3	1202.5	1413.5	880.7	1160.2	978.6	1569.9	1247.5	1022.5	542.6	766.0
55.2	167.0	282.1	179.3	65.1	99.4	145.6	87.7	43.2	45.3	67.4
43.0	620.9	1583.2	680.3	1028.8	1077.5	750.7	1020.2	1060.3	2139.4	445.8
141.1	1471.7	1442.5	1338.3	1854.5	1235.8	1809.0	1719.5	1243.3	912.1	753.7
139.8	1681.6	2284.3	1283.2	3009.2	2082.0	1774.3	2788.8	1621.5	4978.4	1849.2
54.9	1408.1	2255.5	1718.6	1360.3	1773.8	1513.3	2300.7	1837.4	730.3	1703.0
28.5	2261.5	1886.7	1168.6	1684.3	2497.8	1272.3	2065.7	2689.1	2141.1	1562.7
104.6	2659.7	2593.2	2228.9	1653.2	2668.8	2031.6	2237.3	4790.8	2883.9	2588.6
51.2	168.1	193.3	205.0	192.8	172.5	70.8	334.0	402.0	273.2	356.2

3870.2	2407.3	1664.1
4928.0	3645.6	2604.6
94.9	405.4	62.4
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1297.8	1103.3	1822.2
2380.9	2583.1	1390.1
1928.7	3681.0	2346.8
5163.7	4212.9	7509.9
3187.9	3873.8	2081.4
7318.9	8474.1	4796.5
3709.8	2063.3	1109.9
5332.4	5017.6	4435.5
617.2	632.8	1546.6
815.9	970.9	455.9
7917.7	7711.2	6125.7
1705.5	1826.5	3182.0
2566.5	2267.4	1185.5
7386.1	6893.8	5718.8
3778.0	3182.3	3431.0
1142.8	947.3	4789.9
2952.7	3214.6	2873.2
94.7	100.2	89.8
365.5	1750.5	1159.2
1384.4	1331.3	2883.2
2578.4	3471.6	3037.7
8271.4	7766.9	7357.0
2556.8	2366.2	1640.1
1858.1	1517.2	1268.4
5905.6	5316.4	4697.4
7784.8	6745.0	8213.3
157.7	308.0	105.1
3788.3	2276.0	1929.7
1084.2	999.7	801.5
98.6	131.8	106.1
1051.0	1350.5	437.2
1473.6	1242.3	1219.5
2323.0	2037.3	1013.2
1965.1	2092.7	596.0
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1974.2	2058.5	2074.8
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FJ674701.1 gg_id:530399 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
FJ744807.1 gg_id:573297 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
EU290161.1 gg_id:237287 Tenacibaculum marinus str. A31 EU290
AM259823.1 gg_id:212421 Spatial sponge- Mediterranean Tethya aurantium sponge endosome clone TAI-8-51 AM259
GQ452872.1 gg_id:586530 Biodiversity planktonic surface water Northern Bering Sea clone s3 GQ452
EF573073.1 gg_id:231756 Coco's Island site 23 marine clone S23_1172 EF5730
EF571947.1 gg_id:232534 Coco's Island site 23 marine clone S23_46 EF5719
AB073573.2 gg_id:66035 Cytophaga sp. I-545 AB0735
FJ203005.1 gg_id:344393 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2030
GQ331112.1 gg_id:556650 Formosa sp. str. EM151 GQ331
DQ001321.1 gg_id:126861 Psychroserpens mesophilus str. KOPRI 13650 DQ001
GU119362.1 gg_id:576486 Threatened Corals Provide Microbial Habitats reef water clone Reef_G01 GU119
EU512921.1 gg_id:260066 Maribacter sp. str. CL-AP4 EU5129
FM179910.1 gg_id:311773 Biogeochemical processes microbial Gullfaks and Tommeliten methane seeps (Nortl FM179
EU432436.1 gg_id:274302 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU4324
AB294107.1 gg_id:337128 Fulvibacter tottoriensis str. MTT-39 AB2941
DQ015841.1 gg_id:140556 Antarctic lake water clone WLB13-197 DQ015
EU287913.1 gg_id:237293 Lutaonella thermophilus str. CC-MHSW-2 EU2879
AY862745.2 gg_id:160453 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon AY8627
FJ674683.1 gg_id:512822 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
FJ674780.1 gg_id:519316 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
EU287319.1 gg_id:243681 Pacific arctic surface sediment clone S26-19 EU2873
AY883939.1 gg_id:112379 Gaetbulibacter saemankumensis str. SMK-45 AY8839
DQ191182.1 gg_id:139623 Muricauda sp. str. DOKDO 023 DQ191
EU328155.1 gg_id:244757 Formosa crassostrea str. KO3 EU3281
AM990891.1 gg_id:278231 Structure and functions coastal NW Mediterranean ecosystem sea water AM990
AB057592.1 gg_id:18143 Flavobacteriaceae str. SA-0082 AB0575
DQ376560.1 gg_id:154706 Microbial ecology removing phosphate wastewater EBPR process aerobic sequencin DQ376
AY162110.1 gg_id:135966 Cultivating Sargasso Sea clone GMD16C04 AY1621
EU626686.1 gg_id:279532 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
FJ671486.1 gg_id:521135 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6714
GQ009813.1 gg_id:499853 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EU050891.1 gg_id:244501 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_12 EU0508
AM180741.1 gg_id:145434 Cellulophaga sp. UL16 AM180
EU564844.1 gg_id:263680 Muricauda sp. str. CC-HSB-11 EU5648
EU735708.1 gg_id:332107 Biological Arsenic Remediation Project Groundwater Aquifer soil clone 1As26 EU7357
AY922244.1 gg_id:113641 whalefall clone 131828 AY9222
FJ202207.1 gg_id:305797 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
FJ497566.1 gg_id:579831 Microbial Ecology Fe-rich Mats and Basaltic Rock American Samoa Vailulu'u Seamoun FJ4975
EU287015.1 gg_id:251033 Pacific arctic surface sediment clone B78-51 EU2870
FJ744983.1 gg_id:554802 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7449

937.8	5074.1	5225.2	4232.6	5411.1	6587.5	4736.1	5884.6	6238.0	5522.9	4417.8
148.8	295.3	284.4	163.5	338.9	249.4	462.1	284.9	169.0	87.0	186.7
482.9	2019.4	1803.6	1768.6	1880.1	1670.7	2019.5	1868.0	2408.2	2517.8	1872.5
7973.5	6959.3	6060.0	7304.1	6498.6	6170.9	7431.2	5895.1	10178.9	9009.5	6832.8
70.2	590.0	611.7	294.0	363.2	842.5	537.2	728.6	1108.1	894.0	620.0
50.7	3898.4	3122.4	2039.4	3150.0	4020.4	2251.1	3786.0	5249.6	3685.7	2644.4
71.0	2070.7	3884.0	2007.0	1274.0	2126.6	1258.4	2868.7	2715.6	2822.2	2400.2
54.9	190.6	161.2	152.6	82.6	154.6	141.6	131.9	137.0	104.3	217.8
1634.4	4793.3	4272.3	4999.1	4202.7	4354.2	5692.7	4074.1	7205.5	6125.3	4637.2
503.9	2030.0	1950.4	1514.5	1670.3	2719.0	2071.5	1861.2	1744.5	2916.4	1616.8
43.5	2343.5	2697.2	2159.2	2209.4	1888.3	2115.3	2617.1	4415.5	1982.8	1518.6
141.8	4319.6	4068.6	3428.5	3143.4	4157.7	2728.2	4208.8	5442.5	3861.7	3407.8
34.2	823.5	1561.6	1711.0	1589.7	1045.4	1055.1	1654.9	1602.1	1112.0	792.9
37.7	618.7	1521.0	1745.1	1587.6	772.0	2632.2	1125.5	540.5	573.1	689.3
1486.8	3875.1	3884.3	3208.6	3440.8	4208.0	3316.7	4120.0	5844.7	4260.2	3634.4
821.5	2017.0	2325.3	1971.4	1762.5	2023.5	2080.1	2897.3	1788.1	1629.6	1952.6
45.0	125.4	216.8	65.2	103.0	113.0	48.3	117.0	182.0	59.6	62.6
167.9	5290.4	4851.8	5088.1	6552.7	5599.6	6061.7	6297.5	5130.1	5525.1	5984.7
449.6	5114.2	4274.5	5316.6	5141.2	4593.2	5091.2	4405.9	5256.6	4057.7	3755.1
263.2	8310.4	8123.5	6517.0	7343.9	7804.9	5649.7	6621.7	12991.0	7875.6	6278.8
67.5	3330.5	5857.1	2637.6	4449.5	3739.8	2200.0	2219.4	7510.2	2716.6	1779.4
1190.6	5802.9	7219.3	6757.4	7942.6	6695.0	6042.6	6056.6	11654.2	8061.4	5634.9
28.8	165.0	210.3	84.0	155.0	183.9	80.8	132.6	256.7	464.6	75.1
54.6	57.3	67.6	53.7	69.6	53.6	51.4	52.2	42.4	34.9	35.1
80.0	854.1	1813.3	815.3	1273.6	952.6	878.8	1116.7	637.7	1794.6	368.4
221.0	6374.5	6089.5	5483.0	6985.3	6269.4	6421.3	6021.3	8008.0	7135.8	5882.0
64.8	1202.1	1669.7	1656.4	1476.5	1207.9	1199.3	1964.1	1862.3	534.7	1005.0
58.5	99.0	163.7	81.2	133.1	109.7	99.8	193.5	187.2	153.2	131.2
28.5	25.6	25.2	18.7	22.3	28.7	23.8	19.5	25.9	17.0	23.7
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277.3	1410.4	1453.8	1090.1	1546.5	1711.6	1498.9	1641.7	1883.6	1510.0	919.0
53.1	96.7	162.6	122.0	92.4	106.4	262.4	183.3	53.0	29.1	75.5
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56.0	1550.1	1984.1	1116.4	1534.1	1925.9	1340.1	1633.3	1027.2	797.5	1358.1
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215.4	383.8	266.5
1935.8	1896.7	1917.5
5597.6	6658.4	6861.5
541.0	539.8	381.9
3407.0	3942.4	1591.6
2126.5	1738.5	991.4
189.5	281.5	298.3
4298.3	4355.9	4418.0
2475.4	1679.2	1173.0
3824.1	1051.7	2846.4
4229.2	3477.8	2888.2
2171.0	1442.1	1081.1
587.6	965.1	595.3
3345.6	3138.3	2223.1
2316.3	1829.1	1312.3
93.3	382.6	54.6
5686.3	4301.6	6749.8
3688.2	4957.6	4348.5
7176.4	7199.6	4765.9
2441.8	3167.6	2153.3
6982.7	6606.7	4227.9
132.0	417.2	48.2
73.9	52.9	47.5
2101.9	883.3	440.7
5999.3	5886.1	4648.3
1222.9	1309.9	1170.1
283.8	280.0	82.0
21.0	21.7	17.5
5605.5	4905.0	6687.5
5430.9	4395.9	3547.2
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331.3	163.8	52.0
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797.5	716.7	368.9
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FJ671847.1 gg_id:526200 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6718
EU236375.1 gg_id:301867 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91G5 EU2363
GU118047.1 gg_id:586123 Threatened Corals Provide Microbial Habitats clone Apal_M01 GU118
AM259875.1 gg_id:206791 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-74 AM259
FJ624452.1 gg_id:555318 Lau Basin hydrothermal vent sediment clone DY2-180 FJ6244
EU050894.1 gg_id:245177 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_15 EU0508
AB073561.2 gg_id:100504 Cytophaga sp. I-2034 AB0735
AY372917.1 gg_id:144373 marine sponge Pseudoceratina clavata symbiont AY3729
AY372916.1 gg_id:141336 marine sponge Rhabdastrella globostellata symbiont AY3729
AB362815.1 gg_id:552208 Xanthobacillum maris str. Se5-09-15 AB3628
FJ674994.1 gg_id:514212 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6749
GU118571.1 gg_id:563278 Threatened Corals Provide Microbial Habitats clone Mfav_G21 GU118
EF100858.1 gg_id:177653 marine ability degrade oil pollutant Bohai bay Marine CON-A2 EF1008
EF554365.1 gg_id:226929 Antarcticimonas flava str. IMCC3175 EF5543
DQ351797.1 gg_id:148831 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ716956.1 gg_id:539891 L. Bioturbated Mesocosm marine sediment Cullercoats Northumberland United Kingc FJ7169
AM945558.1 gg_id:260584 Winogradskyella sp. MOLA:326 AM945
AB261012.1 gg_id:165728 Marinoxanthomonas ophiurae str. KMM 3046 AB2610
DQ351766.1 gg_id:145981 Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surfac DQ351
FJ202911.1 gg_id:329636 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2029
EF125443.1 gg_id:191828 mangrove soil clone MSB-2E3 EF1254
DQ064789.1 gg_id:130810 Stenothermobacter spongiae str. UST030701-156 DQ064
EU464885.1 gg_id:291250 Hartmann's mountain zebra feces clone AFZEB_aaj72e02 EU4648
EU626642.1 gg_id:278244 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6266
FN433333.1 gg_id:547261 patterns and flavobacterial clades contrasting masses North Atlantic marine water cl FN4333
FJ674283.1 gg_id:530154 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6742
FJ203427.1 gg_id:330755 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2034
EU287285.1 gg_id:243677 Pacific arctic surface sediment clone S11-102 EU2872
AY285940.1 gg_id:87495 Flavobacteriaceae G11A1 AY2859
EU626567.1 gg_id:278602 variation and endosymbiotic phenotypically- sea urchin Strongylocentrotus intermec EU6265
AB017597.1 gg_id:2462 Flavobacterium sp. str. 5N-3 AB0175
AM292405.1 gg_id:308348 Microbial investigations anaerobic nitrate-dependent utilization toluene and n-hexa AM292
EU722656.1 gg_id:346435 Microbial athalassohaline Tirez lagoon (Spain) sediment clone SB80 EU7226
AJ567549.1 gg_id:89871 deep-sea sediment clone MBMPE34 AJ5675
EF123558.1 gg_id:250190 Microbial disease microbial mats on Siderastrea siderea three regions wider Caribbea EF1235
DQ372851.1 gg_id:154027 Pirellula and OM43 are among dominant lineages identified Oregon coast diatom bl DQ372
AB073589.2 gg_id:102971 Cytophaga sp. I-1856 AB0735
FJ674609.1 gg_id:520214 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6746
AY693998.1 gg_id:105007 Subsaximicrobium saxinquilinus str. Y4-5 AY6939
FJ403077.1 gg_id:362103 Disease- changes healthy and diseased colonies Caribbean coral Montastrea faveolat FJ4030

47.1	1777.0	1187.1	960.3	2639.8	2059.2	1264.7	2961.2	5891.6	2936.8	3075.5
4222.5	12210.7	11162.8	9196.1	10303.4	11271.1	10597.6	9922.5	19474.7	13929.7	12138.6
68.4	2142.5	2870.4	3124.0	4041.9	2391.9	3553.9	2666.0	809.5	1044.2	3519.5
2770.4	804.4	986.8	817.0	538.1	845.7	871.1	791.7	934.0	1017.7	633.9
36.0	75.6	114.5	120.1	82.1	97.6	64.9	89.5	59.9	202.7	74.3
1489.4	7618.2	6869.6	5712.2	5630.7	7100.0	5542.0	6097.0	9934.2	5160.7	6834.8
85.5	3373.7	1619.6	1163.9	1938.9	2775.3	1252.4	2556.7	4299.7	2225.2	1815.1
29.6	127.4	256.5	276.5	288.6	230.0	478.6	178.1	74.7	42.7	107.9
5271.3	7333.0	7625.3	8452.2	7894.9	8003.4	8146.5	7413.9	7997.3	6671.5	7722.5
959.6	6231.7	6423.2	5725.6	6313.4	6636.9	5936.5	5959.6	8909.8	8134.5	5734.7
36.8	159.3	565.4	242.3	287.5	163.5	140.5	275.5	95.5	100.6	113.8
416.2	10068.8	7610.2	6504.5	8437.6	9827.4	7573.1	9511.2	14731.4	10936.3	10155.1
36.9	559.1	807.4	940.1	983.7	648.1	1619.9	452.4	257.0	797.1	383.8
52.9	910.9	1660.6	1965.9	1854.6	1294.1	1650.5	1467.7	629.8	377.0	562.2
62.4	48.5	65.0	63.2	61.5	37.5	75.4	39.1	30.9	61.5	55.3
29.9	32.4	63.4	43.9	64.8	74.5	69.8	81.7	53.6	45.5	26.9
56.5	1782.1	1649.3	1851.9	2206.4	1932.6	2442.8	2511.5	1261.3	1464.5	1624.3
58.6	2429.0	2673.1	1890.5	1964.0	1778.0	1676.9	2685.0	4565.9	1990.8	1603.8
30.6	403.2	528.3	480.9	649.7	284.6	774.9	410.4	289.9	698.7	318.8
464.3	2687.7	3116.4	2788.7	2501.3	3283.4	2671.2	3170.0	3930.9	3389.0	3399.9
52.4	589.1	541.0	418.8	585.3	415.8	603.7	499.1	527.3	734.2	319.5
1730.5	5417.9	5305.7	4444.4	4164.2	4784.9	4684.4	4365.3	6668.3	3603.2	5858.4
49.1	34.0	62.5	65.7	31.1	35.3	21.1	58.2	29.0	27.3	46.6
222.1	3090.0	2518.2	1791.0	1964.0	3477.1	1492.3	2818.5	6128.2	3194.7	2312.0
26.7	946.3	648.5	516.6	510.0	767.6	396.7	1312.0	505.9	1162.9	898.5
2397.8	1527.4	1715.5	1709.3	1858.4	1769.6	2293.4	1642.2	2297.6	1618.3	1298.2
1556.7	3674.1	5073.5	2667.9	4154.1	3316.3	2403.0	2272.6	5142.4	2637.4	1962.8
3074.6	6461.4	5684.9	4637.0	5161.1	5786.2	5133.7	6093.1	7724.0	6556.1	4706.1
143.0	4765.7	4646.8	2581.0	4570.2	4135.5	4007.6	4454.8	8381.0	3799.6	2973.9
82.3	2747.9	2133.7	1552.4	1025.2	2111.3	1887.2	2487.2	4217.5	1970.4	1126.3
114.7	3038.2	2820.4	2901.5	2794.2	2515.6	1965.7	3753.5	1498.6	2631.2	2893.3
440.7	207.1	277.2	204.9	292.9	261.5	219.9	265.2	466.5	375.7	222.5
1028.2	5115.9	3660.1	2813.8	2884.0	3137.7	2971.2	2956.8	5064.6	2656.2	2293.6
50.9	3674.6	3259.5	1120.6	3007.7	3377.3	3107.7	3251.2	5471.6	4492.5	4425.9
34.9	1026.8	1062.2	628.2	980.9	903.2	756.1	1341.3	1803.0	1239.6	665.2
34.8	2106.4	2247.1	1227.7	1347.7	1952.6	1259.4	1836.3	1282.9	1704.5	1112.0
300.0	1992.4	2609.7	2582.9	2510.5	1927.2	4076.0	1380.6	1180.3	803.3	1100.6
59.6	4257.5	4629.4	4060.1	3534.2	4665.1	3416.1	4133.1	7312.3	4338.9	3627.4
941.9	7579.0	7689.9	4753.0	5932.5	7317.4	3832.2	5649.7	14616.2	7331.5	4899.1
36.2	26.2	23.9	21.0	26.1	22.5	22.7	18.5	22.3	16.7	22.1
287.5	3884.6	4571.7	4662.7	3462.0	4042.3	3869.2	3792.8	4063.2	2573.9	2781.9

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112.0	124.9	90.5
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1278.7	1625.1	544.5
146.8	244.3	591.6
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6334.2	5872.6	6122.6
197.2	161.9	69.5
8802.2	7869.5	5514.6
587.4	759.5	505.3
1418.6	804.5	1103.7
37.2	73.9	53.0
62.8	92.5	40.4
2015.9	2140.5	1549.5
2380.0	808.7	1066.7
243.4	359.9	869.0
3630.8	2732.0	2416.8
346.7	715.7	1232.6
4806.0	3750.5	2947.6
44.2	30.8	30.8
2228.8	2842.0	1340.3
1182.4	317.5	246.1
2046.7	1868.7	1737.2
2366.1	3206.1	2102.1
6163.2	5695.1	5335.6
3238.3	1614.7	2049.5
2290.3	1225.0	1313.6
2240.7	1565.3	1526.2
215.5	570.3	209.1
2410.3	2344.9	2349.2
3088.1	3184.6	2294.3
778.1	855.8	441.8
1471.4	1740.1	454.3
906.4	1376.6	1738.7
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5407.4	5456.6	3614.1
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EU592336.1 gg_id:535928 Seasonal changes Salton Sea hypersaline water clone SSW3Ap EU592
EU624432.1 gg_id:284011 str. AMSU EU624
FJ545547.1 gg_id:509482 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S2-2 FJ5455
EU005774.1 gg_id:259717 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micrc EU005
FJ826189.1 gg_id:549457 Succession during spring Sea filtered surface sea water decay period after diatom blo FJ8261
AM982605.1 gg_id:279056 microbial and slurry pig saw dust spent bedding clone PISD-AIA05 AM982
FJ744837.1 gg_id:564502 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7448
AM279180.1 gg_id:171189 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
EU440974.1 gg_id:335445 Salegentibacter sp. str. PR54-18 EU440
AF419681.1 gg_id:26293 Guaymas Basin hydrothermal sediment clone CS_B009 AF4196
EF572790.1 gg_id:234993 Coco's Island site 23 marine clone S23_889 EF5727
GU118567.1 gg_id:532684 Threatened Corals Provide Microbial Habitats clone Mfav_B06 GU118
AY280420.1 gg_id:100771 exterior deep-sea hydrothermal vent sulfide chimney Juan de Fuca Ridge Pacific Oce AY2804
AB188215.1 gg_id:103277 Cytophaga sp. str. TUT1214 AB188
AF052742.1 gg_id:39004 Arenibacter latericius str. KMM 426; LMG 19694; CIP 106861 AF0527
EU328040.1 gg_id:279468 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
AY654766.1 gg_id:100882 Oculina mucus isolate 20 AY6547
EU465134.1 gg_id:288740 African elephant feces clone AFYEL_aaj68e07 EU465
FM958432.1 gg_id:544536 olive flies and its major symbiont 'Candidatus Erwinia dacicola adult female headless FM958
FM162560.1 gg_id:540441 Wautersiella falsenii str. MT2 FM162
AJ853512.1 gg_id:110915 landfill leachate clone GZKB17 AJ8535
DQ346496.1 gg_id:155685 during composting libraries compost clone 2B12 DQ346
DQ129251.1 gg_id:137948 microarray level air two cities Texas urban aerosol clone AKIW644 DQ129
EU794729.1 gg_id:330265 Empedobacter sp. str. FM-1 EU794
AM177497.1 gg_id:147208 Empedobacter brevis str. LMG 4011 AM177
EU779437.1 gg_id:337303 Hartmann's Mountain Zebra feces clone AFZEB_aaj72h08 EU7794
FJ999733.1 gg_id:525497 Wautersiella falsenii str. P1785 FJ9997
GQ082931.1 gg_id:385877 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ082
EU293154.1 gg_id:241741 Empedobacter brevis str. Y7D EU293
AY521225.1 gg_id:99909 Winogradskyella eximia str. KMM 3944 AY5212
DQ530465.1 gg_id:161743 Winogradskyella sp. str. gap-f-41 DQ530
DQ073103.1 gg_id:152380 Psychroserpens sp. str. TW-JL-49 DQ073
AY771730.1 gg_id:143056 Winogradskyella thalassocola S4-6 AY7717
DQ356490.1 gg_id:147248 Winogradskyella sp. str. BC1 DQ356
EU195943.1 gg_id:244700 Winogradskyella sp. str. P101 EU1959
AY771731.1 gg_id:143045 Winogradskyella thalassocola S4-7 AY7717
FJ919968.1 gg_id:556977 Winogradskyella sp. str. A73 FJ9199
AY771720.1 gg_id:141948 Winogradskyella thalassocola S3-5 AY7717
AY521224.1 gg_id:99754 Winodgradskyella epiphytica str. KMM 3906 AY5212
AY521223.1 gg_id:99602 Winogradskyella thalassicola str. KMM 3907 AY5212
FJ196009.1 gg_id:315572 Winogradskyella sp. str. NF1-23 FJ1960

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608.4	5091.4	6006.1	4736.0	4324.2	5126.1	4803.8	5684.4	4957.2	9232.4	4836.0
210.7	7819.9	7010.4	6173.5	6977.9	7531.2	7131.2	7078.9	11060.9	11479.0	7238.2
1586.9	7131.6	6118.3	5421.6	4483.8	6469.4	3377.9	5469.4	8144.1	3822.5	7309.0
4166.6	5080.7	5400.6	4567.4	4769.1	4819.4	4640.9	4509.1	7288.0	5129.7	4922.8
682.5	8031.2	6908.3	8362.7	7356.2	6552.6	7478.6	6773.2	8330.7	7676.8	7322.0
115.7	3893.0	3227.3	2989.5	3802.4	3699.2	4100.4	3450.8	4457.1	2664.2	2155.8
267.9	2802.7	4127.3	3393.8	3840.0	3122.1	4952.8	3487.2	2129.9	817.9	2679.9
1683.8	3130.3	3389.1	3308.4	3818.5	3686.5	3866.0	3282.7	6394.2	4577.4	3842.4
67.1	2476.7	1680.4	1583.9	1229.3	2763.4	1748.1	2370.3	1489.8	1163.8	952.2
40.1	994.6	1462.4	1180.2	841.0	871.8	965.3	1381.2	313.2	830.4	1027.8
880.2	4523.8	4275.1	4478.7	4797.3	4717.6	4814.7	5166.7	6196.8	3399.9	4619.7
215.0	5824.8	5999.1	6530.5	7639.4	6331.8	8450.3	6567.5	4342.2	3518.0	5067.9
78.5	1567.0	1897.4	1570.6	1840.5	1979.4	1546.2	2371.1	1515.3	2128.3	1053.5
29.6	29.1	42.0	31.1	65.4	38.5	37.4	28.1	31.1	24.7	27.4
4873.8	4277.8	4259.5	4092.1	5302.9	4255.4	3710.4	5385.7	5167.5	6694.8	5915.6
74.2	3825.3	4834.1	4920.3	5664.5	4220.6	5058.8	5613.2	1526.2	1785.1	8051.8
392.0	3458.2	2958.7	3217.0	2892.1	3081.9	3090.2	3602.6	3974.8	5950.7	2928.7
547.9	3198.5	3428.7	4401.3	3055.0	2721.8	4523.7	3449.5	2354.2	4063.0	2724.7
57.7	3460.8	2759.7	2729.0	2684.4	3600.2	2653.9	2900.7	3455.1	10718.0	2395.9
41.6	188.0	326.7	342.1	294.2	368.8	251.2	221.0	114.3	1839.0	149.0
34.1	351.5	320.5	304.1	343.2	457.0	342.4	402.1	173.7	147.5	259.3
24.3	77.6	74.3	58.7	126.4	48.8	111.4	65.5	34.6	39.0	40.1
65.0	4664.3	6011.9	2764.8	3177.9	6856.4	2044.1	3019.6	7642.0	9686.4	2808.9
102.9	7730.8	6863.6	6247.6	5538.1	6381.6	5697.8	6467.5	10229.5	12524.2	5746.3
35.6	113.4	172.1	224.8	64.0	161.8	69.8	52.3	139.3	156.5	53.3
3628.7	7716.4	6408.6	5419.7	6004.0	6888.3	6701.7	6562.5	8806.3	13795.4	6823.1
1391.8	3679.5	3235.9	3810.6	3116.5	2976.2	4052.4	2673.8	2631.1	9950.7	2708.6
56.5	3345.6	2085.8	1934.4	2177.8	3064.7	2308.6	2854.3	2540.5	10077.7	2037.3
718.6	5810.5	6418.0	5486.2	5672.2	5832.7	7726.7	5997.6	8261.2	8237.7	6897.8
385.6	872.2	763.4	644.3	579.5	546.7	653.5	1714.8	353.9	1634.5	939.4
381.6	2544.8	2168.7	1944.0	2116.4	2729.6	2316.0	3390.3	2990.0	4300.2	2613.9
42.2	447.2	1080.7	1021.6	792.7	1182.3	500.0	1072.6	312.2	339.9	433.6
44.4	382.5	687.4	583.9	489.8	584.4	325.0	642.7	157.0	203.4	428.5
354.8	576.2	518.3	487.6	747.0	726.3	407.8	918.4	233.6	581.6	368.3
56.7	1825.1	2128.3	1270.8	1929.1	2433.9	1620.5	2028.5	2678.0	2138.0	2030.2
402.7	2085.7	3453.3	3264.3	2997.2	2755.6	3118.3	2914.5	4748.1	3609.2	2096.3
57.6	1962.5	1982.9	1763.6	1695.9	2963.9	1071.4	2960.0	1839.9	3084.3	1858.3
70.3	1144.9	935.0	589.1	862.4	1321.8	814.0	936.7	2505.6	1821.9	1050.9
82.9	1899.3	1875.7	918.1	1858.4	2476.3	1339.4	1731.5	3079.6	2217.0	2052.0
76.5	2896.3	2500.4	1891.4	2300.6	3056.3	1450.1	2853.5	4877.8	2419.3	1797.8

4176.4	6375.8	1426.2
5302.5	4968.7	5901.8
7024.9	6232.3	4518.3
3887.0	4504.9	2571.0
4491.6	4981.8	4234.4
7029.0	6752.6	4896.7
2159.7	2863.3	2502.7
2097.0	3043.0	3896.0
3064.5	3888.2	3244.1
1598.4	1404.0	986.0
687.1	1153.6	1515.6
3818.3	4109.3	5223.0
5837.6	5402.8	7887.9
1695.0	2810.8	1254.1
32.5	50.9	28.8
4483.0	4039.4	3479.0
3569.0	2537.4	1879.3
2696.0	3510.6	3878.1
2721.3	2839.6	2811.6
2802.3	3218.6	1296.1
225.0	247.1	609.7
80.9	473.9	1898.3
61.2	49.9	29.1
3370.1	1877.7	861.5
6432.7	5793.9	4504.3
61.0	98.3	86.3
6231.9	5106.0	3685.1
1999.1	2181.0	2256.4
2218.5	2215.8	860.3
7386.3	5872.6	5794.8
1820.4	763.4	565.1
2752.9	2283.8	1470.2
2502.3	442.3	719.4
1405.0	323.6	700.5
940.5	811.5	437.7
3398.7	1567.6	1507.0
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DQ357769.1 gg_id:145482 Psychroserpens sp. MAC17 Mac17 DQ357
AB438962.1 gg_id:360101 Winogradskyella sp. str. R60 (=KMM 3968) AB438
AB255367.1 gg_id:223113 Galbibacter mesophilus str. Mok-17 AB255
DQ097522.1 gg_id:133522 Venteria marina str. En5 DQ097
FJ230837.1 gg_id:325922 Joostella sp. AD3 str. AN4 FJ2308
AB121976.1 gg_id:102893 Zobellia russellii str. KMM 3677 AB121
DQ066625.1 gg_id:150547 Symbiosis and Insect Ancient Symbiont Sap-Feeding Insects Phylum Bacteroidetes U DQ066
EU646081.1 gg_id:552008 symbiont EU646
DQ679965.1 gg_id:162099 Mycoplasma sp. str. B2 DQ679
EU646047.1 gg_id:572398 symbiont EU646
EU646066.1 gg_id:544736 symbiont EU646
DQ066640.1 gg_id:144003 Symbiosis and Insect Ancient Symbiont Sap-Feeding Insects Phylum Bacteroidetes U DQ066
EU646080.1 gg_id:571511 symbiont EU646
EU646049.1 gg_id:560878 symbiont EU646
DQ133563.1 gg_id:149599 Preliminary survey insects (Hemiptera:Coccoidea) scale insect clone DQ133
DQ133559.1 gg_id:147524 Preliminary survey insects (Hemiptera:Coccoidea) scale insect clone DQ133
AY922215.1 gg_id:114215 whalefall clone 131697 AY922
AM990892.1 gg_id:279587 Balneola sp. MOLA 118 AM990
DQ015824.1 gg_id:140368 Antarctic lake water clone ELB19-188 DQ015
DQ015773.1 gg_id:139513 Antarctic lake water clone ELB25-086 DQ015
GQ243712.1 gg_id:554668 consortia immobilizing nitrifying bioreactors designed penaeid and non-penaeid larv GQ243
EU735656.1 gg_id:330672 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
EU735648.1 gg_id:343612 archaeal structures oil contaminated and soils China pristine soil Jidong Oilfield clone EU735
FJ152978.1 gg_id:352504 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1529
EU328034.1 gg_id:278678 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU328
FJ152887.1 gg_id:304760 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4C FJ1528
GQ263633.1 gg_id:560384 Structure Simulated Level Waste Site simulated level waste site clone FW3_192C GQ263
AF449784.1 gg_id:80582 CFB group clone ML615J-21 AF449
EF632720.1 gg_id:237373 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) wate EF6327
GQ263696.1 gg_id:587073 Structure Simulated Level Waste Site simulated level waste site clone FW3_98C GQ263
GQ263661.1 gg_id:592463 Structure Simulated Level Waste Site simulated level waste site clone FW3_49C GQ263
EU723156.1 gg_id:327281 actinobacterium str. kmd_222 EU723
AM237313.1 gg_id:150813 Cytophaga arvensicola str. T2 AM237
AM237311.1 gg_id:153828 Cytophaga arvensicola str. DSM 3695 AM237
AB264798.1 gg_id:164755 Chitinophaga ginsengisegetis str. M1-09 AB264
AB278570.1 gg_id:182778 Chitinophaga sp. str. KP01 AB278
EU133718.1 gg_id:252642 tallgrass prarie soil clone FFCH13611 EU133
EU714260.1 gg_id:328242 Chitinophaga sp. str. JS16-4 EU714
AY238335.1 gg_id:82843 Flexibacter sp. str. MDA2495 AY2383
EU714259.1 gg_id:347504 Chitinophaga sp. str. JS13-10 EU714
AB078067.1 gg_id:58620 Flexibacter sancti str. IFO 16033 AB078

63.5	2038.6	2919.6	2794.5	2835.6	3033.9	2412.2	2619.6	3959.8	2675.6	1663.3
48.3	1162.4	999.6	916.9	905.7	1160.8	549.9	1168.5	818.2	901.4	471.0
75.6	4922.7	4604.7	4092.0	5633.6	4312.4	4865.5	5941.4	5541.3	6377.2	4836.8
780.9	1110.9	1134.4	1076.4	1633.9	1751.1	966.1	1871.2	1144.9	1119.3	929.3
54.0	1911.7	2542.1	1189.7	1042.2	1658.5	727.2	2239.9	3426.1	1918.2	1202.2
133.1	5780.0	3891.3	3015.7	3850.9	3810.3	4219.5	3763.4	6372.1	4033.7	4118.4
46.1	28.9	37.0	44.6	46.7	38.6	45.0	46.7	21.2	16.1	24.3
3398.6	6671.6	6587.3	7180.4	6239.6	6925.1	7501.9	6288.3	7298.6	4820.5	10952.5
166.5	391.1	306.2	231.1	193.4	421.0	238.2	434.5	577.9	378.1	396.2
2061.6	6554.4	5895.4	5844.3	6643.9	5956.3	6593.3	5494.4	6358.2	8317.3	5812.9
20106.5	10066.5	9755.9	10081.2	10238.1	9325.8	9775.6	8747.4	13597.6	11790.2	11439.4
36.5	65.1	23.8	68.2	109.7	79.7	90.1	86.7	32.9	8.8	71.1
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35.6	111.9	164.1	144.8	166.3	137.7	159.1	301.9	73.1	170.3	145.4
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215.8	2620.3	2336.6	2208.4	2746.3	2907.4	2726.4	2352.8	2361.7	4882.4	1245.0
171.3	3462.8	3966.1	3244.3	3059.8	3149.7	3580.0	3330.0	1725.7	2196.4	3618.2
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323.2	1840.5	1968.2	1707.2	2030.3	1779.3	2240.3	1846.8	1482.5	1085.5	1172.6
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40.5	184.7	429.4	176.3	88.5	128.1	97.2	123.0	99.7	35.3	159.5
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8421.0	11171.9	9913.1
223.8	99.6	144.8
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3793.8	3176.4	3322.6
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1729.7	2094.4	2220.9
1388.6	1972.7	1102.5
107.2	200.7	188.8
2017.9	2240.1	2587.7
1384.5	2018.7	1133.6
6592.1	6851.9	7332.5
1738.8	2012.2	2037.5
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2247.0	2205.5	2390.0
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AB245374.1 gg_id:149306 Chitinophaga sp. str. Gsoil 052 AB245
DQ298787.1 gg_id:141868 Effect Nutrient Periodicity upon Microbial Dynamics exposed 14-day nutrient flux DQ298
AF181568.1 gg_id:71851 Flexibacter cf. sancti 1 AF1815
DQ062743.1 gg_id:134254 Chitinophaga sp. str. CC-SG1B DQ062
FM865977.1 gg_id:573131 Chitinophaga sp. str. CS5-B1 FM865
DQ378248.1 gg_id:154761 oil-polluted soil clone M28_Pitesti DQ378
AB267477.1 gg_id:162563 Flavosolibacter ginsengiterrae str. Gsoil 643 AB2674
AY921684.1 gg_id:113437 farm soil clone AKYH1027 AY9216
DQ378235.1 gg_id:152427 oil-polluted soil clone M15_Pitesti DQ378
GQ116342.1 gg_id:434729 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw691f12 GQ116
AY493956.1 gg_id:136598 Fingerprinting aggregates soil clone 1417 AY4939
FJ657758.1 gg_id:532743 Metalworking Fluids and Aerosols Metallurgy Plant metalworking aerosol clone Winte FJ6577
AY211072.1 gg_id:81764 anaerobic VC-degrading enrichment clone VC10 bacterium AY2110
AB485756.1 gg_id:578831 Stratified medicinal leech Hirudo verbana bladder clone 1B-NIA AB4857
FJ457040.1 gg_id:573552 Niabella sp. str. CCBAU 05354 FJ4570
DQ457019.1 gg_id:156950 Niablella koreensis str. R2A15-11 DQ457
EU133632.1 gg_id:250223 tallgrass prarie soil clone FFCH2679 EU1336
AM085477.1 gg_id:140614 microbial subsurface west Pacific warm pool deep sea sediment clone E26 AM085
EU881188.1 gg_id:353494 Karst region natural restoration land soil clone KNR200711-019 EU8811
EU133640.1 gg_id:246952 tallgrass prarie soil clone FFCH4809 EU1336
EU917053.1 gg_id:351981 Niastella sp. str. RHYL-67 EU9170
DQ244076.1 gg_id:141748 Niastella jeongjuensis str. GR20-13 DQ244
AJ583191.1 gg_id:94468 radioactive site ground water clone S15B-MN17 AJ5831
EF516765.1 gg_id:222536 grassland soil clone FCPO489 EF5167
AB267478.1 gg_id:172843 Terribacter koreensis str. Gsoil 664 AB2674
DQ365993.1 gg_id:155441 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3! DQ365
DQ365999.1 gg_id:154794 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone BP DQ365
FJ485120.1 gg_id:558937 microbial autonomous rover world's deepest phreatic sinkhole water column El Zacat FJ4851
AF449772.1 gg_id:80757 CFB group clone ML310M-18 AF4497
AB464942.2 gg_id:338020 Altitudinal changes flora on Gulkana Glacier Alaska analyzed sequencing and -cycle c AB4649
EU104177.1 gg_id:323582 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
AB286623.1 gg_id:208838 Reducing production and domination comamonadaceae reducing oxygen supply was AB2866
AB286615.1 gg_id:205961 Reducing production and domination comamonadaceae reducing oxygen supply was AB2866
AJ007870.1 gg_id:2554 cytophagales clone LD1 AJ0078
EU104150.1 gg_id:342905 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
AF507866.1 gg_id:55727 Mono Lake at depth 17.5 m station 6 July 2000 clone ML617.5J-33 AF5078
CU466754.1 gg_id:327821 Evry wastewater treatment plant anoxic basin clone CU4667
GQ347704.1 gg_id:533454 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
FJ592611.1 gg_id:554348 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
GQ264422.1 gg_id:511320 Structure Simulated Level Waste Site simulated level waste site clone WW3_110 GQ264
AY921733.1 gg_id:113386 farm soil clone AKYG1020 AY9217

113.7	913.5	1104.5	927.7	1912.0	1061.7	1392.1	937.9	954.3	277.9	507.3
75.9	3962.0	2166.2	2282.0	3724.8	2782.3	3148.1	2340.4	2803.0	1784.8	2202.0
38.0	1461.2	263.1	1224.0	2734.6	1617.5	1632.8	1231.9	1148.9	1807.9	1196.0
59.1	214.0	163.8	162.5	208.3	152.0	187.0	120.0	361.4	51.8	125.5
40.1	216.9	71.3	87.8	101.3	76.0	75.3	101.0	63.4	22.3	48.0
53.4	32.8	23.4	27.5	47.9	20.5	35.5	20.5	21.4	18.2	20.5
418.2	11080.4	7531.5	8649.1	13936.8	8640.1	12612.4	7302.9	7087.7	5554.2	7641.3
9598.9	7992.0	7027.6	8017.3	9095.2	7550.3	8305.8	6392.8	8996.7	4891.7	8839.8
133.6	2634.4	2469.0	1761.1	2744.1	1851.0	2116.3	1768.5	2536.1	986.5	1643.5
90.5	1562.6	1878.5	1910.8	1940.8	2080.7	1045.9	2093.5	874.2	421.8	1304.5
73.4	3136.1	1656.8	1341.2	4332.7	2366.7	2647.9	1470.8	509.2	341.0	1061.8
580.8	3778.9	3309.9	2762.8	3071.5	2631.1	2367.6	2202.5	2630.9	1652.9	1568.8
42.7	2277.0	2019.1	1087.0	3087.2	1531.1	1604.8	1630.6	1061.6	314.8	881.1
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187.5	3148.5	2299.2	2546.5	4631.0	2665.5	3521.8	2782.5	1957.5	925.8	2648.0
1973.0	6057.1	6311.0	7850.3	7304.9	5796.6	6585.1	6237.5	5023.7	5374.6	6828.1
1138.1	3917.6	3006.6	3434.2	7394.5	3611.5	4493.9	3511.4	1730.4	1105.0	1911.1
68.7	1289.9	1220.0	1646.0	2344.8	1906.2	1223.0	1469.1	788.0	388.4	1375.5
50.6	1639.1	1365.9	2101.4	6290.6	3024.9	2684.1	1846.7	954.1	513.2	1273.6
46.2	2697.4	2118.4	2231.2	5552.1	2286.0	3165.7	1890.5	1728.6	546.0	667.1
15303.2	9816.5	8030.6	9344.7	10578.5	8821.5	9252.6	8014.8	11119.4	5157.0	12130.1
122.0	4137.0	2990.4	3644.0	6008.3	4105.7	4770.2	3607.7	2326.4	1516.3	3248.3
883.1	2524.0	2096.4	2449.8	5191.0	2688.1	2552.1	2190.3	1611.6	626.8	1164.4
408.5	6543.2	4734.2	3926.1	5939.4	4915.1	5221.9	4696.3	5660.5	2819.8	4206.7
29.7	157.3	238.8	329.5	542.5	487.5	501.0	299.1	56.3	113.4	161.5
41.2	1193.3	456.0	411.1	612.5	379.4	306.7	262.2	108.3	75.3	173.6
10464.9	6141.5	6114.7	6421.1	9267.8	7682.3	8674.4	5783.8	6871.4	5770.7	7154.7
9560.6	6617.6	6291.3	5951.0	5169.5	5945.1	6798.4	5213.8	7231.7	5885.3	6368.0
56.0	291.4	339.6	361.1	415.0	288.3	413.1	376.3	91.7	91.9	552.8
878.0	1867.2	1795.9	2837.7	3151.5	1336.6	2058.1	3259.4	1662.2	679.5	1223.8
1482.1	5925.3	5739.3	7449.5	8777.2	6512.7	7543.4	7061.0	6192.8	5017.8	6929.9
3126.3	7083.0	6064.8	6957.1	8096.0	6794.8	7481.3	6522.7	6984.2	6323.5	6347.1
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3031.1	5355.8	4545.1	4892.7	5755.8	4251.3	4430.5	3560.2	5089.4	2390.7	4930.6
139.7	2138.0	2282.6	2059.2	2398.0	1881.5	3030.1	1523.1	3074.4	1600.1	2851.6
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142.7	49.0	47.6
24.7	33.0	21.7
9201.9	6398.0	7038.4
7041.5	7198.3	6483.0
2062.8	2166.0	1039.3
1816.1	1619.6	1077.1
1421.0	1723.4	1625.4
2676.7	2742.4	2146.6
1081.3	1454.1	822.5
6436.7	5077.0	5648.6
2268.1	2306.9	2328.7
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1234.5	526.9	64.4
8654.1	9617.7	8336.8
5807.5	5750.1	4369.2
4366.1	4579.5	3419.3
2621.0	3507.6	3213.0
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AY056829.1 gg_id:32581 Bifissio spartinae str. AS1.1762 AY056
AJ295511.1 gg_id:25227 rape rhizosphere clone wr0060 AJ2955
EU861847.1 gg_id:343941 effects chronic fertilization on alpine tundra microbial implications carbon and nitrog EU861
GQ396989.1 gg_id:554086 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GU208213.1 gg_id:538684 Study on Sediment Dongping Lake sediment clone 1T1-11 GU208
AB504919.1 gg_id:558029 structure microorganisms reddish-brown iron-rich snow clone oze05B16 AB504
EF516017.1 gg_id:222507 grassland soil clone FCPN444 EF516
DQ298006.1 gg_id:142330 Microbial hydrocarbon contaminated soil clone UA2 DQ298
DQ450747.1 gg_id:161257 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
EF516344.1 gg_id:220513 grassland soil clone FCPS474 EF5163
AB240473.1 gg_id:142837 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
EF520597.1 gg_id:233334 structure lakes: what controls ? acid-impacted lake clone ADK-RXe02-22 EF5205
FM201192.1 gg_id:551880 and distinct induced biofilm fouling operated under conditions laboratory-scale men FM201
GQ396857.1 gg_id:509873 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
DQ450743.1 gg_id:160651 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
DQ501312.1 gg_id:180406 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
AY218618.1 gg_id:81845 penguin droppings sediments clone KD3-81 AY218
GQ043454.1 gg_id:417385 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw97 GQ043
EU133660.1 gg_id:244018 tallgrass prarie soil clone FFCH5150 EU133
EF516340.1 gg_id:225059 grassland soil clone FCPP437 EF5163
EF018461.1 gg_id:204934 aspen rhizosphere clone Amb_16S_1087 EF0184
DQ191824.1 gg_id:140407 Microbial and geochemical heterogeneity 3 km deep South Africa fractured metaba DQ191
GU295962.1 gg_id:540458 Niastella sp. str. JCN-23 GU295
EU015106.1 gg_id:250277 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
FJ479493.1 gg_id:547060 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794
AJ295528.1 gg_id:42289 rape rhizosphere clone wr0086 AJ2955
EU861890.1 gg_id:354903 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
AF529321.1 gg_id:61843 PCE-contaminated site clone CLi112 AF5293
EF516406.1 gg_id:225926 grassland soil clone FCPS640 EF5164
EF516138.1 gg_id:218051 grassland soil clone FCPP411 EF5161
EF018806.1 gg_id:204470 aspen rhizosphere clone Amb_16S_1276 EF0188
DQ640728.1 gg_id:234598 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
AF314428.1 gg_id:41664 aerobic phosphorus-removal ecosystem clone PHOS-HE19 AF3144
AF368190.1 gg_id:58374 non-EBPR sludge clone SBRT303 AF3681
AY211071.1 gg_id:82223 anaerobic VC-degrading enrichment clone VC5 bacterium AY211
AJ295463.1 gg_id:39882 rape rhizosphere clone wr0002 AJ2954
EF018581.1 gg_id:209422 aspen rhizosphere clone Amb_16S_850 EF0185
AM990456.1 gg_id:278060 Solibium sp. str. I-28 AM990
DQ404887.1 gg_id:155209 contaminated sediment clone 654959 DQ404
AB286400.1 gg_id:216923 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
FJ479490.1 gg_id:553534 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4794

33.3	289.0	287.9	180.4	1612.8	450.1	116.0	162.1	95.5	270.7	150.5
170.6	3488.7	3255.7	3148.3	2490.0	3048.2	3100.9	4955.9	3331.0	4146.2	6078.0
447.0	12762.2	10109.8	11314.1	17843.9	11827.0	16192.0	10078.4	8872.6	7024.0	10837.7
1475.3	6995.3	5903.4	5601.7	10088.8	6841.0	8541.1	5490.3	6356.3	3641.2	5343.5
374.3	6109.3	6039.6	6304.2	5704.2	6102.1	6719.1	6010.7	6536.9	6630.3	5158.1
6078.1	5594.4	4806.7	5248.5	11270.2	6422.4	7305.3	4214.6	4553.1	2737.3	4370.4
62.3	1072.9	1467.6	704.4	1582.0	1649.4	1285.6	910.3	590.9	134.4	503.2
19664.5	4484.9	5853.7	6047.7	6138.4	5438.4	6072.0	4727.3	8056.3	8415.8	8536.7
53.6	117.1	177.9	49.3	87.1	102.7	49.3	66.6	29.0	28.2	40.1
144.4	4565.8	3452.9	4011.2	9222.4	5560.6	6299.2	3262.4	1841.2	1791.1	2655.4
57.5	7507.9	4187.7	4747.2	10189.6	3641.8	3959.7	2351.4	1779.1	904.0	1832.8
292.4	451.9	471.9	557.8	1008.9	519.4	766.4	420.6	583.1	277.8	623.3
2279.3	6376.5	5726.5	6767.1	12537.0	8104.0	9756.5	5911.8	4259.1	2858.2	5336.9
260.5	6606.0	5306.8	5128.9	10057.7	6052.0	8020.6	5547.6	3520.1	1830.4	4646.9
2106.4	5953.1	5514.1	5888.8	6126.7	4707.2	5552.0	5406.2	6661.1	2239.8	4870.6
211.6	9054.1	5806.6	6095.6	5771.6	5149.7	4724.5	5812.7	9056.3	3824.4	5520.4
337.0	6363.0	4539.3	5005.8	7199.3	5180.7	5829.9	5136.3	4666.0	1993.1	4338.6
62.4	1939.1	1771.3	2179.7	4796.1	2403.3	2924.7	1989.2	996.3	675.4	1409.5
186.9	6445.8	4229.0	4733.1	8576.5	4919.9	9240.5	4756.3	3645.0	1413.6	4609.8
44.5	523.3	940.4	445.0	1426.5	1365.6	1965.3	1273.0	172.9	45.4	230.5
39.5	849.2	532.1	416.5	771.2	984.2	468.0	503.3	226.2	70.0	271.2
1009.5	5833.4	6003.4	6586.1	8144.3	5544.9	9155.1	5769.7	4596.6	1734.2	5188.1
154.5	4453.1	3554.4	3776.0	6300.5	4203.6	5618.1	3458.3	3151.0	1470.0	2690.4
242.6	6884.1	5566.3	6137.6	10941.9	6828.7	8389.3	5384.3	5329.7	3298.0	5089.0
304.9	3806.5	4012.3	3702.9	8288.4	5496.9	6662.7	4550.9	1999.5	1953.8	2899.0
152.0	1397.9	1871.5	1500.8	1689.5	1245.9	1522.1	1430.6	1300.7	482.5	1618.4
846.1	5160.2	4859.0	4368.0	4674.7	5063.9	4292.7	4137.6	3486.7	4126.6	3585.8
59.4	3828.4	1483.9	1694.3	2750.8	1908.4	1537.7	2209.2	1158.3	525.0	1287.1
42.6	229.7	1534.6	102.5	137.4	813.1	84.4	479.4	40.4	32.8	230.7
37.9	619.5	753.9	477.1	777.5	557.8	660.2	574.9	676.0	185.5	339.5
43.7	980.1	648.4	951.7	1637.8	773.0	3632.4	949.8	169.6	484.4	597.7
3333.1	2823.4	2701.4	1782.7	2137.4	2103.1	2614.0	2413.0	2835.3	1986.3	2395.1
45.1	408.2	411.8	459.0	465.1	288.3	285.4	297.6	171.0	82.4	125.8
41.9	108.0	214.9	150.6	483.2	213.3	230.5	198.8	127.5	280.6	117.9
40.4	856.9	929.4	656.2	3396.5	1591.9	2084.7	790.7	458.1	259.7	658.5
3063.8	2941.6	2590.2	2714.3	3912.6	2564.2	3490.3	2775.5	2437.3	1469.5	2313.2
38.8	1255.5	914.6	1588.0	3026.0	2231.3	1422.5	1918.6	471.3	524.5	1161.3
122.8	785.3	999.3	1313.5	1849.8	1194.7	2082.6	1200.9	600.2	450.1	1199.9
6411.2	5376.9	4923.9	4715.1	9529.2	6159.9	7652.7	6277.4	3843.9	2522.9	6088.2
4555.2	6734.9	5455.4	5565.8	7376.0	5125.7	8552.4	4292.3	5187.0	4993.5	5801.2
130.4	3472.1	3482.7	3609.8	5211.4	3280.7	3923.6	3702.5	2244.6	1094.5	2755.9

216.2	124.4	29.7
4709.3	4856.0	3370.9
12319.1	9451.0	10879.1
6724.0	5348.9	5375.5
5672.1	6020.5	5926.5
4967.6	4755.3	5164.7
1184.1	685.9	992.3
4906.4	6548.4	4639.2
137.2	85.2	50.4
4194.7	3680.2	2730.3
3352.4	2407.0	1658.1
415.5	740.3	561.4
7215.0	5704.3	4813.1
5494.9	4817.9	4279.1
4747.4	5817.4	3829.6
4809.9	5955.3	3945.2
4522.9	4955.4	4013.7
3659.1	1879.7	1414.7
4758.1	3900.6	4267.8
867.5	579.4	266.2
303.0	432.0	441.8
5373.5	5291.8	5878.8
3408.4	3634.4	3359.3
7219.1	5068.8	4792.9
3919.9	2961.6	3092.9
1121.0	1358.0	858.8
4912.5	3900.1	5244.2
2421.3	2371.1	1317.5
294.3	193.7	1403.3
489.0	681.4	384.7
1453.8	326.7	576.4
2065.3	3236.5	3165.0
189.8	164.8	244.4
203.2	262.9	159.5
808.1	1177.4	546.8
2292.2	3354.9	4480.7
2059.0	2267.3	835.4
1071.5	896.5	2619.8
4871.7	4304.2	4539.7
5915.0	5214.0	4482.4
3155.3	3194.1	2900.5

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AB154301.1 gg_id:99400 freshwater clone S9A-31 AB154
GQ264521.1 gg_id:557173 Structure Simulated Level Waste Site simulated level waste site clone WW3_74 GQ264
EU133745.1 gg_id:251459 tallgrass prarie soil clone FFCH9847 EU133
EU283407.1 gg_id:242455 consecutively aerated submerged treating domestic wastewater activated sludge m EU283
EU133736.1 gg_id:235802 tallgrass prarie soil clone FFCH8654 EU133
AB269814.1 gg_id:206019 shal eutorophic Japan freshwater lake AB269
CU922785.1 gg_id:545292 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
AY302126.1 gg_id:109652 sludge dentrifying reactor fed with methanol clone DSBR-B064 AY302
AJ575723.1 gg_id:96745 lake water clone SW56 AJ5757
AY948032.1 gg_id:142590 Synchrony and seasonality two temperate rivers USA: Massachusetts Parker River cl AY948
FJ710768.1 gg_id:580914 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
EF019920.1 gg_id:209940 aspen rhizosphere clone Elev_16S_1292 EF0199
GQ263562.1 gg_id:566521 Structure Simulated Level Waste Site simulated level waste site clone FW3_114C GQ263
AJ575722.1 gg_id:98865 lake water clone SW36 AJ5757
AY792295.1 gg_id:119875 Humic Lake clone CrystalBog2KE10 AY792
FJ478810.1 gg_id:576653 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
DQ640666.1 gg_id:234394 full-scale EBPR sludge clone Skagenf91 DQ640
GQ472392.1 gg_id:541215 Microbial Dongping Lake lake sediment clone 4D4-6 GQ472
GQ115645.1 gg_id:396424 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw689a0 GQ115
FJ478596.1 gg_id:548715 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
EU104030.1 gg_id:345271 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
DQ984541.1 gg_id:236776 Mt. Nan-Jen soil clone IFD_11 DQ984
AM930283.1 gg_id:535708 gradual cooling stage mass and its spatial composting clone SMG23 AM930
EF688340.1 gg_id:250093 soil clone F3-31 EF6883
GQ263274.1 gg_id:570643 Structure Simulated Level Waste Site simulated level waste site clone FW1_a2 GQ263
DQ297996.1 gg_id:143484 Microbial hydrocarbon contaminated soil clone UD10 DQ297
AB286466.1 gg_id:216092 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
GQ339899.1 gg_id:540472 Niastella sp. str. Gsoil 221 GQ339
GQ263497.1 gg_id:578914 Structure Simulated Level Waste Site simulated level waste site clone FW2_191B GQ263
DQ378273.1 gg_id:154846 oil-polluted soil clone M60_Pitesti DQ378
EU644185.1 gg_id:282480 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
GQ263856.1 gg_id:581218 Structure Simulated Level Waste Site simulated level waste site clone WC2_10 GQ263
GU359109.1 gg_id:521439 rhizosphere soil peanut clone 2G87 GU359
AY218661.1 gg_id:82316 penguin droppings sediments clone KD9-169 AY218
EF025264.1 gg_id:190531 Examination microbial ecology avian vivo bromodeoxyuridine intestine clone B5_F26 EF0252
DQ413096.1 gg_id:153532 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
AB286634.1 gg_id:207342 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
AB177144.1 gg_id:129332 seafloor methane hydrate clone ODP1230B11.15 AB177
EU133734.1 gg_id:255322 tallgrass prarie soil clone FFCH7779 EU133
FM866271.1 gg_id:362648 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhC-1 FM866
EF516931.1 gg_id:217839 grassland soil clone FCPN422 EF5169

2848.5	4147.8	1398.2	1422.8	855.3	1190.5	1498.0	1043.7	1793.2	1160.1	1612.8
213.4	7334.4	5155.5	5302.9	7594.6	6193.7	6341.8	5773.6	4798.3	3935.5	4279.6
90.0	3254.9	2635.4	3720.8	5157.2	3915.2	3906.0	3805.1	2198.5	1148.1	2750.0
83.8	7755.2	5391.6	5699.1	11019.3	6204.3	8298.0	5682.3	3937.4	2378.1	4767.2
780.4	2613.7	2743.7	2626.5	5912.5	3442.4	4110.7	2254.7	1541.4	944.4	2269.8
1110.2	7506.4	6022.7	6781.3	5928.8	4747.2	5487.0	5372.1	7426.0	2194.4	5506.5
423.7	11456.1	8466.7	8763.5	11335.8	8603.3	10528.5	7927.0	7936.4	5882.5	8327.8
1457.5	1702.1	1523.3	1361.3	4453.1	2113.4	2509.1	1595.8	1328.1	948.0	1261.1
1355.2	10918.8	9586.7	9514.7	12824.4	9611.6	11495.1	8697.5	11036.3	7092.8	9576.4
8175.4	12486.6	6696.2	5499.8	4240.6	4389.4	4719.0	7552.6	12727.2	3406.9	6095.2
579.7	5687.0	4475.7	5205.3	5844.6	4422.1	4023.7	4408.5	6694.8	1494.6	5723.6
61.2	1367.7	2840.2	1324.2	3937.5	2290.3	1943.7	2094.2	529.9	345.9	1370.3
398.1	5175.4	2531.8	2840.4	2751.0	3301.9	2447.3	3132.2	8940.2	2636.4	3135.2
1327.9	1846.0	1567.7	1731.0	5015.5	2383.5	3066.6	1955.1	723.6	435.1	1362.3
10438.8	4946.9	4705.9	8100.0	5858.8	4669.4	5061.5	7602.0	5860.2	4497.7	7873.0
650.8	5442.2	6215.4	6731.8	8618.8	6666.2	8078.1	6935.6	3800.8	2579.6	5096.9
3468.4	6850.2	4992.7	5861.4	8183.4	5642.0	9177.8	5689.7	6816.6	4268.5	7154.8
9738.0	5076.9	4823.4	4806.9	8931.9	5740.9	7646.5	4517.7	7337.3	3746.2	4702.6
174.2	7407.3	5597.9	5552.5	10342.2	6087.0	7654.9	4771.9	3181.3	2923.8	4696.1
336.6	3024.0	2957.3	3084.2	5637.5	2955.9	4003.4	2731.4	2169.6	1319.8	2351.5
1020.7	5993.8	5949.1	4723.6	5867.3	5673.1	5110.4	4965.3	5349.4	1555.4	4573.9
50.5	359.0	1279.8	786.8	378.7	516.5	196.8	101.7	56.8	94.7	213.4
128.4	3220.4	2575.7	3051.9	4870.8	2826.7	3523.4	2347.7	1620.8	1289.1	1965.7
56.7	3495.8	3510.0	4369.4	7971.6	5590.5	5423.7	3746.8	2390.5	742.7	2425.9
319.4	5695.8	3837.0	4040.9	6538.5	4181.7	5046.3	3795.7	5039.2	1681.9	4092.7
46.5	2075.4	1748.9	2590.9	5531.7	3155.8	3291.9	2231.8	615.1	619.5	1414.0
109.9	1519.4	1515.9	1203.7	5024.0	2186.6	2664.8	1254.3	1195.3	479.3	670.5
15144.6	10070.3	8187.9	9320.8	12166.3	9619.0	10850.1	8301.2	10898.4	9787.8	11056.1
3479.9	5855.9	5364.5	5112.5	5889.5	5289.3	5056.5	5130.2	7934.0	3692.8	5849.5
599.2	5544.8	4848.2	5299.3	13716.2	8064.1	9039.2	4650.3	3317.2	3414.1	4502.1
1065.4	3838.5	3689.9	3973.5	10637.4	5648.0	6495.9	3333.9	2131.9	1460.0	2963.8
66.0	2802.2	2099.0	2384.4	5037.1	3136.3	4330.9	2315.4	1485.3	1072.1	1754.0
18740.7	9639.6	6876.9	7907.7	7117.2	6861.5	7634.6	6614.7	10092.3	7265.4	8718.3
8074.5	6694.9	5992.5	6392.8	6568.1	6480.0	6796.4	5746.2	9212.4	6697.5	6836.7
365.3	4368.5	3426.2	3335.7	4156.3	3048.4	4653.4	3282.8	2682.3	1513.1	2499.4
59.8	881.5	927.8	783.6	1452.9	860.2	1321.2	870.0	594.5	92.3	649.3
441.4	4366.5	2842.4	3641.4	6985.3	3514.9	7867.6	3175.9	1375.5	1494.2	2924.4
2555.7	6361.5	6041.8	6137.8	6530.2	5401.1	5605.8	5281.9	7335.5	5358.6	5869.2
277.2	8275.0	5352.9	6320.4	9998.0	6495.0	9783.0	5853.0	6307.6	2181.5	4966.9
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20166.2	8502.9	8180.3	8438.7	8503.7	7720.5	8494.5	7256.2	12882.9	8809.0	9265.6

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3222.9	2170.5	2110.4
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5308.6	4524.5	3863.9
6075.6	4760.3	4714.3
2763.7	3133.8	4032.0
5127.6	4572.6	4161.0
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4144.5	4444.7	3136.6
2657.7	1807.5	1307.9
1712.3	1459.3	1365.7
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4883.2	5448.3	4818.9
6009.1	4776.1	4642.0
3685.8	4408.9	3457.6
2924.6	2173.5	2183.1
6783.6	7624.3	6070.3
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3511.4	3353.9	2334.2
733.5	1509.1	743.6
4723.1	2235.4	2538.5
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7126.4	4959.0	4693.3
863.9	1369.9	818.2
7078.9	8213.3	8234.7

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AY218658.1 gg_id:81804 penguin droppings sediments clone KD9-156 AY2186
GQ264009.1 gg_id:592173 Structure Simulated Level Waste Site simulated level waste site clone WC3_06 GQ264
EF019155.1 gg_id:211909 aspen rhizosphere clone Amb_16S_1802 EF0191
EU571161.1 gg_id:270708 eubacterium sp. str. 11-14 EU5711
FJ439877.1 gg_id:511214 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M3 FJ4398
GQ402737.1 gg_id:510619 Accessing microbial biodiversity and metabolic potential tropical -based approach p GQ402
EF188431.1 gg_id:348170 Microbial Altamira Cave clone 245 EF1884
AJ318106.1 gg_id:52540 Waste-gas biofilter clone Blai2 AJ3181
EU133735.1 gg_id:248199 tallgrass prarie soil clone FFCH8475 EU1337
EU133756.1 gg_id:254621 tallgrass prarie soil clone FFCH3089 EU1337
DQ378256.1 gg_id:151174 oil-polluted soil clone M39_Pitesti DQ378
GQ113676.1 gg_id:464363 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ113
EF516578.1 gg_id:223554 grassland soil clone FCPP516 EF5165
FJ536911.1 gg_id:550393 Linking performance microbiology biofilters treating dimethyl sulphide presence and FJ5369
EU104318.1 gg_id:324205 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1043
GQ396884.1 gg_id:541963 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GQ488016.1 gg_id:543592 Microbial metal soil polluted heavy metals clone V8-189 GQ488
AB470450.1 gg_id:358964 Sediminibacterium sp. str. TEGAF015 AB4704
EU431807.1 gg_id:540217 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
EF019363.1 gg_id:213634 aspen rhizosphere clone Elev_16S_585 EF0193
FJ716020.1 gg_id:557323 Diet- gut microbiota Lumbricus rubellus fingerprinting technique and cloning intestina FJ7160
EF589974.2 gg_id:231571 changes structure sediments Songhua River contaminated nitrobenzene -DGGE cloni EF5899
EU362136.1 gg_id:317483 and Mesquite Flats Site Death Valley dune sand clone 7 EU3621
EU644197.1 gg_id:280545 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU6441
EF019397.1 gg_id:211598 aspen rhizosphere clone Elev_16S_630 EF0193
EU305589.1 gg_id:255546 Short-term effect organic matter on nitrite oxidation performance structure nitrite-o EU3055
AY493955.1 gg_id:136597 Fingerprinting aggregates soil clone 435 AY4939
EU133639.1 gg_id:241705 tallgrass prarie soil clone FFCH1448 EU1336
EF032765.1 gg_id:193234 cyanobacterial mat in lava cave clone HAVOmat81 EF0327
FJ466261.1 gg_id:567628 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4662
EF516161.1 gg_id:219059 grassland soil clone FCPT501 EF5161
EU881309.1 gg_id:320742 (maize-sweet cropping field) Karst region maize-sweet potato cropland soil clone KM EU8813
AJ290042.1 gg_id:40073 Germany: Lake Fuchskuhle south basin clone FukuS59 FukuS59 AJ2900
FJ612209.1 gg_id:582864 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.3.7 FJ6122
FM253591.1 gg_id:321965 Rock gold mine unusually microbial biofilm clone C11-1 FM253
EF516225.1 gg_id:225377 grassland soil clone FCPU633 EF5162
EU244015.1 gg_id:359585 16SrRNA probes river Leine sediment clone sls1309 EU2440
AF255635.1 gg_id:47339 EBPR sludge clone Ebpr1 AF2556
AJ888562.1 gg_id:113307 lake sediment clone TH451 AJ8885
EF522294.1 gg_id:221611 Endolithic Microbial Ecosystems Rocky Mountain endolithic sandstone clone FQSS07 EF5222
EU861946.1 gg_id:328230 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU8619

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683.0	9177.7	6278.1	7366.2	11147.2	7239.6	10459.5	6999.0	7111.0	4181.2	6891.4
54.3	261.2	384.5	108.5	977.8	425.2	365.5	147.2	58.0	38.1	105.6
82.7	6062.4	5331.2	5754.2	7588.9	4061.5	4734.6	4779.4	3204.9	1075.1	2923.1
3631.0	4661.2	4254.4	4050.6	5706.4	4428.7	5631.0	4601.4	5267.6	5188.7	5132.2
4954.4	4538.0	3042.6	4093.6	6585.7	3885.7	5718.9	3273.0	3142.4	1902.1	3427.6
1086.0	3416.5	3408.7	3657.2	3695.7	3664.9	4288.5	3518.5	2261.1	1528.3	2632.7
2566.9	5560.0	4374.9	4575.6	7070.2	5367.2	5774.7	4955.7	5396.2	4527.1	3627.2
319.8	5803.8	4913.7	5300.2	11183.1	6476.7	8766.6	5005.9	2354.8	2369.5	4641.1
915.2	8108.1	6261.5	7503.1	8726.3	5988.5	7840.3	6368.1	5387.0	2666.4	6582.9
155.6	3075.4	1936.0	2261.2	3321.0	1110.7	3778.3	2392.2	475.5	1537.2	2293.9
57.2	962.2	1133.1	923.9	2425.7	1378.9	1977.8	979.5	503.9	332.1	860.0
33.6	73.6	54.0	43.6	59.3	15.3	44.0	19.1	17.8	21.0	18.2
105.6	7730.3	5462.9	5681.8	12773.8	6835.6	8139.0	4539.0	6192.5	4525.3	3902.1
595.8	4329.1	3993.0	4587.1	5264.0	4059.6	4899.3	4453.4	3797.4	907.0	3655.1
289.5	4185.3	3650.2	3690.8	6744.3	3756.8	5769.4	4023.3	2347.5	1362.2	3157.3
535.6	1969.9	1271.8	1337.2	2544.6	1583.8	2506.0	1150.7	1084.6	671.4	1236.5
417.0	13215.5	8476.6	9933.7	9261.8	7465.9	6013.8	8769.7	16951.5	2532.1	8069.9
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43.0	1014.9	883.4	1353.4	976.0	760.9	2049.6	1293.4	728.7	144.4	932.4
120.0	6400.0	5306.2	5364.5	6507.3	5679.8	6656.1	6485.7	5002.7	2703.1	4784.9
99.4	1832.7	1449.9	1343.1	5713.6	3067.9	3497.2	2436.5	1501.0	970.0	1632.7
75.8	5734.8	4126.4	3129.6	5601.2	3875.6	3671.1	4271.9	3871.8	1561.5	4222.5
5813.3	5330.5	5058.7	4967.2	6340.5	5233.3	6611.7	5130.7	10450.4	5178.6	5086.6
29.6	17.9	19.2	24.7	146.7	23.4	25.5	20.2	23.8	14.4	22.0
72.3	4432.6	3214.7	3723.1	8874.4	4185.5	5370.7	2421.7	2072.9	2044.0	1545.8
45.3	294.8	160.4	166.0	1139.9	274.2	170.6	131.7	98.9	65.5	112.1
3379.2	2797.8	2698.0	2505.1	4267.4	2351.2	5156.6	2735.3	2402.4	1690.3	2767.4
40.7	353.5	205.4	202.6	1542.0	541.5	689.5	194.1	112.4	51.1	44.0
119.2	2609.5	1604.5	1093.4	3035.4	1383.9	1976.4	937.9	2995.3	241.5	584.1
790.1	7380.4	7332.9	7712.6	11614.0	8924.6	8914.4	7402.4	6002.8	2197.1	6720.3
4080.6	3345.5	3431.6	3773.6	5070.9	4101.0	3634.1	4195.3	4672.3	2378.6	2903.5
1261.6	2447.8	1772.4	1886.6	2512.6	1988.4	2458.2	3009.5	2316.9	1312.6	1566.9
63.8	1915.6	5179.6	1436.1	2770.1	3240.4	2693.5	2774.1	1401.8	682.1	1525.4
1536.7	6001.2	4152.6	5381.9	9839.9	5735.8	8600.7	4396.2	2581.6	2584.3	4386.3
171.1	5164.5	4505.9	4760.9	7351.6	4882.6	5464.6	4510.4	3526.4	1261.1	3104.8
2525.6	8769.9	7294.6	7394.0	13097.6	8857.3	10702.0	6768.6	7339.4	6177.6	7134.1
72.1	2067.1	1102.5	1410.0	1821.2	1207.5	1765.3	1230.7	1885.6	332.4	1010.4
9004.1	5444.2	4395.9	4559.3	6324.6	5191.8	5009.5	4141.9	7948.5	5991.5	5672.9
132.3	3668.3	3425.6	3712.7	4919.5	3887.3	5058.1	4682.9	1944.8	3129.8	4056.1
47215.6	12379.7	10986.4	12790.4	14872.8	11994.5	15206.0	10999.9	18901.4	15984.5	14828.6

5535.8	6317.4	4470.2
7456.4	6389.4	6802.5
196.0	229.2	87.9
5714.4	3943.9	3247.2
4579.6	5406.1	3503.0
3911.3	3585.4	2947.4
3199.5	3777.2	3456.6
4784.3	6150.2	5588.0
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6754.5	6083.5	4968.3
2571.0	1627.5	2072.5
807.0	1135.8	786.8
28.9	27.4	19.4
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4059.2	4287.5	3588.8
1305.2	1242.3	1085.5
7487.5	6765.7	4613.8
3503.2	3860.7	5504.0
1061.8	1580.9	1261.6
6674.5	5285.4	4517.8
1912.0	2512.3	1868.0
3875.8	3720.8	2662.3
5122.5	5352.5	4401.7
22.7	25.7	17.9
3421.5	3226.1	2989.1
159.7	168.5	91.5
3115.9	2578.4	2380.4
307.6	304.9	160.2
1101.7	878.0	750.3
7464.4	6995.9	7445.5
3146.0	4145.1	3094.7
1609.6	2808.9	1469.7
2395.1	2028.9	4014.2
5425.5	5494.0	4401.1
4399.2	3640.2	3982.6
7958.0	7219.8	6948.8
1189.2	1815.3	723.3
3975.8	5229.0	3690.1
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GQ264313.1 gg_id:511866 Structure Simulated Level Waste Site simulated level waste site clone WW2_135 GQ264
EF018856.1 gg_id:213892 aspen rhizosphere clone Amb_16S_1338 EF0188
GQ113817.1 gg_id:445860 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw(GQ113
AY177767.1 gg_id:78422 surface soil clone AY1777
EU509144.1 gg_id:273018 cecal contents Mus musculus strain C57BL/6J; MD7 clone MD7_aap44g05 EU5091
FN396945.1 gg_id:557824 integrative isotopic approach study degradation mixed Mixed (US3-M) enriched grou FN3969
AJ581604.1 gg_id:93798 soil near uranium mill tailings clone KCM-B-27 AJ5816
AY302124.1 gg_id:110665 sludge dentrifying reactor fed with methanol clone DSBR-B032 AY3021
EF688336.1 gg_id:242284 soil clone F1-133 EF6883
AY945889.1 gg_id:145905 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal r AY9458
AJ318177.1 gg_id:47356 Waste-gas biofilter clone BIsi8 AJ3181
EF019792.1 gg_id:203786 aspen rhizosphere clone Elev_16S_978 EF0197
EU283359.1 gg_id:246204 consecutively aerated submerged treating domestic wastewater activated sludge m(EU2833
AJ619071.1 gg_id:107742 Brewery bottling plant clone MTAG12 AJ6190
EF174291.1 gg_id:199043 direct activated sludge last compost maturation stage clone J60-814 EF1742
EU133682.1 gg_id:236693 tallgrass prarie soil clone FFCH600 EU1336
FJ793188.1 gg_id:528336 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB87 FJ7931
AY945881.1 gg_id:146138 Thauera and Azoarcus functionally important genera denitrifying quinoline-removal r AY9458
AF423292.1 gg_id:42740 soil clone 760-2 AF4232
FM200897.1 gg_id:560204 and distinct induced biofilm fouling operated under conditions laboratory-scale men FM200
FJ592637.1 gg_id:563390 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
EU978818.1 gg_id:534067 and metabolic potential metagenome glacier ice clone glb330c EU9788
AY326513.1 gg_id:136594 Amazon soil clone 6-1 AY3265
EU639180.1 gg_id:329287 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6391
EU283384.1 gg_id:245356 consecutively aerated submerged treating domestic wastewater activated sludge m(EU2833
AY124340.1 gg_id:55504 identification and Eukarya inhabiting Antarctic glacial cryoconite hole AY1243
EF516915.1 gg_id:222635 grassland soil clone FCPP496 EF5169
EF516498.1 gg_id:225398 grassland soil clone FCPT752 EF5164
AB179522.1 gg_id:105552 sedimentary rock clone MIZ31 AB1795
AY752128.1 gg_id:101380 lake water clone S10.17 AY7521
EU335290.1 gg_id:241123 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU3352
EF516686.1 gg_id:219534 grassland soil clone FCPP584 EF5166
AY796040.1 gg_id:108759 gold mine bore hole clone 47mm40 AY7960
EF492929.1 gg_id:254256 Iron-manganese Nodule and Its Surrounding Soil soil around iron-manganese nodule EF4929
EU133676.1 gg_id:258047 tallgrass prarie soil clone FFCH5267 EU1336
EU431809.1 gg_id:552192 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
AY792299.1 gg_id:122683 Humic Lake clone CrystalBog022A2 AY7922
DQ228370.1 gg_id:142482 microbial compositions two subglacial possible role microbes chemical weathering p DQ228
EU803695.1 gg_id:341876 It's all ranking aquatic Lake Gatun clone 5C231300 EU8036
GQ221080.1 gg_id:578107 consortia immobilizing nitrifying bioreactors designed penaeid non-penaeid larval re GQ221
EU881217.1 gg_id:344260 Karst region natural restoration land soil clone KNR200711-210 EU8812

295.7	6724.1	7142.6	6894.3	10204.1	7821.1	8984.9	6291.1	4591.5	3427.6	5919.2
1113.5	3024.6	2279.5	2512.8	5928.8	3428.7	5020.7	2955.1	1931.0	874.0	2649.6
249.5	4285.2	2966.9	3306.5	6777.9	3831.2	4676.3	2649.3	4268.2	1274.6	2438.3
154.0	1705.5	1575.4	1938.2	4392.8	2221.9	3242.0	2044.1	906.5	894.6	1181.9
352.3	4288.0	5330.6	5208.6	6262.8	5735.8	4663.9	5494.5	4310.8	3876.6	3977.4
54.6	5615.5	3217.3	4076.9	5661.0	4731.3	5225.0	5301.6	4161.8	2643.7	5605.3
425.8	5229.6	4652.4	5089.0	9524.2	5649.9	7386.2	4985.3	2453.8	2616.7	3653.3
181.7	4104.4	4040.7	3877.6	6322.6	4633.2	5389.2	3674.8	1994.7	1675.5	2666.8
267.6	7546.9	5476.4	6157.1	9916.2	6887.8	7032.5	6376.9	8794.8	5574.0	6627.5
189.5	4649.8	3201.5	3752.5	7531.5	4412.8	6313.1	3692.1	1802.8	1232.5	3332.0
169.7	1147.1	1073.4	1050.9	1454.6	1118.9	1637.8	898.9	1183.9	558.0	797.7
43.4	29.1	34.3	28.2	199.2	32.8	159.3	24.9	28.4	16.8	24.8
48.4	155.2	281.1	178.9	914.7	448.4	861.5	128.5	43.6	46.8	72.5
80.5	4730.4	3321.4	4062.8	3993.3	3021.0	3168.1	3187.8	3302.3	1641.7	2963.2
43.7	62.6	62.4	77.4	120.2	56.4	104.5	67.6	28.5	25.3	42.9
1069.9	5777.6	4266.2	5464.9	7620.5	4988.6	7566.3	5518.1	2686.9	2420.0	4804.4
3971.1	7778.4	5941.4	6503.5	11686.4	8331.6	9056.8	6133.6	8284.6	2990.3	5703.9
140.8	3678.7	4446.4	3121.2	6186.3	4557.1	5199.3	3397.2	2195.0	1575.5	2874.8
57.2	301.6	334.5	325.2	630.9	223.1	339.1	67.7	131.2	124.4	236.0
5999.8	9494.6	7133.9	7850.6	11734.2	8430.3	9425.8	6658.6	10675.7	3324.0	6968.1
2834.3	12521.2	9424.9	11113.9	14751.1	10506.4	13910.9	9188.8	13331.8	8295.1	11203.2
6982.9	10282.7	8079.6	8192.3	13327.0	9076.1	10906.4	7598.1	9617.4	5947.7	7282.1
350.3	4414.2	5275.3	3608.3	2440.3	3835.1	2243.0	3950.8	2644.7	796.7	5485.0
2564.5	13238.8	10984.8	11711.3	12715.0	10323.4	10447.3	10410.3	14914.7	7059.0	11601.0
908.2	4882.4	4852.0	5415.9	6244.4	4563.6	4859.4	4866.5	4831.1	2239.5	3638.5
351.9	10602.2	7557.6	8777.0	13290.9	8905.4	11610.8	7785.9	8644.9	5181.1	8077.7
125.5	3598.9	2010.8	2239.3	3459.4	2926.1	4865.9	2507.7	5893.1	652.7	2049.3
552.9	8483.5	7105.2	7342.4	10681.2	8277.1	9314.2	6464.0	7782.6	5316.2	6887.2
37.8	3147.1	68.1	70.1	285.6	143.3	134.7	100.5	79.0	73.9	122.3
52.9	2459.9	1724.7	1801.0	3646.1	2520.6	2494.2	2058.5	1135.8	988.3	1239.0
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45.1	258.1	751.6	88.1	318.4	331.9	155.9	368.2	85.3	51.0	122.1
240.7	3443.1	3227.8	4180.0	4160.3	3331.1	3234.1	4657.7	3120.6	1171.5	3816.7
169.1	6061.6	4470.4	5285.2	8022.2	4609.4	6526.0	4356.3	6898.0	1561.5	4236.9
1078.5	7537.5	6321.2	5864.8	6847.3	7335.9	6156.4	6440.1	10114.7	5457.0	6122.9
30.2	1663.5	789.1	515.9	8136.4	2292.0	2915.3	748.6	596.1	165.6	540.5
602.9	2963.5	2452.3	2290.1	4046.1	3454.8	2907.9	2245.7	3698.5	1712.2	2392.2
42.5	1679.4	761.1	500.8	959.3	1214.2	516.6	680.3	241.0	317.6	299.1
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289.8	4045.8	4605.8	4612.8	7418.2	5783.0	6167.2	5405.0	2769.1	3997.0	4167.0
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2291.4	2034.2	1722.6
6157.6	4693.8	4348.9
3405.2	3807.3	2894.4
5486.6	4327.1	4801.8
3420.4	3759.5	3519.1
5823.2	5515.0	4820.6
4830.2	2961.4	2914.9
971.7	1628.7	702.5
18.1	27.6	56.1
396.6	261.5	141.9
2618.1	3404.6	2479.0
52.7	99.5	101.2
6132.5	4454.3	4682.0
7231.7	5951.4	5274.5
3866.6	3459.7	3604.5
273.4	384.6	230.9
7867.6	6289.5	4492.5
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8870.4	8707.5	7293.1
3405.1	4666.3	2655.2
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69.3	143.1	261.9
2328.1	2511.6	1742.7
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4252.0	3834.6	3603.3
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2552.9	2665.6	1767.1
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GQ264392.1 gg_id:538827 Structure Simulated Level Waste Site simulated level waste site clone WW2_81 GQ264
EU283357.1 gg_id:254735 consecutively aerated submerged treating domestic wastewater activated sludge m EU2833
GQ263619.1 gg_id:540149 Structure Simulated Level Waste Site simulated level waste site clone FW3_175C GQ263
FJ386545.1 gg_id:360124 vaccination sludge backf pumping house Xilang municipal wastewater treatment plar FJ3865
FJ439829.1 gg_id:558682 Investigation estrogen-degrading bioreactors membrane bioreactor biofilm clone M2 FJ4398
AY792298.1 gg_id:123927 Humic Lake clone CrystalBog022H6 AY7922
DQ404910.1 gg_id:152725 contaminated sediment clone 661186 DQ404
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AJ577267.1 gg_id:93561 Algoriphagus antarcticus str. LMG 21482 AJ5772
U85891.1 gg_id:2611 Algoriphagus ratkowskyi str. IC025 U8589
AY771735.1 gg_id:144618 Algoriphagus ratkowskyi S5-5 AY7717
EU636233.1 gg_id:278695 Algoriphagus sp. PR1(2008) str. PR1 EU6362
EU703453.1 gg_id:450855 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH9 EU7034
GQ340168.1 gg_id:585358 Prokaryotic Marathonas Reservoir Greece water column clone K07-34-BAC GQ340
AY699794.1 gg_id:100794 Algoriphagus yeomjeoni str. MSS-160 AY6997
EF392675.1 gg_id:211176 Algoriphagus vanfongensis str. KMM 6241 EF3926
FJ986206.1 gg_id:399883 Algoriphagus sp. str. HMC4223 FJ9862
EF219025.1 gg_id:266307 structure and significance Rhizobiales biofouling biofilms on reverse osmosis membra EF2190
DQ178979.1 gg_id:139018 Algoriphagus dokdonensis str. DS-44 DQ178
AY835923.1 gg_id:110855 Algoriphagus locisalis str. MSS-171 AY8359
AY264839.1 gg_id:85985 Hongiella halophila str. IMSNU 14013 JC2051 AY2648
AY264840.1 gg_id:82949 Hongiella ornithinivorans str. IMSNU 14014 JC2052 AY2648
DQ365899.1 gg_id:156351 Algoriphagus sp. str. RE3 DQ365
GQ396828.1 gg_id:537859 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ396
GQ009408.1 gg_id:500257 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
FJ196000.1 gg_id:346430 Algoriphagus sp. str. ZS3-3 FJ1960
EU800233.1 gg_id:342719 It's all ranking aquatic Delaware Bay NJ clone 2C228256 EU8002
EU880511.1 gg_id:330914 Cyclobacterium sp. str. P81 EU8805
AY133105.1 gg_id:59894 TCE-contaminated site clone ccspost2184 AY1331
EF488486.1 gg_id:221747 Hongiella hitoincola str. 7-UAH EF4884
AJ717393.1 gg_id:110611 Chimaereicella alkaliphila str. AC74 AJ7173
EU283530.1 gg_id:279331 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A507 EU2835
AJ697698.1 gg_id:99104 mesotrophic lake clone SF21 AJ6976
EU161637.1 gg_id:239326 Hongiella aquaeductus str. T4 EU1616
AJ244689.1 gg_id:71214 Cyclobacterium sp. str. V4.MS.32 = MM_2749 AJ2446
GU072591.1 gg_id:556145 Algoriphagus sp. str. LYX05 GU072
GQ340091.1 gg_id:569230 Prokaryotic Marathonas Reservoir Greece water column clone A07-64-BAC GQ340
AY771733.1 gg_id:144558 Algoriphagus antarcticus S4-9 AY7717
AJ744861.1 gg_id:104934 Aquiflexum balticum str. BA160 AJ7448
EU703272.1 gg_id:590303 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU7032

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176.6	3935.0	2692.6	2380.7	4100.1	2984.3	3524.8	3043.6	3122.3	1032.4	2891.3
90.0	6693.6	5594.8	6937.7	8389.0	6071.6	6551.6	6189.9	5485.8	1731.2	5313.1
564.0	4846.9	4222.8	2696.1	3728.6	3922.6	2451.5	2987.9	5879.4	1268.1	2802.4
330.8	4869.2	3968.0	4502.0	6746.2	4303.3	5170.3	3814.8	4963.5	2864.2	3963.7
92.6	4073.5	2565.8	2921.9	7277.3	3792.0	3346.5	2495.5	961.4	376.6	1418.1
52.8	343.0	340.3	303.6	764.1	458.0	701.8	339.1	157.1	199.4	248.9
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288.4	4624.1	4225.1	5111.9	5486.1	5448.3	4904.1	5344.9	5178.8	2768.1	4473.5
1933.8	3755.0	4762.1	4440.2	5725.9	3990.8	4371.7	4700.7	2981.1	5665.3	3285.3
9251.8	10379.8	8429.0	7848.0	7651.7	10085.7	7119.3	9338.9	14090.2	8346.3	9043.3
87.3	2024.0	1536.4	1237.0	2073.2	1401.8	1675.8	1805.1	1510.9	1467.5	1296.2
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271.5	2578.4	3578.1	3326.6	3964.9	3084.8	2382.4	4216.6	2072.2	1926.2	2842.3
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53.7	284.5	394.4	365.0	1055.6	445.6	399.1	968.8	368.3	79.4	218.9
283.8	3266.0	2943.1	3096.7	4461.5	3187.8	4351.3	4724.4	2174.8	1434.5	4078.8
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1600.5	1603.1	1269.1
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s__Persicobacter diffluens	74336
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s__Thermonema rossianum	74261
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EU283502.1 gg_id:278772 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A223 EU283
EU283503.1 gg_id:278764 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1488 EU283
AJ564643.1 gg_id:90126 Belliella baltica str. BA134 AJ5646
EU685336.1 gg_id:291455 Belliella sp. str. CC-SAL-25 EU685
AY533665.1 gg_id:105344 Cyclobacterium marinum str. DSM 745 AY5336
AY960985.1 gg_id:115015 Cyclobacterium amurskyensis str. KMM 6143 AY9609
EU419941.1 gg_id:269319 Cyclobacterium linum str. RW54 EU4199
DQ534063.1 gg_id:160672 Cyclobacterium linum str. HY9 DQ534
AM406795.1 gg_id:183122 Echinicola vietnamensis KMM 6221 AM406
DQ645421.1 gg_id:159952 Echinicola vietnamensis str. KMM 6221 DQ645
FJ152973.1 gg_id:327267 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX4CI FJ1529
FJ152601.1 gg_id:318195 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX1A_ FJ1526
FM991866.1 gg_id:553854 Belliella sp. str. LW7 FM991
FJ671714.1 gg_id:521536 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6717
AY533663.1 gg_id:105029 Hongiella marincola str. SW-2 AY5336
FJ674389.1 gg_id:514663 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6743
DQ112663.1 gg_id:130535 Rhodinella ikkaensis str. GCM70 DQ112
GU112990.2 gg_id:591576 Rhodonellum psychrophilum str. 4-5-25 GU112
AY849869.1 gg_id:110577 Microscilla sp. str. MY04 AY8498
FN554611.1 gg_id:541109 Flammeovirga aprica str. HG4 FN5546
FN377813.1 gg_id:549152 Flammeovirga sp. aga24 MB-Aga24 FN3778
AB251933.1 gg_id:178196 Flammeovirga bosoensis str. YS10 AB2519
AB078077.1 gg_id:58611 Flexithrix dorotheae str. IFO 15987 AB0780
AB078073.1 gg_id:58615 Flexibacter tractuosus str. IFO 16035 AB0780
EU328009.1 gg_id:278936 dynamics during bioremediation crude oil contaminated moderate saline soil clone B EU3280
AB433335.1 gg_id:315738 Fulvivirga kasyanovii AB4333
AB260929.1 gg_id:178637 Persicobacter diffluens str. NBRC 15940 AB2609
AB265183.1 gg_id:176970 Flexibacter sp. str. 37GB AB2651
AB444610.1 gg_id:341062 Rapidithrix sp. str. TISTR 1768 AB4446
AB265184.1 gg_id:175211 Flexibacter sp. str. 58GB AB2651
AB265186.1 gg_id:183407 Flexibacter sp. str. SH1.3.1 AB2651
EU697080.1 gg_id:293250 Roseivirga sp. str. F8 EU6970
AJ310654.1 gg_id:106339 Sporocytophaga myxococcoides str. DSM 11118T AJ3106
FJ372724.1 gg_id:357873 Sporocytophaga sp. str. 4v FJ3727
Y08958.1 gg_id:2630 Thermonema rossianum str. AG3-1 Y08958
U10877.1 gg_id:17215 Riemerella anatipestifer str. ATCC 11845 U10877
AB539957.1 gg_id:518608 Evidence syntrophic acetate oxidation coupled hydrogenotrophic methanogenesis -t AB5399
EU639239.1 gg_id:331320 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6392
AB274511.1 gg_id:214740 packed-bed reactor clone CFB-22 AB2745
AF018199.1 gg_id:2632 hot spring clone env.OPS17 AF0181
CU918589.1 gg_id:568907 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9185

351.2	6526.2	4458.2	5181.9	6493.0	5975.0	4603.5	6404.8	8120.4	5809.4	5387.0
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22.0	12.5	15.4	14.9	20.5	15.6	13.7	26.1	17.7	17.2	15.0
250.4	6285.7	6034.1	4919.8	4303.3	5900.3	3271.9	6389.1	8221.1	3229.7	4913.9
2923.4	10527.2	8797.1	10023.4	9329.2	10368.8	10250.8	10198.5	13034.3	7463.8	8478.6
3496.9	6427.4	7077.6	7816.8	9791.1	8620.7	9042.3	8117.3	5400.5	5672.7	6590.1
134.6	2505.4	1952.1	1564.3	1773.1	2198.4	1082.1	2263.9	4022.9	853.2	1702.9
38.6	103.2	188.7	156.7	242.2	88.0	191.2	161.1	53.0	37.3	84.9
119.6	4260.5	3512.9	4136.7	4020.7	4710.1	4059.7	4292.2	4276.4	3579.5	3885.0
39.1	33.5	30.3	45.2	38.6	40.8	33.9	33.2	22.0	31.1	41.3
286.1	2975.0	3831.9	3652.4	4552.5	3488.6	4751.0	3385.3	2869.2	1783.3	2881.9
74.0	741.1	992.8	803.0	782.7	608.5	552.7	823.4	525.3	328.3	483.9
851.7	3780.3	3489.6	3552.2	4134.3	3629.4	3811.3	3858.1	4466.9	1361.2	3102.3
3904.2	4215.0	4022.5	4066.7	5291.7	4220.2	4381.9	4919.7	6464.8	4645.4	4634.1
48.2	4685.3	3859.7	3622.7	5308.2	3961.0	4390.8	3636.6	3436.9	1645.3	2881.0
905.8	5920.9	6571.0	7748.7	8340.0	6386.1	7805.2	6780.3	5208.4	2421.0	5315.3
34.6	93.1	100.8	117.5	247.5	126.8	146.5	124.4	55.0	52.6	48.1
78.7	1742.7	1826.0	2167.7	3255.8	2010.1	2470.0	2305.2	2047.0	716.9	958.1
103.7	250.8	310.2	337.6	647.9	271.7	475.6	382.9	245.5	279.4	359.8
53.8	1573.9	1253.6	1332.5	1586.2	1153.0	1458.7	1141.5	1305.3	3212.9	883.4
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40.3	45.5	95.7	77.3	53.5	45.8	56.6	69.3	73.6	38.2	99.5
879.4	2338.9	2996.7	3242.7	1922.5	1603.8	3452.6	2753.9	2219.2	711.4	4080.5
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61.1	296.7	427.0	444.2	314.0	112.0	331.4	262.5	131.6	77.8	266.6
51.7	413.2	693.9	642.5	686.8	647.6	657.4	1108.2	231.4	81.2	356.4
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1581.7	1255.1	952.8	1018.7	1708.3	888.1	968.5	1158.1	811.2	651.3	1303.3
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82.4	443.6	538.4	501.4	820.5	464.9	621.4	917.4	474.1	105.3	314.2
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36.2	34.8	77.3	80.1	72.1	43.1	36.5	85.8	44.8	18.2	55.1
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8435.6	5532.2	4985.7	6330.5	9222.0	5715.9	7101.0	6340.4	6769.6	2472.8	5580.2
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6711.5	6813.8	7661.5
1738.8	2039.1	1024.3
73.1	92.3	100.5
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3260.8	2636.1	3690.2
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344.0	309.7	277.1
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4717.3	5204.6	4793.9
16.4	19.2	18.9
46.8	58.6	38.3
2637.5	2958.0	1688.9
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245.9	183.8	167.4
598.8	760.6	483.6
1485.2	1419.1	1242.6
1591.3	1524.1	1292.0
2121.5	1976.7	1809.8
652.3	686.7	199.4
1185.6	1181.3	621.6
4101.8	3936.2	4001.6
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2503.8	3426.6	2564.2
6153.7	5770.6	5988.6
3920.4	5546.1	6339.3

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g__Thermonema
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CU924222.1 gg_id:544947 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EF092232.1 gg_id:275754 Persistent Axinella corrugata Flexibacteraceae clone B2706_D5 EF0922
DQ446174.2 gg_id:169117 Surface Mucopolysaccharide Layer and Band Microbial Mat Black Band-Diseased Sid DQ446
GU118694.1 gg_id:584570 Threatened Corals Provide Microbial Habitats clone Mfav_D23 GU118
FJ203289.1 gg_id:338360 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2032
EU236350.1 gg_id:292109 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A6 EU2363
GU119029.1 gg_id:555927 Threatened Corals Provide Microbial Habitats clone Past_A16 GU119
AY193144.1 gg_id:79737 marine sediment clone Bol18 AY1931
AB276355.1 gg_id:225690 Perexilibacter aurantiacus str. Shu-F-UV2-2 AB2763
FN396961.1 gg_id:376180 Flexibacter sp. str. AMV16 FN3969
GQ261809.1 gg_id:511354 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
FJ202555.1 gg_id:353421 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2025
FJ203032.1 gg_id:303670 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
AB015528.1 gg_id:2588 deep-sea sediment clone BD1-27 AB0155
GU118814.1 gg_id:589137 Threatened Corals Provide Microbial Habitats clone Mfra_M22 GU118
AB359908.1 gg_id:270601 Limibacter armeniacum str. YM11-159 AB3599
AM997917.1 gg_id:571975 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AB078074.1 gg_id:58613 Flexibacter tractuosus str. IFO 16037 AB0780
FJ203593.1 gg_id:322937 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
FJ203538.1 gg_id:356218 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
EU491626.1 gg_id:259009 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU4916
FJ425620.1 gg_id:356937 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata F FJ4256
AB058919.1 gg_id:66996 Reichenbachia agariperforans str. KMM 3525 AB0589
EF208684.1 gg_id:201988 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.C EF2086
FJ612161.1 gg_id:553065 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.4.24 FJ6121
EU801449.1 gg_id:327877 It's all ranking aquatic Chesapeake Bay MD clone 3C002742 EU8014
EU050910.1 gg_id:252466 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_32 EU0509
FJ202064.1 gg_id:332966 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2020
AB530240.1 gg_id:545952 Monitoring Suez and Tokyo bays based on analyses marine sediment clone Tokyo..B AB5302
GU118220.1 gg_id:576352 Threatened Corals Provide Microbial Habitats clone Dstr_K24 GU118
FJ425640.1 gg_id:364885 communnities healthy and diseased colonies Caribbean coral Montastrea faveolata F FJ4256
FJ202278.1 gg_id:334363 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
AM162576.1 gg_id:145556 and role capsules Sepia officinalis cuttlefish egg capsule clone 3iSOMBO27 AM162
AB255370.1 gg_id:239946 Sediminitomix flava str. Mok-1-85 AB2553
EF208685.1 gg_id:200444 Vertical and horizontal structure microbial sandy carbonate sediment clone CI5cm.C1 EF2086
AJ565431.1 gg_id:90078 Bacteroidetes MWH-CFBk5 AJ5654
FJ203647.1 gg_id:346219 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
FJ205242.1 gg_id:540371 Prokaryotic deep-sea region East Lau Spreading Centre inactive hydrothermal field se FJ2052
AM746683.1 gg_id:255630 etiology rosy discoloration ancient wall paintings rosy-discoloured mural clone A5 AM746
EU236347.1 gg_id:287889 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg91A5 EU2363
GQ261768.1 gg_id:512679 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261

2338.5	4742.4	5040.0	5352.9	5577.6	4708.8	5854.2	3999.4	4382.6	2056.3	5320.4
4087.2	8347.1	8667.8	10328.3	7262.7	8605.9	8908.8	8192.9	8219.4	8716.9	8917.9
32.4	211.5	273.2	299.3	183.9	344.7	267.3	423.5	139.5	220.3	218.9
4111.8	4630.8	4446.9	4345.7	4835.3	4153.0	4806.1	4380.3	6670.4	3076.1	3110.8
55.9	360.2	435.3	551.8	592.0	234.9	584.3	415.4	317.3	51.9	233.0
1640.0	4371.8	3989.3	3921.3	3911.7	3559.3	3669.0	3848.2	3854.1	2108.1	3614.1
1146.8	2043.9	2992.0	2260.1	1788.9	1831.9	2045.2	2065.2	2643.2	1557.9	1937.1
298.7	1228.3	1058.8	1052.9	1116.2	1156.0	858.7	1128.4	794.7	376.4	1022.6
297.1	1218.5	1540.5	2088.5	1660.7	1377.4	1394.5	2288.6	1235.0	641.5	1036.2
358.7	3624.4	4544.6	4291.5	4613.1	4331.3	4104.9	4384.4	3131.8	2112.9	3419.6
93.1	2241.5	3066.2	4137.6	3022.8	3659.2	3573.0	3261.4	2119.3	526.5	2069.6
631.6	3080.0	3479.9	3864.1	3271.9	3261.2	3106.3	2729.9	2845.7	998.7	2661.9
10526.9	6027.3	6252.3	5783.0	7424.0	5440.2	7045.5	5702.9	10122.9	5338.3	4973.8
42.5	358.7	564.2	572.8	122.4	736.7	749.8	426.0	221.7	117.5	599.1
4793.6	4664.0	3998.9	3861.8	4077.5	4501.9	4723.9	4609.1	5194.2	2881.2	3749.1
4210.7	7332.6	7059.4	7050.9	6340.6	6649.9	6565.5	6668.0	9476.4	6161.6	6430.6
1559.4	939.0	1185.4	1030.3	1228.4	1490.2	1152.9	1177.8	1334.4	4033.4	778.7
248.0	868.8	926.9	103.7	1096.4	992.5	889.9	1155.8	1065.4	766.2	856.9
1189.4	2395.7	3337.8	3406.8	2827.6	3484.7	3143.8	3166.7	2921.6	2610.6	1913.7
212.7	3106.5	3620.9	4339.8	2759.6	3106.8	2868.0	3908.0	2833.3	1447.0	3595.3
430.8	1808.4	2636.2	2610.1	3165.9	1977.2	3856.3	2598.4	1835.3	1032.4	2369.2
215.2	1883.4	2789.8	2716.3	1685.4	2121.0	1606.7	2611.4	3178.8	2609.4	1526.3
1679.9	4801.5	4953.5	3229.5	4753.9	4059.4	5190.1	4608.1	3997.8	1985.8	4622.8
48.8	76.7	49.5	55.7	45.1	69.2	52.6	60.2	45.8	34.3	45.5
1225.2	1926.2	2869.9	2234.9	2409.5	2309.3	2691.8	2721.8	1563.9	1587.8	1964.9
5952.0	7960.0	6902.9	7471.7	7161.8	7088.8	7004.8	7848.9	9889.3	6001.7	8947.3
504.3	5741.7	5239.5	5504.3	4575.0	5190.8	4807.6	5206.3	6544.3	5061.4	4736.6
60.9	78.7	116.5	137.8	192.1	141.9	156.8	180.7	48.7	42.3	64.0
57.8	1713.9	2205.2	2686.7	1815.6	1180.6	2017.9	2597.7	855.2	687.8	3856.5
814.9	3716.6	4180.0	3917.1	5607.6	4607.7	6677.2	4214.2	4132.9	2589.2	3242.1
44.3	683.2	942.5	1375.2	748.9	636.5	862.6	1025.4	574.6	66.4	557.9
423.1	2729.2	3360.8	3358.7	2564.1	3124.7	3779.6	3098.6	3542.3	2101.1	2158.9
53.5	547.2	997.1	877.5	944.5	515.6	1840.6	991.9	402.7	89.1	371.8
35.6	122.3	110.5	95.5	107.7	93.0	61.8	97.7	167.5	48.0	53.0
40.6	763.8	749.2	494.7	1361.3	760.0	904.7	443.8	553.8	310.4	236.8
92.7	4077.5	3039.2	3213.1	3070.0	3791.7	3026.3	3260.1	5558.1	4044.2	3451.4
263.8	713.4	1141.9	997.5	1289.7	918.9	1919.6	937.4	588.5	409.3	857.4
1190.4	2148.7	2970.3	3373.6	2620.7	2380.5	3415.8	2426.6	1634.7	1391.1	2023.9
1170.4	7074.4	5638.4	5724.4	6105.7	6257.5	6698.6	5464.1	5774.1	7439.8	5147.3
1578.8	3441.4	3467.0	3575.0	3906.3	3703.2	3277.6	3470.3	4503.3	2521.0	3029.9
1586.8	2398.2	2828.3	2864.6	2892.6	2105.7	3917.7	2768.3	1687.2	444.1	2263.7

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444.0	484.5	506.6
3432.9	4447.7	4219.4
506.8	670.3	201.7
3547.0	3790.6	2418.3
1658.3	2480.7	2113.7
922.3	1197.7	849.8
2503.6	1878.1	1737.4
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433.8	553.6	318.4
3925.1	5286.8	3945.0
7319.8	5925.0	4893.9
1150.5	1690.1	623.6
1096.4	1067.1	1304.1
2732.4	2601.0	2210.1
3038.5	2570.7	2162.0
2395.0	2337.7	1467.9
2268.4	3063.1	1676.7
3216.3	3849.3	3935.1
68.0	99.0	111.3
2359.2	1904.5	1824.2
6659.6	7352.9	5770.1
6251.6	4485.0	4112.0
82.3	99.8	82.9
1732.9	1194.3	1406.6
3980.7	4050.8	4308.1
552.4	835.2	438.1
4335.4	3568.2	2811.9
383.1	575.0	479.4
179.5	160.0	69.3
285.8	525.8	485.9
2694.9	2528.2	1999.1
492.6	1123.7	1045.0
1886.5	2130.6	1724.0
6027.5	6850.4	5547.5
4335.1	3919.9	2302.3
1908.7	2474.9	2824.7

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GU369880.1 gg_id:530688 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
EU491708.1 gg_id:277421 Abundance and microbial life ocean crust seafloor lavas East Pacific Rise clone EPR39 EU491
FJ358900.1 gg_id:534943 and redox-stratified sediments marine reef sandy sediment clone AO4 FJ3589
AB078038.1 gg_id:58647 Flexibacter aggregans str. IFO 15974 AB078
DQ269107.1 gg_id:183196 marine macro-alga surface clone DPC168 DQ269
GU118563.1 gg_id:536426 Threatened Corals Provide Microbial Habitats clone Mfav_M18 GU118
DQ415767.1 gg_id:158044 Dominant microbial limestone-corroding biofilms frasassi system Italy Frasassi sulfid DQ415
EU617868.1 gg_id:323057 Seasonal variation microbial Yel Sea sediment clone A13S-92 EU617
EF092163.1 gg_id:270590 Persistent Axinella corrugata Flexibacteraceae clone AC2_G5 EF0921
AB189382.1 gg_id:113510 cold seep sediment clone JT75-329 AB189
AY654823.1 gg_id:103997 Oculina mucus isolate 86 AY654
GU118216.1 gg_id:555186 Threatened Corals Provide Microbial Habitats clone Dstr_F06 GU118
FM209310.1 gg_id:533965 Microbial Negev desert s sand soil clone 3107 FM209
EU362130.1 gg_id:356181 and Mesquite Flats Site Death Valley dune sand clone 1 EU362
CP000383.1 gg_id:169083 Cytophaga hutchinsonii str. ATCC 33406 CP000
AB240469.1 gg_id:141044 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
EU133658.1 gg_id:245770 tallgrass prarie soil clone FFCH5405 EU133
GQ487883.1 gg_id:594352 Microbial metal soil polluted heavy metals clone T1-1 GQ487
FM877553.1 gg_id:356940 Microbial several mining wastes Bulgaria uranium mill tailings clone BuhD-239 FM877
GQ264517.1 gg_id:540980 Structure Simulated Level Waste Site simulated level waste site clone WW3_70 GQ264
AY921921.1 gg_id:112959 farm soil clone AKYG823 AY921
DQ499313.1 gg_id:159655 acidic cave snottite biofilm clone CV74 DQ499
AB286643.1 gg_id:208463 Reducing production and domination comamonadaceae reducing oxygen supply was AB286
GQ264428.1 gg_id:512079 Structure Simulated Level Waste Site simulated level waste site clone WW3_12 GQ264
AY921971.1 gg_id:112979 farm soil clone AKYG1686 AY921
EU644183.1 gg_id:284666 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
FN396950.1 gg_id:546606 integrative isotopic approach study degradation mixed Mixed (US3-M) enriched grou FN396
FM209126.1 gg_id:569376 Dynamics during identified and SSU libraries pilot-scale bioremediation process hydr FM209
EU015107.1 gg_id:247988 Investigation estrogen-degrading bioreactors membrane bioreactor suspension and EU015
CU924663.1 gg_id:552677 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EF516777.1 gg_id:219799 grassland soil clone FCPO734 EF5167
EU335282.1 gg_id:239396 Changes microbial metabolic and along hydrogeochemically variable profile unsatura EU335
FJ529937.1 gg_id:563166 Initial ammonia- and nitrite-oxidizing compromises successful nitritation counter-diffu FJ5299
AB199572.1 gg_id:111136 river water Japan clone RVW-05 AB199
FJ479173.1 gg_id:509032 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4791
FJ516813.1 gg_id:534971 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled biofilm FJ5168
EU133703.1 gg_id:242737 tallgrass prarie soil clone FFCH11302 EU133
EU104264.1 gg_id:351446 Evidence Comamonadaceae determinants settling performance activated sludge clo EU104
AY887012.1 gg_id:114481 fresh water clone 1.9.7 AY887
FJ478744.1 gg_id:510426 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
GQ021719.1 gg_id:487948 Topographical and Temporal Human Skin Microbiome skin antecubital fossa clone n GQ021

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7090.3	4651.3	5632.7	5916.1	4220.8	4594.4	3938.5	4966.5	5380.0	3525.8	6190.1
576.9	3803.0	4340.9	4255.0	3636.6	3809.6	4911.5	4772.6	2845.7	1123.4	3183.4
50.5	722.1	423.2	657.3	2760.6	658.7	1180.6	452.4	191.6	19.3	81.1
89.9	3055.7	1689.5	1497.4	1982.2	1800.6	1775.6	1567.5	2896.2	1101.2	937.0
643.2	2935.8	3607.3	3431.0	3495.0	3265.5	6159.0	3469.2	3926.8	2289.5	2302.6
250.7	1038.7	1915.4	1738.0	3309.2	1885.3	5086.5	1691.7	525.9	296.7	982.1
108.5	5476.2	5268.5	4958.9	4542.6	5429.4	4216.9	5658.6	6131.1	4361.2	4425.4
5189.1	10244.6	8745.7	8372.9	8515.0	8072.4	7971.3	8425.8	11196.4	8374.2	9243.8
155.4	473.0	821.3	994.9	818.9	626.4	717.8	1087.3	510.2	72.7	477.2
40.3	1978.3	3050.9	3252.2	1967.7	1975.3	3003.1	2127.1	892.1	1026.6	1510.4
2378.9	4535.3	4474.7	4578.6	4599.1	4649.2	4274.4	4657.7	3819.5	1865.7	4257.7
451.3	4392.4	4116.7	4004.0	5079.8	3825.7	6605.5	3878.9	4993.9	4855.2	2627.5
178.1	4844.5	4498.1	4768.1	5089.7	3757.5	5631.6	3949.3	3751.2	3791.2	3330.3
4552.5	7648.1	6788.6	6230.3	6998.4	7356.2	7485.5	7528.1	9304.7	5782.0	6989.7
55.5	506.6	342.3	388.0	1527.4	514.2	3134.6	266.9	119.3	133.3	120.3
307.3	5035.0	4251.8	4801.6	6575.8	4258.9	5230.6	4014.6	4156.0	4066.3	2404.4
94.2	4388.6	4621.0	4593.5	5041.1	4311.9	4774.3	4079.2	3026.9	4326.3	3290.3
337.1	3686.1	2867.8	3466.7	3212.3	2574.7	3932.1	2427.3	2610.5	1287.0	2662.8
1232.1	2751.2	3536.9	3846.1	5541.8	3458.6	4261.6	2777.0	1885.6	1455.9	2380.7
1333.0	2311.1	2144.0	2426.4	2663.4	2068.8	2457.7	2211.5	2262.8	1884.2	1620.9
87.2	3077.5	2348.8	2503.5	3185.7	2836.5	2739.1	2560.4	3161.3	2472.3	1590.3
31.7	672.9	239.6	251.3	1190.2	320.7	415.5	166.9	130.4	32.4	32.5
3706.4	1906.6	2468.2	2755.7	3904.7	2509.4	2902.5	3255.5	1865.4	580.1	2660.5
1107.4	14546.1	11190.6	13323.6	14976.4	12270.3	13606.5	12362.1	19585.7	12115.1	13164.6
886.2	3704.7	5092.0	5709.5	9746.3	4389.9	6374.4	3488.1	3174.2	2106.3	3424.5
81.9	2810.2	3366.9	3909.9	4916.6	4393.3	4099.1	3849.1	1587.8	2046.8	2796.2
10201.3	3542.6	3437.8	3571.4	3699.6	3794.6	4249.0	3255.3	4785.0	5179.5	3561.6
9547.7	5781.5	7402.4	5768.2	8159.3	5914.7	7188.3	5674.8	6430.9	7825.8	6342.8
162.5	4869.0	6943.1	5659.7	11120.8	5094.5	6687.8	4479.0	3140.8	5388.8	2890.2
7301.5	4840.4	4768.7	4575.6	5321.2	5491.3	5089.8	6089.5	6304.3	4865.8	6185.6
74.6	3339.3	3165.0	3715.4	5770.9	3247.5	5327.8	3813.1	3357.3	1963.6	2739.7
61.6	63.9	65.1	67.5	238.1	60.8	97.1	33.1	32.9	21.6	34.9
62.5	542.8	810.6	1047.4	1510.5	573.4	935.8	462.5	101.4	39.8	176.8
1476.8	2678.6	2737.5	3167.3	3839.2	1753.3	4011.9	1752.9	1517.8	1044.9	1758.0
245.1	4519.1	3684.4	3694.6	5516.3	3825.0	4345.8	3416.8	2398.8	3857.2	3291.6
62.8	963.1	1474.0	1295.5	2669.3	1324.4	1634.1	1473.0	994.6	978.9	555.8
1691.9	4492.5	5907.3	5754.8	8447.7	4528.7	6178.3	4027.3	4294.7	5099.4	4361.3
39.0	2266.9	1565.5	1854.2	1460.7	1723.6	1395.4	2267.1	2388.7	3599.3	2334.9
892.2	4270.3	3429.4	4655.9	6745.2	3129.5	5607.7	2559.2	2841.6	2096.7	3108.6
83.7	2213.9	4789.9	3491.3	3666.0	4327.9	2843.6	3813.0	1305.2	5239.5	2251.5

1470.3	1732.0	2283.0
4689.2	4774.3	3842.9
3919.7	4365.2	3425.9
605.6	629.2	281.5
2019.5	1051.0	1234.1
4835.5	3281.7	1700.4
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5496.6	4493.7	4442.7
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2819.5	1526.3	4247.0
3843.7	4882.4	3705.1
3458.4	4863.0	5669.9
3730.4	4886.9	5078.7
6281.3	7133.5	5424.0
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4772.3	4435.7	3526.7
3914.2	3689.7	2951.7
2489.6	1795.1	1634.6
2966.6	2459.7	2368.6
1892.2	2449.7	1657.4
2581.0	1733.2	1063.5
179.5	73.5	55.8
2745.4	2643.6	2169.6
11677.6	12063.1	10267.8
4446.2	4119.6	2417.9
2509.3	2792.5	2795.1
3854.8	4695.2	3329.4
6587.2	5351.3	4970.6
5638.1	2728.0	2846.3
4616.2	5129.8	4911.4
3104.8	3009.9	2301.4
59.0	137.2	51.8
582.8	102.6	172.8
2160.7	1924.2	1330.4
3627.3	3522.4	3111.8
1530.1	1780.7	988.5
4533.1	4142.4	4082.0
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AM934889.1 gg_id:544136 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM934
AY493953.1 gg_id:136478 Fingerprinting aggregates soil clone 453 AY4939
FJ710659.1 gg_id:578102 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7106
EU133655.1 gg_id:247445 tallgrass prarie soil clone FFCH599 EU1336
FJ478788.1 gg_id:541511 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4787
AF137029.1 gg_id:2595 Dyadobacter fermentens str. NS114 AF1370
FN421581.1 gg_id:588757 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 1_B12 FN4215
DQ335125.1 gg_id:145990 Dyadobacter sp. str. A54 DQ335
EU344946.1 gg_id:273380 Hepialus gonggaensis guts equalized library larval gut clone Hg5-36 EU3449
GQ389175.1 gg_id:510721 quality deterioration drinking system during serious red water outbreak clone D45 GQ389
FJ719038.1 gg_id:530554 Protozoan grazers alter metabolically active aquifer aquifier sediments clone p03_B0! FJ7190
AY904352.2 gg_id:112685 Tyrosinophaga indica str. GPTSA100-15 AY9043
AF502211.1 gg_id:59352 EBPR sludge lab scale clone HP1A92 AF5022
AB245370.1 gg_id:146568 Kaistomonas ginsengisoli str. Gsoil 085 AB2453
FN547417.1 gg_id:539293 Flectobacillus sp. str. WG3 FN5474
DQ112352.1 gg_id:130977 Flectobacillus sp. str. CL-GP79 DQ112
AB078051.1 gg_id:58637 Flexibacter flexilis str. IFO 16025 AB0780
AB464937.2 gg_id:350565 Altitudinal changes flora on Gulkana Glacier Alaska analyzed sequencing and -cycle c AB4649
EF639389.1 gg_id:235307 Hymenobacter sp. str. BSw20462 EF6393
DQ130048.1 gg_id:137870 microbial biota normal forearm human skin clone PR8 DQ130
GQ097346.1 gg_id:426219 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453h0: GQ097
EF127614.1 gg_id:207271 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE129 EF1276
EF423328.1 gg_id:212044 Hymenobacter sp. str. 1018 EF4233
AF408306.1 gg_id:23691 Hymenobacter group clone KL-94-1-15 AF4083
GQ097378.1 gg_id:408445 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw454c04 GQ097
AF408278.1 gg_id:46108 Taxeobacter sp. clone KL-2-4-3 AF4082
GQ097291.1 gg_id:377316 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw453b1: GQ097
GQ131579.1 gg_id:434806 Hymenobacter sp. str. BZ33r GQ131
EF516581.1 gg_id:219318 grassland soil clone FCPN403 EF5165
AB251884.1 gg_id:151061 Hymenobacter sp. str. PB17 AB2518
GQ097358.1 gg_id:383555 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw454a0: GQ097
Y18837.1 gg_id:2605 Taxeobacter sp. str. Txc1 Y18837
AF408300.1 gg_id:47791 Hymenobacter group clone KL-2-4-4 AF4083
EU370958.1 gg_id:270190 Hymenobacter sp. str. Dae14 EU3709
FJ979849.1 gg_id:418749 Hymenobacter sp. str. tsz19 FJ9798
AM697178.1 gg_id:224467 sequencing libraries indoor dust clone BF0001C019 AM697
Y18836.1 gg_id:2604 Taxeobacter gelupurpurascens str. Txg1 Y18836
GQ097743.1 gg_id:377016 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw456b0: GQ097
DQ365992.1 gg_id:150955 Hymenobacter sp. 21/4 DQ365
Y18835.1 gg_id:2574 Taxeobacter ocellatus str. Myx2105 Y18835
EF127605.1 gg_id:209617 Fossil Genes and Microbes Entombed Oldest Ice on Earth ice clone DLE022 EF1276

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45.2	34.7	47.3	57.3	913.0	169.1	307.4	150.0	48.8	17.3	31.1
64.8	2943.0	2587.5	2438.8	3700.3	2725.6	2705.9	3346.5	1435.6	1219.5	1235.5
2405.1	4367.6	4439.4	5133.1	6645.9	4259.4	5557.6	3860.5	3646.4	1964.5	3071.6
62.8	4935.0	6546.7	5663.3	6945.6	4850.4	8996.8	4773.1	5006.5	691.3	4431.1
164.8	4227.9	3982.2	3516.4	4026.4	5625.8	4363.7	4205.5	2232.9	6393.7	2499.9
1890.2	8546.9	7819.9	8045.3	8554.7	8592.0	7276.8	6946.9	6719.4	7685.7	7466.0
1615.3	8205.1	6071.1	5857.8	5528.4	8795.4	4792.9	5743.4	4050.3	6962.2	4249.5
5009.3	6798.2	6831.0	7203.6	9004.8	6693.7	8584.3	6274.1	6851.2	6513.2	7187.1
298.1	8053.9	7130.2	6199.5	6282.9	7982.0	5663.9	5317.7	3659.3	6975.1	5411.1
773.4	8221.7	7796.1	7873.3	8727.3	7696.5	8501.1	6984.2	8680.3	8307.1	7781.1
37.1	1867.1	1631.8	1498.2	2100.6	3690.5	465.4	2682.9	6683.8	4028.4	1475.7
1100.5	3803.0	3537.2	3213.6	3138.0	5434.4	1762.1	6478.7	6913.6	10723.7	4826.5
804.6	5590.7	6251.5	4379.7	5665.5	6669.5	4117.7	6296.9	11504.8	6402.8	6033.1
1548.0	5563.9	3783.3	4195.3	4321.4	6947.8	2962.7	9632.9	5310.6	15584.8	8915.6
429.6	2388.9	3190.4	3460.3	2196.8	3962.5	1825.4	5566.8	2296.9	8040.6	4258.2
4247.7	4880.4	4815.3	4354.6	3754.7	5352.3	3168.5	4070.3	3526.0	8576.7	2885.5
151.8	13898.0	9057.4	3301.6	6208.2	7709.2	6653.4	5816.0	13891.6	9603.3	4797.1
39.4	45.9	49.9	52.2	99.6	99.2	52.5	122.8	167.8	74.9	44.6
47.6	136.4	136.3	147.5	162.4	165.7	110.8	219.2	102.6	57.0	141.6
302.6	1524.3	1735.3	1825.5	2112.2	2646.7	1917.9	3326.7	1390.3	2506.0	2235.5
438.0	3688.1	3548.2	3634.5	3484.2	2898.8	3441.8	3071.2	3341.8	3900.0	3118.7
104.8	2246.4	1763.7	1696.8	1759.2	2309.5	711.1	2413.3	2802.0	5295.0	2585.5
41.8	473.5	433.0	741.2	588.3	554.0	792.8	875.0	778.9	221.3	364.6
1926.7	3410.6	3122.0	2871.1	3431.1	4679.5	3198.2	4725.0	4734.4	4078.8	4263.7
6692.2	7455.4	6721.6	7346.2	9182.3	7136.3	8773.9	6525.4	9606.8	5827.7	6301.4
6143.9	5373.6	4659.8	4417.4	3953.2	4911.8	4882.8	5560.8	6576.0	7968.4	5227.5
2271.3	7698.9	4884.7	5492.7	5513.8	5590.2	4975.7	4793.1	6943.4	5337.1	3895.2
13708.5	9693.0	6240.1	6037.6	5796.2	9077.2	5846.3	6669.3	11924.1	6605.0	7631.0
50.9	39.2	55.9	51.2	45.4	28.3	31.5	33.1	82.3	78.6	47.8
120.0	2472.9	2651.8	2749.0	2694.7	2420.8	2103.5	3115.9	1717.1	1636.5	1772.7
42.2	685.1	791.6	736.8	1015.7	662.6	1143.3	774.4	673.8	44.6	492.2
46.2	113.9	104.1	115.6	192.1	131.4	204.1	45.0	81.5	38.0	56.0
44.2	151.6	241.6	213.0	361.0	145.4	163.6	167.8	342.7	114.7	93.5
4586.2	6367.9	6013.6	5892.7	6553.7	6221.9	6981.5	5832.1	8284.4	4910.5	7197.6
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49.9	115.2	159.0	167.8	129.9	116.8	268.7	110.8	53.8	49.0	61.4
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4600.6	3268.4	3747.3
4415.5	3071.2	2154.4
5453.3	4100.8	4161.5
9333.5	6793.8	7711.6
8054.6	5912.0	6129.2
7069.9	7281.8	7052.7
8238.7	4716.6	6214.4
7876.7	7772.9	8016.1
1455.4	2135.5	619.7
4511.4	3621.4	2226.7
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5755.7	4090.3	3009.2
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4606.4	3523.0	3139.6
5710.9	2558.5	3737.9
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200.4	263.0	114.4
2425.9	2255.6	1258.2
2664.0	3893.2	3005.3
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605.7	848.2	718.4
3638.8	3729.2	2353.8
7278.7	6162.2	5077.9
5409.3	4189.8	4354.9
4301.7	4498.5	3912.0
6116.9	6996.5	5709.7
70.9	69.5	33.1
4000.5	3005.6	2933.2
723.8	833.8	1085.6
90.7	125.1	104.0
225.9	277.1	193.4
5943.0	6736.3	4504.0
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s__Microscilla marina	75466
s__unclassified	74771
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s__Pontibacter korlensis	73444
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NZ_AAWS01000102.1 gg_id:195845 Microscilla marina str. ATCC 23134 NZ_AA
NZ_AAWS01000012.1 gg_id:188038 Microscilla marina str. ATCC 23134 NZ_AA
FJ202249.1 gg_id:319886 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
FJ202421.1 gg_id:304538 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2024
FJ005077.1 gg_id:306350 Pontibacter sp. str. RCML-11 FJ0050
AM049256.1 gg_id:132838 Sedimentibacter rubrus str. SRC-1 AM049
DQ672723.1 gg_id:161173 Chinabacter akesu str. zy-4 DQ672
DQ365990.1 gg_id:153734 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil DQ365
GU339183.1 gg_id:548681 Pontibacter sp. str. HMD3125 GU339
FJ903178.1 gg_id:567490 Pontibacter sp. str. HMC6020 FJ9031
FM209327.1 gg_id:567720 Microbial Negev desert s sand soil clone 1031 FM209
DQ416803.1 gg_id:265113 Delineation Chromate-Resistant and Clones Cr(VI) Contaminated Sediments landfill : DQ416
AF227830.1 gg_id:42709 str. 47077 AF2278
DQ298339.1 gg_id:153137 studies on and nifH Lasiurus sindicus Sewan grass Thar Desert Rajasthan India rhizos DQ298
EF688348.1 gg_id:247967 soil clone F4-32 EF6883
DQ365989.1 gg_id:154323 Dominant soils Marble Point and Wright Valley Victoria Land Antarctica soil clone J3! DQ365
GQ144416.1 gg_id:448050 Runella sp. str. HMD1032 GQ144
DQ676366.1 gg_id:223870 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AB249681.1 gg_id:153026 Runella sp. str. P.slu-06 AB249
GQ022810.1 gg_id:486859 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbu3 GQ022
DQ847443.1 gg_id:161920 human forearm skin clone GL2-106 DQ847
AM697491.1 gg_id:217969 sequencing libraries indoor dust clone BF0002D002 AM697
AM000023.1 gg_id:146467 Spirosoma linguale str. LMG 10896 AM000
AF445698.1 gg_id:40101 travertine hot spring clone SM1G04 AF4456
EF451726.2 gg_id:259377 Spirosoma sp. str. RODSPM10 EF4517
AY792302.1 gg_id:127534 Temporal Variation and Humic Lake clone CrystalBog1D6 AY7923
EU925903.1 gg_id:309050 sediments sediment station DBS1 northern Bering Sea clone 129H24 EU9259
EF520590.1 gg_id:231977 structure lakes: what controls ? acid-impacted lake clone ADK-BTh02-48 EF5205
FJ592603.1 gg_id:549972 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5926
EU283380.1 gg_id:242384 consecutively aerated submerged treating domestic wastewater activated sludge m EU2833
EF516898.1 gg_id:219243 grassland soil clone FCPS427 EF5168
EU133692.1 gg_id:254714 tallgrass prarie soil clone FFCH7240 EU1336
AY218622.1 gg_id:81939 penguin droppings sediments clone KD3-93 AY2186
EU431819.1 gg_id:543813 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
AF233294.1 gg_id:51029 Tuber borchii symbiont b-10RA AF2332
CU466728.1 gg_id:328392 Evry wastewater treatment plant anoxic basin clone CU466
CU466751.1 gg_id:341696 Evry wastewater treatment plant anoxic basin clone CU466
EF516038.1 gg_id:222673 grassland soil clone FCPT641 EF5160
AF097805.1 gg_id:2488 activated sludge clone 49511 AF0978
GQ259245.1 gg_id:578996 Microbial activities coastal marine sediments and column Svalbard surface water clc GQ259
EF516127.1 gg_id:227169 grassland soil clone FCPS539 EF5161

206.8	808.8	848.0	826.1	610.5	613.4	461.6	844.4	925.2	468.8	360.7
3386.2	8518.3	6336.6	7039.9	9031.0	6010.0	6237.3	8048.7	9494.9	6138.1	4802.7
69.5	1092.3	763.9	806.1	707.8	800.7	469.3	1055.5	941.1	458.8	382.1
10128.0	6648.2	5757.4	5665.5	5911.0	5874.2	7065.9	6683.9	10006.5	8431.1	8124.6
81.4	2865.8	2177.0	1616.0	2253.2	2645.1	2185.4	2235.5	4031.6	1719.8	1509.9
40.5	269.1	315.3	293.7	337.2	278.6	293.4	366.0	200.0	163.0	205.1
284.7	894.6	1104.4	1352.7	1545.8	1107.0	1443.0	1320.9	533.1	571.2	666.7
51.4	83.0	104.8	140.8	116.3	70.1	105.9	111.6	73.2	41.7	62.1
424.1	3592.0	3338.8	3419.7	5330.2	4202.9	4166.1	3760.3	2703.7	1440.7	2739.1
127.2	2050.3	1575.3	1970.7	2167.9	1722.1	2145.6	2163.8	1226.0	371.3	814.8
1654.1	2272.7	2607.2	2381.7	2328.0	2715.8	3016.2	2326.2	1641.0	1732.7	2698.6
165.6	2735.9	3663.1	3400.5	3933.2	2867.5	3807.6	3081.0	2248.3	3577.2	3283.3
57.7	639.5	567.9	666.0	759.4	448.4	903.4	429.6	634.7	516.3	447.0
466.5	1863.0	2142.3	2445.4	3103.0	2082.1	3321.1	2257.6	819.7	1172.2	2520.3
2173.0	5384.0	5816.1	6140.5	5031.4	5070.2	5626.1	5522.1	4555.5	4160.4	6656.8
481.7	2189.8	2349.4	2514.6	2343.0	1387.9	2393.0	2456.1	1690.1	1506.5	2941.8
7982.4	9182.5	7658.5	8475.1	9667.9	10366.1	7703.3	8467.1	10043.5	8503.2	7831.9
5715.7	1622.8	1789.4	1791.0	2433.5	4275.1	116.2	1698.8	2160.8	1432.2	1310.2
551.2	1223.5	1220.5	1482.7	1986.1	1924.6	1486.5	1225.7	1367.2	688.4	1330.7
1033.1	5533.6	4773.9	5938.4	5260.4	6272.7	5315.6	5553.8	7377.9	5573.2	5295.3
4505.8	5410.9	4985.8	5262.3	5907.2	5161.0	5887.7	4893.7	5629.9	4101.6	5255.5
44.1	278.3	586.4	236.1	249.9	335.6	188.1	425.6	124.2	77.6	244.3
82.0	1406.7	6102.5	489.5	907.6	1525.5	669.6	2675.3	234.5	295.3	1521.0
81.3	926.0	1040.8	854.1	3035.6	1414.5	1731.3	786.4	503.2	257.5	718.2
110.6	182.4	364.8	221.1	195.8	155.3	216.3	208.9	179.0	44.8	148.8
390.4	2547.3	5748.1	1388.4	1631.8	3454.9	1523.8	3718.5	963.8	1027.8	2556.1
592.4	8872.2	8455.7	9157.5	8729.1	7062.0	9092.9	8543.8	9046.5	6314.4	9235.6
48.6	860.5	1831.3	2185.5	1447.8	1449.8	2568.0	2747.5	823.3	127.4	838.9
7312.3	4287.9	3983.6	4355.9	6584.4	3843.0	6773.2	4141.3	4553.5	3158.8	4612.5
37.7	837.6	1079.8	1193.7	1884.1	2124.4	2435.3	2190.2	983.0	152.4	462.7
87.9	3811.8	5141.4	5503.0	7020.3	5697.4	5714.4	9372.4	6507.0	2592.0	4519.3
7836.9	14432.7	12514.2	14103.2	15483.6	14318.7	15349.5	13776.9	17725.4	15165.8	15172.9
10816.2	5970.5	7578.7	6184.4	5593.9	6363.9	7149.2	5624.7	7312.4	5823.0	7992.9
210.2	4399.6	3691.6	4581.9	3630.9	3430.2	3231.4	4197.9	2793.3	1666.3	3017.9
3671.2	3601.6	3724.1	4480.4	3397.2	3752.1	3448.7	4447.3	3701.1	1287.6	4271.3
345.3	8655.1	8721.1	10359.2	10354.9	9353.5	10807.0	8753.2	7521.7	4702.4	7915.9
38.3	365.6	675.6	682.5	3496.1	1165.7	2090.0	951.2	195.6	100.0	242.1
9304.2	6833.2	6088.5	7163.3	8031.3	6667.1	8747.4	5964.6	8756.0	5951.2	7879.8
47.3	939.2	1524.1	1977.7	1089.9	968.8	1721.6	1919.7	1102.2	1232.8	991.8
31.7	1448.9	1598.7	2081.9	2380.5	3016.4	1923.6	1998.2	908.8	175.3	1038.1
40.4	1002.6	985.2	785.5	994.5	840.6	709.9	652.2	708.4	347.7	571.8

646.8	962.6	743.1
9444.1	5837.6	6528.4
880.3	910.6	616.6
6599.0	5707.6	4824.9
1932.9	1039.9	1743.9
311.7	339.3	316.8
1006.2	1519.0	1335.8
97.3	100.1	104.9
3729.9	3457.4	2937.6
1817.5	1501.7	1899.3
1905.8	2408.0	1781.5
3614.3	2460.1	2560.9
412.2	843.8	566.9
1846.3	2244.3	2595.1
5041.7	4582.5	4989.2
2152.4	2411.9	2411.8
7586.5	7637.3	7231.0
580.7	2568.2	1576.6
1350.2	1786.9	1266.5
5649.5	4219.8	4032.8
4974.4	6240.6	5658.4
272.1	460.0	200.2
717.1	568.4	500.7
1016.5	1308.2	605.2
157.5	119.6	157.9
1640.9	1106.4	1492.9
6578.5	6687.1	6708.0
2128.8	1511.2	2405.3
3744.9	4212.5	4493.3
1952.0	1230.7	1712.7
6852.6	4997.2	3679.6
13157.2	12655.1	11453.7
5889.5	6087.5	5424.9
3789.7	3418.5	2373.2
1600.4	4118.4	3727.9
8229.4	8026.0	7551.8
1087.9	603.5	677.4
5826.8	6561.2	8219.5
1130.4	1532.0	1467.2
1729.6	1365.9	1060.4
646.9	1241.1	972.1

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AY921825.1 gg_id:113309 farm soil clone AKYH918 AY9218
EF516341.1 gg_id:223126 grassland soil clone FCPP386 EF5163
EU803667.1 gg_id:334320 It's all ranking aquatic Lake Gatun clone 5C231272 EU8036
DQ640737.1 gg_id:228088 full-scale EBPR sludge clone Skagen115 DQ640
EU703356.1 gg_id:419525 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH95 EU7033
EU104255.1 gg_id:307869 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1042
EF020137.1 gg_id:214099 aspen rhizosphere clone Elev_16S_1558 EF0201
GQ340105.1 gg_id:584477 Prokaryotic Marathonas Reservoir Greece water column clone A07-90-BAC GQ340
FM253657.1 gg_id:332717 Rock gold mine unusually microbial biofilm clone E04-2 FM253
DQ521530.1 gg_id:179289 Antarctic lake ice cover clone ANTLV2_H03 DQ521
AM991273.1 gg_id:279186 Microbial groundwater and their potential use biomonitoring karst spring water clo AM991
EU133767.1 gg_id:244639 tallgrass prarie soil clone FFCH4913 EU1337
AF534435.1 gg_id:83335 Toolik Lake main station at 3 m depth clone TLM11/TLMdgge04 AF5344
EF520601.1 gg_id:232505 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-17 EF5206
GQ340151.1 gg_id:581285 Prokaryotic Marathonas Reservoir Greece water column clone B07-94-BAC GQ340
FJ612299.1 gg_id:543271 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.43 FJ6122
FJ612395.1 gg_id:586468 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.3.91 FJ6123
FJ612274.1 gg_id:513523 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.4.20 FJ6122
EU703435.1 gg_id:415279 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH54 EU7034
FJ612336.1 gg_id:547205 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.2.1 FJ6123
AY947930.1 gg_id:142943 Synchrony and seasonality two temperate rivers USA: Massachusetts Ipswich River c AY9479
GQ340219.1 gg_id:577223 Prokaryotic Marathonas Reservoir Greece water column clone VE07-43-BAC GQ340
EU104144.1 gg_id:322475 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1041
AM279196.1 gg_id:169294 Cytophaga-Flavobacterium-Bacteroides coastal North Sea marine water clone NorS AM279
EU091557.2 gg_id:330775 clones IRDE (IW) Western Ghats region India water clone IWENVB11 EU0915
DQ071076.1 gg_id:133154 marine surface water clone PB1.33 DQ071
GU444059.1 gg_id:516417 Effects amendments on fertility and microbial structure cucumber Cucumis sativus L GU444
AB078061.1 gg_id:58627 Flexibacter roseolus str. IFO 16030 AB0780
AY065626.1 gg_id:77370 Flectobacillus speluncae str. GWF20B AY0656
EF636834.1 gg_id:277776 Metagenomic and Namib desert sand clone 6 EF6368
EU289479.1 gg_id:245429 metagenomic approach biosynthesis ansamycin endophytes or symbionts enriched s EU2894
AB078072.1 gg_id:58616 Flexibacter tractuosus str. IFO 15989 AB0780
AJ290033.1 gg_id:20151 Austria: Lake Gossenkoellesee clone GKS2-216 GKS2-216 AJ2900
EU010168.1 gg_id:239504 Biogeography Singapore seawaters seawater clone B49 EU0101
AB078079.1 gg_id:58609 Microscilla furvescens str. IFO 15994 AB0780
AJ535729.1 gg_id:77393 Arcicella aquatica str. NO-502 AJ5357
AB078056.1 gg_id:58632 Flexibacter litoralis str. IFO 15988 AB0780
DQ917821.1 gg_id:221302 Microbial profiles bleached and wild-type Muricea elongata Microscilla clone BME34 DQ917
AJ746140.1 gg_id:112775 Arcicella sp. MG83 AJ7461
AB078059.1 gg_id:58628 Flexibacter polymorphus str. IFO 16703 AB0780
FJ667554.1 gg_id:555655 algae-lysing clone -13 FJ6675

56.0	2751.2	2634.9	2684.6	9399.4	3280.1	6883.8	2623.1	1269.2	761.0	1702.3
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10244.0	10715.5	10488.8	12813.3	12525.4	10871.7	12613.2	11644.9	17101.1	10200.6	12197.0
44.9	281.6	357.3	177.2	220.7	268.8	280.7	331.6	275.6	90.3	137.2
72.8	6989.0	6864.6	7563.7	5752.0	7068.7	6164.3	7740.3	4852.0	5912.9	5288.7
661.8	8237.0	6320.9	4883.7	4719.7	8418.0	4948.0	5648.6	3598.5	5139.3	3270.5
66.3	174.1	318.9	309.1	834.7	449.3	3632.7	416.2	107.9	42.7	205.1
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146.9	3925.4	5387.9	6652.0	6292.7	5314.0	5960.3	7025.4	6371.5	1564.3	4394.7
8710.9	14325.0	12999.0	13062.1	13119.1	13492.0	13307.2	12770.1	17274.9	14392.5	15843.8
7629.3	8181.6	7156.2	7495.2	7692.5	6767.0	7329.2	6706.0	10681.0	7307.8	6848.4
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81.6	1685.6	805.6	1013.5	1223.7	1255.6	1333.3	1164.6	1118.7	247.5	827.4
1909.0	9970.8	6997.5	7323.4	7400.3	7122.6	8309.2	6123.8	7712.2	5674.1	6405.9
493.0	4638.9	4787.4	5252.3	7085.4	4506.2	6501.9	4031.0	2623.1	1676.6	3485.8
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75.0	3398.7	5780.1	7747.8	2705.2	4197.5	2959.7	4322.3	3311.8	492.9	3086.8
16425.6	6247.4	5748.5	6542.7	6734.1	6003.0	6724.0	6072.5	7458.1	5295.0	7502.9
56.2	2102.3	3743.6	5618.2	187.0	3341.5	2053.2	7379.2	238.4	25.1	7371.3
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907.1	4331.3	5600.4	5802.3	4343.9	4617.7	5595.9	3862.5	4739.7	3937.5	4352.1
27.8	62.6	231.6	254.7	349.5	75.0	164.9	141.5	55.6	29.5	67.7
4798.6	7121.6	5948.4	6835.8	7633.4	6672.8	8102.6	6937.1	8388.7	5156.6	4485.1
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180.7	5953.7	4436.4	5044.3	5703.3	4835.2	3134.6	5342.9	5062.9	3997.1	7006.1
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1229.4	6233.9	7062.9	6458.8	5776.9	9176.6	6204.3	8167.7	6021.3	8432.0	7698.8
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33.1	206.8	299.2	318.6	366.7	229.7	233.1	261.0	113.5	52.0	212.8
93.3	1452.9	1695.5	1744.0	1451.9	1913.2	1090.5	2302.4	1052.3	1310.8	1583.2
35.6	142.2	264.6	316.5	85.0	143.6	147.5	223.4	46.2	90.7	267.5
269.5	2450.0	3438.5	1525.6	2610.8	2428.3	2527.0	2088.9	1418.6	915.6	1687.1

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515.3	305.8	665.0
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3684.0	2554.9	2025.4
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5676.5	5567.7	4994.2
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6160.9	6555.4	6224.8
4536.6	4083.3	4334.4
3287.8	2783.8	3283.0
797.3	815.2	958.0
5790.6	6106.1	5976.8
4308.4	3558.3	6597.5
1208.2	2787.6	1254.5
2311.9	2247.0	1470.1
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103.3	126.7	98.6
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47.6	74.7	139.9
5607.3	5767.4	4196.3
168.8	346.8	269.0
3444.6	3158.5	2322.4
4978.7	4596.2	5946.6
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1402.6	1870.0	2256.5
9433.6	6451.8	4087.5
3641.3	2609.3	2481.2
519.5	1417.7	719.0
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83.4	93.9	39.2
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EU371587.1 gg_id:555506 and Structural Changes Oyster Shell during 1-Year Storage oyster shell clone CBFOS-(EU371
DQ990929.2 gg_id:175203 Microbial Rock Varnish Yungay Atacama Desert Chile rock varnish clone AYRV1-015 DQ990
AM259891.1 gg_id:210600 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-5-25 AM259
GQ350621.1 gg_id:555379 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ350
AY167829.1 gg_id:77550 Taxeobacter sp. str. SAFR-033 AY1678
EF635010.1 gg_id:244833 Rudanella aurantiaca str. 5715S-11 EF6350
EU703303.1 gg_id:444025 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH98 EU7033
AB078065.1 gg_id:58624 Flexibacter ruber str. IFO 16677 AB0780
FN421864.1 gg_id:590649 proteogenomics physiology phyllosphere clover clone 2_D07 FN4218
EU004198.2 gg_id:257862 Rhodocytophaga aerolata str. 5416T-29 EU0041
EF683048.1 gg_id:249391 Eastern Mediterranean atmosphere clone F27_4H_FL EF6830
EU722650.1 gg_id:352793 Microbial athalassohaline Tirez lagoon (Spain) sediment clone SB74 EU7226
DQ346479.1 gg_id:155601 during composting libraries compost clone 2B07 DQ346
AM000022.1 gg_id:150422 Larkinella insperata str. LMG 22510 AM000
AB078063.1 gg_id:58625 Flexibacter roseolus str. IFO 16707 AB0780
AY854022.2 gg_id:115032 Leadbetterella byssophila str. 4M15 AY8540
GQ020313.1 gg_id:489354 Topographical and Temporal Human Skin Microbiome skin glabella clone nbu267e04 GQ020
DQ981405.1 gg_id:188216 entrapped Puruogangri ice core clone PIC-D5 DQ981
AF445730.1 gg_id:35334 CFB group clone SM2F08 AF4457
AY168735.2 gg_id:135189 Oxidizing Biofilms: Cultivation Approaches and Rates Arsenite Oxidation arsenite-oxi AY1687
AB078054.1 gg_id:58634 Flexibacter flexilis subsp. pelliculosus str. IFO 16028 subsp. AB0780
AM746475.1 gg_id:252171 Ekhidna lutea str. BiosLi/39 AM746
EU236411.1 gg_id:288687 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92E12 EU2364
FJ203195.1 gg_id:340708 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
AB078082.1 gg_id:58606 Microscilla sericea str. IFO 16561 AB0780
GQ421846.1 gg_id:549650 Adhaeribacter sp. str. 6515J-31 GQ421
AY907776.1 gg_id:136881 identification picoplankton contrasting waters Arabian Sea water clone A712037 AY9077
AB015263.1 gg_id:2577 deepest cold-seep area Japan Trench clone JTB248 sp. AB0152
DQ395524.1 gg_id:154918 deep-sea octacoral clone ctg_CGOCA57 DQ395
EU804292.1 gg_id:324075 It's all ranking aquatic 250 miles Panama City clone 6C232194 EU8042
EF016479.1 gg_id:181596 Near real-time autonomous detection marine on coastal mooring Monterey Bay Calif EF0164
EU804351.1 gg_id:320907 It's all ranking aquatic 250 miles Panama City clone 6C232257 EU8043
EF573031.1 gg_id:233619 Coco's Island site 23 marine clone S23_1130 EF5730
EU404040.1 gg_id:320521 Microbial septic tank effluent and soil biozone infiltrative surface clean water clone (EU4040
AB078048.1 gg_id:55293 Flexibacter elegans str. IFO 15055 AB0780
DQ395539.1 gg_id:153017 deep-sea octacoral clone ctg_CGOCA43 DQ395
EU005886.1 gg_id:274173 Major activity inside and outside natural iron-fertilized phytoplankton bloom 3 micro EU0058
GQ349744.1 gg_id:546322 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ349
AF217497.1 gg_id:29905 Rhodothermus marinus str. PRQ-55 AF2174
EU635948.1 gg_id:279426 Microbiology geochemistry great boiling and mud springs sediment hot spring; temp EU6359
CU467270.1 gg_id:319903 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467

233.2	6945.2	3715.6	5410.4	7077.8	5681.2	5643.7	6535.0	7393.5	5808.5	4572.3
3282.6	7820.4	6046.9	6498.5	7058.9	6078.0	7116.4	5048.9	8859.5	5940.1	6172.9
34.5	13.3	10.0	16.6	20.0	11.2	12.7	15.0	32.2	20.4	10.5
40.8	496.7	402.8	478.3	1091.7	527.6	1093.4	362.6	128.4	194.3	138.9
1480.7	1989.3	1490.4	1759.9	1503.7	1734.5	1235.8	2273.9	2615.1	300.9	1913.9
849.6	7873.4	8776.7	7908.9	9096.3	7855.4	7825.9	7760.4	8174.1	9315.2	6992.4
4194.7	5213.4	4920.1	5873.0	5206.2	4218.6	5626.2	4686.1	7347.2	4458.5	3996.9
39.2	31.6	45.6	55.1	70.0	47.4	77.8	84.5	59.0	21.1	52.0
4043.5	4841.6	6076.5	4133.2	6833.7	5835.9	5858.2	5283.3	5583.3	4500.0	5162.7
372.6	1459.1	826.1	1191.0	1911.3	1039.3	1140.6	1266.9	1294.2	624.3	567.8
690.6	5539.0	6154.2	6228.6	6735.0	5994.9	6844.6	5841.1	5504.1	7329.6	4780.1
313.7	3116.7	3416.2	4165.0	3945.7	2768.0	4682.0	3903.8	3746.2	1991.6	2762.8
187.0	2551.6	2640.8	2594.0	3986.9	2518.8	3956.3	3318.6	2104.9	1949.0	2093.1
87.2	420.0	385.2	451.0	372.7	500.8	324.0	635.2	168.5	267.5	228.7
44.2	146.8	272.2	426.1	705.6	260.3	570.2	405.0	114.0	29.6	174.0
50.4	1108.4	1265.3	1582.5	1678.8	793.8	1807.9	876.7	666.5	615.3	481.7
621.6	4765.6	5860.8	4172.0	5763.3	4933.5	4688.5	5582.4	5298.5	4009.6	4123.6
54.3	2655.5	2813.1	2157.5	1636.6	3361.1	1274.0	3309.2	2576.4	3516.4	2131.2
115.9	173.0	204.4	218.7	223.6	153.1	415.0	182.3	150.5	96.1	117.8
48.9	4809.1	6628.3	10074.4	7440.5	4159.8	7578.5	5655.7	6545.3	7059.0	3791.0
459.3	7741.9	5829.6	7172.8	6389.8	6698.2	6637.2	7638.2	10805.2	6016.4	6267.6
336.7	6475.9	3539.3	3241.6	2996.6	4382.9	2524.9	3532.5	8479.9	4194.6	2634.2
173.4	2325.0	3015.0	3661.5	2599.9	2860.9	2679.1	3144.1	1860.8	1142.4	3016.2
7624.4	6998.6	7813.4	8172.1	6639.6	6394.0	6543.9	6503.5	11220.3	7756.3	8844.4
94.7	245.1	383.7	336.7	254.5	284.3	246.5	484.9	243.8	86.2	178.3
432.3	5323.1	3662.3	4469.9	4791.9	4315.7	4305.6	4665.2	5929.4	3424.7	2867.5
227.9	1300.1	2948.4	1464.5	837.8	1329.6	1113.0	1621.3	1081.5	644.2	1192.0
43.2	238.3	487.1	380.8	226.8	228.5	261.0	530.7	126.8	60.1	158.0
60.1	319.7	417.8	385.9	276.5	252.4	312.5	390.3	499.6	175.9	346.7
105.7	825.2	1571.6	1777.1	1248.4	1262.3	3377.1	1722.5	979.7	263.8	517.9
43.6	1089.6	703.1	396.3	709.0	520.2	303.2	279.0	1068.1	92.0	196.8
37.1	495.7	664.0	501.0	359.4	389.9	498.6	419.6	321.0	96.7	309.4
10431.2	3703.2	4468.6	4093.7	3087.2	3032.4	4142.7	4317.7	7596.3	2979.7	3827.6
1362.8	8003.2	8482.1	9778.0	10476.5	8388.3	11133.5	9079.4	8111.6	4464.6	8354.2
37.4	197.5	236.2	337.6	313.5	267.6	333.7	378.0	164.5	134.9	146.5
292.7	3244.1	3983.9	4349.8	4430.8	3496.9	5246.7	4429.6	3699.6	1249.0	3038.6
4191.0	2395.4	2386.1	2540.2	1991.4	2018.2	1998.8	2204.0	4327.7	3128.4	2017.6
60.2	3933.3	2502.0	1970.0	2934.0	2247.5	2527.6	1427.7	4874.4	892.9	1669.4
50.0	84.6	96.3	129.5	77.1	81.3	425.1	110.6	20.6	49.6	47.9
275.5	3906.6	4174.3	4211.5	4161.3	3699.5	4402.2	5002.1	3932.1	3358.2	3187.3
13407.6	7041.3	5095.7	5967.7	5970.8	6631.1	8612.8	5988.2	7333.1	8116.1	9036.5

5994.5	4993.4	4032.7
5699.6	4350.6	6087.0
120.7	20.5	13.2
293.5	267.2	279.5
1462.9	1205.7	712.9
7008.8	6847.6	6740.1
5167.3	5489.8	3157.4
101.2	66.2	24.1
5191.8	4503.0	4063.6
1124.7	1232.0	1007.6
6498.4	6320.5	7508.3
3711.6	3605.4	2056.9
2536.5	2976.9	2852.5
535.5	478.4	367.9
155.3	514.6	181.2
2098.9	780.3	371.2
5089.5	4739.1	4352.2
2345.8	2664.3	1188.2
141.3	266.5	295.4
7960.0	4842.7	1306.3
5866.1	5501.4	7221.7
5417.0	2643.3	3018.4
2378.0	2681.2	3654.3
6762.7	7003.3	6173.2
273.6	335.1	321.8
4061.6	3496.9	3450.6
1379.0	1417.2	1260.8
195.9	289.0	205.9
255.0	399.7	260.3
1561.3	1587.5	2203.3
381.8	424.2	244.4
400.8	512.8	423.6
3947.7	4487.6	3737.8
7636.5	9121.5	11569.9
402.2	424.4	505.0
3261.5	3698.8	5341.8
1816.9	2986.8	2116.4
1479.8	1381.1	1012.1
67.3	68.5	92.7
3310.1	4071.6	4336.2
6601.3	7088.8	6127.4

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CU467410.1 gg_id:316919 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
AY862787.2 gg_id:161235 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon AY862
AM981339.1 gg_id:274210 Microbial processed Mediterranean seawater based on salt crystal Tunisian solar sa AM981
EF459716.1 gg_id:218096 Prokaryotic Hypersaline Inland Turkey Tuz Lake (hypersaline) clone 3-55B EF4597
AJ242998.1 gg_id:2645 halophilic EHB-2 AJ2429
CU467372.1 gg_id:337266 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
FN393464.1 gg_id:558759 prokaryotic sediments two Tunisian multipond sediment solar saltern clone 188ZA01 FN3934
FN393434.1 gg_id:537260 prokaryotic sediments two Tunisian multipond sediment solar saltern clone 188ZE03 FN3934
FN393524.1 gg_id:550621 prokaryotic sediments two Tunisian multipond sediment solar saltern clone SFD1D0 FN3935
EU869386.1 gg_id:317840 Microbial hypersaline soil Sidi Ameur Salt Lake Algerian Sahara clone ARDBACSS36 EU8693
FN393497.1 gg_id:575327 prokaryotic sediments two Tunisian multipond sediment solar saltern clone SFD1H1 FN3934
CU467411.1 gg_id:318809 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
EF106051.1 gg_id:201165 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1060
CU467386.1 gg_id:354845 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
CU467277.1 gg_id:305812 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
CU467363.1 gg_id:314160 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
AM981385.1 gg_id:273261 Microbial processed Mediterranean seawater based on salt crystal Tunisian solar sa AM981
AM981366.1 gg_id:274224 Microbial processed Mediterranean seawater based on salt crystal Tunisian solar sa AM981
CU467353.1 gg_id:347711 Prokaryotic Tunisian saltern Saltern solar multipond clone CU467
EF106117.1 gg_id:200167 microbial two endoevaporitic salt crusts evaporitic crust Lindsey Lake New Mexico cl EF1061
GU447292.1 gg_id:532169 Salisaeta longa str. BX104 GU447
EF106234.1 gg_id:201362 microbial two endoevaporitic salt crusts evaporitic crust Guerrero Negro Baja clone 3 EF1062
EU050888.1 gg_id:235984 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_01_23 EU0508
FJ745114.1 gg_id:564902 Transporter genes expressed coastal response dissolved organic carbon surface wate FJ7451
GU118662.1 gg_id:577399 Threatened Corals Provide Microbial Habitats clone Mfav_C15 GU118
FJ905760.1 gg_id:570489 s Tonga-Kermadec iron oxide sediments Volcano 1 Tonga Arc clone V1F167b FJ9057
GU061242.1 gg_id:541457 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
EF648151.1 gg_id:257002 dynamics during produced water treatment aerobic activated sludge clone XJ103 EF6481
AF407678.1 gg_id:60618 Great Artesian Basin clone Y30 AF4076
GQ108731.1 gg_id:437088 Topographical and Temporal Human Skin Microbiome skin occiput clone nbw692h0 GQ108
GU118538.1 gg_id:586741 Threatened Corals Provide Microbial Habitats clone Mfav_I11 GU118
EU592405.1 gg_id:536800 Seasonal changes Salton Sea hypersaline water clone SSW6AP EU5924
DQ889917.1 gg_id:172643 natural product producing octocoral Erythropodium caribaeorum Cytophaga clone E DQ889
AJ347046.1 gg_id:60166 sponge clone TK44 AJ3470
EU133663.1 gg_id:249217 tallgrass prarie soil clone FFCH12849 EU1336
GU056052.1 gg_id:592121 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
AB015543.1 gg_id:2649 deep-sea sediment clone BD2-15 AB0155
DQ070835.1 gg_id:148406 Prokaryotic Structures Seafloor Basalts Varying Age East Pacific Rise and Ridge basal DQ070
AM997702.1 gg_id:571736 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
AY493957.1 gg_id:136516 Fingerprinting aggregates soil clone 9 AY4939
FN545882.2 gg_id:588351 un 2 Rupi basin Bulgaria hot spring clone S2R-130 FN5458

13148.4	6973.8	8120.5	8841.6	6217.0	6945.8	6477.1	8034.9	10820.7	8995.4	8612.1
37.9	397.9	437.7	389.7	518.7	411.5	457.8	686.3	285.6	43.3	237.9
514.4	3576.3	3359.0	3526.2	3126.8	4217.6	3637.2	3861.5	3350.2	5424.5	2982.6
20471.0	1561.8	3328.6	3935.6	4340.5	3696.1	4111.3	5749.7	4034.7	5826.4	3802.4
11767.4	8203.1	6889.1	7559.9	7575.3	6006.1	7612.9	7386.9	10602.0	2274.2	5780.8
19702.2	10419.9	9684.3	10901.3	9500.7	10090.2	9622.8	10199.7	10104.1	11699.4	11209.6
12457.9	8820.8	8163.4	7833.8	7509.5	8375.0	7607.0	8118.9	9299.9	9022.7	7803.0
15473.5	7813.3	8470.6	9000.9	8663.5	7369.4	9048.7	7705.0	7966.7	6678.5	9435.4
5603.6	5942.3	5551.3	6381.6	6606.0	5436.0	7279.3	6095.4	4895.1	4149.1	5215.2
28.5	169.8	121.6	93.6	208.4	81.5	192.6	90.8	84.2	40.6	44.2
6139.0	7162.1	6908.2	5404.6	6564.7	6326.3	6828.5	5634.7	7165.2	5598.6	4751.1
115.2	2898.4	2730.2	2292.1	1931.5	2090.3	3476.0	2341.3	1096.3	1895.4	1675.6
42.0	29.5	31.9	39.1	25.8	28.9	34.7	27.0	41.9	26.6	18.2
9023.3	5991.8	6633.9	7150.2	5654.8	5678.7	5837.4	6637.0	5747.6	5479.4	4836.7
1096.7	3774.0	4436.8	3865.2	4181.4	3913.8	4660.6	3988.5	5331.2	5675.2	3402.7
2574.6	3224.1	3119.0	3113.9	3383.4	2949.4	3521.7	3445.9	3330.1	1769.3	2920.5
7549.4	8607.4	8598.8	10534.4	9611.5	9532.2	10711.7	9694.3	7194.4	11968.7	9620.9
658.1	2402.7	1763.4	1481.9	1673.9	2406.1	2770.3	2320.7	2301.6	1546.6	1463.6
10485.8	9171.7	9207.5	11142.9	9304.8	9285.7	9191.4	9789.3	9774.5	11345.8	9597.2
697.0	3481.8	3865.5	3514.1	4954.4	3957.0	4683.1	3295.0	3432.5	4480.2	2959.7
3520.7	7306.6	6323.2	5224.5	4570.3	5240.6	5545.2	6239.2	6722.2	3813.7	7723.8
36.6	944.1	1232.4	1577.6	2095.9	1017.7	1665.6	1762.9	632.6	387.6	753.0
251.6	3383.9	2829.3	2766.3	3506.2	3138.9	4092.4	3479.2	5076.6	1227.1	1854.9
11872.9	5713.5	5029.7	5070.7	5533.5	5767.1	5222.8	4675.0	6190.5	4296.2	6390.4
1004.8	3465.7	4570.7	3994.8	3605.2	3512.9	5000.2	3873.3	3712.7	1926.0	3354.9
76.0	1379.6	1911.0	1995.2	1723.7	1278.0	1524.7	1376.7	687.0	372.9	1068.5
151.1	1553.4	1720.2	1659.9	2022.3	1765.6	2163.6	1759.5	691.7	440.1	1072.1
18316.3	7708.8	6938.2	7347.5	8582.8	8051.4	7509.1	9242.2	5240.3	4546.0	7281.0
582.5	1070.9	1071.9	1287.0	1438.5	1149.0	1389.4	1086.1	801.8	889.8	778.7
54344.8	15552.7	14347.6	15035.9	14389.8	13631.9	16712.6	13222.7	19630.6	16704.8	19272.5
1455.0	3971.2	3909.1	4327.2	3846.5	3485.4	5262.2	3662.8	4708.4	1597.4	4345.2
7163.2	8198.6	7957.1	8694.3	9646.6	9614.5	9503.0	7923.0	8564.3	6704.8	10032.1
40.0	37.4	74.1	80.8	48.0	32.0	121.5	55.3	34.6	19.2	37.3
31.1	34.3	34.1	43.3	58.1	35.1	51.2	25.6	16.6	13.3	18.2
2213.1	3136.1	2734.0	3145.4	4061.0	2934.3	3936.2	2429.7	2967.0	2048.1	3350.5
641.7	3101.4	3092.6	3552.4	3698.0	3017.9	4212.4	3856.3	2321.6	1361.3	2311.0
614.0	3886.3	5398.8	5226.8	4615.7	4425.4	5547.1	4876.5	3198.2	3422.3	4457.3
61.6	1134.3	1549.9	442.3	416.9	478.1	513.3	532.7	605.2	443.6	343.2
7624.8	7446.9	6034.6	6153.1	6318.5	5806.2	5976.3	6827.5	8412.2	5851.0	5524.5
39.7	27.1	46.7	44.1	66.8	47.9	56.5	41.2	16.9	37.4	19.1
8071.8	11881.2	11223.6	11860.7	12639.7	11020.4	13211.4	10301.8	13139.9	11070.1	13365.5

6784.1	9990.0	6961.1
374.4	440.8	742.3
4344.1	3844.1	3174.0
4046.5	5855.0	3265.7
7230.0	7694.7	6223.2
10376.2	10496.3	9487.4
8056.7	8103.0	7104.6
7822.2	8235.1	8135.5
5439.5	5697.4	5759.8
61.6	191.8	421.8
5942.0	6240.0	6353.2
2220.8	2071.1	2602.7
27.8	33.1	25.5
6883.3	6572.7	6295.8
3858.4	4709.2	4360.1
2910.7	3834.3	4344.5
9277.3	10218.8	9828.6
2145.8	2685.7	1650.6
9935.0	9935.5	9003.7
3493.1	4200.9	2910.6
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1034.9	1498.6	1794.1
3034.8	3630.1	4226.2
4846.4	6803.9	5877.2
3539.5	4492.2	5174.9
1334.7	1368.5	1639.4
1866.1	1575.7	2291.9
8666.1	6791.6	6748.0
1249.5	1721.1	1837.7
12946.4	14769.3	14368.4
3946.1	4117.9	3642.8
8129.6	9437.6	10219.2
46.6	52.5	54.7
28.2	24.1	23.4
3263.6	3499.0	3776.5
3093.4	3235.6	3659.0
4482.8	4589.8	4881.6
234.3	239.5	843.1
6454.3	6504.8	5798.1
36.2	40.0	38.6
10834.8	11056.1	11873.6

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EU488070.1 gg_id:574540 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
AB250561.1 gg_id:161044 and ecology Grotta Azzurra Palinuro Cape (Salerno Italy) microbial mat clone #2-11 AB250
DQ890437.1 gg_id:164768 phylotypes Pestarella tyrrhena (Decapoda: Thalassinidea) abdominal setal tuft clone DQ890
DQ395043.1 gg_id:153143 harbor sediment clone VHS-B5-77 DQ395
AB245934.1 gg_id:186116 Aureispira marina str. 62 (= IAM 15390 = TISTR 1728) AB245
AY907809.1 gg_id:136805 identification picoplankton contrasting waters Arabian Sea water clone A714026 AY907
AY527408.1 gg_id:101416 Saprospira grandis str. ATCC 23116 AY527
EU050913.1 gg_id:255567 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_08_95 EU050
AB088636.1 gg_id:63062 Saprospira grandis str. ATCC23116 AB088
FJ905677.1 gg_id:574719 s Tonga-Kermadec iron oxide chimney-like structure on Volcano 19 Tonga Arc clone V FJ9056
AY527409.1 gg_id:101586 Saprospira sp. str. CNJ451 AY527
AB058899.1 gg_id:35418 Saprospira sp. str. SS90-1 AB058
EF574193.1 gg_id:241532 site S25 near Coco's Island marine clone S25_537 EF5741
AY527410.1 gg_id:105211 Saprospira sp. str. CNJ640 AY527
AJ786333.1 gg_id:114960 Lake Taihu freshwater clone MS-Taihu1-L AJ7863
AY863078.1 gg_id:111774 wastewater treatment pool clone SXAU021 AY863
EU703324.1 gg_id:380678 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH240 EU703
EU703352.1 gg_id:411990 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH74 EU703
EU703430.1 gg_id:406875 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH67 EU703
EU703317.1 gg_id:447962 lakes on Eastern Tin Plateau polysaline lake altitude 3204 masl clone XZQH163 EU703
AJ786339.1 gg_id:115067 Lake Loosdrecht freshwater clone MS-Loos1-L AJ7863
AJ786335.1 gg_id:115006 Dunedin: artificial pond freshwater clone MS-NZ1-L AJ7863
EU703341.1 gg_id:439336 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH25 EU703
EU703382.1 gg_id:436730 lakes on Eastern Tin Plateau freshwater lake altitude 4219 masl clone XZXXH171 EU703
EU703380.1 gg_id:440437 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH82 EU703
FJ612203.1 gg_id:574154 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.5.58 FJ6122
EU703204.1 gg_id:538387 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
FJ612189.1 gg_id:557078 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP3.5.22 FJ6121
EU703376.1 gg_id:378092 lakes on Eastern Tin Plateau freshwater lake altitude 4298 masl clone XZTSH97 EU703
FJ612298.1 gg_id:556107 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP7.5.37 FJ6122
AJ786331.1 gg_id:114980 Lake Tanganjika freshwater clone MS-Tang1-L AJ7863
EU703161.1 gg_id:549226 taxon richness -altitude lakes eastern tin plateau predominance Bacteroidetes and S EU703
FJ612411.1 gg_id:554700 and Biogeochemistry Dongping Lake Ecosystems lake water clone DP10.4.26 FJ6124
EF520596.1 gg_id:228517 structure lakes: what controls ? acid-impacted lake clone ADK-MOe02-10 EF5205
AJ290034.1 gg_id:73931 Austria: Lake Gossenkoellesee clone GKS2-217 GKS2-217 AJ2900
AY168729.2 gg_id:76801 arsenite-oxidizing biofilm clone Hot Creek 49 AY168
AJ784892.1 gg_id:115129 Haliscomenobacter hydrossis str. DSM 1100 = ATCC 27775 AJ7848
NR_028693.1 gg_id:556906 Lewinella cohaerens str. II-2; ATCC 23123 NR_02
GQ441283.1 gg_id:584899 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
GQ441322.1 gg_id:584859 and dynamic mat present vs. active nitrogen-fixing microorganisms marine microbia GQ441
AB301614.1 gg_id:223475 Lewinella cohaerens str. NBRC 102661 AB301

331.7	4165.8	3889.5	4085.2	4657.7	3583.6	5767.5	4037.5	3013.5	1320.2	2573.3
1685.0	5406.2	4841.8	5366.0	5337.2	5613.6	5527.7	5165.0	6144.1	4473.2	4615.1
38.5	324.6	410.7	469.2	180.4	321.8	442.8	307.1	221.4	51.8	146.5
43.7	140.5	229.4	273.2	235.8	193.0	384.0	189.7	74.2	30.7	109.1
32.0	19.5	35.5	19.0	25.9	25.3	18.9	42.5	24.7	13.2	23.0
33.6	26.3	33.6	25.6	32.2	22.3	25.4	24.6	32.8	20.5	26.9
37.2	19.4	18.7	17.0	23.6	20.2	20.0	14.9	17.4	14.8	17.8
129.4	3814.9	3716.8	3295.0	3964.2	3997.6	3394.3	3947.0	5766.3	5121.0	2745.0
72.4	295.5	506.1	560.9	358.9	431.5	450.2	439.5	248.6	55.7	242.0
53.4	1255.3	964.1	706.4	1029.5	894.2	1182.2	990.3	684.5	586.4	769.2
113.8	1904.7	2309.4	2395.4	2012.1	2234.8	2479.0	2260.7	1330.9	598.6	1521.6
322.2	2948.3	2866.0	2802.0	2842.8	2925.3	2199.1	3389.6	3663.3	3300.6	2726.6
2128.9	5318.3	4040.3	4649.8	5919.8	5345.6	6262.5	5083.3	6207.7	6065.8	5137.4
33.0	1206.3	1116.3	1098.6	455.9	1005.1	371.7	1311.1	1714.3	628.0	1171.4
23799.9	7971.8	7268.6	7960.7	8674.3	7738.2	9190.1	7546.2	11917.8	8427.7	10507.6
47.7	2019.8	1854.9	1756.4	2459.8	2073.2	2899.1	2569.0	2231.1	856.3	1228.9
2041.3	6358.6	5551.2	5231.4	5895.3	4938.7	6701.9	4698.3	5512.8	5240.1	5669.3
508.4	2285.7	1857.6	2055.4	3188.4	2022.6	3508.5	2334.2	1434.3	575.4	1276.8
985.2	8199.2	7331.1	8008.6	7678.5	8069.1	6885.7	8226.7	11544.1	7093.4	8291.0
483.3	4221.1	3666.5	4208.7	6449.3	3763.4	6302.1	3941.7	3349.1	2158.9	3294.4
494.9	2319.7	1873.4	2055.6	3406.8	2103.8	3408.0	2119.1	1670.5	776.7	1455.2
45.5	631.9	676.3	752.8	1044.9	661.7	1173.7	992.6	488.5	219.2	522.7
511.8	2427.0	1883.3	2077.7	3225.2	2084.4	3493.0	2332.6	1436.7	654.6	1223.7
4554.1	5263.9	4929.6	4795.4	3855.6	4876.9	5421.3	4432.9	6646.0	4966.6	4896.7
81.2	1672.6	1279.0	1376.1	2279.8	1365.9	2322.2	1576.8	876.0	409.2	852.6
38.2	2405.6	1478.9	1440.2	1905.4	1806.5	2056.4	2107.4	1089.1	1084.8	1010.4
48.8	1663.5	1015.9	1027.5	1396.5	1111.0	1781.2	1265.2	1109.1	846.8	874.1
508.6	2325.0	1650.0	1867.3	3013.6	1953.2	3218.3	2037.6	1369.6	612.4	1194.6
9336.4	7762.7	7446.4	8407.5	6928.8	7135.4	8302.9	7100.7	6870.0	5856.8	10349.5
45.4	659.3	593.5	559.6	950.4	521.3	920.2	786.1	421.3	203.2	387.6
48.8	2238.2	1990.5	1798.4	2054.6	2227.6	2479.9	3455.5	3013.4	1687.8	1900.5
507.3	2374.0	1805.5	1995.1	3228.3	2022.4	3452.2	2202.2	1527.4	642.9	1163.4
417.4	2252.8	1715.6	1801.1	2800.1	1827.9	3091.9	1927.5	1385.7	650.6	1171.0
51.6	1148.1	987.4	1089.2	1534.4	1623.2	1388.0	833.8	746.7	163.8	479.5
5999.9	4670.1	5647.5	4647.2	4433.9	5816.0	4723.0	4484.4	7587.7	6030.5	6887.2
405.4	1320.7	1619.4	2993.0	4261.2	2215.1	2096.0	2121.6	3188.0	530.9	983.3
52.5	1094.8	1514.1	2922.2	4095.5	2209.3	2511.0	1466.8	2323.6	382.2	769.8
4350.2	6837.6	5844.2	8080.9	8686.3	6149.4	8908.1	6129.7	5844.2	4338.1	5500.0
130.1	2753.0	3595.7	3601.7	2560.6	3143.2	3633.5	3038.8	2023.0	1182.5	2463.4
440.9	4703.4	4330.7	5546.4	4792.5	4176.4	5176.4	3909.9	4185.0	3269.8	5334.7
1275.1	3383.2	4512.2	5609.3	6731.9	4537.1	6157.1	3773.3	3662.0	3525.0	3144.2

3345.6	3533.7	3979.9
4418.6	5293.7	5046.2
234.8	276.0	274.5
125.2	371.2	372.6
20.6	29.9	25.4
21.7	29.6	20.1
19.6	23.4	20.0
3245.9	4084.0	3260.1
341.0	356.4	386.9
733.4	1155.4	2536.4
2219.8	2853.2	3322.4
2593.3	2776.5	3033.2
4933.2	5176.6	4890.1
646.5	555.3	355.1
6803.0	10020.8	7320.8
1528.1	2291.5	2730.1
4320.7	6848.1	5981.5
2055.8	1930.9	2589.0
7065.9	8166.3	5018.0
3677.1	4182.9	4485.3
2032.3	2107.4	2235.9
597.8	745.5	956.4
2104.1	1970.7	2571.2
3548.9	5528.6	4953.3
1342.8	1381.9	1807.1
1304.3	848.9	2115.0
818.6	1041.0	1634.1
1919.2	1723.1	2428.0
6322.2	8240.9	8054.6
455.7	800.8	715.8
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2072.9	1815.5	2625.0
1535.9	1684.5	2009.2
750.8	1470.8	887.8
4171.0	4737.7	4277.7
1821.8	2878.8	1162.1
1712.1	2880.7	1433.7
5866.9	6269.9	6833.7
3181.7	2266.2	3184.5
3489.8	3773.4	3536.0
3640.2	4640.7	3566.2

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o__Sphingobacteriales	f__Saprospiraceae
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s__Lewinella nigricans	75295
s__Lewinella persicus	74736
s__unclassified	74726
s__unclassified	74947
s__unclassified	75027
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s__unclassified	75535
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s__unclassified	75020
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s__unclassified	75054
s__unclassified	75060
s__unclassified	75064
s__unclassified	75076
s__unclassified	75088
s__unclassified	75132

AM295255.1 gg_id:251371 Lewinella nigricans str. ATCC 23147 AM295
EU371935.1 gg_id:259026 Lewinella persicus EU371
EF554367.1 gg_id:219002 Lewinella antarctica str. IMCC3223 EF5543
NR_028695.1 gg_id:583989 Lewinella nigricans str. SS-2; ATCC 23147 NR_02
AB301494.1 gg_id:236361 Lewinella lutea str. FYK2402M69 (= NBRC 102634 = NCI AB301
GU061593.1 gg_id:586573 and function microbial mesoscale eddy perturbations South China Sea clone CE2-5m GU061
EF092259.1 gg_id:274109 Persistent identical Axinella corrugata on 27-Jun-2002 clone MB255_F10 EF0922
AF445681.1 gg_id:33230 travertine hot spring clone SM1E03 AF4456
AB301495.1 gg_id:255544 Lewinella marina str. MKG-38 (= NBRC 102633 = NCIMB 1 AB301
AM286229.1 gg_id:256191 Lewinella agarilytica str. SST-19 AM286
EU236397.1 gg_id:295985 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92C6 EU2363
EU925862.1 gg_id:307334 sediments sediment station DBS1 northern Bering Sea clone 063F26 EU9258
FJ517043.1 gg_id:568024 semiarid 'Tablas de Daimiel National Park' wetland (Central Spain) unravelled water c FJ5170
EU246289.1 gg_id:243481 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-D05 EU2462
EU245106.1 gg_id:244430 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H2-B08 EU2451
FJ230926.1 gg_id:310337 under Level Antibiotic Selection Pressures river water clone F23 FJ2309
EU246805.1 gg_id:240609 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
EU245082.1 gg_id:245355 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-F08 EU2450
DQ270634.1 gg_id:144512 hydrothermal carbonate chimney clone LC1408B-77 DQ270
GQ261756.1 gg_id:570841 shifts taxa and response localized organic loading deep sea sediment whale falls clo GQ261
FJ535046.1 gg_id:542634 Enhancement protein conversion volatile fatty acids accumulation during addition: ef FJ5350
CU466734.1 gg_id:336473 Evry wastewater treatment plant anoxic basin clone CU466
DQ232756.1 gg_id:194491 Identity abundance and ecophysiology filamentous Cytophaga-Flavobacterium spec DQ232
DQ330422.1 gg_id:159332 Guerrero Negro hypersaline microbial mat clone 01D1q40 DQ330
DQ640668.1 gg_id:228176 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
EU283383.1 gg_id:253723 consecutively aerated submerged treating domestic wastewater activated sludge m EU2833
AM040132.1 gg_id:150023 sandy sediments clone Sylt 36 AM040
EU177704.1 gg_id:274126 Identification and ecophysiological epiphytic protein-hydrolyzing saprospiraceae ('Ca EU177
EU246830.1 gg_id:245374 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2468
CU923649.1 gg_id:557079 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU923
DQ330419.1 gg_id:159352 Guerrero Negro hypersaline microbial mat clone 01D1q39 DQ330
DQ856550.1 gg_id:246616 intestinal microflora Chinese mitten crab (Eriocheir sinensis) clone C3H DQ856
EF020003.1 gg_id:204415 aspen rhizosphere clone Elev_16S_1393 EF0200
AB476221.1 gg_id:568287 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB4762
EU431829.1 gg_id:538448 Troglobitic (Cansiliella) on specialized feeding apparatus calcium carbonate (moonmi EU4318
DQ640679.1 gg_id:232231 full-scale EBPR sludge clone Skagenf44 DQ640
EU101259.1 gg_id:244393 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1012
DQ330510.1 gg_id:159469 Guerrero Negro hypersaline microbial mat clone 072DZ68 DQ330
DQ269109.1 gg_id:200498 marine macro-alga surface clone DPC179 DQ269
DQ640691.1 gg_id:233992 full-scale EBPR sludge clone Skagenf54 DQ640
EU177700.1 gg_id:271904 Identification and ecophysiological epiphytic protein-hydrolyzing saprospiraceae ('Ca EU177

1031.2	3057.0	1690.0	2315.0	2484.4	2109.5	2961.3	2667.5	1999.3	2196.6	1922.3
39.1	412.2	349.4	272.7	318.9	62.9	243.8	633.4	163.9	530.5	382.3
36.0	92.3	79.6	156.1	95.9	89.9	346.1	124.6	73.2	62.0	44.7
811.7	4310.5	3684.2	3874.8	5246.2	4222.7	3629.3	5174.0	4782.2	5074.0	3844.3
908.9	3798.5	4238.2	4061.0	3999.5	4087.3	4113.7	4296.0	5104.1	4795.1	3346.5
81.5	1677.9	1847.9	2330.6	3221.6	1793.3	2580.0	1847.3	1433.2	791.2	1605.3
3487.1	7318.8	6549.5	7620.2	8877.2	7137.1	8864.2	6913.2	7610.3	5425.0	6396.3
113.1	1180.5	1261.6	1615.8	2816.0	1609.7	3328.3	2854.5	3467.2	409.3	621.2
1678.1	4336.4	4341.2	3818.1	4966.8	4253.9	4810.4	4135.6	5462.9	5586.8	4253.4
1523.9	4661.8	4911.1	4093.3	5354.1	4830.8	5361.0	4572.3	6364.3	4999.0	4467.5
1095.0	4227.3	3922.3	4020.6	4690.9	4430.3	4904.9	3852.8	4924.5	2344.6	3346.5
1309.3	5735.6	5593.3	6151.9	7526.3	6539.1	7534.3	5085.4	3720.8	2172.2	4186.1
1219.3	2013.5	2347.5	4400.0	6822.7	4388.5	6810.7	3812.5	2305.0	1759.3	3665.7
3616.9	4196.0	3259.9	3824.0	3552.1	4103.9	4754.3	3201.0	4776.6	3618.0	4459.2
300.2	6198.6	4773.1	5093.5	4637.6	5380.4	6144.1	5116.6	3356.5	5553.4	4778.2
1775.6	10786.0	8581.0	10045.0	12797.3	9527.8	12457.1	9081.6	11617.6	7564.3	8773.9
5294.5	6301.8	6112.0	6776.0	6963.2	5797.5	7784.3	6253.2	7015.4	6369.8	6385.0
3798.2	5006.9	5372.6	5820.1	4425.6	5717.2	8227.8	5057.8	6918.2	6723.9	7416.2
49.6	1238.6	1263.6	783.9	1040.7	1406.1	808.0	1563.4	2643.1	917.3	812.4
736.5	6307.6	4144.0	4729.8	7950.7	5647.0	6703.5	5264.7	6584.3	4116.7	4262.3
1380.7	4028.7	4032.7	3951.9	4833.2	3301.2	5271.6	3784.9	2623.0	2895.5	4387.5
3637.1	5316.2	3977.0	4759.8	6893.8	4772.2	5657.6	4503.4	6511.0	4192.0	4314.6
45.9	112.8	114.7	98.9	119.5	94.2	176.2	115.4	49.3	30.9	60.4
5887.3	3948.2	4181.9	4813.6	4706.4	4053.6	4534.1	4783.2	4241.4	3391.8	6083.9
42.9	37.3	40.3	37.2	48.9	31.2	56.6	35.7	23.9	18.3	21.4
2603.7	12767.4	9424.7	10940.9	13283.6	10821.1	13957.5	9426.1	12881.4	7986.2	10245.2
2070.2	8525.1	7264.5	8109.4	9193.0	7469.9	10638.6	7042.0	9928.8	8567.5	8001.2
6910.9	6750.7	6386.1	6476.2	8049.5	6568.1	7650.8	6057.9	7048.4	6311.5	5926.0
829.3	7669.2	6694.2	5739.3	5064.1	7190.7	6459.6	5751.0	8333.3	3896.9	6459.8
1707.9	6699.3	6675.2	7352.0	8829.4	7374.5	8310.8	7536.8	6818.1	6141.4	7197.3
117.5	1969.9	1874.8	1851.6	1246.4	1969.3	1437.4	1872.2	1569.5	328.2	976.5
46.2	1298.0	879.9	1357.0	1390.4	947.0	1299.5	1321.6	856.6	691.0	609.0
43.8	1293.5	1456.3	1520.3	4203.5	2155.9	2950.1	1551.5	2538.0	1137.4	686.3
44.4	617.1	731.5	738.4	1077.0	719.4	686.5	793.1	578.8	230.9	501.8
222.8	4966.0	3907.8	3125.6	2181.0	2498.0	4805.0	3021.2	4556.0	3779.9	2013.5
221.8	4862.4	5214.1	5871.1	4892.9	4492.0	6859.4	4976.5	5394.5	4286.6	4437.0
536.1	896.3	1284.2	921.9	852.6	876.9	1262.4	861.7	546.6	233.8	1257.5
4377.6	1320.4	1298.0	1659.4	1611.2	1425.4	2199.8	1543.5	67.7	752.6	1520.5
9378.0	7340.8	7090.7	7770.8	8130.4	7144.1	9179.7	7752.6	9816.5	4436.1	6740.5
251.4	6665.3	5927.0	6220.7	6089.3	5715.1	7015.7	6328.2	7976.7	6957.1	5546.8
2551.2	5279.4	4952.1	4458.4	5573.5	4202.9	4136.1	4318.4	4877.8	3268.3	5963.5

2328.5	2497.9	2169.3
352.1	290.7	863.3
135.6	114.7	50.7
3599.9	4332.1	4815.7
4536.4	4724.1	4294.9
1713.8	1729.7	1914.8
6178.8	6347.2	6379.0
1602.3	1554.0	2179.1
3649.5	4249.8	5979.5
4161.0	4695.6	6284.8
3822.6	3610.0	2330.7
4909.7	4395.8	7396.4
3455.8	3285.5	3663.8
3289.1	3899.6	3253.6
4326.7	3578.3	4170.6
9560.9	8623.7	8841.5
5489.6	6194.8	5088.0
4787.7	4907.8	5527.9
638.6	734.4	1341.3
4333.3	5200.8	5190.5
3667.4	3425.4	2915.2
4025.0	6515.5	4282.6
125.5	119.7	129.1
3537.5	3695.0	3304.8
43.5	30.2	36.6
10868.0	10652.7	10661.5
7796.2	8201.0	7130.1
5640.0	6774.6	5838.0
4741.3	4756.6	3516.5
7411.6	6943.4	7244.1
1702.8	2043.0	1095.2
1343.6	1328.8	940.9
1249.6	1144.4	480.4
629.1	672.0	653.2
2560.4	2293.4	1822.3
4158.1	5666.9	4492.7
1015.6	935.5	530.3
1430.0	1447.5	1845.3
7740.5	7062.9	7765.1
4864.8	6082.8	5830.5
4809.4	5334.3	2933.6

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o__Sphingobacteriales	f__Saprospiraceae
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EU246294.1 gg_id:242491 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-E02 EU2462
DQ640669.1 gg_id:228572 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
GU230422.1 gg_id:590902 Multilevel approach along Rio de la Plata-South Atlantic Ocean coastal sediment clo GU230
DQ640739.1 gg_id:228243 full-scale EBPR sludge clone Skagen114 DQ640
EU246796.1 gg_id:249508 polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdon EU2467
DQ269043.1 gg_id:191119 marine macro-alga surface clone UA18 DQ269
DQ270658.1 gg_id:142556 hydrothermal carbonate chimney clone LC1446B-1 DQ270
EU919769.1 gg_id:314728 Kongsfjorden western Spitsbergen Svalbard ocean water clone b29 EU9197
L10944.1 gg_id:2555 marine snow clone agg32 L10944
EU925904.1 gg_id:316764 sediments sediment station DBS1 northern Bering Sea clone 130H27 EU9259
AJ704707.1 gg_id:109301 marine sediment clone HMMVBeg-23 AJ7047
FJ517715.1 gg_id:538346 Disturbing epithelial homeostasis metazoan Hydra leads drastic changes microbiota e FJ5177
EU265797.1 gg_id:268688 epibiotic assemblage recently described Yeti Kiwa hirsuta (Kiwidae) surface crab hyc EU2657
AB476272.1 gg_id:573306 Compositional and functional transition epibiotic microbial hydrothermal vent galath AB4762
DQ640718.1 gg_id:232619 full-scale EBPR sludge clone Skagen118 DQ640
AY921686.1 gg_id:112888 farm soil clone AKYH1028 AY9216
CU466747.1 gg_id:314086 Evry wastewater treatment plant anoxic basin clone CU4667
EU104094.1 gg_id:303752 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
CU466750.1 gg_id:334860 Evry wastewater treatment plant anoxic basin clone CU4667
AB286458.1 gg_id:215105 Reducing production and domination comamonadaceae reducing oxygen supply was AB2864
AF314434.1 gg_id:34106 aerobic phosphorus-removal ecosystem clone PHOS-HE79 AF3144
EU104080.1 gg_id:329138 Evidence Comamonadaceae determinants settling performance activated sludge clo EU1040
EF471455.1 gg_id:262076 Fast Screening and Estuarine Operon Libraries whole surface water Chesapeake Bay (EF4714
DQ640703.1 gg_id:230258 Biodiversity and microbial full-scale enhanced biological phosphorus removal plant a DQ640
AJ318154.1 gg_id:52545 Waste-gas biofilter clone BIjiii32 AJ3181
AM259876.1 gg_id:211973 Spatial sponge- Mediterranean Tethya aurantia sponge cortex clone TAA-10-77 AM259
AY302114.1 gg_id:109536 sludge dentrifying reactor fed with methanol clone DSBR-B007 AY3021
EU283492.1 gg_id:278585 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A1877 EU2834
EU245985.1 gg_id:256252 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P1-B03 EU2459
CU466727.1 gg_id:325671 Evry wastewater treatment plant anoxic basin clone CU4667
DQ295906.1 gg_id:146854 Cohn's Crenothrix filamentous oxidizer unusual methane monooxygenase physical e DQ295
AB058902.1 gg_id:29244 Saprospira sp. str. SS95-4 AB0589
EF523466.1 gg_id:263176 Identification and ecophysiological epiphytic protein-hydrolyzing saprospiraceae ('Ca EF5234
EU340156.1 gg_id:252788 on Aquatic Macrophytes Geothermally Active Area Sedge Bay Yellowstone Lake WY ; EU3401
DQ640672.1 gg_id:234415 full-scale EBPR sludge clone Skagenf45 DQ640
AB058901.1 gg_id:30366 Saprospira sp. str. SS92-11 AB0589
AF087087.1 gg_id:2534 activated sludge clone MK09 AF0870
EU246157.1 gg_id:246729 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P4-E02 EU2461
AF314431.1 gg_id:35871 aerobic phosphorus-removal ecosystem clone PHOS-HE35 AF3144
EU925914.1 gg_id:340563 sediments sediment station DBS1 northern Bering Sea clone 149H54 EU9259

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13529.0	8631.3	6998.3	7348.7	9314.7	8425.9	8981.6	8312.8	9592.6	9366.4	7883.5
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104.5	357.8	646.5	845.4	696.4	392.1	733.4	565.2	2281.1	67.6	261.9
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2130.9	5665.1	6574.3	6088.0	6897.8	6502.0	6462.3	6246.4	5549.7	4742.4	6468.9
185.3	2541.9	3385.5	4043.6	3413.4	2937.1	4911.2	3089.2	1448.6	1927.3	2132.8
537.9	7128.9	7750.9	7522.8	8148.6	7637.7	8045.0	8570.3	8090.4	8292.8	8163.4
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1443.5	7152.2	6449.9	8324.6	17474.5	7735.6	15658.7	5239.8	2476.2	3039.7	6595.9
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3076.1	7228.8	6767.6	7452.5	8552.7	7151.1	8210.1	8080.7	6184.5	7903.6	8877.2
8841.8	4148.5	4068.3	4601.3	5084.7	3733.9	6702.0	3897.4	4720.4	3393.5	4351.6
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67.2	920.5	1184.6	1201.5	1166.7	1015.4	1569.2	1363.9	489.4	655.9	1250.0
271.5	1618.6	1057.7	703.6	1038.8	1379.3	920.5	1025.9	2321.7	1934.8	691.4
2047.7	6172.7	6185.2	6534.3	8199.1	5570.8	8037.6	5896.8	5917.9	4868.0	5841.2
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2743.7	2956.7	2644.8
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4700.1	3959.6	3665.8
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202.5	244.7	87.9
6500.1	6345.3	9217.4
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DQ640709.1 gg_id:230351 full-scale EBPR sludge clone Skagenf40 DQ640
EF644787.1 gg_id:299993 genes and citrate lyase deep-sea microbial MAR Logatchev hydrothermal vent syster EF6447
EU374049.1 gg_id:270239 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment clc EU374
AY929064.1 gg_id:112991 Saprospira sp. str. PdY3 AY929
EU245092.1 gg_id:246699 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-H06 EU245
DQ103646.1 gg_id:136195 hypersaline endoevaporitic microbial mat clone E2aC08 DQ103
AB267714.1 gg_id:169934 Pocheonia terrae str. Jip 13 AB267
GQ263282.1 gg_id:510706 Structure Simulated Level Waste Site simulated level waste site clone FW1_a28 GQ263
GQ263443.1 gg_id:510710 Structure Simulated Level Waste Site simulated level waste site clone FW2_12B GQ263
FJ754321.1 gg_id:574254 Parapedobacter sp. str. 4M40 FJ7543
GQ263506.1 gg_id:541496 Structure Simulated Level Waste Site simulated level waste site clone FW2_28B GQ263
DQ680836.1 gg_id:164618 Pedobacter koreensis str. Jip14 DQ680
FJ754320.1 gg_id:547664 Parapedobacter sp. str. 4M29 FJ7543
EU169155.1 gg_id:240279 Pedobacter cryoconitis str. B52 EU169
AJ438174.1 gg_id:29206 Pedobacter piscium str. DSM 11725T AJ4381
AM491368.1 gg_id:208050 Pedobacter duraquae str. WB2.1-25 AM491
AJ318151.1 gg_id:44075 Waste-gas biofilter clone BIji46 AJ3181
AB255102.1 gg_id:163090 corroded concrete clone SC-85 AB255
DQ298770.1 gg_id:142463 Effect Nutrient Periodicity upon Microbial Dynamics exposed 7-day nutrient flux DQ298
FN421509.1 gg_id:585420 proteogenomics physiology phyllosphere Arabidopsis thaliana clone 12_F02 FN421
EU057838.1 gg_id:237550 Pedobacter sp. CH30-5 EU057
AM237384.1 gg_id:154889 Pedobacter cryoconitis OS-119 AM237
EU030686.1 gg_id:336897 Pedobacter nyackensis str. NWG-II14 EU030
GQ389204.1 gg_id:570755 quality deterioration drinking system during serious red water outbreak clone D78 GQ389
GU377107.1 gg_id:529048 Flavobacterium sp. str. sptzw17 GU377
AF385531.1 gg_id:70559 swab advanced noma lesion clone Av100 AF385
FJ230892.1 gg_id:303672 under Level Antibiotic Selection Pressures river water clone F1 FJ2308
AM491370.1 gg_id:210212 Pedobacter metabolipauper str. WB2.3-71 AM491
FJ979862.1 gg_id:465948 Sphingobacterium sp. str. tsz34 FJ9798
NR_028977.1 gg_id:565000 Pedobacter africanus str. K 1/K2; DSM 12126 NR_02
GQ263646.1 gg_id:562141 Structure Simulated Level Waste Site simulated level waste site clone FW3_33C GQ263
EU652337.1 gg_id:282928 Pedobacter sp. str. JC2491 EU652
FN421692.1 gg_id:535873 proteogenomics physiology phyllosphere soybean clone 3_E10 FN421
AB245371.1 gg_id:148944 Pedobacter ginsengisoli str. Gsoil 104 AB245
GQ009735.1 gg_id:499930 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
EF459523.1 gg_id:207247 Pedobacter sp. KFC-76 EF4595
EU652336.1 gg_id:284420 Pedobacter sp. str. JC2490 EU652
AY571816.1 gg_id:106242 Sphingobacterium sp. 44/35 AY5718
EF154114.1 gg_id:196903 SAR increases fitness Arabidopsis thaliana response natural pathogens leaf clone ME EF1541
AJ438172.1 gg_id:52839 Pedobacter heparinus str. DSM 2366T AJ4381

1659.3	4264.6	3270.5	4832.7	4051.7	4275.5	4807.5	4691.3	3320.7	2739.9	3614.7
1453.3	8718.1	6460.6	5692.4	5726.7	5555.5	8133.3	7325.3	7056.3	9202.7	5703.3
21506.9	8517.8	9801.2	10847.7	12208.8	8144.5	12273.0	9110.7	12116.1	6825.6	9863.9
2193.3	9441.9	8243.1	9154.4	12286.6	9287.7	12895.8	8520.8	12293.0	8567.9	8206.2
30.8	73.8	194.8	160.9	150.5	124.6	213.1	168.0	115.6	28.5	72.5
705.1	3159.3	3866.1	4495.4	4758.1	3114.0	4543.2	4594.5	2969.7	2608.7	3033.1
316.1	713.2	747.9	722.0	718.5	624.7	698.1	670.2	580.6	459.4	566.5
39.5	200.9	154.2	188.2	120.7	234.7	156.9	153.3	41.7	70.1	97.8
43.4	619.8	1764.3	809.2	419.7	933.5	318.4	961.1	378.5	497.7	416.1
59.8	3191.0	3457.0	3102.5	2263.1	2832.2	2451.9	3152.9	1338.9	4192.5	2134.7
70.5	1875.1	2445.2	2404.1	2442.1	1959.5	2889.0	1845.5	820.6	607.3	1226.2
1745.9	5087.1	4994.0	4656.7	4714.5	4816.8	4832.8	4601.1	2497.2	3885.5	3658.3
67.7	3190.8	2439.5	1686.3	1161.5	2616.4	1510.6	1678.8	822.3	4006.0	990.7
101.4	3224.8	3261.3	3014.5	3098.8	3242.2	3565.4	2898.9	1664.4	2756.6	2467.7
50.8	2651.1	2651.5	2103.8	1893.5	5545.8	3348.7	1845.0	650.4	556.0	974.1
70.6	3909.8	4185.5	4375.1	3678.7	4911.5	4057.5	3738.6	1790.9	1440.4	2080.0
292.2	8580.7	4708.0	2900.6	3178.9	9078.7	3824.7	3439.7	2806.0	2790.0	2452.6
179.1	4766.9	4185.2	4661.9	4584.8	5148.8	5377.6	4422.8	2519.1	3904.6	3032.8
45.1	2191.7	818.9	388.8	315.6	5307.4	287.7	591.1	326.3	884.1	520.4
57.4	6121.1	4324.6	3190.8	3913.6	5607.3	3403.0	3595.9	2436.8	3998.7	2714.4
194.9	10420.1	7559.3	5629.9	4717.9	10491.5	5572.6	5821.8	4403.2	8204.6	3732.9
503.3	7857.7	6297.1	7353.9	5176.7	9564.8	6135.1	6347.0	5888.5	4712.6	6240.3
51.1	6851.1	2735.4	1654.2	1753.3	6633.4	1965.2	1897.0	1747.2	6218.0	1066.6
2797.0	10253.1	6564.9	5968.2	5824.3	8164.8	6402.2	6514.8	5262.6	4981.2	4975.9
10909.3	5828.1	6508.3	6751.1	5304.8	6558.0	5956.8	5681.4	7289.2	7531.1	6196.8
47.6	3391.7	3495.2	3357.9	3174.8	6145.9	3622.7	3371.6	1486.8	3625.9	2056.7
36.8	1439.9	2099.8	2056.8	1594.5	3293.1	1491.4	1964.6	497.5	3525.1	1308.4
29.3	3512.0	3225.6	2597.6	2975.5	5523.2	3687.2	2831.9	1468.6	1195.3	1460.4
85.5	3126.3	1882.6	1202.0	759.9	3900.2	506.6	1262.0	450.9	611.8	501.2
59.7	7008.7	6354.1	6744.0	5726.2	7484.8	7936.8	4917.1	3927.1	9125.3	3772.5
198.0	4310.2	3763.2	3530.8	2882.0	6362.6	2961.5	3772.6	1841.6	3121.4	3004.9
854.2	3650.1	2670.6	2766.5	1859.4	6453.5	2672.8	2439.2	1336.7	2950.0	1598.8
425.3	5697.1	4526.7	4837.0	4564.1	6147.3	5613.8	3800.7	3540.5	5902.4	3100.9
215.4	7055.1	5076.8	4005.1	2981.0	9082.8	3640.8	4227.2	2662.2	4132.3	2799.0
125.4	3493.5	4101.6	4104.1	2975.7	5140.9	3761.8	3892.1	2174.4	2725.6	2857.9
1018.9	6766.1	4487.5	4512.4	4389.5	7183.5	4084.3	4642.5	4787.0	5685.8	3610.2
275.2	5285.1	5267.8	4955.3	4534.6	6949.9	4613.7	5063.4	6877.8	6520.8	5256.0
355.7	5598.7	4251.5	3667.6	3003.6	5499.7	1737.3	5033.1	4268.1	5342.9	3307.2
68.1	4179.6	3785.1	2598.3	2837.4	6426.8	2692.2	2667.1	2237.3	3628.3	1797.9
1071.4	10902.7	7597.3	7197.8	6744.9	10471.1	7292.2	6813.2	6997.1	7975.0	5017.6
52.6	5001.4	3517.8	3312.9	2318.1	7297.2	2164.5	3583.4	1570.9	4719.9	1799.9

3713.9	3366.1	4432.1
5593.3	4886.4	4980.1
8029.6	8654.2	8317.2
7668.9	9394.7	7928.0
103.5	195.1	95.6
4280.4	3362.9	3166.2
534.7	767.1	415.5
443.5	287.3	128.6
3177.8	1077.5	716.9
4056.0	2446.4	2487.5
2300.1	1730.1	1705.5
5091.1	4187.4	4146.1
2802.3	1538.2	2576.7
3116.5	2735.0	3210.2
3360.4	889.6	1590.6
3723.6	1849.7	2433.0
5333.1	2661.3	3570.4
5373.3	3912.8	3932.5
1619.2	253.6	474.1
6045.3	3085.5	3356.8
11437.4	4218.8	5139.0
7708.1	4687.1	5506.4
3752.6	1664.1	2485.0
8849.8	5847.2	6025.9
6904.3	6252.5	6102.7
5765.1	2374.7	2661.1
4666.4	1407.0	1150.3
4658.8	1722.7	2870.9
2832.4	769.6	1371.6
7788.4	4218.1	5040.6
6166.3	2773.1	3358.8
5800.9	1372.5	2239.5
6790.1	3199.5	3238.6
8685.8	3161.3	3616.4
5934.9	2745.9	4548.5
6656.8	4406.1	4307.4
5269.9	4880.4	4256.3
7602.7	2856.1	2205.8
3992.6	2162.6	1676.2
10964.6	6002.2	6733.5
7792.1	2367.1	2801.0

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EF459524.1 gg_id:209091 Sphingobacterium sp. KFC-77 EF4595
AM491372.1 gg_id:210540 Pedobacter steynii str. WB2.3-45 AM491
EU538991.1 gg_id:283118 profile human microbiota antecubital fossa (inner elbow) skin clone nbt98a10 EU538
AB485750.1 gg_id:582642 Stratified medicinal leech Hirudo verbana bladder clone 1B-SPH AB485
DQ172992.2 gg_id:152752 Pedobacter sp. str. TSBY-22 DQ172
AM411066.1 gg_id:175904 Sphingobacterium faecium str. Z18zhy AM411
FJ950587.1 gg_id:410685 Sphingobacterium faecium str. c121 FJ9505
AM411995.1 gg_id:192089 Sphingobacterium sp. Z15zhy AM411
AY635870.1 gg_id:99322 Sphingobacterium sp. str. BM-9_2 AY6358
EU918344.1 gg_id:341269 Sphingobacterium sp. str. PM2-P1-29 EU918
DQ366085.1 gg_id:149460 on Oil Degrading Consortium oil polluted soil clone SQ4_Pitesti DQ366
FJ194520.1 gg_id:341712 Sphingobacterium mizutaii str. LCD51 FJ1945
AM286268.1 gg_id:168576 Flavobacterium mizutaii Ch1 AM286
EU467916.1 gg_id:293198 cheetah feces clone CE2_a04 EU467
GQ040665.1 gg_id:401742 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw957c12c GQ040
EF059710.1 gg_id:184233 Sphingobacterium sp. str. cxh-3 EF0597
GQ016558.1 gg_id:493107 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
DQ530064.1 gg_id:159938 Sphingobacterium sp. CI01 DQ530
GQ040745.1 gg_id:417140 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw958b12c GQ040
GQ040990.1 gg_id:393426 Topographical and Temporal Human Skin Microbiome skin elbow clone nbw960h08c GQ040
EU538173.1 gg_id:282651 profile human microbiota antecubital fossa (inner elbow) skin clone nbt81d07 EU538
AB100738.1 gg_id:79272 Sphingobacterium multivorum str. IAM14316 AB100
AY556415.1 gg_id:100180 Sphingobacterium sp. str. SGE3 AY5564
EU536959.1 gg_id:280639 profile human microbiota antecubital fossa (inner elbow) skin clone nbt217f07 EU536
EU834268.1 gg_id:344005 Sphingobacterium siyangense str. DS48 EU834
EU240953.1 gg_id:276940 Sphingobacterium multivorum str. DW-7 EU240
AB100739.1 gg_id:79519 Sphingobacterium multivorum str. IAM15026 AB100
EU240954.1 gg_id:268061 Sphingobacterium multivorum str. DW-1 EU240
FJ894578.1 gg_id:552745 Matriptase-deficient mice exhibit ichthyotic selective shift skin microbiota B2E; ear pu FJ8945
EU306339.1 gg_id:240379 Sphingobacterium sp. str. Y15B EU306
GQ016359.1 gg_id:493307 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
GQ016564.1 gg_id:493101 Topographical and Temporal Human Skin Microbiome skin interdigital web space clc GQ016
AJ459411.1 gg_id:66760 Sphingobacterium spiritivorum str. DSM 2582 AJ4594
DQ984207.1 gg_id:239331 Sphingobacterium sp. str. VA-15b DQ984
AJ438177.1 gg_id:26308 Sphingobacterium thalpophilum str. DSM 11723T AJ4381
GQ339910.1 gg_id:570493 Sphingobacterium sp. str. IBFC2009 GQ339
EU373423.1 gg_id:263070 Sphingobacterium siyangensis str. YRL14 EU3734
EF122436.1 gg_id:178057 Sphingobacterium compostus str. 4M24 EF1224
FJ156081.1 gg_id:348866 Sphingobacterium sp. str. MOL-1 FJ1560
EU046272.1 gg_id:239018 Sphingobacterium siyangensis str. SY1 EU046
AY856847.1 gg_id:109982 Sphingobacterium sp. str. 62 AY8568

162.6	6259.8	4630.9	4988.3	4334.6	7471.6	3870.6	4024.6	3712.2	5285.9	3451.4
121.9	8138.2	3893.1	2359.2	2600.4	4530.5	2968.8	3721.1	3377.9	2800.0	1807.4
122.4	6161.1	4705.9	3770.8	3283.9	8690.2	3521.8	4070.4	2465.2	4268.1	2348.4
31.3	1552.5	487.0	514.1	272.2	1206.0	280.4	400.6	172.4	1020.7	145.4
6365.0	6442.9	4935.6	5245.8	4650.3	5062.4	5439.2	4570.5	5341.5	5006.0	5382.6
158.4	4840.8	4033.3	3551.9	3008.2	3719.7	3147.4	3631.4	4945.1	5409.4	2942.7
1789.9	5041.9	4100.3	2975.5	3053.5	4903.7	2311.7	3300.1	3652.9	6913.8	2517.9
5979.2	9285.3	8704.4	8500.1	9010.7	8929.6	9285.3	7743.2	9155.5	8749.0	10877.0
293.7	3465.4	3657.2	2515.5	2393.0	3552.0	1836.4	3144.2	4072.9	3254.1	2298.9
279.4	5467.4	5980.6	5455.7	4248.2	5802.0	5185.6	5971.9	6084.0	7577.1	5220.5
267.4	1879.4	1565.6	1605.1	2010.3	2065.2	1485.6	1550.6	1409.7	4422.6	1254.0
99.4	2057.9	941.6	901.0	997.2	1446.4	636.7	1591.3	3012.0	2970.0	1157.9
49.8	5280.6	3153.8	3277.5	3407.9	4498.5	1855.5	4007.8	3795.1	7898.1	2855.5
330.9	7466.7	4975.3	4902.1	4833.0	5687.1	3456.5	5443.7	6211.6	7303.3	4227.6
7653.6	12288.3	8872.6	8504.9	8065.5	9426.5	8805.6	7552.5	10117.8	13155.7	8468.8
1639.7	8987.3	6080.0	5828.7	5998.7	7781.3	5909.6	4604.8	4869.5	8915.5	5240.4
213.7	9256.9	5474.4	4889.1	4122.8	7567.0	4457.8	4443.0	4204.2	12731.4	3352.8
9532.4	8672.2	6729.7	7071.1	6173.7	7635.9	6829.9	6670.0	8663.6	11040.0	7911.7
87.1	8538.2	4486.2	3259.9	2734.2	6220.1	3056.0	2875.5	2607.7	11525.1	2168.2
157.9	9152.9	5155.7	3978.4	3327.8	6392.5	4059.8	3553.1	3094.4	10614.4	2836.7
1504.3	10304.2	7794.0	6259.9	6646.7	7852.0	6433.9	5779.8	5727.8	8839.4	5933.0
211.8	7883.0	4332.9	4060.8	3352.8	6929.3	3077.3	3672.6	3589.3	12996.1	2583.3
8008.8	9789.2	6850.7	6721.8	5392.5	8654.7	5531.3	6354.1	6985.0	9174.1	7128.7
124.5	8713.8	5468.6	4191.0	3315.5	6991.1	4072.7	3811.1	2851.4	11371.7	3616.1
136.2	4413.4	3163.7	2670.4	1758.5	4103.8	1577.1	2481.8	1502.2	9573.2	1626.6
2676.3	8239.8	7409.1	6443.1	5445.8	6862.0	5991.6	5754.1	6612.0	11305.9	6089.4
259.2	7880.7	4346.2	4097.3	3034.0	6999.7	3064.6	3653.3	3650.0	12996.1	2598.7
169.6	4067.6	2443.3	2306.2	1734.0	4360.9	1593.3	1918.8	1893.4	11674.2	1393.0
185.6	7759.4	5144.4	4607.7	3971.7	7223.9	3822.8	4247.2	3865.2	13105.0	3456.5
142.9	5818.6	3981.6	3507.8	2744.5	5505.0	2763.9	2845.8	1518.8	9411.8	1829.7
7505.1	8191.8	5787.8	5783.9	5862.5	8723.8	5806.1	5183.9	5943.6	12504.9	6302.3
166.1	8262.5	4937.9	4528.8	3744.6	7200.1	4118.2	3986.3	3265.0	13093.4	2995.6
60.4	833.9	752.3	1020.1	532.2	1384.1	378.5	1916.2	612.4	6905.3	563.2
205.3	5923.4	3648.0	3349.2	2627.5	5361.9	2622.9	3014.4	3124.2	12180.7	2281.5
1058.3	2872.2	2109.9	1972.8	2044.1	2713.5	1870.2	2099.4	2171.0	6794.6	1963.6
34.6	3965.7	3048.7	1963.7	1716.8	3477.5	1555.0	2271.6	2079.4	3942.8	1982.8
269.1	6661.9	3889.4	3702.4	2957.4	5222.0	2807.4	4399.7	4238.7	9537.8	3407.4
41.2	143.5	153.7	91.5	96.3	199.2	80.1	93.7	71.7	223.5	38.9
30.7	592.1	764.9	690.5	734.6	1056.2	342.8	690.2	209.4	2234.7	282.7
7414.4	8183.3	4015.2	3284.0	2610.2	4890.5	3232.7	2908.6	4070.0	7597.7	3516.6
130.4	8975.1	4531.4	3246.6	2557.7	6434.5	2773.1	2674.6	2370.8	10485.1	1806.5

5629.6	3088.1	3489.6
4643.8	2750.6	3541.3
8386.6	3155.7	3344.7
1003.6	420.5	452.3
5378.2	4852.7	4569.5
3681.0	3636.0	2986.5
5335.5	3037.6	2580.2
9121.0	7428.3	6949.5
3509.7	2807.4	2153.6
7542.6	4700.2	4840.0
2118.8	1795.0	1538.8
1693.2	895.8	550.5
4809.2	2982.7	3702.8
6383.7	4219.9	3645.2
9683.5	6456.2	7772.4
6184.5	5300.0	5004.6
8163.1	3632.3	5117.4
6892.0	7098.2	6937.8
5649.6	2609.1	3242.3
6181.2	3090.0	4051.1
7006.8	5820.2	5952.2
6770.7	3202.7	4217.9
7284.6	6470.7	5985.3
6503.4	3346.3	3973.9
5235.4	2006.8	2196.6
8233.0	6159.8	6261.3
6806.9	3233.1	4297.0
3973.8	1828.8	2164.2
7974.4	3598.5	4884.7
6327.3	2348.2	4093.6
7633.5	5653.5	5909.2
7466.8	3169.7	5005.5
972.1	723.4	570.9
5529.9	2915.1	3325.3
3006.7	1888.0	1705.0
3418.7	1987.6	1888.2
4391.6	3275.0	2931.9
332.2	81.2	74.4
1268.9	582.3	682.8
4077.3	2843.9	3117.1
5665.2	2553.1	3376.9

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EU344912.1 gg_id:270982 Hepialus gonggaensis guts equalized library larval gut clone Hg5-02 EU344
EU464820.1 gg_id:291453 Hartmann's mountain zebra feces clone AFZEB_aaj71d10 EU464
FJ816788.1 gg_id:560815 Sphingobacterium shayense str. HS39 FJ8167
AB249372.1 gg_id:155740 Sphingobacterium daejeonense str. TR6-04 AB249
EU595360.1 gg_id:277106 Sphingobacterium sp. str. 35 EU595
GU353117.1 gg_id:576006 Sphingobacterium sp. str. CH14 GU353
GQ058131.1 gg_id:410722 Topographical and Temporal Human Skin Microbiome skin volar forearm clone nbw GQ058
EU465049.1 gg_id:291433 African elephant feces clone AFYEL_aaj67c03 EU465
EU464925.1 gg_id:302702 African elephant feces clone AFYEL_aaj65c07 EU464
DQ168834.1 gg_id:138761 Fermentative biohydrogen production heated anaerobic sludge clone J16 DQ168
FJ859899.1 gg_id:442126 Sphingobacterium sp. str. XH4 FJ8598
AY838458.1 gg_id:109338 fruiting body Pleurotus eryngii clone PE02 AY8384
GQ988781.1 gg_id:573731 Sphingobacterium sp. str. LQY-18 GQ988
DQ824722.1 gg_id:183740 human fecal clone RL185_aaj72c06 DQ824
AB078046.1 gg_id:56235 Flexibacter canadensis str. IFO 15130 AB078
GQ263715.1 gg_id:543870 Structure Simulated Level Waste Site simulated level waste site clone WC1_a30 GQ263
DQ450752.1 gg_id:160802 Microbial Alpine Tundra Wet Meadow Soil: Chloroflexi Cold Water-Saturated satura DQ450
FN400860.1 gg_id:550032 Mucilaginibacter sp. str. FT2.2 FN400
GQ263411.1 gg_id:540688 Structure Simulated Level Waste Site simulated level waste site clone FW2_03B GQ263
GQ396878.1 gg_id:575305 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts GQ396
AF170741.1 gg_id:2485 Cytophagales str. QSSC5-1 AF1707
AJ295641.1 gg_id:50974 uranium mill tailing clone KF-Gitt2-34 AJ2956
EU861966.1 gg_id:347195 effects chronic fertilization on alpine tundra microbial implications carbon and cyclin EU861
AM490402.1 gg_id:205748 Mucilaginibacter paludis str. TPT56 AM490
GQ009469.1 gg_id:500195 Topographical and Temporal Human Skin Microbiome skin plantar heel clone nbw77 GQ009
AB267717.1 gg_id:163173 Sphingoterrabacterium daejeonensis str. Jip10 AB267
GQ263331.1 gg_id:568750 Structure Simulated Level Waste Site simulated level waste site clone FW1_a85 GQ263
EF151805.1 gg_id:184347 Parapedobacter soli str. DCY14 EF1518
AM936258.1 gg_id:564970 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM936
EU133724.1 gg_id:236952 tallgrass prarie soil clone FFCH1521 EU133
EF516352.1 gg_id:223975 grassland soil clone FCPN446 EF5163
DQ421387.1 gg_id:154665 Olivibacter itius str. AW-6 DQ421
AF409002.1 gg_id:106893 Sphingobacteriaceae str. Ellin160 AF409
GQ129977.1 gg_id:405895 Genetic inventory 'JPL-SAF' during MSL mission spacecraft assembly clean room floc GQ129
EU196345.1 gg_id:238897 Ginsengisolibacter sp. NP11 EU196
EF516964.1 gg_id:223783 grassland soil clone FCPN666 EF5169
AY509377.1 gg_id:99619 freshwater clone LiUU-3-212 AY5093
AF492000.1 gg_id:68384 Sphingobacterium sp. str. HC-6155 AF492
FJ466361.1 gg_id:534367 and carbon monoxide-oxidizing across successional on recent Hawaiian 1959 Kilauea FJ4663
EU802122.1 gg_id:341582 It's all ranking aquatic Chesapeake Bay MD clone 3C003531 EU802
AB330392.1 gg_id:243196 Pedobacter mucosus str. SCK AB330

132.8	6490.4	4127.7	3198.8	2267.4	6273.2	2260.1	2746.5	2218.2	11254.6	2129.9
237.1	4629.1	4479.3	4575.2	3706.4	5386.6	3444.0	4276.6	2857.2	8674.9	3131.4
149.2	3506.6	3238.1	3222.8	2718.1	3033.7	2859.6	2733.1	2633.2	5087.3	1915.8
52.3	2386.9	2104.0	1668.3	2285.0	2916.1	2236.1	2006.4	859.9	1994.6	1274.7
17.0	5640.3	4877.0	5087.5	6679.6	5300.1	6102.5	4732.1	2713.1	3887.2	3104.2
147.6	5272.3	3986.1	3793.9	3370.4	5185.3	2400.4	3805.6	3464.3	8000.1	2883.6
160.0	1932.7	1950.6	1608.3	2223.4	2553.3	2019.4	1958.3	2204.4	2798.4	1254.2
543.7	6405.1	3571.5	2675.0	2645.5	4472.7	2241.4	3068.4	3044.9	4109.8	2053.7
10947.5	8505.4	6275.7	6097.6	5954.1	6961.5	5985.6	5394.7	7325.1	5712.2	7429.3
67.9	789.9	785.9	852.6	1089.9	1384.9	486.5	979.2	305.5	4624.8	346.6
40.1	1450.1	1746.0	1066.5	1162.4	1781.6	527.8	929.9	618.7	5147.4	477.1
18000.9	5541.1	5145.7	5628.0	5424.1	5741.6	5896.0	5454.2	6598.1	9108.9	6379.3
35.6	3715.0	2024.2	2148.8	1803.7	2902.5	1668.0	1783.9	730.0	3599.5	650.9
10425.7	7560.5	5852.4	6108.8	6241.4	7080.0	5706.1	5376.7	7886.8	9967.3	6487.1
101.9	1246.6	1016.1	1104.2	782.7	1248.3	1549.0	456.9	423.2	191.9	480.8
3064.6	7176.8	6240.0	7153.4	5386.2	7392.1	5951.6	6649.6	6166.6	7149.0	6554.2
55.9	48.8	77.4	90.9	58.1	56.7	68.2	95.0	36.6	38.6	40.9
409.7	10263.9	10053.6	8959.7	7487.1	9474.8	7412.5	9455.1	9750.3	9992.0	9262.7
167.7	1783.9	2950.4	2344.4	2181.4	3357.3	2068.8	2893.3	2406.3	3590.8	2373.8
40.6	8837.7	5608.9	3685.9	2207.7	5559.5	3964.9	3288.4	2186.6	3902.2	1901.4
8857.2	7347.1	5580.7	6516.6	7225.3	6813.5	7404.1	6804.1	7084.4	4648.9	6325.1
1678.4	9147.3	6536.1	5559.9	4476.5	7079.2	5120.4	5545.6	3846.0	2975.9	3378.8
89.7	6909.9	5003.9	3576.0	2028.6	4803.7	2280.3	3857.8	2998.1	3408.3	2386.1
7343.1	4604.6	5822.4	4185.9	2557.0	3979.0	2658.7	4453.6	4051.0	2843.2	4430.8
2231.4	6503.9	6654.1	6825.7	5347.3	5973.9	5307.9	6319.7	7710.3	5328.8	5803.7
59.6	968.1	1808.6	1231.1	1754.2	2212.7	2236.7	777.4	438.4	353.8	654.6
29.7	58.0	85.0	84.9	185.6	68.2	31.4	84.8	58.7	24.9	57.3
1668.6	4784.7	4025.4	4457.1	3652.8	4846.9	4052.8	4503.2	5660.6	3992.5	4393.5
37.1	1598.2	3389.5	1827.3	305.6	1356.7	517.3	1329.7	511.2	1707.4	679.2
124.9	9877.7	7204.5	6497.6	6295.2	8869.5	7906.9	6691.3	6500.4	6751.9	5289.3
36.1	552.6	1403.5	473.5	211.0	1103.1	115.8	709.9	218.8	280.1	271.8
103.7	2047.8	1696.2	1217.9	1867.7	2073.9	1713.7	1827.3	1546.8	1383.2	1089.7
131.3	3021.0	2362.0	3086.4	2744.9	2738.2	2061.3	3459.5	3550.6	2616.3	1562.6
1221.1	8946.6	7030.6	7411.9	5126.6	7559.5	6150.1	7558.5	7185.4	4219.7	7053.5
11909.9	11586.3	9458.8	9152.0	8858.5	9600.0	9650.3	8588.5	12872.4	14025.2	10077.6
224.1	5959.8	6494.5	4452.7	3630.4	5564.3	3308.9	5748.2	3110.8	7021.0	4060.8
58.9	6190.3	2654.6	1227.3	1362.8	4314.8	715.6	2363.7	2165.5	4432.8	2086.2
255.2	2690.6	3475.0	4003.1	3518.3	4990.2	2762.9	3827.2	2057.8	3450.3	3360.3
28.0	4474.1	5906.8	5648.0	4594.2	5179.3	3904.2	5306.4	4289.2	4384.6	4720.6
181.1	6908.4	5850.6	6542.5	5691.7	6145.5	4076.3	7778.5	5215.8	4381.7	5724.8
4983.9	4457.9	5356.2	5628.9	4904.6	4478.1	4916.9	4281.9	4281.8	3619.9	4641.3

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6711.9	3691.1	3106.1
3853.3	2982.7	3221.3
3228.7	2360.7	2614.1
6715.4	3775.0	3437.8
7413.0	3319.2	3219.2
1967.7	2423.3	1703.0
3848.7	2969.6	3117.0
6985.0	6998.5	5863.5
1761.4	814.5	953.0
3140.5	561.6	972.1
5933.3	6023.5	6031.3
2974.0	2061.3	5227.9
7865.5	6641.2	5438.7
524.2	938.0	1381.6
6872.9	6372.0	5914.9
211.9	114.5	154.5
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2409.4	3025.0	1634.2
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7816.5	3977.9	7005.4
7367.9	2395.1	4032.4
5342.0	2971.4	3682.1
6753.4	6097.7	4997.6
1826.7	744.7	1051.5
189.1	159.1	99.3
4882.9	4207.2	4312.7
9475.5	754.6	572.1
8314.0	5894.3	6892.2
1360.8	342.1	296.7
1842.7	2490.4	2036.5
3029.6	2801.2	1918.2
6713.9	5972.6	7206.8
9778.3	8404.8	9685.5
6597.0	4856.2	4012.2
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3584.1	3034.8	2742.5
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EF516467.1 gg_id:222163 grassland soil clone FCPP433 EF5164
GQ263305.1 gg_id:591613 Structure Simulated Level Waste Site simulated level waste site clone FW1_a53 GQ263
DQ234507.2 gg_id:580066 Mucilaginibacter sp. RA1BR4 DQ234
AB240499.1 gg_id:143639 microbial structure rhizosphere biofilm Sapporo root-base (80 160 mm) Phragmites S AB240
DQ311009.1 gg_id:147488 Flavobacterium sp. str. Xb-5 DQ311
EU787448.1 gg_id:332533 Flexibacter sp. str. R2A36-4 EU787
EF125948.1 gg_id:512727 Biofilm-reactor Based Enrichment Utilizing Oligotrophic Concentrations Acyl-homose EF1259
AJ575720.1 gg_id:97995 lake water clone SW30 AJ5757
EF446146.1 gg_id:212927 Pedobacter lentus str. DS-40 EF4461
EU636060.1 gg_id:278598 Antarctic str. GA082 EU636
EU734803.2 gg_id:305278 Pedobacter sp. str. 12157 EU734
FJ674761.1 gg_id:523152 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6747
EF516106.1 gg_id:221402 grassland soil clone FCPO447 EF5161
AJ318181.1 gg_id:19131 Waste-gas biofilter clone BIsii5 AJ3181
EF157093.1 gg_id:240268 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF157
FJ377315.1 gg_id:370124 Pedobacter sp. str. L2b-1 FJ3773
EU769182.1 gg_id:321863 velvetleaf seed clone S3-10-CL5 EU769
DQ297969.1 gg_id:141304 Microbial hydrocarbon contaminated soil clone UA8 DQ297
EF516092.1 gg_id:225889 grassland soil clone FCPU417 EF516
DQ984593.1 gg_id:238033 Mt. Nan-Jen litterfall clone IYF111 DQ984
NC_010830.1 gg_id:342865 Candidatus Amoebophilus asiaticus str. 5a2 NC_01
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FJ203649.1 gg_id:334714 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2036
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GU118732.1 gg_id:547706 Threatened Corals Provide Microbial Habitats clone Mfra_I15 GU118
EU236302.1 gg_id:302378 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg1a1A4 EU236
FJ203161.1 gg_id:329500 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2031
FJ203340.1 gg_id:347250 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
FJ203020.1 gg_id:355518 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203043.1 gg_id:311355 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203017.1 gg_id:330094 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203331.1 gg_id:315090 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
GU119035.1 gg_id:568584 Threatened Corals Provide Microbial Habitats clone Past_F02 GU119
GU118657.1 gg_id:570612 Threatened Corals Provide Microbial Habitats clone Mfav_D13 GU118
EU925836.1 gg_id:315126 sediments sediment station DBS1 northern Bering Sea clone 005E9 EU925
GU118611.1 gg_id:582732 Threatened Corals Provide Microbial Habitats clone Mfav_A15 GU118
GU118827.1 gg_id:559549 Threatened Corals Provide Microbial Habitats clone Mfra_D03 GU118
FJ202283.1 gg_id:345661 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2022
FJ202772.1 gg_id:319915 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata k FJ2027
FJ203070.1 gg_id:342735 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2030
FJ203358.1 gg_id:356575 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2033

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2063.5	7257.3	6471.2	6644.7	6688.5	8174.9	6504.5	6668.3	10661.0	10957.2	7361.7
3007.7	3558.6	3924.8	3564.9	2034.3	3121.1	2236.1	2591.4	3508.6	2310.3	3296.4
94.2	4514.3	4489.6	4798.3	1567.3	3990.0	3174.3	4054.1	2756.3	2419.9	2538.1
201.2	5270.7	5789.4	5873.6	5901.8	5141.4	5740.4	5423.8	5980.1	4119.4	4833.4
368.8	8318.9	6440.5	6339.1	5185.4	7648.3	5299.1	6873.6	6445.0	10523.3	6928.7
39.2	2645.4	3895.3	2897.5	920.6	2875.9	627.7	4065.2	2383.1	1876.1	1855.6
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147.8	5332.4	5889.4	6183.2	3653.8	5579.0	3762.0	5748.3	3247.6	4633.2	4216.2
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FJ203306.1 gg_id:313726 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata c FJ2033
AM040120.1 gg_id:148599 sandy sediments clone Sylt 24 AM040
AF215634.1 gg_id:33872 Acanthamoeba spp. symbiont AF2156
FJ203542.1 gg_id:348635 and White Plague Disease-Induced Changes Caribbean Coral Montastraea faveolata h FJ2035
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AY862784.2 gg_id:161615 prokaryotic genetic Salar de Atacama Northern Chile athalassohaline lake water clon AY8627
AB015585.1 gg_id:2576 deep-sea sediment clone BD7-10 AB0155
EU236422.1 gg_id:290158 Haliclona gellius: sponge and symbionts 13 m depth Pacific Ocean clone Hg92G12 EU2364
EU156156.1 gg_id:250980 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
AY862060.1 gg_id:202103 Hydrogen and bioenergetics Yellowstone geothermal ecosystem Washburn Spring 3 AY8620
EU245415.1 gg_id:238437 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M1-D0 EU2454
EF648019.1 gg_id:253575 dynamics during produced water treatment aerobic activated sludge clone HB5 EF6480
GQ356162.1 gg_id:582163 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
FJ902777.1 gg_id:561726 phreatic limestone sinkholes northeastern Mexico wall biomat >195m deep cenote Z FJ9027
AB240228.1 gg_id:143475 microbial structure rhizosphere Phragmites bulk soil reed bed reactor laboratory clo AB2402
AY218548.1 gg_id:82144 penguin droppings sediments clone KD1-1 AY2185
EU181485.1 gg_id:255060 Prokaryotic enhanced organic matter remineralization continental margin marine se EU1814
EU385882.1 gg_id:261758 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3858
EF157182.1 gg_id:247643 Microbial natural asphalts rancho la brea heavy oil seeps Rancho La Brea tar pits clon EF1571
AF445671.1 gg_id:74751 travertine hot spring clone SM1D02 AF4456
AJ390445.1 gg_id:30354 soil clone PBS-II-34 AJ3904
GU172181.1 gg_id:591575 Microbial Eucalyptus plantation soil clone DSM-R9 GU172
EU156145.1 gg_id:254219 thermal spring microbial and functional genes Coffee Pots Hot Spring clone pCOF_65 EU1561
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EF515667.1 gg_id:217919 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5156
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EU522662.1 gg_id:262018 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU5226
EU638713.1 gg_id:349253 Ecological Role Firmicutes Identified Thermophilic Microbial Fuel Cells thermophilic n EU6387
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CU922950.1 gg_id:538588 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9229
EF515591.1 gg_id:227180 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
AY713479.1 gg_id:151718 first genome fragment marine sponge- candidate phylum Poribacteria transposase s AY7134

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FJ652532.1 gg_id:536466 aerobic and anaerobic ammonia-oxidizing marine sponges Atlantic Ocean water colu FJ6525
FJ479322.1 gg_id:569418 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4793
AB177139.1 gg_id:134010 seafloor methane hydrate clone ODP1230B10.20 AB177
AY093477.1 gg_id:63105 deep marine sediment clone MB-C2-106 AY0934
FJ873292.1 gg_id:564399 Vertical and archaea methane-rich cold seep located base sediments Okhotsk Sea clo FJ8732
EU491224.1 gg_id:263735 Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount Pisces Peak EU491
EU385929.1 gg_id:260188 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
AB177164.1 gg_id:134487 seafloor methane hydrate clone ODP1230B2.02 AB177
U68437.2 gg_id:3042 Chlamydia muridarum str. SFPD U6843
AY661797.1 gg_id:103676 Chlamydia suis str. 32XII AY661
U76710.2 gg_id:3022 Chlamydophila abortus str. EBA U7671
AB001785.1 gg_id:2944 Chlamydophila felis str. Fe-145 AB001
AB001775.1 gg_id:3035 Chlamydophila pecorum str. Bo-Maeda AB001
AE017160.1 gg_id:90574 Chlamydophila pneumoniae str. TW-183 AE017
AB001779.1 gg_id:2966 Chlamydophila psittaci str. Bud-1 AB001
AB001791.1 gg_id:2976 Chlamydophila psittaci str. Ohmiya AB001
AB001807.1 gg_id:2992 Chlamydophila psittaci str. PCM55 AB001
U68419.2 gg_id:3019 Chlamydophila psittaci str. turkey strain NJ1; Tk-NJ U6841
E17339.1 gg_id:44021 Chlamydia psittaci Prt/GCP1 E17339
E17340.1 gg_id:36508 Chlamydia psittaci Prk/Daruma E17340
E17343.1 gg_id:36991 Chlamydia pecorum Bo/Maeda E17343
DQ011662.1 gg_id:158932 Chlamydia sp. CH301104 DQ011
NC_005861.1 gg_id:471187 Candidatus Protochlamydia amoebophila str. UWE25 NC_00
FJ532294.1 gg_id:579758 Protochlamydia naegleriophila str. CRIB41 S156 FJ5322
FJ976105.1 gg_id:561599 Parachlamydia acanthamoebae str. cvE20 FJ9761
AF478463.2 gg_id:580742 New parachlamydial phylotypes detected s human clinical nasal washing clone cvC7 AF4784
AF177275.1 gg_id:24341 Neochlamydia hartmannellae str. A1Hsp AF1772
AY223862.1 gg_id:83246 Candidatus Rhabdochlamydia porcellionis clone RKPsHep porcellionis AY2238
EU090707.1 gg_id:249365 Chlamydia-Like Respiratory Pneumonia Patients clinical respiratory s German patient EU090
EU133918.1 gg_id:253897 tallgrass prarie soil clone FFCH17845 EU1339
AY140911.1 gg_id:89923 Fritschea eriococci AY1409
EF177461.1 gg_id:217851 Xenoturbella westbladi UUZM 57848 symbiont EF1774
U68460.2 gg_id:2935 Simkania negevensis str. Z U68460
DQ124300.1 gg_id:152262 Criblamydia sequanensis str. CRIB-18 DQ124
EU074225.1 gg_id:320922 Estrella lausannensis str. CRIB 30 EU0742
AF448722.3 gg_id:583814 New chlamydial lineages s freshwater clone cvE6 AF4487
DQ444442.1 gg_id:171324 Anaerobic ammonium oxidation tropical freshwater system (Lake Tanganyika) fresh DQ444
AF448723.3 gg_id:584073 New chlamydial lineages s freshwater clone cvE9 AF4487
AY184804.1 gg_id:100535 Waddlia sp. str. G817 AY1848
AF042496.1 gg_id:2936 Waddlia chondrophila str. WSU 86/1044 AF0424

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314.1	802.7	793.3	855.8	832.5	846.3	954.6	904.7	490.6	478.0	863.0
2320.3	8470.9	8667.7	10580.4	10772.1	9344.3	11437.8	7939.0	6282.5	4732.2	10841.3
5868.8	2831.0	2844.0	3050.5	3487.6	2545.0	3959.0	2990.1	3699.5	1778.2	3507.0
3982.1	2984.3	2442.2	3161.2	2846.7	2210.1	3479.2	2515.7	1492.8	862.4	2700.5
220.5	711.5	378.2	599.7	684.6	612.7	772.6	908.9	202.0	148.0	500.1
43.2	242.0	396.5	540.3	391.1	276.1	469.1	345.4	127.3	30.2	186.2
4274.4	5407.4	5151.9	5827.4	6928.5	5497.1	6828.8	5468.3	4890.1	5875.3	7813.0
34.3	1550.0	1329.6	1527.5	1545.7	1667.9	1816.7	1592.0	598.8	230.5	1393.4
2105.0	2608.1	2522.2	2811.8	2802.5	2487.5	2760.9	2705.7	3460.0	2543.8	2392.0
927.2	4004.5	4024.5	4185.7	4187.6	3901.1	4653.4	3950.5	4403.6	3612.5	3831.7
781.9	1838.8	1907.0	1797.9	1752.3	1946.4	2162.6	2138.1	1626.6	1731.7	1842.5
52.2	1299.3	1948.3	1663.2	908.9	1399.8	1088.0	2540.5	676.1	228.3	1136.0
5318.4	4510.7	4158.5	4021.0	2652.4	4657.9	4074.8	4035.4	6289.9	5345.5	4417.0
413.1	1900.1	2118.4	1873.6	2104.1	1865.1	2428.0	2125.5	3026.6	2251.2	1869.4
747.6	2077.4	2211.2	2102.8	2313.8	2176.1	2604.0	2270.0	2582.1	1685.8	2197.6
459.1	1590.8	1594.1	1620.5	1835.1	1666.9	2012.0	1774.5	1980.5	885.2	1631.7
804.4	2128.0	2339.3	2251.8	1657.4	2256.7	2462.8	2204.1	3241.2	2115.4	2246.1
776.7	1834.4	1885.9	1780.7	1741.4	1927.0	2157.2	1993.7	1736.8	1606.8	1832.4
2688.3	3014.5	2958.6	2976.6	3473.1	3164.0	3183.8	3211.7	2553.7	3009.0	2412.3
733.4	1989.8	2183.9	2094.9	2292.5	2103.3	2585.4	2223.5	2575.8	1794.7	2187.4
1473.8	1947.9	1948.6	2173.8	1813.1	2035.1	2194.3	2557.5	1135.2	936.1	1598.6
36.7	122.6	171.9	173.6	138.1	115.0	215.1	171.8	76.8	43.0	115.7
84.2	1592.2	1550.2	1586.0	1888.8	1419.5	2324.3	1306.3	1151.0	736.6	1031.7
120.1	1425.7	1828.0	1557.6	1392.2	1462.2	1794.8	1753.0	946.2	700.7	1178.4
37.2	39.2	47.8	51.7	48.0	44.0	54.4	55.6	21.3	25.0	35.7
11140.8	9610.0	8717.2	9461.0	10085.4	8504.2	11572.1	9829.3	11794.1	10734.3	10595.6
48.2	183.3	235.3	206.0	305.9	207.7	278.8	235.7	84.0	62.3	190.8
39.6	86.6	125.7	76.2	67.3	70.7	71.6	68.8	29.5	20.1	50.2
125.1	1153.1	1279.2	1437.3	1450.3	1367.0	1356.1	1553.3	617.5	1516.6	780.2
8312.9	7447.0	7381.2	7300.7	7292.1	7092.0	7636.1	7142.5	7195.0	6734.6	8992.7
3624.0	5421.9	6107.9	6464.3	6042.0	5629.3	6322.4	6477.7	6619.1	4522.5	6376.0
146.7	534.3	822.6	980.3	867.5	729.6	819.6	743.6	491.6	259.7	574.6
188.1	2787.1	3373.4	3121.8	3325.6	2796.8	4057.5	2903.6	1442.7	783.8	2062.3
201.2	451.9	434.0	424.7	386.9	494.3	336.5	411.7	370.1	169.5	477.1
344.2	4728.2	3374.1	3975.8	3465.3	3128.4	3407.6	4499.9	2928.1	3447.8	3771.2
174.3	3464.0	3706.9	4504.6	3539.2	3542.9	4559.3	3918.8	1814.2	536.5	2445.7
56.6	85.5	78.0	81.9	88.5	84.5	94.6	112.0	93.8	27.5	68.1
1826.3	3016.4	3441.5	3772.2	3562.2	3204.3	4003.3	3537.9	3555.5	2151.6	4323.0
1212.4	3042.1	3472.8	3425.8	2995.7	3289.9	4129.6	3365.8	3400.9	6085.0	4045.2
773.2	1161.5	967.2	1073.8	1442.1	1265.2	1329.8	1114.2	706.8	621.1	948.0

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7753.8	9430.9	11033.7
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2371.2	1921.6	3258.6
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367.4	516.9	805.0
5466.4	5716.7	7505.4
1349.8	1049.1	1973.8
2336.4	2997.3	3415.3
4078.3	4456.6	4966.7
1761.7	2273.1	2298.7
1692.6	1726.9	1697.7
2909.3	4477.7	4355.5
1883.1	2200.3	4102.5
2208.2	2438.5	2564.6
1761.9	1761.4	2197.5
2078.6	2413.8	2525.7
1756.1	2263.2	2285.3
3440.4	3756.2	3981.5
2109.5	2379.4	2304.9
2087.8	2280.3	3048.7
118.6	149.9	299.5
1268.1	1049.4	1561.6
1713.2	1517.7	1825.9
31.8	39.5	71.1
8902.1	9207.2	9699.4
148.9	262.9	304.5
48.8	90.3	103.9
1392.7	1532.4	1786.6
6880.3	7679.7	7463.7
5583.5	6702.4	7432.7
684.5	844.5	873.2
2308.8	2447.7	4318.5
442.7	573.9	355.5
3931.1	4961.1	3727.9
2680.6	3382.6	5145.5
79.9	115.9	77.5
3234.0	3557.3	4312.0
3149.2	4657.4	3162.0
979.9	1224.4	1432.7

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s__Chlorobium ferrooxidans	57079
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s__Chloroherpeton thalassium	56512
s__Chloroherpeton thalassium	56669
s__Pelodictyon luteolum	56587
s__Pelodictyon phaeoclathratiforme	56565
s__Prosthecochloris aestuarii	57451
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FJ172861.1 gg_id:354398 Qinghai Yak Ruminal and Fungi China rumen clone RB-5B9 FJ1728
FJ810559.1 gg_id:408758 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GU208405.1 gg_id:560369 Study on Sediment Dongping Lake sediment clone Fh2-11 GU208
AM490699.1 gg_id:565618 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
DQ640726.1 gg_id:230544 full-scale EBPR sludge clone Skagen107 DQ640
FJ810562.1 gg_id:467449 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
FM207902.1 gg_id:310286 Anaerobic p-xylene mineralization activated sludge and fresh water sediment denitr FM207
GU208220.1 gg_id:581318 Study on Sediment Dongping Lake sediment clone 3C3-5 GU208
AM490708.1 gg_id:565419 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
AM162482.1 gg_id:152302 and situ identification acidic sphagnum peat bog clone B44 AM162
DQ501337.1 gg_id:196940 Seasonal dynamics free-living and particle- four lakes northeastern Germany freshw DQ501
AB486984.1 gg_id:578382 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCORC AB486
AB252950.1 gg_id:172221 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 392 AB2529
AY221073.1 gg_id:83562 Mammoth cave clone CCM9b AY221
AB252951.1 gg_id:170662 Identification Shibayama lagoon Ishikawa Japan iron-oxidation biofilm clone 397 AB2529
FJ810563.1 gg_id:373685 Subsurface ecosystem resilience: Long-term attenuation subsurface contaminants su FJ8105
GU208359.1 gg_id:561793 Study on Sediment Dongping Lake sediment clone Td4-4 GU208
FJ485389.1 gg_id:509237 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4853
AF445702.1 gg_id:46550 green sulfur clone SM1H02 AF445
AY555793.1 gg_id:106021 Bor Khlueng hot spring clone PK74 AY555
DQ088767.1 gg_id:134457 subsurface clone BE325FW032701CTS_hole1-17 DQ088
AY741701.1 gg_id:99903 borehole water gold mine clone TTMF57 AY741
EF560699.1 gg_id:225651 Chlorobaculum parvum str. L EF5606
NC_002932.3 gg_id:143083 Chlorobium tepidum str. TLS NC_00
AM050125.1 gg_id:188667 Chlorobium limicola str. C1 AM050
EF560696.1 gg_id:226020 Chlorobaculum macestae str. M EF5606
AM050131.1 gg_id:192472 Pelodictyon luteolum str. E1P1 AM050
AY693833.1 gg_id:103776 anaerobic sludge clone EUB42 AY6938
NR_029321.1 gg_id:540816 Chlorobaculum thiosulfatiphilum str. 6230; DSM 249 NR_02
EF560700.1 gg_id:222254 Chlorobaculum parvum str. X EF5607
NC_007514.1 gg_id:141021 Chlorobium chlorochromatii str. CaD3 NC_00
NZ_AASE01000013.1 gg_id:171289 Chlorobium ferrooxidans str. DSM 13031 NZ_AA
NZ_AAJD01000008.1 gg_id:131048 Prosthecochloris vibrioformis str. DSM 265 NZ_AA
NC_011026.1 gg_id:347501 Chloroherpeton thalassium str. ATCC 35110 NC_01
AF170103.1 gg_id:202092 Chloroherpeton thalassium AF170
CP000096.1 gg_id:143111 Pelodictyon luteolum str. DSM 273 CP000
NZ_AAIK01000026.1 gg_id:132219 Pelodictyon phaeoclathratiforme str. BU-1 NZ_AA
AAIJ01000002.1 gg_id:133741 Prosthecochloris aestuarii str. DSM 271 AAIJ01
AJ291827.1 gg_id:19433 Prosthecochloris vibrioformis str. CHP 3402 AJ2918
FJ716270.1 gg_id:513209 Chlorobi dominate shal chemocline Bahamas Sawmill Sink column 10.3 m water dept FJ7162
AJ888468.1 gg_id:113834 Prosthecochloris sp. str. 4Vi AJ8884

1104.7	6801.6	6402.5	6053.3	4040.7	6264.9	5407.0	6030.1	4788.7	3048.6	4892.4
3112.8	5324.3	5665.4	6472.6	7070.6	5099.2	7377.7	5375.1	4984.3	3578.4	5932.5
13311.4	6253.2	6436.7	7368.0	7570.0	5644.4	9573.0	5819.2	6532.0	8262.1	5895.8
6946.5	5081.8	5111.4	5931.0	5570.2	4533.2	8314.8	4625.8	7321.2	5250.5	5625.4
61.1	79.8	229.2	204.3	517.2	131.1	2099.2	140.0	62.8	18.6	56.2
1675.6	4187.6	4519.1	4991.4	5045.1	4055.6	5905.4	4251.4	3965.3	3722.8	4423.5
3921.9	7900.0	7132.4	7305.2	6448.0	6826.7	7369.5	6842.1	10872.4	5815.4	8018.1
233.8	4362.7	5299.9	5257.4	6326.3	4181.1	8744.5	4545.0	2912.9	2815.2	3429.4
619.5	6028.8	6219.6	7620.5	8154.5	5647.4	11871.0	5959.4	4036.3	3168.6	5569.4
27.6	248.9	675.4	1174.2	818.0	781.6	687.7	459.2	100.4	161.1	219.9
10579.7	5022.3	4351.2	4822.7	4974.1	3200.8	7039.3	3430.1	5360.2	4443.5	5093.5
101.9	4431.7	4181.8	4547.1	5406.6	3167.4	8997.6	3316.9	2684.8	1071.7	2086.2
51.3	194.0	463.4	1241.5	517.7	192.9	1605.3	280.1	112.0	28.5	101.0
627.7	3038.2	3558.1	4154.1	4625.9	3269.0	4417.4	3579.2	2633.7	1688.7	2532.7
46.0	1607.7	2619.4	3008.9	3217.9	1778.2	5206.1	1990.7	1213.7	551.2	1149.2
8611.0	6620.0	6898.2	7734.4	6228.6	6133.4	6942.4	6359.8	7233.1	5511.5	9525.6
49.5	2628.6	3671.7	4671.0	5068.7	1579.7	7478.1	1393.6	417.1	248.0	996.2
92.4	3822.1	3609.8	3434.1	5688.0	3021.3	7553.1	3377.5	2700.1	3976.1	2535.7
19956.6	11936.2	8697.0	8036.8	8263.0	8811.6	9017.0	8384.2	11517.9	9186.6	16527.5
6219.0	7618.1	6669.1	6678.5	6209.2	6282.6	6954.6	6378.9	7054.7	4310.6	9922.0
1325.7	2631.8	2004.3	1529.1	1547.3	2064.8	1826.6	1926.1	1927.3	1426.8	1277.0
4806.8	3498.3	2603.7	2469.5	2711.3	3094.7	2742.5	2855.7	3091.1	2059.0	4681.3
80.6	1913.2	1982.7	2800.9	2380.1	2485.7	3032.8	1830.2	379.9	195.8	1285.1
60.7	196.2	168.7	147.9	222.8	282.0	913.6	275.7	48.3	47.2	87.9
500.9	1159.5	1138.6	1235.2	1094.7	1415.4	3398.0	1410.1	698.5	307.0	1068.1
1587.0	4130.1	4298.6	4888.0	3946.8	4241.8	6318.8	5053.5	3137.0	2128.4	4805.6
54.4	46.4	61.4	46.2	81.5	194.7	3593.8	39.0	47.5	32.2	44.6
1128.6	1098.9	997.5	948.0	782.8	905.5	1842.7	941.7	960.2	873.6	821.8
1403.9	1265.9	1105.5	822.4	1175.7	1117.8	5281.6	726.7	1265.3	702.6	1166.5
221.0	250.5	224.6	186.8	193.7	283.9	1349.4	254.2	153.7	76.7	137.1
1409.6	1219.5	1263.4	1353.2	1351.5	1676.2	5187.7	1405.7	795.2	611.2	1238.9
192.1	1658.0	1269.9	1924.5	1369.3	1695.0	3469.9	1690.3	1129.2	619.1	1236.4
365.9	1756.9	2157.0	3037.7	2191.3	2513.8	3997.7	2283.6	845.4	233.2	1613.2
56.7	2518.4	1485.1	1173.6	2228.3	1227.1	3395.9	705.9	2010.7	191.5	554.0
4392.9	8042.6	8527.1	8716.7	8841.6	8371.3	9312.8	7692.4	7439.8	5764.3	9081.5
2636.7	3617.3	4885.3	4264.3	4939.5	3838.1	5730.2	3924.1	4408.6	3364.0	4585.1
129.3	1079.8	1001.6	1571.5	972.0	1236.0	2596.8	1155.7	638.1	303.9	1001.3
43.8	133.5	227.5	191.1	298.4	438.5	497.0	198.9	51.9	34.0	94.6
3212.6	3320.4	3459.5	3561.7	3615.0	3225.1	4109.5	3327.2	3845.4	1135.5	2311.5
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48.3	36.6	56.4	53.2	55.1	31.0	84.8	36.2	22.0	26.0	26.9

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3832.1	5224.4	4850.7
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3523.2	3260.3	4723.3
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AB301726.1 gg_id:222703 Prosthecochloris sp. str. 5H2 AB301
EF205522.1 gg_id:212646 among geographically regions central Tibet geothermal spring mat clone DTB149 EF2055
AY293405.1 gg_id:88021 travertine terrace Yellowstone Hot Springs clone SM2B09 AY2934
NC_010803.1 gg_id:292136 Chlorobium limicola str. DSM 245 NC_01
EF153291.1 gg_id:189071 Chlorobium sp. str. ShCl03 EF1532
EF654662.1 gg_id:256699 Chlorobium phaeobacteroides str. G-gCphb03 EF6546
AY509521.1 gg_id:103210 freshwater clone LiUU-9-330 AY5095
DQ676424.1 gg_id:217425 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AB286365.1 gg_id:216447 Reducing production and domination comamonadaceae reducing oxygen supply was AB2863
GQ339136.1 gg_id:515456 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
GU183591.1 gg_id:582049 Structures Reduced and Oxidized Aquifer lower Aqueous Arsenic Titas Bangladesh a GU183
GQ339118.1 gg_id:529782 Comprehensive Investigation on Iron Cycling Freshwater Seep ing Microscopy Cultiv GQ339
AB240289.1 gg_id:144037 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB240
AF234699.1 gg_id:25315 sludge clone A12b AF2346
DQ520166.1 gg_id:160290 shal China sequences hypertrophic freshwater lake clone ML-5-66.2 DQ520
EF648096.1 gg_id:255310 dynamics during produced water treatment aerobic activated sludge clone HB107 EF6480
AB288917.1 gg_id:202747 termite gut homogenate clone BOf8-10 AB2889
AF445657.1 gg_id:30516 travertine hot spring clone SM1B09 AF4456
EF126253.1 gg_id:277457 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
AF234130.1 gg_id:41844 arid soil clone #0319-6E22 AF2341
AY921840.1 gg_id:114305 farm soil clone AKYH1119 AY9218
EF126257.1 gg_id:263133 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
EU133924.1 gg_id:253338 tallgrass prarie soil clone FFCH3953 EU1339
EF018268.1 gg_id:203705 aspen rhizosphere clone Amb_16S_627 EF0182
EU133919.1 gg_id:239595 tallgrass prarie soil clone FFCH12071 EU1339
EF126256.1 gg_id:273696 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
EF632929.1 gg_id:241447 Unique microbial contrasting aquatic altitude Andean Altiplano (northern Chile) fresh EF6329
AY118151.1 gg_id:60815 benzene-degrading nitrate-reducing consortium clone Cart-N2 bacterium AY1181
AB240328.1 gg_id:141738 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clon AB2403
AB192128.1 gg_id:142983 termite gut homogenate clone M2PB4-57 AB1921
DQ413108.1 gg_id:153791 Microbial -dependent and Approaches Anaerobic/Aerobic SBR Reactor EBPR sludge DQ413
FJ356024.1 gg_id:360408 Targeted FACS enrichment groups lab scale systems anaerobic:aerobic lab-scale EBPR FJ3560
AY118152.1 gg_id:60814 benzene-degrading nitrate-reducing consortium clone Cart-N3 bacterium AY1181
DQ676315.1 gg_id:222624 Archaeal and plankton freshwater pond suboxic freshwater-pond sediment clone M DQ676
AB192127.1 gg_id:141121 termite gut homogenate clone M2PT2-67 AB1921
GQ356164.1 gg_id:588073 biomarkers ammonia oxidation activity anaerobic ammonium-oxidation (Anammox) GQ356
EF515342.1 gg_id:224048 Electricigen Enrichment MFC upf microbial fuel cell anode clone 23b07 EF5153
AB192126.1 gg_id:142772 termite gut homogenate clone M1NP2-57 AB1921
DQ018819.1 gg_id:135521 Unique Microbial Anaerobic Swine Lagoons anaerobic swine lagoon clone C-156 DQ018
AF027006.1 gg_id:2640 hot spring clone OPB88 AF0270

54.6	1054.3	1752.8	1988.4	1974.9	1400.9	2129.0	1509.0	821.2	310.3	1195.8
680.9	2075.8	1563.8	2078.6	2319.9	1978.3	2905.3	2427.8	2661.2	908.0	2094.8
43.8	276.8	360.6	472.2	565.1	456.2	344.0	496.0	269.9	183.2	252.8
53.9	50.2	56.0	52.7	71.8	88.9	148.8	66.2	25.1	27.8	32.7
769.3	2491.6	2978.9	3875.7	3349.6	3424.5	4895.2	3227.9	2430.5	1650.9	2534.8
197.9	1649.8	1647.4	2165.2	1275.1	1766.9	2624.3	1450.9	1234.8	930.5	1567.0
253.7	2936.6	3650.6	3736.9	3018.1	2928.4	4581.2	3470.2	1925.8	1416.6	3315.2
8056.7	6694.4	6939.0	7786.7	7948.7	9235.6	8888.4	6412.4	9789.6	7335.3	9056.3
5337.7	6527.9	7272.7	7683.4	7526.1	6993.7	7219.1	7673.9	6583.6	6076.9	6990.3
60.1	460.2	856.7	469.1	1566.4	787.9	642.9	6086.8	1008.8	58.6	1969.3
3096.9	5151.7	6259.2	6238.1	6119.3	5866.1	6211.6	6784.8	4372.3	3105.9	6224.6
2195.9	7481.6	8691.5	9775.5	9095.0	8599.8	9330.7	8379.9	7132.7	7264.4	9208.0
12583.0	4814.3	4575.5	6002.2	5253.9	5255.0	6271.5	5223.6	6680.2	7507.5	6235.5
14412.8	4240.4	4380.8	4628.0	5643.6	4716.1	5479.2	5526.5	3992.1	3644.5	4692.7
4513.3	3246.3	2825.7	3209.1	4055.6	3224.3	4912.2	3485.7	4548.8	3477.8	4064.9
2912.8	2942.0	3536.6	3343.7	3558.0	2976.0	3101.3	3502.2	2190.0	1203.2	3711.2
34.0	711.6	1174.2	1616.9	787.6	618.2	689.9	1665.4	149.7	102.9	335.1
29.2	100.2	321.0	124.0	96.5	378.8	223.8	2721.9	545.3	11.8	522.5
1362.9	2484.6	2928.7	3052.5	3815.0	2628.3	3147.5	2994.1	2402.2	1938.2	3627.4
3689.3	6770.7	6332.8	6737.2	6083.3	6285.1	6652.7	6281.2	7267.5	4865.2	7260.8
12779.2	3137.2	4148.4	4638.6	4210.0	3267.0	4453.3	3457.7	4169.8	1739.4	2926.8
911.3	4537.3	4688.6	5228.4	6297.7	4425.2	6199.2	4480.7	4164.8	2002.1	4338.3
1274.6	6254.1	5288.7	5658.8	6312.0	5512.0	5661.3	5477.0	7132.8	5900.6	5268.7
5581.8	2335.5	1984.7	2354.5	1897.4	2566.8	1774.7	2354.4	1172.4	455.5	1839.6
48.7	511.3	651.2	688.0	2071.7	792.3	1690.1	623.3	613.6	568.7	322.7
187.2	1657.5	2290.1	2559.7	2410.0	2415.5	3011.9	1970.9	427.2	376.1	1732.3
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49.0	2315.6	2937.1	1772.8	2670.7	2748.6	2501.9	1755.2	984.6	1341.0	922.3
9755.4	5938.1	6333.5	6577.1	6649.3	5904.8	6527.0	5757.2	7773.6	5892.2	7408.3
53.4	404.1	869.3	787.8	1276.0	626.6	1204.3	590.0	163.5	114.5	302.8
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317.2	235.7	439.4	669.1	849.7	385.4	772.6	616.1	152.0	142.3	1006.9

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341.4	502.4	326.0
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1956.5	2803.9	4900.4
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2393.6	3043.4	4033.3
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7258.3	7975.2	7206.9
1100.8	210.1	291.7
5718.3	6975.5	6616.3
8262.4	7772.3	7080.3
5109.2	5934.6	5018.3
5405.7	4605.7	6125.5
3917.2	3621.1	2954.3
2407.8	3920.9	2612.7
1037.7	273.8	929.8
948.5	267.7	217.7
2837.2	4224.6	2802.8
5227.2	6330.4	5819.8
3188.7	3544.4	4260.8
4542.3	4528.9	6135.7
5136.4	6830.3	5764.8
1436.8	1646.0	2662.5
697.0	664.7	1282.2
1390.3	2441.4	2557.3
6629.7	7949.8	7299.0
6535.1	8394.7	10552.7
1381.2	694.3	1263.2
1449.5	1184.6	2132.2
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471.9	624.3	527.6
361.0	289.5	231.4
73.8	99.7	75.2
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DQ324902.1 gg_id:148867 Geochemical and bioenergetic variability across systems Yellowstone National Park DQ324
DQ645243.1 gg_id:164804 Microbial and oxidation activity biofilms within Alvord Desert Basin Southeastern Or DQ645
AY861796.1 gg_id:112647 Obsidian Pool prime community clone OPPB063 AY8617
EU283596.1 gg_id:278344 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A309 EU2835
FN429794.1 gg_id:588053 Biogeochemistry -activity cold seep Larsen B area western Weddell Sea Antarctica m FN4297
EU937844.1 gg_id:337082 Biogeochemistry Iron Oxidation Circumneutral Freshwater Habitat riparian iron oxidi EU9378
AM490707.1 gg_id:564034 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
AB195898.1 gg_id:109186 Anaerobic sludge clone N25 AB1958
EU234260.1 gg_id:255151 river and un techniques downstream Wang Yang River receiving penicillin G producti EU2342
AM997556.1 gg_id:572568 and biogeography deep-sea surface sediments South Ocean Atlantic Ocean:South-A AM997
EF562071.1 gg_id:256995 Subsurface microbial deep-granitic-fracture water colorado Henderson Molybdenum EF5620
FJ710780.1 gg_id:540639 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
AB234252.1 gg_id:149719 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AB486936.1 gg_id:577176 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSCOR(AB4869
EF467561.1 gg_id:216233 situ microelectrode voltammetry sulfur-oxidizing biofilms Frasassi sulfidic cave strear EF4675
FJ710734.1 gg_id:591641 Abundance and microbial long-term operated anammox biofilm reactors initiated ino FJ7107
FJ416082.1 gg_id:363429 sediments sediment station NEC5 Northern Bering Sea clone 014K15 FJ4160
EF203206.1 gg_id:213866 phylotypes sediments Lake Kastoria Greece sediment clone Kas175B EF2032
DQ404811.1 gg_id:154683 contaminated sediment clone 655939 DQ404
EU644107.1 gg_id:282378 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU6441
GQ487886.1 gg_id:578784 Microbial metal soil polluted heavy metals clone T1-6 GQ487
AB186805.1 gg_id:101101 polychlorinated dioxin dechlorinating microcosm clone TSAC14 AB1868
AY340841.1 gg_id:91023 sulfate-reducing fluidized-bed reactor clone SR_FBR_L83 AY3408
AY741700.1 gg_id:99743 borehole water gold mine clone TTMF87 AY7417
EU101178.1 gg_id:255842 Sulfide/oxygen supply ratio predicts outcome competition among sulfur-oxidizing wa EU1011
DQ925883.1 gg_id:252875 Microbes and Thermal Gradients Temperature Hydrothermal Chimneys hydrotherm DQ925
GU369881.1 gg_id:517364 and mats vents Arc white filamentous microbial mat photic shal hydrothermal vent GU369
AB355060.1 gg_id:247813 Monitoring and archaeal two heavy polluted areas lake Egypt based on sediment Ma AB3550
AY327874.1 gg_id:88595 surface vent snail foot clone SF_C4-C6 AY3278
FJ545477.1 gg_id:547407 Diveristy Seawater and Sediment Northern North Yel Sea sediment clone S1-48 FJ5454
DQ337042.1 gg_id:147607 subsurface water clone EV818EB5CPSAJJ39 DQ337
AB179693.1 gg_id:102361 groundwater 0.2 m-captured fraction clone KNA6-EB22 AB1796
FJ484546.1 gg_id:533163 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4845
AB117714.1 gg_id:103839 autotrophic nitrifying biofilm clone NB-10 AB1177
DQ521481.1 gg_id:185950 Antarctic lake ice cover clone ANTLV1_C12 DQ521
AF234733.1 gg_id:53925 sludge clone S14 AF2347
FJ481330.1 gg_id:565487 Microbes marine sponges sponge tissue clone XB3E04F FJ4813
EU134161.1 gg_id:248283 tallgrass prarie soil clone FFCH18628 EU1341
AF445738.1 gg_id:47497 travertine hot spring clone SM2G06 AF4457
AM490723.1 gg_id:540671 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490

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314.0	1769.4	1600.5	1480.1	1608.7	1317.6	1999.9	1618.2	1685.1	1078.5	1247.8
118.6	601.2	913.5	952.8	916.0	992.8	1208.2	1198.1	307.7	2090.6	406.7
402.4	4349.4	4676.3	5835.2	6883.9	4913.2	8448.6	5610.8	3889.6	1233.6	3697.4
1549.0	4755.2	4803.1	5267.3	7174.9	5274.6	7699.1	5684.4	9199.4	3903.2	3892.1
720.7	4195.5	4878.7	4959.9	6138.3	3739.5	7359.2	3728.3	2697.5	2887.5	3771.7
1978.4	9695.4	10269.8	9985.6	10526.9	8814.2	11942.1	9571.0	8583.2	7226.0	9917.2
4393.2	7142.9	7449.3	7457.9	7236.2	6199.0	10524.2	6418.9	7090.0	5685.7	7444.1
10995.6	3451.4	4477.8	4990.7	6176.8	4059.4	8045.9	4085.8	2461.7	2155.4	4063.6
6136.5	6766.1	6343.6	7053.1	7928.0	5815.1	9718.4	6061.4	6871.0	4572.9	5985.8
146.9	3216.3	3180.5	3941.0	5384.0	2860.6	5787.8	2991.0	1784.6	447.0	2555.9
10894.2	7911.1	7735.4	9002.4	9454.7	7703.8	9920.8	7016.9	8779.1	8468.1	9300.6
790.1	3629.1	3813.3	4342.7	4686.8	3275.3	5626.6	3615.2	2844.6	981.4	3611.2
3290.0	5922.4	5665.4	6831.2	6592.1	4994.8	7123.2	5039.0	4975.3	3905.5	5348.5
6038.0	4524.6	4851.1	5716.1	6775.0	4227.3	9068.0	3769.9	4345.6	3188.3	4491.6
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23561.7	4655.7	5672.7	6141.8	6804.2	4296.2	8235.7	4725.2	3210.1	1642.3	5084.1
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4564.2	7979.8	7823.2	8829.0	9497.8	7135.2	11215.8	7550.8	6781.1	4814.0	7573.0
131.0	2347.9	2968.0	3605.1	6050.5	1534.1	7646.3	1519.5	847.1	527.0	1788.0
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CU466712.1 gg_id:324279 Evry wastewater treatment plant anoxic basin clone CU466
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DQ404819.1 gg_id:154220 contaminated sediment clone 655947 DQ404
EU134165.1 gg_id:243950 tallgrass prarie soil clone FFCH1946 EU134
FJ478663.1 gg_id:583735 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4786
AJ347035.1 gg_id:60174 sponge clone TK16 AJ3470
EF516563.1 gg_id:223701 grassland soil clone FCPT422 EF5165
EF516958.1 gg_id:219899 grassland soil clone FCPS653 EF5169
AF173817.1 gg_id:2727 Antarctic lake ice clone LB3-100 AF1738
GQ397094.1 gg_id:535410 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts s GQ397
EU133974.1 gg_id:251353 tallgrass prarie soil clone FFCH9554 EU1339
DQ017911.1 gg_id:131339 upland stream clone S-Rwb_62 DQ017
EU134013.1 gg_id:248412 tallgrass prarie soil clone FFCH5168 EU1340
EU051342.1 gg_id:249472 soil clone BJ-204 EU0513
AY921746.1 gg_id:113259 farm soil clone AKYH905 AY9217
AY922012.1 gg_id:113017 farm soil clone AKYG434 AY9220
EU134153.1 gg_id:249503 tallgrass prarie soil clone FFCH17716 EU1341
FM253644.1 gg_id:308698 Rock gold mine unusually microbial biofilm clone C04-2 FM253
FJ479099.1 gg_id:576689 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4790
FJ481242.1 gg_id:546971 Microbes marine sponges sponge tissue clone XA2F07F FJ4812
AM490722.1 gg_id:584712 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
EF019589.1 gg_id:215379 aspen rhizosphere clone Elev_16S_1110 EF0195
AY921926.1 gg_id:114246 farm soil clone AKYH973 AY9219
EF126266.1 gg_id:270948 Phototrophic microbial build laminated Fe-formations on Sulawesi Indonesia mesoph EF1262
FM253645.1 gg_id:316115 Rock gold mine unusually microbial biofilm clone C05-2 FM253
FJ152730.1 gg_id:306793 Changes ly soil (Mexico) flooding alkaline saline soils former lake Texcoco clone TX5A_ FJ1527
AF445676.1 gg_id:30131 travertine hot spring clone SM1D10 AF4456
AM259916.1 gg_id:240136 Chondrilla nucula-specific sponge mesohyl clone CN69 AM259
AY921673.1 gg_id:112841 farm soil clone AKYG659 AY9216
EF515553.1 gg_id:227415 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
AM935617.1 gg_id:534001 Dynamics during identified and SSU libraries pilot-scale bioremediation process hyd AM935
AY426440.1 gg_id:105100 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone B15 AY4264
AJ306749.1 gg_id:66944 DCP-dechlorinating consortium clone SHA-147 AJ3067
AB046413.1 gg_id:44630 Anaerolinea thermophila AB0464
CU922908.1 gg_id:564996 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU9225
AB274513.1 gg_id:214594 packed-bed reactor clone CFB-24 AB2745
AB234255.1 gg_id:149727 Biotransformation Polychlorinated Dioxins Microbial Dynamics Sediment Microcosm AB2342
AY921672.1 gg_id:113861 farm soil clone AKYH789 AY9216
AY921883.1 gg_id:112889 farm soil clone AKYG493 AY9218
AB240304.1 gg_id:143935 microbial structure Phragmites rhizosphere biofilm reed bed reactor laboratory clone AB2403

163.4	792.7	1253.2	1032.7	1149.5	1022.5	1235.6	1098.1	362.1	688.9	834.4
467.2	2976.0	2971.4	3366.8	4220.0	3276.1	5582.3	2939.3	1546.4	1385.1	3213.5
706.1	3815.4	3811.0	4110.1	4883.2	3849.2	4689.1	3958.3	3916.9	4546.9	4983.4
36.4	79.4	146.9	44.0	189.7	48.5	115.3	38.5	35.3	25.7	39.4
425.2	4336.6	4420.0	4368.5	8453.0	4655.5	9185.4	4144.3	2534.0	2025.0	3631.0
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33.5	104.0	92.2	98.6	223.3	113.7	176.8	156.9	53.0	31.8	76.8
405.1	5413.5	6221.6	6543.9	9666.3	6331.2	9952.2	5532.6	4065.0	3171.5	4861.6
4014.9	6791.1	6610.9	6738.4	8273.4	6588.2	9191.7	6438.8	6595.9	7066.5	6778.3
40.2	60.1	71.8	54.8	315.2	73.4	218.5	55.5	46.5	35.6	51.3
3571.1	5097.6	5141.7	5062.0	6858.1	4708.0	7660.7	4742.2	2568.8	4024.1	4806.2
1362.7	4381.8	4851.8	5527.9	7984.0	4511.6	7619.1	5124.6	4178.0	1159.7	3304.5
40.0	50.7	208.8	57.9	202.9	54.9	120.1	48.4	30.9	21.7	42.0
30747.8	14754.8	13439.3	14788.4	14792.6	14132.7	15699.9	12846.8	18886.6	15141.6	20414.3
78.7	90.8	118.5	81.1	335.6	236.9	92.9	467.0	51.5	47.0	94.8
6981.7	5969.3	5396.5	7339.8	6905.0	6239.8	7495.0	5752.8	4442.6	4169.3	6716.7
3208.1	3677.7	2387.7	3775.2	6401.7	3660.4	5498.6	3421.0	4601.4	2744.8	3867.7
641.5	2564.5	2660.8	2847.4	2981.9	2671.2	3585.8	3102.3	2342.5	1742.3	2080.6
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1060.1	8567.3	8768.7	9470.6	12156.0	9214.0	13719.0	8164.8	5549.2	7070.9	9032.3
1614.0	8238.1	8763.7	8927.2	13206.9	8946.8	15151.5	8454.3	4180.8	4871.8	7681.0
947.6	3808.5	3641.0	3388.9	5840.6	4882.5	5780.3	4731.7	2502.4	4688.4	1843.1
8306.1	7411.7	7473.1	8326.9	8973.5	8102.3	9222.7	7095.2	8584.2	6844.8	8449.1
42.6	264.7	260.2	272.4	918.5	247.7	1067.4	163.1	87.0	65.2	149.7
13806.7	8746.1	9003.7	9105.2	9821.8	8429.2	11190.4	10659.0	8153.0	9097.3	11349.8
1104.5	3504.8	4149.4	4267.5	5198.3	3953.8	5660.4	3899.8	2858.2	2244.4	3295.1
9214.9	6544.0	6218.7	7306.3	8945.6	6919.3	8994.8	6401.0	6135.3	5953.7	8109.8
197.2	191.3	197.0	164.6	257.6	176.8	273.0	203.8	87.9	82.8	122.6
215.4	2363.5	2403.5	2884.8	4278.9	2558.0	4151.7	2350.5	1667.1	535.4	1728.9
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50.3	176.2	176.1	171.8	315.4	112.9	189.4	92.5	77.2	54.6	57.3
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116.6	1751.2	3100.1	1934.9	2192.4	1370.7	2406.9	1563.3	630.3	286.8	1151.4
42.0	264.0	438.6	337.6	634.6	352.5	630.6	260.6	265.6	29.7	135.5
179.5	1717.7	2242.0	2251.6	3268.5	2218.8	4071.1	2016.8	778.8	573.1	1071.1
37.7	223.8	328.1	387.4	386.1	233.6	688.3	282.9	133.0	65.6	159.1
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3847.9	2404.2	2347.6	2724.0	2535.2	2778.1	3466.4	2916.2	2684.4	2589.0	2416.1
38.2	145.3	189.5	176.9	308.6	107.0	418.4	108.4	28.8	24.8	43.3
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4634.1	5601.2	6012.9
7212.2	7665.8	10301.5
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1111.3	1511.5	2412.6
180.8	596.4	790.7
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GU061267.1 gg_id:593453 Evaluation culturing methods cultivate previously Yel Sea intertidal beach seawater GU061
AF154084.1 gg_id:13740 hydrocarbon seep clone BPC110 AF154
FN396699.1 gg_id:549125 constant flux thermophilic cold seabed Arctic marine surface sediment clone s5_0_V FN396
CU924021.1 gg_id:544436 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
AY592357.1 gg_id:105404 deep-sea mud volcano clone Amsterdam-1B-56; BC20-1B-56 AY592
EF198026.1 gg_id:195376 Microbial structures and thermophilic methanogenic consortia anaerobic mesophilic EF198
EU542512.1 gg_id:264526 Effects chemical structure concentration on pathways microbial during dechlorinatio EU542
DQ478736.1 gg_id:158754 UASB reactor treating brewery wastewater clone CLONG3 DQ478
AB447642.1 gg_id:579753 Microbial Structure and Dynamics Granules Expanded Granular Sludge Bed (EGSB) R AB447
AB274515.1 gg_id:214216 packed-bed reactor clone CFB-26 AB274
EF688367.1 gg_id:242454 soil clone F6-01 EF6883
GU118185.1 gg_id:587139 Threatened Corals Provide Microbial Habitats clone Dstr_N04 GU118
DQ811864.1 gg_id:168417 mangrove soil clone MSB-3D4 DQ811
FJ542942.1 gg_id:519946 Microbiomic intestine earthworm Eisenia fetida fed ergovaline treatment gut clone B FJ5429
EF125394.1 gg_id:193982 soil naked tidal flat sediment near mangrove clone MSB-1B8 EF1253
GU455152.1 gg_id:525242 Understanding short-chain fatty acids accumulation enhanced alkaline digestion: kir GU455
EF125459.1 gg_id:191839 mangrove soil clone MSB-2G5 EF1254
EU283567.1 gg_id:278710 Model Early Earth Harbors Deeply Divergent Divisions Anderson Lake clone A379 EU283
FJ478574.1 gg_id:582447 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4785
DQ833488.1 gg_id:167645 detected analyses depth sediment Guanting Reservoir clone 35-35 DQ833
AY221613.1 gg_id:89830 metal and hydrocarbon contaminated soil clone HS9-66 AY221
GQ093932.1 gg_id:430848 Topographical and Temporal Human Skin Microbiome skin toe web space clone nbw GQ093
GU390735.1 gg_id:529542 Dark hot springs: structure biofilms caves Acquasanta Terme (Italy) sulfidic cave stre GU390
GQ347430.1 gg_id:588075 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ347
AM162480.1 gg_id:153300 and situ identification acidic sphagnum peat bog clone B71 AM162
EF594055.1 gg_id:231772 mixed granule anammox reactor clone KIST-JJY023 EF594
FJ793156.1 gg_id:518088 Archaea and Hot Spring Thailand Tao Dam hot spring clone TDB09 FJ7931
AY531577.1 gg_id:99031 Indian Ocean hydrothermal vent clone SF_C23-G2 AY531
GQ396855.1 gg_id:559525 Functional unvegetated perhumid recently-deglaciated soils do not correlate shifts GQ396
CU466710.1 gg_id:341107 Evry wastewater treatment plant anoxic basin clone CU466
FJ264602.1 gg_id:323817 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2646
GQ351059.1 gg_id:535853 Metagenome versatile chemolithoautotroph expanding oceanic dead zones Saanich GQ351
EU245299.1 gg_id:244008 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-F01 EU245
AM943597.1 gg_id:269159 Microbial dolomite formation Lagoa Vermelha Brazil carbonaceous sediments hype AM943
GQ246419.1 gg_id:510365 Temporal and spatial China North Yel Sea sediments clone Ld1-24 GQ246
EF125407.1 gg_id:182748 soil naked tidal flat sediment near mangrove clone MSB-1E5 EF1254
EU050928.1 gg_id:253945 libraries sediment Kings Bay Svalbard Arctic clone SS1_B_03_41 EU050
GU180177.1 gg_id:534587 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
AJ441227.1 gg_id:72863 hydrothermal vent polychaete mucous clone P. palm C 37 AJ4412
AF154100.1 gg_id:1295 hydrocarbon seep clone GCA112 AF154

41.0	233.5	608.3	352.8	1241.8	367.3	2747.8	138.1	44.7	36.7	133.5
2340.6	5794.1	5879.0	5779.2	7147.9	5703.4	9703.7	5546.0	4798.1	4048.9	5211.2
44.3	201.3	352.2	291.9	483.2	353.4	1111.8	245.1	76.3	55.6	123.9
1731.9	3353.9	3574.0	3744.4	4797.0	3708.4	5006.5	3426.6	3585.5	2850.9	3750.9
728.4	1210.4	966.8	1081.6	1206.4	1143.4	2033.6	911.6	904.7	421.9	133.5
42.7	318.5	728.3	422.6	1458.7	637.4	2121.9	857.2	163.0	89.4	218.8
79.8	425.8	598.5	511.1	452.6	623.5	563.7	536.4	295.3	1952.4	286.7
1340.5	4675.7	5276.2	5325.5	6168.5	4597.7	7924.9	3985.5	4409.5	3104.1	4832.9
44.0	60.9	84.0	76.9	138.3	79.7	236.4	31.2	24.0	20.1	60.2
969.5	2191.3	2777.0	2696.5	3582.1	2324.2	5014.5	1979.5	1478.1	1583.9	2069.3
546.9	2296.6	2668.3	2616.6	2595.4	2583.1	3317.2	2650.5	1117.3	1746.8	2091.5
1386.5	4367.0	4503.7	5162.4	6967.6	4735.5	6767.5	5790.0	4680.6	3328.1	4078.8
52.8	759.3	1011.5	1271.1	908.2	677.8	5121.4	364.5	598.7	551.0	454.0
201.0	2722.9	2843.1	3085.5	3424.4	2897.6	3787.9	3201.6	3011.9	3984.4	2249.5
617.4	5434.2	6467.9	6825.2	8843.3	6120.9	10633.5	5950.9	3859.3	3615.4	6528.5
80.5	292.3	432.5	393.4	438.2	314.6	546.2	369.1	128.2	122.7	225.8
72.9	463.9	581.5	450.2	415.4	383.3	746.6	399.3	399.7	231.0	771.0
38.8	114.0	208.1	92.7	146.5	73.8	348.8	48.8	28.9	19.2	48.4
2058.2	4624.5	4295.4	5235.1	5420.1	5304.8	5760.1	4828.6	2769.9	1965.1	4860.8
672.4	6970.9	7604.6	7779.3	11758.4	7369.4	13398.3	6644.2	3714.5	2746.4	5838.1
62.3	180.5	218.4	248.2	189.7	160.7	197.4	173.0	96.9	82.3	155.2
68.4	694.8	402.8	231.4	1489.6	900.5	1065.8	200.1	55.1	40.5	200.6
40.8	444.4	1430.0	737.5	4439.7	1779.8	3743.1	1247.9	83.0	151.7	769.4
85.3	2064.6	2959.0	2357.2	4431.8	2699.2	6290.0	2150.1	566.9	380.8	1560.1
193.0	2297.8	1712.4	1166.9	2133.4	1929.7	2590.5	1524.5	1726.4	704.6	897.2
159.9	424.3	410.5	379.6	976.8	595.6	649.1	377.5	189.6	64.8	306.0
59.9	508.1	528.4	277.0	749.4	736.6	1661.3	1071.0	143.9	120.6	490.2
51.2	2959.1	3596.3	2816.8	7389.0	3606.0	8311.1	2423.8	655.3	458.9	2085.8
60.7	475.2	862.5	641.2	1594.7	819.4	1906.3	846.5	138.7	189.7	445.9
1978.7	5106.9	5771.4	5407.6	10337.9	6119.8	12577.2	4648.2	2584.6	1719.5	3275.8
70.2	1839.6	1729.0	1293.5	3732.2	1969.5	3895.8	2306.3	1748.6	399.3	1408.5
607.0	3927.1	3737.3	4089.4	4568.1	3682.4	5435.1	3245.8	3606.8	3002.9	3345.7
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126.8	1131.9	1594.9	1291.1	2058.1	1203.2	2012.8	1315.2	541.4	373.1	1117.4
64.2	317.7	427.3	351.7	547.2	325.2	712.9	377.8	93.4	68.7	189.4
496.5	1304.9	1747.8	1863.6	1118.7	1499.4	2055.6	1628.4	1438.4	1032.3	1655.1
34.2	1420.6	2160.3	1642.4	2576.6	2501.0	3702.0	1559.4	333.2	298.2	848.7
1511.1	5419.4	5713.1	6243.7	8313.4	6085.5	10157.3	5503.6	4001.0	2843.3	5262.3
352.2	2888.3	3116.1	3303.3	4493.3	2869.2	5611.2	2640.0	1268.5	1090.8	2006.1
146.7	682.4	897.0	718.3	758.1	706.6	1276.1	806.9	512.8	185.9	505.8
57.9	437.5	621.5	486.1	563.0	463.1	1128.4	362.6	143.3	188.8	222.2

79.7	83.0	156.6
4674.3	5376.3	6472.6
98.2	97.7	192.7
3008.7	3507.6	4018.6
67.3	1058.4	802.3
695.6	460.7	379.1
964.9	828.7	533.8
3750.4	4285.0	5774.8
27.7	44.0	73.8
1948.8	2782.0	3274.5
1775.7	2370.4	2936.1
5252.2	5222.6	7360.1
272.5	884.6	147.7
2665.8	3199.7	5102.6
5940.7	5651.7	6310.0
277.5	468.5	435.4
293.6	402.9	338.3
40.7	51.6	68.5
4029.9	5123.0	5136.0
7085.5	5683.1	9885.7
149.7	246.5	239.0
115.2	195.0	1049.4
3060.7	591.9	769.0
2012.3	2029.7	4066.7
971.8	1083.6	1309.7
193.0	525.6	595.6
349.4	254.5	480.2
1838.3	1631.7	2874.7
380.7	776.9	791.5
4035.9	4185.9	5805.5
726.9	1235.2	1455.5
3158.2	4239.6	5023.4
2245.8	2354.6	3431.0
886.2	1006.8	1922.8
304.1	364.9	469.5
1327.7	1959.1	2045.3
1517.1	943.6	1144.5
5260.1	4728.6	8191.6
2088.5	2822.9	4014.5
513.2	494.1	630.8
298.3	278.4	515.6

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FJ264751.1 gg_id:319179 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
EU925873.1 gg_id:353087 sediments sediment station DBS1 northern Bering Sea clone 076F60 EU925
EU385891.1 gg_id:274098 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU385
AB426184.1 gg_id:267008 -situ identification study benzene-degrading s under methanogenic condition anaerc AB426
EU812967.1 gg_id:324201 Microbial structure mesophilic reactors biogas reactor fed corn silage clone TUM-Mb EU812
EU181507.1 gg_id:255643 Prokaryotic enhanced organic matter remineralization continental margin marine se EU181
DQ833486.1 gg_id:163647 detected analyses depth sediment Guanting Reservoir clone 35-26 DQ833
AJ306746.2 gg_id:55534 DCP-dechlorinating consortium clone SHA-36 AJ3067
EU385730.1 gg_id:260028 Stratified microbes sediments Core MD05-2896 subseafloor sediment South China S EU385
DQ297988.1 gg_id:144633 Microbial hydrocarbon contaminated soil clone UD6 DQ297
EU134003.1 gg_id:250810 tallgrass prarie soil clone FFCH610 EU134
AY221060.1 gg_id:82558 Mammoth cave clone CCM2b AY221
EF019253.1 gg_id:207036 aspen rhizosphere clone Elev_16S_434 EF0192
FJ484492.1 gg_id:559629 microbial autonomous rover world's deepest phreatic sinkhole wall biomat El Zacator FJ4844
FN563384.1 gg_id:549137 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
CU920961.1 gg_id:544167 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
AJ249113.1 gg_id:21437 DCP-dechlorinating consortium clone SHA-105 AJ2491
EU245353.1 gg_id:237424 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H6-E05 EU245
EU488497.1 gg_id:549616 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
GU056107.1 gg_id:584240 Biologic Techniques Applied Microbial Prospecting China: Ban 876 Gas Oil Field Bein GU056
DQ330063.1 gg_id:159211 Guerrero Negro hypersaline microbial mat clone 062DZ89 DQ330
EU245784.1 gg_id:256129 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M6-C0 EU245
EU245957.1 gg_id:243597 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-F1 EU245
EU245567.1 gg_id:252001 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-B0 EU245
EU488065.1 gg_id:573706 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
FJ264758.1 gg_id:333224 Manganese and Iron Dependent Anaerobic Oxidation Methane methane seep sedim FJ2647
EU245923.1 gg_id:240978 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-C0 EU245
DQ330138.1 gg_id:159294 Guerrero Negro hypersaline microbial mat clone 072DZ94 DQ330
FN563361.1 gg_id:560750 Impact changing HRT OLR on prokaryotes involved biomethanizitaion and fuzzy logic FN563
GQ850583.1 gg_id:571883 bottom water northern Bering Sea clone d147 GQ850
EU245598.1 gg_id:252162 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-E0 EU245
EU245751.1 gg_id:239123 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M5-H0 EU245
GQ249578.1 gg_id:550014 Microbial anaerobic sediments Bay Cadiz (Spain) marine sediment: 12-14 cm layer c GQ249
DQ330139.1 gg_id:159200 Guerrero Negro hypersaline microbial mat clone 072DZ46 DQ330
DQ330158.1 gg_id:159124 Guerrero Negro hypersaline microbial mat clone 072DZ38 DQ330
DQ330169.1 gg_id:159407 Guerrero Negro hypersaline microbial mat clone 08D2Z40 DQ330
DQ394929.1 gg_id:151554 harbor sediment clone VHS-B3-9 DQ394
DQ330199.1 gg_id:159389 Guerrero Negro hypersaline microbial mat clone 10D2Z16 DQ330
FJ638585.1 gg_id:512964 Temperature dependent succession sulfate reducing muddy southwestern Taiwan hc FJ6385
DQ330198.1 gg_id:159395 Guerrero Negro hypersaline microbial mat clone 10D2Z17 DQ330
EU246094.1 gg_id:243415 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P3-C04 EU246

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6859.2	4977.8	5796.5	6163.4	7062.4	5435.7	9139.2	4862.1	4542.9	3091.6	6138.0
716.8	6363.1	6319.5	7050.6	7329.1	6298.1	9726.0	6064.2	4002.0	2246.6	5315.6
177.3	2508.0	3221.3	2959.8	5050.0	3732.7	5709.9	2709.4	882.5	449.5	1910.8
7483.5	5757.4	6092.2	6654.5	6823.3	5550.7	7625.0	5703.7	6089.3	4383.5	5923.2
599.7	3528.6	3676.8	4378.3	4837.6	3570.9	5549.2	4023.8	5160.0	996.2	3403.2
43.5	84.2	149.0	130.6	148.2	106.3	275.3	77.5	32.5	27.7	56.0
238.0	408.8	509.8	523.6	1084.4	427.7	937.9	380.1	158.8	95.4	242.5
3734.8	10028.7	9398.7	10418.3	9851.7	9484.9	10881.3	8610.7	9214.1	5284.9	10108.6
42.7	160.7	169.0	230.0	503.1	404.1	433.7	131.8	96.3	22.6	87.3
21966.4	11561.7	11418.6	12218.6	13227.6	10741.8	15970.1	9991.1	13068.9	9243.4	14036.1
2271.1	5900.9	4365.5	4821.7	5137.4	4650.2	5912.4	4417.6	4922.4	3307.8	6080.4
123.4	722.3	1031.1	799.3	1999.5	853.3	3350.1	908.2	288.0	233.0	509.5
627.3	4628.6	3825.6	3937.0	5047.3	4778.9	5036.7	3673.3	4042.9	2336.1	4818.2
228.9	4282.4	5120.0	5323.0	6402.0	4029.1	8047.9	4090.5	4225.7	2756.3	4462.2
1763.8	7350.7	8280.5	8759.4	6458.2	6850.3	8097.4	7515.0	5431.8	6525.6	9446.8
51.6	322.9	369.8	449.0	774.6	428.0	820.8	243.3	206.3	89.1	326.9
576.0	4045.9	5032.0	5508.5	6582.4	5052.8	8407.9	4954.9	2050.2	1530.4	3344.5
62.6	747.6	683.6	602.2	1381.7	695.8	1188.4	893.8	250.0	96.9	411.1
451.6	3744.8	5079.6	4513.8	6515.5	4670.9	7257.9	4067.8	3218.1	4408.0	2903.9
150.4	425.8	456.5	536.6	915.2	844.4	503.9	307.6	144.5	140.2	168.1
47.7	353.8	337.0	461.9	642.5	335.8	703.0	199.2	344.5	66.4	208.6
41.4	38.1	35.4	45.0	49.0	36.1	42.5	51.8	34.1	29.6	36.7
300.5	2013.6	2037.0	2201.7	2883.3	2334.9	4676.8	2185.2	1663.8	1333.3	1872.4
1130.7	7239.5	7077.9	6806.6	8077.6	6853.4	8740.7	6192.9	7779.8	4092.6	6556.7
583.0	8928.6	8207.8	8622.4	8553.1	8544.2	10293.2	8718.1	6138.9	5118.1	11033.8
2699.4	2640.6	2420.2	2616.0	3198.5	2493.1	4976.8	2768.7	2798.3	2697.9	3023.5
34.2	38.5	57.0	47.3	79.9	47.5	123.1	56.4	34.7	25.3	61.7
119.3	399.6	421.7	543.2	788.6	538.5	837.4	579.9	153.7	592.5	280.2
11613.4	6764.8	5970.1	6175.6	9777.0	6074.5	7988.5	5803.6	6181.5	5088.5	6852.8
608.2	4255.7	4988.8	4375.5	6041.5	4146.7	7155.4	4287.1	2914.6	2377.4	4027.3
195.3	3219.7	3568.3	3415.3	5798.1	3152.5	5033.2	4407.3	2730.0	2901.1	2683.2
1193.1	5115.2	4703.5	3999.7	5501.7	4387.2	4919.2	4207.5	5486.6	3545.7	2944.4
49.4	172.7	202.3	198.4	303.4	319.3	294.7	208.9	78.7	40.1	151.4
56.9	386.9	414.0	445.2	742.5	407.9	707.5	608.4	151.2	87.2	287.0
35.7	504.2	510.0	478.0	1214.0	449.8	1195.5	398.5	118.6	139.7	171.7
39.6	49.8	57.4	62.0	101.0	53.6	167.0	29.3	27.2	30.5	44.1
280.5	3222.9	4201.4	4465.7	4611.1	3842.1	4432.1	4095.8	1721.4	861.8	2930.4
53.2	73.8	150.6	200.2	298.4	133.3	245.5	201.8	67.2	56.8	100.7
568.4	2429.4	3118.0	3234.6	3341.8	2549.8	4567.1	2764.4	2597.8	2392.3	3259.6
125.3	2820.9	3233.7	2590.8	3889.3	2865.0	4371.0	2330.7	1363.9	723.4	2143.8

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6124.5	6054.4	8594.8
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5428.8	7617.7	8307.4
217.6	381.1	1092.6
3990.3	4550.0	6307.5
501.5	546.9	816.0
3601.1	3655.8	4523.1
611.9	635.3	517.4
459.9	453.6	548.6
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6241.8	6018.1	6906.0
8546.8	8236.8	10100.2
2122.5	3347.2	2960.7
36.3	61.2	85.4
520.6	483.3	582.5
6459.5	6885.7	8520.2
4183.2	3943.5	5529.7
3424.6	3810.0	5455.8
4043.0	5484.9	4758.5
125.8	331.2	451.1
425.7	508.1	979.1
473.1	564.6	783.1
29.5	49.1	59.1
4476.6	3839.8	4878.5
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DQ811879.1 gg_id:162071 mangrove soil clone MSB-5G10 DQ811
DQ811873.1 gg_id:162958 mangrove soil clone MSB-4F5 DQ811
EU245596.1 gg_id:241036 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M3-E0 EU245
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EU245343.1 gg_id:235444 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H6-C11 EU245
EU245948.1 gg_id:239373 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-M8-E1 EU245
GQ848217.1 gg_id:536506 and Archaeal Xiarinur Soda Lake Water-sediment Interface water-sediment interfac GQ848
EU245058.1 gg_id:238582 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H1-C02 EU245
GQ143765.1 gg_id:443913 Level Continental Shelf Sediment and Phylum-level lineages Phylum Planctomycetes GQ143
EU488090.1 gg_id:543473 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
DQ330166.1 gg_id:159319 Guerrero Negro hypersaline microbial mat clone 08D2Z72 DQ330
FM242278.1 gg_id:322996 sequences sediment clone 17bis T0h-oil FM242
FJ478819.1 gg_id:574527 species richness estimates obtained nearly and simulated pyrosequencing-generated FJ4788
EU979011.1 gg_id:312328 Effects intercropping Rhizobium inoculation on microbial biomass and rhizosphere b EU979
EU245378.1 gg_id:248966 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H6-H0 EU245
EU669650.1 gg_id:304270 soil clone S8-80 EU669
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EU134007.1 gg_id:241530 tallgrass prarie soil clone FFCH5447 EU134
EF594052.1 gg_id:233441 mixed granule anammox reactor clone KIST-JJY020 EF594
EU374068.1 gg_id:272558 southern Cretan margin (eastern Mediterranean Sea) canyon and slope sediment cl EU374
DQ811866.1 gg_id:164467 mangrove soil clone MSB-3H11 DQ811
EU488398.1 gg_id:550672 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EF061968.1 gg_id:184557 Xiamen China mangrove sediment clone XME13 EF0619
EF205579.1 gg_id:211551 among geographically regions central Tibet geothermal spring mat clone TP7 EF2055
DQ463699.2 gg_id:173719 distinct Lake Tanganyika anoxic hypolimnion clone TK-SH16a DQ463
EU488293.1 gg_id:533639 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
AY193182.1 gg_id:80115 thermal spring mat clone O1aA2 AY193
AM490737.1 gg_id:570248 Linking and functional nutrient spiraling mats (USA) microbial mat sulfidic cave sprir AM490
AY592366.1 gg_id:101396 deep-sea mud volcano clone Amsterdam-2B-06; BC20-2B-06 AY5923
FJ746327.1 gg_id:509084 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7463
FJ746247.1 gg_id:509572 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
EU385894.1 gg_id:268805 Stratified microbes sediments Core MD05-2902 subseafloor sediment South China S EU3858
FJ746244.1 gg_id:553966 Microbial oligotrophic marine sediments: South Pacific Gyre ocean sediment 5306 m FJ7462
FJ455877.1 gg_id:513961 Variations archaeal and sulfate-methane transition zone continental margin sediment FJ4558
DQ811877.1 gg_id:171074 mangrove soil clone MSB-5B1 DQ811
AM176852.1 gg_id:161058 Recovery mangrove sediment clone SZB52 AM176
EF208698.1 gg_id:202905 Vertical and horizontal structure microbial sandy carbonate sediment clone CI75cm.2 EF2086
EF061971.1 gg_id:192578 Xiamen China mangrove sediment clone XME55 EF0619
EF061967.1 gg_id:199390 Xiamen China mangrove sediment clone XME3 EF0619

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34.6	108.4	161.3	153.2	247.7	93.1	358.8	191.7	59.8	35.2	76.2
183.1	2797.4	3166.8	3730.3	4568.4	3404.4	5574.8	3570.2	2605.3	2708.3	2192.8
3017.4	6507.5	5956.1	7344.1	10106.3	6593.5	10384.2	6534.3	3915.4	4785.4	5839.0
50.2	1911.6	1911.0	1840.6	2462.6	1392.8	2802.7	1598.3	714.4	291.1	937.3
211.8	4884.3	3842.4	3840.0	4323.3	4599.4	4826.8	3940.9	2425.3	1732.7	3260.8
547.9	6772.5	6763.5	7943.0	9785.5	7275.5	11481.5	6126.3	4398.2	3190.7	6030.9
3642.7	8537.1	8245.2	9323.5	11479.3	8446.7	13306.6	8784.9	8990.2	3929.8	7707.6
10525.4	12052.9	10068.8	11497.4	12730.0	10830.9	12678.9	10270.2	11005.2	10883.0	12050.5
113.1	1850.3	1977.9	2198.4	3358.8	2252.7	3841.4	1923.9	932.4	1018.9	1779.0
272.1	4696.3	4367.0	4987.5	7310.0	4638.2	8524.3	4321.0	1401.0	1426.0	3335.3
274.2	3522.5	3951.2	3613.4	3922.3	3114.1	4160.4	3573.3	3317.6	2257.9	2832.4
249.7	1719.3	1895.1	1855.7	2003.7	1736.5	2108.0	2069.4	906.5	432.1	1260.0
95.0	5208.9	4619.0	2691.9	2128.3	2899.8	3382.0	3348.2	3985.6	2774.2	2830.2
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3372.7	5942.4	4946.9	5364.1	5994.5	5101.2	8893.2	4974.4	4581.5	3126.8	5351.6
247.3	3895.2	4699.4	4708.4	3122.6	3623.2	4140.8	3705.3	2261.4	1776.0	3481.4
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89.0	4075.7	4264.3	4164.3	5764.8	3849.2	7198.9	3342.2	1809.2	1872.6	3484.6
51.0	271.2	339.4	337.3	1998.2	345.6	3148.1	228.9	73.4	39.3	90.0
1479.8	5722.4	5617.3	5038.7	5709.3	4875.4	8572.0	4758.7	5567.4	4395.7	4124.1
734.9	3757.1	3988.3	4121.7	4950.5	3446.3	6149.1	2451.5	1171.9	1047.9	2665.4
140.9	2351.2	3092.2	3025.3	4104.1	2674.8	4906.8	2493.5	637.7	279.9	1518.9
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46.4	230.0	267.8	218.5	437.3	213.1	651.3	215.2	54.7	43.6	118.0
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153.1	2515.8	3165.8	2963.6	4735.0	3138.4	5147.7	2741.8	1346.0	815.3	2052.2
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94.0	3986.9	3897.1	4573.8	5693.2	4733.3	6694.2	3509.5	1581.3	1521.0	2850.3
42.2	76.3	85.6	85.4	55.4	81.6	106.4	90.2	29.7	35.1	49.6
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71.0	1241.1	1886.3	1944.2	1981.6	1452.0	2609.1	1524.7	588.1	156.1	949.9
6408.7	2054.5	2871.3	2447.9	3167.8	2380.0	4135.5	1949.3	1615.1	2222.1	2271.7
146.0	1987.7	1569.0	1350.5	1444.6	1510.0	1822.0	1807.5	1092.9	1224.3	1454.6
7623.5	3635.2	3517.6	3507.8	3654.6	3496.4	4461.3	3314.7	3714.7	2811.6	4278.0
57.0	116.1	157.7	123.5	124.5	109.9	155.8	133.9	92.4	121.4	125.8
164.0	1546.8	2735.9	2578.7	3177.9	1767.6	4264.7	1938.0	654.1	313.1	1007.9
112.3	1058.1	1399.3	1674.8	1770.6	1358.7	2495.4	1272.0	395.3	344.8	1089.5
33.0	50.2	74.0	47.3	53.6	37.4	50.3	48.2	41.2	16.1	36.3
924.8	3232.1	4002.2	3233.0	4039.4	2614.9	5717.5	2669.2	1594.5	1076.4	2046.7

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2428.6	1861.2	2691.3
7541.5	5094.7	10808.3
4569.2	4794.3	6847.6
3485.3	3643.8	4455.8
7717.0	8467.7	8772.8
3410.4	3125.7	3814.7
119.2	324.3	303.4
4437.7	5038.7	7014.1
2595.8	3382.1	4702.2
2265.5	2176.4	4683.3
5427.3	5300.2	5992.1
105.2	152.3	335.4
3691.1	4173.4	5228.1
2570.3	2750.9	4385.9
193.5	413.7	373.6
3436.2	3505.3	5307.8
60.4	105.3	64.3
6155.6	5456.3	8851.0
1378.0	1958.5	2227.2
1432.7	2649.9	3925.8
869.7	1372.6	1316.1
3147.6	3695.8	3837.9
79.6	155.0	56.7
1203.6	1775.1	2937.0
988.7	1032.2	1577.6
33.6	61.4	55.7
1656.6	2605.9	2923.7

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DQ394932.1 gg_id:151229 harbor sediment clone VHS-B3-15 DQ394
EU488019.1 gg_id:558101 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
EF644517.1 gg_id:236900 Structure and performance microbial involved reductive dechlorination 1122-tetrach EF6445
AF050568.1 gg_id:2707 contaminated aquifer clone WCHB1-63 AF0505
DQ080134.1 gg_id:133917 sediment clone BFA-K16 DQ080
EU465609.1 gg_id:300528 argali sheep feces clone AS1_aao39f02.Contig1 EU465
FN436174.1 gg_id:554498 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
CU920557.1 gg_id:563752 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
DQ330038.1 gg_id:159256 Guerrero Negro hypersaline microbial mat clone 05D2Z82 DQ330
EU245271.1 gg_id:252689 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H5-B02 EU245
EU245259.1 gg_id:235632 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H4-H07 EU245
FJ671130.1 gg_id:516109 Synecology primary and secondary habitats Escherichia coli O157:H7 feedlot surface I FJ6711
AY297975.1 gg_id:88752 thermophilic anaerobic terephthalate-degrading sludge clone TTA_B60 AY297
FN436181.1 gg_id:551775 Molekularbiologische Charakterisierung der bakteriellen Populationsdynamik eines t FN436
FJ821660.1 gg_id:551191 hot spring sediment clone R24 FJ8216
DQ330143.1 gg_id:159346 Guerrero Negro hypersaline microbial mat clone 072DZ41 DQ330
DQ330141.1 gg_id:159239 Guerrero Negro hypersaline microbial mat clone 072DZ16 DQ330
EU245338.1 gg_id:258151 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-H6-C02 EU245
AF323767.2 gg_id:34771 benzoate-degrading consortium clone BA046 AF323
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EF515579.1 gg_id:222893 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
CU924204.1 gg_id:548965 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU924
EF515624.1 gg_id:224860 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5156
EU522648.1 gg_id:264388 hydrocarbon-degrading methanogenic microbial consortia settling basin Northern Al EU522
EU644236.1 gg_id:281467 and Samoylov Island Lena active layer -centred polygon near surface horizon; Rim_T EU644
CU918081.1 gg_id:567834 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
FJ234904.1 gg_id:334279 Microbial structure mesophilic biogas mesophil anaerobic reactors fed corne silage cl FJ2349
EF515525.1 gg_id:217391 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EU246296.1 gg_id:248667 Miniprimer new lens viewing world hypersaline microbial mat clone MAT-CR-P6-E04 EU246
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CU925406.1 gg_id:565436 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU925
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CU922134.1 gg_id:554888 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU922
CU918551.1 gg_id:552199 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
CU919033.1 gg_id:534657 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU919
CU920569.1 gg_id:569566 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU920
EF515594.1 gg_id:218815 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155

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4112.6	5312.9	6134.1	5445.2	5615.3	5425.4	7723.7	5364.7	4963.3	3696.7	5698.5
85.8	213.1	328.8	485.9	379.1	283.0	815.2	239.3	113.3	58.5	145.1
1437.0	5073.2	6030.2	6533.4	7002.2	5143.1	8496.0	6915.8	4525.5	4733.9	5336.4
395.7	3139.2	3707.9	3108.7	3730.6	3741.8	4741.9	3571.8	4668.6	4273.7	3490.9
194.2	1805.8	2323.3	1964.8	3423.8	1704.2	4550.7	1333.1	801.5	439.6	1008.8
50.0	606.8	511.8	383.1	746.4	390.6	1376.6	671.7	380.3	31.1	312.1
21897.1	7651.5	7257.5	7632.2	8741.3	7511.2	9551.5	7758.1	12018.5	7046.2	9698.2
62.0	45.3	63.3	50.8	68.4	51.7	64.0	53.0	45.2	33.4	47.4
60.3	193.3	322.9	342.1	369.8	425.8	240.4	399.6	223.3	599.6	149.7
69.7	387.7	553.8	595.1	581.4	396.8	736.6	416.0	113.0	60.9	191.8
58.4	592.2	433.9	349.1	485.6	423.4	566.0	505.7	103.7	85.0	354.5
76.3	1418.5	1089.7	1053.4	1448.5	1419.2	1012.5	1034.8	865.8	648.9	704.1
283.7	2859.4	2631.1	2505.3	4266.9	2940.5	4801.6	2561.5	1912.6	2007.0	1788.6
6416.6	7780.4	8268.8	8574.0	12636.0	8573.3	14490.4	7906.4	6510.9	4640.4	8166.9
52.1	738.3	993.3	800.6	1514.4	1031.7	1807.9	858.6	379.4	1045.6	590.4
55.1	160.7	212.7	160.8	215.9	230.9	253.7	136.2	60.5	39.0	98.3
51.1	57.2	54.0	51.7	84.3	52.5	148.9	41.2	40.0	25.5	48.5
60.7	3343.7	3624.4	3384.9	2549.2	2433.9	5492.0	2664.2	407.4	420.0	2030.0
14488.7	4787.0	4470.7	4829.1	4693.2	4535.0	5890.4	4169.6	5902.4	4013.2	5675.8
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407.1	4674.0	4674.0	4751.1	5188.0	4526.1	7072.9	3805.1	2574.3	1742.6	3227.9
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18845.3	7610.9	7747.7	7649.0	8870.2	5697.9	10838.9	6734.2	9288.9	7189.1	9670.5
114.5	1713.7	2242.6	2104.8	2459.9	1501.7	3643.3	1257.2	904.1	577.2	1016.6
247.9	3970.1	4991.4	4681.0	7442.7	4050.7	10973.2	3743.4	1780.7	815.9	3080.3
36.5	185.0	268.6	256.4	178.9	202.2	383.7	141.7	59.5	39.8	98.6
110.2	1685.6	1674.0	1607.4	3071.1	1756.3	3050.1	1659.7	1097.8	703.8	1040.7
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565.8	5488.8	4929.1	5866.0	8307.8	5682.6	8279.1	5113.6	6962.7	2600.2	4423.9
27917.4	8871.0	8928.6	9086.2	9047.9	8447.4	10475.3	7721.7	11687.7	9645.9	11829.7
570.5	2091.0	2346.1	2282.8	3323.3	2516.7	3133.4	3290.0	1719.9	3211.1	2320.3
26271.9	8432.9	8439.9	8974.3	8890.2	8714.5	9549.8	7773.6	11612.8	11383.0	11705.8
1253.5	3282.7	3753.5	3700.7	3463.2	3534.3	4318.7	3838.3	3165.8	4138.3	3424.6
358.0	2362.3	2439.2	2662.7	2496.4	3245.3	2443.8	2780.8	1631.2	1246.6	1131.9
6879.5	3828.1	4067.7	3896.7	4085.9	3996.7	5187.6	4155.9	3947.3	3006.6	5266.4
11224.4	6832.9	7032.4	7468.6	8723.9	6977.1	11006.1	6771.4	7675.9	6717.5	8612.3
30925.3	10565.6	10029.7	10394.5	9851.4	9275.4	11443.0	8920.8	13938.3	11653.0	12870.5
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3003.0	4399.4	4516.7
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150.7	459.3	5097.5
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EU644092.1 gg_id:282676 and Samoylov Island Lena active layer -centred polygon near permafrost table; Rim_ EU644
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FM178831.1 gg_id:310689 Monitoring abundance and expression 'dehalococcoides' species chloroethene-redu FM178
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EU487924.1 gg_id:549880 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU487
EU488227.1 gg_id:565887 lucinid bivalve- symbiotic system: significance geochemical habitat on symbiont and EU488
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AF445659.1 gg_id:74684 travertine hot spring clone SM1B12 AF445
AB240467.1 gg_id:143650 microbial structure rhizosphere biofilm Sapporo root-tip (0 40 mm) Phragmites Sosei AB240
EF515524.1 gg_id:222764 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
AY426459.1 gg_id:102678 full-scale anaerobic UASB bioreactor treating paper mill wastewater clone E15 AY426
DQ811858.1 gg_id:162841 mangrove soil clone MSB-3F12 DQ811
DQ329898.1 gg_id:159186 Guerrero Negro hypersaline mat clone 02D2Z14 DQ329
AY921832.1 gg_id:113374 farm soil clone AKYG1561 AY921
AJ431247.1 gg_id:103391 Dehalococcoides sp. str. BHI80-52 AJ4312
CU921045.1 gg_id:553193 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU921
AJ009480.1 gg_id:2710 chlorobenzene-degrading consortium clone SJA-101 AJ0094
EF125425.1 gg_id:185193 mangrove soil clone MSB-2B11 EF1254
GU180178.1 gg_id:555085 Impact coplanar PCBs on microbial activity anaerobic estuarine sediments sediment GU180
AJ306793.1 gg_id:66911 DCP-dechlorinating consortium clone SHD-14 AJ3067
FM955656.1 gg_id:563339 Study Prokaryotic Some Selected Niches Western Ghats India water clone BCWCSP1 FM955
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EF515576.1 gg_id:226739 Electricigen Enrichment MFC full-scale anaerobic bioreactor sludge treating brewery EF5155
EF203180.1 gg_id:208032 phylotypes sediments Lake Kastoria Greece sediment clone Kas19B EF2031
AY214200.1 gg_id:81161 benzene-contaminated groundwater clone ZZ14AC19 AY2142
CU918692.1 gg_id:560513 Towards definition core microorganisms involved digestion mesophilic anaerobic dig CU918
AY548939.1 gg_id:100980 ANAMMOX sludge clone 1-20 AY548
AY921711.1 gg_id:114347 farm soil clone AKYG535 AY9217

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75.8	1157.2	2173.0	1366.6	1520.3	1013.4	5016.2	1142.5	376.5	584.6	947.0
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62.0	45.0	117.1	85.2	180.3	66.4	546.8	45.8	34.3	16.3	64.4
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45.0	211.6	355.4	282.8	440.4	176.8	682.9	223.4	53.0	54.9	84.5
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AB525472.1 gg_id:574788 Segregated ANME-1 and -2 cold-seep marine sediments deep-sea methane seep sed AB525
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EF520628.1 gg_id:232744 structure lakes: what controls ? acid-impacted lake clone ADK-IHh02-60 EF5206
AB286334.1 gg_id:211661 Reducing production and domination comamonadaceae reducing oxygen supply was AB2863
AB487122.1 gg_id:594201 Microbial responsive denitrification-inducing conditions rice paddy soil clone TSNIR0 AB4871
FJ592893.1 gg_id:572435 Fumarole-supported islands biodiversity within hyperarid -elevation landscape on Pu FJ5928
AJ009460.1 gg_id:2751 chlorobenzene-degrading consortium clone SJA-35 AJ0094
EF516324.1 gg_id:225605 grassland soil clone FCPU564 EF5163
EF516490.1 gg_id:219565 grassland soil clone FCPS418 EF5164
DQ128817.2 gg_id:186887 no tillage soil clone HSB NT53_E04 DQ128
EU134243.1 gg_id:242432 tallgrass prarie soil clone FFCH2524 EU1342
EF515997.1 gg_id:217684 grassland soil clone FCPP418 EF5159
DQ906813.1 gg_id:251412 Oman subsurface soil clone 5B-12 DQ906
EU134012.1 gg_id:250099 tallgrass prarie soil clone FFCH5198 EU1340
AY922056.1 gg_id:113502 farm soil clone AKYG705 AY9220
AY922073.1 gg_id:113276 farm soil clone AKYG885 AY9220
AY921805.1 gg_id:112836 farm soil clone AKYG617 AY9218
AY921706.1 gg_id:112949 farm soil clone AKYH1185 AY9217
AY922118.1 gg_id:113599 farm soil clone AKYH1480 AY9221
EU134246.1 gg_id:235741 tallgrass prarie soil clone FFCH477 EU1342
AB257647.1 gg_id:261663 Microbial few millimeters be surface dolomite rock 'Val Piora' Alps 1965 meters abo AB2576
GQ015160.1 gg_id:494503 Topographical and Temporal Human Skin Microbiome skin palm clone nbw765b09c GQ015
AY921657.1 gg_id:114052 farm soil clone AKYG631 AY9216
AY922170.1 gg_id:113170 farm soil clone AKYH910 AY9221
EF019661.1 gg_id:217133 aspen rhizosphere clone Elev_16S_815 EF0196

711.4	5880.0	5525.7	6229.6	6250.6	5634.9	7943.9	5973.9	4233.7	3752.0	5881.1
112.2	1262.8	1606.5	1575.2	2713.0	1410.9	4003.7	1461.6	535.4	227.6	998.0
72.4	705.3	1113.9	755.2	2569.4	837.5	3515.7	1196.4	220.0	140.1	476.1
7680.2	5990.6	5691.9	7187.9	8207.0	6821.3	7186.9	4972.0	4153.7	2760.9	4020.0
332.0	1984.9	3302.2	2302.7	3136.7	2153.5	4431.3	1842.3	1032.9	680.5	1584.0
45.7	51.7	142.2	213.9	41.6	83.5	67.5	47.6	35.1	30.1	46.8
53.3	1366.8	1940.2	1652.3	2574.5	1688.8	5420.2	1399.7	614.3	272.5	832.1
101.0	154.9	203.6	149.7	271.0	213.6	313.2	180.2	95.2	106.5	87.7
73.7	3121.1	3830.7	3238.1	4551.2	2313.2	6319.7	1761.9	520.7	358.0	1285.0
543.3	6258.5	6515.1	7143.0	8523.2	6082.8	8969.1	6744.7	6934.5	4873.1	6772.6
2787.0	2169.1	2122.7	2397.8	2126.3	2140.6	4936.5	2074.2	1899.1	1398.9	2630.5
918.2	5285.2	6326.4	6812.7	8380.4	5454.7	10579.7	5429.0	4643.4	3012.4	5270.9
8656.2	1971.6	1654.2	2016.2	2153.9	2486.4	2466.8	1521.0	2699.3	1779.2	2627.4
34.5	117.3	151.1	162.5	210.7	145.8	844.4	80.0	82.4	36.6	74.4
37.9	513.9	741.6	498.6	5313.2	1150.5	1691.3	947.6	75.3	386.2	821.5
5037.4	5579.3	6130.5	5728.6	6530.7	5874.6	7002.4	4949.4	4815.7	3742.8	6428.5
655.7	212.5	293.8	371.5	829.7	299.0	751.7	213.0	176.2	134.7	349.8
3755.6	2870.6	3193.7	2895.1	4062.8	3129.9	5988.7	3114.2	2779.5	1835.6	3083.7
265.3	3413.4	3491.1	4096.3	6511.9	4350.4	7524.4	4278.0	2676.0	1066.7	4544.0
67.8	619.8	440.6	315.2	1746.7	836.3	2779.3	1133.6	148.7	82.5	342.0
199.3	5227.7	3431.0	4049.9	5825.3	4489.4	8745.6	4423.1	1145.3	1666.6	4288.2
4993.5	4043.5	3373.6	3202.1	4699.0	3668.4	6193.9	4210.5	2729.4	2277.3	4165.8
42.3	75.8	88.7	64.0	91.6	55.0	227.7	90.5	29.9	18.9	29.1
37.4	319.0	278.0	299.4	290.2	279.3	312.1	193.3	65.1	43.6	278.7
624.1	2523.6	3202.8	3083.2	4133.5	3472.2	4554.5	2801.6	2899.6	1436.4	2869.6
3104.8	5714.4	4754.1	5445.6	5953.9	5331.9	5485.0	5181.5	3707.2	3481.6	4475.4
4488.7	5758.5	5114.3	5264.5	5982.2	5701.8	6172.2	6099.9	4379.0	2702.3	4744.3
23415.4	11195.1	8533.0	9652.9	8685.0	10471.5	10038.4	7985.3	12510.3	9515.3	14210.4
229.7	2880.9	3365.8	4049.7	5575.2	3328.4	5780.5	2634.7	1261.9	1036.6	1994.2
286.4	3528.0	3308.3	3655.7	4953.8	3926.6	5235.1	3918.4	1613.2	1171.7	2956.3
850.2	2078.7	1570.9	1708.9	2306.8	2256.2	2689.3	1476.9	858.8	622.2	1340.8
812.9	4061.5	5122.5	4406.2	4937.8	4348.4	5425.7	4573.7	2488.3	2371.1	3333.4
2128.8	3979.0	3591.1	3967.0	4576.2	4100.2	4808.3	3727.4	3362.2	3139.8	3376.5
1608.2	2267.9	2953.4	2664.6	2631.2	2699.5	3023.3	2985.2	1759.7	1686.4	2114.2
7176.1	6652.3	6639.2	7302.3	8108.2	7039.9	8332.0	6493.9	6933.2	4185.5	7745.8
2503.2	6734.4	6285.6	7355.2	7995.8	6612.7	8867.4	5523.1	4553.8	3921.7	6126.8
106.2	1273.9	1281.7	1344.1	2046.7	1306.8	1928.9	1404.2	988.3	475.2	996.3
1659.2	4040.7	3680.2	3227.8	4037.7	3547.2	4570.7	3395.2	2395.4	2674.5	2740.8
495.7	2196.0	2081.0	2215.1	3083.5	2054.0	3146.3	2197.1	1127.7	714.8	1764.4
1015.9	4230.0	4143.8	4466.1	6040.5	4448.8	5596.2	3434.4	2499.6	1664.1	3338.9
105.0	867.6	1180.0	1053.1	1965.2	1046.2	1957.8	999.1	787.8	189.0	619.0